FINAL

WORKSHOP REVIEW REPORT

California Gnatcatcher Facilitated Science Panel Workshop

US FISH AND WILDLIFE SERVICE

November 9, 2015

Prepared for:

U.S. Fish & Wildlife Service
Carlsbad Fish and Wildlife Office
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Executive Summary

The coastal California gnatcatcher (*Polioptila californica californica*) was listed by the US Fish & Wildlife Service (Service) in 1993. A new genetic analysis of the subspecies was published in 2013 (Zink et al. 2013) that disputes its current taxonomic status. This phylogeographic study integrated new nuclear gene-sequence data with the mtDNA analysis from Zink et al. (2000) with some morphology data. Zink et al. (2013) concluded that their analysis does not support the coastal California gnatcatcher as a distinct subspecies. The Service published a 90-day finding (USFWS 2014) indicating that a petition to delist the subspecies, which was based largely on the conclusions of Zink et al. (2013), contained substantial information and a status review as initiated. A large number of public comments were received in response to the Service's 2014 90-day finding including a paper published by McCormack and Maley (2015) that disputed the conclusions drawn by Zink et al. (2013). As part of the Service's process to evaluate the status of the coastal California gnatcatcher, the Service requested assistance from a science panel to evaluate this new information in the context of avian and coastal California gnatcatcher genetics and taxonomy.

The Service prepared a Statement of Work for an independent contractor to convene a panel to provide an external, independent scientific review of the genetics data described above, as well as evaluate the taxonomic status of the coastal California gnatcatcher. The review included a 1.5 day science panel Workshop with a facilitator in Carlsbad, California. The panelists, who all have expertise in molecular genetics and birds, considered and individually responded to five Discussion Questions, provided to the contractor by the Service prior to the Workshop. These responses were provided through the preparation of an individual memorandum by each panel member.

The panelists and facilitator were selected by a contractor (without input from the Service) to provide a balance of skills and expertise to accomplish the review. The panelists had no contact with the Service during their review, except for a brief question and answer session during the Workshop.

As described in their individually prepared memoranda, the panel members were in agreement that the currently available genetic data is not sufficient to overturn long standing subspecific recognition based on morphology. The panelists were in agreement that additional research was required to definitively settle the status of the subspecies, but accepted that the current morphological data indicate at least two subspecies with a division at 30ºN. Although all panelists suggested additional research and analyses, the panelists expressed some differences as to the appropriate use of particular genetic techniques, and their utility for providing insight into the taxonomy of California gnatcatchers.

1.0 Summary of Scope and Objectives

The coastal California gnatcatcher (*Polioptila californica californica*) was listed by the US Fish & Wildlife Service (Service) in 1993. It is one of at least two subspecies of California gnatcatchers (*Polioptila californica*) that occurs in California and Baja California. Its taxonomic status has been the subject of numerous reviews.

Zink et al. (2000) examined the mitochondrial DNA (mtDNA) control region and three mtDNA genes and provided new information on geographic structure throughout the entire range of the California gnatcatcher. Zink et al. (2000, pp. 1394, 1402) concluded that “northern populations [of California gnatcatchers] do not appear to constitute a unique component of gnatcatcher biodiversity” and the authors stated that their results suggest that “not all currently recognized subspecies are equivalent to evolutionarily significant units.”

In the Service’s 5-year status review (USFWS 2010) and in a 2011 90- day finding (76 FR 66259; October 26, 2011), the Service concluded that the information presented in Zink et al. (2000) alone did not provide sufficient information to disregard the existing taxonomic data and conclusions contained in previous scientific papers before 2000.

A subsequent phylogeographic study regarding the California gnatcatcher by Zink et al. (2013) integrated new nuclear gene-sequence data with the mtDNA from Zink et al. (2000). The results of this study found that there were no subspecies groups within the California gnatcatcher. In contrast, a paper published by McCormack and Maley (2015) disputed the conclusions drawn by Zink et al. (2013).

The purpose of this review was to provide a formal, independent, scientific panel review of the genetic data described above, and to evaluate the taxonomic status of the coastal California gnatcatcher. The review included a 1.5 day panel Workshop in Carlsbad, California. The agenda and discussion questions for the Workshop are provided in Appendix A. The material provided by the Service is included in Appendix B. Each scientist on the panel provided his or her individual expert review of the available data and responses to the questions presented. The memoranda are found in Appendix C.

Coastal California gnatcatcher.

Photo from USFWS (2010).

2.0 Description of the Process

Amec Foster Wheeler Infrastructure and Environment, Inc. (Amec Foster Wheeler) was contracted by the Service to provide a panel of scientists and facilitator for the Workshop to review the publications described above. Amec Foster Wheeler personnel identified potential panelists following the process described in Section 2.1 and based on a Statement of Work provided by the Service. During this process, no identifying information was provided to the Service about the potential panelists; only their areas of expertise and general qualifications were included. Upon award, potential dates for the Workshop were identified and panel selection was finalized. One panelist was replaced due to scheduling conflicts.

All communication between the Service and the panelists was performed by the Amec Foster Wheeler project manager (PM), with the exception of a brief question and answer period during the Workshop (described in Section 2.3), to ensure the independence of the panelists.

2.1 Panel Selection

The selection of panelists followed the guidance provided in the Office of Management and Budget's *Final Information Quality Bulletin* (OMB Bulletin; December 16, 2004) to ensure scientific integrity of peer reviews. Relevant expertise and an appropriate balance of that expertise was identified for this science panel based on the Statement of Work from the Service and used to identify potential panelists. Panelists with expertise in conservation, molecular genetics, taxonomy, systematics, phylogeography, and population evolution were essential for this panel, with an emphasis on experience with birds. The elements considered for producing a balanced panel included:

- Avian experience: two primarily avian research, four multiple taxa including birds
- Experience with federally listed species: four previous experience, two no previous experience
- Areas of expertise: six with avian conservation, four with conservation genetics, one with taxonomy, six with phylogeography, six with population genetics, and two with systematics. All panelists and the facilitator had experience with a range of molecular genetic techniques. All panelists had experience in at least two areas of expertise.
- Years of experience: Ranged from 19 years to 35 years.

The facilitator was selected based on experience with facilitation and on expertise with the genetics techniques and the general topics (particularly with rare species, conservation genetics, and population genetics), but with no experience with birds. Expertise in these areas was necessary to assist and guide the panelists in discussion of the information and issues. The facilitator was selected from universities in the San Diego area, while the panelists were selected from candidates at universities across the United States and not in southern California. All panelists and the facilitator were provided the language from the OMB Bulletin (2004) with regard to independence and conflicts of interest and any potential issues were identified and evaluated during the selection of the panelists, with respect to both the Service and the material under review. The facilitator and panelists are all independent of the Service, have not taken an advocacy position with respect to the California gnatcatcher, and have no conflict of interest, which was documented in a Conflict of Interest statement completed and submitted by each panelist and the facilitator.

To maintain the independence and objectivity of the science panel, the panelists requested that their input be anonymous; thus, a number was randomly assigned to each panelist and this report and the individual memoranda reference that assigned number.

2.2 Workshop Preparation

The facilitator and each panelist reviewed the Panel Review Questions (Section 2.4) provided by the Service prior to the Workshop. The PM relayed questions and answers between the Service and the panelists regarding the discussion questions and the materials provided. The PM and the facilitator developed a draft agenda, which was then reviewed by the panelists and the Service. This resulted in the final agenda provided in Appendix A. The Service provided the materials listed in Appendix B to the PM, who then distributed them to the panelists and the facilitator. , In an email communication to the Service from the PM, the panelists requested that the Service also provide four summaries on the following topics: 1) taxonomic history of the California gnatcatcher, 2) listing history of the coastal California gnatcatcher, 3) summary of definitions of listable entities under the Endangered Species Act, and 4) a summary of recent comments received from the 2014 90-day finding (USFWS 2014) for the coastal California gnatcatcher. These documents were provided in electronic format to the PM prior to the Workshop and were reviewed during the Workshop by the panel, but the Service did not present them to the panel at the Workshop as originally requested. These documents are included in Appendix B.

2.3 Workshop

The purpose of the Workshop was to provide a forum for panel members to discuss the various topics related to the coastal California gnatcatcher’s taxonomic status. The Workshop was intended to assist the panelists in increasing their familiarity with the materials; discuss the issues; review the charge given to them; provide an opportunity for the panelists to ask questions regarding the materials, issues, and charge; and to allow panelists the opportunity to hear the viewpoints and/or analyses of the other panelists. The panelists were not asked to reach consensus or to develop conclusions regarding the issues/charge during the Workshop. Following the Workshop, each panelist was asked to provide their own individual responses to the questions through an individual memorandum.

The PM coordinated the science panel Workshop, which was led by the facilitator. The Workshop was one and a half days and held at the Carlsbad Fish and Wildlife Office of the Service located in San Diego County in southern California. The panelists reviewed the papers identified above (McCormack and Maley 2015; Zink et al. 2000, 2013), as well as other relevant recent avian genetics and taxonomy publications and other publications specific to coastal California gnatcatchers, all of which are included in Appendix B. Section 4.0 summarizes the major points of discussion during the Workshop.

2.4 Panel Review Questions

In a Statement of Work, five written questions for discussion were suggested by the Service to guide discussions by the panelists during the Workshop.

1. What, if any, do you consider to be the most reliable features and methods to delimit infraspecific entities in songbirds or avian species in general?

2. What are the strengths and weaknesses of these approaches, particularly with the issues presented with the coastal California gnatcatcher (*Polioptila californica californica*)?

3. Different methodologies may be suited to discriminate between taxa at various ranks while others are best suited to show close relationships among taxa. With this in mind, assess the extent to which the methods, data and conclusions of Zink et al. (2013) apply to these two approaches. How does your assessment apply to the taxonomic status of the California gnatcatcher?

4. There is an array of scientific information that could be used to determine the taxonomic status of animals listed as the coastal California gnatcatcher. Using the available evidence, describe how the coastal California gnatcatcher represents a recognizable entity (e.g., subspecies) or specifically why no infraspecific taxa warrant recognition within California gnatcatcher (*Polioptila californica*). In addressing this question, we ask that you consider the following: the discreteness, significance, and conservation status of the species' (or subspecies) population segments.

5. What additional information or analysis, if any, would clarify the taxonomic status of the California gnatcatcher?

2.5 Preparation of Individual Memoranda

After the Workshop, each panelist provided an individual memorandum that addressed the Panel Review Questions. Each individual memorandum was based on the information provided and discussed during the Workshop, based on the individual panelist's area(s) of expertise.

This science panel did not reexamine the morphological data from earlier publications (Atwood 1988, 1991; Mellink and Rea 1994), or the various re-analyses of those data (Link and Pendleton 1994; McDonald et al. 1994; Messer 1994). The panelists noted that the analysis of the available morphological data for the California gnatcatcher had previously been subject to two peer reviews (as described in USFWS 2011) and determined that there was no new information to justify a reevaluation of these morphological data. This was confirmed by the Service on Day 2 of the Workshop (see summary below).

3.0 Panelists

The facilitator was Andrew J. Bohonak from San Diego State University. The curricula vitae for the panelists are presented in Appendix D and the panelists were:

- H. Lisle Gibbs, PhD, from Ohio State University;
- M. Zachariah Peery, PhD, from University of Wisconsin - Madison;
- Michael D. Sorenson, PhD, from Boston University;
- Garth M. Spellman, PhD, from Denver Museum of Nature and Science;
- Sabrina S. Taylor, PhD, from Louisiana State University; and
- Samantha M. Wisely, PhD, from University of Florida at Gainesville.

4.0 Major Points of Discussion

The Workshop started on August 17, 2015 at 8:15 am and ended at 11:00am on August 18, 2015. There were no Service employees present on Day 1. There was a brief question and answer session with Service employees on Day 2 (described below).

Day 1 - Morning Session

The facilitator and panelists reviewed the agenda and the questions. The panelists then reviewed the documents previously provided by the Service on the taxonomic history of the California gnatcatcher and the listing history of the coastal California gnatcatcher. The panelists also reviewed the document previously provided by the Service regarding the definitions of listable entities.

Additional discussion during the morning session:

- Discussion of completeness and conclusions of the morphology data (taxonomy summary)
    - Panel discussion about the role of morphology data and its importance as a data type for subspecies definition. Panel members were in agreement that morphology is an important data type and sets the historical standard for the subspecies definition.
    - Panel discussion about whether the published morphology was appropriate and adequate at the time. There was also discussion about any limitations of the morphology data that could be corrected using current standards and/or methods for analyzing morphology and morphological variation.

- Panelists began discussing how to define species versus subspecies and distinct population segments (DPS). On a related note, panelists also started discussing the role and value of different types of data in evaluating species/subspecies/DPS.

- After reviewing the document previously provided by the Service summarizing the listing history of the coastal California gnatcatcher, the panelists discussed what constitutes 'best available data'.

Day 1 - Afternoon Session

The panelists reviewed the Service's document summarizing comments received on the 90-day finding for the coastal California gnatcatcher (USFWS 2014).

- Panel discussed the criteria for defining subspecies:
    - The panelists reviewed American Ornithological Union (AOU) criteria for subspecies.
    - Panel members discussed the following questions: Are the same criteria used for subspecies and DPS but different thresholds? What criteria really matter for subspecies definition? Is diagnosability essential for subspecies and should subspecies be diagnosable across multiple lines of evidence?
    - Panel members noted that, in birds, subspecies definition is generally founded on phenotypic differences that are associated with biogeographic patterns. Additional discussion by the panel on the related questions:
        - Can one define a subspecies on phenotypic data only (if no genetic data are available or genetic data are not appropriate)?
        - Can one define a subspecies on phenotypic data plus limited neutral genetic data (vs. adaptive genetic data which would be similarly informative like phenotypic data)? How much neutral genetic data and what type is informative? How much weight should it have relative to the phenotypic data?
        - Panel members also discussed clinal variation versus discrete breaks and how that might relate to subspecies definition. Based on AOU criteria, discrete breaks appeared to be the standard.
    - In contrast to Zink, each of the panelists concluded that (1) a subspecies cannot be defined on the basis of neutral genetics alone and (2) reciprocal monophyly of mtDNA lineages is not a necessary criterion for the recognition of subspecies.

- The panelists discussed Zink et al. (2000) paper. The panel members noted that the data were generally consistent with south Baja being ancestral with dispersion/expansion to the north. The panelists discussed the sample sizes and methods used and whether the conclusions were supported.

- The panelists discussed Zink et al. (2013) paper. Panel members noted the following:

    - Generally very low statistical power for the type of analyses and number of samples. Did not perform significance testing. Did not account for limitations of STRUCTURE analysis.

    - Some of the G_{ST} and F_{ST} indicate some weak evidence of genetic differentiation. This is not surprising given recent divergence among subspecies.

    - Partial Mantel test or other more sophisticated analysis (several options) would be an interesting analysis of the data and would be more informative regarding subspecies question.

    - The publication focused on testing for reciprocal monophyly, with very limited analysis regarding restricted gene flow.

    - Niche modeling presented in the publication was bare bones and this field has advanced considerably since this paper was published. The methods were not sufficiently described in the publication. However, the overall results probably would not change. The current subspecies are currently as divergent as expected based on the divergence of habitat (which is considerable). The panel members were in agreement that the conclusion in the publication that the species is a ‘habitat generalist’ is not supported.

- The panelists discussed McCormack and Maley (2015) paper. Each of the panel members noted that the primary criticisms of Zink et al. (2013) described by McCormack and Maley (2015) were that the relevant markers to test for subspecies were not used in Zink et al. 2013 and there was a lack of hypothesis testing.

- The panelists discussed Zink’s criticism of McCormack and Maley (2015) as they were presented in comments to the Service.

- The day ended with a review of the discussion of Question 1 (subspecies definition and criteria).

Day 2 – Morning Session

The panelists requested a brief question and answer session with Service personnel.[1] This session was approximately 20 minutes. The panel members requested verification that the morphological data had undergone external scientific review previously and whether the Service had evaluated the results in Skalski et al. 2008. The Service confirmed the morphological data had been reviewed twice previously, which was summarized in the 2011 90-day finding (USFWS 2011), where the Service also responded to the Skalski et al. 2008 paper. The Service noted that the panel should look at the best available information to answer the discussion questions. The panel members also asked some clarifying questions regarding DPS criteria, particularly significance and discreteness. The Service generally referred the panelists to the summary document already provided. The panel members also requested a summary of the role of this panel in the current process the Service is undergoing. The Service explained the steps and timeline of the current process they are completing, in which the panel plays one part.

After this discussion, the panel members determined it was unnecessary to reexamine data that had been reviewed repeatedly and there was also no new morphology data to modify those original datasets.

The panelists then reviewed the Individual Memorandum template and discussed the requirements for completion and the expected contents. The session ended with a round table review of Questions 2 through 5. Each panelist summarized their current response to each question and the panel discussed key points as they arose.

5.0 Individual Memoranda

Each panel member considered and responded to the five Discussion Questions provided by the Service and provided an individual memorandum to the Amec Foster Wheeler PM. The responses were proofread for errors and formatted for consistency across all memoranda. Responses ranged from 4 pages to 25 pages. These are included in their entirety in Appendix C.

6.0 Summary of Agreements and Disagreements

The panelists were in agreement that using only phylogenetic criteria (e.g., reciprocal monophyly) to define subspecies was not appropriate. In the Workshop discussions and in their individual memoranda, the panel members noted that subspecies are in the process of evolving to new species and, therefore, some level of gene flow and/or incomplete lineage sorting is expected. All panelists noted that any intraspecific divergence in California gnatcatchers would be of recent origin, so neutral genetic variation is likely to have a limited signal with respect to genetic differentiation between subspecies. Panel members were also in agreement that genetic information, particularly neutral genetic variation, does not overturn phenotypic variation, particularly in species where phenotypic variation provides a sufficient signal to distinguish subspecies. There was some disagreement among the panelists as to whether neutral genetic

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[1] Bradd Bridges and Betty Grizzle (Carlsbad Fish and Wildlife Office)

variation had any value in answering the question of defining subspecies generally. Some of the panelists said not at all; some said it could provide supportive data but the lack of distinguishing neutral genetic variation was not essential for defining subspecies; and one panel member said that some divergence in neutral genetic variation (given a large enough genetic dataset) was important to confirming subspecies delineations.

In the Workshop discussion and in their individual memoranda, all of the panelists said there were significant limitations with the available genetic data and that the data did not provide enough information to evaluate the population structure or any adaptive divergence between populations of California gnatcatchers. Most panelists noted that the type of loci and analyses were not suited to identifying recent, intraspecific divergence. One panelist noted concerns about sample deterioration for those used by Zink et al. (2013). Most panelists noted concerns that Zink et al (2013) did not contain sufficient methodology to evaluate the data well. Most panelists also noted that the current data, when analyzed appropriately, did show some signs of genetic structure that supported the subspecies classification. Different panelists performed different analyses (as presented in their individual memoranda), in addition to those presented in McCormack and Maley (2015), but generally found indications that specific loci showed breaks between populations.

The panel members were in agreement that the current sub-specific taxonomy of California gnatcatchers remains valid. In their individual memoranda, they noted that the currently available genetic data is not of sufficient quality or of the appropriate type to overturn long standing conclusions based on phenotypic data. Based on the information presented in the individual memoranda, there was also agreement that additional research was required to definitively settle the status of the subspecies; although all of the panel members noted that at the present time the available morphological information indicates at least two subspecies with a division at 30^{o}N. Panelists who provided comments as to whether the coastal California gnatcatcher would qualify as a DPS stated that it would meet more than one of the Service’s criteria for a DPS designation.

In the Workshop discussions and the individual memoranda, there was disagreement among the panelists as to which genetic approaches would offer the most insight into the subspecies (or lack thereof) of California gnatcatchers. Two panelists stated that RAD-seq would be valuable, whereas another stated the method would be unlikely to capture “adaptive loci.” There was similar disagreement between panelists as to the use of microsatellites. All the panel members were in agreement that any analysis needs to be based on the appropriate conceptual framework for delineating subspecies. The panel members were in agreement that reciprocal monophyly at mtDNA is not a necessary criterion for delineating subspecies.

Most panelists noted in their individual memoranda that additional analyses and research would provide more insight into the status of subspecies of California gnatcatcher. Some of the proposed analyses were phenotypic and some were genetic. Almost all panelists noted that this research would likely to confirm the subspecies designations as described; however, one panelist indicated that further research was likely to show a cline rather than diagnosable break.

7.0 References

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McCormack, J. E., and J. M. Maley. 2015. Interpreting negative results with taxonomic and conservation implications: Another look at the distinctness of coastal California Gnatcatchers. The Auk **132**:380–388.

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APPENDIX A

Meeting Agenda

California Gnatcatcher Facilitated Science Panel Workshop

U.S. Fish & Wildlife Service

Coastal California Gnatcatcher Facilitated Expert Panel Workshop
U.S. Fish & Wildlife Service
Carlsbad, California

Date: August 17-18, 2015

Location:
U.S. Fish and Wildlife Service Office
2177 Salk Avenue, Suite 250
Carlsbad, California 92008
Telephone: 760-431-9440

Goal: Evaluate the taxonomy and systematics of the California gnatcatcher (*Polioptila californica*) and its subspecies, with emphasis on recent research.

Agenda

Day 1 (August 17, 2015)

8:00	Welcome and introductions
8:10	Overview of the workshop objectives, agenda, and process
8:30	Review history of California gnatcatcher taxonomy and systematics
8:50	Review listing history of coastal California gnatcatcher
9:20	Review recent public comments relative to the genetics of California gnatcatcher
9:50	Break
10:00	Review of general process used to make listing decisions (including determining DPS)
10:30	Panelist discussion
12:00	Lunch
1:00	Subspecies definition and criteria (in birds)
1:30	Review recent genetic studies in gnatcatchers
2:30	Discussion of other relevant genetics studies
3:00	Identification of questions for or information needed from USFWS
3:15	Break
3:45	Discussion
5:00	End of Day 1

Day 2 (August 18, 2015)

8:00	Individual panelist interim evaluations (10 minutes per panelist)
9:00	Discussion Question Review
9:45	Break
10:00	(Continued) Discussion Question Review
11:45	Individual Memoranda and Summary Report
12:00	End of Workshop

Discussion Questions (for Individual Memoranda)

1. What, if any, do you consider to be the most reliable features and methods to delimit infraspecific entities in songbirds or avian species in general?
2. What are the strengths and weaknesses of these approaches, particularly with the issues presented with the coastal California gnatcatcher (*Polioptila californica californica*)?
3. Different methodologies may be suited to discriminate between taxa at various ranks while others are best suited to show close relationships among taxa. With this in mind, assess the extent to which the methods, data and conclusions of Zink et al. (2013) apply to these two approaches. How does your assessment apply to the taxonomic status of the California gnatcatcher?
4. There is an array of scientific information that could be used to determine the taxonomic status of animals listed as the coastal California gnatcatcher. Using the available evidence, describe how the coastal California gnatcatcher represents a recognizable entity (e.g., subspecies) or specifically why no infraspecific taxa warrant recognition within California gnatcatcher (*Polioptila californica*). In addressing this question, we ask that you consider the following: the discreteness, significance, and conservation status of the species' (or subspecies) population segments.
5. What additional information or analysis, if any, would clarify the taxonomic status of the California gnatcatcher?

APPENDIX B

Materials Provided

California Gnatcatcher Facilitated Science Panel Workshop
U.S. Fish & Wildlife Service

Documents for Distribution Prior to Workshop

Primary Peer-Reviewed Papers and Book Sections on Gnatcatchers:

AOU. 1957. Genus *Polioptila* Sclater. Pages 450–452 Check-list of North American Birds, 5th Edition. American Ornithologists' Union, Baltimore, MD.

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U.S. DEPARTMENT OF THE INTERIOR
MARCH 3, 1849

Taxonomy and systematic history of the coastal California gnatcatcher

Prepared by U.S. Fish and Wildlife Service
Carlsbad Fish and Wildlife Office
August 2015

Pre-Brewster (1881)

The non-blue-gray gnatcatchers of southern California were combined with those of western North America and were recognized as various taxa under different treatments:

- **Heermann (1853)** – identified a specimen from San Diego, CA (#7191 NMNH*) and one from Fort Yuma, CA (#7192 NMNH*) as *Culicivora atricapilla*
    - *see Baird (1858), p. 383, *List of specimens*
- Sclater (1855) – describes the genus *Polioptila* (but does not mention any gnatcatcher species from the western U.S.)
- **Baird (1858)** – recognized Heermann's specimens as *Polioptila melanura*
- **Cassin (1862)** – borrowed info from Heermann, but this time under the species name *Culicivora mexicana*.

Brewster (1881)

Described *Polioptila californica*, the California black-capped gnatcatcher, as a new species.

- Cotypes:
  - Male: Riverside, CA (collected by F. Stephens in 1878)
  - Female: Fort Yuma [CA] (Heermann's specimen from that location, #7192 NMNH) [note: this is outside the range of the taxon as currently recognized]
  - Young male: Saticoy, CA (collected by J.G. Cooper in 1872)
- Distinguished the California birds from other western gnatcatchers
  - differences in plumage (esp. darker undersides)
  - differences in bill, tarsi, tail, and wings.

Post-Brewster (1881)

The birds of southern California and the northern Baja California peninsula were consistently recognized as *P. californica:*

- Bendire (1887) Description of the nest and eggs (San Bernardino, CA)
- Anthony (1895) Birds of San Fernando, Lower California
- Grinnell (1898) Birds of the Pacific Slope of Los Angeles Co.
- Thayer and Bangs (1907) Catalog of birds collected by W.W. Brown, middle Lower California [noted that some were intermediate between *P. californica* and *P. plumbeus*]
- Grinnell (1915) (Birds of California)

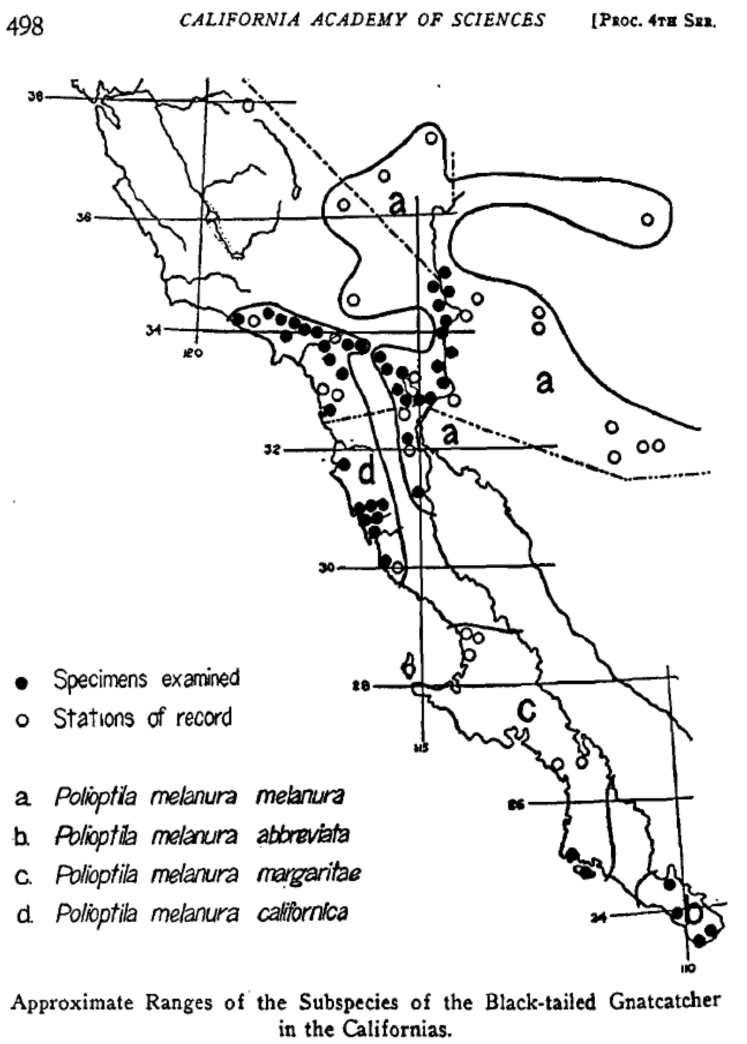
The birds of the southern Baja California peninsula were treated as *P. plumbeus*. Example:

- Brewster (1902) Birds of the Cape Region of Lower California

Grinnell (1926)

A major revision:

- Noted that P. *melanura* should be used instead of *P. plumbea*, per Penard (1923).
- Demoted *P. californica* and *P. margaritae* to subspecies.
- Described *P. m. abbreviata*.
- Mapped the ranges of the subspecies. [Updated in Grinnell 1928.]



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● Specimens examined
○ Stations of record

a. *Polioptila melanura melanura*
b. *Polioptila melanura abbreviata*
c. *Polioptila melanura margaritae*
d. *Polioptila melanura californica*

Approximate Ranges of the Subspecies of the Black-tailed Gnatcatcher in the Californias.

Atwood (1988)

"Re-split" *P. melanura*:

- Interior forms = *P. melanura*, the black-tailed gnatcatcher.
- Coastal and Baja California peninsular forms = *P. californica*, the California gnatcatcher.

2 ORNITHOLOGICAL MONOGRAPHS NO. 42

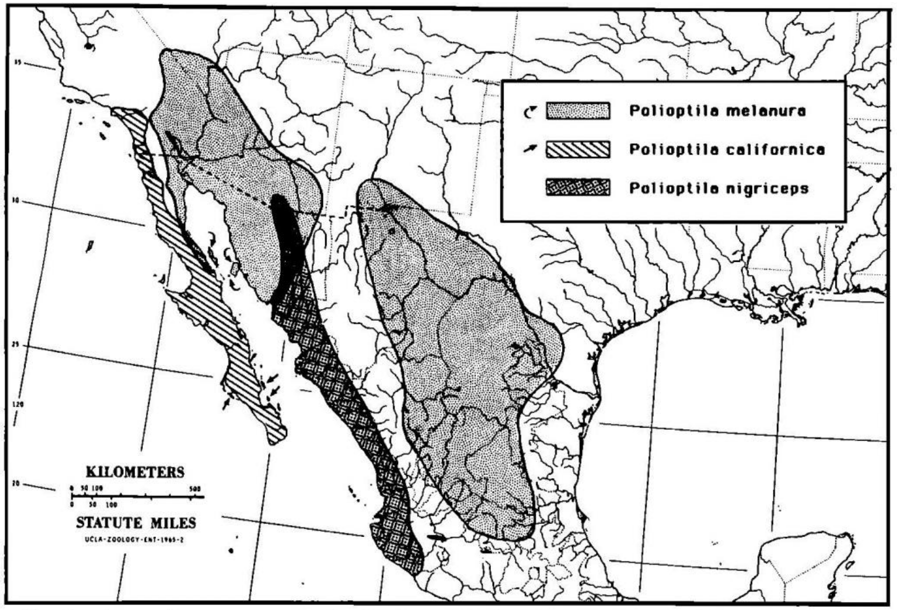

FIG. 1. Approximate geographic distributions of *Polioptila melanura, P. californica,* and *P. nigriceps.*

Focused less on subspecies, but recommended two for *P. californica*:

- *P. c. californica*
- *P. c. margaritae*

Atwood (1991)

Reanalyzed data from Atwood (1988) and revised circumscription of subspecies, returning to Grinnell's three subspecies:

- *P. c. californica*, the Coastal California gnatcatcher (north of 30°N)
- *P. c. margaritae* (30°N to 24°N)
- *P. c. abbreviata* (south of 24°N)

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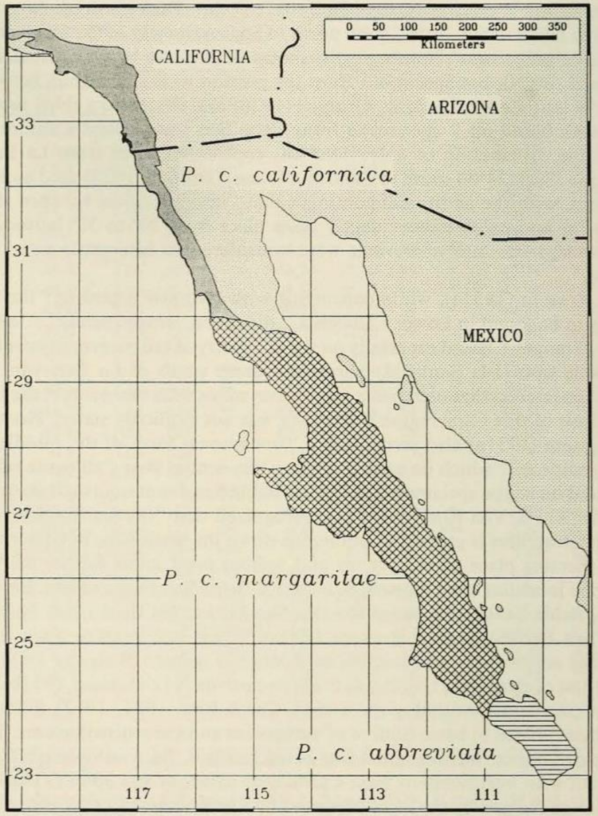


Fig. 7. Approximate geographic limits of California Gnatcatcher subspecies. Due to habitat loss, the indicated range of *P. c. californica* represents historic, not current, distribution. Mapped distributions of *P. c. margaritae* and *P. c. abbreviata* are similarly approximate, and include various areas characterized by habitat known to be unsuitable for California Gnatcatchers. For discussion of distributional patterns on islands in the Sea of Cortez, see Atwood (1988).

Responses to Atwood (1991)

Published papers and unpublished comments received by the Service have criticized *and* defended Atwood's (1991) analyses:

- Barrowclough (1994)
- McDonald et al. (1994)
- Cronin (1997)
- Skalski et al. (2008)

Mellink and Rea (1994)

Revised the subspecies of northern populations, “splitting” *P. c. californica*:

- *P. c. californica*, north of about 32°N
- *P. c. atwoodi,* about 32°N to 30°N
- *P. c. pontilis,* 30°N to an undetermined latitude farther south
- *P. c. margaritae* (not analyzed but recognized by the authors)

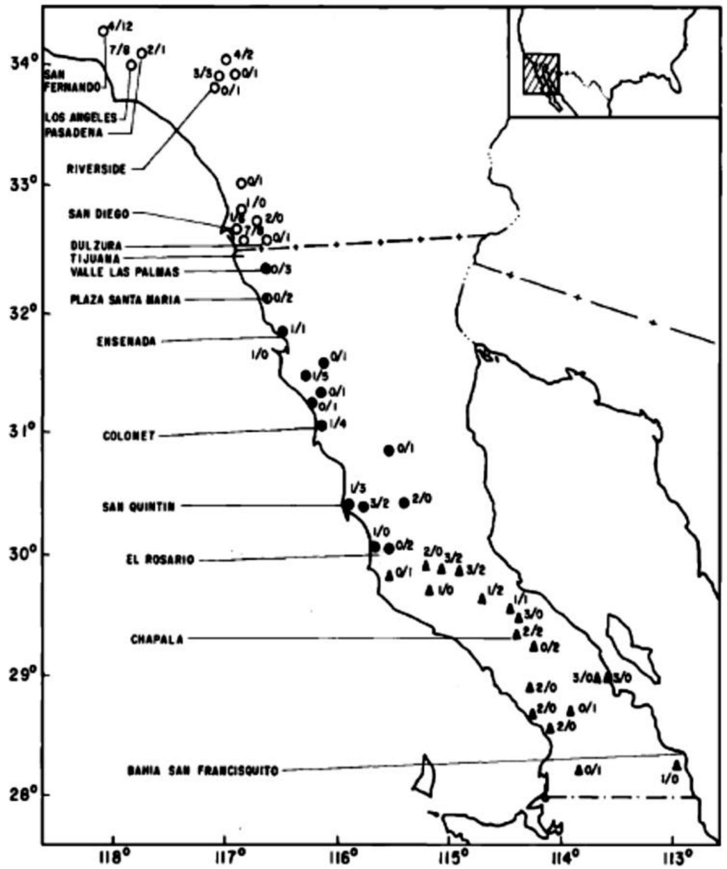


Figure 2. The distribution of California Gnatcatchers in Baja California, Mexico, and California, U.S.A. Open circles, *P. c. californica*; solid circles, *P. c. atwoodi* subsp. nov.; half-filled circles, intermediates between the above two; triangles, *P. c. pontilis.* Numbers indicate numbers of males, then females, examined from each locality. Some localities in close proximity have been lumped.

Am. Ornithologists' Union

- **AOU (1886; 1st Ed.)** – *P. californica*, Southern California and Pacific coast of Lower California.
- **AOU (1895; 2nd Ed.)** – *P. californica*, Southern California and Pacific coast of Lower California.
- **AOU (1910; 3rd Ed.)** – *P. californica*, Southern and Lower California .
- **AOU (1931; 4th Ed.)** – *P. melanura californica*, San Diegan district of southern California from Ventura south to about lat. 30° in northwestern Lower California.
- **AOU (1957; 5th Ed.)** – *P. melanura californica*, southwestern California from the lower Santa Clara Valley and San Gorgonio Pass south into northwestern Baja California, to about lat. 30° N.
- **AOU (1983; 6th Ed.)** – *P. melanura*,* [californica group] from southwestern California (north to Los Angeles County, formerly to Ventura County) and northwestern Baja California south locally to southern Baja California.
- **AOU (1998; 7th Ed.)** – *P. californica**, southwestern California (north to Los Angeles County, formerly to Ventura County) and northwestern Baja California south locally to southern Baja California.

*subspecies not addressed in this edition

Recent treatments and basis for the two recent petitions to delist

- Zink et al. (2000)
- Zink et al. (2013)

(Both documents previously provided)

U.S. DEPARTMENT OF THE INTERIOR
MARCH 3, 1849

Listing History: coastal California gnatcatcher

1982-2014

Prepared by U.S. Fish and Wildlife Service
Carlsbad Fish and Wildlife Office
August 2015

Candidate for Listing – 1982-1991
First Petitions – 1990
90-day Finding – 1991

- Initially, Service recognized the entity as coastal black-tailed gnatcatcher (*Polioptila melanura californica)*
    - Reason for proposed candidacy not described
    - AOU recognized the taxonomic "split" in 1989
    - Coastal population became *P. californica* (based on Atwood 1988)
- Three petitions received in 1990 requesting listing
    - Cited **Atwood 1980**, **Atwood 1988**, **Brewster 1881**
- Status review to assess vulnerability/threats (1991)
- Substantial 90-day finding (i.e., may be warranted for listing)(1991)

First Proposed Listing Rule - 1991

- coastal California gnatcatcher (*Polioptila californica californica or P.c.c.)*
  - Proposed as <u>Endangered</u>
  - Taxonomic and species distribution based on **Atwood 1988**, **Atwood 1990**, **AOU 1957**, **1989**, and **USFWS status review (citing Atwood)**
  - restricted to coastal southern California and northwestern Baja California, Mexico, from Los Angeles County south to El Rosario at about 30°N latitude
- Primary threats:
  - Habitat loss and fragmentation
  - Inadequate existing regulatory mechanisms

First Proposed Listing Rule - 1991

- Selected/highlighted discussion from **Atwood 1988**:
  - The use of subspecies in avian taxonomy has similarly [referring to debate surrounding biological and phylogenetic species concepts] been debated recently…and their application in the present context is dependent upon how species are defined…(p. 60).
  - Clinal variation in <u>multiple morphological characters</u> was found in populations of *P. californica* north of the Cape region of Baja California; at approximately 25°N latitude, many characters showed a relatively sharp transition or step (p. 61). [**Note**: Atwood's (1991) reanalysis changed this to 30°N]
  - <u>Under the biological species concept</u>, two subspecies of *P. californica* would be reasonably recognized: *P. c. californica* in the northern portions of the species' range, and *P. c. margaritae* in the Cape region (p. 61).

First Science Review, Banks and Gardner (1992)

- Historical Review
- Review of **Atwood 1991** (Bull. So. Calif. Acad. Sci. 90:118-133) *aka* Atwood's reanalysis
    - Atwood's (1991) procedures and methods
        - well within the norm for systematic/taxonomic reviews of geographic variation in birds.
    - All readily available pertinent specimen material was used
    - Population samples were assembled properly
    - All important variable morphological characters were examined, and
    - Statistical treatments were appropriate…"although we might have done some things differently" (p. 7).

First Science Review, Banks and Gardner (1992) (continued)

- Responded to "Biological Questions" in letter sent to USFWS from R. Thornton (representing 2 So. Calif. transportation corridor agencies):
  - Designation of *P.c.c.* as a subspecies was as valid as any subspecific designation
  - No reason to review Atwood's primary data
  - No…questions have been raised in the scientific 1iterature [re comparing average measurements of 18 characters], which would be necessary for Atwood's conclusions or methods to be questioned by reputable scientists
  - Stated they had serious doubts that examination of Atwood's data by any reputable ornithological taxonomist would lead to any different conclusions
  - Clarified the AOU/CCN position on species/subspecies and its recognition by Service as "best scientific source of taxonomic information on birds"

First Final Listing Rule - 1993

- Proposed as Threatened (vs. endangered b/c of conservation actions)
  - Taxonomic and species distribution based on **Atwood 1991**, **AOU 1957**, **Phillips 1991**, **Banks and Gardner 1992**
  - Distribution - same as proposed rule
- Primary threats – same as proposed rule
- Critical habitat – not prudent, not proposed

- *NOTE – This final rule declared invalid by court ruling in 1994 because Service did not obtain and make available for public review and comment the data underlying Atwood's 1991 report.*

First Final Listing Rule (excerpts)- 1993

- "Whether or not the abrupt changes in morphological variation reported by Atwood (1991) for the California gnatcatcher are genetically-based is not known at this time."
- "The traditional scientific approach to defining avian subspecies has been based almost exclusively on the identification of morphological differences in body measurements and plumage characters between geographically distinct populations of a species irrespective of whether these differences have a demonstrated genetic origin…"
- "The distributional limits of subspecies have been traditionally determined largely by the correlation between diagnostic morphological characters (including those associated with color) and the environment (May 1971)."

First Final Listing Rule (excerpts) - 1993

- "Atwood's conclusions are strengthened by congruent patterns in geographic variation among several species at 30°N latitude, which represents the southern range limit of the coastal sage scrub community and an important transition zone for various birds, plants, terrestrial insects, land mammals, reptiles, and scorpions (Atwood 1991 and references cited therein)."
- Additional comments/responses addressed concerns of amount of lost and remaining CSS habitat.

Proposed and Final 4(d) Rules - 1993

- Provides for a limited amount of incidental take of the gnatcatcher within subregions actively engaged in preparing a NCCP plan
  - Thus, not a violation of section 9 of the ESA.
- Permits the take of the gnatcatcher resulting from land use activities (regulated by State/Local government) conducted under conservation guidelines for the Coastal Sage Scrub NCCP program.
- Conditions for this Special Rule are published in 50 CFR §17.41(b)

1994 - Responses to invalidation of 1993 final listing rule

- Notice for Soliciting Comments and availability of Atwood's Data

- Notice for Responses/Analyses received

- Service charged with evaluating whether Atwood's data supported his conclusions
- Service received several comments and new analyses of Atwood's data, methods, or results
  - Link and Pendleton (1994)
  - Atwood (1994)
  - Messer (1994)
  - McDonald et al. (1994)
  - Barrowclough (comments) (1994)

Link and Pendleton (1994)

- Objective of this review – Are there apparent groupings in Atwood's data that are consistent with the existence of such subspecies?
- Concluded – 1) the morphological characters in Atwood's data set vary along the geographical gradient, and 2) the changes in characters are more reasonably represented by discrete groupings than by a gradual pattern of change and are thus consistent with the existence of subgroups within the population
  - There appear to be distinct northern, central, and southern groupings of the California Gnatcatcher.
  - The AIC based procedures were the most objective and most creditable of the methods used.
  - These procedures provided results that argue strongly against the aggregation of sites 1 through 5 (Atwood’s LA23, SD24, ST25, ER26, BG27).
- An unanswered question - how well the data represent the existing population of birds.

Atwood (1994)

- Provided his raw data to the Service (in light of court decision to vacate listing)
- Compared/interpreted sample sizes represented in his documents (since 1986) to help establish integrity of submitted data
    - Noted problems with Atwood 1988 on subspecific taxonomy, which was corrected in **Atwood 1991**
        - populations of *P. californica* occurring in central Baja Calif. should not be included within the subspecies *P.c.c.*
- Recommended Service consider Phillips (1991) and Mellink and Rea (1994) re intraspecific variation of *P. californica*
    - *Discussed problems with spectrophotometer measurements (see Mellink and Rea)*
- All of the conclusions are consistent among authors re the existence of a recognizable step in the species' morphology at 30°N latitude.
- His **reanalysis** supports recognition of an identifiable step in gnatcatcher morphology at this latitude.

Messer (1994)

- Independent analysis of Atwood's data
    - Found birds north of 30°N latitude well distinguished from those to the south based on: amount of white on tail, brightness of breast
    - Strong evidence of step-change of several morphological characteristics at about this latitude
    - Classification analysis – birds north of this latitude may be correctly distinguished from those to the south at 92% success rate
- Her findings consistent with Mellink and Rea (1994)
- Sharp criticism of McDonald's comments and analysis ("seriously misrepresented Atwood's work")

McDonald et al. Comment/Analysis (1994)

- Not able to duplicate some of Atwood’s (1991) analyses that involved several variables simultaneously (i.e., multivariate analyses)
- Many of the measurements of morphological characteristics change as a function of latitude
- Original data on specimens show substantial variation with considerable overlap of measurements collected at different latitudes
- If decisions concerning subspecies limits and geographic patterns of morphological variation of California Gnatcatchers (*P. californica*) are to be made based on data provided, then inferences must come from steps in trend of **mean** values because measurements of variables on individual specimens overlap substantially
- The strongest evidence for statistically significant steps in trends of mean morphological characteristics is for steps between approximately 24° and 28°N latitude

Barrowclough Comments (1994)

- Interpretation of McDonald et al.’s (1994) statistical analysis
- Atwood's (1991) analysis and McDonald et al.'s reanalysis of Atwood's individual character measurements are in reasonable agreement.
- But no subspecific taxa should be based on such single measurements
- More appropriate to base subspecific taxa on patterns of geographic variation that are general to several variables
- The geographic patterns common to the measured (Calif. gnatcatcher) variables are clinal ones, or at least not discrete, patchy ones.
    - size and shape, pattern variables, and color variables
- Recognizing subspecies within the Calif. gnatcatcher would imply that subspecies are a reasonable summary of the pattern of geographic variation in this species, but would be a serious misrepresentation of the species’ actual pattern of spatial variation.

Messer (1995) Additional Technical Comments

- Submitted 6-page technical comment letter addressing 3 statistical analyses of Atwood data submitted to the Service
  - Messer 1994 – addressed *a priori* model, with few univariate variables
  - Link and Pendleton 1994 – most integrated and consistent approach, fully multivariate, "state of the art" procedure
  - McDonald et al. 1994 – several univariate approaches
- Compared the discriminant analyses used
  - Messer and McDonald et al. both used ordinary discriminant function analyses
    - But McDonald et al. performed considerable data reduction first
  - Link and Pendleton method allowed data to decide where break is and how many groups

1995 Determination (FR Notice) – Affirming March 1993 Final Listing Rule

- Subspecies is distinct, citing Atwood (1991)
  - **Darker body plumage**
  - **Less extensive white on tail feathers (rectrices 5 and 6)**
  - **Longer tail**
- *P.c.c.* recognized as distinct race/subspecies since Grinnell's 1926 publication
- Addressed Atwood's sample size discrepancies
- Additional analyses adjusting for date of collection support break at 30 °Latitude, the southern subspecific boundary for *P.c.c.*
- Determination summarizes 4 analyses received (Link and Pendleton, Atwood, Messer, McDonald et al.) and varying statistical tests used
- Service found that conclusions by Atwood (1991)
  - Were reasonable
  - Generally supported by additional analyses we received

2010 Petition to Delist (erred in our taxonomic classification)

- Petitioners - Coalition of Labor, Ag, & Business (COLAB; Riverside County Property Owners Assn.; and one individual land owner in SD County
- Petition based on:
  - Subspecies status paper of *P.c.c.*, prepared by M. **Cronin** (NW Biotech Co.) and its appended literature (including **Zink et al. 2000** publication)
- Atwood (1991) wrong on 3 points:
  - Observed morphological characteristics changes are not representative of genetic differentiation (citing Zink et al. 2000)
  - Atwood's statistical analyses seriously flawed (citing **Skalski et al. 2008**)
    - Diagnostic characters support a geographic cline, not a distinct break in character distribution markers
  - Atwood's data sets were confounded, that is, many of Atwood's specimens may not have been representative of wild gnatcatchers (citing Skalski et al.)
- "New science" (Zink et al. 2000) indicates that the California gnatcatcher does not qualify as an evolutionarily significant unit (based on mtDNA haplotype tree)

90-day Finding on 2010 Petition (2011)

- **Not Substantial** Finding based on:
  - Our previous determinations re Atwood's data (see 1995 Determination)
    - Previously recognized morphological variation is indicator of distinctiveness
  - Cronin's unpublished review not reasonable; not new information but rather incomplete interpretation of old data
  - Conclusions of Science Panel
  - Conclusions in our 2010 5-year review
- 7 Federal scientists convened in 2004 (see VanderWerf 2004 reference):
  - Overall, panelists supported retaining subspecies of *P.c.c.*
  - Zink et al. 2000 mtDNA results not sufficient by itself to overturn the existing taxonomy
    - Additional analyses of morphological, genetic (nuclear and mtDNA) and behavior evidence needed
  - Science Panel process criticized by Ramey (see his comment letter re 2014 90-day finding)
- Service also received copy of comment letter from UCLA Professor sent to NRDC re Zink et al. 2000 (Jacobs *in litt*. 2004)
  - Additional molecular and ecological info needed
  - Lack of obvious geographic partitions in the limited genetic data <u>does not</u> preclude the possibility of ESU, or subspecies in northern part of range

2014 Petition to Delist (claiming Service erred in our taxonomic classification)

- Petitioners – COLAB; Center Environ Science. Accuracy & Reliability; Prop. Owners Assn.; National Assn. Home Builders; Calif. Building Industry
- Petition asserts:
  - Original scientific data used to classify *P.c.c.* was flawed
  - Best available scientific data show no support for *P.c.c.* as a distinguishable subspecies; thus, no basis to list under the ESA
  - Service cannot continue to rely on morphological measurements to determine *P.c.c.* is a distinguishable subspecies
  - California gnatcatcher is a single historical entity throughout its geographic range
  - Zink et al. (2000) and Zink et al. (2013) provide best available scientific data that support petition's assertions
    - 2000 paper – mtDNA does not support subspecies
    - 2013 paper – additional genetic analyses did not identify geographic groupings (for previously suggested subspecies)
  - Niche divergence model results indicates no significant niche divergence, thus ecological distinction not valid basis for taxonomic subdivision

90-day Finding on 2014 Petition (2014)

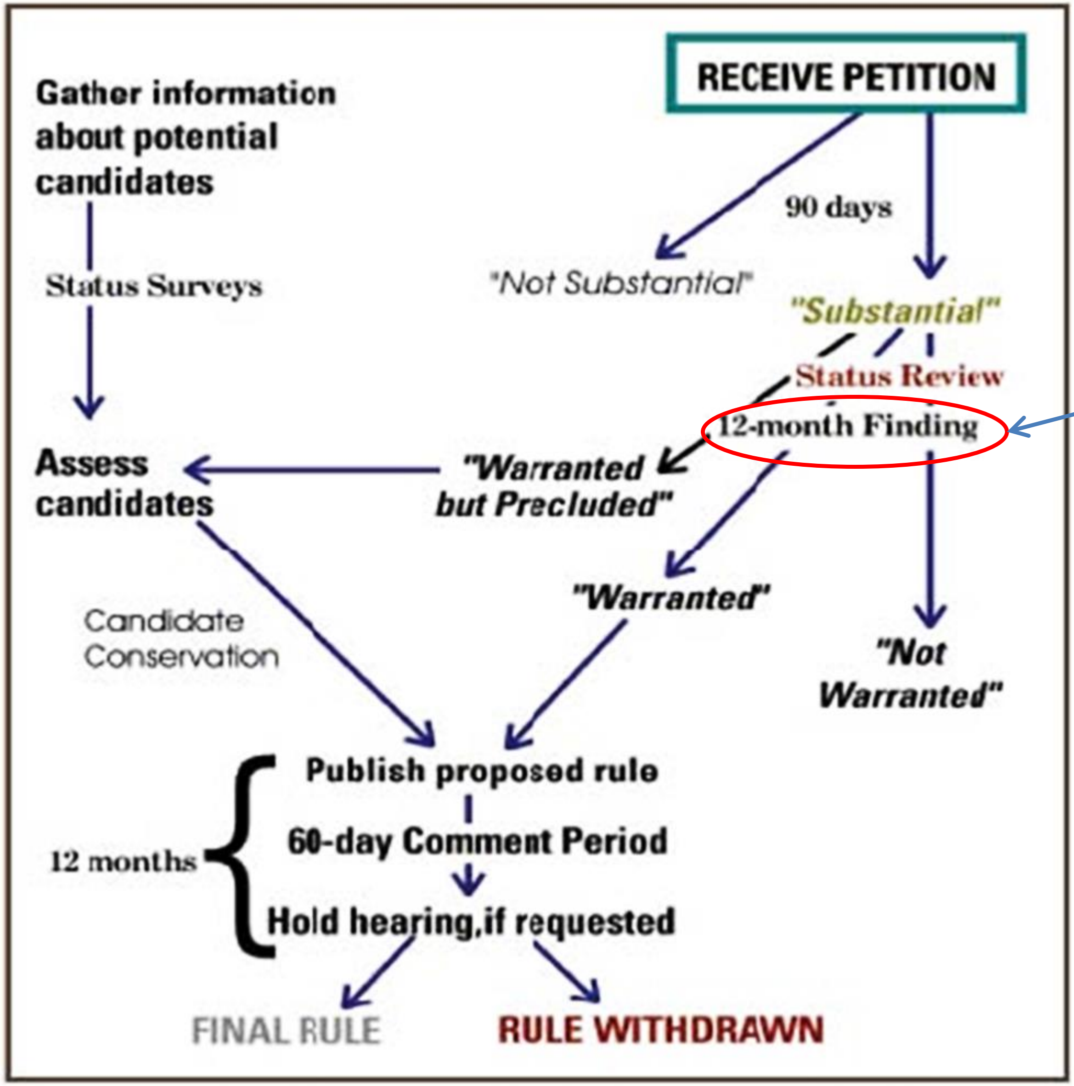
- **Substantial** Finding (i.e., petitioned action may be warranted) based on information presented
  - Petition primarily relies on Zink et al. 2013 to assert *P.c.c.* is not a valid subspecies
    - Nuclear DNA analyses
    - Ecological niche model results
- Current process:
  - 90-day finding requested information regarding taxonomic issues and other listing factors
    - See Public Comments, including publications submitted
  - Initiated12-month Review of Status of Species

U.S. DEPARTMENT OF THE INTERIOR
MARCH 3, 1849

Determining “listable entities” under the Endangered Species Act

Prepared by U.S. Fish and Wildlife Service
Carlsbad Fish and Wildlife Office
August 2015

General Listing Process



RECEIVE PETITION

90 days

"Not Substantial"

"Substantial"

Status Review

12-month Finding

"Warranted but Precluded"

"Warranted"

"Not Warranted"

Gather information about potential candidates

Status Surveys

Assess candidates

Candidate Conservation

12 months

Publish proposed rule

60-day Comment Period

Hold hearing,if requested

FINAL RULE

RULE WITHDRAWN

Next step for coastal California gnatcatcher review

Statutory, Regulatory, Policy Elements

- Definition of species (under ESA/regulations) includes:
  - Any species or subspecies of fish, wildlife, or plant, and any distinct population segment of any vertebrate species…*(more later on DPS)*
- General guidance on whether taxon or population is a species or subspecies
  - **Standard taxonomic distinctions, expertise of the DOI and the scientific community concerning the relevant taxonomic group** (50 CFR § 424.11)
- Relevant Service policies
  - *Interagency policy for peer review in ESA activities* (1994)
  - *Interagency policy on information standards under the ESA* (1994)
  - *Final Information Quality Bulletin for Peer Review* (2004, OMB)
- "Best available scientific and commercial data" standard for all listing and delisting decisions

“Non-regulatory” World

(best understanding is established through science)

Species and Subspecies

- Taxonomically defined
- Different authorities for different taxa
- Varying interpretations may exist simultaneously

Memorialized in the scientific literature (published and unpublished)
-subject to change based on new studies, scientific debate, etc.

“Regulatory” World (ESA)

(applies values, risk assessment/tolerances/management through laws, regulations, and policies, as interpreted by agencies and courts)

Endangered Species

- Includes taxonomically-defined species and subspecies
- Also, Distinct Population Segment (DPS)
- Determined through threats analysis and rule-making

Memorialized in Code of Federal Regulations (50 CFR 17.11 and 17.12)
-species on list can only be added, removed, revised through rule-making

“Species” Under the ESA

- *ESA definition of species*: includes any subspecies of fish or wildlife or plants, and any DPS of any species of vertebrate fish or wildlife which interbreeds when mature.
  - So, the Act defines WHAT can be listed as endangered species or threatened species
    - species, subspecies, and DPSs
  - But, does NOT define species or subspecies
- No legal or policy definition of species or subspecies.
- FWS/NMFS (Services) rely on best available scientific and commercial information regarding species and subspecies classification.
- Because DPSs are not taxonomically-recognized entities, they are defined by policy…(*more later*)
- The Services evaluate the validity of species and subspecies in status reviews.

Species and Subspecies

- General current **species** definitions/concepts:
  - Individuals within a species share an evolutionary history with each other more so than they do with organisms of another species
  - Most taxonomic classification conclusions are inferred by examining variation in one or more traits among groups
  - Some species concepts may not be applicable to all groups of taxa or for all situations or speciation processes
- Divergent opinions on what is a **subspecies** (see *Haig et al. 2006*)
  - Multiple concepts/criteria for identifying subspecies, with varying results due to application of different criteria
  - Subspecies must be discernible from one another
  - Generally, based on morphological, behavioral, geographic, and, more recently, molecular genetic distinctiveness
- Service follows an operational approach and **evaluates all data** available for listing/delisting as species or subspecies, or DPS (see next slide)

Evaluating Validity of Species or Subspecies*

- General Guidance for evaluating opinion and conflicting information:
  - Standard taxonomic distinctions, our expertise, expertise of scientific community, but
  - The **Service bears responsibility** for deciding what taxonomic entities are protected under ESA
- Evaluating taxonomic information – *What if taxonomic distinction is not clearly defined, or conflicting data exist?*
  - Evaluate the reliability of the information
  - Factors to consider in weighing lines of evidence:
    1) ***Clarity of hypothesis;***
    2) ***Validity of research design;***
    3) ***Quality of data collection (sample sizes, sample sources);***
    4) ***Appropriateness of methods and analyses for hypothesis being tested (consider statistical power);***
    5) ***Do conclusions follow from the analysis?;***
    6) ***Has information been peer reviewed and what were results of peer review?***

**** No official written Service policy***

Columbia Basin pygmy rabbit

Canada lynx

Distinct Population Segments

Southern rockhopper penguin

History of DPS

- The ESA allows listing of populations as endangered species or threatened species
  - As noted earlier: “species” includes any subspecies of fish or wildlife or plants, and **any distinct population segment** of any species of vertebrate fish or wildlife which interbreeds when mature
- Congress determined that the Service needed to be able to adopt different management practices for different populations, based on their need
- 1978 ESA Amendments - DPS restricted to vertebrates
- DPSs are to be used “sparingly and only when the biological evidence indicates that such action is warranted”

DPS – Defined by Policy*

- Policy identifies principles that guide the Services' listing, delisting, and reclassification of DPSs of vertebrate species

- Three Elements:
  - **Discreteness** - Discreteness of the population segment in relation to the remainder of the species to which it belongs;
  - **Significance** - The significance of the population segment to the species to which it belongs
  - **Conservation Status** - The population segment's conservation status in relation to the ESA standards for listing

Grizzly bear

*Joint FWS/NMFS policy published February 7, 1996 (61 FR 4722)

Discreteness

- Markedly separate from other populations of same taxon
  - Physical, physiological, ecological, or behavioral factors
  - Genetic or morphological information may be used
- Delimited by international boundaries within which differences in control of exploitation, management of habitat, conservation status, or regulatory mechanisms exist that are significant in light of section 4(a)(1)(D) of the Act (that is, are existing regulatory mechanisms designed to protect a species adequate)

Red tree vole

Marbled murrelet

Significance

- Consider biological and ecological significance
- May include, but not limited to:
  - Persistence of DPS in an ecological setting **unusual or unique** for the taxon
  - Evidence that loss of the DPS would result in a **significant gap** in the range
  - Evidence that the DPS represents the only surviving natural occurrence of a taxon that may be more abundant elsewhere as an introduced population outside its historical range
  - Evidence that the DPS **differs markedly** from other populations of the species in its genetic characteristics

Data relevant to Discreteness and Significance

- Genetics
- Morphology/morphometrics
- Biogeography
- Behavior
- Ecology
- Each is sufficient, not all (including genetics) are required

Conservation status

- Does it does it meet the Act's definitions of "endangered species" or "threatened species”?
- Example: **Black-footed albatross**
  - Hawaiian Islands DPS and Japanese Islands DPS
  - Determined discrete and significant
    - <u>Discrete</u> based on behavior of strong nest fidelity, physical separation, genetics
    - <u>Significant</u> because loss of 1 population would result in significant gap in range, and markedly different genetics
  - After evaluation, neither of these DPSs warranted listing under the ESA

- Different DPSs of the same vertebrate taxon can be assigned different ESA classifications (E or T).
  - **Example: Atlantic sturgeon**
    - Endangered
      - New York Bight DPS
      - Chesapeake Bay DPS
      - Carolina DPS
      - South Atlantic DPS
    - Threatened
      - Gulf of Maine DPS
    - Discreteness based on genetic differences
    - Unique ecological settings

DPS Summary

- Discreteness, Significance, and Conservation Status Criteria
- Include DPS Analysis in 90-Day Petition Finding, 12-Month Finding, Proposed Listing, and Final Listing (if applicable)

Fisher

Southern resident Killer whales

Arctic grayling

Summary of Information & Comments Received

coastal California gnatcatcher 90-day petition finding (Dec. 2014)

Prepared by U.S. Fish and Wildlife Service

Carlsbad Fish and Wildlife Office

August 2015

90-day Finding - Overview

What is a 90-day finding?

- Evaluates whether the petition presents substantial information that the action (in this case, delisting) *may* be warranted
  - Based on information provided in the petition, and info available in our files
    - Does information in the petition appear to support the claim?
    - We do not seek additional information at this point.
- **If substantial**, then we notify the public we've initiated a status review (Federal Register Notice)

What does the notice mean?

- It's a request to all interested parties to submit any information we should consider:
  - No document to comment on, so it's not really a "comment" period
  - Doesn't ask whether or not there is support for the action considered
    - But information and comments received are important as they can provide relevant scientific information/analyses in support of their position

Overall Summary of Reponses

- Received information from: one agency, many environmental groups, general public, scientists, and other professionals
  - Environmental groups
    - Over 38,000 form-type letters (mostly Audubon)
    - Asked Service to reject the petition, not delist, or provided information related to coastal California gnatcatcher's (*P.c.c.)* conservation status and habitat conditions
  - General Public – all but two supported continued listing
  - Variety of responses from professionals/scientists
    - See details in upcoming slides

Only one agency response

- US Navy
  - Activities at its installations provide information on coastal California gnatcatcher biology, range, and population status
  - Prepares/executes natural resource management plans for its installations
    - plans include measures benefitting the gnatcatcher (e.g., invasive species management).

Non-profit conservation organizations

- Audubon (and many chapters)
- Sierra Club
- Natural Resources Defense Council
- Center for Biological Diversity
- and others, such as Endangered Habitats League, Center for Natural Lands Management, Calif. Native Plant Society

Summary of general issues (environmental groups and public)

- 1) Zink et al. (2013) [Study] doesn't provide scientific grounds for delisting (data insufficient)
- 2) Alternate regulatory mechanisms to ensure protection are not in place over large portions of its range
- 3) Multiple threats such as repetitive fires and type conversion still exist; permanent habitat loss still a threat
- 4) Climate change is now a threat, not identified at time of listing; some models project loss of coastal sage scrub (CSS) habitat.
- 5) Petition based on Study that has sponsorship bias/conflict of interest

Summary of general issues (continued)

- 6) Study not consistent with decades of [independent] data and previous evaluations (e.g., 2004 science panel)
    - need to consider other characteristics besides mtDNA and nuclear DNA (too narrow) that better reflect and determine differentiation based on more recent history, ecological role(s), and adaptive differences
- 7) Additional studies and science review needed
    - Decision to list or delist a species should be based on peer-reviewed research that has been demonstrated to fit the rigorous ESA standard of "best available science"
    - Such science should be supported by multiple lines of evidence and rigorous analysis that has been discussed and accepted by more than one or two experts in the field.
    - Many commenters agreed with McCormack and Mack's published analysis and conclusions (see slide #14).
- 8) Service needs to err on the side of caution; one study is not adequate given potentially permanent adverse consequences

Summary of general issues (continued)

- 9) Service needs to consider Mexico's ability to protect this subspecies if it's delisted in U.S.,
- 10) Species has value
  - important to economy, such as birdwatchers and leaders of nature hikes, and artists, photographers,
  - natural predators (gnats and mosquitoes).
- 11) Personal observations indicate populations are becoming rarer
  - species not able to interact genetically with the Mexican population
- 12) Ethical concerns
  - all creatures deserve not just the right to live, but also to thrive
  - preservation of wildlife diversity, especially Southern California endemism

Additional Comment Received

- **Specific questions from one Audubon Chapter that they believe the Service should address:**
  - How current are population models being used by Service?
  - How much does Service currently know about status of this subspecies or California gnatcatchers on regional and statewide scales?
  - What do current dispersal and fecundity models say about the success or recovery since listing?
  - Are isolation impacts between Baja and California being studied?
  - What is known about gene flow between large scale and local populations?

Two public commenters supported the petition to delist

- Erroneous classification has the direct effect of reducing housing affordability in southern California.
- Gnatcatcher is not threatened; population is increasing
- Delisting would have limited practical impact, if any at all, on the gnatcatcher since most CSS is protected

Responses from Scientists or Other Professionals

- Atwood
- J. Remsen
- K. Winker
- M. Patten (with publication)
- McCormack (with publication)
- UC Berkeley (two)
- Others (Putnam, Ryder)
- **R. Thornton** (representing 2 petitioners)
- **Zink**
- **Ramey**

All opposed delisting (except Thornton, Zink, Ramey) and most supported McCormack and Maley's (2015) analysis/critique/conclusions

Atwood

- "No doubt" that the species occurs in very different ecological settings north and south of 30°N latitude on the Baja California peninsula (citing Atwood 1988, 1991, Atwood and Bontrager 2001)
  - long-accepted southern limit of the *P.c.c.* (citing Mellink and Rea 1994)
  - also represents a recurring distributional boundary reflected in numerous other plant and animal taxa
- (at minimum) Calif. gnatcatchers found north of this latitude represent a DPS that should be protected under the ESA
- Citing coauthored paper with Zink (Zink et al. 2000)
  - All of the recent subspecies schemes suggest that the northern part of the range, including the CSS populations, include 1 or 2 subspecific units
  - Paper's analysis found little variation in the mtDNA control region and 3 mtDNA genes
  - Concluded that the genetic [mtDNA] data show that the species poorly reflects the endemism of the CSS community
- Reviewed a draft of the Zink et al. (2013) paper
  - Raised concerns about the ecological niche modeling sections of the manuscript; some fundamental flaws that should be addressed; most suggestions ignored

Remsen

- Zink et al. 2013 is flawed on many levels, citing critique by McCormack and Maley (2015)
  - Any notion that the two forms do not differ genetically based on a pitiful number of neutral genetic loci is intellectually dishonest
  - Study used a few mitochondrial and nuclear loci that are typically selected in studies of relationships BECAUSE they are presumably neutral, i.e. not relevant to natural selection and adaptation at the population level
  - That two phenotypically distinct but recently diverged populations would not differ at these neutral loci is a widespread result in birds
- We do not yet have the tools to locate and sequence those genetic loci associated with the characters that show phenotypic differentiation, e.g. coloration in this case
  - Inappropriate to declare that two populations do not differ genetically when the genes that are responsible for their differences haven't been found, much less analyzed
- Zink's 'mtDNA-only' view of how animals should be classified is an extreme outlier

Winker

- Zink's views of the value and existence of subspecies as a taxonomic category do not predominate in the field of ornithology
- Subspecies descriptions are based on phenotype; in birds we most frequently examine plumage variation
  - difficult to test the validity of a named subspecies using genetics, because typically only a very tiny portion of genome is sampled, and
  - usually know that this tiny sample is not connected to the phenotypic characters used to describe the subspecies
  - thus, a negative result does not mean that the subspecies is not valid, it just means that you did not find a genetic difference that corresponds with the described phenotypic difference
- Study chose genetic markers and analyses more suited to questions about old divergences, not the shallow divergences that we usually expect subspecies to represent.
- Did not apply the full suite of population genetics analyses available to answer their question of the validity of the subspecies
  - **The question was not adequately addressed by their approach**
- Conclusions regarding niche analysis were unconvincing
- As with others, expressed concerns about funding source and potential for bias

Patten

- Key problem with Zink et al. (2013) is failure to incorporate an alternative hypothesis that would allow for a finding of "valid subspecies."
- Submitted in-press paper, *Subspecies and the philosophy of science* (Patten 2015)
    - need for a clear and consistent philosophical approach as to how genetic data are used to assess subspecies limits
    - any adopted framework should allow a full range of alternatives to be either supported or rejected
- In Patten 2015, an amendment was proposed to the *phylogenetic species concept* to include a subspecies category
    - under the phylogenetic species concept, a (morphologically) diagnosably distinct, geographically circumscribed clade that does not form a distinct (neutral) genetic cluster or is not reciprocally monophyletic in relation to other such clades be deemed a subspecies and not a species
- Only after a failure to achieve both phenotypic and genotypic distinctiveness—a large effect size (Patten 2010, Tobias et al. 2010)—should a researcher conclude that a subspecies is taxonomically invalid.

McCormack Comments (with submitted paper, McCormack and Maley 2015)

- Summary of arguments from their paper (critique of Zink et al. 2013)
  - genetic or ecological analysis does not provide compelling evidence for a lack of distinctness of *P.c.c.*
  - nuclear markers chosen were not ideal for addressing differentiation at the subspecies level, and too few in number to conclude that no differences exist
  - overinterpreted negative results in their genetic/ecological analyses
- Presented a separate analysis that found distinctness of *P.c.c.* in several of the DNA regions
- Discrepancy between their results and Study seems to lie in the threshold chosen for distinctness
  - Threshold for Zink et al. seems to be that *P.c.c.* must possess a set of gene copies that is completely different from those of other populations
- Recommended additional, more detailed analyses

UC Berkeley (Andersen)

- Concluded that Study was based upon faulty analysis and interpretation of the molecular results
  - Four of the polymorphic loci were omitted from the results
  - Study lacks sufficient sample sizes to conduct the analyses presented
- Reanalyzed the results from Study using a population genetic framework
    - Found that *P.c.c.* is significantly differentiated from other subspecies
  - Presented alternative approach for determining whether two populations/subspecies should be considered as genetically distinct or as a single panmictic population
    - Results from simulated datasets based on California Gnatcatcher population parameters support the subspecies designation
- Also prepared simulations as to whether two survey populations should be considered unique
  - His calculated value of genetic differentiation (F_{st}) between subspecies of California Gnatcatcher for the two subspecies scenario was greater than simulations' average estimate

UC Berkeley (Cicero)

- Markers used in Study not well-suited to address distinctiveness of the subspecies
  - Many studies note that mtDNA does not sort out cleanly into distinct (reciprocally monophyletic) groups at the subspecies level
  - Nuclear markers chosen were not appropriate for the shallow taxonomic level of subspecies
    - These genes represent only a tiny portion of the genome, and the lack of differences in these genes does not necessarily reflect genome-wide patterns
  - Next-generation sequencing approaches would provide a much broader picture of genetic variation in populations of California Gnatcatchers
- Other differences including phenotype, ecology, and behavior must be considered when reviewing a petition to delist a subspecies
  - Most subspecies are described on the basis of phenotypic differences
- Further analysis is needed to address the question of ecological distinctiveness
  - CSS occupied by *P.c.c.* is different in vegetation and climate from the habitat of other subspecies
- Song or other behavioral traits can also separate subspecies and can serve as a mechanism for reproductive isolation
- Further study is needed re genetics, morphology and plumage, ecology, and song to comprehensively assess the taxonomic status of this subspecies.

Others – Putnam

- Interpretation of genetic data over-reaches given the genetic markers and methods used
- Genetic markers chosen were not appropriate
    - Number and type of genetic marker would not necessarily be expected to show significant population differentiation at the subspecies level.
        - Sequencing a small number of introns/exons is suitable for delineating species, *not* subspecies
    - Given the low genetic diversity of *P.c.c.* many microsatellite markers (which have much higher mutation rates) or genome-wide data using at least many 100's of SNPs would be required for delineating subspecies
- Study estimated genetic differentiation (using G_{ST}) by combining all individuals from all populations for each genetic marker
        - Pooled G_{st} values among loci were very variable, which may also indicate differentiation across some chromosomal regions and the need to examine more genetic markers.
- If genetics alone is used to invalidate a subspecies designation, a clear standard should be set regarding what the genetic research must show.

Others – Ryder

- Study's negative findings are not informative regarding phylogeographic differentiation of northern and southern populations of California gnatcatcher
  - Methods used are inadequate for the purpose of identifying intra-specific population structure
  - Analysis based on limited number of nuclear-encoded loci that generally do not evolve sufficiently/rapidly to provide a significant indication of population divergence
- Concerned about the lack of disclosure of the financial supporters for the Study, normally considered standard practice in scientific publication
- Commented on continued threats to *P.c.c.* and need for ESA protections to ensure long-term survival

Zink (two letters submitted; ***these should be read in their entirety since both delisting petitions were based on his studies***)

- Listing of *P.c.c.* was based on original data error; reanalysis of historical data as well as newly acquired data shows that the best available scientific information does not support its listing
- In the history of describing avian subspecies, existing subspecies were not all created equal (citing Zink 2015 *Condor* article re SW willow flycatcher)
    - Only those subspecies that are discrete and evolutionarily significant meet the qualifications for listing under the ESA, by virtue of showing significant genetic differences and being significant to the species
    - Before a subspecies is considered as qualified for listing, it must either be tested for its significance and validity using modern methods and must meet certain criteria
        - Molecular genetic characters are the "industry standard" (Avise 2000) for providing independent checks on patterns suggested by morphological characters upon which subspecies descriptions were based, or in describing new taxa that could be considered as subspecies or species

Zink

- Several factors compromise inferences and conclusions that have been drawn from Atwood (1991) (also cites Skalski et al. 2008 reanalysis)
    - No support for discrete boundaries (step clines) or distinct subspecies based on morphological characteristics
    - Despite claims to the contrary (McCormack and Maley 2015), Atwood (1991) does not establish support for *P.c.c.*in either univariate or cluster analyses; this has been shown in McDonald et al. 1994 and Skalski et al. 2008.
    - Mellink and Rea's (1994) description not compelling
- No reason to discount the conclusion that the mtDNA data are correct in indicating no genetic gaps in the range of the California gnatcatcher and thus there is no support for described subspecies or any other evolutionarily significant divisions
    - mtDNA data of Zink et al. (2000) were no different than those used in other species
    - Service has relied on mtDNA studies in over 90 ESA listing decisions

Zink

- Re nuclear DNA study (Zink et al. 2013)
  - The pattern of DNA variation is strikingly similar to the morphological data in supporting a continuous pattern of intergradation throughout the range
  - the STRUCTURE results reported by Study show that there are no supported groups other than the entire species
  - the nDNA data corroborates the mtDNA data (Zink et al. 2000) and supports the view that the California gnatcatcher is a species without significant genetic or historical divisions
- Criticized McCormack and Maley's (2015) critique and described results to be presented in an article submitted for publication, including a "in prep" article regarding SNP loci
- Niche model – Not significantly divergent in their <u>climatic</u> ecological niche characteristics, though he states that results depend on the environmental layers and sample sites used to build the model
- DPS discussion – a DPS designation would require evidence that the named population segment is "significant to the species," which the genetic data reveal is not the case (e.g., 1.3% to 5% of total genetic variance); *P.c.c.* does not qualify as either DPS or subspecies
- Conservation status remarks
  - there are better ways to both aid the preservation of this habitat and retain scientific credibility than by recourse to shoddy taxonomy and selective or biased manipulation of data
  - the species has a widespread distribution south of Ensenada, and high population levels; long-term existence not threatened when species considered as a whole

Zink (June 2015 Comment Letter)

- Reviewed comments on www.regulations.gov that support listing; responded to detailed comments submitted by several scientists
- States that the single scientific question is whether the best available scientific or commercial data support the validity of *P.c.c.*
- General remarks:
  - None of the letter writers are alpha taxonomists; only one author has personally described a subspecies
  - None of the letter writers provided any new data
  - Some writers have confused issues (this is not about whether subspecies are useful or whether CSS habitat should be saved)
  - Addressed criticisms of using "wrong markers"
- For the two re-analyses of molecular data (Andersen and McCormack and Maley, Zink et al. (submitted) shows that the conclusions in these reanalyses are incorrect regarding support for *P.c.c.* using any known definition of subspecies
- Manuscript is in preparation – over 6,000 SNPs in nuclear DNA have been analyzed for geographic structure in California gnatcatchers; there is no support for subspecies
  - Also, rebuttal by Zink et al. to McCormack and Maley is making its way through the publication process and deserves to be evaluated before the Service determines whether the delisting petition is warranted.

Thornton (representing 2 petitioners)

- 2014 Petition based on Zink et al. 2013
  - Presents analysis of nuclear DNA obtained from gnatcatcher specimens throughout the range of the species
  - Study concluded that there is no genetic basis for maintaining a subspecies classification for *P.c.c.*
  - Information and conclusions relied upon in the 1994 and 1995 listing determinations are in error
    - Does not comply with ESA best scientific data available mandate
  - Study important because Service suggested that a nuclear DNA analysis would provide the best available scientific data to resolve the subspecies' classification
    - Reliance on genetic data in ESA listing decisions reflects the broad acceptance of use of DNA evidence by the scientific community and by the courts

Thornton (representing 2 petitioners)

- Other Comments
  - A delisting determination will not undermine the conservation of the gnatcatcher or other coastal sage scrub species
    - So Calif. HCPs provide unprecedented levels of conservation to hundreds of thousands of acres of the CSS habitat of the gnatcatcher
  - Issue is not whether the CSS habitat of the gnatcatcher is conserved, but whether the Service will comply with the mandate of the ESA to base listing/de-listing determinations on the best scientific data available
    - Not consistent with best available science mandate to rely on qualitative analyses or outdated methods when current scientific methods and quantitative data are now available
    - The scientific process, including the publication of peer-reviewed papers, is the principal mechanism recognized by the scientific community for identifying the best available scientific information
  - No longer legally/scientifically defensible to continue to rely on measurements of characteristics such as brightness of breast feathers and purity of back feathers from differently aged museum specimens to determine whether *P.c.c.* is a valid subspecies.
  - The Service should not conclude that de-listing *P.c.c.* is not warranted because some as yet uncollected data in the future might support listing
  - Reiterated Zink's submitted public comments criticizing McCormack and Maley (2015)

Ramey

- Supports Zink's analyses/conclusions
  - Data and analyses in Zink's publications provide three lines of corroborating evidence that falsify the hypothesis of uniqueness of this subspecies, relative to California gnatcatchers elsewhere in Baja, whether its boundaries are based on Atwood (1991) or Mellink and Rea (1994).
    - Zink's two genetic data sets (2000 and 2013) represent the best available scientific data on genetic differentiation across the range of the California gnatcatcher species that was not available at time of listing
- Critiqued analysis and conclusions of McCormack and Maley (2015)
- Discussed substantial data quality and scientific integrity issues with the data originally used to list the subspecies as endangered in 1993, and peer review of those data in 2004.

Comments available at www.regulations.gov

Docket Number FWS-R8-ES-2014-58

APPENDIX C

Complete Individual Memoranda

California Gnatcatcher Facilitated Science Panel Workshop

U.S. Fish & Wildlife Service

Unless otherwise noted, references cited in the individual memoranda are provided in Appendix B: Materials Provided.

Individual Memorandum
Coastal California Gnatcatcher Expert Panel

Panelist 1
18 August 2015

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1) What, if any, do you consider to be the most reliable features and methods to delimit infraspecific entities in songbirds or avian species in general?

In its most recent publication of taxonomic guidelines, the American Ornithologists' Union (AOU) Committee on Classification and Nomenclature writes that "Subspecies should represent geographically discrete breeding populations that are diagnosable from other populations on the basis of plumage and/or measurements, but are not yet reproductively isolated. Varying levels of diagnosability have been proposed for subspecies, typically ranging from at least 75% to 95%. Because subspecies represent relatively young points along an evolutionary time scale, genetic differentiation between subspecies may not necessarily parallel phenotypic divergence. Thus, subspecies that are phenotypically but not genetically distinct still warrant recognition if individuals can be assigned to a subspecies with a high degree of certainty. Described subspecies that represent points along a phenotypic continuum (cline) probably would not warrant recognition given further study." This opinion differs slightly from the peer reviewed exchanges of Haig (2006), Patten and Unitt (2002), and Patten (2015) which ask for concordance of two or more datasets. In the case of Patten (2015), these datasets should include phenotypic, genetic and geographic data.

By contrast, Zink and Blackwell (1998) suggest that genetic distinctness is paramount to taxonomic distinctiveness. Zink et al. (2000, 2013) use this opinion to refute taxonomic distinctness of coastal California gnatcatchers (CCG). This representation of a subspecies supplied by Zink and his colleagues is a minority opinion in ornithology. My opinion is that Zink's representation of subspecies status is erroneous. Subspecies by definition are not reproductively isolated, a status afforded only to species and higher levels of taxonomic classifications. I believe a liberal interpretation of subspecies is proposed by AOU and a conservative definition is proposed by Patten (2015). I suggest a middle path where two or more concordant datasets be used to identify subspecies status.

If using genetic data is to be a feature of diagnosing subspecies (as one of the concordant features), then the features and methods used to delimit infraspecies entities should follow a logical framework of hypothesis testing that answers the following questions:

1) Does the avian species have phenotypic variation that is geographically discrete?
    a. If yes, then this species may be a valid subspecies. Concordance with genetic data may be tested.
    b. If no, but the species has variation that is clinal and represents potential adaptations to different environments, and one portion of that cline is threatened, then the species may be a valid DPS.
2) To test for concordance of genetic data, it is imperative that one first asks: What are the evolutionary forces driving phenotypic distinctness? If discreteness is found, then hypotheses need to be proposed that support the type of evolutionary forces that are

suspected. If inappropriate hypotheses are tested, inappropriate methods will be used and erroneous inferences will be made.

  a. If vicariance and drift are suspected to be the driving force of distinctness, then moderate to strong levels of neutral differentiation may be expected along a contemporary or geologically aged barrier.
  b. If selection is suspected as the driving force, then the number of genes under selection would be suspected to be very small compared to the total genome and level of gene flow would be expected to be restricted but only to a small degree. Thus neutral variation and distinctiveness may be expected to be quite low. Scanning for and identifying genes under selection may be a diagnostic tool, but it could very well be a search for “a needle in a haystack”. A negative finding would not indicate that selection was not operating.
  c. If the biogeographic phenomenon that has driven the differentiation is suspected to be of late Pleistocene origin, then a signature of differentiation (as measured by neutral markers) may be detectable and divergence deep.
  d. If the biogeographic phenomenon is more recent, say of Holocene origin, then a signature of differentiation (as measured by neutral markers) may be difficult to detect without using many markers (e.g. thousands to tens of thousands of SNP’s) that are representative of a large portion of the genome.

Thus, it becomes apparent that a one size fits all approach to subspecies designation does not work. The appropriate morphological characters must be measured, and the proper a priori hypotheses about patterns of differentiation must be applied based on proposed mechanisms of evolution and the geologic age at which those events occurred, and the appropriate tools that adequately test those hypotheses must be applied. This approach was not used by Zink et al. (2000, 2013).

2) What are the strengths and weaknesses of these approaches, particularly with the issues presented with the coastal California gnatcatcher (*Polioptila californica californica*)?

The strengths of the morphological approaches for coastal California gnatcatcher (CCG) lie in the morphological (n=31) measurements made by Atwood (1991), Mellink and Rea (1994), and McDonald (1994). These have been reviewed by the Service and 2 panels of scientists who agree with the subspecies designation, but other scientists (Barrowclough 1994, Cronin 1997, and Skalski et al. 2008) disagree. Three papers with dissenting opinions have weaknesses, but cannot be ignored. Skalski’s opinion is based on one characteristic and therefore that analysis is not robust. Cronin and Barrowclough point to deficiencies in the data, but each acknowledge that the analyzed data show patterns that have breaks in variation. They may not agree as to the robustness of those data, however. Erring on the side of caution, I would tend to agree with the opinion of Atwood and the Service and not rescind the subspecific status of the taxon based on morphological data.

The genetic data analyzed Zink et al. (2000, 2013) have no strengths. Inappropriate markers were used to test inappropriate hypotheses (see response to first and third question).

3) Different methodologies may be suited to discriminate between taxa at various ranks while others are best suited to show close relationships among taxa. With this in mind, assess the extent to which the methods, data and conclusions of Zink et al. (2013) apply to these two approaches. How does your assessment apply to the taxonomic status of the California gnatcatcher?

The fundamental flaw with Zink et al. (2013) is that they never test the hypothesis that CCG are part of a subspecies complex (n=2 or n=3 subspecies). All of the analyses are designed to test hypotheses about effective population size, genetic diversity, and isolation by distance. Global tests of population differentiation (G_{ST}) overlook pairwise differences in populations and obscure single locus signals of differentiation. Using a handful of slowly evolving nuclear markers is inappropriate for use in a question where we know, based on biogeographic history of the region, that any divergence is recent (< 12,000 ybp; Axelrod 1978) and therefore effect sizes will be small.

McCormack and Maley (2015) provide an excellent overview of the flaws in logic and analysis of Zink et al. (2013). They provide two compelling pieces of evidence using the Zink et al. (2013) data that provide an effective argument that incipient genetic divergence is taking place. First McCormack and Maley (2015) use an AMOVA to specifically test the hypotheses of subspeciation set forth by both Atwood (1991) and Mellink and Rea (1994). They find significant differentiation in 2 of 7 markers that correspond to Atwood (1991) and the Mellink and Rea (1994) observations of morphological differentiation. Inspection of allele frequencies shows private alleles among subspecies. These data robustly show that there is evidence of incipient differentiation along biogeographical boundaries in concordance with morphological data. Using the middle path criteria of subspecies, CCG in my opinion are a subspecies.

4) There is an array of scientific information that could be used to determine the taxonomic status of animals listed as the coastal California gnatcatcher. Using the available evidence, describe how the coastal California gnatcatcher represents a recognizable entity (e.g., subspecies) or specifically why no infraspecific taxa warrant recognition within California gnatcatcher (*Polioptila californica*). In addressing this question, we ask that you consider the following: the discreteness, significance, and conservation status of the species' (or subspecies) population segments.

Reinspection of the Zink et al. (2013) data conducted by McCormack and Maley (2015) show that genetic data in agreement with morphological data of Atwood (1991) and Mellink and Rea (1994). Using the middle path criteria (Response 1) of subspecies designation, I conclude that CCG are a distinct subspecies based on the available data. There is strong evidence for a subtle but diagnosable difference. One would expect the difference to be subtle and of small effect based on the rapid biogeographic changes to this region that occurred recently (during the Holocene). I would not predict *a priori* that differences would be large, that there would be reciprocal monophyly, or that they are a distinct evolutionary unit. California gnatcatchers do appear to be a species that has diverging evolutionary pathways that can rightly be called subspecies. These pathways are already producing populations which are diagnosable by two characteristics and have discrete geographical locations. By AOU criteria and criteria proposed by Haig et al. (2006) and Patten (2015), CCG are a subspecies.

5) What additional information or analysis, if any, would clarify the taxonomic status of the California gnatcatcher?

I do not believe that further analysis is needed given the morphological and genetic data in hand. Public comments from Zink indicate that he is developing a 16,000 SNP molecular assay to further analyze CCG samples. It is imperative that these genetic data be analyzed in such a way that appropriate hypotheses be tested, appropriate statistical tests be performed (sensu McCormack and Maley (2015) and my response to question 1) and that the data be made available for independent analysis. The conflict of interest from funding sources that consistently shows up in genetic publications makes it imperative that the data be publically available. I do not question the ethics of Zink, however. There is a gamut of viewpoints on the definition of subspecies and Zink’s viewpoint is a minority and fringe one. This viewpoint taints the way he views and analyzes the data. I question the ethics of the funding source. They have clearly found a scientist who fits their world view and exploit that scientist.

Additional Comments

I believe that one of the reasons that the taxonomic classification is so contentious is that geographic differences in characteristics are of small effect size and therefore large sample sizes are needed to produce robust conclusions. Large sample sizes of threatened species are rarely available. The differentiation among lineages that is occurring is very recent and therefore only incipiently distinct. The subspecies status may be found to be not warranted if new data using more robust sampling strategies for populations and genes are used. Those data are not available at this time. Nonetheless, I have no doubt that this species has distinct population segments that represent unique lineages in unique habitats with unique political boundaries. The populations have already been shown to be discrete; the north population is significant because it represents a population in a mesic habitat as opposed to the more southernly xeric habitat.

Axelrod, D. I. (1978). The origin of coastal sage vegetation, Alta and Baja California. American Journal of Botany, 1117-1131.

Individual Memorandum
Coastal California Gnatcatcher Expert Panel

Panelist 2
18 August 2015

1) What, if any, do you consider to be the most reliable features and methods to delimit infraspecific entities in songbirds or avian species in general?

For bird subspecies, I favor the definition reported in Haig et al. (2011): "subspecies is generally defined as a breeding population that has measurably distinguishable genotypes or phenotypes (or both) and occupies a distinct geographic area within its species range (Avise 2004, Patten 2010, Remsen 2010)". This captures the sense that subspecies reflect evolutionarily (but not necessarily phylogenetically) distinct units within species that have undergone some amount of adaptive divergence (reflected in their phenotypes and genotypes) and could potentially (but not necessarily) end up as distinct species detectable as phylogenetically distinct lineages. An important goal of conservation genetics is to preserve the adaptive potential in the form of fitness-related variation within species of conservation concern (Frankham et al. 2010) and indirect (or direct) evidence of adaptive divergence in the form of phenotypic or ecological distinctiveness of proposed conservation units is essential. Genetic differentiation assessed using neutral genetic markers does not necessarily reflect adaptive divergence – confirmation of adaptive divergence requires detecting differentiation in other phenotypic traits or characteristics like ecology that suggest distinct selection regimes.

I do not agree with the extreme view of Zink and others that subspecies are only real if they reflect phylogenetically separate lineages and hence can only be identified using phylogenetic criteria such as reciprocal monophyly in mtDNA (Zink 2004). I agree with McCormack and Maley (2015) and others that this is an excessively restrictive criteria which, if applied to identifying conservation units, will result in a failure to identify population segments that are important to protect from a conservation perspective. Specifically, sets of populations below the species level that show evidence of adaptive divergence, but yet have not necessarily achieved phylogenetic distinctiveness, collectively represent the adaptive potential of a species of concern. Application of the phylogenetic distinctiveness criterion of Zink and others would fail to identify and protect such units that potentially contain adaptive variation within species of conservation concern, hence would constitute a failure to meet the goals of the US Endangered Species Act.

In terms of criteria I share the frustration of many that that the criteria for defining subspecies are vague and qualitative. Of the recent papers that I have read about quantitative approaches for defining subspecies, I am most impressed by the papers by Haig et al. (2006) and Sackett et al. (2014). Both apply more quantitative and explicit criteria for evaluating subspecies that I think represents an important step in applying the concept in conservation applications. They also reflect a general opinion in the conservation community that multiple types of data are needed to evaluate the conservation status of taxa (Crandall et al. 2000). The Haig et al (2006) paper stresses the use of congruent differentiation in different types of variation. Hackett et al (2014) take this further by laying out a clear set of predictions, tests and specific analytical methods for assessing whether two groups of organisms represent distinct subspecies. The methods and data used are not novel – rather it is the hypothesis-testing approach that lays out specific predictions across different data types that is compelling to me. The specific methods and data used for an evaluation could vary but what is useful is that the study lays out an example of a possible common "Gold Standard" for these types of evaluations that represents starting point for decisions about the distinctiveness of a putative subspecies. It could also be up-dated as different types of data and new methods of analyses become available.

2) What are the strengths and weaknesses of these approaches, particularly with the issues presented with the coastal California gnatcatcher (*Polioptila californica californica*)?

The coastal California gnatcatcher (*Polioptila c. californica* – hereafter CCG) presents challenges in assessing its status as a distinct conservation entity. All available evidence points to CCGs as being recently evolved likely within the last 10,000 ybp (Zink et al. 2000; 2013) and so it potentially represents the earliest stages of a taxon undergoing adaptive differentiation. In such situations evolutionary biologists believe the process follows a sequence of steps each of which is reversible: first, adaptation via natural selection leads to adaptive differences between putative subspecies; second, this leads to restricted gene flow between groups; which, third, is finally reflected in differentiation in neutral genetic markers as a result of genetic drift resulting from isolation.

The strength of a "multi-evidence" approach to identifying subspecies (e.g. Haig et al. 2006; Sackett et al. 2014) is that it applies a range of tests and evidence that are able to assess in a more comprehensive manner if two populations that are being considered for protection show adaptive divergence and what stage in the process outlined above they have reached. For example, if two populations show differences in morphology but no genetic or ecological differentiation it would suggest that they are not isolated from each other or have only been so for a very brief period of time and hence may not be deserving of protection. In contrast, groups of populations showing significant differentiation in phenotype, ecology, and genetics provide strong evidence for adaptive differentiation hence separate protected status. A weakness of this approach is that it relies on indirect evidence based on phenotype, ecology, and genetics to make inferences about the evolutionary distinctiveness hence conservation value of populations. However, this is a general problem in evolutionary studies of natural populations. While progress is being made in identifying the genetic basis of adaptations in natural populations (Barrett and Hoekstra 2011) evolutionary and conservation biologists still heavily rely on indirect measures of adaptive variation such as morphology to assess whether potential conservation units are distinct.

This approach contrasts with the more restrictive "subspecies as monophyletic units" approach advocated by Zink and others. The strength of this definition is its clarity. It is certainly true that two isolated populations that show adaptive divergence will eventually show reciprocal monophyly. The key weakness is that this process can take a substantial amount of years ($\geq 2 N_e$ generations, where N_e is the genetically effective size of the organisms undergoing differentiation – Avise 2004). The point is that even if two entities show differentiation in adaptive traits that justifies their protection, phylogenetic distinctiveness (the criteria used by Zink et al. 2000; 2013) is the most conservative criteria that can be used to diagnose entities deserving of protection. Further (as described above) there are multiple other types of analyses and data that can be used to evaluate the conservation status of groups of organisms that reflect earlier stages in the process of adaptive differentiation. Specifically, direct tests of differentiation in traits that may reflect adaptive differentiation (e.g. morphology) and whether the two entities exist in environments that impose different selective regimes (e.g. differences in ecological niches) can provide evidence as to whether adaptive differences are likely to be present (first step in the sequence outline above). Further, direct comparisons of allele frequency differences between groups of populations representing putative subspecies can test the hypothesis of isolation (step three) for populations that show evidence for differentiation in adaptive traits and which occupy different niches. These analyses are among those suggested by Sackett et al. (2014).

3) **Different methodologies may be suited to discriminate between taxa at various ranks while others are best suited to show close relationships among taxa. With this in mind, assess the extent to which the methods, data and conclusions of Zink et al. (2013) apply to these two approaches. How does your assessment apply to the taxonomic status of the California gnatcatcher?**

After reading the three recent papers (Zink et al. 2000; Zink et al. 2013; and McCormack and Maley 2015) my conclusion is as follows: The analyses by Zink et al. strongly suggest that the coastal California Gnatcatcher subspecies (*Polioptila californica californica*) is not a phylogenetically distinct lineage. Therefore, under the restrictive "subspecies are phylogenetically distinct lineages" definition their conclusion that CCG are not a subspecies is supported. However, I agree with the view of McCormack and Maley (2015) that the data and methods of analyses used were either inappropriate for testing the whether these birds were distinct under a more widely-used definition of subspecies (see above) or in fact supported the genetic and ecological distinctiveness of these birds under the ESA. I support the conclusion of McCormack and Maley (2015) that "…the genetic markers they [Zink et al. 2013] chose were not well suited to the question of distinctiveness" and that they "…over-interpreted negative results in their genetic and ecological analyses".

Specifically I feel the following three points are key issues with the Zink et al. (2013) study:

1) *Genetic Markers Used Were Inappropriate for Assessing Recent Divergence*: The small number of nuclear introns used by Zink et al (2013) have low levels of variation relative to other types of nuclear makers (e.g. microsatellites) or assay a very limited portion of the genome in relation to high dimension markers such as those based on RADseq (Baird et al. 2008). Why they chose this type of maker is unclear – as noted by McCormack and Maley (2015), Zink and Barrowclough (2008) have stated in print that these types of markers are far less appropriate for assessing evidence for recent divergences than mtDNA because of the four-fold greater N_e – nDNA markers are "lagging" indicators of differentiation in such situations. Given the lack of phylogenetic distinctiveness in mtDNA shown by Zink et al. (2000) the result in terms of a lack of phylogenetic distinctiveness seems likely to be foregone conclusion.

2) *Direct Tests of the Genetic Distinctness of Gnatcatcher Subspecies Were Not Conducted*: The most direct test of whether putative subspecies are genetically distinct (see subspecies discussion above) is to compare levels of differentiation between sets of populations that fall within the ranges of each putative subspecies. Zink et al. (2013) did not do this but rather conducted global tests across all populations with no grouping by

subspecies. In fact, when McCormack and Maley (2015) conduct such tests they find evidence (albeit limited) for such differentiation. Zink et al. (2013) did use a Structure analyses using all loci – if there are genetic clusters in the data that correspond to subspecies then they should be present as clusters that match the geographic distribution of each subspecies. They did not find this pattern. But, again only a small number of loci with low levels of variation were used. The program Structure has also been shown to be conservative in terms of detecting genetic structure in populations and so this negative result is not unexpected given the limited variation in the data set to which it was applied (Waples and Gagiotti 2006). The same analyses performed on a RADseq dataset would be very revealing.

3) *Interpretation of Ecological Niche Modeling Results was Incorrect*: As pointed out by McCormack and Maley (2015), Figure 7 in Zink et al. (2013) shows that gnatcatcher subspecies have different ecological niches based on BioClim temperature and precipitation variables not that they are ecological indistinguishable. What the background test (developed by McCormack et al. 2010) shows is that they are not MORE different than predicted from existing spatial variation in the variable used to build the models. This is of interest when trying to test whether taxa show evidence for niche conservation or divergence following divergence (see McCormack et al. 2010) but doesn't negate the conclusion that the subspecies are ecologically distinct at least using this representation of their niches.

4) There is an array of scientific information that could be used to determine the taxonomic status of animals listed as the coastal California gnatcatcher. Using the available evidence, describe how the coastal California gnatcatcher represents a recognizable entity (e.g., subspecies) or specifically why no infraspecific taxa warrant recognition within California gnatcatcher (*Polioptila californica*). In addressing this question, we ask that you consider the following: the discreteness, significance, and conservation status of the species' (or subspecies) population segments.

The strongest evidence for the distinctiveness of the CCG remains the data that shows phenotypic differentiation between subspecies north and south of 30^{o} latitude suggesting the possibility of adaptive divergence between subspecies. Although the analysis and interpretation of this data has been controversial (discussed by McCormack and Maley (2015)), repeated consideration of these data by a range of experts has led to the conclusion that there are some discrete morphological differences between populations that represent *P. c. californica* and *P. c. atwoodi*. The fact that recent analyses of environmental niche variation suggests that this morphological variation supports the idea that the observed differences in phenotype may have resulted from selection pressures related to ecological differences. These morphological and ecological differences meet the "two-criteria" metric proposed by Haig et al. (2006) for distinctiveness of subspecies deserving protection under the ESA and satisfy several of the criteria listed by Sackett et al. (2014).

The genetic evidence for distinctiveness is weaker largely because the appropriate type of genetic data has yet to be generated and comprehensive population-level comparisons of differentiation between subspecies have yet to be completed (see above). Nonetheless reanalysis of Zink et al.'s (2013) data by McCormack and Maley (2015) provided weak evidence for genetic differentiation at several loci. Thus there is weak evidence for a third distinct characteristic of these birds (genetics) showing evidence for differentiation between gnatcatcher subspecies.

Finally, the discussion above has been framed in terms of evaluating the conservation status of CCG in terms of whether it represents a distinct subspecies. However, an alternative is designation as a Distinct Population Segment (DPS) (Joint FWS/NMFS policy published February 7, 1996 (61 FR 4722) which is based on three criteria: Discreteness, Significance and Conservation Status of the populations in question. Based on the points discussed above, the CCG clearly meets all three criteria – it is phenotypically, ecologically, and genetically distinct; constitutes a significant portion of the range of the species; and due to low population numbers is of conservation concern.

5) What additional information or analysis, if any, would clarify the taxonomic status of the California gnatcatcher?

I see two analyses that clarify the taxonomic and conservation status of the CCG.

1. Assay genetic variation among putative subspecies of gnatcatchers using a technique such as RADseq which yields a high dimension data set (>1000s of loci) and then analyze the data following an approach (e.g. Sackett et al. 2014) that explicitly allows for an evaluation of the genetic distinctiveness (not just the phylogenetic distinctness) of the CCG. Based on comments by Zink it sounds as if this type of data has already been generated. It is important to stress that HOW this data is analyzed (see above) is just as important as the generation of it per se.

2. Sequence genomes of 2-3 individuals from each putative subspecies and look for evidence of adaptive divergence in protein coding genes. This would provide a direct assessment of evidence for adaptive divergence between subspecies. An example of this "population genomics" approach applied to birds is a recent study on Darwin's finches (Lamichhaney et al. 2015). Note: Not as far-fetched as it sounds as multiple bird genomes have now been sequenced (Zhang et al. 2014) and US Department of Interior has funded sequencing of a Golden Eagle genome (Doyle et al. 2014). I would strongly suggest consulting with Dr. Scott Edwards, Harvard University if this is a direction that is under consideration because of his expertise in bird genomics.

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Individual Memorandum
Coastal California Gnatcatcher Expert Panel

Panelist 3
1 September 2015

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1) What, if any, do you consider to be the most reliable features and methods to delimit infraspecific entities in songbirds or avian species in general?

To address this question, one first needs a working definition of subspecies in ornithology. As avian systematists and taxonomists, we generally look to the American Ornithologists' Union Committee on Classification and Nomenclature for the current recognized definition of various taxonomic entities in Ornithology. While not all ornithologists will agree with these definitions or how the definitions are applied to real data, the definitions do give us a common language in which to couch our arguments as to why we may agree or disagree with a given taxonomy for a biological entity.

The AOU taxonomic review board provides the following guidance for the classification of subspecies.

> "Subspecies should represent geographically discrete breeding populations that are diagnosable from other populations on the basis of plumage and/or measurements, but are not yet reproductively isolated. Varying levels of diagnosability have been proposed for subspecies, typically ranging from at least 75% to 95%. Because subspecies represent relatively young points along an evolutionary time scale, genetic differentiation between subspecies may not necessarily parallel phenotypic divergence. Thus, subspecies that are phenotypically but not genetically distinct still warrant recognition if individuals can be assigned to a subspecies with a high degree of certainty. Described subspecies that represent points along a phenotypic continuum (cline) probably would not warrant recognition given further study." (http://www.aou.org/committees/nacc/subspecies.php)

If we breakdown this guidance there are a number of things that are important for the designation of subspecies status. I believe what is most important, and gets to the heart of what the hypothesis of a subspecies is, is that a subspecies is phenotypically distinct. That is a subspecies is a phenotypic hypothesis. A phenotype arises through an interaction between the environment and the genetic basis for a particular trait (Johansson 1911). If a trait arises in a particular environment and there is no genetic variation at the loci that correspond to this trait (that is, it is all environment), then we call this plasticity. If, however, there is genetic variation and different genetic variants produce a distinct phenotype and the environment selects in favor of certain phenotypes, then the phenotype is under environmental selection and is considered adaptive (Johansson 1911). Subspecies are believed to correspond to the former: an adaptive phenotype or locally adapted population. This is why subspecies descriptions focus on morphology or other measureable phenotypes that presumably have an adaptive basis.

The next important point made by the AOU concerns the fact that although a subspecies must be phenotypically distinct that it does not need to be genetically distinct. This is especially true with regards to neutral genetic variation. Since a subspecies is an adaptive hypothesis linked to an interaction between the environment and genetic variation, the only type of genetic differentiation that will mirror the phenotypic pattern will be found in the loci responsible for producing the phenotype. Genetic variation unlinked to phenotype should not be expected to be concordant with the phenotypic pattern (Winker 2010, Patten 2015). This does not mean that some unlinked genetic variation might show a concordant pattern but one should not expect this pattern nor expect it to be particularly strong.

The third point made by the AOU has to do with the level of diagnosability and the fact that the phenotypic variation must be discreet and not clinal in nature. The level of diagnosability varies across studies with some researchers favoring strict levels (95%) and others favoring more lenient levels (75%) (Winker 2010). I agree with Patten that a 75% threshold is more appropriate given the nature of evolutionary change given standing variation (Przeworski 2005) and that this level of variation is consistent with the commonly used 5% level of statistical significance. Therefore a rigorous statistical analysis of phenotypic variation that supports the distinction of a breeding population is sufficient to warrant subspecies status. Clinal variation can cause problems with subspecies classification. However, I think it important to point out that hybrid or contact zones between recognized biological species can result in clinal variation existing between good species (Harrison 1990). Therefore if subspecies are very young entities then we may expect clinal variation to exist between them. The question is whether the clines are steep or extremely gradual which will require a very dense sampling. Most subspecies studies have less than dense sampling (the Atwood and Zink examinations are perfect examples of this) and so the question of whether the variation is clinal or discreet can be difficult to assess.

After breaking down the AOU guidance on subspecies, it becomes clear that a subspecies must be a diagnosably distinct phenotype that is geographically restricted. Therefore the best or most appropriate methods or approaches for diagnosing a subspecies are a rigorous phenotypic assessment of variation. Whether the measured phenotype is morphology, physiology or life history traits does not matter, as long as a phenotype is measured and compared to samples from the rest of the distribution. A genetic analysis of variation should be considered subpar to phenotype, unless the loci examined are demonstrated to be directly linked to the phenotype in question. A study of neutral genetic variation should never be considered a direct test of the subspecies hypothesis because it is antithetical to the concept of subspecies as a taxonomic entity that describes local adaptation (Winker 2010).

2) What are the strengths and weaknesses of these approaches, particularly with the issues presented with the coastal California gnatcatcher (*Polioptila californica californica*)?

The strengths and weaknesses of the approaches are not germane to the approaches themselves. They are germane to the definition of the taxonomic level of subspecies. A subspecies is a geographically restricted, locally adapted population; therefore, the approaches used to diagnose a subspecies absolutely must measure phenotype. If we disregard the early publications of Brewster (1881, 1902), Grinnell (1926, 1928), and others because they did not sample well across the distribution of the California gnatcatcher, then the only relevant phenotypic data, and thus the most appropriate data, come from Atwood (1988, 1991). Atwood was the only investigator to directly measure phenotype (morphology in this case). Atwood's original studies and subsequent reanalyses of his data (see Mellink and Rea 1994, Link and Pendleton *in litt.*

1994, McDonald *et al. in litt.* 1994; Messer *in litt.* 1994, Newton *in litt.* 1994) all support the subspecies status of the coastal California Gnatcatcher. I do not include a response to the Skalski et al. (2008) reanalysis of a single measurement in the gnatcatcher because this was addressed in a previous finding by the FWS in 2011 and I concur with this decision.

Since the phenotype hypothesis is linked to the environment, then the next most appropriate data would be a measure of environmental variation. The closest thing we have to environmental data in the case of the coastal California gnatcatcher is the Ecological Niche Modeling analysis performed by Zink et al. (2013). Zink et al.'s interpretation of these data and analyses is confusing. The data clearly demonstrate that the environment occupied by the coastal California gnatcatcher is indeed different than the southern subspecies. The results show that the environments the gnatcatcher occupies are as different as you would expect given the background environments available to them (McCormack and Maley 2015). Zink et al. (2013) interprets this to mean that there is no difference when in reality there is a difference. The environmental data support the phenotypic data of Atwood and Zink et al.'s conclusion is perplexing given this. The different environments across the distribution of the California gnatcatcher set the stage for natural selection to act and could lead to local adaptation in the coastal California gnatcatcher.

The next most appropriate data to assess would be adaptive genetic variation, that is genetic loci that are linked to the phenotypic traits that vary across environments. This data does not exist for the coastal California gnatcatcher. Given that a very small portion of the genome could be responsible for the phenotype (see Carneiro et al. 2014 regarding genomic divergence between hare subspecies), only a very dense genomic sampling or whole genome sequencing are likely to uncover the genetic basis of the phenotypic traits.

The methods that are most inappropriate for testing questions regarding subspecies designations are those that investigate neutral genetic variation. Subspecies are an adaptive hypothesis and one would not expect neutral loci to capture adaptive divergence. In fact it is counterintuitive to believe neutral loci would mirror the pattern observed in phenotype. Zink et al. (2008, 2013) does exactly this. The loci used are insufficient to test the subspecies hypothesis (Winker 2010, Patten 2015).

3) **Different methodologies may be suited to discriminate between taxa at various ranks while others are best suited to show close relationships among taxa. With this in mind, assess the extent to which the methods, data and conclusions of Zink et al. (2013) apply to these two approaches. How does your assessment apply to the taxonomic status of the California gnatcatcher?**

My response to this question is rather straightforward (see all my responses above as a preface). The only data in Zink et al. (2013) appropriate to test the subspecies hypothesis for the California gnatcatcher is the environmental data in the Ecological Niche Model and contrary to what Zink et al. suggest these data do demonstrate the coastal California gnatcatcher does occupy a different environment.

The genetic data generated and analyzed by Zink et al. (2013) is not appropriate for testing the subspecies hypothesis. As I have stated before the subspecies hypothesis suggests the phenotype is locally adapted and the best and most appropriate genetic data to test this hypothesis would consist of data from genetic loci directly linked to the phenotype of interest (adaptive genetic loci). Zink et al. (2013) examine genetic variation at eight putatively neutral loci, which would not be expected to co-vary with phenotype (Winker 2010, McCormack and Maley 2015). I also agree with McCormack and Maley (2015) that Zink et al. do not directly test the subspecies hypothesis and McCormack and Maley do a good job of testing the hypothesis directly using AMOVA in their reanalysis of Zink et al.'s data. Since the genetic data comes from putatively neutral loci, it is surprising that the reanalysis by McCormack and Maley (2015) finds at least one locus that supports the subspecies boundaries in the California gnatcatcher. It is important to point out that I do not concur with McCormack and Maley (2015) that a RAD analysis would somehow be most appropriate for assessing subspecies. While RAD certainly samples more loci, the genomic coverage is still low and unlikely to reveal adaptive loci.

The statistical methods employed by Zink et al. (2013) - clustering methods, gene tree networks, and frequency based methods - are not direct tests of the subspecies hypothesis. These methods are most appropriate for examining the demographic history of a species. They can reveal patterns of population expansion or barriers to gene flow, which can be important contributors to the evolution of a subspecies. However, they are not a direct test of the hypothesis. Given that we know that local adaptation or even population divergence can occur in the presence of gene flow (Savolainen et al. 2013), it is disappointing to see Zink et al. (2013) suggest the contrary. Recombination in sexually reproducing organisms allows for selection to act on very small portions of the genome and provides a means for selection to occur even while gene flow among populations can be high (for review see Savolainen et al. 2013).

My overall assessment is that the genetic data analyzed by Zink et al. (2013) are inappropriate to test the subspecies hypothesis. However, a direct test of the subspecies hypothesis (as conducted by McCormack and Maley 2015) does find at least one of these loci supports the subspecies status of the California gnatcatcher. The environmental data analyzed by Zink et al. (2013) does indicate that the coastal subspecies occupies a different environment, even though Zink et al. (2013) conclude the opposite. Therefore, even though the data analyzed are not the most appropriate for testing the hypothesis; analysis of this data supports the subspecies status of the coastal California gnatcatcher.

4) **There is an array of scientific information that could be used to determine the taxonomic status of animals listed as the coastal California gnatcatcher. Using the available evidence, describe how the coastal California gnatcatcher represents a recognizable entity (e.g., subspecies) or specifically why no infraspecific taxa warrant recognition within California gnatcatcher (*Polioptila californica*). In addressing this question, we ask that you consider the following: the discreteness, significance, and conservation status of the species' (or subspecies) population segments.**

Available data substantially supports the subspecies status of the California gnatcatcher. Morphological data indicates that the coastal California gnatcatcher is discrete from other populations (Atwood 1988, 1991, Mellink and Rea 1994, Link and Pendleton *in litt.* 1994, McDonald *et al. in litt.* 1994; Messer *in litt.* 1994, Newton *in litt.* 1994). Environmental data and neutral genetic data presented by Zink et al. (2013) if analyzed appropriately (McCormack and Maley 2015) suggest that the coastal gnatcatcher occupies a different environment and that there is a small but significant portion of neutral genetic variation partitioned among California Gnatcatcher subspecies.

As for the significance of the subspecies, I concur with VanderWerf.

> "Loss of the coastal California gnatcatcher would substantially decrease the species' range and, since it occurs in a somewhat different habitat type from other populations, would diminish the ecological range of characteristics present in the species. Although the adaptive significance of the morphological differences has not been investigated, it is possible they represent important adaptations to the local environment, and that their loss would diminish the species evolutionary legacy.'' (VanderWerf, *in litt.* 2004, pp. 1–2).

I cannot speak to the conservation status of the coastal California gnatcatcher because of the paucity of literature on the subject. There are definite threats to the populations with urban areas (Tijuana, San Diego, and Los Angeles) occupying a large portion of the subspecies range. However, there is little current census data regarding the health and size of current populations.

5) What additional information or analysis, if any, would clarify the taxonomic status of the California gnatcatcher?

I believe a more comprehensive and complete phenotypic analysis of variation in the species is warranted. This should include an in depth investigation of life history traits, morphology, behavior, and habitat use. As for genetics, you are looking for the proverbial needle in a haystack and any amount of negative results are unlikely to overturn the phenotypic data if the pattern still holds after a more complete, modern analysis of phenotype.

References (Those not included in our pre-panel reading list).

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Individual Memorandum
Coastal California Gnatcatcher Expert Panel

Panelist 4
4 September 2015

Preface. In my responses below, I limit my comments to the paper that prompted the petition to delist *P c. californica* (Zink et al. 2013), the subsequent comment by McCormack and Maley (2015), and relevant peer-reviewed and Federal Register publications. In doing so, I assume that the Service's previous assessments (USFWS 2011) of the morphological studies that provided the basis for designating *Polioptila californica californica* as a subspecies stand. I also assumed that re-analysis of the Atwood's (1991) morphological data by Skalski and co-workers (2008) – cited by Zink et al. (2013) as evidence for a lack of morphological distinctness in *P. c. californica* – is not sufficient for removing the subspecific designation (USFWS 2011).

1) What, if any, do you consider to be the most reliable features and methods to delimit infraspecific entities in songbirds or avian species in general?

The American Ornithologists' Union (AOU), which represents the definitive authority in avian taxonomy in the US, uses a criteria based on phenotypic diagnosability in subspecies designations:

> "Subspecies should represent geographically discrete breeding populations that are diagnosable from other populations on the basis of plumage and/or measurements, but are not yet reproductively isolated" (http://aou.org/committees/nacc/subspecies.php)

In many cases, regional variation in morphologic features is believed to represent additive genetic variation at multiple loci that has evolved in response to regional differences in environmental conditions and selection pressures (Remsen 2010). However, not all morphological traits have a genetic basis and geographic variation in avian morphology has also been attributed to phenotypic plasticity and differences in gene expression (Mason and Taylor 2015). As a result, support exists for the use of multiple sources of information in addition to morphology such as spatial patterns of genetic variation, ecology (e.g., habitat associations), and behavior in subspecific taxonomy (Haig et al. 2006, Haig and Winker 2010). To the extent possible, careful consideration should be given to traits that may be adapted to local environments. Ideally, concordance would be observed among traits and some authors have suggested that at least two criteria (e.g., morphological and genetic) should point to similar designations (Haig et al. 2006, Haig and Winker 2010). However, the AOU does not consider genetic divergence as a necessary prerequisite for subspecies designations:

> "Because subspecies represent relatively young points along an evolutionary time scale, genetic differentiation between subspecies may not necessarily parallel phenotypic divergence. Thus, subspecies that are phenotypically but not genetically distinct still warrant recognition if individuals can be assigned to a subspecies with a high degree of certainty" (http://aou.org/committees/nacc/subspecies.php)

In other words, the absence of genetic structure is not considered sufficient for removing subspecific status when groups are diagnosable using morphology, behavior, etc. While there is agreement that specific, repeatable, and defensible criteria are needed to determine whether traits are diagnostic (e.g., the 75% rule; Mayr et al. 1953), the 'messy' nature of evolution may preclude the use of standard criteria across species, not to mention ESA listings. Thus, in practice, subspecies decisions in birds will generally be based on the level of agreement among avian taxonomists, evolutionary biologists, and ecologists considering a wide range of information (genetics, phenotypic traits, etc.).

2) **What are the strengths and weaknesses of these approaches, particularly with the issues presented with the coastal California gnatcatcher (*Polioptila californica californica*)?**

An important consideration when using genetic information to designate subspecies hinges on the fact that most studies (including Zink et al. 2013) describe population genetic structure using a comparatively small number markers that are likely selective neutral, despite recent advances in next-generation-sequencing and the field of conservation genomics. These markers, which include mitochondrial DNA sequences, nuclear introns, and microsatellites, remain common in taxonomic and conservation genetics studies because they are easier to screen than genes known to be under selection or that are linked to a phenotypic trait of interest. When sufficient loci are screened, neutral genetic markers can provide valuable insight into several aspects of the demographic history of a species, including current and historic gene flow, population expansions and bottlenecks, and vicariance. However, they are unconnected to morphology (and more broadly phenotype), are not likely to reflect adaptive among differences among groups of individuals, and can be poor proxies for adaptive divergence (McKay and Latta 2002). Indeed, emerging research indicates that adaptive traits are likely encoded by a small fraction of the genome (Santure et al. 2013, Robinson et al. 2013, Poelstra et al. 2014) and the chance of targeting these genes, even via physical linkage, with for example 6-8 loci is very low.

When spatial patterns of neutral genetic variation differ from unobserved patterns of adaptive genetic variation, delineating conservation units on results solely based on neutral markers can lead to the under-protection of important alleles and traits (Crandall et al. 2000). Indeed, many species appear "panmictic" (i.e., are genetically homogenous across their range or much of their range) at neutral genetic markers, but exhibit population genetic structure at genes under selection (Ekblom et al. 2007, Vasquez-Carrillo et al. 2013). In these cases, treating all groups as equivalent runs the risk of effectively ignoring potentially important adaptive differences among populations and the loss of alleles and traits that could be important in the context of a changing environment (e.g., emerging pathogens and climate change).

As described above, a strength of using morphological criteria in subspecies designations lies in the fact that features such as plumage coloration, body size, and bill shape can reflect adaptations to local environmental conditions. By delineating groups of individuals that are morphologically distinct from other conspecific groups, one increases the likelihood of conserving the evolutionary history of species and the ability of the species to adapt to changes in environmental conditions (Crandall et al. 2000). A weakness of morphological criteria, again, is that geographic differences in morphology can also represent phenotypic plasticity or variation in gene expression.

****Below I respond to Questions 3 and 4 jointly because they both address whether panel members support maintaining or removing the subspecies designation based on the new data presented by Zink and co-workers (2013).****

3) Different methodologies may be suited to discriminate between taxa at various ranks while others are best suited to show close relationships among taxa. With this in mind, assess the extent to which the methods, data and conclusions of Zink et al. (2013) apply to these two approaches. How does your assessment apply to the taxonomic status of the California gnatcatcher?

4) There is an array of scientific information that could be used to determine the taxonomic status of animals listed as the coastal California gnatcatcher. Using the available evidence, describe how the coastal California gnatcatcher represents a recognizable entity (e.g., subspecies) or specifically why no infraspecific taxa warrant recognition within California gnatcatcher (*Polioptila californica*). In addressing this question, we ask that you consider the following: the discreteness, significance, and conservation status of the species' (or subspecies) population segments.

Genetic Analyses. I do not believe that the negative genetic results of Zink et al. (2013) invalidate the designation of coastal California gnatcatchers (*Polioptila californica californica*) as a subspecies. The apparent absence of global (species-wide) genetic structure at a handful of neutral markers unconnected to phenotype does not necessarily indicate the absence of important adaptive differences among specific groups, that populations are not on different evolutionary trajectories, and are not genetically diagnosable in some part of their genome. Even so, McCormack and Maley (2015), in a re-analysis of Zink and co-workers' data, found modest genetic structure between *P. c. californica* and southern subspecies at two nuclear loci [ACON (Fst = 0.062, p = 0.014) and TGFB-2 (Fst = 0.077, p = 0.0049)]. Moreover, stronger divergence and quite high F_{ST} values were observed for the nuclear locus MC1R ($F_{ST} = 0.195$, $p = 0.001$) and the mitochondrial locus ND2 ($F_{ST} = 0.336$, $p = 0.016$) when *P. c. californica* was compared to *P. c. atwoodi* under Mellink and Rea's (1994) classification. Under this scheme, two additional loci (CEPUS and ACON) exhibited significant or nearly significant differentiation. Thus, moderate genetic divergence appears to exist between *P. c. californica* and southerly subspecies at several loci suggesting that recent restrictions to gene flow may indeed have occurred despite low global (species-wide) differentiation.

In addition, Zink and coworkers' Bayesian clustering (i.e., program STRUCTURE) analysis, which supported a single "genetic population", is not a statistically powerful approach for identifying genetically distinct groups when divergence is modest (as appears to the case in California gnatcatchers), particularly given the modest sample size of individuals and loci and level of polymorphism in mtDNA and nuclear introns. Even using highly polymorphic microsatellite markers and larger sample sizes, the ability to identify population structure with the program STRUCTURE is limited in moderately structured populations (Latch et al. 2006). For example, STRUCTURE frequently underestimates the number of genetically divergent groups when $F_{ST} < 0.03$, even with a sample size of 100 individuals/population that are genotyped at 10 microsatellite loci (Latch et al. 2006). (Note that $F_{ST} = 0.02$ based on microsatellites can be indicative of moderate population structure and restricted gene flow given the F_{ST} has an upper limit equal to homozygosity in multi-allelic markers). Moreover, several examples exist where populations are divergent based on F_{ST} and related measures, but where STRUCTURE indicates that the most likely number of genetic populations is equal to one (e.g., Miller et al. 2012, Siegle et al. 2013). Thus, Zink and coworkers' finding of a single genetic population in California gnatcatchers should be interpreted with caution.

Finally, I found the choice of nuclear introns (in addition to mtDNA) curious as this class of markers does not seem particularly well suited for the purposes of evaluating subspecies designations in California gnatcatchers in light of the species' recent demographic history. Comparatively slow mutation rates in nuclear introns (as well as mtDNA) limit the ability to detect recent divergence, as is likely the case in California gnatcatchers given their apparent post-LGM northward range expansion. Microsatellites, despite longer coalescent times (than mtDNA), are more likely to detect recent isolation and restrictions to gene flow because they have high mutation rates and, as a result, are commonly used in intraspecific taxonomic studies. In fact, greater geographic concordance has been observed between morphology and microsatellite variation than between morphology and mitochondrial DNA among subspecies of song sparrows and Gunnison's prairie dogs (Pruett and Winker 2013, Sackett et al. 2014). In both of these cases, authors concluded that microsatellites provided reasonable evidence to support existing morphologically-based subspecies designations. Given the relative ease (and modest cost) of developing microsatellite libraries, not testing for recent restrictions in gene flow with this marker seems like a shortcoming of Zink and coworkers' analysis – particularly given the call for screening rapidly evolving nuclear markers to resolve uncertainties in California gnatcatcher taxonomy (USFWS 2011).

<u>Ecological Niche Modeling</u>. Zink and coworkers (2013) used ecological niche modeling to suggest coastal sage scrub and southern populations of California gnatcatchers did not use environments that were more distinct than expected based on geographic differences in climatic niches. However, the presentation of these analyses lacked the detail I would expect in a paper with such weighty conservation implications. Specifically, the spatial distribution of "presences", the biological rationale behind variable selection, the level of support for the selected model, and measures of model assessment are not reported in sufficient detail to evaluate the analysis critically. Indeed, there are have been several recent calls to provide more transparent reporting of MAXENT settings, environmental input and modelled relationships, methods to control for sample bias, interpretation of output, and treatment of pseudo-absences (Elith et al. 2011, Yackulic et al. 2012, Merow et al. 2013). Without these details, it is not possible to fully evaluate the rigor of Zink and coworkers' modeling exercise or the strength of their conclusion that subspecies' niches are no more divergent than expected based on geographical differences in climate.

Perhaps more importantly, Zink and co-workers argued that niche divergence did not exceed expectations based on niches calculated using only bioclimatic variables. While theirs is a reasonable approach for testing divergence in "bioclimatic" niches (notwithstanding the issues described above), the question from an ESA listing perspective is whether groups of gnatcatchers are "ecologically" distinct. Ecological distinctiveness is much broader than bioclimatic distinctiveness and includes, for example, associations with vegetation type, structure, and composition. Stating that two avian niches are equivalent without consideration of habitat variables seems like an over-interpretation of the authors' negative results. In the case of California gnatcatchers, the northerly subspecies clearly occupies different habitats (coastal sage scrub versus desert scrub). While studies of niche composition based only on bioclimatic variables are published in ecological journals, in my opinion, high-visibility assessments of ecological distinctiveness with major conservation implications require more thorough analysis.

Distinct Population Segment. Regardless of subspecies designation, there is strong justification for considering California gnatcatcher populations in the US as a Distinct Population Segment (DPS) based on their *discreteness* and *significance*. A component of *discreteness* involves the presence of "marked separation from other populations of the same taxon resulting from physical, physiological, ecological, or behavioral factors, including genetic discontinuity". These criteria are very similar to commonly used subspecies definitions, and per my comments above, I believe *P. c. californica* (with a major portion of its range in the US) is indeed distinct from other conspecific groups. Even so, a second component of *discreteness* pertains to whether the population is delimited by international boundaries or whether there are significant differences in (i) the control of exploitation, (ii) management of habitat, (iii) conservation status, or (iv) regulatory mechanisms. There are clear international differences in habitat management and regulatory mechanisms. Take of individuals and loss habitat are not controlled in Mexico nearly to the extent that they are in the US. This difference would seem to qualify *P. c. californica* for DPS status alone because *discreteness* can be determined based on the presence of an international border ***or*** phenotypic, genetic, and ecological differences (USFWS and NMFS 1996). In other words, there is no requirement that both criteria be satisfied to meet the *distinctiveness* criteria. US populations of California gnatcatchers would also seem to meet the *significance* criterion for DPS status given that they - to a large extent - occupy a "unique ecological setting" (coastal sage scrub) and the loss of these populations and habitats could compromise the ability of the species to shift northwards in response to climate change. Moreover, ESA policy does not require that both the *distinctness* and *significance* criteria be satisfied for DPS designation (although I believe both are) – one is sufficient (DOI and DOC 1996).

Zink and co-workers (2013) argue that "The U.S. Congress directed the Fish and Wildlife Service to use the ESA ''sparingly'' when listing DPSs (Bernhardt 2008). Given that the coastal California gnatcatcher lacks morphological, genetic, and ecological significance, it becomes difficult to justify its listing." While the first sentence in this statement is true, there is precedent for designating coastal California gnatcatchers as a DPS given that marbled murrelets (*Brachyramphus marmoratus*) were listed (as DPSs) under similar circumstances (no genetic divergence but differences in regulatory mechanism across international borders). The second part of Zink and coworker's statement is simply their opinion and does not recognize the broader definition of DPSs described above. Moreover, I am not convinced that requiring hard geographical discontinuities in morphology/genetics for DPS designations (as implied by the second sentence in the above quote) is consistent with the intent and spirit of the ESA (even though I believe such discontinuities exist in California gnatcatchers). Clinally varying species without observable discontinuities in morphology or genetics may still harbor important local adaptations in different portions of their range. Ignoring this variability risks losing alleles or combinations of alleles that could be important for the survival of the species in the context of future environmental change (i.e., emerging diseases, climate change, etc). Even if a break in morphology is not observed at approximately 30 degrees north latitude, we run the risk of putting all of the gnatcatcher's "evolutionary eggs" into a single basket by limiting the species' future gene pool to what is currently represented in southern populations.

In sum, I believe genetic, morphological, and ecological information provide concordant evidence for a discrete taxonomic unit of California gnatcatchers above 30°N. Based on the criteria of multiple lines of evidence (Haig et al. 2006), the argument for maintaining subspecific status for *P. c. californica* is compelling, and the case for assigning DPS status (in the absence of subspecific designation) appears even stronger.

5) What additional information or analysis, if any, would clarify the taxonomic status of the California gnatcatcher?

Below I discuss the potential application of new information and analyses to the question of subspecific designations in California gnatcatchers. I believe these three concerns were generally shared by members of the review panel and hope that future analyses will address these points.

First, genomic data have the potential to provide valuable insights into the delineation of conservation units (Funk et al. 2012) and I support the use of genomic approaches to help resolve subspecific taxonomy in California gnatcatchers. Specifically, genomic methods provide opportunities for identifying "candidate genes" of known function and/or the screening of many thousands of single nucleotide polymorphism (SNP) loci and can thus provide a more thorough perspective on population structure than traditional markers. They have the potential to identify adaptive genetic differences resulting from different selection pressures on populations as well as to more precisely estimate the magnitude and timing of isolation. Presumably because of this promise, Zink and coworkers state that it will "be of interest to observe whether *genomic* studies that fail to support subspecies limits are also considered inadequate in some way". The implication being that some may consider lack of divergence at, for example, thousands of SNPs loci as insufficient for pooling previously described subspecies. However, the ability of genomic approaches to help resolve subspecific taxonomy depends on how rigorously and thoroughly SNP data are analyzed. Simply testing for global population structure or conducting clustering analyses will be unlikely to identify adaptively divergent groups even with genomic data (Funk et al. 2012). Again, the vast majority of SNP loci in genomic-scale datasets will be selectively neutral such that the absence of detectable genetic population structure across populations does not indicate that populations have not begun responding to local environmental differences. They may, in fact, be diverging at important adaptive loci and traits and, even with thousands of loci, the probability of screening the few key genes responding to local selection pressures may still be low. More definitive assessments would involve tests for adaptive genetic divergence at markers likely under divergent selection. One method for identifying adaptively divergent populations is to search for outlier loci that exhibit higher levels of linkage or divergence than is typical of the genome (Luikart et al. 2003, Hohenlohe et al. 2010, Prunier et al. 2011). Nevertheless, some outliers may be statistical artifacts that are not representative of divergent selection pressures, and some apparent adaptive variation may go undetected due to weak differences in selection among groups (Narum and Hess 2011). Indeed, many questions about how best to analyze and interpret genomic data in the context of delineating conservation units remain unresolved and await further study (Funk et al. 2012). Thus, despite the exciting potential for genomic data to inform intraspecific taxonomy in California gnatcatchers, the results of such analyses - even those based on large SNP datasets - should be considered carefully in conjunction with geographic variation in morphology, ecology, and behavior.

Second, additional population genetic analyses in California gnatcatchers should treat existing subspecific designations as the null hypothesis instead of simply testing for global population structure. Directly evaluating support (with genetic data) for existing subspecific boundaries is not “circular” (Zink 2015); rather, it is in my opinion the specific conservation question at hand.

Third, Zink and coworkers (2013) expressed concern that a double standard exists because the Service has relied on the results of mtDNA studies in numerous subspecies designations but did not accept mtDNA evidence suggesting that the coastal California gnatcatcher was not distinct in a previous review. At face value, this seems like a reasonable concern. However, I suspect that genetic structure was found in many of these listed subspecies and that genetic data was generally concordant with patterns of morphological variation (and therefore used to support subspecies designations). I doubt that many cases exist where an absence of genetic structure was used to support delisting because there is recognition that mtDNA does not necessarily reflect adaptive genetic differences among populations. The review panel generally agreed that information from neutral genetic markers (particularly when divergence is not detected) should not override pre-existing morphologically-based subspecies assignments. Nevertheless, divergence at neutral markers lends credence to the designation of morphologically-assigned subspecies because restricted gene flow can allow for more rapid response to selective pressures in different environments and enhance the effects of genetic drift. Thus, I do not believe that using evidence for restricted gene flow to support existing subspecies designations, but not treating neutral markers as overriding morphology is a double standard – rather, it is simply sound conservation practice rooted in the “principle of precaution”.

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Individual Memorandum
Coastal California Gnatcatcher Expert Panel

Panelist 5
8 September 2015

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1) What, if any, do you consider to be the most reliable features and methods to delimit infraspecific entities in songbirds or avian species in general?

In the United States, the American Ornithologists' Union (AOU) is the authority that evaluates avian taxonomic rank (http://aou.org/committees/nacc/). The AOU's criteria for subspecific designations are phenotypic diagnosability based on "plumage and/or other measurements" in "geographically discrete breeding populations… (that) are not yet reproductively isolated" (http://aou.org/committees/nacc/subspecies.php). That is, the AOU (the industry standard) considers the best available science for the diagnosability of subspecies to be morphology. I agree that morphology is an important diagnostic tool because it is the embodiment of genetic and epigenetic variation at multiple loci across the genome (Remsen 2010, Tobias et al. 2010).

Most morphological traits are quantitative traits that are influenced by variation at a number of genes (e.g. Robinson et al. 2013, Roulin and Jensen 2015, Vergara et al. 2015) as well as by the environment. Because the influence of genetic factors may be unknown, and the influence of the environment may important (e.g. James 1983, Mason and Taylor 2015), some authors have suggested that two or more categories of biological criteria should be used to evaluate a population's discreteness (Haig et al. 2006, Haig and Winker 2010). These criteria could include morphological, genetic, physiological, life history, ecological, or behavioral factors (Haig et al. 2006). The rationale for including two or more criteria is to guard against recognizing populations that are discrete due to environmentally induced traits.

In my view, the use of two or more categories of biological criteria to evaluate discreteness or diagnosability is more convincing than relying on morphology alone. I also consider "geographically discrete breeding populations…(that) are not yet reproductively isolated" to be a critical feature of subspecific designations. Finally, although the presence of genetic structure lends support to subspecific designations, its absence does not preclude a subspecific designation. If morphological variation is present that diagnoses a population, but the available genetic data do not corroborate it, this should not be taken as evidence that genetic or epigenetic causes of the morphological variation are absent. It is also not evidence that morphological variation is produced by environmental causes. It simply illustrates the limitations of screening a handful of (often neutral) loci. In comparison to the paltry amount of genetic data available for natural populations of non-human organisms, including birds, billions of research dollars are being used to identify the underlying genetic and epigenetic causes of human traits and diseases. Despite that level of funding, the genetic or epigenetic causes remain completely unknown for many, or even most, traits and diseases.

2) What are the strengths and weaknesses of these approaches, particularly with the issues presented with the coastal California gnatcatcher (*Polioptila californica californica*)?

For subspecies designations in general, concordant results from two or more categories of biological criteria provide good evidence that differentiation between lineages is genuine and subspecific designations are appropriate (e.g. Sackett et al. 2014). This requirement becomes problematic when evidence among criteria appears to be inconsistent, for example if morphological differences are present but genetic structure appears to be lacking. However, data can be evaluated based on quality, and in the case of genetic data, a lack of genetic structure at a small number of neutral and/or slowly evolving loci is inconclusive and is not a good basis for rejecting subspecific status. A small number of loci represent a vanishingly small fraction of the genome (e.g. the zebra finch genome is 1.2 billion base pairs (Warren et al. 2010)), neutral loci may be entirely unrelated to genetic variation associated with adaptation, and slowly-evolving loci can be ineffective for identifying subspecific-level population structure. When morphological and genetic data do not produce concordant results, and the genetic data are inconclusive, differences in phenotype and the environment are more likely to reflect adaptive divergence and should be used to designate subspecies (Haig et al. 2006).

The type of genetic data that is currently available for most subspecies (and species) usually consists of a small number of loci (e.g. sequence data from mitochondrial DNA and/or a handful of nuclear loci, microsatellite loci, AFLPs), which may lack power to detect population structure, and so in these situations, phenotypic and environmental parameters will be critical for subspecific designations. However, the field of genetics is rapidly changing and as genomic-level data become available, it will be important to critically evaluate those data, and potentially reassess decisions about, and criteria for, subspecies (and species) designations.

Recent genomic analyses in birds have shown that much of the genome may be relatively undifferentiated, but small areas of genetic differentiation and/or gene expression may have a large effect on morphology, which may or may not lead to assortative mating and speciation. One example concerns a genomic study of the redpoll finches (*Acanthis* spp.; Mason and Taylor 2015). While morphological differences exist among the three currently accepted species (not subspecies), genetic structure at 20,712 loci is absent. Although potentially important areas of genetic differentiation may have been overlooked, this study is particularly interesting because differences in morphology could be attributed to the differential expression of genes under different environmental conditions (Mason and Taylor 2015). That is, morphological differences appeared to depend on the environment, and moreover, they do not appear to cause assortative mating leading reproductive isolation (Lifjeld 2015, Mason and Taylor 2015). In contrast, research on carrion (*Corvus corone*) and gray-coated hooded crows (*Corvus cornix*) has shown that genetic differentiation and differential expression of genes in a small area of the genome (related to visual perception and pigmentation) causes differences in plumage coloration, and since the two crow species mate assortatively with respect to plumage coloration, these small areas of genetic differentiation and expression are crucially important to speciation because they cause reproductive isolation (Poelstra et al. 2014). Such studies show that it can be utterly incorrect to dismiss a low level of overall sequence divergence as trivial – instead, small islands of genetic differentiation may be key drivers of speciation.

With respect to coastal California gnatcatchers, the current data we have are concordant for three types of biological criteria: morphological and environmental differences exist and the available genetic data provide evidence for differentiation at the subspecific level (see #4 below).

3) Different methodologies may be suited to discriminate between taxa at various ranks while others are best suited to show close relationships among taxa. With this in mind, assess the extent to which the methods, data and conclusions of Zink et al. (2013) apply to these two approaches. How does your assessment apply to the taxonomic status of the California gnatcatcher?

Subspecies definition

The underlying philosophical position of Zink (e.g. Zink 2004) is that minimum diagnosable taxonomic units should be reciprocally monophyletic. As a consequence of this position, Zink typically does not identify subspecies: he either elevates a taxonomic unit to the species rank or dispenses with it all together (e.g. Zink et al. 1997). However, reciprocal monophyly is a criterion seldom required or used in practice by most avian taxonomists, even for species level designations (e.g. Helbig et al. 2002, Sangster 2014). Indeed, in a recent review of 1,313 avian taxonomic studies, no single taxonomic criterion (such as reciprocal monophyly) was considered necessary or sufficient by any taxonomist to designate taxa (Sangster 2014).

Subspecies are generally considered by the ornithological community to be incipient species that are not yet reproductively isolated, that is, gene flow continues to occur among subspecies. Because gene flow generally impedes or prevents lineage sorting, reciprocal monophyly is unlikely to occur. In theory, when populations become reproductively isolated (i.e. become different species as defined by the Biological Species Concept), gene flow ceases, lineage sorting eventually occurs, and reciprocal monophyly follows.

Choice of loci

Zink et al. (2013) sequenced mitochondrial DNA (mtDNA) and eight nuclear loci to assess genetic structure in California gnatcatchers. Two of the nuclear loci were unsuitable for genetic analyses, either because they were monomorphic (Zink et al. 2013) or paralogous (McCormack and Maley 2015), and therefore, data on genetic structure and diversity consists of one mtDNA and 6 nuclear loci.

The panel of nuclear loci that Zink et al. (2013) examined provides information for species-level differences; however, these loci are less useful for identifying subspecific-level population structure for two reasons. First, the nuclear loci used by Zink et al. (2013) have a slower mutation rate than the mtDNA used by Zink et al. (2000), not a high mutation rate as recommended by the scientific panel and as requested by the US Fish and Wildlife Service (USFWS 2011). If only a small number of loci are used, nuclear loci with a high mutation rate are more effective than nuclear loci with a slow mutation rate for identifying subspecific population structure with Bayesian clustering techniques, such as the program Structure (Pritchard et al. 2000) employed by Zink et al. (2013). The nuclear loci used by Zink et al. (2013) also have a larger effective population size than the mtDNA used by Zink et al. (2000), which is important for coalescent-based methods. Given that Zink et al. (2000) did not observe genetic structure with mtDNA, it is no surprise that Zink et al. (2013) failed to observe genetic structure with their choice of nuclear loci.

Second, the small number of loci used by Zink et al. (2013) impedes the power of population-level statistical analyses. A small number of loci can hamper clear estimates of the number of populations in the Bayesian clustering program, Structure (Pritchard et al. 2000), and it can also lead to high stochasticity in coalescent-based methods, which are often capable of identifying fine-scale population structure if a large number of loci are employed.

Although the loci employed by Zink et al. (2013) are regularly used to explore species-level structure, they are generally inadequate for detecting recent subspecific-level population structure, the question of interest with respect to California gnatcatchers. Rather than choose a panel of loci that could resolve subspecific structure, Zink et al. (2013) chose a panel of loci more effective for detecting deep phylogenetic breaks at the species level.

Genetic analyses

Studies of population structure below the species level typically use multivariate methods and/or Bayesian clustering programs, which can very effectively identify population structure when fast-evolving (Guichoux et al. 2011) and/or a large number of loci are used (Edwards and Bensch 2009). Zink et al. (2013) attempted a Structure analysis (Pritchard et al. 2000), but as noted above, they lacked power to detect subspecific structure because they used a small number of slowly mutating loci. Consequently, it is necessary to assess the genetic data in Zink et al. (2013) by examining the alleles present in the coastal California gnatcatcher subspecies versus populations farther south.

Zink et al. (2000) sampled 29 individuals north of 30°N, where the coastal CA gnatcatcher occurs, and 35 individuals south of 30°N: samples that were re-used in Zink et al. (2013). A sample size of 29 individuals is the sample size required to have a 95% chance of sampling an allele with a frequency of 0.051 with nuclear diploid markers (Allendorf et al. 2013), i.e. 29 individuals is adequate for detecting fairly rare alleles. Zink et al. (2013) provided pie charts of allele frequencies for 3 nuclear loci (MC1R, CRYAB and TGFß2) and the mtDNA control region locus (Figure 1). These charts show private alleles south of 30°N (MC1R) and north of 30°N (MC1R, CRYAB and TGFß2). McCormack and Maley (2015) identified additional private alleles in northern populations for two additional loci (ACON and ND2) not shown in Figure 2 (Zink et al. 2013). The presence of private alleles north of 30°N is an indication that coastal CA gnatcatcher populations are genetically differentiated and provides evidence for subspecies designations (Crandall et al. 2000), especially when observed in such slowly evolving loci. Moreover, given that there are fewer gnatcatchers north of 30°N than to the south (Zink et al. 2013), and that the small population size in the north is partially attributed to population declines (USFWS 2010) or bottlenecks, which typically remove rare alleles (Allendorf et al. 2013), the presence of rare, private alleles in the north is noteworthy.

Zink et al. (2013) noted "greater diversity of rare alleles in the north" but because Zink et al. (2013) chose 28°N to divide northern from southern populations it is unclear whether this pattern would have changed if 30°N (the latitude of interest) had been chosen. Zink et al. (2013) discounted their observation of increased diversity in the north on the grounds that sample size was larger in the north versus the south, although differences in sample size could have been controlled by calculating allelic richness (El Mousadik and Petit 1996).

Zink et al. (2013) also provided estimates of nucleotide diversity (π) for each sampling location (Table 1 and Figure 2) and G_{ST} values for each locus across nine populations in Table 2 (Zink et al. 2013), but they did not provide any explicit tests of genetic differentiation between sampling locations of interest. Analysis of Molecular Variance (AMOVA)(Excoffier and Lischer 2010) could have been performed and G_{ST} values calculated between putative subspecies of California gnatcatchers, although given the small sample sizes, a comparison between individuals north and south of 30°N would be most meaningful in terms of ensuring sufficient statistical power. McCormack and Maley (2015) used AMOVA to compare individuals north and south of 30°N and to compare individuals assigned to the *P. c. californica* and the adjacent *P. C. atwoodi* subspecies. They found significant F_{ST} values for a number of loci, and quite high F_{ST} values for MC1R ($F_{ST} = 0.195$, $p = 0.001$) and ND2 ($F_{ST} = 0.336$, $p = 0.016$). Note that F_{ST} and G_{ST} are often used interchangeably. F_{ST} was developed for two alleles at a locus, G_{ST} was later developed for multiple alleles at a locus, and is equivalent to the weighted average of F_{ST} at all alleles (Takahata and Nei 1984).

DNA Samples

Background on the defined range of the coastal CA gnatcatcher and sampling locations

The USFWS defines the geographic limits of the coastal California gnatcatcher from Los Angeles County (and formerly Ventura County) south to 30°N latitude (USFWS 1993, 1995, 2010). Thus, sampling locations 1-6 in Zink et al. (2000) and Zink et al. (2013) correspond to the coastal California gnatcatcher range whereas populations 7 (Misión San Fernando, at approximately 29° 59’) to 13 do not. The US-Mexican border at the Pacific Ocean lies at approximately 32°32’N latitude.

DNA samples

Zink et al. (2000) state that they “collected gnatcatchers in Mexico and plucked feathers from nestlings in the United States”. They further state that “mtDNA was isolated from tissue or feather pulp”. Presumably the DNA that Zink et al. (2000) isolated from tissue was from the Mexican birds as only feathers were collected from US birds. A disparity in the DNA source between the US and Mexican gnatcatcher populations could create a serious systematic bias in the measures of genetic diversity observed for subspecies because 4 of 6 coastal California gnatcatcher populations were sampled for feathers whereas all putative subspecies south of the US-Mexican border were sampled for tissue. Feathers are an inferior source of DNA typically providing very low amounts of poor quality DNA in comparison to tissue such as blood, muscle or liver samples (McDonald and Griffith 2011). Low quality and quantity DNA increases the risk of contamination and causes allelic dropout to occur, a phenomenon in which only one allelic form amplifies when two are actually present at a locus (Taberlet et al. 1999, McDonald and Griffith 2011). Zink et al. (2013) used samples collected by Zink et al. (2000) and they used heterozygous nuclear loci: if allelic dropout occurred, the number of rare or private alleles detected in the northern CA gnatcatcher subspecies may have been underestimated.

The problem of low quantity/quality feather DNA is compounded by the sample degradation that Zink et al. (2013) reported. As DNA was presumably stored for approximately 13 years prior to use, it may have degraded from freezing/thawing, evaporation, or hydrolysis depending on the pH of the storage buffer. Given that DNA had degraded to the point that it was unusable for some samples (Zink et al. 2013), contamination and allelic dropout could also be issues, especially for low copy number DNA from feathers relative to tissues.

Researchers can and do use DNA from feathers to successfully calculate genetic variation and structure. The problem with Zink et al. (2000) and Zink et al. (2013) is that the methodology provided is inadequate to evaluate whether a systematic bias exists and whether Zink et al. (2013) underestimated the presence of rare alleles in the coastal CA gnatcatcher subspecies. No information was given describing:

a) DNA extraction or amplification methodology and whether it differed for each sample type.
b) Whether controls were taken to observe and account for allelic dropout, for instance via polymerase chain reaction (PCR) replicates.
c) Whether there were differences in the amount and quality of DNA obtained from feathers versus tissue as measured by quantitative PCR (Beja-Pereira et al. 2009) or Bioanalyzer and Qubit platforms.
d) Whether there were differences in amplification success between DNA isolated from feathers or tissue.

Furthermore, Zink et al. (2013) identified alleles at heterozygous loci, so they could have calculated observed/expected heterozygosity and departures from Hardy-Weinberg Equilibrium, calculations that would help to indicate whether a homozygote excess existed, and consequently whether there was a potential problem with allelic dropout.

In summary, a serious and thorough examination of subspecific-level population differentiation has yet to be undertaken for coastal California gnatcatchers.

4) There is an array of scientific information that could be used to determine the taxonomic status of animals listed as the coastal California gnatcatcher. Using the available evidence, describe how the coastal California gnatcatcher represents a recognizable entity (e.g., subspecies) or specifically why no infraspecific taxa warrant recognition within California gnatcatcher (*Polioptila californica*). In addressing this question, we ask that you consider the following: the discreteness, significance, and conservation status of the species' (or subspecies) population segments.

Given the current data available, the coastal California gnatcatcher represents a valid, recognizable subspecies. This conclusion is based on:

a) Morphological data: The US Fish and Wildlife Service thoroughly reviewed morphological data, including several re-analyses of the Atwood (1991) data (including Skalski et al. 2008), and determined that coastal California gnatcatcher morphological features were diagnosable (USFWS 2011).
b) Ecological data: Coastal California gnatcatchers are ecologically distinct because they occupy coastal sage scrub habitat whereas populations south of 30°N (the southern limit of coastal sage scrub) occupy drier habitat similar to the Sonoran Desert (Zink et al. 2013). The ecological distinctiveness of coastal sage scrub habitat presents conditions amenable to divergence and speciation. Indeed, a genetic break at *ca*. 29-30°N has been associated with genetic differentiation in other species, including pocket gophers (*Thomomys nigricans* subspp.) (Trujano-Alvarez and Alvarez-Castaneda 2013) and Le Conte's thrasher (*Toxostoma lecontei*)(Zink et al. 1997).

c) Genetic data: The geographic area currently occupied by coastal California gnatcatchers was probably colonized during a population expansion from the south to the north sometime following the last glacial maximum (*ca*. 20,000 years ago; Hewitt 2000), perhaps as recently as 3,000 years ago (Zink et al. 2013). On an evolutionary time-scale, coastal California gnatcatchers represent a recent taxonomic unit that may be only beginning to diverge from subspecies to the south. Indeed, post-glacial recolonization appears to have caused low levels of genetic differentiation generally for subspecies in Nearctic and Palearctic regions (Pianka 1966, Phillimore and Owens 2006). Given a timescale of approximately 3,000-20,000 years, most DNA sequences in recently colonized areas will lack new mutations (Hewitt 2000) and are unlikely to be reciprocally monophyletic from southern populations; therefore, it is still too early for coastal California gnatcatchers to have diverged into distinct species, a process that typically takes hundreds of thousands to millions of years (Price 2008). However, in spite of a very short evolutionary time-scale, coastal California gnatcatchers have private alleles at slowly evolving loci even though population bottlenecks have occurred, which typically remove rare, private alleles. In other words, Zink et al. (2013) present evidence that coastal California gnatcatchers are on a different evolutionary trajectory from populations found to the south.

In summary, three categories of biological criteria (morphology, ecology, and genetic variation) provide concordant evidence for a diagnosable, discrete taxonomic unit north of 30°N, thereby supporting the designation of the coastal California gnatcatcher as a legitimate subspecies.

5) What additional information or analysis, if any, would clarify the taxonomic status of the California gnatcatcher?

To date, a thorough analysis of subspecific population structure has not been undertaken for California gnatcatchers with modern genetic techniques. The genome has not been broadly sampled for neutral and/or adaptive genetic variation, and no data on historic variation exist, despite considerable advances in technology since Zink et al. (2000). Additionally, data on behavior appears to be lacking. Below are some modern approaches available to clarify the taxonomic status of the coastal California gnatcatcher.

1) *Population structure at neutral loci with known high mutation rates*: Nuclear loci with a high mutation rate have been previously recommended by a scientific panel and requested by the USFWS (2011) for analyses of genetic structure in California gnatcatchers. Microsatellite loci are one of the most popular types of nuclear loci for population genetic studies (Guichoux et al. 2011). Microsatellite loci have a high mutation rate, and when a panel of 10-20 loci is used (depending on the variation of each locus), subspecific-level population structure can be much better resolved than what is possible with the slowly evolving mtDNA and nuclear introns/exon used by Zink et al. (2013). Microsatellite variation is typically analyzed with AMOVA, multivariate, and Bayesian clustering approaches, which do not depend on coalescent theory and therefore do not rely on the effective population size of the locus. Multivariate and Bayesian clustering approaches are particularly rigorous because they can be used without any *a priori* assumptions about population structure.

2) *Variation across the genome including adaptive variation*: Powerful genetic techniques have been recently developed to sample a large number of loci across the genome. Known as genotyping by sequencing (GBS), this approach can identify thousands of single nucleotide polymorphisms (SNPs) representing both adaptive and neutral variation across broad regions of the genome (Funk et al. 2012). This approach is more powerful than microsatellite analysis not only because many more loci are used, but also because adaptive loci are captured, which allows researchers to link genetic variation to the adaptive divergence underlying speciation (Funk et al. 2012). GBS has proven to be more effective for detecting subspecific population structure than mtDNA (Ruegg et al. 2014), such as that used by Zink et al. (2000), and for dealing with taxa that have experienced recent diversification and may lack coalescence or complete lineage sorting (Mason and Taylor 2015), such as is the case for the coastal California gnatcatcher. GBS is advantageous because the number of loci used lends great power to multivariate/Bayesian clustering techniques, and decreases the stochasticity of coalescent models.
3) *Historic population structure*: Historic DNA is increasingly used to examine population structure in a variety of species. This approach is valuable because it can clarify whether patterns of genetic variation and structure currently observed on the landscape are a consequence of recent anthropogenic effects (e.g. habitat loss and fragmentation) or the result of longer term evolutionary processes such as genetic drift or adaptation. The methodology involves extracting DNA from historic samples (for e.g. museum specimens) and comparing genetic variation and structure to recent samples. For example, Goldstein and Desalle (2003) demonstrated that a single SNP fixed in northern contemporary populations of federally threatened northeastern beach tiger beetles (*Cicindela dorsalis dorsalis*) was historically present in southern populations, and thus, the diagnosability of this locus for northern populations was simply an artefact of recent habitat change and loss. Other studies have shown that contemporary population structure is not the result of recent anthropogenic changes, but has been present on the landscape for a long time, thereby confirming the legitimacy of subspecies (e.g. Sacks et al. 2010, Volkmann et al. 2015). Historic samples usually have low quantity/quality DNA, therefore, appropriate safeguards must be taken such as those outlined by Taberlet et al. (1996) and Champlot et al. (2010).
4) *Behavior*: To date, little or no information appears to have been collected on behavioral differences among California gnatcatcher subspecies, such as acoustic differences in song. Because behavioral differences can play an important role in assortative mating leading to reproductive isolation, research in this area may provide important clues to the discreteness of subspecies.

In addition, I would recommend that researchers planning new genetic studies should obtain high quantity/quality DNA (such as blood) comparable in copy number and quality for all California gnatcatcher sampling locations. This may be particularly important for next-generation sequencing approaches, which may produce better results with high quantity/quality DNA. Finally, it is important to underline that if a researcher will only designate taxonomic units based on reciprocal monophyly, then any analysis with any type of data will fail to identify subspecies. We expect gene flow among subspecies, a process that is largely incompatible with reciprocal monophyly, and therefore reciprocal monophyly is an inappropriate standard for designating subspecies.

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Individual Memorandum
Coastal California Gnatcatcher Expert Panel

Panelist 6
8 September 2015

Background discussion: contrasting views on avian subspecies

Increasingly informed by molecular genetic data, taxonomists organize the diversity of living things by giving names to distinctly different kinds of organisms that we call species. At least in birds, which have sexual reproduction, species reflect an important biological reality — i.e., the fact that individual organisms generally fall into a non-overlapping sets of distinct forms, at least within in a given geographic area. This organization results because interbreeding among individuals of the same species (and a general, but not necessarily absolute, lack thereof between individuals of different species) results in each species having shared traits and an independent evolutionary trajectory. It is within these interbreeding groups of organisms that the standard evolutionary processes of mutation, genetic drift and natural selection generate differences in morphology, ecology, physiology, life history and behavior. Concern for conserving this diversity of form and function was presumably the basis for the Endangered Species Act of 1973, which afforded protections for not only for endangered species, but also subspecies and, in the case of vertebrates, "distinct population segments."

Historically, ornithologists have used the subspecies category to recognize/describe/catalog geographic variation in phenotype (most often variation in traits such as plumage color and pattern) among populations that are thought to be part of the same species. By definition, subspecies occur in different geographic areas because the coexistence of distinct forms in sympatry provides strong evidence of reproductive isolation and hence, evidence of distinct biological species. The classic test of reproductive isolation, however, is generally unavailable for populations living in different geographic areas, which has made the taxonomic status of closely related, allopatric populations a longstanding challenge (e.g., Tobias *et al*. 2010). Nonetheless, many avian species have clearly originated through a process of allopatric speciation, in which geographically isolated populations gradually diverge into distinct forms. Thus, clear geographic differences within a species are of biological interest and provide a potential basis for conservation concern because such variation may represent the initial stages of the speciation process, in addition to representing an important component of biodiversity in its own right. It is critically important to recognize that speciation is a continuous process, such that closely related allopatric populations may fall anywhere along a continuum from zero divergence/differentiation to clearly distinct forms that nearly all would agree are distinct species.

Given this continuum, it is perhaps not surprising that ornithologists have varied perspectives on the necessary and sufficient criteria for recognizing avian subspecies, leading to disagreements about the value of the subspecies category in general and the validity of named subspecies, particularly in cases of subtle divergence representing the earliest stages of the speciation continuum. Indeed, the growing scientific controversy surrounding the coastal California gnatcatcher (*Polioptila c. californica*) largely stems from these different perspectives and their application to a case in which the divergence between populations is relatively subtle and likely recent on an evolutionary timescale.

It is also useful to note that the subspecies concept developed long before scientists had access to molecular genetic data and thus differences in phenotype (primarily morphology) have served as the primary basis for recognizing subspecies. According to Mayr (1943), for example: "*The subspecies is composed of a group of local populations and can be distinguished from other such groups by one or several taxonomic characters.*" For a more current, but similar definition, the American Ornithologists' Union Checklist Committee defines subspecies as follows: "*Subspecies names denote geographic segments of species' populations that differ abruptly and discretely in morphology or coloration; these differences often correspond with differences in behavior and habitat.*" (AOU 1983). Thus, according to these definitions, the recognition of subspecies is warranted when the populations of a given species can be organized into morphologically distinct groups between which there is some break (i.e., non-continuous variation) in the defining trait(s). While there is an implicit assumption that the morphological differences defining subspecies have a genetic basis, patterns of molecular genetic variation are not explicitly considered in these definitions.

With this background in mind, one can contrast the divergent perspectives on subspecies that contribute to the scientific controversy over California gnatcatchers. These perspectives implicitly emphasize either **mutation and genetic drift** or **natural selection** (including sexual selection, for those that consider it a distinct process) as the key processes generating divergence between populations, and result in very different views on the level of neutral genetic divergence that is considered necessary (or sufficient) to provide evidence that populations are evolving independently.

The continuum from panmixia to reciprocal monophyly: To understand these different perspectives, it is helpful to understand the process of divergence for neutral genetic markers (i.e., variable portions of the genome that presumably have no effect on organismal fitness). Consider a simplified model in which a large ancestral population is divided in two either by the formation of a new geographic barrier or the expansion of the population across an existing barrier followed by little or no subsequent gene flow between the two descendant populations (Fig. 1).

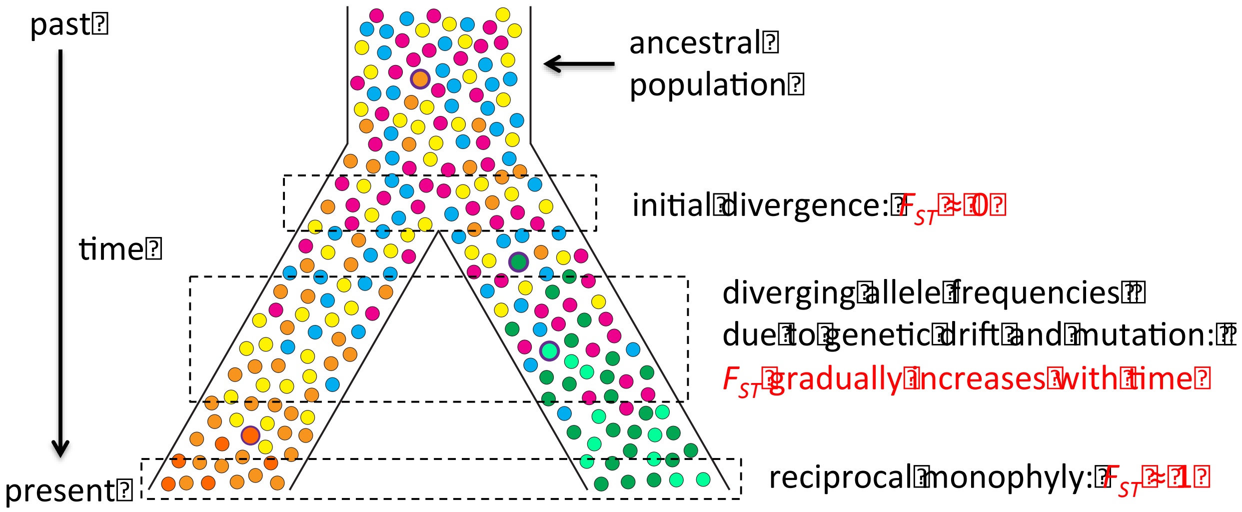

Figure 1: Highly simplified conceptual model of genetic divergence between two populations descending from a common ancestor. Differently colored dots represent allelic variants at a single gene (or genetic locus). Four new mutations generating new alleles are indicated with bold outline at first appearance. Eventually, population 1 has only orange alleles, which trace back to the ancestral population, whereas population 2 has only green alleles, which originated in population 2 after the initial divergence. Such patterns are expected to be highly variable from one genetic locus to the next due to the stochastic nature of both mutation and genetic drift.

Immediately after the split, genetic variation in the ancestral population is represented in both descendant populations, which are thus genetically indistinguishable (this assumes that a reasonable number of individuals move into the new area such that loss of genetic variation due to a founder effect is small). Over time, through a process called genetic drift (or, equivalently, "lineage sorting"), certain alleles (i.e., variants of the same gene or small genomic region) will by chance become more or less common in each of the two populations. In addition, new alleles will appear as a result of mutation, but these will be restricted to one population or the other in the absence of gene flow.

Basic coalescent theory (a cornerstone of modern population genetics) predicts that over the course of ~$4N_e$ generations (where N_e is the effective size of each population, approximately the number of breeding individuals), the populations will progress to a point at which all of the alleles in each population are more closely related to each other than to any of the alleles in the other population. At this point, the two populations are said to be reciprocally monophyletic and individuals from the two populations should be easily "diagnosable" based of the DNA sequences of appropriate genetic markers. This process is expected to occur more quickly for mitochondrial DNA (mtDNA) due to its maternal inheritance, with reciprocal monophyly expected after only ~$1N_e$ generations (assuming no strong deviations from a simple demographic model).

It is also important to note that the lineage sorting/genetic drift process is stochastic and, because of genetic recombination, occurs largely independently for each small portion of the nuclear genome. Thus, reciprocal monophyly is achieved at different times for different loci and with substantial variance around the $4N$ and N expectations for nuclear and mtDNA, respectively. In addition, as the populations are diverging, differences in allele frequencies (as measured by the classic population genetic metric F_{ST}, for example) are expected to be highly variable from one locus to the next.

The phylogenetic perspective: Zink and colleagues have consistently advocated a phylogenetic perspective on subspecies, with an emphasis on mtDNA as the best means of assessing whether populations have experienced sufficient historical isolation (and therefore potential for independent evolution) to be recognized as subspecies. In Zink's view, "*…the ultimate determinant of whether a subspecies is valid is whether it is genetically distinct*." (Zink comment letter, March 2015). In earlier work, Zink clearly defined reciprocal monophyly in mtDNA as an absolute criterion for concluding that subspecies are genetically distinct. For example, in Zink *et al*. (2000):

> "*…is the species uniform throughout its range or is it subdivided into smaller units…? …phylogenetic analysis of mtDNA haplotypes must show that haplotypes from a given region are more closely related to each other than they are to haplotypes from other regions*

> *(termed reciprocal monophyly). If haplotypes from a given region do not form such an exclusive group, then either gene flow is ongoing or it has ceased recently. In either of the latter two cases, there are no geographic units that have had significant periods of isolation and independent evolution*."

Likewise in Zink (2004):

> "*Analysis of mitochondrial DNA (mtDNA) sequence variation within and among subspecies reveals whether subspecies are evolving independently, are freely exchanging breeding individuals or are at some intermediate stage of isolation. In particular, if a subspecies has been evolving independently… an mtDNA gene tree should show that all sequences from a subspecies share a common ancestral sequence not found in individuals from any other subspecies, a pattern termed reciprocal monophyly (Avise 2000). This expectation, that subspecies will be monophyletic, provides a way to evaluate named subspecies. Subspecies should be judged to fail as meaningful units if they do not predict the evolutionary history of the populations they represent*."

Note that under this framework, it does not matter whether putative subspecies are freely exchanging breeding individuals or are at some intermediate stage of isolation — in both cases they "*fail as meaningful units*" (Zink 2004). Thus, McCormack & Maley (2015) argue that Zink simply leaves no room for a subspecies category: "…*Zink has advocated that all populations showing reciprocal monophyly should be recognized as species, whereas all potential taxa not meeting this criterion should go without taxonomic recognition (McKitrick and Zink 1988, Zink 2004, Zink and Johnson 2006).*"

Unfortunately, Zink's more recent work on California gnatcatchers is much less clear on what he considers sufficient evidence of genetic "distinctiveness" or "discreteness." On one hand, the use of STRUCTURE (Pritchard *et al*. 2000), which can often discriminate individuals from different populations based on allele frequency differences at multiple loci even if none of the loci are reciprocally monophyletic, suggests that Zink *et al*. (2013) might accept some intermediate level of divergence as supporting subspecies recognition. On the other hand, many of the expected results illustrated in Zink (e.g., Figs. 9, 10, 11 in March 2015 comment letter) imply that reciprocal monophyly is still his standard.

<u>The "divergence-with-gene-flow" perspective</u>: An alternative perspective on subspecies is based on basic theory in population genetics, which specifies the conditions under which natural selection can be effective in producing adaptive divergence between populations living in different physical and/or biotic environments. This theory also makes different predictions about patterns of neutral genetic variation (i.e., variation that has no effect on fitness) as compared to functionally important genetic variation that is subject to divergent selection. First, consider the case of neutral loci in a model of population divergence with some level of ongoing gene flow (Fig. 2). Any appreciable level of gene flow will tend to homogenize the populations and obscure the historical record of divergence. Basic theory indicates that gene flow on the order of $Nm \approx 1$ (i.e., just one migrant individual per generation regardless of population size) is sufficient to prevent substantial divergence in allele frequencies.

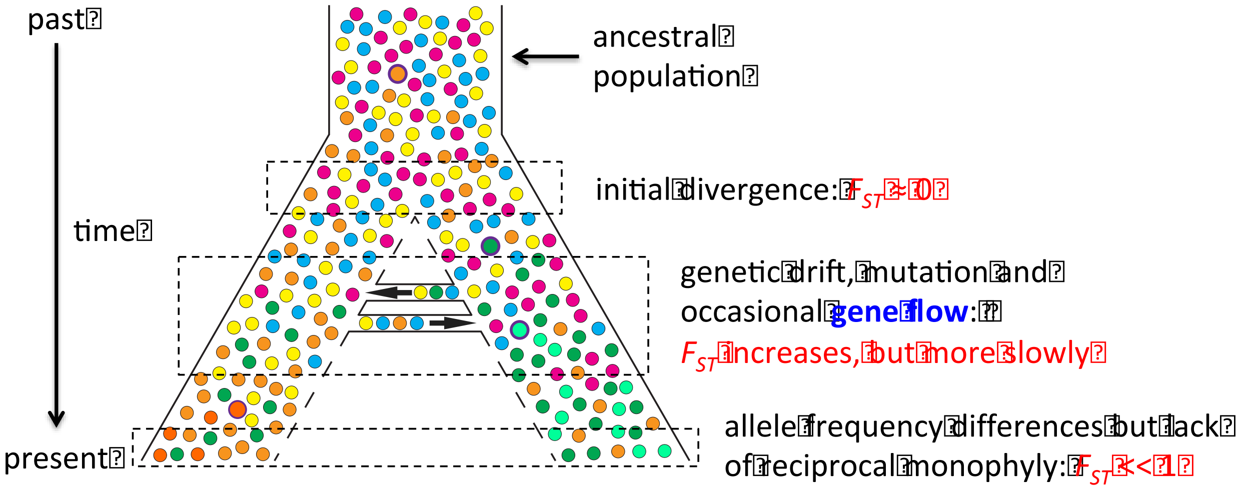

Figure 2: Same model as in Fig. 1 but with some level of ongoing gene flow between the descendant populations. In this simplistic diagram, green alleles move into population 1 and orange alleles move back into population 2, tending to homogenize genetic diversity in the two populations and preventing or at least slowing progress towards reciprocal monophyly.

In contrast, a much higher level of gene flow, on the order of $m > s$, where m is the migration rate and s is the coefficient of selection, is needed to prevent the adaptive divergence of populations. To better illustrate this difference, consider two populations, each with an effective size of ~10,000 individuals. If the migration rate is just 0.001 (i.e., one in a thousand individuals moves to the other population each generation), this translates to a relatively large Nm value of 10 and an expected F_{ST} value for neutral loci of just 0.024. Nonetheless, an allele that conferred a 1% survival advantage in a new environment could still be taken nearly to fixation despite the ongoing gene flow because $s = 0.01$ is substantially greater than $m = 0.001$. Thus, for populations of any appreciable size, there is **a relatively large range of migration rates that are sufficient to prevent the divergence of neutral genetic variation but not large enough to prevent adaptive divergence**.

Similarly, basic theory shows that natural selection can generate divergence between recently isolated populations far more quickly than genetic drift, but selection is generally expected to affect a small portion of the genome. Across the rest of the genome, populations may remain essentially indistinguishable for up to thousands of generations (with or without migration after the initial divergence). Access to genomic data, including whole genome sequencing data, is now providing evolutionary biologists the opportunity to test these ideas with empirical data, and there is a growing consensus that patterns of divergence between incipient species are often highly heterogeneous across the genome due to the effects of natural selection at a small fraction of genomic loci, in comparison to the combined effects of recombination, genetic drift, gene flow, demographic history and hybridization, which shape genome-wide patterns of variation (e.g., Ellegren *et al*. 2012; Poelstra *et al*. 2014; Lamichhaney *et al*. 2015).

These theoretical possibilities and growing body of empirical evidence lead other investigators, including McCormack & Maley (2015) and Patten (2015), to suggest that long-term isolation of populations (and associated divergence in neutral genetic markers) is not a necessary condition for the recognition of subspecies. Instead, these authors highlight the potential for selection to produce adaptive phenotypic divergence between populations. Indeed, Patten (2015) takes what might be considered an extreme view in suggesting that genetic divergence at neutral loci is neither a necessary or sufficient criterion for subspecies: "*Use of such neutral genes might reasonably yield no difference among populations, even if those populations differ markedly in phenotype, so a finding of no difference in neutral markers cannot be construed to mean anything. (Conversely, finding a difference in neutral markers means only that sufficient time has elapsed since the sampled populations were isolated but does not necessarily mean that the subspecies are valid, and they would not be valid unless phenotype differed.)*" Under this view, phenotypic differences (which are assumed to have a genetic basis) are the primary criterion for the description of subspecies, whereas the relatively small genetic data sets typically collected for analyses of phylogenetic relationships or population structure provide only a supporting role; evidence of long-term isolation (e.g., reciprocal monophyly of mtDNA lineages) or evidence of limited gene flow (e.g., F_{ST} values significantly greater than 0) support the recognition of subspecies whereas a lack thereof is considered inconclusive. Again, there is an underlying assumption that the phenotypic differences have a genetic basis, along with an expectation that anything short of whole genome sequencing on appropriate population samples is unlikely to capture the relevant genes.

At the risk of belaboring the point, this is a radically different perspective from Zink, who views historical isolation of populations as measured by genetic data as the primary criterion for recognizing subspecies, whereas phenotypic differences are not only of secondary importance, but can be viewed as an antiquated proxy for making inferences about historical isolation: "*The morphological characters used by taxonomists are simply proxies or markers for recognizing these geographically localized populations. Any character with a genetic, inherited basis can provide an assessment of the existence and geographic boundaries of a subspecies. In fact, the validity of a subspecies increases with concordant support from different character systems, especially molecular characters (mitochondrial DNA, nuclear DNA, microsatellites, SNPs, etc.). There is no question among practicing systematists that molecular characters today provide the most rigorous tests of limits and relationships of subspecies…*"

To briefly summarize the foregoing discussion, disagreements about the taxonomic status of California gnatcatcher subspecies are to a large extent based on radically different perspectives on the nature of subspecies, which carry different implicit assumptions about the evolutionary processes and timescales involved in the generation of biodiversity. One view is based in molecular systematics and emphasizes long-term historical isolation as a necessary condition for concluding that populations are evolutionarily independent, whereas the other is based in population genetics and emphasizes the potentially important role of natural selection in generating phenotypic divergence (with or without continuing gene flow between populations). Thus, there is a broad range of possible scenarios in which investigators looking at the same data and results, but holding these contrasting views will reach different conclusions.

1) What, if any, do you consider to be the most reliable features and methods to delimit infraspecific entities in songbirds or avian species in general?

Based on the above discussion and my experience and expertise as an evolutionary biologist and population geneticist, I would suggest the following outline of important criteria ("features") and methods for the recognition of avian subspecies.

- Divergence in one or more phenotypic traits is a necessary condition for the recognition of subspecies. In ornithology, the description of subspecies has been used as a way of cataloging significant geographic variation in phenotype, most often involving differences in plumage color and pattern. Behavioral and/or ecological traits are also of interest but will often be more difficult to assess. The intraspecific phenotypic variation represented by subspecies is an important component of existing biodiversity, and may influence the future evolutionary trajectory of populations in a changing world, both of which provide a basis for conservation.
- Concordance among multiple morphological traits and/or behavioral and ecological traits provides a stronger basis for recognition of subspecies, but a single trait that is biologically significant (e.g., a discrete difference in coloration that influences mate choice) could provide a reasonable basis for subspecies designation.
- Analyses of divergence in ecological niche may provide additional evidence supporting divergence in phenotype between subspecies, but a positive result is not a necessary condition of subspecies recognition.
- Concordance of phenotypic and genetic data provides a stronger basis for the recognition of subspecies, but genetic evidence remains secondary to the primary question of phenotypic divergence. Phenotypic-genetic concordance includes not only reciprocal monophyly of mtDNA lineages, but at least two additional forms of highly relevant evidence (*contra* Zink):
    - Genetic evidence for long-term isolation (e.g., reciprocal monophyly of mtDNA lineages and significant divergence, $F_{ST} > 0$, at most nuclear loci) between populations that differ discretely in phenotype (see Licona-Vera *et al*. 2014 and Feo *et al*. 2015 for recent examples). Such results will often provide a basis for elevating subspecies to species (e.g., Gohli *et al*. 2014; Feo *et al*. 2015).
    - Evidence of significant genetic structure between populations that differ discretely in phenotype (overall F_{ST} significantly greater than zero across multiple genetic loci, but not necessarily at all individual loci). Ideally, individuals of different subspecies can be discriminated on the basis of multi-locus genotypes (e.g., Ruegg *et al*. 2014). As shown in simulation results presented below, current genotype-by-sequencing (GBS) data sets including thousands of SNPs (still a tiny fraction of genomic variation) should be suitable to discriminate among recently isolated subspecies when overall F_{ST} values are as small as ~0.05.
    - Identification of genetic variants that are strongly correlated with phenotypic traits (e.g., Poelstra *et al*. 2014; Lamichhaney *et al*. 2015). As noted above, in cases of divergence with gene flow, it is expected that only a small fraction of the genome will be divergent and whole genome sequencing may be needed to detect these regions (i.e., "islands of divergence"). Concordance among multiple genetic variants associated with multiple traits provides a stronger basis for the recognition of subspecies.

- Additional evidence of population structure and estimates of historical parameters such as population divergence times and subsequent rates of gene flow (if any) can be obtained from coalescent analyses of multi-locus genetic data sets using programs such as ∂a∂i (Gutenkunst *et al*. 2009) and IMa/IMa2 (Hey & Nielsen 2007). Ideally, such analyses should be based on large single nucleotide polymorphism (SNP) data sets comprising thousands of SNPs generated with GBS methods such as restriction site associated DNA sequencing (RAD-seq) (Baird *et al*. 2008), but smaller data sets (e.g., 20 nuclear sequence loci) generated using standard Sanger sequencing methods may also be useful. Evidence of little or no recent gene flow between phenotypically discrete populations would provide a stronger basis for the recognition of subspecies. These methods have not been applied to California gnatcatchers.
- There appears to be general agreement that recognition of avian subspecies is only appropriate when there is discontinuous phenotypic variation across geographic space (e.g., "*…populations that differ abruptly and discretely in morphology or coloration*," AOU 1983). This condition helps avoid the need to arbitrarily divide continuous clines into an uncertain number of named subspecies and may better align subspecies with isolated populations that are more likely to diverge into incipient species. While one might ask why the populations at either end of a continuous cline are not also worthy of conservation if they show the same level of phenotypic divergence as two subspecies on either side of an abrupt transition in phenotype, it seems clear that discontinuity is an agreed upon criterion in avian taxonomy and thus should be explicitly evaluated.
- Appropriate sampling of individuals and populations and rigorous analysis of both phenotypic and genetic data is critical to evaluating all of the above criteria. Unfortunately, the need to assess whether geographic patterns of phenotypic and genetic variation are discontinuous will tend to increase the number of localities/populations that should be sampled.
    - Morphological analyses should be based on a sufficient number of individuals to characterize variation both within and between populations and between males and females. Statistical analyses should be based on quantitative measurements of both morphometric traits and plumage colors. With respect to the question of discontinuity, it seems reasonable to ask whether the geographic pattern of phenotypic variation differs from a null hypothesis of clinal variation rather than a null hypothesis of no differences between populations (Skalski *et al*. 2008).
    - Genetic data should likewise be based on a sufficient number of individuals to characterize patterns of variation within and among populations. Felsenstein (2005) showed that the optimal strategy for estimating theta ($\theta = 4N\mu$), a classic population genetic parameter, in a single population is to sample the largest number of independent genetic loci possible for as few as eight individuals. Generalizing from this result to estimating other aspects of population structure and history, the number of individuals that need to be sampled per population/locality can be relatively small, whereas more effort should be invested in sampling additional genetic loci and/or populations. For applications based on the allele frequency distribution (e.g., Gutenkunst *et al*. 2009), a somewhat larger sample of individuals per population may be desirable. With sufficient sampling, discontinuities in genetic population structure should be easy to detect using PCA (e.g., Patterson *et al*. 2006) or STRUCTURE (Pritchard *et al*. 2000), even when overall genetic differentiation is low (see simulation results presented under question #5 below).

Note: this summary of criteria and methods largely reflects the "divergence-with-gene-flow" perspective outlined above, but my views are less extreme than those of Patten (2015), for example. I continue to see an important role for analyses of neutral genetic variation in analyses of avian subspecies. Statistically significant evidence of population structure supports the plausibility of "divergence-with-gene-flow," whereas adaptive divergence remains unlikely if gene flow is sufficiently high to fully homogenize neutral genetic variation among populations (i.e., $F_{ST} \approx 0$).

2) What are the strengths and weaknesses of these approaches, particularly with the issues presented with the coastal California gnatcatcher (*Polioptila californica californica*)?

The phylogenetic perspective: The fundamental weakness in Zink's phylogenetic perspective and emphasis on divergence in neutral genetic markers is that it fails to recognize that populations can adapt to different physical and biotic environments and/or diverge in sexually selected traits even when there is an appreciable level of ongoing gene flow. In other words, complete isolation is not necessary for populations to have largely independent evolutionary trajectories. This is a well-established result of theoretical population genetics and an increasingly common empirical result with the expansion of genomics research in evolutionary biology.

Likewise, the phylogenetic perspective shifts the emphasis from phenotype to genetics and focuses on long-term historical divergence rather than functional divergence in phenotype as the primary object of species-level conservation efforts. Thus, this view implicitly assumes that phenotypic differences and reproductive isolation between incipient species evolve on the same timescale (e.g., Barrowclough 1982: "*…this may require tens of thousands of years or more*") as neutral genetic divergence, which would be the case only if these differences accumulate by chance through the process of genetic drift rather than natural selection. In fact, we know that natural and/or sexual selection can produce adaptive phenotypic divergence on a scale of decades rather than thousands of years (e.g., Yeh 2004).

The one strength of the phylogenetic perspective and its focus on mtDNA as an important yardstick for assessing historical isolation is the simple, unambiguous criterion it provides. Unfortunately, reciprocal monophyly places the critical threshold near the end of the process of divergence and rejects all intermediate stages of divergence as being insufficient. While it is true that mtDNA has provided clear inferences about the relationships of closely related populations and species in thousands of scientific studies and that these inferences are often corroborated by subsequent analyses of nuclear loci, this is not always the case (e.g., Irwin *et al*. 2009; Brelsford *et al*. 2011; Dong *et al*. 2014). More importantly, however, mtDNA is effectively a single, non-recombining genetic locus, the history of which represents a single stochastic outcome of the lineage sorting process. Thus, it may provide useful information in the majority of cases, but it is ultimately limited and provides poor resolution of recent history. Zink (March 2015 comment letter) argues that: "*…mtDNA is better able to capture recent population or subspecies splits, usually the purview of conservation biology, than nuclear loci.*" This statement is generally true if one is comparing mtDNA with a single nuclear locus (or perhaps a few nuclear loci), but it is absolutely incorrect if one is comparing mtDNA to a modern GBS data set with thousands of SNPs (e.g., Novembre *et al*. 2008; see also simulation results below). The combined information content from thousands of minimally informative SNPs provides for a substantially richer set of inferences than can be obtained from mtDNA alone. As collecting GBS data becomes routine, the key advantage of mtDNA (i.e., smaller effective population size) for analyses of population structure will be entirely outweighed by the statistical power of combining information from large numbers of loci.

The "divergence-with-gene-flow" perspective: In its most extreme form (e.g., Patten 2015), the "divergence-with-gene-flow" perspective proposes a problematic hypothesis-testing framework, in which any level of population structure/divergence is taken as supporting evidence of subspecies recognition, whereas a lack thereof is discarded as inconclusive. Strong inference (Platt 1964) requires the simultaneous testing of alternative hypotheses with an opportunity to reject either hypothesis. Therefore, I suggest above that failure to find any evidence of significant genetic differentiation should generally lead to a conclusion that the description of subspecies is not warranted because adaptive divergence is not expected in a truly panmictic (random mating) population. However, the level of divergence necessary to show significant structure, including discontinuity or breaks in population structure, may be quite low (see simulation results below).

A related weakness of the "divergence-with-gene-flow" perspective is that it replaces long-term historical divergence (which is easy to detect using genetic data) with divergence at the presumably small number of genetic loci responsible for phenotypic differences between populations. While it is increasingly feasible to identify genomic regions showing elevated divergence between closely related species using whole genome sequencing data, this remains a costly and computationally challenging undertaking at present and yields only correlations between genetic variation and phenotypic traits. Breeding experiments and/or molecular genetic analyses of development are needed to support a direct causal link between a particular genetic variant and a phenotypic trait (see Poelstra *et al*. 2014 for an example using gene expression data). Further, genetic data sets comprising dozens or up to several thousand loci are generally too small to detect divergent regions between closely related species, providing little opportunity to test the assumption that phenotypic differences have a genetic basis.

Analyses of population history and structure based on thousands of genetic loci generated by GBS methods such as RAD-seq are becoming increasingly feasible and will likely become the new standard for routine phylogeographic analyses on a wide range of organisms. The large data sets generated by these approaches provide entirely new opportunities for analysis (e.g., coalescent analyses based on the allele frequency spectrum, Gutenkunst *et al*. 2009), and substantially increased power for resolving population structure and history on much more recent evolutionary timescales. Ideally, evaluation of subspecies should be based on these new methods in combination with rigorous quantitative assessments of phenotypic variation.

I agree with Zink (June 2015 comment letter), albeit for somewhat different reasons, that one specific kind of molecular marker, rapidly evolving microsatellite loci, offers no special advantages for analyses of population structure and history, but instead are characterized by significant disadvantages related to their high mutational rate and extreme homoplasy (i.e., independent derivation of identical alleles through independent mutations) (e.g., Balloux *et al*. 2000).

3) Different methodologies may be suited to discriminate between taxa at various ranks while others are best suited to show close relationships among taxa. With this in mind, assess the extent to which the methods, data and conclusions of Zink et al. (2013) apply to these two approaches. How does your assessment apply to the taxonomic status of the California gnatcatcher?

One of the advantages of the phylogenetic perspective on subspecies is that it requires relatively little genetic data to test for evidence of long-term historical isolation (if long-term means sufficient time to achieve reciprocal monophyly in mtDNA lineages). Thus, the data presented by Zink *et al*. (2013) are entirely sufficient to reach the conclusion that putative California gnatcatcher (CAGN) subspecies have not experienced such long-term isolation, and it is highly unlikely that additional genetic data would change that conclusion. Zink *et al*. (2013) present additional mtDNA data from the ND2 gene, which is consistent with previously published control region data (Zink *et al*. 2000) in showing shared haplotypes among CAGN populations along with a tendency towards greater haplotype diversity in southern populations. The latter pattern is potentially consistent with a historical range expansion from south to north, although a similar pattern could be generated by differences in effective population size among geographic regions. DNA sequences from eight nuclear loci, including seven introns and one exon, are also consistent with the conclusion of no long-term historical isolation based on a pattern of shared alleles among populations.

These results were presumably more than sufficient for Zink *et al*. to be conclude that no CAGN subspecies are warranted, but perhaps anticipating criticism from investigators holding more expansive views of subspecies criteria (see above), Zink *et al*. (2013) press the case further, arguing that there is **no evidence of any population genetic structure**, such that CAGN populations do not meet any reasonable genetic standard for subspecies. The conclusion that there is no evidence of any structure is one focus of the critique by McCormack & Maley (2015), who point out that Zink *et al*. (2013) reported standard metrics for measuring population structure (i.e., G_{ST}, F_{ST}) from analyses comparing allele frequencies across all individual populations (each of which has relatively small sample size) rather than making pairwise comparisons between recognized subspecies. McCormack & Maley (2015) go on to report results of their own analyses of the Zink *et al*. (2013) data and suggest that there is some evidence of significant population differentiation. Specifically, they report significant results for two of seven nuclear loci (ACON, $F_{ST} = 0.062$, $P = 0.014$; TGFB-2, $F_{ST} = 0.077$, $P = 0.0049$) in comparisons of the *P. californica* subspecies versus all southern populations combined. Likewise, they find significant evidence of structure at two nuclear loci and the mitochondrial ND2 gene ($F_{ST} = 0.336$, $P = 0.016$) in comparisons of four California versus two northern Mexico populations, corresponding to a further division of *P. c. californica* into two northern subspecies, as proposed by Mellink & Rea (1994). Zink (March 2015 comment letter) harshly criticizes these analyses for not adhering to the currently accepted taxonomy comprising three subspecies (as in Atwood 1991) and characterizes McCormack & Maley's analysis as "*selective and biased manipulation of the data*." Indeed, the *californica* versus *atwoodi* comparisons perhaps deserve to be criticized as *ad hoc*, particularly given the small sample sizes (e.g., 15 versus 5 samples for the ND2 result noted above). In addition, Zink (March 2015 comment letter) suggests that comparisons of *P. c. californica* versus all southern populations combined are not valid. Given the generally limited sampling across the range, I disagree with this latter criticism. If the principal question at hand is whether *P. c. californica* is genetically distinct, then it is reasonable to combine other subspecies when faced with limited sampling. Both McCormack & Maley and Zink place too much significance on the results from single locus comparisons. For example, Zink (March 2015 comment letter) notes: "*…taken one-by-one, the nDNA loci do not support subspecies or any other genetically discrete or diagnostic pattern of geographic variation*." Given the mtDNA results, there is no reasonable expectation that any single nuclear locus (expect those underlying phenotypic traits) would yield a diagnostic pattern, so these single locus results do nothing more than knock down a straw man.

Nonetheless, whether the **currently available** genetic data provide any evidence of significant (i.e., non-zero) population genetic structure among *P. californica* subspecies remains a critical question. As noted, analysis of individual nuclear loci is not particularly informative, whereas the combined set of available nuclear loci is too small to test for subtle/recent patterns of gene flow (see below). Thus, I focus below on a re-analysis of the available mtDNA data, which as repeatedly argued by Zink is the single locus that is most likely to reveal evidence of population structure. Similarly careful and clear re-analyses of the available nuclear loci are also warranted for the sake of completeness, but again, individual locus analyses are of little value in comparison to combined analyses of multilocus data.

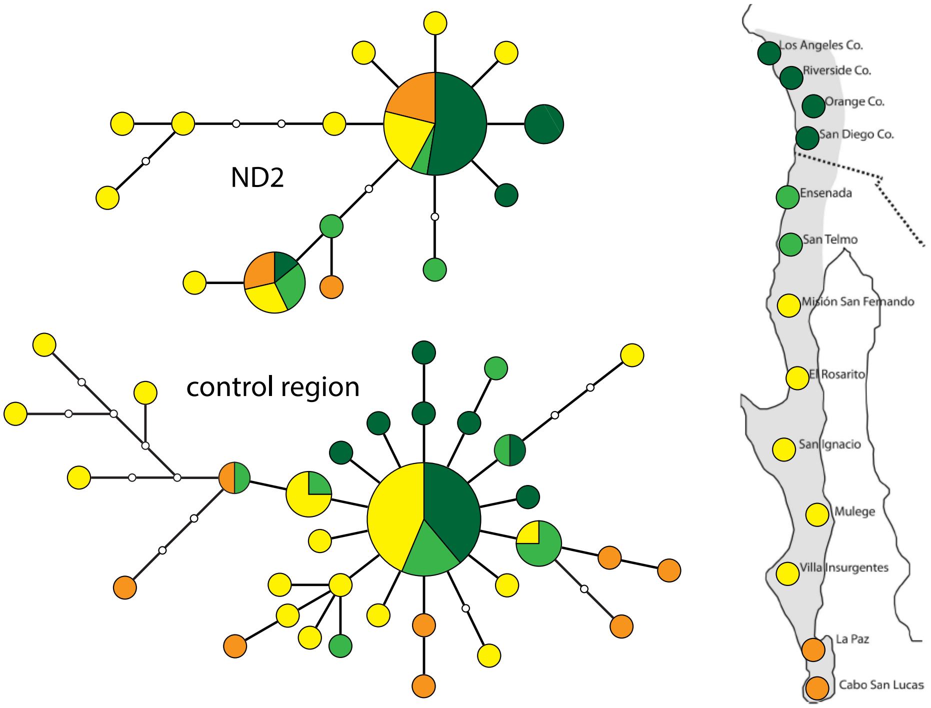

Figure 3: Networks illustrating the relationships among mtDNA haplotypes and their frequencies in populations of *P. californica*. Haplotypes are color-coded by geographic region, a different perspective on the data than provided in Zink et al. (2013), in which haplotypes were arbitrarily colored and their distribution across populations indicated on the map. Both mtDNA regions are consistent in finding greater haplotype diversity in southern populations (particularly within the range of *P. californica margaritae*, yellow), but otherwise suggest only weak evidence of population structure. ND2 data from Zink *et al*. (2013) was downloaded from GenBank. Control region data are from the appendix of Zink *et al*. (2000) with adjustments made to equalize the length of the aligned sequences (the alignment was apparently reproduced incorrectly by the journal). The actual alignment used to produce the control region network above is provided as an appendix to this document. Note that the control region network was simplified by eliminating several alternative connections between haplotypes.

Table 1: F_{ST} and Φ_{ST} values for the ND2 and control region data illustrated in Fig. 3. Calculations completed in Arlequin (Excoffier & Lischer 2010) using either two groups as in "test 1" of McCormack & Maley (2015), or three groups corresponding to the subspecies recognized by Atwood (1991).

Pairwise comparisons

ND2 (F_{ST})	*californica*	*margaritae*
margaritae	0.200***	
abbreviata	0.319***	0.188***
ND2 (Φ_{ST})	*californica*	*margaritae*
margaritae	$0.058^{\text{n.s.}}$	
abbreviata	$0.011^{\text{n.s.}}$	$0.014^{\text{n.s.}}$
CR (F_{ST})	*californica*	*margaritae*
margaritae	$\sim 0.000^{\text{n.s.}}$	
abbreviata	0.064*	$0.023^{\text{n.s.}}$
CR (Φ_{ST})	*californica*	*margaritae*
margaritae	0.032*	
abbreviata	0.139***	0.016

*p < 0.05; **p < 0.01; ***p < 0.001

	F_{ST}	*p*-value	Φ_{ST}	*p*-value
ND2				
2 groups	**0.236**	**<0.0001**	0.023	0.171
3 groups	**0.231**	**<0.0001**	0.039	0.143
control region (CR)				
2 groups	0.008	0.165	**0.042**	**0.007**
3 groups	0.017	0.128	**0.050**	**0.006**

Table 1 provides F_{ST} and "Φ_{ST}" values for comparisons based on mitochondrial ND2 and control region sequences, respectively. Similar results are obtained in comparisons of two groups (*P. c. californica* versus other subspecies) versus three groups (three subspecies), suggesting that this is not a serious issue. Results vary, however, depending on the specific metric used to measure population structure. In the table above, F_{ST} refers to the conventional population genetic statistic based on haplotype (or allele) frequencies, whereas Φ_{ST} refers to an alternative approach that takes the genetic distance between haplotypes as well as their frequencies into account. Both metrics can be interpreted as the proportion of genetic variation that is explained by differences between groups, but Φ_{ST} is generally regarded as the more appropriate measure for DNA sequence data because it incorporates the additional information available in the level of genetic divergence among haplotypes. In contrast, F_{ST} treats different haplotypes exactly the same regardless of whether they are closely or more distantly related. As such, it may be more sensitive to changes in haplotype frequencies on a more recent timescales (i.e., on shorter timescales than involved in the evolution of the haplotypes). Neither Zink *et al*. (2013) or McCormack & Maley (2015) provide a clear and direct statement about which metric they use, although both specify the use of the software Arlequin, which calculates Φ_{ST} values by default in the context of an AMOVA (Analysis of Molecular Variance; Excoffier *et al*. 1992), but is also capable of calculating conventional F_{ST} values. A check on McCormack & Maley's ND2 result for "*californica*" versus "*atwoodi*" confirms that the reported F_{ST} value of 0.336 is actually a Φ_{ST} value (this is a common issue in the molecular ecology literature). Zink *et al*. (2013) report a low "F_{ST}" value ($F_{ST} = 0.021$, $P = 0.37$) for a comparison of ND2 across all sampled populations, but with only 41 samples spread across 13 localities, this test presumably had limited power to detect subtle differences in haplotype frequencies.

Given that currently recognized subspecies represent an a priori taxonomic hypothesis, it is entirely reasonable to test that hypothesis with comparisons among subspecies rather than individual populations. The results shown above indicate that there is some signal for significant (non-zero) population structure in the mtDNA data, albeit with some inconsistency between the two mtDNA loci and alternative metrics. In pairwise comparisons, the largest value is obtained between *californica* and *abbreviata* in three of four comparisons, including all three analyses in which there are any significant pairwise differences. This is consistent with an expectation of greater divergence for geographically distant populations and counters Zink's argument based on a single nuclear locus that a lack of differentiation between *californica* and *abbreviata* is a "*fatal twist*" that "*makes no geographic or taxonomic sense*" (Zink, March 2015 comment letter).

The degree of divergence in mtDNA is relatively low and this result will not change with additional sampling, but it provides some basis for further analysis of the genetic structure of CAGN populations using more robust data sets such as those generated by GBS methods.

Additional comments on Zink *et al*. (2013):

<u>Nuclear data</u>: As shown in simulations presented below, most individual nuclear loci are expected to have F_{ST} values in the 0 to 0.05 range in cases of recent population divergence, including models in which there has been a recent cessation of gene flow between populations. Given that the mtDNA data clearly indicate a lack of deep historical divergence, the eight nuclear loci included in Zink *et al*. (2013) provide no significant new insights because they represent an insufficient sample of the genome to test for subtle differentiation due to more recent isolation of populations. They are sufficient only to corroborate the lack of deep historical divergence.

In attempting to extract additional information from the available nuclear data, Zink (March 2015 comment letter) makes an argument that is incompatible with basic coalescent theory: "*Examining the loci one-by-one, it is clear that the most common allele is found in all populations, which reveals a high degree of gene exchange (i.e., lack of geographic divergence).*" On average, the most common allele/haplotype at a given locus is at the center of the haplotype network and is an older, ancestral allele from which other, less common alleles have more recently originated via mutation. These common ancestral alleles are the most likely to be shared among populations, as they were already present when, for example, an ancestral population expanded. Thus, observing rare alleles in different geographic areas is a much stronger indication of recent gene exchange (e.g., Slatkin 1985). Because they are rare, however, greater sampling of individuals and/or loci may be needed to exploit this potentially powerful evidence for recent gene flow (or a lack thereof).

<u>Functional loci</u>: The following passage in Zink *et al*. (2013) implies a failed test for divergence at a functionally significant locus: "*The locus MC1R has been associated with darker-colored*

phenotypes in some organisms (Baião et al. 2007); this locus also lacked geographic structure in California Gnatcatchers, despite the CSS populations being characterized as having somewhat darker plumage (Atwood 1991)." This passage represents faulty logic at best and is disingenuous at worst. The MC1R gene has been associated with dark plumages in other bird species, most often all black plumages (e.g., Theron *et al*. 2001; Uy *et al*. 2009), but a lack of divergence at this particular locus offers essentially no insight on whether differences in melanin-based plumage traits in CAGN have a genetic basis. The melanogenesis pathway includes dozens of genes, changes in any one of which might explain variation in plumage phenotype (e.g., Poelstra *et al*. 2014).

Historical demographic analysis: Zink *et al*. (2013) present the results of an extended Bayesian skyline analysis in their Fig. 5. The analysis suggests relatively recent (~3,500 years before present) expansion of southern populations and perhaps even more recent expansion of northern populations. The y-axis of Fig. 5, however, raises a concern about whether this analysis was correctly calibrated. Point estimates of current effective population sizes for northern and southern populations are shown as 20 and 60, respectively. These are implausibly small values for effective population size (i.e., N_e) of populations that have survived for at least thousands of years.

Niche modeling: In addition to nuclear sequence data, Zink *et al*. (2013) offer a test for divergence in ecological niche. The test is potentially interesting and worthwhile but is ultimately of somewhat limited significance because it is based on climatic variables only. There are strong climatic differences across the full range of CAGN and thus *P. c. californica* lives in a significantly different environmental niche than populations to the south. The environments it inhabits, however, are neither more similar to nor more divergent from expectations given the "background" latitudinal variation in climate. Zink *et al*. (2013) interpret this as another line of evidence showing a lack of divergence between CAGN subspecies, whereas McCormack & Maley (2015) see the result as inconclusive with respect to the question of whether CAGN is a habitat generalist or has evolved ecological adaptations to differing habitats. My reading of the exchange between McCormack & Maley (2015) and Zink (March 2015 comment letter) suggests that there is no real disagreement or misunderstanding by either party on what the analysis shows, only a disagreement on the interpretation of the results. More importantly, however, because it is based on climatic variables only, the analysis is of limited value. A more interesting test would include biotic variables such as habitat structure and plant species composition. Ultimately, however, habitat use and the possibility of associated ecological adaptation is just one of many possible axes of divergence between avian subspecies and is therefore not a necessary condition for the recognition of subspecies.

Morphology: Zink *et al*. (2013) provide no new information on patterns of morphological variation but rely on Skalski *et al*. (2008) to conclude that there is no evidence for discrete (non-continuous) geographic variation in CAGN plumage coloration (see below).

Funding source: McCormack & Maley (2015) and Winker (March 2015 comment letter) raise the issue of possible bias or conflicts of interest resulting from the private source of funding for the Zink *et al*. (2013) study. I agree that Zink *et al*. (2013) should have provided more information about the source(s) of their funding and should have commented on any potential financial interests of the individuals or organizations who funded the work. Nonetheless, I see no evidence of bias related to the source of funding in the data analyses or interpretation of results in Zink *et al*. (2013). The paper is consistent with Zink's earlier work and strong views on the value and validity of subspecies in general. On the other hand, the overall quality of the data and analyses in Zink *et al*. (2013) is generally unimpressive in comparison to the best current research in the fields of molecular ecology and phylogeography.

To summarize, the primary contribution of the Zink *et al*. (2013) study is to add a small amount of nuclear DNA sequence data to the evidence available for evaluating CAGN subspecies. These data are sufficient to corroborate previous mtDNA results showing no evidence of long-term historical isolation of CAGN subspecies, but are otherwise insufficient (i.e., lack sufficient power) to detect more subtle patterns of genetic structure that may have developed due to more recent isolation of populations. Thus, the study does not represent a major advance in understanding or a strong basis for changing the currently accepted taxonomy of the species.

4) **There is an array of scientific information that could be used to determine the taxonomic status of animals listed as the coastal California gnatcatcher. Using the available evidence, describe how the coastal California gnatcatcher represents a recognizable entity (e.g., subspecies) or specifically why no infraspecific taxa warrant recognition within California gnatcatcher (*Polioptila californica*). In addressing this question, we ask that you consider the following: the discreteness, significance, and conservation status of the species' (or subspecies) population segments.**

As a preface to answering this question, I think it is important to restate that my primary expertise is in evolutionary genetics and genomics rather than avian morphology and taxonomy. Thus, my remarks above and below focus on an evaluation of the genetic data reported by Zink *et al*. (2000, 2013), and more generally on what molecular genetic data can reveal about the structure and history of avian populations in relation to the divergent perspectives on avian subspecies evident in recent papers on CAGN.

With this caveat in mind, my overall assessment is that there are clear differences in a number of morphological traits among populations of CAGN, but it is uncertain whether these populations are connected by continuous phenotypic and/or genetic clines. While perhaps subtle, the phenotypic basis for CAGN subspecies apparently falls within the range of what has historically been standard practice in avian taxonomy, a conclusion supported by the 2004 review of the status of CAGN subspecies (VanderWerf 2004). It is also worth noting that the genus *Polioptila* comprises a number of morphologically similar species, suggesting that even subtle intraspecific variation may warrant description based on the notion that interspecific differences within a given genus provide a standard against which to judge the significance of intraspecific variation (Mayr 1943).

Since 2004, the only new information relevant to phenotypic divergence in CAGN is the limited reanalysis of Atwood's data by Skalski *et al*. (2008). Skalski *et al*. focus on the question of explicitly testing for discontinuity in the geographic pattern of phenotypic variation through comparison to a null hypothesis of clinal variation rather than a null hypothesis of no differences between populations. This is conceptually interesting and potentially important as discontinuity appears to be an agreed upon criterion for recognizing avian subspecies (e.g., AOU 1983).

Unfortunately, there is some concern about the objectivity of Skalski *et al*. because they uncritically accept the conclusions of Zink *et al*. (2000), and assume *a priori* that CAGN subspecies provide a convenient case study in which we know that subspecies were erroneously described: "*In these unique cases where advances in science (i.e., DNA analysis) let us look back at earlier decisions, we are provided with the opportunity to learn from our mistakes*." Nonetheless, the one character analyzed in detail (length of white spot on 5th retrix) appears to show a pattern of clinal variation rather than abrupt changes across the species' range.

Given these observations, there does not appear to be a strong basis for reversing conclusions about the morphological basis for subspecies recognition reached by the 2004 review panel. A key question, however, is whether there is discontinuity in phenotypic traits. If not, then variation in CAGN may not be consistent with a key criterion for subspecies recognition. Nonetheless, the clear pattern of clinal variation in phenotype increases the significance of population segments at the extreme ends of the species' range. With or without discontinuity, these phenotypic differences represent a component of biodiversity that may be at risk without appropriate protections.

The currently available genetic data are likewise inconclusive about the status of CAGN subspecies. While these data are sufficient to reject subspecies under the relatively extreme phylogenetic framework advocated by Zink and colleagues, they are not sufficient to test for recent/current isolation of populations and/or the adaptive divergence of populations (with or without a low level of ongoing gene flow). Zink's consideration of CAGN subspecies almost entirely neglects natural selection as an important evolutionary process and/or assumes that selection produces divergence between populations on the same timescale as divergence in neutral genetic markers. Most evolutionary biologists now recognize the relevance and generality of the "divergence-with-gene-flow" model and the importance of ecological and sexual selection in the diversification of species. An increasing number of empirical examples support the conclusion that evolutionarily independent trajectories are possible for populations showing low levels of genome-wide divergence, and the genetic data needed to test these ideas are increasingly feasible to collect.

As with the morphological data, new genetic evidence since the 2004 status review provides only an incremental advance in understanding. A second mtDNA locus serves only to confirm the results reported in Zink *et al*. (2000), whereas a limited number of nuclear sequence loci show entirely predicable patterns of variation given the mtDNA results. Advancing our understanding of CAGN population structure and history will require the much larger data sets now available from GBS methods. If such analyses reveal a complete lack of genetic structure between subspecies and/or a lack of any breaks in the geographic distribution of genetic variation, I would agree that CAGN subspecies are not warranted. Based on the currently available evidence (i.e., some indication of geographic structure in the mtDNA data and perhaps one or two of the available nuclear loci) it seems likely that GBS data will provide additional insights into CAGN population structure and demographic history, assuming these data are analyzed appropriately using modern coalescent methods.

To summarize, differences among CAGN subspecies appear to be relatively subtle and no amount of additional data collection and analysis will change that basic result. While it is possible that more robust genetic and morphological analyses will provide evidence of concordant, discontinuous and evolutionarily recent divergence among populations, and thereby support the recognition of subspecies, this seems relatively unlikely given all of the currently available evidence. To clarify, I predict that GBS data sets will provide evidence of significant clinal structure among CAGN populations but not necessarily discontinuous structure. Such results would increase the evolutionary significance of populations at either end of the species range, whereas ongoing anthropogenic habitat modification may reduce the likelihood of continuing gene flow between US and Mexican populations, increasing the discreteness of the US population segment. I do not have sufficient expertise or knowledge of US CAGN populations to evaluate their conservation status.

5) What additional information or analysis, if any, would clarify the taxonomic status of the California gnatcatcher?

Unfortunately, none of the currently available morphological or genetic analyses of CAGN subspecies meet the highest current scientific standards for robust sampling of populations or the quality of data collection and analysis.

With respect to morphological variation, rigorous statistical analysis of morphological clines (and the presence or absence of abrupt breaks) is needed for all traits proposed to vary among CAGN subspecies. This should be based on all available museum specimens, should include specimen age as a covariate, and should also include simultaneous analyses of multiple traits (e.g., principal component analysis, discriminant function analysis).

With respect to genetic data, analysis of a large GBS data set is the next logical step. Zink (June 2015 comment letter) reports that a California gnatcatcher data set comprising over 16,000 SNPs is now in the process of being analyzed and prepared for publication. This is a promising development, but it is critical that these data are analyzed using appropriate methods that objectively consider alternative frameworks for subspecies recognition. Thus, a finding of consistently low genome-wide F_{ST} values in the GBS data may lead Zink to conclude that "[t]*here is no support for subspecies*." (Zink, June 2015 comment letter), but other investigators may reach different conclusions through the application of different methods and criteria. Indeed, I would recommend that Zink release the unprocessed GBS data as soon as possible to allow others the opportunity to replicate his analyses (or not) and to conduct additional kinds of analyses using these data (there is a substantial range of potentially informative analyses that can be based on large GBS data sets). This might prevent further delays in reaching a scientific consensus on CAGN subspecies.

To illustrate the potential of GBS data sets to detect recent events in the history of populations and to highlight the kinds of analyses I would like to see in Zink's forthcoming analysis of 16,000 SNPs, I conducted the simulation study described below.

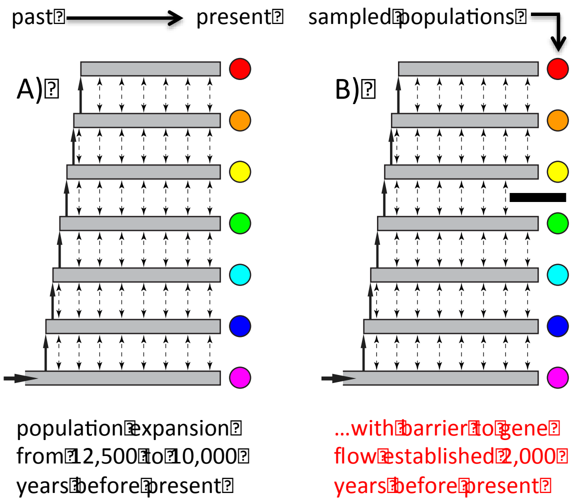

Figure 4. Highly simplified models of recent population expansion (A) without or (B) with a subsequent barrier to gene flow. These models were used in coalescent simulations to generate data sets comparable to those obtained by current GBS methods. Note that the intent is not to precisely model the history of CAGN populations but to illustrate the power of GBS data sets to detect subtle patterns of population structure and recent historical events. Both models consider the geographic expansion of a single species across a linear geographic range. Each successive population is founded at 500-year intervals from 12,500 to 10,000 years before present. Effective population size (N_e) of each population is set at 5,000 diploid individuals (10,000 gene copies) with no population growth or contraction. Because each population originates with 5,000 individuals, there are no founder effects in the model. Instead the model is designed to compare the effects of different levels and patterns of ongoing gene flow (dotted lines with arrows). In model (B), a barrier to gene flow between the "yellow" and "green" populations is introduced at 2,000 years before present (generation time is assumed to be one year). Gene flow continues among populations on either side of the barrier. DNA sequence data for 5,000 x 150 base pair loci was simulated for a sample of 10 individuals (20 gene copies) per population using fastsimcoal2 (Excoffier *et al*. 2013). The mutation rate was set as 10^{-8} per site per generation. Diploid multilocus genotypes were assembled by pairing the simulated alleles for each of the 5,000 loci, and these data were used in principal component analysis in R (R Core Team 2015) following the approach of Novembre & Stephens (2008). Finally, overall and locus-specific F_{ST} values were calculated in Arlequin (Excoffier & Lischer 2010) treating individual SNPs as independent loci. Simulations used one of three different migration matrices: 1) a "stepping stone" model in which gene flow at rate m = 0.005 per generation (Nm = 25) occurs only between adjacent populations; 2) an "island" model in which any two populations may exchange migrants, but with low migration rates varying from 0.0001 between the most distant populations to 0.0006 between adjacent populations (Nm = 0.5 to 3); and 3) the same model with tenfold higher rates of migration, varying from 0.001 to 0.006 in the same manner (Nm = 5 to 30).

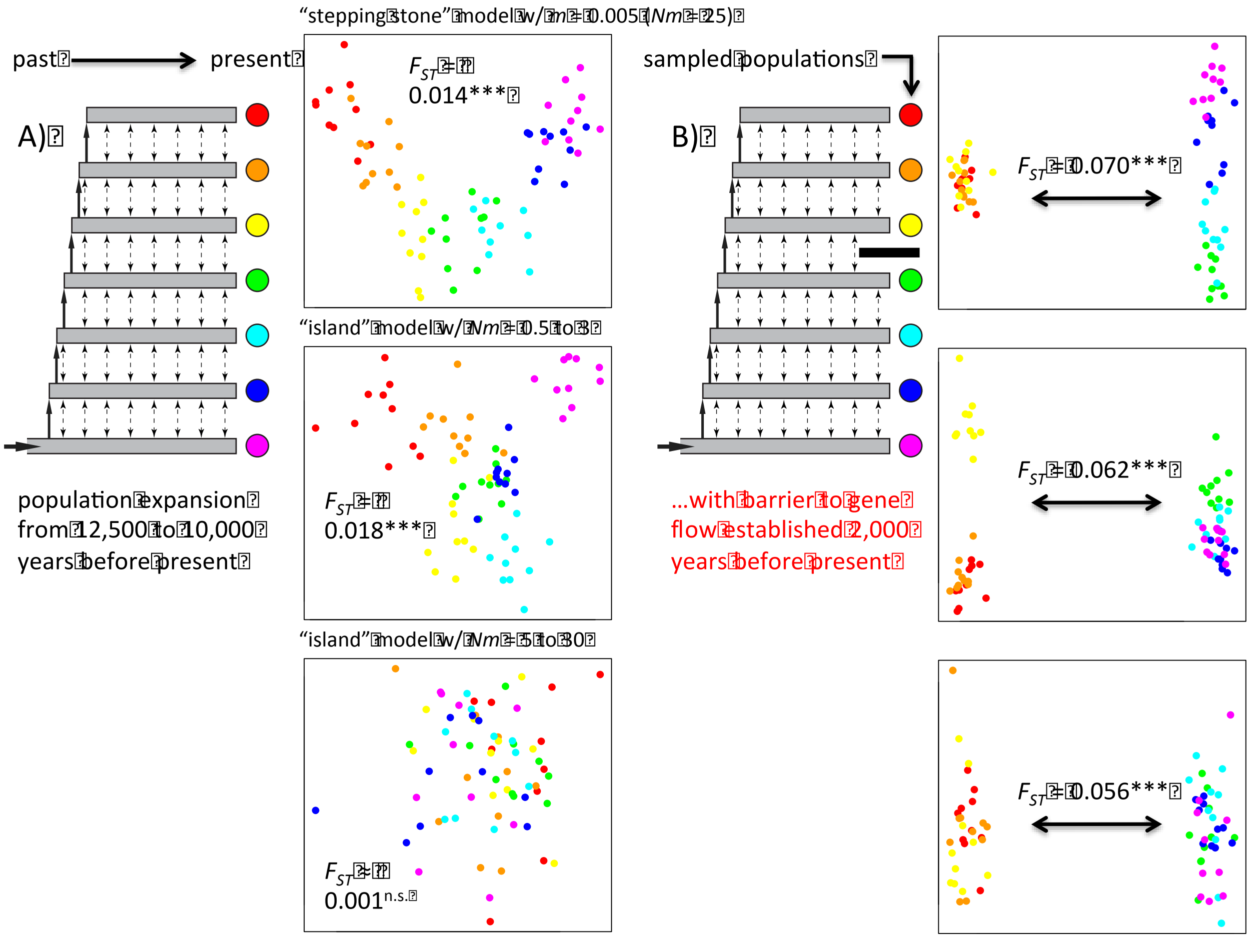

Figure 5. Results of principal components analyses based on simulated SNP data modeled as described in Fig. 4. Each simulated data set comprised ~5,800 SNPs across 5,000 independent loci. The population of origin of each individual sample is color-coded as in the population tree. Each panel includes the overall F_{ST} value for a comparison of the three "northern" populations versus the four "southern" populations.

Fig. 5 shows the results of PCA analyses of simulated SNP data. Note that with no barriers to gene flow, a clear pattern of population structure consistent with "isolation-by-distance" is evident in both the "stepping-stone" model and the island model with low rates of migration, despite overall F_{ST} values less than 0.02. Only with high rates of migration in the island model is there no signal of population structure (bottom left panel in Fig. 5). Under all three models, a barrier to gene flow over the past 2,000 generations is sufficient to generate significant divergence in allele frequencies between populations on either side of the barrier. In addition, populations on either side of the barrier can clearly be discriminated, with all individual samples grouping appropriately based on their multilocus genotypes (no *a priori* information on population of origin is included in the PCA). In addition, there are **zero fixed SNPs** among the ~5,8000 simulated SNPs in each of the simulated data sets. Note that PCA is more sensitive than STRUCTURE in revealing these patterns in large SNP data sets.

A comparison of the top two panels (left and right) provides a simple visual illustration of the contrasting expectations for a continuously distributed population and one with a barrier to gene flow and shows one how a large SNP data set could be used to test for a break in the distribution of genetic variation across the landscape. A more rigorous approach, however, will be to test the fit of the empirical data to alternative historical models using an explicit coalescent framework as implemented, for example, in ∂a∂i (Gutenkunst *et al*. 2009).

These simulations illustrate at least three additional significant points with respect to the results of Zink *et al*. (2013) and his subsequent commentaries (March 2015 comment letter, June 2015 comment letter). In his commentaries, Zink repeatedly argues that small F_{ST} values are biologically meaningless (e.g., "*The overall amount of genetic variance partitioned among localities was 1.3%, a biologically trivial and statistically insignificant level*.") This is indeed true when the analysis is based on a handful of genetic loci, but the above simulations show that large SNP data sets may contain valuable information about population structure and history even when F_{ST} values are quite small (e.g., < 0.02 in the top two panels on the left of Fig. 5). Second, with or without a recent barrier to gene flow and under the model parameters analyzed here, the majority of nuclear loci are expected to have F_{ST} values < 0.05 (Fig. 6), such that a sample of eight nuclear loci may or may not include any showing significant evidence of population structure. In contrast, the overall distributions of F_{ST} values are clearly different in the models with and without a barrier to gene flow (Fig. 6), highlighting the importance of analyses that consider all the data combined rather than individual loci. Third and consistent with the above observation, it is important to point out that the nuclear loci analyzed by Zink *et al*. (2013) included on the order of ~45 non-independent SNPs across 8 nuclear loci (based on allele numbers in their Table 2). Randomly selected sets of 50 SNPs from the simulated data illustrated in the bottom, right panel of Fig. 5, for example, generally fail to detect any evidence of structure using the PCA approach.

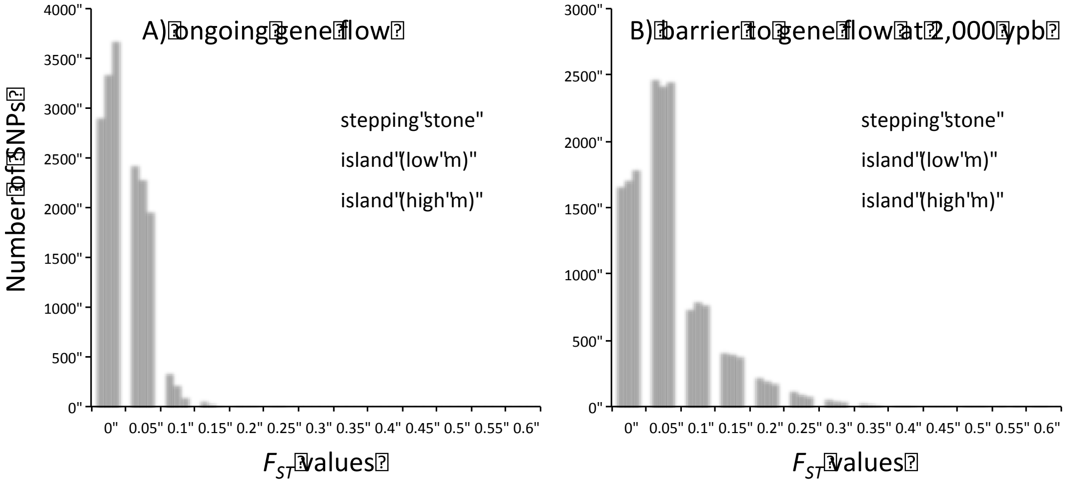

Figure 6. Distribution of individual SNP F_{ST} values for the six simulations presented in Fig. 5.

Additional Comments

Throughout his career, Zink (e.g., Zink & Barrowclough 2008) has advocated the use of mtDNA in studies of phylogeography, population structure and taxonomic relationships. Arguments about the special advantages of mtDNA remain valid if an investigator is faced with choosing the **single** most informative locus available, but they are no longer valid if the question is whether to use mtDNA or large multilocus data sets as the best available data for assessing historical isolation. While the information content of each individual nuclear SNP is minimal, thousands of SNPs analyzed in combination allow far richer inferences of population structure and demographic history and allow those questions to be addressed with much greater temporal resolution. It is not clear that Zink recognizes this distinction; for example, he writes: "*If two populations are isolated, but for less than 1Ne generations, no molecular marker will likely show them to be evolving independently, because all molecular markers have a "lag time" (Zink and Barrowclough 2008).*" (March 2015 comment letter). Implicit to this statement is the notion that an inference of independent evolution requires finding **individual genetic markers** showing reciprocal monophyly, but this is simply incorrect. Large panels of SNPs from across the genome are capable of providing strong evidence of a cessation of gene flow long before reciprocal monophyly is achieved at any individual locus. In contrast, Zink's view limits our analyses of evolutionary processes to relatively ancient timescales because anything more recent than N_e generations is beyond the reach of mtDNA. Under siege in 2008, the time has come for mtDNA to be permanently dethroned.

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Appendix: control region alignment used to generate control region network and analyses – see Zink *et al*. (2000) for more information.

```
CAGN3LA  TTTGCCATCA-GCTAT-G--T--CTT
CAGN2LA  TTTACCATCA-GCTAT-G--T--CTT
CAGN39RV TTTGCCATCA-GCTAT-A--T--CTT
CAGN42RV TTTGCCATCA-GCTAC-G--T--CTT
CAGN60R  TTTGCCATCA-GCTAT-A-----CTT
CAGN70R  TTTGCCATCA-GCTAT-G--T--ATT
CAGN43SD TTTGTCATCA-GCTAT-G--T--CTT
CAGN45SD TTTGCCATCA-GCCAT-G--T--CTT
CAGN48ES TTTGCCATCA-GCTAT-G-TT--CTT
CAGN51ES TTTGCCATCA-GCTAT-G----CCTT
CAGN13ST TTTGCCATCA-GCTGTCG--T--CTT
CAGN14ST TTTGCCATCA-GCCAT-G-TT--CTT
CAGN34ST TTTGCCATCA-GCTAT-G-----CTT
CAGN23MS TTTGCCATCA-GCTGT-G--T--CTT
CAGN17ER TTTGCCATTA-GCTAT-G--T--CTT
CAGN27SI TTTGCCATCA-GCTGT-G-TT--CTT
CAGN28SI TTCGCCATCAAGCTAT-G--T--CTT
CAGN38SI TCTACCATCA-GCTAT-G----CCTC
CAGN56SI TTTGCCATCA-GCTGT-G-----CTT
CAGN64MU TTTGCTATCC-GCTAT-G----CCTC
CAGN65MU CCTACTATCA-GCTAT-G--T--CTT
CAGN68MU TTTGCCACCA-GCTAT-G--T--CTT
CAGN19VI CCTGCCATCA-GTTAT-G--T-CCTC
CAGN57VI TTTGCCGTCA-GCTAT-G--T--CTT
CAGN58VI TTTGCCATCA-ATTAT-G----CCTC
CAGN69VI TTTGCTATCA-GCTGT-G--T--CTT
CAGN21LP TTTGCCATCA-GCTAT-G-TT-CCTT
CAGN22LP TTTGCCATCA-GCTGT-G-----CTC
CAGN29LP CTTGCCATCA-GTTAT-G---CCCTT
CAGN31LP TTTGCCATCA-GCTAT-G--T-CCTT
CAGN60CL TTTGCTATCA-GCTAT-G-TT--CTT
CAGN61CL TTTGCTATCA-GCTAT-GTTT--CTT
CAGN62CL TTTGCCATCA-GCTAT-G-TT--CCC
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APPENDIX D

Reviewer’s Curricula Vitae (Alphabetical)

California Gnatcatcher Facilitated Science Panel Workshop
U.S. Fish & Wildlife Service

CURRICULUM VITAE

Harold Lisle Gibbs

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Columbus, Ohio USA 43210-12393
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fax: (614) 292-2030
email: gibbs.128@osu.edu

Education:

1988	Ph.D.	University of Michigan (Ecology & Evolutionary Biology)
1981	M.S.	University of Michigan (Natural Resources)
1980	B.Sc. (Hons)	Queen's University (Biology)

Positions:

Professor, Ohio State University, 2006 - present
Associate Professor, Ohio State University, 2001-2006
Associate Professor, McMaster University, 1997-2001
Assistant Professor, McMaster University, 1992-1997

Fulbright Scholar, Instituto Butantan, São Paulo, Brazil, 2013. 2014
Director, Ohio Biodiversity Conservation Partnership, Ohio State University, 2011-
Long Term Visitor, Mathematical Biosciences Institute, Ohio State University, 2009-2010
Visiting Scientist, University of Arizona, 2005
Visiting Scientist, Royal Ontario Museum, 1997-1998

Post-doctoral Research Associate
  Department of Biology, McMaster University, 1991-1992
  Department of Biology, Queen’s University, 1988-1991

Research Interests:

Evolutionary Biology, Molecular Ecology, Molecular Evolution, Conservation Genetics

Fellowships and Awards:

2013	Awarded US-Brazil Fulbright – Science without Borders Program Research Fellowship
2012	Fellow of the American Association for the Advancement of Science
2009-10	Long Term Visitor Fellowship, Mathematical Biosciences Institute, Ohio State University
2002	Fellow of the American Ornithologists' Union
2000	Nominated for an E.W.R. Steacie Award (NSERC) by McMaster University
1999	Premier’s Research Excellence Award, Province of Ontario
1993	Elected Member of the American Ornithologists' Union

1991 Young Investigators' Prize, American Society of Naturalists
1990-91 Natural Sciences & Engineering Research Council of Canada Postdoctoral Fellowship
1988-90 A.P. Sloan Foundation Postdoctoral Fellowship for Molecular Studies of Evolution

Professional Training:
2012 Next-Generation Sequencing Course, National Center for Evolutionary Synthesis Center. Duke University, 11- 19 June.
2009 Statistical Phylogeography course. Southwest Research Station, Portal, Arizona, 5-10 April.
2006 Workshop on Molecular Evolution. Marine Biological Laboratory, Woods Hole, Massachusetts, 22 July – 2 August.

Professional Organizations:
Member: Society for the Study of Evolution, American Association for the Advancement of Science

Editorial and Reviewer Positions:
Editorial Review Board, *Conservation Genetics*, 2006- present
Associate Editor for *Conservation Genetics*, 2004- 2006
Associate Editor for *Evolution*, 2000-2002

Ad hoc journal reviewer for: *Auk, American Naturalist, Animal Behavior, Animal Conservation Genetics, Behavioral Ecology, Behavioral Ecology and Sociobiology, BMC Genomics, Canadian Journal of Zoology, Condor, Evolution, Ecology, Genetics, Genome, Journal of Herpetology, Journal of Venom Research, Journal of Proteomics, Journal of Proteomics Research, Journal of Wildlife Management, Molecular Biology and Evolution, Molecular Ecology, Molecular Ecology Resources, Nature, Nature Communications, Science, Proceedings of the National Academy of Science (USA), Proceedings of the Royal Society of London, Series B., Toxicon, Wilson Bulletin.*

Member of the Evolution and Population Ecology Panel, Division of Environmental Biology, National Science Foundation, November 2003 and April 2005

Ad hoc grant reviewer for: Austrian Science Foundation, EU EUROCORES Genomics Program, BBSRC (UK), Natural Environmental Research Council (UK), Leverhulme Foundation (UK), National Science Foundation (USA), Natural Sciences and Engineering Research Council (Canada), Ohio Department of Natural Resources, Sigma Delta Epsilon Eloise Gerry Fellowships for Graduate Women in Science, Netherlands Organization for Scientific Research, and the US-Israel Binational Research Foundation.

Advisory Panels:
Scientific Advisor to Black Rat Snake Recovery Team, Canadian Wildlife Service, Environment Canada, 1999 – 2001.

Scientific Advisor to Massasauga Rattlesnake Recovery Team, Canadian Wildlife Service, Environment Canada 1999 – 2001.

Natural Areas Inventory Evaluation Group, advisory group to Planning Department, Hamilton-Wentworth Municipality, December 1993 - 1996.

Red Hill Creek Scholarship Committee, Hamilton Region Conservation Authority, September 1995.

Other Service Activities

Co-organized (with M. Daly) a NESCent Catalysis Meeting on ““Integrating Organismal and Applied Perspectives on Animal Venom Diversity”, Duke University, Durham, NC, September 2014.

Co-organized (with I. Junqueira de Azevedo) a workshop on “Applications of Next Generation Sequencing to Venomous Snakes”, Instituto Butantan, Sao Paulo, Brazil, December 2013.

Organized the Annual OBCP Research Review Meeting from 2011 - present

Provided scientific advice to US Fish and Wildlife for preparation of petition for listing the eastern massasauga rattlesnake as an endangered species, January 2011. Continue to provide advice on an ongoing basis.

Wrote promotion evaluations for faculty at Capital University, Florida State University, University of Cincinnati, Louisiana State University, Kent State University, University of Michigan, University of South Carolina, Cornell University, Indiana University-Fort Wayne, Louisiana State University 2008-present.

Served as an External Examiner for the Ph.D. exam of Bonnie Fraser, Department of Biology, University of Western Ontario, July 2009

Served as an External Examiner for the Ph.D. exam of Gunnhild Marthinsen, Natural History Museum, University of Oslo, Norway, November 2007

Established and organized (with A. Snow and E. Marschall) Population Biology Seminar Group in Department of EEOB, Ohio State University from 2001 to 2003

Established and organized Evolution, Ecology and Behavior Seminar Series in Biology Department, McMaster University from 1995 to 2000

Co-organized two local one day meetings on Molecular Ecology at Queen's University Biology Station in 1991and 1996

Grants Received (OSU – amounts in US$):

2014 Ohio Biodiversity Conservation Partnership. Ohio Division of Wildlife. H. L. Gibbs (PI and/or co-PI on individual components of proposal). 1 yr. $885,459.

2013 Award to organize a Catalysis Meeting on “Integrating Organismal and Applied Perspectives on Animal Venom Diversity” from the National Center for Evolution Synthesis (NESCent) located at Duke University in Durham NC. M. Daly and H. L. Gibbs (co-PIs). 1 yr, amount not specified.

2013 Ohio State University-FAPESP (Brazil) Collaborative Research Grant. Ohio State University. H.L. Gibbs and I. Azevedo (co-PIs). 2 yrs. $17,000.

2013 Ohio Biodiversity Conservation Partnership. Ohio Division of Wildlife. H. L. Gibbs (PI and/or co-PI on individual components of proposal). 1 yr. $737,317.

2012 Ohio Biodiversity Conservation Partnership. Ohio Division of Wildlife. H. L. Gibbs (PI and/or co-PI on individual components of proposal). 1 yr. $834, 720.

2011 Ohio Biodiversity Conservation Partnership. Ohio Division of Wildlife. H. L. Gibbs (PI and/or co-PI on individual components of proposal). 1 yr. $981,707.

2011 Ohio Biodiversity Conservation Partnership. Ohio Division of Wildlife. H. L. Gibbs (PI and/or co-PI on individual components of proposal). 1 yr. $591,284.

2011 NIH-MCEIRS. Host, agent, and environmental factors influencing the presence, persistence and diversity of low-pathogenic influenza A virus in migratory waterfowl. R. Slemons (PI), H.L. Gibbs (Co-PI), 1 yr, $806,017.

2010 Columbus Zoo-Ohio State University. Conservation genetics, habitat modeling and venomics of an endangered tropical snake. H. L. Gibbs (PI) and D. Salazar (co-PI). 1 yr.. $10,000.

2009 Ohio Department of Natural Resources; “Genetics as a tool for the conservation of state-listed species in Ohio”; 2 yr.; $190,309.

2008 NIH-MCEIRS. Strategically Increase the Breadth and Depth of the MCEIRS Influenza A Virus Research Network: Swine flu surveillance. R. Slemons (PI), W. Gebreyes (Co-PI), H.L. Gibbs (Co-PI), 3 yr, $168, 657.

2008 NIH-MCEIRS. Strategically Increase the Breadth and Depth of the MCEIRS Influenza A Virus Research Network in Wild Birds. R. Slemons (PI), H.L. Gibbs (Co-PI), 3 yr, $806,017.

2008 NIH-MCEIRS. Strategically Increase the Breadth and Depth of the MCEIRS Influenza A Virus Research Network in Wild Birds (AIV Reservoir Project). R. Slemons (PI), H.L. Gibbs (Co-PI), 3 yr, $211, 003.

2007 Ohio Department of Natural Resources; “Genetics as a tool for the conservation of state-listed species and to identify management strategies for urban wildlife in Ohio”; 2 yr.; $200, 058.

2005 Ohio Department of Natural Resources; “Conservation genetics of Ohio populations of eastern massasauga rattlesnakes” 3 yrs; $127, 006.

2004 National Science Foundation (USA) – Integrated Behavior and Neurosciences Panel; “Evolution of Animal Cultures”; Co-PI with D. Nelson (Primary PI – D. Nelson); 5 yrs.; $439,000.

2004 Columbus Zoo/Ohio State University; “Gene flow and habitat connectivity in salamanders”; Co-PI with T. Waite and K. Greenwald (Primary PI – H.L. Gibbs); 2 yrs.; $15,000.

2003 Ohio Department of Natural Resources; “Genetic analyses to determine the racial composition of Canada Geese Harvested in Ohio”; 5 yrs.; $483, 084.

2003 Hillsdale Foundation; “North American Bird Conservation”. ; $25,000

2003 Columbus Zoo/Ohio State University; “Evolution of venom genes and proteins in massasauga rattlesnakes”; 1 yr.; $5,145.

2002 Columbus Zoo/Ohio State University; “Evolution of venom genes in massasauga rattlesnakes”; 1 yr.; $10,000.

Grants Received (McMaster – amounts in CDN$):

2000 Environment Canada; “Songbird conservation genetics”; Co-PI with K. Hobson (Primary PI – H.L. Gibbs); 1 yr.; $28,000.

2000 Premier’s Research Excellence Award, Province of Ontario; “Evolution and conservation genetics of the wood warblers“; 3 yrs.; $150,000.

1999 Environment Canada; “Songbird conservation genetics”; Co-PI with K. Hobson (Primary PI – H.L. Gibbs); 1 yr.; $28,000.

1999 Environment Canada; “Snake conservation genetics”; Co-PI with P. Weatherhead, and K. Prior (Primary PI – P. Weatherhead); 1 yr.; $15,000.

1999 Natural Sciences and Engineering Research Council of Canada – Major Facilities Access Grant; “University of Manitoba Delta Marsh Field Station”; Co-PI with G. Goldsbourgh and 6 others (Primary PI - G. Goldsbourgh); 3 yrs.; $96,800.

1999 Natural Sciences and Engineering Research Council of Canada – Major Facilities Access Grant; “Queen’s University Biology Station”; Co-PI with R.J. Robertson and 8 others (Primary PI – R.J. Robertson); 3 yrs.; $165,300.

1998 Massachusetts Audubon Society; “Conservation genetics of grasshopper sparrows”; 3 yrs.; $60,500.

1998 Parks Canada; “Conservation genetics of black ratsnakes”; 1 yr.; $19,500.

1998 Arizona State University (sub-contract); “Conservation genetics of rattlesnakes”; 1 yr.; $20,000.

1998 University of Saskatchewan; “Songbird conservation genetics”; 1 yr.; $13,000.

1997 Natural Sciences and Engineering Research Council of Canada – Research Grant; “Evolutionary genetics of wild bird populations”; 4 yrs.; $145,200.

1996 Parks Canada; “Conservation genetics of black ratsnakes”; 1 yr.; $25,000.

1996 Parks Canada; “Rattlesnake conservation genetics”; 1 yr.; $18,500.

1996 Natural Sciences and Engineering Research Council of Canada – Major Facilities Access Grant; “University of Manitoba Delta Marsh Field Station”; Co-PI with G. Goldsbourgh and 6 others (Primary PI - G. Goldsbourgh); 3 yrs.; $75,000.

1996 Natural Sciences and Engineering Research Council of Canada – Major Facilities Access Grant; “Queen’s University Biology Station”; Co-PI with R.J. Robertson and 13 others (Primary PI – R.J. Robertson); 3 yrs.; $138,000.

1995 Natural Sciences and Engineering Research Council of Canada – Collaborative Research Grant; “DNA profiling of wildlife species”; Co-PI with P.T. Boag and 7 others (Primary PI – P.T. Boag); 3 yrs.; $324,000.

1995 Natural Sciences and Engineering Research Council of Canada – Research Grant; “Evolutionary and conservation genetics of vertebrates”; 2 yrs.; $58,800.

1995 Natural Sciences and Engineering Research Council of Canada – Equipment Grant; “DNA thermal cycler”; 1 yr.; $8,500.

1995 Parks Canada; “Snake conservation genetics”; 1 yr.; $26,400.

1995 Natural Sciences and Engineering Research Council of Canada – Equipment Grant; “Computer workstation”; Co-PI with G.B. Golding and 3 others (Primary PI –G.B. Golding); 1 yr.; $35,000.

1994 Environment Canada; “Conservation genetics of songbird populations”; Co-PI with K. Hobson (Primary PI – H.L. Gibbs); 3 yrs.; $192,000.

1994 Natural Sciences and Engineering Research Council of Canada – Major Facilities Access Grant; “University of Manitoba Delta Marsh Field Station”; Co-PI with G. Robinson and 8 others (Primary PI - G. Robinson); 1 yr.; $25,000.

1993 Max Bell Foundation; “Delineation of Neotropical songbird populations”; Co-PI with K. Hobson (Primary PI – H.L. Gibbs); 3 yrs.; $100,000.

1992 Parks Canada/Carleton University (sub-contract); “Snake conservation genetics”; 1 yr.; $20,000.

1992 Natural Sciences and Engineering Research Council of Canada – Research Grant; “Molecular and evolutionary genetics of brood parasitic birds”; 3 yrs.; $112,500.

1992 Natural Sciences and Engineering Research Council of Canada – Equipment Grant; “DNA thermal cycler and ultracold freezer”; 1 yr.; $21,600.

Peer-Reviewed Publications

2015 Fries, A.C., Nolting, J.M., Bowman, A.S., Lin, X., Halpin, R.A., Wester, E., Fedorova, N., Stockwell, T.B., Das, S., Dugan, V.G., Wentworth, D.E., Gibbs, H.L., Slemons, R.D. The spread and persistence of influenza A viruses in waterfowl hosts in the North American Mississippi Migratory Flyway*. Journal of Virology* (accepted).

2015 Sovic, M.G., Fries, A.C., Gibbs, H.L. AftrRAD: A pipeline for accurate and efficient de novo assembly of RADseq data. *Molecular Ecology Resources* (in press).

2014 Denton, RD, HL Gibbs, and TC Glenn. Development of 31 new microsatellite loci for two mole salamanders (*Ambystoma laterale* and *A. jeffersonianum*). *Conservation Genetics Resources.* DOI: 10.1007/s12686-014-0320-7.

2014 Camargo, C, C Mariellen, C Costa, GC Del Rio, HL Gibbs, TC Glenn, U Bagal, LF Silveira, AP Wasko and MR Francisco. Novel and cross-amplified microsatellite loci for the critically endangered Sao Paulo marsh antwren *Formicivora paludicola* (Aves: Thamnophilidae). *Conservation Genetics Resources*. DOI 10.1007/s12686-014-0310-9.

2014 Salazar-Valenzuela, D., Mora-Obando, D., Fernández, M. L., Loaiza-Lange, A., Gibbs. H. L., and Lomonte, B. 2014. Proteomic and toxicological profiling of the venom of *Bothrocophias campbelli*, a pitviper species from Ecuador and Colombia. *Toxicon* 90: 15-25.

2014 Denton, RD, LJ Kenyon, KR Greenwald, and HL Gibbs. Evolutionary basis of mitonuclear discordance between sister species of mole salamanders (*Ambystoma sp.*). *Molecular Ecology* 23: 2811-2824.

2014 Lamonte, B, W-C Tsai, J.M. Ureña, L. Sanz, D. Mora-Obando, E. E. Sanchez, B. G. Fry, J.M. Gutiérrez, H.L. Gibbs, M.G. Sovic, J.J. Calvete. Venomics of New World pit vipers: Genus-wide comparisons of venom proteomes across *Agkistrodon*. *Journal of Proteomics* 96: 103-116.

2013 Gibbs, H.L., L. Sanz, M.G. Sovic, and J.J. Calvete. Phylogeny-based comparative analysis of venom proteome variation in a clade of rattlesnakes (*Sistrurus sp*.). *PLoS ONE* 8: e67220.

2012 Munafo, K. M. and H. L. Gibbs. Lack of stable-isotope differences between Canada Goose populations nesting in the subarctic and temperate zones. *Condor* 114: 491-499.

2012 Gibbs, H.L. and J.E. Chiucchi. Inbreeding, body condition, and heterozygosity-fitness correlations in isolated populations of the endangered eastern massasauga rattlesnake (*Sistrurus c. catenatus*). *Conservation Genetics* 13: 1133 – 1143.

2012 Poesel, A., D.A. Nelson, and H.L. Gibbs. Song sharing correlates with social but not extra-pair mating success in the white-crowned sparrow. *Behavioral Ecology* 23: 627-634.

2012 Wooten, J.A. and H.L. Gibbs. Niche divergence and lineage diversification among closely-related *Sistrurus* rattlesnakes. *Journal of Evolutionary Biology* 25: 317-328.

2012 Greenwald, K.R. and H.L. Gibbs. A single nucleotide polymorphism assay for the identification of polyploid unisexual *Ambystoma* salamanders*. Molecular Ecology Resources* 12: 354-362.

2011 Gerard, D., H.L. Gibbs, and L.S. Kubatko. Estimating hybridization in the presence of coalescence using phylogenetic intraspecific sampling. *BMC Evolutionary Biology* 11: 291.

2011 Poesel A., H.L. Gibbs, and D.A. Nelson. Extrapair fertilizations and the potential for sexual selection in a socially monogamous songbird. *Auk* 128: 770-776.

2011 Gibbs, H.L., L. Sanz, J.E. Chiucchi, T.M. Farrell, J.J. Calvete. Proteomic analysis of ontogenetic and diet-related changes in venom composition of juvenile and adult Dusky Pigmy rattlesnakes (*Sistrurus miliarius barbouri*). *Journal of Proteomics* 74: 2169-2179.

2011 Gibbs, H.L. and J.E. Chiucchi. Deconstructing a complex molecular phenotype: population- level variation in individual venom proteins in eastern massasauga rattlesnakes (*Sistrurus c. catenatus*). *Journal of Molecular Evolution* 72: 383-397.

2011 Kubatko, L.S., H.L. Gibbs, and E.W. Bloomquist. Inferring species-level phylogenies and taxonomic distinctiveness using multilocus data in *Sistrurus* rattlesnakes. *Systematic Biolog*y 60: 393-409.

2011 Gibbs, H.L., M. Murphy, J.E. Chiucchi. Genetic identity of endangered massasauga rattlesnakes (*Sistrurus sp.*) in Missouri. *Conservation Genetics* 12: 433-439.

2010 Kubatko L. S. and H. L. Gibbs. Estimating species relationships and taxon distinctiveness in *Sistrurus* rattlesnakes using multilocus data (Chapter 12, pgs. 193-207). In *Estimating Species Trees: Practical and Theoretical Aspects*, edited by L. L. Knowles and L. S. Kubatko, Wiley-Blackwell.

2010 Chiucchi, J. E. and H. L. Gibbs. Similarity of contemporary and historical gene flow among highly fragmented populations of an endangered rattlesnake. *Molecular Ecology* 19: 5345-58.

2010 Anderson, C.S., Gibbs, H.L, and J. Chiucchi. Nineteen polymorphic microsatellite loci isolated from the Eastern Massasauga Rattlesnake, *Sistrurus c. catenatus*. *Conservation Genetics Resources* 2: 243-245.

2010 Gibbs, H.L. and Diaz, J. Identification of single copy nuclear DNA markers for North American pit vipers. *Molecular Ecology Notes* 10: 177-180.

2009 Anderson, C.D., Gibbs, H.L., Douglas, M.E., Holycross, A.T. Conservation genetics of the Desert massasauga rattlesnake (*Sistrurus catenatus edwardsii*). *Copeia* 2009: 740–747.

2009 Greenwald, K.R., Gibbs, H.L., Waite, T.A. Simple land cover models reliably predict isolation of salamanders in a fragmented landscape. *Conservation Biology* 23:1231-1243.

2009 Tieleman, B.I., Versteegh, M.A., Fries, A., Helm, B., Dingemanse, N.J., Gibbs, H.L., Williams, J.B. Genetic modulation of energy metabolism in birds through mitochondrial function. *Proceedings Royal Society of London, Series B*. 276: 1685-1693

2009 Gibbs, H.L. and Mackessy, S.P. Functional basis of a molecular adaptation: prey-specific toxic effects of venom from *Sistrurus* rattlesnakes. Toxicon 53: 672-679.

2009 Weatherhead, P.J. Knox, J.M., Harvey, D.S., Wynn, D., Chiucchi, J., Gibbs, H.L. Diet of *Sistrurus catenatus* in Ontario and Ohio: effects of body size and habitat. *Journal of Herpetology* 43: 693–697.

2009 Gibbs, H. L. Sanz, L. and Calvete, J.J. Snake population venomics: Proteomics-based analyses of individual variation reveals gene regulation effects on venom protein expression in *Sistrurus* rattlesnakes. *Journal of Molecular Evolution* 68: 113-125.

2009 Poesel, A., Gibbs H.L, Nelson, D.A. Twenty-one novel microsatellite DNA loci isolated from the Puget Sound white-crowned sparrow *Zonotrichia leucophrys pugetensis*. *Molecular Ecology Resources* 9:795-798

2009 Francisco, M.R., Gibbs H.L., P. M. Galetti, Jr. Patterns of individual relatedness at blue manakin (*Chiroxiphia caudata*) leks*. Auk* 126:47-53.

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2008 Colbeck G.J., Gibbs H.L., Marra P.P., Hobson K.A., Webster, M. Phylogeography of a widespread North American migratory songbird (*Setophaga ruticilla*). *Journal of Heredity* 99: 453-463

2008 Mylecraine, K.A., Gibbs H.L., Anderson C.S., Shieldcastle M.C. 2008. Using 2 genetic markers to discriminate among Canada goose populations in Ohio. Journal of Wildlife Management 72: 1220-1230.

2008 Durrant K.L., Marra P.P., Fallon S.M., Colbeck G.J., Gibbs H.L., Hobson K.A., D. Ryan Norris D.R., Bernik, B., Lloyd, V.L. and Fleischer, R.C. Parasite assemblages distinguish populations of a migratory passerine on its breeding grounds**.** *Journal of Zoology* 274**:** 318-326.

2008 Moksnes A., Røskaft E., Rudolfsen E.G., Skjelseth S, Stokke B.G., Kleven O., Gibbs H.L., Honza M., Taborsky B, Teuschl Y., Vogl W., Taborsky M. Individual female common cuckoos Cuculus canorus lay constant egg types but egg appearance cannot be used to assign eggs to females. *Journal of Avian Biology* 39:238-241.

2007 Francisco, M.R., H. L. Gibbs, M. Galetti, V.O. Lunardi and P. M. Galetti, Jr. Genetic structure in a tropical lek-breeding bird, the blue manakin (*Chiroxiphia caudata*) in Brazilian Atlantic Forest. *Molecular Ecology* 16: 4908-4918.

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2006 Boulet, M., Gibbs, H.L., Hobson, K.A. Integrated analysis of genetic, stable isotope, and banding data reveal migratory connectivity and flyways in the Northern Yellow Warbler (*Dendroica petechia; aestiva* group). *Ornithological Monographs* 48:29-78.

2006 Sanz L., Gibbs H.L., Mackessy S.P., Calvete, J. Venom proteomes of closely related Sistrurus rattlesnakes with divergent diets. *Journal of Proteome Research* 5: 2098-2112.

2006 Gibbs H.L., Corey S.J., Blouin-Demers G., Prior, K.A., Weatherhead, P.J. Hybridization between mtDNA-defined phylogeographic lineages of black ratsnakes (*Pantherophis sp*.). *Molecular Ecology* 15: 3755-3767.

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2005 Weatherhead, P.J., K. Kissner, and H.L. Gibbs. Experimental assessment of ecological and phenotypic factors affecting male mating success and polyandry in northern watersnakes, *Nerodia sipedon*. *Behavioral Ecology and Sociobiology* 59: 207-214.

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2005 Schriver, W.G., J.P. Gibbs, P. Vickery, H.L. Gibbs, T. Hodgman, P.T. Jones, and C. Jacques. Concordence between morphological and molecular markers in assessing hybridization between Sharp-tailed Sparrows in New England. *Auk* 122:94-107.

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2004 Francisco, M.R., P.M. Galetti Jr., and H. L. Gibbs. Isolation and characterization of microsatellite loci in the Blue manakin, *Chiroxiphia caudata* (Aves, Pipridae). *Molecular Ecology Notes* 4:758-760.

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2003 Smith, T.B., P. Marra, M.S. Webster, I. Lovette, H.L. Gibbs, R.T. Holmes, K.A. Hobson, and S. Rohwer. A call for feather sampling. *Auk*. 120:218-221.

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2000 Milot, E., H.L. Gibbs, and K.A. Hobson. Phylogeography and genetic structure of northern populations of the yellow warbler (*Dendroica petechia*). *Molecular Ecology* 9:667-682.

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1998 Marchetti, K., H. Nakamura, and H.L. Gibbs. Host race formation in the Common Cuckoo. *Science* 282:471-472.

1998 Gibbs, H.L., L. DeSousa, K. Marchetti and H. Nakamura. Isolation and characterization of microsatellite DNA loci for an obligate brood parasitic bird, the common cuckoo (*Cuculus canorus*). *Molecular Ecology* 7: 1437-1439.

1998 Price, T.D., H.L. Gibbs, L. De Sousa, and A. Richman. Different timings of the adaptive radiations of North American and Asian warblers. *Proceedings of Royal Society of London, Series B* 265:1969-1975.

1998 Gibbs, H.L., K. A. Prior, and C. Parent. Characterization of DNA microsatellite loci from a threatened snake, the eastern massasauga rattlesnake and their use in population studies. *Journal of Heredity* 89:169-173.

1997 Gibbs, H.L., K. Prior, P.J. Weatherhead and G. Johnnson. Genetic structure of populations of the threatened eastern massasauga rattlesnake, *Sistrurus c. catenatus*: evidence from microsatellite DNA markers. Molecular Ecology 6:1123-1132.

1997 Hobson, K.A., H.L. Gibbs, and M.L. Gloutney. Preservation of blood and tissue samples for stable-carbon and nitrogen isotope analysis. *Can. J. Zool*. 75:1720-1723

1997 Dawson, R., H.L. Gibbs, K.A. Hobson, and S. Yezerinac. Isolation of microsatellite DNA markers from a passerine bird, the Yellow Warbler. *Heredity* 79:506-514.

1997 Prior, K.A., H.L. Gibbs, and P.J. Weatherhead. Population genetic structure in a threatened snake: biological and management implications. *Conservation Biology* 11:1147-1158.

1997 Jones, D. A. and H.L. Gibbs. Inter- and intraspecific variation in a portion of the mitochondrial ND6 gene in cuckoos. *Condor* 99:815-818.

1997 Gibbs, H.L., P. Miller, G. Alderson, and S.G. Sealy. Genetic analysis of putative host races in the Brown-headed Cowbird: Evidence from mitochondrial and microsatellite DNA markers. *Molecular Ecology* 6:189-193.

1997 Jones, D.J., H.L. Gibbs, T. Matsuda, M. Brooke, H. Uchida, and M. Bayliss. The use of DNA fingerprinting to determine the possible mating system of an obligate brood parasite, the Common Cuckoo. *Ibis* 139:560-562.

1996 Gibbs, H.L., M. Brooke, and N.B. Davies. Analysis of genetic differentiation of host races of the common cuckoo *Cuculus canorus* using mitochondrial and microsatellite DNA variation. *Proceedings of the Royal Society of London, Series B* 263:89-96.

1994 Weatherhead, P.J., R.D. Montgomerie, H.L. Gibbs and P.T. Boag. The cost of extra-pair fertilizations to female Red-winged Blackbirds. *Proceedings of the Royal Society of London, Series B*. 258: 315-320.

1994 Gibbs, H.L., A.W. Goldizen, C. Bullough and A.R. Goldizen. Parentage analysis of multi-male social groups of Tasmanian Native Hens: Genetic evidence for monogamy and polyandry. *Behavioural Ecology and Sociobiology* 35: 363-371.

1994 Gibbs, H.L., K.A. Prior and P.J. Weatherhead. Genetic analysis of threatened snake species using RAPD markers. *Molecular Ecology* 3: 329-337.

1993 Gowaty, P. and H.L. Gibbs. DNA fingerprinting and behavioural ecology: two cultures arise. *Auk* 110: 252-255.

1991 Gibbs, H.L., P.T. Boag, P.J. Weatherhead, B.N. White and L.M. Tabak. Detection of a hypervariable DNA locus in birds by hybridization with a mouse MHC probe. *Molecular Biology and Evolution* 8: 433-446.

1991 Galbraith, D.A., P.T. Boag, H.L. Gibbs and B.N. White. Sizing bands on autoradiographs: A study of precision for scoring DNA fingerprints. *Electrophoresis* 12: 210-220.

1990 Gibbs, H.L., P.J. Weatherhead, P.T. Boag, B.N. White, L.M. Tabak and D.J. Hoysak. Realized reproductive success of polygynous Red-winged Blackbirds revealed by DNA markers. *Science* 250: 1394-1397.

1990 Gibbs, H.L. Cultural evolution of male song types in Darwin's Medium Ground Finches (*Geospiza fortis*). *Animal Behaviour* 39: 253-263.

1989 Gibbs, H.L. and P.R. Grant. Inbreeding in Darwin's Medium Ground Finches. *Evolution* 43: 1273-1284.

1988 Gibbs, H.L. Heritability and selection on clutch size in Darwin's Medium Ground Finches. *Evolution* 42: 750-762.

1987 Gibbs, H.L. and P.R. Grant. Oscillating selection on Darwin's Finches. *Nature* 327: 511-513.

1987 Gibbs, H.L. and P.R. Grant. Ecological consequences of an exceptionally strong El Nino event on Darwin's Finches. *Ecology* 68:1735-1746.

1987 Gibbs, H.L. and P.R. Grant. Adult survivorship in Darwin's Ground Finch populations in a variable environment. *Journal of Animal Ecology* 56: 797-814.

1987 Gibbs, H.L., S.C. Latta and J.P. Gibbs. Effects of the 1982-83 El Nino event on Blue-footed and Masked Booby populations on Isla Daphne Major, Galapagos. *Condor* 89: 440-442.

1987 Price, T.D. and H.L. Gibbs. Brood division in Darwin's Finches. *Animal Behaviour* 35: 299-301.

1987 Gibbs, H.L. and J.P. Gibbs. Prey robbery by nonbreeding Magnificent Frigatebirds (*Fregata magnificens*). *Wilson Bulletin* 99: 101-104.

1986 Robertson, R.J., H.L. Gibbs, and B.J. Stuchbury. Spitefulness, altruism, and the cost of aggression: Evidence against superterritoriality in Tree Swallows. *Condor* 88: 104-105.

1985 Muldal, A., H.L. Gibbs, and R.J. Robertson. Preferred nest spacing of an obligate cavity-nesting birds, the Tree Swallow (*Tachycineta bicolor*). *Condor* 87: 356-363.

1984 Gibbs, H.L., P.R. Grant, and J. Weiland. Breeding of Darwin's Finches at an unusually early age in an El Nino year. *Auk* 101: 872-874.

1984 Price, T.D., P.R. Grant, H.L. Gibbs and P.T. Boag. Recurrent patterns of natural selection in a population of Darwin's Finches. *Nature* 309: 787-789.

1982 Robertson, R.J. and H.L. Gibbs. Superterritoriality in Tree Swallows: A re-examination. *Condor* 84: 313-316.

Published Abstracts

1991 Gibbs, H.L., L.M. Tabak, P.J. Weatherhead, P.T. Boag, B.N. White, and D.J. Hoysak. Realized reproductive success in polygynous Red-winged Blackbirds revealed by DNA fingerprinting. *Journal of Canadian Forensic Science* 23:127.

1989 Gibbs, H.L., P.T. Boag, Y. Plante, and B.N. White. Parentage analysis in birds and mammals using murine MHC probes. *Journal of Cellular Biochemistry* 13C:118.

Invited Presentations (* presentor)

2015 Gibbs, H.L. Rare snakes that rattle: Conservation genetics of Massasauga Rattlesnakes. Invited talk, Department of Biology, Case Western Reserve University.

2014 Gibbs, H.L. Rare snakes that rattle: Conservation genetics of Ohio Rattlesnakes. Invited talk for 3rd Annual Meeting of the Ohio Biodiversity Conservation Partnership, Ohio State University, Columbus, Ohio.

2013 Sovic, M.G.* and H.L. Gibbs. RAD Sequencing: Data generation and analysis. Workshop on “Next Generation Genomics Sequencing (NGGS) Techniques: Applications to Venomous Snakes”, Instituto Butantan, Sao Paulo, Brazil.

2013 Gibbs, H.L.* and M.G. Sovic. RAD Sequencing: Applications to *Sistrurus* and *Bothrops*. Workshop on “Next Generation Genomics Sequencing (NGGS) Techniques: Applications to Venomous Snakes”, Instituto Butantan, Sao Paulo, Brazil.

2013 Gibbs, H.L. Phylogeny-based comparative analysis of venom proteome variation among New World pitvipers. 4th Symposium of the Post-Graduate Program in Toxionology of the Butantan Institute, Sao Paulo, Brazil.

2013 Gibbs, H.L.*, L. Sanz, M. Sovic, and J. Calvete. Phylogeny-based comparative analysis of venom proteome variation in a clade of rattlesnakes (*Sistrurus sp*.). 11th Congress of the Pan-America Section of the International Society on Toxinology and 12th Congress of the Brazilian Society of Toxinology, Guaruja, Brazil.

2012 Gibbs, H.L. Beak of the snake: Evolution of venom proteins in *Sistrurus* rattlesnakes. Invited Talk, Federal University of Western Pará, Santarem, Brazil.

2012 Gibbs, H.L. Beak of the snake: Evolution of venom proteins in *Sistrurus* rattlesnakes. Invited Talk, Instituto Butantan, São Paulo, Brazil.

2012 *Greenwald, K, and H.L. Gibbs. Abundance, distribution, and habitat associations of unisexual mole salamanders (*Ambystoma*) in Ohio. Ohio Amphibian Research and Conservation Conference. Columbus, Ohio.

2012 *Gibbs, H.L., D. Gerard, and L.S. Kubatko. Multilocus analyses of species relationships and hybridization in *Sistrurus* rattlesnakes. Invited talk for Workshop on Estimating Species Trees: A Phylogenetic Paradigm for the 21st Century, Ohio State University, Columbus, Ohio.

2011 Gibbs, H.L. Deconstructing a complex molecular phenotype: snake venom proteins. Keynote Invited Speaker, 17th Congress of the European Section of the International Society on Toxinology, Valencia, Spain.

2011 Gibbs, H.L. Rare snakes that rattle: conservation genetics of the eastern massasauga rattlesnake (*Sistrurus c. catenatus*). Department of Biology, Kenyon College, Gambier, Ohio.

2011 Gibbs, H.L. Integrating genetics as a tool for managing biodiversity: examples from Ohio's snakes and salamanders. Ohio Wildlife Diversity Conference, Columbus, Ohio.

2011 Gibbs, H.L. Rare snakes that rattle: conservation genetics of the eastern massasauga rattlesnake (*Sistrurus c. catenatus*). Department of Biology, Wright State University, Dayton, Ohio.

2010 Gibbs, H.L. Rare snakes that rattle: conservation genetics of the eastern massasauga rattlesnake (*Sistrurus c. catenatus*). Science Seminar Series, Ohio Weslayan University, Delaware, Ohio.

2010 Chiucchi, J.E.* and H. L. Gibbs. Conservation genetics of the eastern massasauga rattlesnake. Ohio Reptile Conservation Meeting, Columbus, Ohio.

2010 Gibbs, H. L. Deconstructing a complex molecular phenotype: population-level variation in individual venom proteins in eastern massasauga rattlesnakes (*Sistrurus. c. catenatus*). Instituto Biomedicina de Valencia – CSIC, Valencia, Spain.

2010 Gibbs, H.L.* and J.E. Chiucchi. Conservation genetics of the eastern massasauga rattlesnake. Invited presentation to Ohio Division of Wildlife Field Site Managers, Killdeer Plains Wildlife Area, Inkster, Ohio.

2010 Gibbs, H.L.*, and Chiucchi, J. Deconstructing a complex molecular phenotype: Population-level variation in individual venom proteins in eastern massasauga rattlesnakes (*Sistrurus. c. catenatus*). Keynote Invited Speaker for Biology of the Vipers- 3rd Conference, Calci (Pisa), Italy.

2010 Gibbs, H.L. Venom evolution and ecology in *Sistrurus* rattlesnakes. Department of Biology, University of Dayton, Dayton, Ohio.

2009 Gibbs, H.L.* and L. Kubatko. Species trees and speciation history in *Sistrurus* rattlesnakes inferred from multilocus data. Invited talk for Workshop on Estimating Species Trees: A Phylogenetic Paradigm for the 21st Century, University of Michigan, Ann Arbor, Michigan.

2007 Gibbs, H.L. DNA-based Tales of Scales and Feathers: Genetic structure of a lek-breeding tropical bird and venom gene evolution in *Sistrurus* rattlesnakes. Invited Talk, Natural History Museum, University of Oslo, Norway.

2007 Gibbs, H.L. DNA-based Tales of Scales and Feathers: Genetic structure of a lek-breeding tropical bird and venom gene evolution in *Sistrurus* rattlesnakes. Invited Talk, Department of Biology, University of Trondheim (NTNU), Norway.

2006 Gibbs, H.L. Beak of the snake: Evolution of venom proteins in *Sistrurus* rattlesnakes. Invited Talk, Instituto de Biomedicina de Valencia, Valencia, Spain.

2006 Gibbs, H.L. Bird conservation genetics. Invited Talk, Departamento de Ciências Biológicas, Universidade Federal de São Carlos at Sorocaba, Sao Paulo, Brazil.

2006 Gibbs, H.L. Beak of the snake: Evolution of venom proteins in *Sistrurus* rattlesnakes. Invited Talk, Departamento de Genética e Evolução, Universidade Federal de São Carlos, Sao Paulo, Brazil.

2006 Gibbs, H.L. Beak of the snake: venom variation in *Sistrurus* rattlesnakes. Invited talk, Ohio Reptile and Conservation Conference, Columbus, Ohio.

2005 Gibbs, H.L. Conservation genetics of endangered Florida Grasshopper sparrows. Invited talk, Department of EEB, University of Arizona.

2005 Gibbs, H.L. Topics in Conservation Genetics. Invited Lectures, Departamento de Genética e Evolução, Universidade Federal de São Carlos, Sao Paulo, Brazil.

2005 Gibbs, H.L. Beak of the Snake: Evolution of venom proteins in *Sistrurus* rattlesnakes. Invited talk for Grantfest – Celebration of the Research of Peter and Rosemary Grant, University of British Columbia, Vancouver, BC.

2004 Gibbs, H.L. Bird conservation genetics. School of Natural Resources, Ohio State University.

2004 Gibbs, H.L. Host race evolution in a brood parasitic bird, the common cuckoo (*Cuculus canorus*). Invited talk, Department of Biology, Kenyon College.

2003 Gibbs, H.L. Host race evolution in a brood parasitic bird, the common cuckoo (*Cuculus canorus*). Invited talk, Department of Zoology, Miami University.

2003 Gibbs, H.L. Host race evolution in a brood parasitic bird, the common cuckoo (*Cuculus canorus*). Invited talk, Department of Biological Sciences, University of Cincinnati.

2003 Gibbs, H.L. Host race evolution in a brood parasitic bird, the common cuckoo (*Cuculus canorus*). Invited talk, Department of Life Sciences, Indiana State University.

2002 Gibbs, H.L. Co-leader for Roundtable on “Tools for Assessing Connectivity of Migratory Bird Populations”. Birds of Two Worlds Conference sponsored by the Smithsonian Institution, Shepardstown, WV.

2002 Gibbs, H.L. Host race evolution in a brood parasitic bird, the common cuckoo (*Cuculus canorus*). Invited talk, Department of Biology, University of Missouri at St. Louis.

2002 Gibbs, H.L. Host race evolution in a brood parasitic bird, the common cuckoo (*Cuculus canorus*). Invited talk, Department of Biology, Bowling Green State University.

2002 Gibbs, H.L. Host race evolution in a brood parasitic bird, the common cuckoo (*Cuculus canorus*). Invited talk, Department of Biological Sciences, Wright State University.

2002 Gibbs, H.L. Host race evolution in a brood parasitic bird, the common cuckoo (*Cuculus canorus*). Invited talk, Department of EEB, University of Arizona.

2001 Gibbs, H.L. Host race evolution in a brood parasitic bird, the common cuckoo (*Cuculus canorus*). Invited talk, Department of Zoology, University of Washington.

2001 Gibbs, H.L. Host race evolution in a brood parasitic bird, the common cuckoo (*Cuculus canorus*). Invited talk, Department of Biology, San Francisco State University.

2001 Gibbs, H.L. Host race evolution in a brood parasitic bird, the common cuckoo (*Cuculus canorus*). Invited talk, Department of Biology, University of Rochester.

2000 Gibbs, H.L.*, M. Boulet. and K. Hobson. Genetic structure of breeding populations of a migrant bird, the Yellow Warbler: Insights from mtDNA and microsatellite DNA. Invited Talk for NSF Biocomplexity Incubation Activity Meeting on “Connectivity of migratory populations and its consequences for population dynamics and microevolutionary processes”. Smithsonian Environmental Research Center, Edgewater, MD.

2000 Gibbs, H. L.* and P.J. Weatherhead. Sex and serpents: parentage and kinship studies in snakes using DNA markers. Invited Talk for the American Genetics Association Presidential Symposium on “Genetic Parentage, Mating Systems and Behavioral Ecology of Poikilothermic Vertebrates”, AGA Annual Meeting, Yale University, New Haven, CT.

2000 Gibbs, H. L.* and P.J. Weatherhead. Population structure in snakes determined using DNA markers. Invited Talk for Snake Ecology Group Annual Meeting, University of Arkansas, Fayetteville, AR.

2000 Gibbs, H.L. Host race evolution in a brood parasitic bird, the common cuckoo (*Cuculus canorus*). Invited talk, Department of EEOB, Ohio State University.

2000 Gibbs, H.L. Host race evolution in a brood parasitic bird, the common cuckoo (*Cuculus canorus*). Invited talk, Department of Biology Sciences, Brock University, University.

1999 Gibbs, H.L. Host race evolution in a brood parasitic bird, the common cuckoo (*Cuculus canorus*). Invited talk, Department of EEOB, Ohio State University.

1999 Gibbs, H.L. Host race evolution in a brood parasitic bird, the common cuckoo (*Cuculus canorus*). Invited talk, Department of Zoology, University of Toronto.

1998 Gibbs, H.L. Interpreting genetic data for population management of the eastern massasauga rattlesnake. 2nd International Symposium on the Conservation of the Eastern Massasauga Rattlesnake, Metro Toronto Zoo, Toronto, ON.

1998 Gibbs, H.L. Eastern massasauga rattlesnake population genetics: Implications for conservation and management. Conference on “Managing Human-Rattlesnake Interactions”, Killbear Provincial Park, Parry Sound, ON.

1996 Gibbs, H.L. DNA-based studies of wild animal populations. Invited talk, Department of Zoology, University of Western Ontario.

1996 Gibbs, H.L. DNA-based studies of wild animal populations. Invited talk, Department of Zoology, University of Guelph.

1995 Gibbs, H.L. Conservation genetics of migrant birds and snakes. H.R. Macmillan Invited Lecture in Conservation Biology. Faculty of Forestry, University of British Columbia.

1995 Gibbs, H.L. Of Cuckoos and conservation: DNA studies of wild bird and snake populations. Invited talk, Department of Zoology, University of British Columbia.

1995 Gibbs, H.L. Of Cuckoos and conservation: DNA studies of wild bird and snake populations. Invited talk, Department of Biological Sciences, Simon Fraser University.

1995 Gibbs, H.L. DNA-based studies of wild bird populations. Invited talk, Department of Biology, Queen’s University.

1994 Gibbs, H.L. DNA-based studies of wild bird populations. Invited talk, Department of Biology, York University.

1992 Gibbs, H.L. Sex, lies and autoradiographs: Parentage analyses in Red-Winged Blackbirds using DNA markers. Invited talk, Department of Zoology, University of Toronto.

1991 Gibbs, H.L. Genetic analysis of host races in the Common Cuckoo. Invited talk for Symposia on Molecular Genetics and Social Behaviour of Birds and Co-evolution and Brood Parasitism in Birds, 22nd International Ethological Conference, Kyoto, Japan.

1991 Gibbs, H.L. Behavioural ecologists' expectations versus what DNA fingerprinters can deliver. Roundtable on Use of DNA Technology in Behavioural Studies, 22nd International Ethological Conference, Kyoto, Japan.

1991 Gibbs, H.L. Sex, lies and autoradiographs: Parentage analyses in Red-Winged Blackbirds using DNA markers. Invited talk in a symposium for ASN Young Investigator Prize Winners, Joint Meeting of the Society for the Study of Evolution and the American Society of Naturalists, Hilo, Hawaii.

1991 Gibbs, H.L. Sex, lies and autoradiographs: Parentage analyses in Red-Winged Blackbirds using DNA markers. Invited talk, Department of Biology, Concordia University.

1991 Gibbs, H.L. Sex, lies and autoradiographs: Parentage analyses in Red-Winged Blackbirds using DNA markers. Invited talk, Canadian Wildlife Service, Ottawa.

1991 Gibbs, H.L. Sex, lies and autoradiographs: Parentage analyses in Red-Winged Blackbirds using DNA markers. Invited talk, Department of Zoology, University of New Hampshire.

1991 Gibbs, H.L. Sex, lies and autoradiographs: Parentage analyses in Red-Winged Blackbirds using DNA markers. Invited talk, Department of Biology, McMaster University.

1990 Gibbs, H.L. Sex, lies and autoradiographs: Parentage analyses in Red-Winged Blackbirds using DNA markers. Invited talk, Department of Ecology, Evolution and Marine Biololgy, University of California at Santa Barbara

1990 Gibbs, H.L. Sex, lies and autoradiographs: Parentage analyses in Red-Winged Blackbirds using DNA markers. Invited talk, Department of Biology, University of Ottawa.

1990 Gibbs, H.L. Sex, lies and autoradiographs: Parentage analyses in Red-Winged Blackbirds using DNA markers. Invited talk, Department of Zoology, University of Tasmania.

1990 Gibbs, H.L. Sex, lies and autoradiographs: Parentage analyses in Red-Winged Blackbirds using DNA markers. Invited talk, Department of Biology, Carleton University.

1990 Gibbs, H.L. Sex, lies and autoradiographs: Parentage analyses in Red-Winged Blackbirds using DNA markers. Invited talk, Division of Biological Sciences, University of California at San Diego.

1988 Gibbs, H.L. Oscillating selection in Darwin’s Finches. Invited talk, Division of Biological Sciences, University of California at San Diego.

1986 Hall, G.A.*, H.L. Gibbs, P.R. Grant, L.W. Botsford, and G.S. Butcher. Effects of the El Nino Southern Oscillation on terrestrial birds. Invited talk in a symposium on Birds and the El Nino Southern Oscillation, XIX International Ornithological Congress, Ottawa.

1986 Gibbs, H.L. Adult survivorship in Darwin’s Finches. Invited talk, Department of Zoology, Oxford University.

1985 Gibbs, H.L. Adult survivorship in Darwin’s Finches. Invited talk, Department of Wildlife, University of Maine.

(b) Contributed Papers/Posters at Professional Meetings (* denotes presentor)

2014 Fries, AC. *, Nolting, J.M., Bowman, A.S., Gibbs, H.L., Slemons, R.D. The movement and persistence of avian-origin influenza A viruses in the Mississippi Migratory Flyway. Great Lakes Partners Forum: Waterfowl and Wetlands Research. Winous Point Marsh Conservancy, Port Clinton, OH, USA.

2014 Fries, AC. *, Nolting, J.M., Bowman, A.S., Gibbs, H.L., Slemons, R.D. The movement and persistence of avian-origin influenza A viruses in the Mississippi Migratory Flyway. Advances in Veterinary Medicine. College of Veterinary Medicine, The Ohio State University, Columbus, OH, USA.

2014 Pham, M.T. *, Fries. A.C., Gibbs, H.L. Lack of genetic structure in northwestern Ohio mallards commonly infected by influenza A virus. The Natural and Mathematical Sciences (NMS) Undergraduate Research Forum. The Ohio State University, Columbus, OH, USA.

2014 Fries, A.C *., Nolting, J.M., Bowman, A.S., Gibbs, H.L., Slemons, R.D. The movement and persistence of avian-origin influenza A viruses in the Mississippi Migratory Flyway. Multinational Influenza Seasonal Mortality Study (MISMS). NIH – Fogarty International Center, Washington, D.C.

2014 Sovic, M.G. *, Fries, A.C, Gibbs, H.L. Genomic scale phylogeographic analysis of the endangered eastern massasauga rattlesnake (*Sistrurus catenatus*). Evolution 2014, Raleigh, NC, USA.

2014 Sovic, M.G. *, Fries, A.C, Gibbs, H.L. Phylogeographic analysis using genomic-scale data of the endangered eastern massasauga (*Sistrurus catenatus*) rattlesnake. Biology of the Pitvipers 2, Tulsa, OK, USA.

2014 Salazar-Valenzuela, D.*, Mora-Obando, D., Fernández, M. L., Loaiza-Lange, A., Gibbs. H. L., and Lomonte, B. Proteomic analysis of the venom of the Ecuadorian toadheaded pitviper, *Bothrocophias campbelli*. Poster presented at the Biology of the Pitvipers 2, Tulsa, Oklahoma, USA

2014 Holding, M.L*., Gibbs, H.L., Biardi, J.E. 2014. Testing for Local Adaptation of Pitviper Venoms to Resistant Prey: Interactions between Northern Pacific Rattlesnakes and California Ground Squirrels. The Biology of the Pitvipers 2, Tulsa, OK.

2014 Denton, RD and HL Gibbs. Sexuality on the move: Dispersal of sexual and unisexual mole salamanders (Ambystoma) across a fragmented landscape. Joint Meeting of Ichthyologists and Herpetologists - Chattanooga, TN.

2014 HL Gibbs and RD Denton. Cryptic sex? Estimates of gene exchange between sexual and asexual mole salamanders (Ambystoma sp.)" Evolution 2014 - Raleigh, NC.

2014 Denton, RD and HL Gibbs. Using genetics to track the movement of unisexual Ambystoma salamanders in fragmented landscapes. 2014 Ohio Biodiversity Conservation Partnership Research Review - Columbus, OH

2014 Smiley, Sarah A.*, Terence M. Farrell, and H. Lisle Gibbs. Differential response of prey to rattlesnake venom: comparisons across and within taxanomic prey groups. Oral Presentation: Biology of the Pitvipers 2. Tulsa, OK.

2014 Zinenko, O., M. Sovic, and H.L. Gibbs. Phylogenetic analysis and estimation of hybridization in small European Vipers (Vipera sp.) based on Restriction site Associated DNA (RAD) sequencing. Biology of the Pitvipers 2. Tulsa, OK.

2013 Calvete, J.J, L. Sanz, H.L. Gibbs, J.M. Gutierrez, and B. Lomonte. Venomics of snakes of the Americas. 11th Congress of the Pan-America Section of the International Society on Toxinology and 12th Congress of the Brazilian Society of Toxinology, Guaruja, Brazil.

2012 Sovic, M.G. and H.L. Gibbs. Genomic approaches for assessing conservation units in eastern massasauga rattlesnakes (*Sistrurus s. catenatus*). Ohio Biodiversity Conservation Partnership Meeting, Columbus, Ohio.

2012 Denton, R.*, L.J. Kenyon, K.R. Greenwald, L.S. Kubatko, and H.L. Gibbs. Using multilocus, coalescent-based methods to test for hybridization between two salamander species in Ohio, USA. 2012 Ohio Biodiversity Conservation Partnership Meeting, Columbus, Ohio.

2012 Greenwald, K.* and H. L. Gibbs. Abundance, Distribution, and Habitat Associations of Unisexual Mole Salamanders (*Ambystoma*) in Ohio. World Herpetological Congress, Vancouver, British Columbia.

2012 Denton, R.*, L. Kenyon, K. Greenwald, L. Kubatko, and H. L. Gibbs. Using multilocus, coalescent-based methods to test for hybridization between two *Ambystoma* salamander species in Ohio, USA. World Herpetological Congress, Vancouver, British Columbia.

2011 Greenwald, K.*, and H.L. Gibbs. A New DNA-based method to identify polyploid unisexual *Ambystoma* salamanders. American Society of Icthyology and Herpetology Annual Meeting, Minneapolis, MN, July 2011.

2011 Chiucchi, J. and Gibbs, H.L.* Inbreeding, fitness and fatness in historically isolated populations of eastern massasauga rattlesnakes (*Sistrurus c. catenatus*). Society for the Study of Evolution Meetings, Oklahoma City, OK, June 2011.

2011 Fries, A.C.*, Slemons, R.D., Gibbs, H.L. Use of trace element profiles in feathers to establish residency status of mallards (*Anas platyrhynchos*) in an influenza A virus surveillance study. 5th Annual NIAID Centers of Excellence for Influenza Research and Surveillance Network Meeting, April 17-21, 2011. Stone Mountain, GA.

2010 Gibbs, H.L.*, and Chiucchi, J. Conservation genetics of a highly-fragmented species: the eastern massasauga rattlesnake (*Sistrurus c. catenatus*). Biology of the Vipers-3rd Conference, April 2010, Calci (Pisa), Italy.

2010 Anderson, C.S.*H. L. Gibbs, and M. J. Tonkovich. Using DNA markers to identify management units of white-tailed deer (*Odocoileus virginianus*) in Ohio. Ohio Fish and Wildlife Conference, Feb 2010, Columbus, OH

2009 Anderson, C.S*., S. Prange, and H. L. Gibbs. Using DNA markers to identify management units of bobcats in Ohio. Poster presentation. Ohio Fish and Wildlife Conference, Feb 2009, Columbus, OH

2009 Anderson, C.S*., H. L. Gibbs, and M. J. Tonkovich. Using DNA markers to identify management units of white-tailed deer (*Odocoileus virginianus*) in Ohio. Poster presentation. 70th annual Midwest Fish and Wildlife Conference, 6 - 9 Dec 2009, Springfield, IL.

2009 Fries, A.C.*, H.L. Gibbs, and R.D. Slemons. Geographic sourcing of AIV-infected mallards using genetic, trace element and stable isotopic markers. 3rd Annual Center for Excellence in Influenza Research and Surveillance Network Meeting June 22 – 26, 2009, Minneapolis, MN.

2009 Prange, S.*, Christine S. Anderson, and H. Lisle Gibbs. The Ohio Bobcat: Distribution, Abundance, and Genetic Structure of a Recovering Population. Oral presentation. 70th annual Midwest Fish and Wildlife Conference. 6 - 9 Dec 2009, Springfield, IL

2009 Fries, A.C.*, H.L. Gibbs, and J.B. Williams. Molecular evolution of mitochondrial proteins in tropical and temperate birds: thermal adaptation to climate? June 3-7, 2009 Annual Meeting of the Society for Molecular Biology and Evolution, Iowa City, IA.

2009 Fries, A.C.*, H.L. Gibbs, and J.B. Williams. Molecular evolution of mitochondrial proteins in tropical and temperate birds: thermal adaptation to climate? 127th Meeting of the American Ornithologists' Union August 12-15, 2009, Philadelphia, PA.

2009 Gibbs, H.L.* and Mackessy, S.P. Functional Basis of a Molecular Adaptation: Prey-specific Toxic Effects of Venom from *Sistrurus* Rattlesnakes. Poster presented at the Society for the Study of Evolution Meetings, Moscow, ID, June 2009.

2008 Anderson, C.* and Gibbs, H.L. Noninvasive Genetic Sampling Methods Using Hair Samples: Dealing with Potential Issues. 69th Midwest Fish and Wildlife Conference, Columbus, OH, December 2008.

2008 Gibbs, H.L.* and Chiucchi, J.E. Is Intraspecific Variation in Snake Venom PLA2 Proteins Due to Gene Regulation? Poster presented at the Society for the Study of Evolution Meetings, Minneapolis, MN, June 2008.

2008 Kubatko, L.*, and Gibbs, H.L. Phylogenetics of Recently-Evolved Taxa: Relationships among *Sistrurus* Rattlesnakes Inferred from 19 Gene Trees. Poster presented at the Society for the Study of Evolution Meetings, Minneapolis, MN, June 2008.

2007 Chiucchi, J.E.*, Gibbs, H.L. and Wynn, D. Diet of Eastern Massasauga Rattlesnakes (*Sistrurus c. catenatus*) Inferred from Stable Isotope Analysis. Poster Presented at the Joint Meeting of the American Society of Ichthyologists and Herpetologists, St. Louis, MO. July 2007.

2007 Gibbs, H.L.* and Rossiter, W. Rapid Evolution by Positive Selection and Gene Gain and Loss: PLA2 Venom Genes in Closely Related Sistrurus Rattlesnakes with Divergent Diets. Talk at the Joint Meeting of the American Society of Ichthyologists and Herpetologists, St. Louis, MO. July 2007.

2007 Mylecraine K.A.*, HL Gibbs, C.S. Anderson, and M.C. Shieldcastle. Spatial and temporal variation in Ohio Canada goose harvest composition. Talk at Ohio Fish and Wildlife Conference; Columbus, Ohio; February 2, 2007.

2007 Greenwald KR*, HL Gibbs and TA Waite. Gene flow and habitat connectivity in a fragmented landscape. Poster presentation at Understanding Agriculture's Effects on Amphibians and Reptiles in a Changing World USGS Conference/Workshop; St. Louis, MO (February 2007).

2006 Mylecraine, K.A., H. L. Gibbs, C.S. Anderson and M.C. Shieldcastle. Discriminating among Canada goose populations in Ohio harvests: a comparison of two genetic markers. Ohio Fish and Wildlife Meeting, Columbus, Ohio, February 2006. (poster)

2006 Mylecraine, K.A., H.L. Gibbs, M.C. Shieldcastle and C.S. Anderson. Using genetic markers to determine the composition of Ohio Canada goose harvests. Mississippi Flyway Technical Section Meeting, St. Louis, Missouri, July 2006.

2006 Mylecraine, K.A., H.L. Gibbs, M.C. Shieldcastle and C.S. Anderson. Using genetic markers to determine the composition of Ohio Canada goose harvests. Research Forum, Ohio Division of Wildlife and Terrestrial Wildlife Ecology Laboratory, Ohio State University.

2005 Mylecraine, K.A.*, H.L. Gibbs, C.S. Anderson. Using genetic analysis to identify resident and migrant Canada geese harvested in Ohio. Ohio Avian Ecology and Conservation Conference, Columbus, Ohio.

2005 Mylecraine, K.A.*, H.L. Gibbs, C.S. Anderson, M.C. Shieldcastle. Using genetic analysis to determine the stock composition of Ohio Canada goose harvests. The Wildlife Society Annual Conference, Madison, Wisconsin.

2005 Mylecraine, K.A.*, H.L. Gibbs, C.S. Anderson. Genetic stock identification of Canada geese harvested in Ohio. Ohio Fish and Wildlife Meeting, Columbus, Ohio.

2005 Gibbs, H.L.* and W. Rossiter. Venom evolution in *Sistrurus* rattlesnakes. Society for the Study of Evolution Meeting, University of Alaska.

2005 Gibbs, H.L. Venom evolution in *Sistrurus* rattlesnakes: conservation implications. Mid-West Massasauga rattlesnake Meeting. Squaw Creek National Wildlife Refuge, Mound City, Missouri.

2004 Ketcham, K.D.*, H. L. Gibbs, R. C. Fleischer, R. S. Greenberg, P.D. Vickery. MC1R variation is not linked to small-scale melanin-based plumage patterns in two passerine birds. Genomes and Evolution 2004 Conference, Penn State University.

2004 Rossiter, W* and H.L. Gibbs. PLA_2 venom loci show evidence for positive selection in *Sistrurus* rattlesnakes with different diets. Genomes and Evolution 2004 Conference, Penn State University.

2004 Corey, S.* and H.L. Gibbs. Phylogenetic evaluation of eastern and western fox snakes: evidence for cryptic lineages. Snake Ecology Group IV Conference, University of Southern Illinois.

2004 Gibbs, H.L.*, S. Corey, G. Blouin-Demers, P.J. Weatherhead, and K.A. Prior. Phylogeographic Analysis of Canadian Black Ratsnake (*Elaphe obsoleta*) Populations Reveals a Hybrid Zone Between Phylogenetic Species. Snake Ecology Group IV Conference, University of Southern Illinois.

2004 Boulet, M.*, H.L. Gibbs, and K. Hobson. Stable-hydrogen isotopes and genetic markers reveal migratory connectivity and flyways in Yellow Warbler populations. American Ornithologist's Union Meeting, Laval University.

2003 Gibbs, H.L.*, N.L Bulgin, P. Vickery and A.J. Baker. Ancestral polymorphisms in genetic markers obscure detection of evolutionarily distinct populations in the endangered Florida grasshopper sparrow. Society for the Study of Evolution Meeting, Chico State University.

2003 Gibbs, H.L.*, N.L Bulgin, P. Vickery and A.J. Baker. Ancestral polymorphisms in genetic markers obscure detection of evolutionarily distinct populations in the endangered Florida grasshopper sparrow. Conservation Genetics Conference, American Genetic Association, Front Royal, Virginia.

2003 Corey, S.* and H.L. Gibbs. Phylogenetic analysis of the Eastern and Western Fox Snake using DNA sequences: Evolutionary and conservation implications. Conservation Genetics Conference, American Genetic Association, Front Royal, Virginia.

2002 MacDougall-Shackelton, B., H.L. Gibbs*, and T.D. Price. Melanistic plumage patterns in old world leaf warblers do not correspond to sequence variation at melanocortin-1 receptor locus. Society for the Study of Evolution Meeting, University of Illinois.

2002 Schulte-Hostedde, A.I.*, J. S. Millar, and H.L. Gibbs. The role of male reproductive success in the evolution of female-biased sexual size dimorphism in the yellow-pine chipmunk. International Society for Behavioral Ecology Meeting, Montreal.

2002 Kissner, K.J.*, P.J. Weatherhead and H.L. Gibbs. Increased offspring survival associated with multiple paternity in the water snake, *Nerodia sipedon.* International Society for Behavioral Ecology Meeting, Montreal.

2002 Boulet, M.*, H.L. Gibbs, and K. Hobson. Where do yellow warblers go? An application of genetic markers as a tool to assess migratory connectivity among breeding and wintering grounds**.** North American Ornithological Conference, New Orleans, Louisiana.

2001 Pearce, R. L.* and H. L. Gibbs. Conservation genetics of the Eastern Massassauga Rattlesnake. Society for Conservation Biology Meeting, Hilo, Hawaii.

1999 Gibbs, H. L.*, M. D. Sorenson, K. Marchetti, M. de L. Brooke, N. B. Davies, and H. Nakamura. Female-specific genetic differentiation between host races of the Common Cuckoo. American Ornithologists' Union Meeting, Cornell University.

1999 Bulgin, N.*, H. L. Gibbs, P. Vickery, and M. Valliantos. Microsatellite DNA analysis of population structure among Grasshopper Sparrows. American Ornithologists' Union Meeting, Cornell University.

1999 Woolfenden, B.E.*, H.L. Gibbs, and S.G. Sealy. Laying patterns of female Brown-headed Cowbirds. American Ornithologists' Union Meeting, Cornell University.

1999 Woolfenden, B.E.*, H.L. Gibbs, and S.G. Sealy. Laying patterns of female Brown-headed Cowbirds. Animal Behavor Society Meeting, Bucknell University.

1999 Gibbs, H.L.*, M.D. Soreson, K. Marchetti, M. de L. Brooke, N.B. Davies, and H. Nakamura. Genetic analyses of host races in the Common Cuckoo. Society for the Study of Evolution Meeting, University of Wisconsin.

1998 Marchetti, K.*, H. Nakamura, and H.L. Gibbs. Incipient host race formation in the Common Cuckoo. International Society for Behavioral Ecology Meeting, Asilomar, California.

1998 Woolfenden, B.E.*, H.L.Gibbs, and S.G. Sealy. The genetic mating system of the brood parasitic Brown-headed Cowbird. International Society for Behavioral Ecology Meeting, Asilomar, California.

1998 Marchetti, K.*, H. Nakamura, and H.L. Gibbs. Incipient host race formation in the Common Cuckoo. Society for the Study of Evolution Meeting, University of British Columbia.

1998 Price, T.D.*, H.L. Gibbs, and A.D. Richman. Adaptive radiations of warblers on two continents. Society for the Study of Evolution Meeting, University of British Columbia.

1998 Prosser, M.R.*, H.L. Gibbs, and P.J. Weatherhead. Estimates of male and female reproductive success in the northern water snake using microsatellite DNA makers. American Society of Ichthyologists and Herpetologists, University of Guelph.

1998 Lougheed, S.C., H.L. Gibbs*, K.A. Prior, and P.J. Weatherhead. Hierarchical patterns of genetic population structure in black rat snakes as revealed by microsatellite DNA markers. American Society of Ichthyologists and Herpetologists, University of Guelph.

1998 Prior, K.A.*, H.L.Gibbs, and P.J. Weatherhead. Scales of diversity: the role of parks in conserving genetic population structure of threatened snakes. American Society of Ichthyologists and Herpetologists, University of Guelph..

1998 Prior K.A.*, Gibbs H.L., and Weatherhead P.J. Scales of diversity: the role of parks in the conservation of population genetic structure in threatened snake species. SAMPA III Conference, Calgary, Alberta.

1997 Gibbs, H.L.*, R. Dawson, and K.A. Hobson. Continent-wide patterns of population genetic structure in a neotropical migrant bird: data from microsatellite DNA markers. American Ornithologists' Union Meeting, University of Minnesota.

1997 Woolfenden, B.*, H.L. Gibbs, and S.G. Sealy. Demography of an individually-marked Brown-headed Cowbird population at Delta, Manitoba. Canadian Ornithologist’s Union Meeting, Trent University.

1997 Prosser, M.R.*, H.L. Gibbs, and P.J. Weatherhead. Determination of microgeographic population structure in the northern water snake using DNA markers. Ontario Ecology and Ethology Colloquium, University of Western Ontario.

1996 Milot, E.*, H.L. Gibbs, and K.A. Hobson. Phylogeography of the Yellow Warbler as determined using mtDNA control region sequences. American Ornithologists' Union Meeting, Boise State University.

1996 Alderson, G.A.*, H.L. Gibbs, and S.G. Sealy. Host choice and mating system of the Brown-headed Cowbird as determined using DNA genetic markers. American Ornithologists' Union Meeting, Boise State University.

1995 Gibbs, H.L. Genetic analyses of putative host races in the Common Cuckoo. Society for the Study of Evolution Meeting, McGill University.

1995 Gibbs, H.L. Genetic analyses of putative host races in avian brood parasites: examples from cuckoos and cowbirds. Ontario Ecology and Ethology Colloquium, McMaster University.

1995 Dawson, R.*, H.L. Gibbs, and K.A. Hobson. Population structure of Yellow Warblers: evidence from microsatellite DNA markers. American Ornithologists' Union Meeting, University of Cincinnati.

1992 Gelter, H.*, H.L. Gibbs and P.T. Boag. Evolution of mtDNA control regions in Darwin's Finches. Society for the Study of Evolution Meeting, University of California, Berkely.

1990. Gibbs, H.L., P.T. Boag* and P.J. Weatherhead. Realized reproductive success of Red-winged Blackbirds as revealed by DNA markers. International Ornithological Congress, Christchurch, New Zealand.

1990 Gibbs, H.L., L.M. Tabak*, B.T. Boag and B.N. White. Parentage analysis of Red-winged Blackbirds using DNA markers. Canadian Society for Forensic Science, Ottawa.

1990 Gibbs, H.L.*, L.M. Tabak, P.T. Boag and B.N. White. Parentage analysis of Red-winged Blackbirds using a single locus hypervariable DNA marker. International Congress of Systematic and Evolutionary Biology, University of Maryland.

1990 Gibbs, H.L.*, L.M. Tabak, P.T. Boag and B.N. White. Parentage analysis of Red-winged Blackbirds using a single locus hypervariable DNA marker. American Ornithologists' Meeting, UCLA.

1989 Gibbs, H.L. Inbreeding in Darwin's Medium Ground Finches. American Ornithologists' Union Meeting, University of Pittsburgh.

1989 Gibbs, H.L*., Y. Plante, P.T. Boag and B.N. White. Parentage analysis in birds and mammals using mouse MHC probes. UCLA Molecular Biology Symposium on Molecular Evolution, Lake Tahoe, Nevada.

1987 Gibbs, H.L. Oscillating selection on Darwin's Finches. American Ornithologists Union Meeting, San Francisco State University.

1986 Gibbs, H.L. Survivorship in Darwin's Finches. XIX International Ornithological Congress, Ottawa.

Courses Taught

McMaster University (1992 – 2001)

Undergraduate

1996-2001	Biology 3FF3 – Evolution
1993-2001	Biology 4AA3 – Conservation Biology
1993-94	Env Sci 1A06 – Introduction to Environmental Science
1994-2001	Senior Thesis
1994	Community Ecology
1991, 93, 95	Biology 3R03/4J03 – Field Course – Molecular Ecology of Birds

Graduate

1994, 96, 99	Biology 724 – Molecular Ecology

Ohio State University (2001 – present)

Undergraduate

2013-	EEOB 4410 – Conservation Biology
2011	EEOB 661 – Conservation Biology
2002 – 07, 09	EEOB H400 - Honors Evolution
2010	EEOB 713 – Molecular Ecology
2003 - 07	EEOB 694, 713 - Molecular Ecology (with A. Wolfe)
2008- 09	Biology 402 – Integrated Biology

Graduate

2014	EEOB 8896 – Graduate Seminar: Venom Evolution (with M. Daly)
2012	EEOB 881 – Graduate Seminar: Programming in Perl
2011	EEOB 881 – Graduate Seminar: Next Generation Sequencing in Ecology and Evolution
2007- 09	EEOB 881 – Graduate Seminar: Population Genetic Analyses (with L. Kubatko and P. Furest).
2007	EEOB 881 – Graduate Seminar: Coalescent Theory (with L. Kubatko).
2005	EEOB 881- Graduate Seminar: Analysis of Population Genetic Data
2004	EEOB 881 – Graduate Seminar: Adaptive Evolution of Genes and Genomes (with P. Fuerst)
2003	EEOB 881 – Graduate Seminar: Molecular Markers and Genetic Diversity in Plant Populations (with A. Snow)
2002	EEOB 881 – Graduate Seminar: Dispersal (with T. Grubb)

Graduate Students:

McMaster University (1992-2001)

Cindy Bullough, M.Sc., 1993. “Inter- and intrapopulation analysis of bird species: results from VNTR and MHC genetic markers”
Paul Miller, M.Sc., 1993. “Molecular genetic analysis of a Brown-headed Cowbird population”
Gerry Alderson, M.Sc., 1996. “Parentage analyses of Brown-headed Cowbirds using microsatellite DNA markers”
Emmauel Milot, M.Sc., 1997. “Population genetic structure and phylogeography of Yellow Warblers inferred from mtDNA”
Melanie Prosser, Ph.D. 1999. “Sexual selection in Northern water snakes.”
Kevin Shonk, M.Sc., 2001. “Movement patterns, behavior and genetic measures of space use by Brown-headed Cowbirds”
Natalie Bulgin, M.Sc., 2000. “Conservation genetics of Grasshopper Sparrows”
Bonnie Woolfenden, Ph.D. 2000. “Host use and mating patterns of Brown-headed Cowbirds”
Rebecca Pearce, M.Sc. 2001. “Conservation genetics of eastern massasauga rattlesnakes”
Marylene Boulet, Ph.D. 2004. “Evolutionary history and migration patterns in Yellow Warblers”

Ohio State University (2001- present)

Kelly Ketcham, M.S. 2004. “MC1-R variation in relation to small-scale melanin-based plumage variation in two passerine birds.”
Wayne Rossiter, M.S. 2005. “Evolution of PLA2 venom genes in *Sistrurus* rattlesnakes.”
James Chiucchi, Ph.D. 2011. “Conservation genetics of snakes”.
Kody Kuehnl Ph.D. 2004 - 2006. “Conservation genetics of freshwater mussels” (jointly supervised with Tom Watters).
Katherine Greenwald, Ph.D. 2010. “Conservation genetics of salamanders”.
Tony Fries, M.S. 2009 “Evolution of bird mitochondrial genomes”.
William Keen, Ph.D. 2007-08. “Rattlesnake venom evolution”.
Tony Fries, Ph.D. 2009- present. “Ecology of avian flu in mallard ducks”
David Salazar. Ph.D. 2009 – present. “Tropical viper venom ecology and evolution”
Eric McClusky. Ph.D. 2009- 2011. “Snake Conservation biology”.
Sarah Simley, Ph.D. 2010 – present. “Ecology and evolution of snake venom toxicity”
Robert Denton, Ph.D. 2011- present. “Salamander molecular ecology”
Laura Kenyon, Ph.D. 2011- 2012. “Salamander molecular evolution”
Mathew Holding, Ph.D. 2011-present. “Rattlesnake venom evolution”

I have also served as a member of the committee of 4 EEOB graduate students (Chen, Macrander, Hellman, and Pelletier), and a PhD student in SENR (Graziano) and have served as external committee member for Heather Farrington (Ph.D., Dept. Biology, University of Cincinnati; 2006 - 2011), Lucia Orantes (MS., Dept Entomology, OARDC, OSU; 2009-11); Phillip Lavertsky (PhD. Candidate, Dept Biology, Wright State University; 2010- 2014), and Evan Wong (PhD. Candidate, Dept Biology, University of Cinicinnati; 2011-2012)

Postdoctoral Researchers
McMaster University (1992-2001)

Dr. Robert Dawson (Ph.D., Nottingham University), 1993-96. “Conservation genetics of Neotropical migrant birds”
Dr. Karen Marchetti (Ph.D., University of California – Davis). 1997-98. “Host race evolution in a brood parasitic bird, the Common Cuckoo”. NATO Post-doctoral Fellow.
Dr. Beth MacDougall-Shackelton (Ph.D., Princeton University). 2000-01. “Melanistic plumage patterns in old world leaf warblers in relation to MC1R”. NSERC Postdoctoral Fellow.

Ohio State University (2001- present)

Dr. Gabriel Blouin-Demers (Ph.D., Carleton University). 2001-02. “DNA-based parentage analysis of black ratsnakes”. OSU Postdoctoral Fellow and NSERC Postdoctoral Fellow.
Dr. Kristin Mylecraine (Ph.D., Rutgers University). 2004 – 2008. “Genetic analyses to determine the racial composition of Canada Geese Harvested in Ohio”.
Dr. Christine Anderson (Ph.D., Miami University). 2004 – 2009. “Conservation genetics”.
Dr. Angelika Posel (Ph.D., University of Copenhagen). 2005 – 2009. “Song dialect evolution in White-crowned sparrows”.
Dr. Katy Greenwald (Ph.D. Ohio State University). 2009-2010. “Conservation genetics”.
Dr. Michael Sovic (Ph.D. Ohio State University). 2011-present “Conservation genetics”.

Undergraduate Honors Advisees:
McMaster University (1992-2001)

Supervised 17 4th Year Undergraduate Honours Thesis (4F06 and 4C09) students who completed research projects in my lab.

Ohio State University (2001- present)

Sarah Corey, 2002-03. Honor’s Thesis: “Phylogenetic evaluation of eastern and western fox snakes”.
Aubrey Griffin, 2004-05. Honor’s Thesis: “Isolation of single nucleotide polymorphisms from massasauga rattlesnakes”.
Mike Murphy, 2008-09. Honor’s Thesis: “Genetic analysis of hybridization in *Sistrurus* rattlesnakes”.
David Gerard, 2009-2010. NSF-RUMBA Undergraduate Fellow: “Theoretical and empirical studies of hybridization in snakes” (co-supervised with L. Kubatko).
Tia Sinclair, 2009-2010. Research on bird globin gene evolution.
Paul Anderson, 2010. Senior Thesis “Varied response to habitat degradation in the genus *Ambystoma*”
Edward Kern, 2013-14. Senior Honors Thesis “Behavioral responses of rattlesnakes to prey scents” (co-supervised with Matt Holding).
Monica Saccucci, 2013-14. Senior Honors Thesis “Morphological variation in larval *Ambystoma*”

Administrative Responsibilities

McMaster University (1992 – 2001)

Biology Undergraduate Studies Committee, 1992 - 01; Chair of Committee, 1999-2000
Health Physics Advisory Committee, 1996-97
Undergraduate Advisor, Faculty of Science, Honours (Science) Programme, 1996-98
Animal Research Ethics Board, 1995-96
Biology Plant Ecologist Search Committee, 1994-95
Biology Department Coordinator for Ontario Universities Program in Field Biology, 1991-98
Biology Representative to Faculty of Science Curriculum Review Committee, 1992-94
Biology Representative to Faculty of Science Undergraduate Admissions and Liaison Committee, 1992-94

Ohio State University (2001 – present)

College and University Committees:
Institutional Laboratory Animal Care and Use Committee, 2002-03
Graduate School, University Postdoctoral Fellowship Committee, 2003 – 04
College of Biological Sciences Faculty Advisory Committee, 2004-07
Division of Natural, Mathematical, and Physical Sciences, Center for Biodiversity Science Proposal Committee, 2012 -13
Office of International Affairs, Brazil Faculty Advisory Committee, 2012-

Director, Ohio Biodiversity Conservation Partnership, 2011- present

Department Committees:
EEOB Promotion and Tenure Committee: 2001- present; Chair of Committee: 2013-present
EEOB Seminar Committee, 2001-03; Chair of Committee: 2002 - 03
EEOB Advisory Committee, 2002 – 04, 2006-08, 2013- present.
EEOB Graduate Studies Committee, 2001-02, 2005-2009; Chair of Committee 2005-2009
EEOB Graduate Admissions Committee 2005-2006, 2010-11
EEOB Animal Systematics Search Committee, 2002-03
EEOB Communications Committee, 2003 - 05; Chair of Committee: 2004-05
EEOB Department Chair Search Committee 2009, 2013
EEOB Evolutionary Genomics Search Committee 2011; Chair of Committee
EEOB Aquatic Ecology Search Committee 2014-15
EEOB Targeted Hire Search Committee 2014-15

30 January 2015

M. Zachariah Peery
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EDUCATION

Ph.D. Environmental Science, Policy, and Management 2004
University of California, Berkeley
M.Sc. Wildlife Biology 1996
Humboldt State University
B.Sc. Ecology, Behavior, and Evolution 1993
University of California, San Diego

PROFESSIONAL POSITIONS

Associate Professor, University of Wisconsin-Madison 2014 -
(Department of Forest and Wildlife Ecology)
Assistant Professor, University of Wisconsin-Madison 2008 - 2014
(Department of Forest and Wildlife Ecology
Post-doctoral Researcher, University of California, Berkeley 2006 - 2008
(Museum of Vertebrate Zoology)
Post-doctoral Researcher, Moss Landing Marine Laboratories 2005 - 2008
Assistant Project Leader, Humboldt State University Foundation 1996 - 1999

PEER-REVIEWED PUBLICATIONS (**indicates student author*)

In Review (6)

Reid*, B. N., R. Theil, and **M. Z. Peery**. *In Review*. Combining genetic kinship and demographic methods to estimate cryptic dispersal rates. Methods in Ecology and Evolution.

Fountain, E. D., J. N. Pauli, P. J. Palsbøll and **M. Z. Peery**. *In Review*. Finding the right coverage: The impact of read depth and sequence quality on SNP genotyping error rates. Molecular Ecology Resources.

Reid*, B. N., R. P. Thiel, and **M. Z. Peery**. *In Review*. If you build it, they will (slowly) come: population dynamics of endangered Blanding's turtles in a restored area. Biological Conservation.

Jones*, G., R. J. Gutierrez, D. Tempel, B. Zuckeberg, and **M. Z. Peery**. *In Review*. Modeling climate change impacts and adaptation strategies in complex environments: A dynamic occupancy approach. Ecological Applications.

Tempel, D. J., R. J. Gutiérrez, J. J. Battles, D. L. Fry, Q. Guo, M. J. Reetz, S. A. Whitmore, G. M. Jones*, B. M. Collins, S. L. Stephens, M. Kelly, W. J. Berigan, and **M. Z. Peery**. *In Review*. Assessing the short- and long-term impacts of fuel treatments and wildfire on an old-forest species. Ecological Applications.

Dill-McFarland, K. A, J. N. Pauli, **M. Z. Peery**, P. J. Weimer, and G. Suen, *In Review*. A specialized diet selects for a unique and simplified gut microbiota in sloths. PLoS Biology.

Published or In Press (45)

Mendoza, J.*, **M. Z Peery**, G. A. Gutiérrez, G. Herrera, and J. N. Pauli. 2015. Resource use by two- and three-toed sloths differ in a shade-grown agro-ecosystem. Journal of Tropical Ecology 31:49-55.

Stoelting, R.*, R. J. Gutiérrez, W. L. Kendall, and **M. Z. Peery**. 2015. Life-history trade-offs and reproductive cycles in spotted owls. The Auk 132:46-64.

Tempel, D., R. J. Gutierrez, S. Whitmore, M. Reetz, W. Berigan, R. Stoelting*, M. E. Seamans, and **M. Z. Peery**. 2014. Effects of forest management on California spotted owls: Implications for reducing wildfire risk in fire-prone forests. Ecological Applications. 24:2089–2106.

Reid, B. N.*, and **M. Z. Peery**. 2014. Land use patterns skew sex ratios, decrease genetic diversity, and trump the effects of recent climate change in an endangered turtle. Diversity and Distributions. 20:1425-1437.

Tempel, D., **M. Z. Peery**, and R. J. Gutierrez. 2014. Integrated population models for wildlife conservation: An example with the California spotted owl (*Strix occidentalis occidentalis*)**.** Ecological Modelling 289:86-95.

Peery, M. Z., and J. N. Pauli. 2014. Shade-grown cacao supports a self-sustaining population of two-toed but not three-toed sloths. Journal of Applied Ecology. 51:162-170

Pauli, J. N., J. E. Mendoza*, S. A. Steffan, C. Carey, P. J. Weimer, and **M. Z. Peery**. 2014. A syndrome of mutualism reinforces the life-history of a sloth. Proceedings of the Royal Society, B. 281.

Vasquez-Carrillo, C.*, V. L Friesen, L. A. Hall, **M. Z. Peery.** 2014. Variation at MHC class II B genes in marbled murrelets: Implications for delineating conservation units. Animal Conservation. 17:244-255.

Vasquez-Carrillo, C.*, R. W. Henry, L. Henkel, **M. Z. Peery**. 2013. Integrating population and genetic monitoring to understand demographic changes in a threatened seabird. Biological Conservation. 167:173–178.

Peery, M. Z., B. N. Reid*, R. Kirby, R. Stoelting***,** E. Doucet-Bëer*, S. J. Robinson, C. Vasquez-Carrillo*, J. N. Pauli, P. J. Palsbøll. 2013. More precisely biased: increasing the number of markers is not a silver bullet in genetic bottleneck testing. Molecular Ecology. 22:3451-3457.

Peery, M. Z. and R. J. Gutiérrez. 2013**.** Life-history trade-offs in California spotted owls: Implications for assessment of territory quality. The Auk. 130:132-140. ***Featured as "Editor's Choice"***

Palsbøll, P. J., **M. Z. Peery**, M. T. Olsen, and S. R. Beissinger, and M. Bérubé. 2013. Inferring recent historic abundance from current genetic diversity. Molecular Ecology: 22:22-40. ***Invited Review.***

Peery, M. Z. and J. N. Pauli. 2012. The mating system of a "lazy" mammal, Hoffmann's two-toed sloth. Animal Behaviour. 84:555-562.

Peery, M. Z., R. Kirby, B. N. Reid*, R. Stoelting***,** E. Doucet-Bëer*, S. J. Robinson, C. Vasquez-Carrillo*, J. N. Pauli, P. J. Palsbøll. 2012. Reliability of genetic bottleneck tests for detecting recent population declines. Molecular Ecology. 21:3403–3418. ***Invited Review***.

Peery, M. Z., R. J. Gutiérrez, R. Kirby, O. E. LeDee, and W. S. LaHaye. 2012. Climate change and spotted owls: potentially contrasting responses in the southwestern United States. Global Change Biology. 18:865-880.

Pauli, J. N., and **M. Z. Peery**. 2012. Unexpected strong polygyny in the brown-throated three-toed sloth. PLoS One. 7:e51389

Popescu, V. D., P. de Valpine, D. Tempel, and **M. Z. Peery**. 2012. Estimating population impacts via dynamic occupancy analysis of Before-After Control-Impact studies. Ecological Applications. 22:1389-1404.

Moss*, W. E., J. N. Pauli, G. A. Gutiérrez, C. Vaughan, G. Herrera, **M. Z. Peery**. 2012. Development and characterization of 18 microsatellites for the brown-throated three-toed sloth, *Bradypus variegatus*. Conservation Genetics Resources 4:1037-1039.

Moss*, W. E., J. N. Pauli, G. A. Gutiérrez, A. Young, C. Vaughan, G. Herrera, **M. Z. Peery**. 2011. Development and characterization of 16 microsatellites for Hoffman's two-toed sloth, *Choloepus hoffmanni*. Conservation Genetics Resources 3:625-627.

Peery, M. Z., L. A. Hall*, A. Sellas, S. R. Beissinger, C. Moritz, M. Bérubé, M. G. Raphael, S. K. Nelson, R. T. Golightly, L. McFarlane-Tranquilla, S. Newman, P. J. Palsbøll. 2010. Genetic analyses of historic and modern marbled murrelets suggest decoupling of migration and gene flow after habitat fragmentation. Proceedings of the Royal Society, Biological Series 277:697-706.

Peery, M. Z. and R. W. Henry. 2010**.** Recovering the Marbled Murrelet via corvid management: a PVA-based assessment. Biological Conservation. 143:2414–2424.

Palsbøll, P. J, **M. Z. Peery**, and M. Bérubé. 2010. Detecting populations in the "ambiguous" zone: kinship-based estimation of population structure at low genetic divergence. Molecular Ecology Resources. 10:797–805. ***Invited Review***.

Hall*, L. A., S. R. Beissinger, P. J. Palsbøll, J. T. Harvey, M. Bérubé, M. G. Raphael, S. K. Nelson, R. T. Golightly, S. Newman, L. McFarlane-Tranquilla, and **M. Z. Peery.** 2009. Characterizing dispersal patterns of a threatened seabird with limited genetic structure. Molecular Ecology. 18:5074–5085.

Peery, M. Z., S. H. Newman, C. Storlazzi, and S. R. Beissinger. 2009. Meeting reproductive demands in a dynamic upwelling system: foraging strategies of a pursuit-diving seabird, the Marbled Murrelet. The Condor. 111:120–134.

Peery, M. Z., S. R. Beissinger, R. F. House, M. Bérubé, L. A. Hall, A. Sellas, and P. J. Palsbøll. 2008. Characterizing source-sink dynamics with genetic parentage assignments. Ecology. 89: 2746–2759.

Peery, M. Z., L. A. Henkel, S. H. Newman, B. H. Becker, J. T. Harvey, C. Thompson, and S. R. Beissinger. 2008. Effects of rapid flight-feather molt on post-breeding dispersal in a pursuit-diving seabird. The Auk. 125:113-123.

Peery, M. Z., B. H. Becker, and S. R. Beissinger. 2007. Age ratios as estimators of productivity: testing assumptions on a threatened seabird, the Marbled Murrelet. The Auk.124:224-240.

Beissinger, S. R., and **M. Z. Peery.** 2007. Reconstructing the historical demography of an endangered seabird. Ecology. 88:296-305.

Becker, B. H., **M. Z. Peery**, and S. R. Beissinger. 2007. Ocean climate affects trophic level and reproductive success of an endangered seabird, the Marbled Murrelet. Marine Ecology Progress Series. 329:267-279.

Peery, M. Z., B. H. Becker, and S. R. Beissinger. 2006. Combining demographic and count-based approaches to identify source-sink dynamics for a threatened seabird. Ecological Applications. 16:1516-1528.

Peery, M. Z., S. R. Beissinger, E. Burkett, S. H. Newman. 2006. Local survival rates of Marbled Murrelets: roles of oceanographic conditions, sex, and radio-tagging. Journal of Wildlife Management. 70:78-88.

Cooper, B. A., M. G. Raphael, and **M. Z. Peery**. 2006. Trends in radar-based counts of Marbled Murrelets in the Olympic Peninsula, Washington, 1996-2004. Condor 108:936-947.

Baker*, L. M., **M. Z. Peery**, S. R. Beissinger, E. Burkett, S. W. Singer, and D. L. Suddjian. 2006. Nesting habitat characteristics of Marbled Murrelets in central California redwood forests. Journal of Wildlife Management 70:939-946.

Rew, M. B., **M. Z. Peery**, S. R. Beissinger, M. Bérubé, J. D. Lozier, E. M. Rubidge, and P. J Palsbøll. 2006. Cloning and characterization of twenty-nine tetranucleotide and two dinucleotide polymorphic microsatellite loci from the endangered marbled murrelet (*Brachyramphus marmoratus*). Molecular Ecology Notes 6:241-244.

Bigger, D., **M. Z. Peery,** J. Baldwin, S. Chinnici and S. P. Courtney. 2006. Power to detect trends in marbled murrelet populations using audio-visual and radar surveys. Journal of Wildlife Management 70:493-504.

Bigger, D., **M. Z. Peery**, S. Chinnici and S. P. Courtney. 2006. Efficacy of audio-visual and radar surveys for studying marbled murrelets in inland habitats. Journal of Wildlife Management 70:505-516.

Peery, M. Z., S. R. Beissinger, S. H. Newman, E. B. Burkett, and T. D. Williams. 2004. Applying the declining population paradigm: diagnosing causes of low reproductive success in Marbled Murrelets. Conservation Biology 18:1088-1097.

Peery, M. Z., S. R. Beissinger, S. H. Newman, B. H. Becker, E. Burkett, and T. D. Williams. 2004. Individual and temporal variability in inland flight behavior of Marbled Murrelets: implications for population monitoring. Condor 106:344-353.

Seamans, M. E., R. J. Gutiérrez, C. A. Moen, and **M. Z. Peery**. 2001. Spotted owl demography in the central Sierra Nevada. Journal of Wildlife Management 65:425-431

Peery, M. Z., 2000. Factors affecting interspecific variation in raptor home range size. The Auk 117:511-517.

Peery, M. Z., R. J. Gutiérrez, and M. E. Seamans. 1999. Habitat composition and configuration around spotted owl nests and roosts in the Tularosa Mountains, New Mexico. Journal of Wildlife Management 63:36-43.

Smith, R., **M. Z. Peery,** R. J. Gutiérrez, and W. S. LaHaye. 1999. The relationship between spotted owl diet and reproductive success in the San Bernardino Mountains, California. Wilson Bulletin 111:22-29.

Seamans, M. E., R. J. Gutiérrez, C. M. May, and **M. Z. Peery**. 1999. Demography of two Mexican spotted owl populations. Conservation Biology 13:744-754.

Gutiérrez, R. J., M. E. Seamans, and **M. Z. Peery.** 1996. Intermountain movements by Mexican spotted owls. Great Basin Naturalist. 56:87-89.

May, C. M., **M. Z. Peery,** R. J. Gutiérrez, M. E. Seamans, and D. Olson. 1996. Feasibility of a random quadrat design to estimate changes in density of Mexican spotted owls. USDA Forest Service Research Paper RM-RP-322.

RESEARCH GRANTS

Pending

2016-2018	**Inferring the structure and dynamics of pre-European forests with population genomics.** *Amount*: TBD (pre-proposal stage); *PI:* **M. Z. Peery**, *co-PI*: R. J. Gutierrez; *Source:* National Science Foundation, Division of Environmental Biology.
2016-2018	**Do upslope shifts in fitness outpace occupancy in warming environments?** *Amount*: TBD (pre-proposal stage); *PI:* **M. Z. Peery**, *co-PI*: R. J. Gutierrez, B. Zuckerberg; *Source:* National Science Foundation, Division of Environmental Biology.
2016-2018	**Linking nutrient flow to gut microbiota structure and function in two species of herbivorous tree sloths.** *Amount*: TBD (pre-proposal stage); *PI:* G. Suen, *co-PI*: J. N. Pauli, **M. Z. Peery;** *Source:* National Science Foundation, Division of Integrative Organismal Systems.

Awarded

2013-2015	**The ABCs of dispersal: Developing an approximate Bayesian computation approach for estimating recent migration from the distribution of related individuals.** *Amount:* $500,000; *PI:* **M. Z. Peery,** *Co-PI:* J. N. Pauli, P. J. Palsbøll. *Source*: National Science Foundation, Division of Environmental Biology.
2010-2018	**Spotted Owl population dynamics in the central Sierra Nevada.** *Amount:* $3,035,786. *PI*: **M. Z. Peery**; *Source:* U.S. Forest Service
2007-2015	**The Sierra Nevada Adaptive Management Project** *Amount*: ~$14,000,000 *PI*: J. Battles, co-PI: **M. Z. Peery** and 9 others. *Source:* US Forest Service and California Department of Water.
2014-2020	**Will bat population declines from white-nose syndrome benefit pests in Wisconsin agriculture?** *Amount*: $250,557*; PI:* **M. Z. Peery**; *Source*: UW-Madison Agricultural Experiment Station, Hatch Formula Funds. UW-Madison Graduate School.
2015-2019	**Integrating genetic and demographic methods to model agricultural and climate change impacts on native species: Wisconsin turtles as a case study.** *Amount*: $115,556*; PI:* **M. Z. Peery;** *Source*: UW-Madison Agricultural Experiment Station, Hatch Formula Funds.
2015-2018	**Assessing the impacts of the King Fire on California Spotted Owls.** *Amount*: $183,000*; PI:* **M. Z. Peery**, *co-PI*: R. J. Gutierrez; *Source*: US Forest Service

2015-2018	**Assessing the impacts of wildfire on California Spotted Owls in the Sierra Nevada.** *Amount*: $149,034*; PI:* **M. Z. Peery**, *co-PI*: R. J. Gutierrez; *Source*: State Wildlife Grant Program: California Department of Fish and Wildlife.
2015-2016	**Assessing the impacts of a long-term Marbled Murrelet conservation strategy**. *Amount*: $60,000*; PI:* **M. Z. Peery**; *Source*: Washington Department of Natural Resources.
2012-2015	**Foraging and population ecology of Steller's Jays in redwood forests: implications for the conservation of Marbled Murrelets** *Amount*: $223,700; *PI*: **M. Z. Peery**; *Sources*: Save the Redwoods League, US Fish and Wildlife Service, California Department of Fish and Wildlife, private donor, UW-Madison Graduate School, US Geological Survey
2014-2016	**Sloth conservation and shade-grown agriculture**. *Amount:* $25,000; *Source*: Disney World Conservation Fund. *PI:* J. N, Pauli, *Co-PI:* **M. Z. Peery**
2015-2016	**Characterizing the foraging ecology of Marbled Murrelets in coastal waters adjacent to old-growth redwoods.** *Amount*: $25,000; *PI*: **M. Z. Peery**; *Source*: Save the Redwoods League.
2014-2017	**An ecological 'time machine' to restore cyclical population dynamics.** *Amount:* $170,094. *PI*: J. N. Pauli, *Co-PIs*: B. Zuckerberg, **M. Z. Peery.** *Source*: UW-Madison, CALS McIntire-Stennis Formula Funds
2011-2013	**Population viability analysis of Wisconsin cave bats: implications for the management of white-nose syndrome**. *Amount*: $38,002; *PI*: **M. Z. Peery**, *co-PI*: T. R. VanDeelen; *Source*: WI Department of Natural Resources
2010-2013	**Assessing the effects of SPLATs on California Spotted Owls and Pacific fisher.** *Amoun*t: $475,290; *PI*: **M. Z. Peery**, *co-PI*: R. J. Gutierrez *Source*: California Department of Fish and Game and UC Berkeley
2010-2012	**Role of sustainable agriculture in the conservation of sloths in Costa Rica** *Amount*: $62,400; *PI*: **M. Z. Peery**; *co-PI*: J. N. *Source*: UW-Madison Graduate School and the Milwaukee Public Museum
2010-2013	**Developing single nucleotide polymorphisms (SNPs) as tools for assessing the impacts of environmental stressors on native species**. *Amount*: ~$111,000; *PI*: **M. Z. Peery**, Graduate Student: B. N. Reid *Source*: U.S. Environmental Protection Agency STAR Fellowship
2010-2011	**Identification of migrant Marbled Murrelets in central California** *Amount*: $32,653, *PI*: **M. Z. Peery,** *Source:* National Fish and Wildlife Foundation
2010-2012	**Adaptive genetic diversity of the Marbled Murrelet (*Brachyramphus marmoratus*).** *Amount*: $83,000, *PI:* **M. Z. Peery**, *Source*: AK Department of Fish and Game
2009-2014	**An assessment of genetic variation in Blanding's turtle populations in Wisconsin**. *Amount*: $98,626*; PI:* M. Z. Peery; *Source*: UW-Madison Agricultural Experiment Station, Hatch Formula Funds
2007-2009	**At-sea surveys of Marbled Murrelets in central California** *Amount:* $50,000; *PI:* **M. Z. Peery**; *Source*: CA State Parks and Recreation
2006-2007	**Modeling spatial and temporal variation in mercury concentrations in fish inhabiting the Sacramento Delta**. *Amount:* $20,000; *PI:* **M. Z. Peery**; *Source:* San Francisco Estuary Institute

2002-2009	**Ecology and conservation of Marbled Murrelet populations** *Amount*: $582,000; *PI:* **M. Z. Peery**; *Source*: Pacific Lumber Company
2004	**Power analysis for sturgeon populations in the Missouri River** *Amount*: $14,000; *PI:* **M. Z. Peery**; *Source*: Sustainable Ecosystems Institute
2003-2004	**Using genetic techniques to determine if the central California Marbled Murrelet population is a sink**. *Amount*: $21,500; *PI*: S. R. Beissinger, co-PI: **M. Z. Peery**; *Source*: U. S. Fish and Wildlife Service
2002-2003	**Conservation genetics of Marbled Murrelet in northern California** *Amount:* $38,000; *PI:* V. L. Friesen, *co-PI*: T. Birt, **M. Z. Peery**, S. R. Beissinger; *Source:* Pacific Lumber Company
2002-2003	**Post-breeding season movements and distribution of Marbled Murrelets in central California.** Amount: $40,000; *PI*: S. R. Beissinger, co-PI: **M. Z. Peery.** *Source*: Oiled Wildlife Care Network, U. S. Coast Guard
2000-2002	**Using radio-telemetry and mark-recapture to determine factors affecting the central California Marbled Murrelet population**. *Amount*: $143,000; *PI*: S. R. Beissinger, co-PI: **M. Z. Peery**; *Source:* CA Department of Fish and Game, California State Parks

SCIENTIFIC PRESENTATIONS (*indicates student author)

Invited Presentations

Tempel, D., R. J. Gutiérrez, **M. Z. Peery**. 2014. Forest fuel reductions, spotted owls, and adaptive management: where are we? Oral presentation at the Ecological Society of America Annual Meeting. Sacramento, CA.

Tempel, D., R. J. Gutiérrez, **M. Z. Peery**. 2014 Spotted owl research update for the Sierra Nevada Adaptive Management Project (SNAMP). Oral presentation at the SNAMP public outreach meeting, Sacramento, CA.

West*, E. and **M. Z. Peery.** 2014. A Tale of Two Birds. Big Basin Redwoods State Park Wings Over the Basin Celebration. Big Basin, CA.

G. M. Jones*, R. J. Gutierrez, B. Zuckerberg, **M. Z. Peery.** 2014. Do physiography and habitat buffer spotted owls from adverse weather? Department of Forest & Wildlife Ecology, UW-Madison.

Peery, M. Z. 2013. Conservation status of marbled murrelets. Pacific Seabird Group Annual Conference. Portland, OR. ***Invited plenary presentation.***

Doucet-Beer, E*, R. W. Henry, and **M. Z. Peery**. 2013. Foraging ecology of Steller's jays in redwood forests: Implications for marbled murrelet conservation. Annual Meeting of the Luckenbach and Cosco Busan Trustee Council. Fairfield, CA.

Vasquez-Carrillo, C.*, R. W. Henry, L. Henkel, **M. Z. Peery**. 2013. Integrating population and genetic monitoring to understand demographic changes in a threatened seabird. Annual Meeting of the Luckenbach and Cosco Busan Trustee Council. Fairfield, CA.

D. Tempel, R. J. Gutierrez, S. Whitmore, M. Reetz, W. Berigan, R. Stoelting*, M. E. Seamans, and **M. Z. Peery**. 2013. Effects of forest management on California spotted owls: Implications for reducing wildfire risk in fire-prone forests._Annual Meeting of the Sierra Nevada Adaptive Management MOU Partners. Sacramento, California.

D. Tempel, R. J. Gutierrez, S. Whitmore, M. Reetz, W. Berigan, R. Stoelting*, M. E. Seamans, and **M. Z. Peery**. 2013. Effects of forest management on California spotted owls: Implications for reducing wildfire risk in fire-prone forests. Annual Meeting of the Sierra Nevada Adaptive Management Science Team. Sausalito, California.

Peery, M. Z. and J. N. Pauli. 2012. The mating system of a "lazy" mammal, Hoffman's two-toed sloth. California Academy of Sciences, San Francisco, California.

Peery, M. Z. 2011. Integrating genetic and demographic methods in threatened species research. Department of Wildlife, Fish, and Conservation Biology, University of California, Davis.

Peery, M. Z., R. J. Gutiérrez, D. Tempel, S. Whitmore, V. Berigan, R. Stoelting. 2011. SNAMP: A landscape-scale experiment to assess the effects of forest fuel treatments on the Sierra Nevada ecosystem. University of Wisconsin Biology Colloquium.

Peery, M. Z. 2011. Demography and genetics of Marbled Murrelets in central California. Pacific Seabird Group, Marbled Murrelet Technical Committee Meeting.

Peery, M. Z., E. Doucet-Beer, R. W. Henry. 2011. Impacts of food subsidies on the foraging ecology of Steller's Jays in the Santa Cruz Mountains. Pacific Seabird Group, Marbled Murrelet Technical Committee Meeting.

Peery, M. Z., R. J. Gutiérrez, D. Tempel, S. Whitmore, V. Berigan, R. Stoelting. 2010. SNAMP: A landscape-scale experiment to assess the effects of forest fuel treatments on the Sierra Nevada ecosystem. University of Wisconsin Ecology Group.

Peery, M. Z. 2010. Genetic analyses of historic and modern marbled murrelets suggest decoupling of migration and gene flow after habitat fragmentation. University of Wisconsin-Madison Behavior Series Seminar.

Peery, M. Z. 2009. Genetic analyses of historic and modern marbled murrelets suggest decoupling of migration and gene flow after habitat fragmentation. University of Wisconsin-Madison Evolution Series Seminar.

Peery, M. Z. 2009. Genetic analyses of historic and modern marbled murrelets suggest decoupling of migration and gene flow after habitat fragmentation. Swedish Environmental Protection Agency.

Peery, M. Z. 2009. Immigration without gene flow leads to cryptic extinction in an endangered seabird. Wisconsin Department of Natural Resources.

Contributed Oral Presentations

Reid*, B. N. and **M. Z. Peery.** 2015. A tale of three turtles: conservation and genetics of wetland chelonians in the Midwest. Oral presentation at Joint Annual Meeting, Minnesota and Wisconsin Chapters of The Wildlife Society, Duluth, MN.

Reid*, B. N. and **M. Z. Peery**. 2015. A tale of three turtles: conservation and genetics of wetland chelonians in Wisconsin. Oral presentation at Wisconsin Wetland Association Annual Meeting, Madison, WI.

West*, E. and **M. Z. Peery.** 2014. Food for thought: The influence of resource subsidies on the ecology and behavior of Steller's jays in protected areas. Joint meeting of the American Ornithologists' Union, Cooper Ornithological Society and Society of Canadian Ornithologists. Estes Park, CO.

Reid*, B. N. and **M. Z. Peery.** 2014. Urbanization skews sex ratios, decreases genetic diversity, and trumps the effects of recent climate change in an endangered turtle. Oral presentation at Wisconsin Ecology Symposium, Madison, WI.

Reid*, B. N. and **M. Z. Peery.** 2014. Using genetic and demographic methods to characterize nesting philopatry in a long-lived turtle (*Emydoidea blandingii*). Oral presentation at Joint Meeting of Ichthyologists and Herpetologists, Chattanooga, TN.

Reid, B. N.* and **M. Z. Peery**. 2013. Comparing the effects of urban development on turtles across Wisconsin. Oral presentation at: Midwest Partners in Amphibian and Reptile Conservation Meeting; 2013 August 2-4, Port Washington, WI.

Doucet-Beer, E*, R. W. Henry, and **M. Z. Peery**. 2013. Foraging ecology of Steller's jays in redwood forests. Pacific Seabird Group Annual Conference. Portland, OR.

Popescu, V. D., P. de Valpine, D. Tempel, and **M. Z. Peery**. 2012. Estimating population impacts via dynamic occupancy analysis of Before-After Control-Impact studies. Ecological Society of America, Portland Oregon.

Vasquez-Carrillo,* C., **M. Z. Peery** and V. Friesen. 2012 Adaptive genetic variation of marbled murrelet: Implications for conservation unit delineation. Student Conference on Conservation Science, New York, USA (October -12, 2012).

Pauli, J. N. and **M. Z. Peery** 2011. Novel approaches for studying the population ecology of sloths. American Society for Mammalogists. Portland, Oregon.

Reid*, B. N. and **M. Z. Peery**. 2011. Estimating population connectivity using kinship methods in Blanding's Turtle (*Emydoidea blandingii*). Poster presentation at the Joint Meeting of Ichthyologists and Herpetologists, Minneapolis, Minnesota.

Reid*, B. N. and **M. Z. Peery**. 2011. Novel genetic markers and methods for species and ecosystem conservation. Poster presentation at the 2011 EPA STAR Graduate Fellowship Conference, Washington, DC (September 19-20th).

Peery, M. Z. 2009. Immigration without gene flow leads to cryptic extinction in an endangered seabird. University of Bergen, Norway.

Peery, M. Z. 2009. Immigration without gene flow leads to cryptic extinction in an endangered seabird. Wisconsin Chapter of The Wildlife Society.

Peery, M. Z., L. A. Henkel, S. H. Newman, B. H. Becker, J. T. Harvey, C. Thompson, and S. R. Beissinger. 2007. Effects of rapid flight-feather molt on post-breeding dispersal in a threatened seabird. Pacific Seabird Group 34nd Annual Conference, Monterey, California

Peery, M. Z., B. H. Becker, and S. R. Beissinger. 2005. Age ratios as estimators of productivity: assumptions and applications to Marbled Murrelets. 131st Annual Meeting of the American Ornithologists' Union. Santa Barbara California.

Peery, M. Z., B. H. Becker, and S. R. Beissinger. 2005. Age ratios as estimators of productivity: assumptions and applications to Marbled Murrelets. Cooper Ornithology Society Meeting. Humboldt State University.

Peery, M. Z., S. R. Beissinger, B. Becker, S. H. Newman, and E. Burkett. 2005. Survival rates and rates of population change for Marbled Murrelets in central California, evidence for a sink population? Pacific Seabird Group 32nd Annual Conference in Portland, Oregon.

Peery, M. Z., S. R. Beissinger, S. H. Newman, and C. S. Storlazzi. 2005. Foraging ecology of Marbled Murrelets: meeting energy demands in a dynamic ocean environment. Pacific Seabird Group 32nd Annual Conference in Portland, Oregon.

Peery, M. Z., S. R. Beissinger, B. H. Becker, E. Burkett, and S. H. Newman. 2003. Demography of the Marbled Murrelet in central California. Pacific Seabird Group 30th Annual Conference in Parksville, British Columbia.

Peery, M. Z., S. R. Beissinger, B. H. Becker, E. Burkett, and S. H. Newman. 2002. Demography of the Marbled Murrelet in central California. The Wildlife Society, Pacific Northwestern Section, Annual Meeting in Spokane Washington

Peery, M. Z., S. R. Beissinger, S. H. Newman, and E. Burkett. 2001. Population dynamics of the Marbled Murrelet in central California. Pacific Seabird Group 28th Annual Conference in Kuaii, Hawaii.

ACADEMIC SOCIETIES

The Wildlife Society,
The Society for Conservation Biology
The American Ornithologists' Union

SCHOLASTIC AND PROFESSIONAL AWARDS

2003 - Budweiser Conservation Scholarship ($10,000)
2003 - American Museum of Natural History - Chapman Award ($3,000)
2001 - Environmental Protection Agency - *STAR* PhD Fellowship ($102,000)
2001 - Starker Leopold Award, University of California, Berkeley ($10,000)
1996 - Humboldt State University - Koplin Award for Outstanding Graduate Student

TEACHING EXPERIENCE

Course	**Enrollment**	**Credits**	**Semester**
Extinction of Species (FWE/ZOO/ENV ST 360)	~300	3	Fall 2009, 2010, 2011, 2013, 2013, 2014
Conservation Genetics (FWE 875)	8-20 gr	1-2	Spring 2010, Fall 2013
Demographic Methods (FWE 875)	19 (gr)	3	Fall 2012

MENTORSHIP

Graduate Students

Brendan Reid, PhD Candidate and EPA STAR Fellow	2010 - present
Elena Doucet-Beer, PhD Canditate, co-advised with William Karasov	2010 - present
Gavin Jones, MSc Student	2013 – present
Mario Restrepo, PhD Student, co-advised with Jonathan Pauli	2014 – present
Evan Wilson, PhD Student, co-advised with Jonathan Pauli	2014 – present
Rebekah Moses, PhD Student, co-advised with Claudio Gratton	2015 – present
Nathan Byers, PhD Student	2015 - present
Ricka Stoelting, PhD Student	2010 - 2014

Jorge Mendoza, MSc Student, co-advised with Jonathan Pauli	2011 - 2014
Catalina Vasquez-Carrillo, MSc Student	2010 - 2102

Post-docs

Emily Fountain	2013 – present
Doug Tempel	2013 - present
Jungkoo Kang	2013 – 2014
Matthew Reetz	2012 – 2014
Jonathan Pauli	2009 - 2010

Research Associates and Interns (all full time UW-Madison employees)

William Berigan	2011 - present
Sheila Whitmore	2011 - present
Wynne Moss	2011 - 2012

Graduate Thesis Committees

Vera Pfeiffer	2013 - present
Michael Hardy	2013 - present
Wynne Moss	2012 - present
Hoa Nguyen-Phuc	2011 - present
Rebecca Kirby	2011 - present
John Pokallus	2011 - present
Andrew Cassini	2010 - present

*Undergraduats Research Interns (UW-Madison) *published paper from research*

Wynne Moss**	2011 - 2012
Rob Dugenske	2011 - 2012
Sara Matasick	2011 - 2012
Cristina Vaughan	2011
Megan Evansen	2010
Nick Kryshack	2010
Anthony Swichtenberg	2010
Anthony Colon	2010
Jessica Steig	2009 - 2010

Non-UW Graduate Students and Selected Undergraduate Students

Laurie Hall. M.Sc, Moss Landing Marine Labs.	Currently a PhD student at UC Berkeley
Lauren Baker. Undergraduate Intern, UC Berkeley	Currently a PhD student at Yale.

UNIVERSITY AND PROFESSIONAL SERVICE

Professional Service

2013 Scientific advisor the US Fish and Wildlife Service regarding Section 7 Consultations under the US Endangered Species Act (Lacey, WA; Aug 22-23)

2013	Comment on California State Parks General Plan for Big Basin Redwoods State Park (6 pages).
2013	Led 1-day workshop on status of California Spotted Owls for US Forest Service (Jan 7, 2013)
2012	Co-Instructor of an intensive, week-long course titled “Population Viability Analysis” for endangered species biologists from state and federal resource agencies. Taught at the US Fish and Wildlife Service’s Regional Office in Portland, Oregon
2011	Expert Panelist for the US Fish and Wildlife Service on “Reducing Threats to Marbled Murrelets” (Oct 17-21, 2011)
2011-	Marbled Murrelet Recovery Implementation Team
2011	Co-Instructor of an intensive, week-long course titled “Population Viability Analysis” for endangered species biologists from state and federal resource agencies. Taught at the US Fish and Wildlife Service’s Regional Office in Denver, Colorado
2011	Expert Panelist for the US Fish and Wildlife Service on “Impacts of Pile Driving to Marbled Murrelets” (Aug 9-14, 2011)
2010	Co-Instructor of an intensive, week-long course titled “Population Viability Analysis” for endangered species biologists from state and federal resource agencies. Taught at the US Fish and Wildlife Service’s National Conservation Training Center in West Virginia
2009	Co-Instructor of an intensive, week-long course titled “Population Viability Analysis” for endangered species biologists from state and federal resource agencies. Taught at the US Fish and Wildlife Service’s National Conservation Training Center in West Virginia
2008	Co-Instructor of an intensive, week-long course titled “Population Viability Analysis” for endangered species biologists from state and federal resource agencies. Taught at the US Fish and Wildlife Service’s National Conservation Training Center in West Virginia
2007	Co-Instructor of an intensive, week-long course titled “Population Viability Analysis” for endangered species biologists from state and federal resource agencies. Taught at the US Fish and Wildlife Service’s National Conservation Training Center in West Virginia
2007	Steering Committee for Pacific Seabird Group’s Annual Conference
2007	Review of Washington Department of Natural Resources’ proposed management strategy “Conservation recommendations for a long-term conservation strategy for Marbled Murrelets on Washington DNR lands”
2003	Review of US Forest Service’s proposed management strategy “Impact of the amended Sierra Nevada Framework on California Spotted Owls” for the Natural Resources Defense Council
1999	Review of the US Forest Service’s proposed management strategy “Impact of the Sierra Nevada Framework and Quincy Library Group’s Forest Plan on California Spotted Owls” for the Sierra Nevada Protection Campaign.

University Committees

2013 - present	Alternate Academic Senator
2013- present	Graduate Wildlife Ecology Curriculum Committee, Forest and Wildlife Ecology

2011 Search Committee Member, UW-Madison Climate Scientist position

Guest Lectures

(1) FWE 379 (Principles of Wildlife Management), Spring 2010 and 2011, 5 lectures on Conservation Genetics;
(2) ZOO 651 (Conservation Biology), Spring 2009, 2010, and 2011 Conservation Genetics;
(3) FWE 799 (Population Analysis), Spring 2010, Population Viability Analysis
(4) FWE 655 (Animal Population Dynamics), Spring 2010 and Spring 2012, Population Viability Analysis.

Journals Refereed (since 2009)

Auk, Animal Conservation, Avian Conservation and Ecology, Biological Conservation, Canadian Journal of Zoology, Condor, Conservation Biology, Conservation Genetics, Diversity and Distributions, Ecology, Ecological Applications, Heredity, Journal of Applied Ecology, Journal of Heredity, Journal of Wildlife Management, Marine Ecology Progress Series, Marine Ornithology, Molecular Ecology, Molecular Ecology Resources, Wilson Journal of Ornithology.

REFERENCES

Dr. Steven Beissinger, Professor and A. Starker Leopold Chair in Wildlife Biology and Professor of Conservation Biology
Department of Environmental Science, Policy, and Management
147 Mulford Hall #3114
University of California, Berkeley, CA 94720-3114
510-643-3038
beis@nature.berkeley.edu

Dr. Ralph Gutierrez, Professor and Gordon Gullion Endowed Chair in Forest Wildlife Research
Department of Fisheries, Wildlife, and Conservation Biology
1980 Folwell Avenue
University of Minnesota
St. Paul, Minnesota 55108
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Department of Genetics, Microbiology and Toxicology
Stockholm University
106 91 Stockholm, Sweden
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MICHAEL D. SORENSON

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Boston University
5 Cummington St.
Boston, MA 02215

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Fax (617) 353-6340

e-mail: msoren@bu.edu

EDUCATION

University of Minnesota, Minneapolis
Ph.D. in Ecology, Evolution and Behavior, August 1990

Luther College, Decorah, Iowa
B.A. in Biology, May 1984
Honors: Summa Cum Laude, Phi Beta Kappa

PROFESSIONAL EXPERIENCE

Department of Biology, Boston University (1998 — present)
Professor, September 2010 — present
Department Chair, June 2010 — present
Associate Chair, September 2007 — May 2010
Associate Professor, September 2004 — August 2010
Assistant Professor, January 1998 — August 2004
Courses taught:

BI107	Biology I: Ecology, Behavior & Evolution (Fall 1999—2004, 2006—2009, 2014)
BI303	Evolutionary Ecology (Fall 1998)
BI508	Behavioral Ecology (Spring 1999—2004, 2006—2008, 2010, 2012, 2014)
BI515	Population Genetics (Spring 2009, 2013; Fall 2014)
BI549	Molecular Phylogenetics and Evolution (Fall 1999, 2001, 2003, 2005, 2007)
BI581	Seminar in Biology: Phylogeography (Fall 2000)
BI581	Seminar in Biology: Beyond the Modern Synthesis (Fall 2008)
BI582	Seminar in Biology: Molecular Ecology (Spring 2003, Fall 2004)
BI582	Seminar in Biology: Population Genetics (Spring 2007)

Adjunct Research Investigator, University of Michigan Museum of Zoology, January 2001—

Research Associate, Department of Conservation and Research, National Zoological Park, Smithsonian Institution, March 1998—

Visiting Scholar, Harvard University Museum of Comparative Zoology, January—May 2005

Postdoctoral Fellow, Museum of Zoology, University of Michigan, July 1995—Dec 1997

National Science Foundation Postdoctoral Fellow, Molecular Genetics Laboratory, U.S. National Zoological Park, July 1993—June 1995

Smithsonian Institution Postdoctoral Fellow / Research Associate, Conservation and Research Center, U.S. National Zoological Park, August 1990—June 1995

Dissertation Research in Manitoba, 1986—1989:

Teaching Assistant, University of Minnesota, 1984—1988

Research Assistant, Delta Waterfowl and Wetlands Research Station, Manitoba, 1985

Research Assistant, University of Minnesota (fieldwork on sea otters in Alaska), 1984

FELLOWSHIPS & GRANTS

DISSERTATION RESEARCH: Parent-embryo interactions in glassfrogs - female mating strategies, paternal effort, and adaptive plasticity in hatching, NSF (PI: K.M. Warkentin, co-PI: Sorenson; PhD Candidate: J.R.J. Delia)	2015—2017	$16,380
EAGER: The Genomic Landscape of Species Divergence in an Extraordinary Avian Radiation, NSF (PI: Sorenson)	2014—2016	$149,902
White-nose Syndrome Research at Boston University, Bat Conservation International (PI: Sorenson)	2013—2016	$225,000
DISSERTATION RESEARCH: Bats, Bugs and Pecans: Using Next-Generation Pyrosequencing to Evaluate Ecosystem Services of Insectivorous Bats, NSF (PI: Sorenson; PhD Candidate: E.C. Braun de Torrez)	2012—2015	$14,969
DISSERTATION RESEARCH: Speciation Genomics: Expanded Sampling of a Remarkable Avian Radiation, NSF (PI: Sorenson; PhD Candidate: K.F. Stryjewski)	2012—2014	$14,426
Assessing population genetic structure and gene flow in the little brown myotis, Myotis lucifugus, Morris Animal Foundation (PI: T.H. Kunz; co-PI: Sorenson)	2010—2014	$196,759
Sponsor for Martina Boerner, Postdoctoral Fellow, Marie Curie Actions – International Outgoing Fellowships, European Union	2011—2013	$148,232
Speciation in Lonchura *munias, an extraordinary example of rapid evolutionary diversification*, National Geographic Society (PI: Sorenson)	2011—2012	$21,670
DISSERTATION RESEARCH: RAD Phylogenetics: Harnessing Next-Generation Sequencing for Molecular Systematics, NSF (PI: Sorenson; PhD Candidate: J.M. DaCosta)	2010—2013	$13,223
Multilocus Analyses of Speciation, Hybridization, and Population Structure in Brood Parasitic Indigobirds, NSF (PI: Sorenson)	2007—2013	$440,966
REU supplements, NSF	2007, 2008, 2011	$19,500
ROA supplement, NSF	2011	$10,352
Immune Function, Body Composition and Genetic Correlates of Bat White-nose Syndrome, US Fish & Wildlife Service (PI: T.H. Kunz; co-PI: Sorenson)	2010	$105,000
Ecology of Infectious Diseases: Ecological Influences on Rabies Infections in Bats, NSF/NIH (PI: G.F. McCracken, University of Tennessee)	2004—2007	$1,496,000
(Boston University sub-award: co-PI: T.H. Kunz; senior persons: E.P. Widmaier, M.D. Sorenson)	2004—2007	$578,503
Development of Additional Genetic Markers to Differentiate Mottled Ducks from Mallards and Hybrids in Florida, Florida Fish and Wildlife Conservation Commission (PI: Sorenson)	2005—2006	$20,000
Conflicting Evidence in Waterfowl Systematics, NSF (PI: Sorenson; co-PI: H.F. James, Smithsonian Institution)	2001—2006	$190,970
Speciation in Brood Parasitic Indigobirds, NSF (PI: Sorenson)	2001—2005	$269,714
DISSERTATION RESEARCH: Genetic Diversity and Population Structure of Ectoparasitic Lice Associated with Brood Parasitic Finches Viduidae and their Estrildid Finch Hosts, NSF (PI: Sorenson; PhD Candidate: C.N. Balakrishnan)	2003—2005	$11,955
An Automated DNA sequencer for the Department of Biology at Boston University, NSF (PI: Sorenson; co-PIs: Celenza, Finnerty, Schneider)	2003—2005	$102,887
Hybridization Between Florida Mottled Ducks and Feral Mallards: An Assessment of the Florida Mottled Duck Genome, Wildlife Foundation of Florida & Florida Fish & Wildlife Conservation Commission (PI: Sorenson)	2003—2004	$24,329
Population Genetics, Phylogeography, and Systematics of Black Ducks and Mallards, Delta Waterfowl Foundation (PI: Sorenson)	2001—2004	$56,500

Collaborative Cross-Disciplinary Research in Ecology, Endocrinology, and Molecular Biology, NSF REU Sites Program (PI: Kunz; co-PI: Sorenson)	2000—2003	$163,500
Sponsor for Kristina Sefc, Postdoctoral Fellow, Austrian Science Fund	2000—2002	$64,500
Avian Ordinal Phylogeny Based on Mitochondrial DNA Sequences, NSF (PI: D.P. Mindell, University of Michigan; co-PI: Sorenson)	1998—2002	$210,803
REU supplements, NSF	1998—1999	$15,000
National Science Foundation Postdoctoral Fellowship	1993—1995	$69,600
Friends of the National Zoo (PI: SR Derrickson; co-PI: Sorenson)	1991—1994	$41,000
Smithsonian Institution Postdoctoral Fellowship	1990—1991	$21,000
Graduate Fellowships & Research Grants (various sources)	1984—1989	$71,937

GRADUATE STUDENTS

Marina Ramon (MA, 1999—2000, phylogeography of Caribbean hamlet fish *Hypoplectrus* spp., co-advised with Phil Lobel)

Becki French (MA, 2001—2002, analysis of population differentiation among sympatric indigobird populations using amplified fragment length polymorphisms)

Christopher N. Balakrishnan (PhD, 1999—2005, behavioral and population genetic tests of reproductive isolation among indigobird species in Cameroon)

Violeta Muñoz-Fuentes (PhD, 2001—2005, visiting student from Estacion Biologica de Doñana, Spain, population genetics and hybridization of white-headed ducks and introduced ruddy ducks in Europe)

Ryan J. Harrigan (PhD, 2001—2006, phylogeography and hybridization of mallards, black ducks, and mottled ducks)

Kevin Yana Njabo (PhD, Jan. 2002—2006, phylogeography and systematics of montane forest birds in Cameroon)

Tejashree Modak (MA, 2009—2011, molecular systematics and biogeography of Samoan land birds)

Heather C. Shull (PhD, 2004—2012, molecular evolution and phylogenetics of estrildid and brood parasitic finches)

Jeff DaCosta (PhD, 2007—2014, coalescent analyses of population structure and history in brood parasitic indigobirds)

Aryn Wilder (PhD, 2009—2014, population genomics of little brown myotis, co-advised with T. H. Kunz, BU)

Katherine Faust Stryjewski (PhD, 2008—present, speciation in the *Lonchura* munias of Papua New Guinea)

POSTDOCTORAL ASSOCIATES

Kristina M. Sefc (2000—2003, indigobird speciation and population structure)

Heidi Fisher (2006—2007, hybridization in swordtails *Xiphophorus*, co-advised by Gil Rosenthal, Texas A&M University)

Marianne Moore (2010, MHC and white-nose syndrome in bats, co-advised with T. H. Kunz)

Martina Boerner (2011—2013, genetic variation for fitness in buzzards, co-advised with Oliver Kruger, University of Bielefeld, Germany)

Aryn Wilder (2014—present, immunogenomics of little brown myotis in relation to white-nose syndrome)

MEMBERSHIPS & PROFESSIONAL SERVICE

American Ornithologists Union
  Elected Fellow, August 2009
  Elective Member, April 1998
  Student Awards Committee, 2002
Society for the Study of Evolution
Society of Systematic Biologists
  Council Member, 2007-2009
  Ernst Mayr Award Committee, 2008
Associate Editor, *Evolution: International Journal of Organic Evolution*, 2004—2006
Associate Editor, *Ibis: The International Journal of Avian Science*, 2009—2010
Evolutionary Genetics Panel – National Science Foundation, April 2010
Evolutionary Genetics Panel – National Science Foundation, October 2008
Evolutionary Genetics Panel – National Science Foundation, November 2007
Systematic Biology Panel – National Science Foundation, October 2003

BOSTON UNIVERSITY SERVICE

Charles River Campus IACUC (2008—2011), Chair (2009—2011)

Undergraduate Research Opportunities Program (UROP)
  Faculty Advisory Committee (2004—2007)

Judge for Science Day poster competitions (2000—2004, 2009)

Co-director (with Prof. Thomas H. Kunz) of National Science Foundation Research Experience for Undergraduates Site program (2000—2002)

Biology Department
  Department Chair (2010—2016)
  Chair, Integrative Neurobiology Search Committee (2013—2015)
  Chairman's Advisory Committee (2005—2010)
  Director, DNA Sequencing Core Facility (1998—2007)
  Computer / Web Page Committee (1998—1999, 2007 - 2010)
    Chair, Web Page Redesign Committee (2007—2008)
    Supervisor for Departmental IT Support Staff Person (2007—2010)
  APT Committee (2005—2007)
  Chair, Evolutionary Genomics Search Committee (2009—2010)
  Chair, Marine Biology Search Committee (2008—2009)
  Evolutionary Biology Search Committee (2000—2001)
  Evolutionary Ecology Search Committee (1999—2000)
  Evolutionary Developmental Biology Search Committee (1998—1999)
  Graduate Admissions Committee (1998—2000)
  Ecology, Behavior and Evolution Seminar Series Coordinator (2001—2002)
  Faculty Merit Review Committee (2006, 2007)
  Library Committee (1999—2000, 2003—2004)
  Honors Biology (BI107 HC) Participating Faculty (2000—2009)

FIELD EXPERIENCE

Waterfowl: Manitoba (7 seasons, 22 months total), Alberta, Wisconsin, Nevada, Minnesota, New York; Bahamas (4 trips, New Providence, Abaco, Great Inagua, Long Island)

Songbirds: Papua New Guinea; Africa (7 trips): Cameroon (3 trips), Tanzania (2 trips), Zimbabwe/Zambia, Gambia/Guinea

PUBLICATIONS

DaCosta, J.M. & M.D. Sorenson. Accepted/in revision. ddRAD-seq phylogenetics based on nucleotide, indel, and presence-absence polymorphisms: analyses of two avian genera with contrasting histories. *Molecular Phylogenetics and Evolution.*

Ebel, E.R., J.M. DaCosta, M.D. Sorenson, R.I. Hill, A.D. Briscoe, K.R. Willmott & S.P. Mullen. 2015. Rapid diversification associated with ecological specialization in Neotropical *Adelpha* butterflies. *Molecular Ecology* 24: 2392-2405.

DaCosta, J.M. & M.D. Sorenson. 2014. Amplification biases and consistent recovery of loci in a double-digest RAD-seq protocol. *PLoS One* 9: e106713.

DaCosta, J.M. & M.D. Sorenson. 2014. An experimental test of host song mimicry as a species recognition cue in brood parasitic indigobirds (*Vidua* spp.). *The Auk: Ornithological Advances* 131: 549-558.

Spottiswoode, C.N., K.F. Stryjewski, S. Quader, J.F.R. Colebrook-Robjent & M.D. Sorenson. 2011. Ancient host specificity within a single species of brood parasitic bird. *Proceedings of the National Academy of Science USA* 43: 17738-17742.

Sorenson, M.D. & J.M. DaCosta. 2011. Genotyping HapSTR loci: phase determination from direct sequencing of PCR products. *Molecular Ecology Resources* 11: 1068-1075.

Turmelle, A.S., T.H. Kunz & M.D. Sorenson. 2011. A tale of two genomes: Contrasting patterns of phylogeographic structure in a widely distributed bat. *Molecular Ecology* 20: 357-375.

Culumber, Z.W., H.S. Fisher, M. Tobler, M. Mateos, P.H. Barber, M.D. Sorenson & G.G. Rosenthal. 2011. Replicated hybrid zones of *Xiphophorus* swordtails along an elevational gradient. *Molecular Ecology* 20: 342-356.

Mertl, A.L., M.D. Sorenson & J.F.A. Traniello. 2010. Community-level interactions and functional ecology of major workers in the hyperdiverse ground-foraging *Pheidole* (Hymenoptera, Formicidae) of Amazonian Ecuador. *Insectes Sociaux* 57: 441-452.

Sorenson, M.D., M.E. Hauber & S.R. Derrickson. 2010. Sexual imprinting misguides species recognition in a facultative interspecific brood parasite. *Proceedings of the Royal Society of London, Series B* 277: 3079-3085.

McCracken, K.G., C.P. Barger & M.D. Sorenson. 2010. Phylogenetic and structural analysis of the HbA (a^A/b^A) and HbD (a^D/b^A) hemoglobin genes in two high-altitude waterfowl from the Himalayas and the Andes: bar-headed goose (*Anser indicus*) and Andean goose (*Chloephaga melanoptera*). *Molecular Phylogenetics and Evolution* 56: 649-658.

Bulgarella, M., M.D. Sorenson, J.L. Peters, R.E. Wilson & K.G. McCracken. 2010. Phylogenetic relationships of *Amazonetta*, *Speculanas*, *Lophonetta*, and *Tachyeres*: four morphologically divergent duck genera endemic to South America. *Journal of Avian Biology* 41: 186-199.

McCracken, K.G., C.P. Barger, M. Bulgarella, K.P. Johnson, S.A. Sonsthagen, J. Trucco, T.H. Valqui, R.E. Wilson, K. Winker & M.D. Sorenson. 2009. Parallel evolution in the major hemoglobin genes of eight species of Andean waterfowl. *Molecular Ecology* 18: 3992–4005.

PUBLICATIONS (CONT.)

Krüger, O., M.D. Sorenson & N.B. Davies. 2009. Does coevolution promote species richness in parasitic cuckoos? *Proceedings of the Royal Society of London, Series B* 276: 3871-3879.

Njabo, K.Y. & M.D. Sorenson. 2009. Origin of Bannerman's turaco in relation to historical climate change and the distribution of West African montane forests. *Ostrich: Journal of African Ornithology* 80: 1-7.

Campbell, B.C., P.B. Gray, D.T.A. Eisenberg, P. Ellison & M.D. Sorenson. 2009. Androgen receptor CAG repeats and body composition among Ariaal men. *International Journal of Andrology* 32: 140-148.

Balakrishnan, C.N., K.M. Sefc & M.D. Sorenson. 2009. Incomplete reproductive isolation following host shift in brood parasitic indigobirds. *Proceedings of the Royal Society of London, Series B* 276: 219-228.

Harrigan, R.J., M.E. Mazza & M.D. Sorenson. 2008. Computation versus cloning: evaluation of two methods for haplotype determination. *Molecular Ecology Resources* 8: 1239-1248.

Muñoz-Fuentes, V., A.J. Green & M.D. Sorenson. 2008. Comparing the genetics of wild and captive populations of white-headed ducks *Oxyura leucocephala*: consequences for recovery programmes. *Ibis* 150: 807-815.

Njabo, K.Y., R.C.K. Bowie & M.D. Sorenson. 2008. Phylogeny, biogeography and taxonomy of the African wattle-eyes (Aves: Passeriformes: Platysteiridae). *Molecular Phylogenetics and Evolution* 48: 136-149.

Eisenberg, D.T.A., B. Campbell, P.B. Gray & M.D. Sorenson. 2008. Dopamine receptor genetic polymorphisms and body composition in undernourished pastoralists: An exploration of nutrition indices among nomadic and recently settled Ariaal men of northern Kenya. *BMC Evolutionary Biology* 8: 173.

Brown, J.W., J.S. Rest, J. García-Moreno, M.D. Sorenson & D.P. Mindell. 2008. Strong mitochondrial DNA support for a Cretaceous origin of modern avian lineages. *BMC Biology* 6: 6.

Chilton, G. & M.D. Sorenson. 2007. Genetic identification of eggs purportedly from the extinct Labrador duck. *The Auk* 124: 962-968.

Sefc, K.M., R.B. Payne & M.D. Sorenson. 2007. Single base errors in PCR products from avian museum specimens. *Conservation Genetics* 8: 879-884.

Krüger, O., N.B. Davies & M.D. Sorenson. 2007. The evolution of sexual dimorphism in parasitic cuckoos: sexual selection or coevolution? *Proceedings of the Royal Society of London, Series B* 274: 1553-1560.

Brennan, P.L.R., R.O. Prum, K.G. McCracken, M.D. Sorenson, R.E. Wilson & T.R. Birkhead. 2007. Coevolution of male and female genital morphology in waterfowl. *PLoS ONE* 2: e418.

Payne, R.B. & M.D. Sorenson. 2007. Integrative systematics at the species level: plumage, songs and molecular phylogeny of quail-finch *Ortygospiza*. *Bulletin of the British Ornithological Club* 127: 4-26.

Muñoz-Fuentes, V., C Vilà, A.J. Green, J.J. Negro & M.D. Sorenson. 2007. Hybridization between white-headed ducks and introduced ruddy ducks in Spain. *Molecular Ecology* 16: 629-638.

Sefc, K.M., R.B. Payne & M.D. Sorenson. 2007. Genetic differentiation after founder events: an evaluation of F_{ST} estimators with empirical and simulated data. *Evolutionary Ecology Research* 9: 21-39.

Balakrishnan, C.N. & M.D. Sorenson. 2007. Dispersal ecology versus host specialization as determinants of ectoparasite distribution in brood parasitic indigobirds and their estrildid finch hosts. *Molecular Ecology* 16: 217-229.

Muñoz-Fuentes, V., A. J. Green, M. D. Sorenson, J. J. Negro & C. Vilà. 2006. The ruddy duck *Oxyura jamaicensis* in Europe: natural colonisation or human introduction? *Molecular Ecology* 15: 1441-1454.

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Balakrishnan, C.N. & M.D. Sorenson. 2006. Song discrimination suggests premating isolation among sympatric indigobird species and host races. *Behavioral Ecology* 17: 473-478.

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Muñoz-Fuentes, V., A.J. Green, J.J. Negro & M.D. Sorenson. 2005. Population structure and loss of genetic diversity in the endangered white-headed duck, *Oxyura leucocephala*. *Conservation Genetics* 6: 999-1015.

Kulikova, I.V., S.V. Drovetski, D.D. Gibson, R.J. Harrigan, S. Rohwer, M.D. Sorenson, K. Winker, Y.N. Zhuravlev & K.G. McCracken. 2005. Phylogeography of the mallard (*Anas platyrhynchos*): hybridization, dispersal, and lineage sorting contribute to complex geographic structure. *The Auk* 122: 949-965.

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McCracken, K.G. & M.D. Sorenson. 2005. Is homoplasy or lineage sorting the source of incongruent mtDNA and nuclear gene trees in the stiff-tailed ducks (*Nomonyx-Oxyura*)? *Systematic Biology* 54: 35-55.

Payne, R.B., C.R. Barlow, C.N. Balakrishnan & M.D. Sorenson. 2005. Song mimicry of black-bellied firefinch *Lagonosticta rara* and other finches by brood-parasitic indigobirds *Vidua camerunensis* in West Africa. *The Ibis* 147: 130-143.

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García-Moreno, J., M.D. Sorenson & D.P. Mindell. 2003. Congruent avian phylogenies inferred from mitochondrial and nuclear DNA sequences. *Journal of Molecular Evolution* 57: 27-37.

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Balakrishnan, C.N., S.L. Monfort, A. Gaur, L. Singh & M.D. Sorenson. 2003. Phylogeography and conservation genetics of Eld's Deer (*Cervus eldi*). *Molecular Ecology* 12: 1-10.

Sorenson, M.D. & R.B. Payne. 2002. Molecular genetic perspectives on avian brood parasitism. *Integrative and Comparative Biology* 142: 388-400.

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Sorenson, M.D., A. Cooper, E. Paxinos, T.W. Quinn, H.F. James, S.L. Olson & R.C. Fleischer. 1999. Relationships of the extinct moa-nalos, flightless Hawaiian waterfowl, based on ancient DNA. *Proceedings of the Royal Society of London, Series B* 266: 2187-2193.

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Johnson, K.P. & M.D. Sorenson. 1999. Phylogeny and biogeography of the dabbling ducks (Genus: *Anas*): A comparison of molecular and morphological evidence. *The Auk* 116: 792-805.

Johnson, K.P., F. McKinney & M.D. Sorenson. 1999. Phylogenetic constraint on male parental care in the dabbling ducks. *Proceedings of the Royal Society of London, Series B* 266: 759-763.

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Mindell, D.P., M.D. Sorenson & D.E. Dimcheff. 1998. An extra nucleotide is not translated in mitochondrial ND3 of some birds and turtles. *Molecular Biology and Evolution* 15: 1568-1571.

Mindell, D.P., M.D. Sorenson & D.E. Dimcheff. 1998. Multiple independent origins of mitochondrial gene order in birds. *Proceedings of the National Academy of Science USA* 95: 10693-10697.

Johnson, K.P. & M.D. Sorenson. 1998. Comparing molecular evolution in two mitochondrial protein coding genes (Cytochrome *b* and ND2) in the dabbling ducks (Tribe: Anatini). *Molecular Phylogenetics and Evolution* 10: 82-94.

Sorenson, M.D. 1998. Patterns of parasitic egg laying and typical nesting in redhead and canvasback ducks. Pp. 357-375 *in* S.I. Rothstein & S.K. Robinson, eds. *Parasitic birds and their hosts*. Oxford University Press: New York.

Sorenson, M.D. & T.W. Quinn. 1998. Numts: A challenge for avian systematics and population biology. *The Auk* 115: 214-221.

Young, H.G., M.D. Sorenson & K.J. Johnson. 1997. A description of the Madagascar teal *Anas bernieri* and examination of relationships with the grey teal *A. gracilis*. *Wildfowl* 48: 174-180.

Worthy, T.H., R.N. Holdaway, M.D. Sorenson & A.C. Cooper. 1997. Description of the first complete skeleton of *Cnemiornis calcitrans* (Aves: Anatidae), and a reassessment of the relationships of *Cnemiornis*. *Journal of Zoology* (London) 243: 695-723.

Mindell, D.P., M.D. Sorenson, C. J. Huddleston, H. Miranda, A. Knight, S. J. Sawchuk & T. Yuri. 1997. Phylogenetic relationships among and within select avian orders based on mitochondrial DNA. Pp. 213-247 *in* D.P. Mindell, ed. *Avian Molecular Evolution and Systematics*. Academic Press: New York.

Sorenson, M.D. 1997. Effects of intra- and interspecific brood parasitism on a precocial host, the canvasback, *Aythya valisineria*. *Behavioral Ecology* 8:153-161.

Sorenson, M.D. & R.C. Fleischer. 1996. Multiple independent transpositions of mitochondrial DNA control region sequences to the nucleus. *Proceedings of the National Academy of Science USA* 93:15239-15243.

Cooper, A., J.M. Rhymer, H.F. James, S.L. Olson, C.E. McIntosh, M.D. Sorenson & R.C. Fleischer. 1996. Ancient DNA and island endemics. *Nature* 381: 484.

Arnold, T.W., M.G. Anderson, R.B. Emery, M.D. Sorenson & C. de Sobrino. 1995. The effect of late-incubation body mass on reproductive success of canvasbacks and redheads. *The Condor* 97: 953-962.

Sorenson, M.D. 1995. Evidence of conspecific nest parasitism and egg discrimination in the sora. *The Condor* 97: 819-821.

Arnold, T.W., M.D. Sorenson & J.J. Rotella. 1993. Relative success of overwater and upland mallard nests in southwestern Manitoba. *Journal of Wildlife Management* 57: 578-581.

Sorenson, M.D. 1993. Parasitic egg laying in canvasbacks: frequency, success and individual behavior. *The Auk* 110: 57-69.

Sorenson, M.D. 1992. Comment: Why is conspecific nest parasitism more common in waterfowl than in other birds? *Canadian Journal of Zoology* 70: 1856-1858.

Sorenson, M.D. 1991. The functional significance of parasitic egg laying and typical nesting in redhead ducks: an analysis of individual behaviour. *Animal Behaviour* 42: 771-796.

Sorenson, M.D. 1990. Parasitic egg laying in redhead and canvasback ducks. PhD Thesis, University of Minnesota: Minneapolis.

Sorenson, M.D. 1989. Effects of neck-collar radio transmitters on female redhead ducks. *Journal of Field Ornithology* 60: 523-528.

PUBLICATIONS (CONT.)

Arnold, T.W. & M.D. Sorenson. 1988. A record early season for marsh-breeding birds in southwestern Manitoba. *Blue Jay* 46: 133-135.

COMPUTER PROGRAM

Sorenson, M.D. & E.A. Franzosa. 2007. *TreeRot*, version 3. Boston University, Boston, MA. (Available at: http://people.bu.edu/msoren/TreeRot)

Sorenson, M.D. 1999. *TreeRot*, version 2. Boston University, Boston, MA.

Sorenson, M.D. 1996. *TreeRot*. University of Michigan, Ann Arbor.

This program generates constraint statements that aid in the determination of support indices in phylogenetic analysis. Systematists have used the program extensively for analyses of both molecular and morphological data. The three versions of the program have been cited in over **1000** journal articles to date.

POPULAR ARTICLES

Payne, R.B. & M.D. Sorenson. 2006. Song lines. *NATURAL HISTORY* 115(7): 41 (September 2006).

Sorenson, M.D. 1992. The parasitic tactics of redhead ducks. *ANIMA: Magazine of Natural History*. No. 237: 78-81 (June 1992). Heibonsha Limited, Publishers: Tokyo.

Sorenson, M.D. 1989. Brood parasitism in the redhead duck. *IMPRINT* 6(4): 4-5. James Ford Bell Museum of Natural History: Minneapolis.

MANUSCRIPT/PROPOSAL REVIEWS

Acta Zoologica Sinica
American Naturalist
Animal Behaviour
Animal Conservation
The Auk: An International Journal of Ornithology
Behavioral Ecology
Behavioral Ecology and Sociobiology
Biological Journal of the Linnean Society
Biology Letters
Bird Behavior
BMC Evolutionary Biology
Canadian Journal of Zoology
Cladistics
Climatic Change
The Condor
Conservation Genetics
Ecology
Emu: Austral Ornithology
Ethology
Evolution
Evolutionary Ecology
Genetics
Genome
Hormones and Behavior
The Ibis: The International Journal of Avian Science
Journal of Avian Biology
Journal of Biogeography
Journal of Biological Systems
Journal of Experimental Biology
Journal of Field Ornithology
Journal of Great Lakes Research
Journal of Heredity
Journal of Theoretical Biology
Journal of Wildlife Management
Journal of Zoological Systematics and Evolutionary Research
Mitochondrial DNA
Molecular Biology and Evolution
Molecular Ecology
Molecular Ecology Resources
Molecular Phylogenetics and Evolution
Nature
PLoS Biology
PLoS Genetics
Prairie Naturalist
Proceedings of the National Academy of Sciences USA
Proceedings of the Royal Society of London B*, Biological Sciences*
Quarterly Review of Biology
Scopus (East African Journal of Ornithology)
Systematic Biology
Trends in Ecology and Evolution
Wilson Bulletin
Zoological Studies

The American Ornithologists Union
Chilean National Fund for Scientific & Technological Development (FONDECYT)
Delta Waterfowl & Wetlands Research Station
Finnish Academy of Science
Marsden Fund, Royal Society of New Zealand
National Geographic Society
National Science Foundation
Netherlands Organisation for Scientific Research (NWO)

INVITED CONFERENCE SYMPOSIA

Symposium: Genomic Approaches to Understanding Avian Speciation. AOU, COS, SCO Joint Meeting, Estes Park, Colorado, September 2014 (presentation by PhD student Katherine Stryjewski)

Symposium: Avian Diversification in the Old World Tropics. American Ornithologists' Union, Chicago, Illinois, August 2013

International Symposium on Avian Brood Parasitism, Haikou, Hainan, China, November 2012

Symposium: Speciation. American Ornithologists' Union, Laramie, Wyoming, August 2007

Symposium: Phylogenies and Behaviour. Association for the Study of Animal Behaviour, London, December 2004

Symposium: Problems and Opportunities in Avian Deep Phylogenetics. 3rd North American Ornithological Conference, New Orleans LA. September 2002

Symposium: Untangling Coevolutionary History. Society for Systematic Biology, Champaign-Urbana, Illinois, June 2002

Symposium: Living Together: the Dynamics of Symbiotic Interactions. Society for Integrative and Comparative Biology, Chicago, Illinois, January 2001

Symposium: Coevolution in Brood Parasitism, 22nd International Ethological Conference, Nagano, Japan, August, 1991

Symposium: Parasitic Birds and Their Hosts, American Ornithologists' Union, Los Angeles, California, June, 1990

RECENT INVITED LECTURES (2007—2015)

CIBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Portugal, December 2014

Hoslett Memorial Lecture, Luther College, Decorah IA, October 2014

Department of Biological Sciences, Wright State University, October 2013

Department of Ecology and Evolution, Stony Brook University, December 2012

Guest Lecture, OEB 190, Biology and Diversity of Birds, Harvard University, March 2012

Department of Evolution Ecology and Organismal Biology, Ohio State University, April 2011

31st Annual Darwin Festival, Salem State College, Salem, MA, February 2010

Department of Ecology and Evolutionary Biology, University of California Santa Cruz, September 2009

Department of Ecology and Evolutionary Biology, University of California Los Angeles, September 2009

California Academy of Sciences, San Francisco, September 2009

Museum of Vertebrate Zoology, University of California Berkeley, September 2009

National Geographic Society, Committee for Research and Exploration, Washington D.C., July 2009

Institute for Genomic Biology, University of Illinois at Urbana-Champaign, May 2009

Field Museum of Natural History, Chicago, IL, May 2009

Guest Lecture, OEB 190, Biology and Diversity of Birds, Harvard University, April 2009

"BioMixer", Department of Biology, Boston University, December 2008

Guest Lecture, OEB 190, Biology and Diversity of Birds, Harvard University, April 2007

1. Name and Professional Address.

Garth Michael Spellman
Curator of Ornithology
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2100 Colorado Blvd
Denver, CO 80205-5798
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Garth.spellman@dmns.org

Rank.

Curator

Education.

Ph.D. University of Nevada, Las Vegas, Las Vegas, NV. 2006. Biological Sciences.
M. S. University of Alaska Fairbanks, Fairbanks, AK. 2000. Zoology.
B. A. Carleton College, Northfield, MN. 1996. Biology.

Professional Experience.

Program Director, Evolutionary Processes Cluster, Division of Environmental Biology, Biological Sciences Directorate, National Science Foundation. 2013 – 2015.
Associate Professor, Black Hills State University, School of Natural Sciences. 2012 – 2015.
Program Director, Master's of Science in Integrative Genomics, Black Hills State University. 2009 – 2013.
Assistant Professor, Black Hills State University, Department of Biology. 2008 – 2012.
Research Assistant Professor, Black Hills State University, Department of Biology, Center for the Conservation of Biological Resources. 2006 – 2008.
Research Associate, Marjorie Barrick Museum of Natural History, University of Nevada, Las Vegas. 2006 – 2012.
Visiting researcher, Dr. Scott V. Edwards' lab, Museum of Comparative Zoology, Harvard University. 2007 (April).
DNA Laboratory Manager and Genetic Resources Collections Manager, Marjorie Barrick Museum of Natural History, University of Nevada, Las Vegas. 2001 – 2006.
Instructor, Department of Biological Sciences, University of Nevada, Las Vegas. 2004.
Graduate Teaching Assistant, Department of Biological Sciences, University of Nevada, Las Vegas. 2000.
Graduate Research Assistant, University of Alaska Museum. 1999 – 2000.
Graduate Teaching Assistant, Department of Biology, University of Alaska, Fairbanks. 1998 – 1999.

2. Research, Scholarly, and Creative Activities.

Scopus h index = 14 with 423 total citations. Google Scholar h index = 15 with 550 total citations, avg./cit./article~ 27. Multi-author Annotation: U= undergraduate mentee, G = graduate student mentee and * = senior author.

a. Articles in Refereed Journals.

J.D. Manthey, J. Klicka, and **G.M. Spellman*.** 2015. Chromosomal patterns of diversity and differentiation in creepers: a next-gen phylogeographic investigation of *Certhia Americana*. *Heredity.* doi:10.1038/hdy.2015.27

P. Van Els, **G.M. Spellman**, B.T. Smith, and J. Klicka. 2014. Extensive gene flow characterizes the phylogeography of a widespread North American migrant bird: Black-headed Grosbeak (*Pheucticus melanocephalus*). *Molecular Phylogenetics and Evolution*. **78**: 148-159. http://dx.doi.org/10.1016/j.ympev.2014.04.028

J.D. Manthey^G, J. Klicka, and **G.M. Spellman*.** 2014**.** Effects of climate change on the evolution of Brown Creeper (*Certhia americana*) lineages. *The Auk: Ornithological Advances*.**131**(3): 559-570. http://dx.doi.org/10.1642/AUK-13-242.1

J.D. Manthey^G and **G.M. Spellman***. 2014. Increased efficacy of fixation in Z-linked markers between lineages of the Brown Creeper (*Certhia americana*): the fast-Z effect? *Journal of Avian Biology*. **45**(2): 149-156. doi: 10.1111/j.1600-048X.2013.00233.x

P.C. Pulgarín-R^U, B.T. Smith, R.W. Bryson, Jr., **G.M. Spellman***, and J. Klicka*. 2013. Multilocus phylogeny and biogeography of the New World *Pheucticus* grosbeaks (Aves: Cardinalidae). *Molecular Phylogenetics and Evolution*. **69:** 1222-1227. http://dx.doi.org/10.1016/j.ympev.2013.05.022.

J.D. Manthey^G, J. Klicka, and **G.M. Spellman*.** 2012. Is gene flow promoting the reversal of Pleistocene divergence in the Mountain Chickadee (*Poecile gambeli*)? *PLoS ONE* **7**(11): e49218.

V.W. Walstrom^G, J Klicka, and **G.M. Spellman***. 2012. Speciation in the White-breasted Nuthatch (*Sitta carolinensis*): a multilocus prospective. *Molecular Ecology*. **21**:907-920.

J.D. Manthey^G, J. Klicka, and **G.M. Spellman*.** 2011**.** Isolation driven divergence: speciation in a widespread North American songbird (Aves: Certhiidae). *Molecular Ecology*. **20**:4371–4384.

J. Klicka, **G.M. Spellman**, K.S. Winker, V. Chua, and B.T. Smith. 2011. Phylogeography and population-genetic analysis of a widespread, sedentary North American bird: The Hairy Woodpecker (*Picoides villosus*). *The AUK* **128**(2):346−362.

J.D. Manthey^G, J. Klicka, and **G.M. Spellman***. 2011. Cryptic diversity in a widespread North American songbird: phylogeography of the Brown Creeper (*Certhia americana*). *Molecular Phylogenetics and Evolution*. **58,** 502-512.

J. J. Stone, S. A. Clay, **G.M. Spellman**. 2010. Tylosin and chlortetracycline effects during swine manure digestion: influence of sodium azide. *Bioresource Technology*. **101**, 9515–9520. doi:10.1016/j.biortech.2010.07.116

R. Mettler^{UG} and **G.M. Spellman***. 2009. A hybrid zone revisited: molecular analysis of the maintenance, movement, and evolution of a Great Plains avian (Cardinalidae: *Pheucticus*) hybrid zone. *Molecular Ecology*. **18**, 3256-3267. DOI: 10.1111/j.1365-294X.2009.04217.x

J. M. DaCosta, **G.M. Spellman**, P. Escalante-Pliego, and J. Klicka. 2009. A molecular systematic revision of two historically problematic songbird clades: *Aimophila* and *Pipilo*. *Journal of Avian Biology*. **40**, 206-216.

J. J. Stone, S. A. Clay, Z. Zhu, K. Wong, L. Porath, **G.M. Spellman**. 2009. Effect of Antimicrobial Compounds Tylosin and Chlorotetracycline during Batch Anaerobic Swine Manure Digestion. *Water Research* **43,** 4740-4750.

G.M. Spellman*, A. Cibois, R. Moyle, K. Winker, and F.K. Barker. 2008. Clarifying the systematics of an enigmatic avian lineage: What is a Bombycillid?. *Molecular Phylogenetics and Evolution.* 49,1036-1040.

C.M. Anderson, **G.M. Spellman**, C. Ferrell, K. Strickler, and S.K. Sarver. 2008. Conservation genetics of American Dipper (*Cinclus mexicanus*): the genetic status of a population in severe decline. *Conservation Genetics*. **9,** 939-944. DOI 10.1007/s10592-007-9429-5

A. Maj, **G.M. Spellman**, and S.K. Sarver. 2008. The complete CDS of the prion protein (PRNP) gene of the African lion (*Panthera leo*). *Virus Genes*. **36**, 433-434.

G.M. Spellman and J. Klicka. 2007. Phylogeography of the White-breasted Nuthatch (*Sitta carolinensis*): diversification in North American pine and oak woodlands. *Molecular Ecology* **16**(8), 1729-1740.

G.M. Spellman, B. Riddle, and J. Klicka. 2007. Phylogeography of the Mountain Chickadee (*Poecile gambeli*): diversification, introgression, and expansion in response to Quaternary climate change. *Molecular Ecology***, 16,** 1055-1068.

G.M. Spellman and J. Klicka. 2006. Testing hypotheses of Pleistocene population history using coalescent simulations: phylogeography of the pygmy nuthatch (Sitta pygmaea). *Proceedings of the Royal Society Series B.* **273**, 3057-3063.

J. Klicka, K. Burns, and **G.M. Spellman**. 2007. Defining a monophyletic Cardinalini: A molecular perspective. *Molecular Phylogenetics and Evolution* **45**, 1014-1032.

J.M. DaCosta, **G.M. Spellman**, and J Klicka. 2007. Bilateral Gynandromorphy in a White-ruffed Manakin (*Corapipo altera*). *The Wilson Journal of Ornithology*. **119,** 290-292.

J. Klicka and **G. M. Spellman**. 2007. A molecular evaluation of the North American "grassland" sparrow clade. *The AUK* **124**, 537-551.

J. Klicka, G. Voelker, and **G.M. Spellman**. 2005. A systematic revision of the true thrushes (Aves: Turdinae). *Molecular Phylogenetics and Evolution* **34,**486-500.

G. Voelker and **G.M. Spellman**. 2004. Nuclear and mitochondrial DNA evidence of polyphyly in the avian superfamily Muscicapoidea. *Molecular Phylogenetics and Evolution* **30**(2), 386-394.

i. Manuscripts in Review or Nearing Completion.

J.A. Chaves, E. Birmingham, P. Escalante, **G.M. Spellman**, and J. Klicka. *In Review*. Climate driven ecological shift yields a rapid and recent radiation in the New World's most widely distributed songbird, the House Wren (*Troglodytes aedon*). *Systematic Biology*.

G.M. Spellman*, A. Howe^{G}, K. Kennedy^{G}, J. McAllister^{G}, J. Nies^{G}, and J.Sheets^{G}. *In prep.* Insights into the shared evolutionary history of birds and their gut microbiota. *Intended for ISME.*

b. Monographs, Reports, and Extension Publications.

G.M. Spellman. 2010. Are subspecies still of interest to Ornithology today? *South Dakota Bird Notes* **62(2)**, 25-26.

C. Cicero, T. Jervis, and **G.M. Spellman**. 2010. Split Mountain Chickadee (*Poecile gambeli*) into two species. Report reviewed by the American Ornithologists Union taxonomic review board.

G.M. Spellman. 2006. Comparative phylogeography of pine-oak birds. Dissertation. University of Nevada, Las Vegas.

c. Talks, Abstracts and Other Professional Papers Presented.

i. Invited Talks.

2014	NSF Division of Integrative Organismal Systems, Arlington, VA.
2013	American Museum of Natural History, New York, NY.
2012	NSF Division of Environmental Biology, Arlington, VA.
2012	Department of Biology, Augustana College, Sioux Falls, SD.
2011	Institute of Agricultural and Natural Resources, University of Nebraska Lincoln, Lincoln, NE.
2011	Department of Biology, Concordia College, Moorhead, MN.
2011	Department of Biology, University of South Dakota, Vermillion, SD.
2009	Black Hills State University Lunch Lecture Series, Spearfish, SD.
2008	Department of Physiology and Zoology, University of Wyoming, Laramie, WY.
2007	Black Hills State University, Spearfish, SD.
2007	Museum of Comparative Zoology, Harvard University, Cambridge, MA.
2006	Black Hills State University, Spearfish, SD.
2005	American Museum of Natural History Ornithology lecture series, New York, NY.

ii. Presented Papers and Posters.

2014

Kin Han, **G.M. Spellman**, and Rebecca Kimball. A bird’s eye view of habitat fragmentation: comparing the effects at ecological and evolutionary timescales in two sister species. Evolution 2014, Raleigh, NC.

Raeann Mettler, John Klicka, and **G.M. Spellman***. RADTag sequencing to study phylogenetic relationships and diversification within the House Wren (*Troglodytes aedon*) complex. Evolution 2014, Raleigh, NC.

2013

Christine Bubac^{G} and **G.M. Spellman***. How habitat connectivity shapes genetic structure during range expansion: insights from Virginia’s Warbler in the Black Hills. One Hundred and Thirty-first Stated Meeting of the American Ornithologists' Union, Chicago, IL.

Joseph D. Manthey and **G.M. Spellman***. A genomic perspective on the phylogeography of the Brown Creeper. One Hundred and Thirty-first Stated Meeting of the American Ornithologists' Union, Chicago, IL.

Lindsey Kreun^{G}, Joseph D. Manthey, John Klicka, and **G.M. Spellman***. Comparative genomics of Pleistocene divergence. One Hundred and Thirty-first Stated Meeting of the American Ornithologists' Union, Chicago, IL.

2012

G.M. Spellman*, Amanda Howe, Kyle Kennedy^{G}, Joseph McAllister, Jason Nies, Jordan, SheetsG. Insights into the shared evolutionary history of birds and their gut microbiota. Fifth North American Ornithological Congress, Vancouver, BC.

Christine Bubac^G and **G.M. Spellman***. How habitat connectivity shapes genetic structure during range expansion: insights from Virginia's Warbler in the Black Hills. Fifth North American Ornithological Congress, Vancouver, BC and South Dakota Ornithologists Fall Meeting.

Kelsey Prosser^G and **G.M. Spellman***. Molecular characterization of avian gut parasites (Eimeria). Fifth North American Ornithological Congress, Vancouver, BC and South Dakota Ornithologists Fall Meeting.

Kyle Kennedy^G and **G.M. Spellman***. Examining the modes of selection maintaining the Pheucticus Great Plains hybrid zone using genomic cline analysis of AFLP data. Fifth North American Ornithological Congress, Vancouver, BC and South Dakota Ornithologists Fall Meeting.

Kyle Kennedy^G and **G.M. Spellman***. Estimating Hybrid Zone Origins using Ecological Niche Models. Fifth North American Ornithological Congress, Vancouver, BC.

Joseph MantheyG, Scott V. Edwards, John Klicka, **G.M. Spellman***. Ecological selection or environmental drift in western North American phylo-species? Fifth North American Ornithological Congress, Vancouver, BC.

Brian Byrne^U, Kelsey Prosser^G**, G.M. Spellman***. Survey of Avian Gut Borne Parasites: Insights into Codiversification and Diversity. 2012 South Dakota Biomedical Research Infrastructure Network Annual meeting.

Heather Weisser^U and **G.M. Spellman***. West Nile Virus in House Wren nestlings. 2012 South Dakota Biomedical Research Infrastructure Network Annual meeting.

G.M. Spellman. Describing the influences of host natural history and phylogeny on the bird gut microbiome. 2012 South Dakota Biomedical Research Infrastructure Network Annual meeting.

2011

Van Els, P.; B.T. Smith; **G.M. Spellman**; J Klicka, A multilocus phylogeography of the Black-Headed Grosbeak. 129th Stated Meeting of the American Ornithologists' Union, Jacksonville, FL.

Joseph Manthey^G & **G.M. Spellman***. The fast-Z effect: increased efficacy of fixation in Z-linked markers in Certhia americana. Evolution 2011. Norman, OK.

Justin Tibbits^U, Joseph Manthey^G, Christine Bubac^U, J. Klicka, **G.M. Spellman***. Testing alternative hypotheses of niche evolution in the Hairy Woodpecker. Evolution 2011, Norman, OK.

2010

G.M. Spellman*, Daniel Turveen^U, Pankaj Mehrotra^G, Chirstine Bergeon Burns, and Ellen Ketterson. Malaria in the Black Hills: pathogen mediated selection in the White-winged Junco. Evolution 2010, Portland, OR.

Joseph Manthey^G and **G.M. Spellman***. Asymmetric gene flow following secondary contact in the Mountain Chickadee. Evolution 2010, Portland, OR.

John Duvall-Jisha^G and **G.M. Spellman***. Polygyny and population structure in the ant Camponotus modoc. Evolution 2010, Portland, OR.

Laura Kramer*, J Klicka, **G.M. Spellman***. A multilocus study of demographic and evolutionary history in the Black-headed Grosbeak (Pheucticus melanocephalus). Evolution 2010, Portland, OR.

V. Woody Walstrom[G] and **G.M. Spellman***. Speciation in the White-breasted Nuthatch. Joint meeting of Cooper Ornithological Society, American Ornithologists' Union, and Society of Canadian Ornithologists / Société des Ornithologistes du Canada. San Diego, CA.

Joseph Manthey[G] and **G.M. Spellman***. Multilocus phylogeography of the Brown Creeper. Joint meeting of Cooper Ornithological Society, American Ornithologists' Union, and Society of Canadian Ornithologists / Société des Ornithologistes du Canada. San Diego, CA.

Vivien Chua, B.T. Smith, **G.M. Spellman**, K. Winker, and J. Klicka. Phylogeography of a widespread North American woodpecker: Picoides villosus. Joint meeting of Cooper Ornithological Society, American Ornithologists' Union, and Society of Canadian Ornithologists / Société des Ornithologistes du Canada. San Diego, CA.

G.M. Spellman*, K. Burns, S. Cameron, J. Hudon, and J. Klicka. Glacial isolation and postglacial expansion enhance genetic diversity in a Neotropical migrant passerine. 128th Stated meeting of the American Ornithologists' Union, San Diego, CA.

2009

G.M. Spellman* and Raeann Mettler[G]. Grosbeak hybridization in the Great Plains: the roles of intrinsic and extrinsic selection in the narrowing of a transition zone. South Dakota Ornithologists Union Annual Meeting, Pierre, SD.

V. Woody Walstrom[G] and **G.M. Spellman***. Speciation in the White-breasted Nuthatch (Sitta carolinensis): a multilocus study of diversification in North American pine and oak woodlands. 127th Stated Meeting of the American Ornithologists Union, Philadelphia, PA the Ecological Genomics Symposium 2009 Kansas City, KS.

Joseph Manthey[G] and **G.M. Spellman*.** Complex speciational history in the Brown Creeper inferred from multilocus sequence data. 127th Stated Meeting of the American Ornithologists Union, Philadelphia, PA and the Ecological Genomics Symposium 2009 Kansas City, KS.

Laura Kramer[U] and **G.M. Spellman***. Comparison of the evolutionary rates of anonymous and intron loci for the usefulness in avian evolutionary biology. South Dakota Academy of Sciences.

Daniel Turveen[U], Pankaj Mehrotra[G], Chirstine Bergeon Burns, Ellen Ketterson, and **G.M. Spellman***. Malarial Parasites in the Endemic White-winged Junco: the impacts of seasonality, sex, and body condition on infection rates. NIH-INBRE Summer Research Fellow Convocation, Vermillion, South Dakota.

2008

G.M. Spellman and J. Klicka. Speciation in a western (US) woodland songbird (Bushtit, Psaltriparus minimus): comparing patterns and process inferred from mtDNA and 19 anonymous nuclear loci. Evolution 2008, University of Minnesota.

R. Mettler[G] and **G.M. Spellman***. A hybrid zone revisited: molecular analysis of the maintenance, movement, and evolution of a Great Plains avian (Cardinalidae: Pheucticus) hybrid zone. Evolution 2008, University of Minnesota.

M. Mika, **G.M. Spellman**, P. Escalante-Pliego, J. Klicka. Phylogeography and diversification in the red-eyed towhee species complex. 126th Stated meeting of the American Ornithologist Union, Portland, Oregon.

C. Cicero, M. Koo, **G.M. Spellman,** K. Winker, J. Klicka. Linking phylogeography and distributional ecology. 126th Stated meeting of the American Ornithologist Union, Portland, Oregon.

L. Kramer[U] and **G.M. Spellman***. Multilocus comparative phylogeography of the Black-headed Grosbeak. Undergraduate research Day, Pierre, SD and NCUR, Salisbury Unviersity, MD.

J. Moser[U] and **G.M. Spellman***. Evolution of opsin genes in the Cardinalidae. NIH-INBRE Summer Research Fellow Convocation, Vermillion, South Dakota.

2007

G.M. Spellman* and J. Klicka. Speciation in North American Certhiid(s): Is the Brown Creeper a single morphologically diverse species? 125th Stated Meeting of the American Ornithologists' Union, Laramie, Wyoming.

J. Moser[U] and **G.M. Spellman***. Evolution of avian malarial parasites in geographically structured host species: a phylogenetic approach. 125th Stated Meeting of the American Ornithologists' Union, Annual Meeting, Laramie, Wyoming; NIH-INBRE Summer Research Fellow Convocation, Vermillion, South Dakota; Evolution 2008, University of Minnesota.

G. M. Spellman*, C. Cicero, K. Winker, and J. Klicka. Clarifying the evolutionary history of a morphologically diverse species: Phylogeography of the Steller's Jay. 125th Stated Meeting of the American Ornithologists' Union, Laramie, Wyoming.

J. Moser[U], J. Klicka, **G.M. Spellman***. Phylogeography of the Bushtit (Psaltriparus minimus). 125th Stated Meeting of the American Ornithologists' Union, Laramie, Wyoming and BHSU Undergraduate Research symposium.

R.D. Mettler[G] and **G.M. Spellman***. Molecular analysis of Grosbeak (Cardinalidae: Pheucticus) hybridization in South Dakota. 125th Stated Meeting of the American Ornithologists' Union. Laramie, WY.

R.D. Mettler[G] and **G.M. Spellman***. Molecular analysis of Grosbeak (Cardinalidae: Pheucticus) hybridization in South Dakota. ConGen3: The 3rd International Conservation Genetics Symposium. New York, NY.

R.D. Mettler[G] and **G. M. Spellman***. Genetic charactization of an avian hybrid zone (Pheucticus): the importance of endogenous selection. Ecological Genomics Symposium. Kansas City, KS.

G.M. Spellman, R. Mettler[G], S. Sarver, J. Klicka. Cryptic genetic variation in a coniferous forest management indicator species (Aves, Certhiidae: <u>Certhia americana</u>). Evolutionary Change in Human Altered Environments, An International Summit. Institute of the Environment, University of California, Los Angeles.

S. Sarver**, G.M. Spellman**, C. Ferrell, R. Mettler[G], C. Anderson,. Conservation genetics of the American Dipper (<u>Cinclus mexicanus</u>): declining population size in an impacted population in the Black Hills of South Dakota. Evolutionary Change in Human Altered Environments, An International Summit. Institute of the Environment, University of California, Los Angeles.

J.R. Jaeger, D.F. Bradford, **G.M. Spellman,** B. Riddle. Population Structure of the Red-spotted Toad, <u>Bufo punctatus</u>, in a Naturally Fragmented Desert Landscape. California/Nevada Amphibian Population Task Force 2007 Annual Meeting, Las Vegas, NV.

J.J. Stone, S. Clay**, G.M. Spellman.** Impact of antimicrobial compounds Tylosin and Chlortetracycline during swine manure treatment. Presented at the Joint Meeting of the Eastern South Dakota Water Conference and the 52nd Annual Mid-West Groundwater Conference, Sioux Falls, SD.

J.J. Stone, S. Clay**, G.M. Spellman.** Impact of antimicrobial compounds Tylosin and Chlortetracycline during swine manure treatment. Presented at the Association of Environmental Engineering and Science Professors Bi-Annual Conference, Blacksburg, VA.

2000-2006

J. Klicka, R. Ricklefs, E. Birmingham, P. Escalante, and **G.M. Spellman**. The evolutionary history of the Troglodytes aedon complex. North American Ornithological Congress, Vera Cruz, Mexico.

G.M. Spellman and J. Klicka. Phylogeography of the Pygmy Nuthatch. American Ornithologists Union Annual Meeting, Santa Barbara, CA.

J. Klicka and **G.M. Spellman.** Temperate and tropical New World sparrows (Emberizini), two separate clades? American Ornithologists Union Annual Meeting, Santa Barbara, CA.

G.M. Spellman and J. Klicka. Phylogeography of the Mountain Chickadee. Society for the Study of Evolution Annual Meeting, Fairbanks, AK.

G.M. Spellman and J. Klicka. Genetic consequences of the Late Quaternary: lessons from phylogenetic and coalescent analyses of the Mountain Chickadee (Poecile gambeli). American Ornithologists Union Annual Meeting, Quebec, Quebec and BIOS Symposium, UNLV Department of Biological Sciences.

J. Klicka and **G.M. Spellman.** Molecular systematics of the Cardinalidae. American Ornithologists Union Annual Meeting, Quebec, Quebec.

G.M. Spellman and J. Klicka. Comparative phylogeography of the North American pine-oak avifauna: exploring patterns of genetic and geographic variation in eight co-distributed species. BIOS Symposium UNLV.

G.M. Spellman and G. Voelker. A molecular test of the superfamily Muscicapoidea: a minor tear in the tapestry. American Ornithologists Union Annual Meeting, New Orleans, LA.

G.M. Spellman and J. Klicka. Does morphology track phylogeny in Emberizine sparrows? American Ornithologists Union Annual Meeting, Seattle, Washington and BIOS Symposium UNLV.

G.M. Spellman. Intercontinental colonization and molecular systematics of the avian family Bombycillidae. Cooper Ornithological Society Annual Meeting, Riverside, California.

d. Past and Current Grants and Fellowships. (Funding Source in Bold.)

2012 TCUP: Biology, Ecology, Conservation Genetics and Management of the Ornate Box Turtles (*Terrapene ornata ornata*) in South Dakota. **NSF 1153443** $191,572. Spellman, Co-PI. PI Allessandra Higa at Oglala Lakota College, Kyle, SD.

2012 South Dakota Sustainability Initiative: building sustainable practice throughout the Missouri River watersheds of South Dakota. SD EPSCoR RII T1 Proposal Planning Grant, March 2012 to August 2012. PI: Stone, J.J., co-PIs: Clay, D. and Johnson, C. South Dakota State University; Spellman, G. and Sarver, S. Black Hills State University; Kerby, J. and Sulak, B. University of South Dakota. **SD Epscor** $7,997.

2011 SNAAP: Strengthening Native American Access to the Professoriate. **NSF AGEP 1111231**. Award total $140,879. SUBAWARD to Spellman. PI Idaho State University Extension Office.

2011 REU Supplement - COLLABORATIVE RESEARCH: Multilocus comparative phylogeography of North American pine and oak woodland birds. **NSF DEB1112162** $7,500.

2010 REU Supplement - COLLABORATIVE RESEARCH: Multilocus comparative phylogeography of North American pine and oak woodland birds. **NSF DEB1026957** $13,856.

2009 REU Supplement - COLLABORATIVE RESEARCH: Multilocus comparative phylogeography of North American pine and oak woodland birds. **NSF DEB0924306** $18,231.

2008 COLLABORATIVE RESEARCH: Multilocus comparative phylogeography of North American pine and oak woodland birds. PIs: Garth M. Spellman, John Klicka (UNLV), and Scott V. Edwards (Harvard). **NSF DEB 0814841, 0815705, 0815057**. Grant total $500,000. PI Spellman awarded $207,229.

2008 Evolution of UV sensitive opsin genes in the Cardinalidae (Aves). **NIH-INBRE**, Summer Salary grant. $4,500.

2007 BHSU Integrative Genomics Transition Scholarship Program, **NSF S-STEM Program**, Co-PI. **DUE-0728553** $598,000.

2007 Comparative phylogeography of pine-oak birds. **NIH-INBRE**, Summer Salary grant. $8,666.

2006 Phylogeography of the Bushtit (*Psaltripaurs minimus*). Faculty Research Grant. **Black Hills State University**. $3,000.

2006 Phylogeography of the sky-islands of Western North America: implications of geographic and genetic variation in thirteen avian taxa. **NIH-INBRE**, Summer Salary grant. $4,333.

2004 Marsha Brady Tucker Travel Award – **AOU**. AOU Annual Meeting, Quebec, Quebec.

2003 Comparative phylogeography of North American montane birds. Chapman Memorial Ornithological Grant. **American Museum of Natural History**. $2,000.

2002 Comparative phylogeography of North American montane birds. Chapman Memorial Ornithological Grant. **American Museum of Natural History**. $2,013.

2001 Phylogeography of the sky islands of western North America: implications of geographic and genetic variation in eight avian taxa. **Marjorie Barrick Museum of Natural History Foundation**. $20,000.

2000 Summer research tuition award. **University of Alaska, Fairbanks**.

1999 Comparative Phylogeography of Aleutian Island Birds. **Angus Gavin Memorial Bird Research Grant**. $15,000.

1999 Summer research tuition award. **University of Alaska, Fairbanks**.

i. Grant Proposal Submissions (since 2011).

NSF DIMENSIONS:COLLABORATIVE RESEARCH: Frugivory, sexual selection and diversification of manakins and their gut microbiome. G.M. Spellman one of many PIs: Chris Balakrishnan (East Carolina University), Bette Loiselle (University of Florida), W. Alice Boyle (Kansas State University), Michael Braun (Smithsonian Institute) and Emily Duval (Florida State University). Submitted April 2013. $2,000,000.

NSF DEB Preproposal submitted January 2012 with Matt Carling as PI and G.M. Spellman and Ben Zuckerberg as co-PIs. Climate-change velocity, environmental heterogeneity and hybridization.

NSF CAREER: From the top down: Exploring the connections between host genetic diversity and gut microbial diversity and using a vertical mentorship program to broaden participation and enhance science teacher training in South Dakota. Submitted July 2011. $681,508.

The South Dakota NASA Space Grant Research Scholars Program. Improving STEM Retention through Early Immersion in Research. PIs G.M. Spellman and Daniel Howard (Augustana College, Sioux Falls, SD). $500,000.

The South Dakota NASA Space Grant Research Scholars Program. One teacher at a time: Improving recruitment, retention, and STEM scientific inquiry in South Dakota pre-service high school teachers. PIs G.M. Spellman and Carrie Hall (Augustana College, Sioux Falls, SD). $500,000.

ii. Student Research Awards and Grants.

2012 NIH-INBRE (SD) 9 Month Undergraduate Research Fellowship. **Nicole Deidrich**. $4500.
2012 NIH-INBRE (SD) Summer Undergraduate Research Fellowship. **Heather Weisser**. $4500.
2012 NIH-INBRE (SD) Summer Undergraduate Research Fellowship. **Brian Byrne**. $4500.
2011 NASA-EPSCOR Graduate Stipend Award. **Joseph Manthey.** $1750.
2010 South Dakota Ornithologists Union Graduate Scholarship. **Joseph Manthey.** $500.
2010 Whitney Small Grant South Dakota Ornithologists Union. **Joseph Manthey.** $500.
2010 NIH-INBRE (SD) 9 Month Undergraduate Research Fellowship. **Jeffery Herr**. $3800.
2009 NIH-INBRE (SD) 9 Month Undergraduate Research Fellowship. **Jess Moser**. $3800.
2009 NIH-INBRE (SD) Summer Undergraduate Research Fellowship. **Daniel Turveen**. $3200.
2008 NIH-INBRE (SD) 9 Month Undergraduate Research Fellowship. **Laura Kramer**. $3200.
2008 NSF Native American and Pacific Islander Research Experience (NAPIRE) – Summer undergraduate research fellow. Organization for Tropical Studies (OTS). Andrew Elk Shoulder.
2008 NIH-INBRE (SD) Summer Undergraduate Research Fellowship. **Jess Moser**. $4000.
2008 Nelson Summer Scholarship Research Fellow (BHSU). **Laura Kramer**. $4000.
2007 NIH-INBRE (SD) 9 Month Undergraduate Research Fellowship. **Laura Kramer**. $3200.
2007 NIH-INBRE (SD) 9 Month Undergraduate Research Fellowship. **Jess Moser**. $3200.
2007 American Ornithologists Union Student Membership Award. **Raeann Mettler**.
2007 American Ornithologists Union Student Travel Award. **Raeann Mettler**. $250.
2007 NIH-INBRE Summer Undergraduate Research Fellowship. **Jess Moser**. $4000.

e. Fellowships, Prizes, Awards, and Acknowledgments.

2013 Black Hills State University, Outstanding Faculty Research Award.
2012 Top Reviewer for Molecular Ecology.
2011 Elective Member of the American Ornithologists' Union.
2010 Faculty Fellowship, South Dakota NIH-INBRE.
2009 Faculty Fellowship, South Dakota NIH-INBRE.

2009 NSF EPSCoR Young Investigator Award. South Dakota EPSCoR Program.
2004 Student presentation award – BIOS Symposium. UNLV Department of Biological Sciences.

3. Teaching and Advising

a. Black Hills State University Courses.

- Biology Survey I, BIOL 101
  - 2 sections each semester (~90 students each section), Fall 2009, Fall 2011.
- Biology Survey Lab, BIOL 101L
  - 10 sections (~20 students per section), Fall 2012.
- Scientific Writing & Advanced Evolutionary Biology, BIOL 491
  - 1 course (10 students), Spring 2010.
- Population and Quantitative Genetics, BIOL 710
  - 1 course in alternating years (~10 students per course), Spring 2008, 2010, 2013.
- Genomic Techniques, BIOL 724L
  - 1 course every year (~10 students per course), Fall 2006-2012.
- Evolutionary Genomics, BIOL 735
  - 1 course every year (~10 students per course), Spring 2007-2013.
- Evolution, BIOL 371
  - 1 course in alternating years (~25 students per course), Spring 2009, 2011.
- Evolution Lab, BIOL 371L
  - 1 course in alternating years (~25 students per course), Spring 2009, 2011.
- Ornithology with lab, BIOL 492
  - Course started at BHSU in 2012 (24 students).
- Climate Change and Biodiversity, SCI 592
  - 1 course (20 students), Summer 2011.

i. Teaching at other institutions.

a. University of Nevada, Las Vegas

- Phylogenetic Inference, BIOL 799. Fall 2005. (15 students)
- Ornithology, Guest Lecturer and Teaching Assistant, BIOL 433. Fall 2000 (26 students).

b. University of Alaska, Fairbanks

- Ornithology, Teaching Assistant, BIOL 426. Spring 1999. (25 students)
- Fundamentals of Biology, Teaching Assistant, BIOL 105. Fall 1998. (2 sections ~25 students each section.)

b. Course and Curriculum Development.

All course development for graduate level courses at BHSU and UNLV were new designs for the University. Ornithology was also a newly approved course for BHSU.

Served on the working group that designed the course curriculum for the new Masters of Science in Sustainability at BHSU.

Designed the course Climate Change and Biodiversity, SCI 592 at BHSU. This was a course offered to high school science teachers seeking Masters degrees and helped the teachers design educational modules focusing on climate change.

c. Advising (Research Direction).

i. Graduate

Catherine Geisik (2013-) Population genomics of the Hairy Woodpecker.

Lindsey Kreun (2012-) Genomic architecture of phylospecies: assessing the impact of genetic drift versus ecological selection.

Christine Bubac (2011-) Population genetics of Virginia's Warbler.

Kelsey Prosser (2011-) Co-diversification of birds and their gut microbiota.

Kyle Kennedy (2010-2012) The role of selection in the maintenance of a Great Plains avian hybrid zone.

Jordan Sheets (2010-2012) Malaria and MHC: pathogen mediated selection in a North American songbird. PhD candidate at Sanford School of Medicine, Department of Basic Biomedical Sciences.

John Duvall Jisha (2009-2011) Landscape genetics and ecology of facultatively polygynous colonies of carpenter ants (*Camponotus modoc*). Currently a Research Technician at BIOO Scientific, Austin, TX.

Joseph Manthey (2009-2011) Complex speciational history in the Brown Creeper inferred from multilocus sequence data. Currently a PhD candidate at the University of Kansas.

Pankaj Mehrotra (2008-2010) Malarial Parasites in the Endemic White-winged Junco: the impacts of seasonality, sex, and body condition on infection rates. Currently a PhD Candidate at the University of Aberdeen, Scotland.

V. Woody Walstrom (2008-2010) Speciation in the White-breasted Nuthatch (*Sitta carolinensis*): a multilocus study of diversification in North American pine and oak woodlands. Currently a PhD Cadidate at Mississippi State University.

Raeann Mettler (2006-2008) Molecular analysis of Grosbeak (Cardinalidae: *Pheucticus*) hybridization in the Great Plains. Currently a Post-doctoral Associate at Black Hills State Unviersity.

ii. Undergraduate

Nicole Deidrich (Academic year 2012-2013) Morphological and molecular characterization of avian *Eimeria* parasites. NIH-INBRE Undergraduate Research Fellow.

Heather Weisser (Spring and Summer 2012) Epidemiology of West Nile Virus in experimental House Wrens. NIH-INBRE Undergraduate Research Fellow. Currently a Masters student at the University of Manitoba.

Brian Byrne (Spring and Summer 2012) Morphological and molecular characterization of avian gut parasites. NIH-INBRE Undergraduate Research Fellow. Currently an undergraduate Biology major at BHSU.

Jeffery Herr (Academic year 2010-2011) Malaria and MHC: pathogen mediated selection in the Dark-eyed Junco. NIH-INBRE Undergraduate Research Fellow.

Justin Tibbits (Summer 2010-11) Multilocus comparative phylogeography of North American pine and oak woodland birds. REU Student.

Daniel Turveen (Summer 2009 & Summer 2010) Roles of hormone induced immune suppression and seasonality in Malarial infection rates of the Black Hills Dark-Eyed Junco. NIH-INBRE Undergraduate Research Fellow. Currently a Medical School student at Sanford School of Medicine, Vermillion, SD.

Jordan Sheets (Summer 2009) Multilocus comparative phylogeography of North American pine and oak woodland birds. PhD candidate at Sanford School of Medicine, Department of Basic Biomedical Sciences.

Jenna Eddy (Summer 2009) Multilocus comparative phylogeography of North American pine and oak woodland birds. REU Student. Currently a Masters of Biotechnology student at Colorado State University.

Andrew Elk Shoulder (2008) Multilocus comparative phylogeography of North American pine and oak woodland birds.

Ronald Scott (2008-2009) Multilocus comparative phylogeography of North American pine and oak woodland birds.

Laura Kramer (2007-2009) Multilocus phylogeography of the Black-headed Grosbeak (*Pheucticus melanocephalus*); Multilocus comparative phylogeography of North American pine and oak woodland birds. REU Student. Currently an administrative assistant at the Center for the Conservation of Biological Resources, BHSU, Spearfish, SD.

Jess Moser (2006-2008) Phylogeography of the Bushtit (*Psaltriparus minimus*) and Evolution of avian malarial parasites in geographically structured host species: a phylogenetic approach; Multilocus comparative phylogeography of North American pine and oak woodland birds. REU Student. Currently in Optometry student at the Illinois Institute of Optometry.

Jennifer Jensen (2007) Phylogeography of the Western Tanager (*Piranga ludoviciana*). Currently a nurse in Rapid City, SD.

4. Service.

a. Professional.

i. **Journal Review:** (I conduct ~10 reviews annually and have reviewed for these journals in the last 5 years) Evolution and Ecology, The Auk, The Condor, Current Biology, Evolution, Ibis, Journal of Avian Biology, Journal of Biogeography, Molecular Phylogenetics and Evolution, Proceedings of the Royal Society, Series B, Molecular Ecology, Molecular Ecology Resources, BMC Genetics, PLOS One.

ii. **Granting Agency Review:** NSF DDIG Program, NSF Population Biology and Systematics Program, NSF Environmental Genomics Program, NSF CAREER

Program, NSF Population and Evolutionary Processes Program, NSF Dimensions of Biodiversity Program, National Geographic Society.

iii. **Panel Participation:** NSF Division of Environmental Biology (4 panels). Evolutionary Processes Cluster: full proposal panel (x2), pre-proposal panel and DDIG panel.

iv. **Memberships held in Professional Organizations.**

American Ornithologists Union
South Dakota Ornithologists Union
Cooper Ornithological Society
International Biogeography Society
Society of Field Ornithologists
Society for the Study of Evolution

b. Campus.

i. Departmental.

BHSU Systematic Botanist Search, Committee Chair (2009)
Integrative Genomics Graduate Operations Committee (2007-2013)
BHSU Science Seminar Series, Committee Chair (2006-2013)
BHSU NSF S-STEM Integrative Genomics scholarship program, Chair (2008-2013)
BHSU, Integrative Genomics, Program Director (2009-2013)
Employee Search Committee Member
    BHSU Research Associate I (2008)
    BHSU Research Associate II (2008)

ii. College.

Graduate Curriculum Committee (2007-2013)
Public Relations Committee (2011-2013)
Steering Committee for the Masters of Science in Sustainability (2011-2013)
Judge BHSU Research Symposium (2007-2013)

iii. University.

Graduate Council (2009-2013)
Faculty Senate (2009-2010)
Dean of Educational Outreach and Graduate Programs Search Committee member (2012-2013)
Elected to the University Promotion and Tenure Committee (2012-2013)
BHSU Faculty Representative to the Board of Regents Research Committee (2012)
IRB and IACUC Committee Member (2010-2013)
BHSU Soccer Club Faculty Representative (2007-2013)

c. Community Service.

Judge, Spearfish Middle School Science Fair, 2007-2013
Guest Lecture, Children First Kindergarten, Spearfish, SD 2007-2013
Guest Speaker, Black Hills Birding Club and Audubon Society, 2010-2013
Guest Speaker, Black Hills Parrot Center, 2012-2013
Exhibitor, Spearfish Friday Nights Downtown, Spearfish, SD 2012-2013
Coordinator of Nerd Nite Spearfish 2012-2013
Career Day, NSF Science Careers Day, Dulles Mall, Dulles, VA, 2013
Facilitator, International Funding Agency Symposium, Arlington, VA, 2014
Volunteer and Judge, Glebe Elementary School Science Fair, Arlington, VA, 2014

5. Collaborators and Mentors.

Anderson, Cynthia	Black Hills State University
Barker, F. Keith	University of Minnesota
Balakrishnan, Chris	Eastern Carolina University
Bergeon Burns, Christy	Louisiana State University
Bryson, Robert	University of Washington
Burns, Kevin	San Diego State University
Carling, Matt	University of Wyoming
Cicero, Carla	University of California, Berkeley
DaCosta, Jeffery	Boston University
Dor, Roi	University of Colorado
Edwards, Scott V.	Harvard University
Escalante, Patricia	Universidad Nacional Autonoma de Mexico
Ferree, Elise	Claremont Colleges
Higa, Allesandra	Oglala Lakota College
Ketterson, Ellen	Indiana University
Klicka, John	University of Washington
Manthey, Joseph	University of Kansas
Miller, Matthew	Smithsonian Tropical Research Institute
Moyle, Robert	University of Kansas
Riddle, Brett	University of Nevada, Las Vegas
Sarver, Shane	Black Hills State University
Smith, Brian Tilston	Louisiana State University
Stone, James	SD School of Mines and Technology
Thompson, Charles	Illinois State University
Townsend, Andrea	University of California, Davis
Walstrom, Woody	Mississippi State University
Winker, Kevin	University of Alaska Fairbanks
Zuckerburg, Ben	University of Wisconsin, Madison

6. Administrative Experience.

Program Director – Evolutionary Processes Cluster in the Division of Environmental Biology, National Science Foundation. Maintain a dynamic, high quality and effective merit review system. Serve as an ongoing advisor to applicants and grantees concerning NSF policies and program objectives. Promote and support excellent science ethics. Participate in outreach visits and educational activities designed to broaden participation in NSF activities.

Master's of Integrative Genomics Program Director. Duties include recruitment and monitoring of enrolled student progress, serving as an active member on the university Graduate Council, chair of the Graduate Progress Committee, and fund raising and grant writing to sustain the nascent master's program. 2009-2013.

Chair of NSF-STEM Graduate and Undergraduate Scholars Program. Duties include organization and execution of activities focusing on the recruitment and retention of promising Biology majors from underrepresented groups, especially Native American students, at BHSU. 2007-2013.

7. Field Experience.

Black Hills State University. Associate, Assistant Professor and Research Assistant Professor. Organization and funding of a rigorous research program integrating modern molecular techniques to address many questions in avian evolutionary biology and molecular ecology. Started the Black Hills State University Ornithological Collection. 2006-present.

Barrick Museum of Natural History and University of Nevada – Las Vegas. DNA Lab Manager, Genetic Resources Collections Manager, Collections Assistant, and PhD Candidate. Organization and maintenance of a fully operational molecular systematics laboratory. 2001 – 2006.

Barrick Museum of Natural History and University of Nevada, Las Vegas. Collection and preparation of avian specimens. Collecting was conducted on several trips throughout the United States and Canada, and included expeditions to Honduras, Guatemala, Mexico (3), Panama, and Malawi. International expeditions were often in collaboration with other research institutions including UNAM – National Ornithological Collection (Dra. Patricia Escalante), UNAM – Department of Ecology (Dr. Adolfo Navarro), Smithsonian Tropical Research Institution – Panama, and the Malawi National Museum of Natural History. 2000 – 2006.

University of Alaska, Fairbanks, Alaska. Phylogeography of the resident avifauna of the Queen Charlotte Islands, British Columbia, Canada. Approximately 50 birds prepared; mtDNA analyses conducted. 1999 – 2000.

Cordova, Alaska, Prince William Sound. Part of a University of Alaska Museum and USDA study of avian viruses in migrating shorebirds. Approximately 200 birds collected and cloacal swabs taken for viral screening. 2000.

Aleutian Islands, Alaska Peninsula, and Prince William Sound. Phylogeography of 8 landbirds of the Aleutian Islands. Approximately 300 birds collected and 100 prepared. 1999.

Northfield, Minnesota, U.S.A. A test of the ideal free distribution model in Mallards (*Anas platyrynchos*). 1995 – 1996.

a. Technical Experience.

Museum specimen preparation. Prepared 5000 bird specimens for the Barrick Museum and University of Alaska Museum research collections and the Black Hills State University teaching collection as skins and tissues.

Museum database management. Assisted curator in updating specimen information for the Barrick Museum bird collection database.

Museum Collections management/curation. Managed and organized the tissue collection for the Barrick Museum bird collection. A collection that grew from 5000 to 18000 tissues during my tenure.

CURRICULUM VITAE

Dr. Sabrina S. Taylor

Associate Professor
School of Renewable Natural Resources
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staylor@lsu.edu

EDUCATION

Ph.D., Department of Zoology, University of Otago, Oct 2006.
Thesis subject: The genetic and conservation consequences of species translocations in New Zealand saddlebacks and robins. Supervisor: Dr. Ian Jamieson.

M.Sc., Department of Biology, Dalhousie University, Dec. 1, 2000
Thesis subject: Parental care and foraging behaviour during incubation and chick rearing in endangered Humboldt Penguins (*Spheniscus humboldti*). Supervisors: Dr. M. Leonard and Dr. D. Boness (Smithsonian Institution).

B.Sc. (Hons. First Class), Biology Co-op Programme, University of Victoria, 1995
Minor in Environmental Studies
Thesis subject: Speciation in Garter Snakes (*Thamnophis sirtalis*). Supervisor: Dr. P. Gregory

PROFESSIONAL EXPERIENCE

Associate Professor, Conservation Genetics. Louisiana State University AgCenter, Baton Rouge, Louisiana. July 2015 - present.

Assistant Professor, Conservation Genetics. Louisiana State University AgCenter, Baton Rouge, Louisiana. March 2009 – June 2015.

NSERC Postdoctoral Fellow. University of British Columbia, Vancouver, British Columbia. July 2007 to March 2009.

PUBLISHED REFEREED SCIENTIFIC ARTICLES

Names of students and post-doctoral fellows (current and former) under my supervision/co-supervision are given in bold. Last author position indicates research that I directed or co-directed.

Brzeski, K.E., M.B. DeBiasse, D.R. Rabon Jr., M.J. Chamberlain, and S.S. Taylor. In press. Mitochondrial DNA variation in southeastern pre-Columbian canids. Journal of Heredity.

Wilson, A.S., Y. Chan, S.S. Taylor, and P.A. Arcese. In press. Genetic divergence of an avian endemic on the Californian Channel Islands. PLoSONE.

Elbers, J. and S.S. Taylor. 2015. GO2TR: a gene ontology-based workflow to generate target regions for target enrichment experiments. Conservation Genetics Resources DOI 10.1007/s12686-015-0487-6.

Brzeski, K., R. Harrison, W. Waddell, K. Wolf, D. Rabon Jr., and S.S. Taylor. 2015. Infectious disease and red wolf conservation: assessment of disease occurrence and associated risks. Journal of Mammalogy 96:751-761.

Rogers, H.A., S.S. Taylor, J.P. Hawke, and J.A. Anderson Lively. 2015. Variations in prevalence of viral, bacterial, and rhizocephalan diseases and parasites of the blue crab (*Callinectes sapidus*). Journal of Invertebrate Pathology 127: 54-62.

Chua, V. L., Q. Phillipps, H.-C. Lim, S.S. Taylor, D.F. Gawin, M.A. Rahman, R.G. Moyle, and F.H. Sheldon. 2015. Phylogeography of three endemic birds of Maratua Island, a potential archive of Bornean biogeography. Raffles Bulletin of Zoology 63: 259-269.

Rogers H.A., S.S. Taylor, J.P. Hawke, and J.A. Anderson Lively. 2015. Prevalence and distribution of three protozoan symbionts in blue crab (*Callinectes sapidus*) populations across Louisiana, USA. Diseases of Aquatic Organisms 114:1-10.

Rogers, H.A., S.S. Taylor, J.P. Hawke, E.J.Schott, and J.A. Anderson Lively. 2015. Disease, parasite, and commensal prevalences for blue crab *Callinectes sapidus* at shedding facilities in Louisiana, USA. Diseases of Aquatic Organisms 112: 207-217.

Woltmann, S., P.C. Stouffer, **C.M. Bergeon Burns**, M.S. Woodrey, M.F. Cashner, and S.S. Taylor. 2014. Population genetics of Seaside Sparrow (*Ammodramus maritimus*) subspecies along the Gulf of Mexico. PLoS ONE 9(11): e112739. doi:10.1371/journal.pone.0112739

Bergeon Burns C.M., J.A. Olin, **S. Woltmann**, P.C. Stouffer, and S.S. Taylor. 2014. Effects of oil on terrestrial vertebrates: predicting impacts of the Macondo blowout. BioScience 64:820-828.

Brzeski, K.E., D.R. Rabon, M.J. Chamberlain, L.P Waits, and S.S. Taylor. 2014. Inbreeding and inbreeding depression in endangered red wolves (*Canis rufus*). Molecular Ecology 23:4241-4255.

Cerame, B., J.A. Cox, R.T. Brumfield, J.W. Tucker, and S.S. Taylor. 2014. Adaptation to ephemeral habitat may overcome natural barriers and severe habitat fragmentation in a fire-dependent species, the Bachman's Sparrow (*Peuceae aestivalis*). PLoS ONE 9:e105782.

Taylor, S.S., **S. Woltmann**, A. Rodriguez, and W.E. Kelso. 2013. Hybridization of white, yellow and striped bass in the Toledo Bend Reservoir. Southeastern Naturalist 12:514-522.

Sheldon, F.H., C.H. Oliveros, S.S. Taylor, B. McKay, H.-C. Lim, M.A. Rahman, H. Mays, and R.G. Moyle. 2012. Molecular phylogeny and insular biogeography of the lowland tailorbirds of Southeast Asia (Cisticolidae: Orthotomus). Molecular Phylogenetics and Evolution 65:54-63.

Taylor, S.S., D.A. Jenkins and P.A. Arcese. 2012. Loss of Mhc and neutral variation in Peary caribou: genetic drift is not mitigated by balancing selection or exacerbated by Mhc allele distributions. PLoS ONE 7:e36748.

Moyle, R.G., S.S. Taylor, C.H. Oliveros, H.-C. Lim, C.L. Haines, M.A. Rahman and F.H. Sheldon. 2011. Diversification of an endemic Southeast Asian genus: Phylogenetic relationships of the Spiderhunters (Aves: Nectariniidae). Auk 128:777–788.

Taylor, S.S., R. Sardell, J.M. Reid, T. Bucher, N.G. Taylor, P.A. Arcese, and L.K. Keller. 2010. Inbreeding coefficient and heterozygosity-fitness correlations in unhatched and hatched song sparrow nestmates. Molecular Ecology 19:4454-4461.

Lim, H.-C., F. Zou, S.S. Taylor, B.D. Marks, R.G. Moyle, G. Voelker, and F.H. Sheldon. 2010. Phylogeny of Magpie-Robins and Shamas (Aves: Turdidae: *Copsychus* and *Trichixos*): implications for island biogeography in Southeast Asia. Journal of Biogeography 37:1894-1906.

Jamieson, I.G., S.S. Taylor, L. Tracy, D.P. Armstrong, and H. Kokko. 2009. Why some species of birds do not avoid inbreeding: data and new theory from New Zealand robins and saddlebacks. Behavioural Ecology 20:575-584.

Taylor, S.S., S. Boessenkool, and I.G. Jamieson. 2008. Genetic monogamy in two long-lived New Zealand passerines. Journal of Avian Biology 39:579-583.

Taylor, S.S. and I.G. Jamieson. 2008. No evidence for loss of genetic variation following sequential translocations in extant populations of a genetically depauperate species. Molecular Ecology 17:545-556.

Taylor, S.S., I.G. Jamieson, and G.P. Wallis. 2007. Historical and contemporary levels of genetic variation in two New Zealand passerines with different histories of decline. Journal of Evolutionary Biology 20:2035–2047.

Taylor, S.S. and I.G. Jamieson. 2007. Factors affecting the survival of founding individuals in translocated New Zealand saddlebacks. Ibis 149:783–791.

Boessenkool, S., S.S. Taylor, C.K. Tepolt, J. Komdeur, and I.G. Jamieson. 2007. Large mainland populations of South Island robins retain greater genetic diversity than offshore island refuges. Conservation Genetics 8:705-714.

Taylor, S.S. and I.G. Jamieson. 2007. Discriminant function analysis for sexing South Island saddlebacks. Notornis 54:61-65.

Taylor, S.S., I.G. Jamieson, and D. Armstrong. 2005. Successful island reintroductions of New Zealand robins and saddlebacks with small numbers of founders. Animal Conservation 8:415-420.

Taylor, S.S., M.L. Leonard, D.J. Boness, and P. Majluf. 2004. Humboldt penguins *Spheniscus humboldti* change their foraging behaviour following breeding failure. Marine Ornithology 32:63-67.

Taylor, S.S., M.L. Leonard, D.J. Boness, and P. Majluf. 2002. Foraging in Humboldt penguins (*Spheniscus humboldti*) during the chick-rearing period: general patterns, sex differences, and recommendations to reduce incidental catches in fishing nets. Canadian Journal of Zoology 80:700-707.

Taylor, S.S., M.L. Leonard, D.J. Boness, and P. Majluf. 2001. Foraging trip duration increases for Humboldt penguins tagged with recording devices. Journal of Avian Biology 32:369-372.

Taylor, S.S., M.L. Leonard, and D.J. Boness. 2001. Aggressive nest intrusions by male Humboldt penguins. Condor 103:162-165.

PUBLICATIONS IN REVIEW

Elbers, J. and S.S. Taylor. Major histocompatibility complex polymorphism in reptile conservation. Herpetological Conservation and Biology.

Weston, K.A., S.S. Taylor, and B.C. Robertson. Identifying populations for management: fine-scale population structure in the New Zealand alpine rock wren (*Xenicus gilviventris*). Conservation Genetics.

OTHER PUBLICATIONS IN REFEREED JOURNALS

Taylor, S.S. 2014. Book review: “The Birds of New Zealand: A Photographic Guide” by Paul Scofield and Brent Stephenson. Journal of Field Ornithology 85:224-225.

Taylor, S.S. 2012. Book review: “Seabird Genius: The Story of L.E. Richdale, the Royal Albatross, and the Yellow-eyed Penguin” by Neville Peat. Journal of Field Ornithology 83:327-328.

Taylor, S.S. 2012. Book review: "Avian Architecture: How Birds Design, Engineer, and Build" by Peter Goodfellow. Journal of Field Ornithology 83:102-103.

MAGAZINE ARTICLES

Taylor, S.S. 2012. Genetics and the management of birds, reptiles and mammals. Louisiana Agriculture 55:16-17.

Taylor, S.S. 2003. Book review: "Crows and Jays" by Steve Madge and Hilary Burn. Nova Scotia Birds 45:42.

Taylor, S.S., I. McLaren, and K. Dillon. 2002. Return of breeding Laughing Gulls to Atlantic Canada. Birder's Journal 11:58-60.

Taylor, S.S. 2002. Book review: "Who killed the Great Auk?" by Jeremy Gaskell. Nova Scotia Birds 44:39.

CONFERENCE PROCEEDINGS

Stouffer, P.C., S.S. Taylor, **S. Woltmann**, and **C.M. Bergeon Burns**. 2013. Staying alive on the edge of the earth: response of Seaside Sparrows (*Ammodramus maritumus*) to salt marsh inundation, with implications for storms, spills, and climate change. Pages 82-93 in Proceedings of the 4th Louisiana Natural Resources Symposium (T. F. Shupe, and M. S. Bowen, Eds.).

PUBLISHED CONFERENCE ABSTRACTS

Bergeon Burns, C.M., J. Olin, **S. Woltmann**, P.C Stouffer, and S.S. Taylor. 2015. Annual variation in CYP1A gene expression and fatty acid composition in liver of Seaside Sparrows from oiled and unoiled salt marsh following the BP Deepwater Horizon spill. Midwest Ecology and Evolution Conference, Bloomington, Indiana, USA, March 28-29. Conference poster presentation.*

Bergeon Burns, C.M., S. Woltmann, P.C Stouffer, and S.S. Taylor. 2015. Seaside Sparrow CYP1A gene expression on oiled and unoiled salt marsh in Barataria Bay, Louisiana. Gulf of Mexico Oil Spill and Ecosystem Science Conference, Houston, Texas, USA, February 16-19. Conference oral presentation (presented by S. Taylor).

Woltmann, S., P.C Stouffer, **C.M. Bergeon Burns**, and S.S. Taylor. 2015. A modern view of diversity and research needs among Seaside Sparrow populations along the Gulf of Mexico. Gulf of Mexico Oil Spill and Ecosystem Science Conference, Houston, Texas, USA, February 16-19. Conference poster presentation.

Olin J.A., **C.M. Bergeon Burns**, W. Bam, L. Hooper-Bui, S.S. Taylor, and P.C. Stouffer. 2015. Intraspecific differences in the food resources used by Seaside Sparrow (*Ammodramus maritimus*): a consequence of prey availability? Gulf of Mexico Oil Spill and Ecosystem

Science Conference, Houston, Texas, USA, February 16-19. Conference poster presentation.

Brzeski, K.E., B. Bartel, D.R. Rabon, K. Wolf, W. Waddell, and S.S. Taylor. 2014. Infectious disease and red wolf conservation: baseline pathogen prevalence. The Wildlife Society Annual Conference, Pittsburgh, PA. October 24-30. Conference poster presentation.*

Bergeon Burns, C.M., S. Woltmann, P.C Stouffer, and S.S. Taylor. 2014. Physiological and ecological effects of the Deepwater Horizon oil spill on Seaside Sparrows. American Ornithologists' Union, Estes Park, Colorado, USA, September 23-28. Conference oral presentation (presented by S. Taylor).

Woltmann, S., P.C Stouffer, M.S. Woodrey, **C.M. Bergeon Burns**, and S.S. Taylor. 2014. Population genetics of the Gulf Coast subspecies of the Seaside Sparrow (*Ammodramus maritimus*): subspecies validity and conservation implications. American Ornithologists' Union, Estes Park, Colorado, USA, September 23-28. Conference oral presentation.

Ford, R., W. Selman, and S.S. Taylor. 2014. Hybridization and population structure of western Gulf Coast Mottled Ducks. Southeastern Association of Fish and Wildlife Agencies, Destin, Florida, USA, October 19-22. Conference oral presentation.

Olin J.A., **C.M. Bergeon Burns**, W. Bam, L. Hooper-Bui, P.C. Stouffer, and S.S. Taylor. 2014. Stable isotopes reveal intra-specific differences in the food webs utilized by Seaside Sparrows (*Ammodramus maritimus*). Society of Limnology & Oceanography, Portland, Oregon, USA, May 18-23. Conference oral presentation.*

Olin J.A., **C.M. Bergeon Burns**, P.C. Stouffer, and S.S. Taylor. 2014. Variation in resource use by Seaside Sparrows (*Ammodramus maritimus*) in Louisiana marshes based on stable isotopes and fatty acid profiles. North American Benthological Society, Jacksonville, Florida, USA, March 18-23. Conference oral presentation.*

Bergeon Burns, C.M., S. Woltmann, P.C. Stouffer, and S.S. Taylor. 2014. Consequences of the Deepwater Horizon oil spill on breeding Seaside Sparrows. Gulf of Mexico Oil Spill and Ecosystem Science Conference, Mobile, Alabama, 26-29 January. Conference oral presentation.

Bergeon Burns, C.M., S. Woltmann, S.S. Taylor, and P.C Stouffer. 2014. Physiological responses of Seaside Sparrows to the Deepwater Horizon oil spill. Society for Integrative and Comparative Biology, Austin, Texas, 3-7 January. Conference poster presentation.*

Taylor, S.S., D.A. Jenkins and P.A. Arcese. 2013. Loss of variation at neutral and Mhc loci in Peary caribou over 100 years: drift is more important than selection. Congress of the European Society for Evolutionary Biology, Lisbon, Portugal, 19-24 August. Conference poster presentation.

Brzeski, K.E., D.R. Rabon, M.J. Chamberlain, and S.S. Taylor. 2013. MHC variation and its effects on red wolf fitness. Congress of the European Society of Evolutionary Biology, Lisbon, Portugal, 19-24 August. Conference poster presentation.

Bergeon Burns, C.M., S. Woltmann, S.S. Taylor, and P.C. Stouffer. 2013. Seaside Sparrow responses to the Deepwater Horizon oil spill. 131st Meeting of the American Ornithologists' Union, Chicago, Illinois, 13-17 August. Conference poster presentation.

Taylor, S.S., **S. Woltmann**, P.C. Stouffer, and **C.M. Bergeon Burns**. 2013. Effects of the Macondo oil spill on Seaside Sparrows. Gulf of Mexico Oil Spill & Ecosystem Science Conference, New Orleans, Louisiana, 21-23 January. Conference oral presentation.

Woltmann, S., S.S. Taylor, and P.C Stouffer. 2012. Seaside Sparrow biology following the BP Deepwater Horizon oil spill. 5th North American Ornithological Conference, Vancouver, Canada, 14-18 August. Conference poster presentation.

Cerame, B., R.T. Brumfield, J.A. Cox, J.W. Tucker, and S.S. Taylor. 2012. Genetic structure of Bachman's Sparrow populations in Louisiana. 5th North American Ornithological Conference, Vancouver, Canada, 14-18 August. Conference poster presentation.

Taylor, S.S., D.A. Jenkins and P.A. Arcese. 2011. Using historical and contemporary DNA in Peary caribou to examine the relative loss of microsatellite and Mhc variation following population bottlenecks. 25th International Congress for Conservation Biology, Auckland, New Zealand, 5-9 December. Conference oral presentation.

Woltmann, S., K. Daroca, and S.S. Taylor. 2011. A preliminary assessment of hybridization of *Morone* species in the Toledo Bend Reservoir, Louisiana. Southeastern Fishes Council, Chattanooga, Tennessee, 10-11 November. Conference poster.*

Brzeski, K.E., D.R. Rabon, M.J. Chamberlain, and S.S. Taylor. 2011. Inbreeding in wild red wolves. The Wildlife Society Annual Conference, Waikoloa, Hawaii, 5-10 November. Conference poster presentation.*

Elbers, J.P. and S.S. Taylor. 2011. Genetic variation at Mhc loci and susceptibility to mycoplasmal upper respiratory tract disease in gopher tortoises. 33rd Annual Gopher Tortoise Council Meeting. Orlando, Florida, 15 October. Poster presentation.*

Taylor, S.S., D.A. Jenkins and P.A. Arcese. 2010. Loss of microsatellite and Mhc variation following population bottlenecks in Peary caribou. Fourth International Symposium on Biomolecular Archaeology, Copenhagen, The Netherlands, 8-10 September. Conference poster presentation.

Taylor, S.S., and I.G. Jamieson . 2005. Genetic variation in saddlebacks following population bottlenecks. 8th Annual New Zealand Molecular Ecology Meeting, Wainui, New Zealand, 2-4 December. Conference oral presentation.

Taylor, S.S., I.G. Jamieson, and D. Armstrong. 2005. Successful reintroductions of New Zealand saddlebacks and robins with small numbers founders. XIX Annual Meeting of the Society for Conservation Biology, Brasilia, Brazil, 15-19 July. Conference oral presentation.

Taylor, S.S. and I.G. Jamieson. 2004. Genetic variation in saddlebacks following population bottlenecks. NZ Ecological Society Conference, Invercargill, New Zealand, 29 August - 2 September. Conference oral presentation.

Taylor, S.S. and I.G. Jamieson. 2004. Genetic variation in saddlebacks following population bottlenecks. 7th International Conference on Ancient DNA & Associated Biomolecules, Brisbane, Australia, 10-17 July. Conference poster presentation.

Taylor, S.S. 2001. Current status of the Nova Scotia Herpetofaunal Atlas. 6th Annual Meeting of the Canadian Amphibian and Reptile Conservation Network, Cornwall, PEI, Canada 18-22 October. Oral presentation.

Taylor, S.S. 2000. Humboldt penguin foraging patterns: identifying conflicts with fisheries. 2000. 118th Meeting of the American Ornithologists' Union, St. John's, Canada, 14-19 August. Conference oral presentation.

*Did not attend the meeting.

WORKSHOPS AND INVITED SEMINARS

Workshops

National Science Foundation CAREER Workshop, Louisiana State University, 8-9 November 2011.

Advanced Bird Banding Workshop with Peter Pyle, 16-18 April 2011.

National Science Foundation CAREER Proposal Writing Workshop, Connecticut, 4-5 April 2011.

Conservation Genetics Workshop, Flathead Lake BioStation, Montana, 31 August-4 September 2009.

Invited Seminars

Taylor, S.S. 2015. A tale of two sparrows: population structure in two local sparrow species, the Seaside and Bachman's Sparrow. LSU Museum of Natural History, Baton Rouge, LA, 6 March.

Taylor, S.S. 2013. Genetics and the conservation, management, and ecology of species. LSU Science Club, Baton Rouge, LA, 10 October.

Taylor, S.S., D.A. Jenkins and P.A. Arcese. 2012. Using historical and contemporary DNA in Peary caribou to examine the relative loss of microsatellite and Mhc variation following population bottlenecks. Biology Department, University of Louisiana at Lafayette, 4 October.

Taylor, S.S. 2012. Exploring the world by degrees. Baton Rouge Audubon Society, Baton Rouge, LA, 27 September.

Taylor, S.S. 2010. Bottlenecks, translocations and genetic variation in New Zealand saddlebacks and robins. Biology Department, Southeastern Louisiana University, 19 February.

Taylor, S.S. 2008. Bottlenecks, translocations and genetic variation in New Zealand saddlebacks. Ecology, Evolution and Behaviour Seminar Series, University of British Columbia, Vancouver, BC, 26 March.

Taylor, S.S. 2008. Ancestral genetic variation in New Zealand saddlebacks and robins and its consequences for management. Canadian Wildlife Service, Delta, BC, 18 March.

Taylor, S.S., S. Boessenkool, and I.G. Jamieson. 2008. Genetic variation and management of saddlebacks and robins. Department of Conservation, Te Anau, New Zealand, 26 February.

Taylor, S.S. 2006. The genetic and conservation consequences of species translocations in New Zealand. Department of Zoology, University of Otago, Dunedin, New Zealand, 22 September.

Taylor, S.S., and I.G. Jamieson. 2006. Genetic variation and management of saddlebacks and robins. New Zealand Ornithological Society, Dunedin, New Zealand, 23 August.

Taylor, S.S. 2002. The Nova Scotia Herpetofaunal Atlas. Blomidon Naturalist Society, Wolfville, NS, June.

Taylor, S.S. 2002. Humboldt penguins: diving behaviour and male nest intruders. Nova Scotia Bird Society, Halifax, NS, 28 March.

RESEARCH SUPPORT

Gulf of Mexico Research Initiative. 1 January 2015 – 31 December 2017. Coastal Waters Consortium, RFP-IV: Marsh Vertebrates. **Funded** for $851,616. **PI: Sabrina S. Taylor**; Co-PI: Philip Stouffer.

National Science Foundation Doctoral Dissertation Improvement Grant (to PhD student Kristin Brzeski). 1 July 2013 – 30 June 2015. Understanding mate choice and hybridization in the endangered red wolf. **Funded** for $17,040. **PI: Sabrina S. Taylor**; Co-PI: Kristin Brzeski.

Gulf Coast Joint Venture. August 2012 – July 2015. Hybridization in western Gulf Coast Mottled Ducks. **Funded** for $29,900. **PI: Sabrina S. Taylor**; Co-PI: William Selman.

Louisiana Department of Wildlife and Fisheries. July 2012 – June 2015. Stock identification of Louisiana's largemouth bass fisheries. **Funded** for $192,000. PI: William E. Kelso; **Co-PIs: Sabrina S. Taylor** and Michael Kaller.

Louisiana Department of Wildlife and Fisheries State Wildlife Grant. July 2012 – June 2014. Effective population size and genetic connectivity of Seaside Sparrows in Louisiana. **Funded** for $34,398. **PI: Sabrina S. Taylor**; Co-PIs: Philip Stouffer and Stefan Woltmann.

Gulf of Mexico Research Initiative. September 2011 – December 2014. The effects of the Macondo oil spill on coastal ecosystems: marsh birds. **Funded** for $503,571. **PI: Sabrina S. Taylor**; Co-PI: Philip Stouffer.

LA Board of Regents Research Competitiveness Subprogram. July 2011 – June 2014. Genetic population structure in Bachman's Sparrow. **Funded** for $74,000. **PI: Sabrina S. Taylor**.

US Fish and Wildlife Service. January 2011 – December 2014. Inbreeding and mate choice in red wolves. **Funded** for $12,160. **PI: Sabrina S. Taylor**.

Louisiana Department of Wildlife and Fisheries. July 2010 – June 2012. Assessment of the hybrid status of Toledo Bend Reservoir striped bass. **Funded** for $120,000. **PI: Sabrina S. Taylor**; Co-PI: William Kelso.

LA EPSCoR Pilot Fund. January 2010 – September 2010. Mhc variation, microsatellite variation and incidence of avian malaria in song sparrows. **Funded** for $10,000. **PI: Sabrina S. Taylor**.

LA Board of Regents Link Fund. July 2009 – August 2009. Measuring avian Mhc variation for conservation genetics. **Funded** for $3000. **PI: Sabrina S. Taylor**.

OTHER AWARDS AND SCHOLARSHIPS

LSU Alumni Association Rising Faculty Research Award, 2015 ($5,000)
Gamma Sigma Delta Award of Merit Teacher Honor Roll, 2015
Tiger Athletic Foundation Award for Outstanding Teacher, LSU College of Agriculture 2014 ($1000)
NSERC Postdoctoral Fellowship, 2007-2009 ($80,000)
University of Otago Division of Science International Fees Scholarship, 2005-2006 ($25,500)
International Federation of University Women, A. Vibert Douglas Fellowship, 2005 ($12,000)
NSERC Julie Payette Award, 2003-2004 ($50,000)

Dalhousie Graduate Scholarship, 1998-2000 ($14,000)
Innovative Research Award, 1999, Canadian International Development Agency ($10,000)
Kathleen S. Anderson Award, 1999, Manomet Center for Conservation Sciences ($500)
Oregon Zoo Range Country Conservation Grant 1999-2000 ($6,500)
American Ornithologists' Union, Marcia Brady Tucker Travel Award 2000 ($200)

POST-DOCTORAL FELLOWS AND THESES/DISSERTATIONS DIRECTED

A total of three post-doctoral fellows, two PhD, four MS, and three Honor's students advised.

MEMBERSHIP IN PROFESSIONAL ORGANIZATIONS

LSU Science Club 2014 - present
Society for Conservation Biology 2003-present
American Ornithologists' Union 1999-2001 and 2010-present
    AOU Elective Member 2014-present
Association of Field Ornithologists 2014-present
Canadian Federation of Graduate Women 2007-2009
New Zealand Federation of Graduate Women 2003-2007
New Zealand Society for Biochemistry and Molecular Biology 2003-2007
New Zealand Ecological Society 2003-2006
Society of Canadian Ornithologists 2000-2009
Nova Scotia Federation of Naturalists 2000-2003
Nova Scotia Bird Society 2000-2003
Animal Behavior Society 1999-2001

OUTREACH

Gulf Lagniappe Adult Education, Seaside Sparrows, LUMCON, 8 March 2014

Marsh Edge-U-Cation Teacher Professional Development, Seaside Sparrows, LUMCON, 1-2 March 2013

Superintendent of the Environmental Threats Contest, LSU 4-H University, 2010 – present.

Judge at the Louisiana Region VII Science and Engineering Fair, 2010, 2011 & 2012

AgMagic Volunteer, May 2011 and April 2010.

LSU Day Volunteer, November 2010.

Volunteer fund-raiser for the Nova Scotia Nature Trust, 2002 & 2003

Judge at the Halifax Regional Science Fair, 1998 & 1999

UNIVERSITY SERVICE

LSU Institutional Animal Care and Use Committee 2015 - present

LSU Faculty Senate 2013-present.

Organizer of the School of Renewable Natural Resources Seminar Series, 2013-present.

Editor for the School of Renewable Natural Resources “Newsletter” and “Research Matters” publications, 2012-present.

Undergraduate Faculty Advisor 2011-present.

Organized electrical modifications to provide emergency generator power for fridges and freezers in the School of Renewable Natural Resources, 2013.

College of Agriculture Student Recognition and Awards Committee Member, 2010-present.

School of Renewable Natural Resources Outreach/Communications Committee Member, 2010-present.

School of Renewable Natural Resources Recruitment Committee Member, 2010-present.

LSU AgCenter Biotechnology Laboratory Advisory Committee Member, 2009-2010.

PROFESSIONAL SERVICE

NSF Panelist 2013 & 2014

Book Review Editor for the Journal of Field Ornithology 2013-present

Associate Editor for Animal Conservation 2012-present

Reviewer for Auk, Behavioral Ecology and Sociobiology, Biological Journal of the Linnean Society, Bioscience, BMC Evolutionary Biology, Condor, Conservation Genetics, Fisheries, Heredity, Ibis, International Journal of Immunogenetics, Journal of Avian Biology, Journal of Fish Biology, Journal of Wildlife Management, Molecular Ecology, PLoSONE, Southeastern Naturalist, and Trends in Ecology and Evolution.

Curriculum vitae
Samantha M. Wisely

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***Research Interests*:** conservation genetics, molecular ecology, biogeography, wildlife biology

Education:

Ph.D. Zoology and Physiology, University of Wyoming, August 2001. Dissertation: Conservation genetics of the black-footed ferret.
M.S. Wildlife Ecology, Humboldt State University, August 1997. Thesis: Comparative physiology, ecology and behavior in two species of plethodontid salamander.
B.A. Ecology, Evolution and Animal Behavior, University of California, San Diego. June 1991.

Appointments:

2011-present	**Associate Professor**, Dept. of Wildlife Ecology and Conservation, University of Florida
2011-present	**Associate Director**, Ordway Swisher Biological Station, University of Florida
2013-present	**Affiliate Associate Curator**, Dept. of Mammalogy, Florida Museum of Natural History
2013-present	**Research Affiliate**, Emerging Pathogens Institute, University of Florida
2004-present	**Research Associate**, National Zoological Park, Smithsonian Institution
2010-2011	**Associate Professor**, Division of Biology, Kansas State University
2004- 2010	**Assistant Professor**, Division of Biology, Kansas State University
2002-2003	**Postdoctoral Associate**, National Zoological Park, Smithsonian Institution
2001-2002	**Smithsonian Postdoctoral Fellow,** National Museum of Natural History
1997-2001	**Research Assistant**, University of Wyoming
1993-1997	**Teaching Assistant**, Humboldt State University

Publications (**Corresponding Author, *Avian or Conservation Genetic related (n=30 pubs)):

Miller, S., Zieger, U., Ganser, C., Satterlee, S.A., Bankovich, B., Amadi, V., Hariharan, H., Stone, D., **Wisely, S.M.**** 2015. The Influence of Land Use and Climate on Salmonella Carrier Status in the Small Indian Mongoose (*Herpestes auropunctatus*) in Grenada, West Indies. Journal of Wildlife Diseases 51:60-68.

Peng, X., Alfoldi, J., Gori, K., Eisfeld, A.J., Tyler, S.R., Tisoncik-Go, J., Brawand, D., Law, G.L., Skunca, N., Hatta, M., Gasper, D.J., Kelly, S.M., Chang, J., Thomas, M.J., Johnson, J., Berlin, A.M., Lara, M., Russell, P., Swofford, R., Turner-Maier, J., Young, S., Hourlier, T., Aken, B., Searle, S., Sun, X., Yi, Y., Suresh, M., Tumpey, T.M., Siepel, A., **Wisely, S.M**., Dessimoz, C., Kawaoka, Y., Birren, B.W., Lindblad-Toh, K., DiPalma, F., Engelhardt, J.F., Katze, M.G., Palmero, R.E. 2014. Insights from the ferret genome (*Mustela putorius furo*) for biomedical models of human respiratory disease. Nature Biotechnology. doi:10.1038/nbt.3079.

*Lounsberry, Z.T., Almeida, J.B., Grace, A., Lanctot, R.B., Liebezeit, J., Sandercock, B.K., Strum, K.M., Zack, S., **Wisely, S.M.**.** 2014. Museum collections reveal that Buff-breasted Sandpipers (*Calidris subruficollis*) maintained mtDNA variability despite large population declines during the past 135 years. Conservation Genetics DOI :10.1007/s10592-014-0611-2.

*McNew, L.B., L.M. Hunt, A.J. Gregory, **S.M. Wisely**, and B.K. Sandercock. 2014. Effects of wind energy development on the nesting ecology of Greater Prairie-Chickens in fragmented grasslands. Conservation Biology 28: 1089-1099.

*Tucker, J.M., Schwartz, M.K., Truex, R.L., **Wisely, S.M.**, Allendorf, F.W. 2014. Sampling affects the detection of genetic subdivision and conservation implications for fisher in the Sierra Nevada. Conservation Genetics 15:123-136.

*Winder, V.L., L.B. McNew, A.J. Gregory, L.M. Hunt, **S.M. Wisely**, and B.K. Sandercock. 2013. Space use of female Greater Prairie-Chickens in response to wind energy development. Ecosphere 5(1):art3.

*Winder, V., McNew, L.B., Gregory, A., Hunt, L., **Wisely, S.M.,** Sandercock, B.K. 2013. Effects of wind energy development on survival of female Greater Prairie-Chickens. Journal of Applied Ecology 51:395-405.

Caldus, Marcellus M.**, Goodin, Douglas G., Sherwood, Steven, Campos Krauer, Juan M. and **Wisely, Samantha M.** 2013. Land-cover change in the Paraguayan Chaco: 2000-2011. Journal of Land Use Science. DOI: 10.1080/1747423X.2013.807314

Ganser, C., **Wisely, S.M.**** 2013. Patterns of spatio-temporal distribution, abundance, and diversity in a mosquito community from the eastern Smoky Hills of Kansas. Journal of Vector Ecology 38:229-236.

*Lounsberry, Z.T., Almeida, J.B., Grace, A., Lanctot, R.B., Liebezeit, J., Sandercock, B.K., Strum, K.M., Zack, S., **Wisely, S.M.**** 2013. Range-wide conservation genetics of buff-breasted sandpipers. Auk 130:429−439.

Santymire, R.M. **, **Wisely, S.M.,** Livieri, T.M., Howard, J.G. 2012. Using canine width to determine age in the black-footed ferret, *Mustela nigripes*. Small Carnivore Conservation 46:17-21.

*McNew,L.B.**, Gregory, A.J., **Wisely, S.M**., Sandercock, B.K. 2012. Demography of Greater Prairie-Chickens: Regional Variation in Vital Rates, Sensitivity Values, and Population Dynamics. Journal of Wildlife Management 76:987-1000. (Wildlife Publications Award - Outstanding Article of the Year).

Gregory, A.J., Kaler, R.S.A., Prebyl, T.J., Sandercock, B.K., **Wisely, S.M.**** 2012. Influence of translocation strategy and mating system on the genetic structure of a newly established population of island ptarmigan. Conservation Genetics 13:465-474.

*Statham, M.J., Sacks, B.N., Aubry, K.B, Perrine, J.D., and **Wisely, S.M.****. 2012. The origin of recently established red fox populations in the United States: Translocations or natural range expansions? Journal of Mammalogy 93:38-51.

Barton, H.D., and **Wisely, S.M.**.** 2012. Phylogeography of striped skunks (*Mephitis mephitis*) in North America: Pleistocene dispersal and contemporary population structure. Journal of Mammalogy 93:52-65.

*Blevins, E.**, Wisely, S.M., and With, K.A. 2011. Historical processes and landscape context influence genetic structure in peripheral populations of the collared lizard (*Crotaphytus collaris*). Landscape Ecology 26:1125-1136.

*McNew, L.B., Gregory, A.J., **Wisely, S.M.**, Sandercock, B.K.** 2011. Reproductive biology of a southern population of Greater Prairie-chickens. In Studies in Avian Biology, Vol. 39. Ecology, Conservation and Management of Grouse, eds. Sandercock, B.K., Martin, K., and Segelbacher, G., Pp. 209-222.

*McNew, L.B., Gregory, A.J., **Wisely, S. M.,** Sandercock, B.K.** 2011. Human-mediated selection on life history traits of the Greater Prairie-chicken. In Studies in Avian Biology, Vol. 39. Ecology, Conservation and Management of Grouse, eds. Sandercock, B.K., Martin, K., and Segelbacher, G., Pp. 255-266.

*Gregory, A.J., McNew, L.B., Prebyl, T., Sandercock, B.K., **Wisely, S.M.**** 2011. Hierarchical modeling of lek habitats of Greater Prairie-chickens. In Studies in Avian Biology, Vol. 39. Ecology, Conservation and Management of Grouse, eds. Sandercock, B.K., Martin, K., and Segelbacher, G., Pp. 21-32.

*Casey, A.E., Sandercock, B.K., **Wisely, S.M.**** 2011. Genetic parentage and local population structure in the socially monogamous Upland Sandpiper. Condor 113: 119-128.

*Klug, P.E.**, **Wisely, S.M.,** With K.A. 2011. Population genetic structure and landscape connectivity of the Eastern Yellowbelly Racer (*Coluber constrictor flaviventris*) in the tallgrass prairie of northeastern Kansas. Landscape Ecology 26:281.

Campos-Krauer, J.M., **Wisely, S.M.**** 2011. Deforestation and cattle ranching drive rapid range expansion and secondary contact of vicariant populations of a semiaquatic rodent in the Gran Chaco ecosystem. Global Change Biology 17: 206-218.

Apple, J.L., Grace, T., Joern, A., St. Amand, P., **Wisely, S.M.**** 2010. Genome scan detects host-related divergent selection in the grasshopper *Hesperotettix viridis*. Molecular Ecology 19: 4012-4028.

Grace, T., **Wisely, S.M**., Brown, S.J., Dowell, F., Joern, A.** 2010. Divergent host plant adaptation drives the evolution of sexual isolation in the grasshopper *Hesperotettix viridis* (Orthoptera: Acrididae) in the absence of reinforcement. Biological Journal of the Linnean Society 100:866-878.

*Conard, J., Statham, M.J., Gipson, P.S., **Wisely, S.M.****. 2010. The influence of translocation strategy and management practices on the genetic health of a re-established elk (*Cervus elaphus*) population. Restoration Ecology 18 (S1): 85-93.

*Sacks, B.**, Statham, M.J., Perrine, J., **Wisely, S.M**., Aubry, K.B. 2010. North American montane red foxes: expansion, fragmentation, and the origin of the Sacramento Valley red fox. Conservation Genetics. 11:1523-1539.

Barton, H.D., Gregory, A.J., Davis, R., Hanlon, C.A., **Wisely, S.M.**** 2010. Contrasting landscape epidemiology of two sympatric rabies virus strains. Molecular Ecology 19:2725-2738.

Coolon, J.D., Jones, K.L., Narayanan, S., **Wisely, S.M**.** 2010. Microbial ecological response of the intestinal flora of *Peromyscus maniculatus* and *P. leucopus* to heavy metal contamination. Molecular Ecology, Special Issue on next generation technology 19:67-80.

Grace, T., Joern, A., Apple, J.L., Brown, S.J., and **Wisely, S.M.**** 2009. Highly polymorphic microsatellites in the North American Snakeweed Grasshopper, *Hesperotettix viridis*. Journal of Orthoptera Research 18:19-21.

Dragoo, J., Coan, K., Moore, K., Henke, S., Fleischer, R., **Wisely, S.M.**** 2009. Polymorphic microsatellite markers for the striped skunk, *Mephitis mephitis*, and other mephitids. Molecular Ecology Resources 9:383-385.

Casey, A.*, Sandercock, B., Jones, K., **Wisely, S.M.**** 2009. Heteroduplex molecules cause sexing errors in a standard molecular protocol for avian sexing. Molecular Ecology Resources 9:61-65.

*McNew LB, Gregory AJ, **Wisely SM**, Sandercock BK. 2009. Estimating the stage of incubation for nests of greater prairie-chickens using egg flotation: a float curve for grousers. Grouse News 38:12-14

*Aubry, K. B., Statham, M. J., Sacks, B. N., Perrine, J. D., & **Wisely, S. M.**** (2009). Phylogeography of the North American red fox: vicariance in Pleistocene forest refugia. Molecular Ecology 18: 2668-2686.

Wisely, S.M.*, Santymire, R.M., Livieri, T.M., Mueting, S.A.*, Howard, J.G. 2008. Genotypic and phenotypic consequences of reintroduction history: case study of the black-footed ferret. Conservation Genetics 9:389-399.

Wisely, S.M.*, Howard, J.G., Williams, S.A., Bain, O., Santymire, R.M., Bardsley, K.D., Williams, E.S. 2008. An unidentified filarial species and its impact on fitness in wild populations of the black-footed ferret (*Mustela nigripes*). Journal of Wildlife Diseases. 44:53-64.

Wisely, S.M.*, Statham, M.J., Fleischer, R.C. 2008. Pleistocene refugium and Holocene expansion of a grassland dependent species, the black-footed ferret (*Mustela nigripes*). Journal of Mammalogy. 89:87-96.

*Schwartz, M.K.**, Aubry, K.B, McKelvey, K.S., Pilgrim, K.L., Copeland, J.P., Squires, J.R., Inman, R.M., **Wisely, S.M.** 2007. Inferring geographic isolation of wolverines in California using ancient DNA. Journal of Wildlife Management 71:2170-2179.

Parker, M.W.**, Kress, S.W., Golightly, R.T., Carter, H.R., Parsons, E.B., Schubel, S.E., Boyce, J.A., McChesney, G.J., and **Wisely, S.M.** 2007. Assessment of social attraction techniques used to restore a Common Murre colony in central California. Waterbirds 30:17-28.

Bronson E.**, Bush M., Viner T., Murray S., **Wisely S.M.**, Deem S.L. 2007. Mortality of captive black-footed ferrets (*Mustela nigripes*) at Smithsonian's National Zoological Park: 1989-2004. Journal of Zoo and Wildlife Medicine 38:169-176.

Li, Z., Sun, X., Chen, J., Liu, X., **Wisely, S.M.**, Zhou, Q., Renard, J.P., Leno, G.H., Engelhardt, J.F.** 2006. Full-term development of ferret embryos cloned by cell nuclear transfer. Developmental Biology. 293:439-448.

Wisely, S.M.* 2005. The genetic legacy of the black-footed ferret: past, present, and future. Pages 37-43 *in* Recovery of the Black-Footed Ferret: Progress and Continuing Challenges. U.S.G.S. Scientific Investigations Report 2005-5293.

***Wisely, S.M.**,** Santymire, R.M., Marinari, P., Kreeger, J. Livieri, T., Wildt, D.E., Howard, J.G. 2005. Environment influences morphology and development of *in situ* and *ex situ* populations of the black-footed ferret. Animal Conservation 8:321-328.

Buskirk, S.W. and **Wisely, S.M.** 2005. Appraising the conservation value of private lands. Pages 174-190 In: Species at risk: using economic incentives to shelter endangered species on private lands. J. Shogren, ed., Austin TX: University of Texas Press.

*Aubry, K.**, **Wisely, S.**, Raley, C. and Buskirk, S. 2004. Zoogeography, spacing patterns, and dispersal in fishers: insights gained from combining field and genetic data. Pages 201-220 in D.J. Harrison, A.K. Fuller, and G. Proulx, eds. Martens and fishers (Martes) in human-altered environments: an international perspective. Springer Science+Business Media, New York, NY. 279 pp.

Wisely, S.M.*, Buskirk, S.W., Russell, G.*, Aubry, K. and Zielinski, W. 2004. Phylogeography and genetic diversity of the fisher (*Martes pennanti*) in a peninsular and peripheral metapopulation. Journal of Mammalogy 85: 640-648.

Wisely, S.M.**, Maldonado, J.E., and Fleischer, R.C. 2004. Turbinal bones as a source of ancient DNA. Conservation Genetics 5:105-107.

Wisely, S.M.** and Golightly, R.T. 2003. Behavioral and ecological adaptations to water economy in two species of plethodontid salamander. Journal of Herpetology 37:659-665.

Wisely, S.M.*, McDonald, D.B., and Buskirk, S.W. 2003. Evaluation of the species survival plan and captive breeding program for the black-footed ferret. Zoo Biology 22:287-298.

***Wisely, S.M**.**, Fleming, M.A., McDonald, D.B., Buskirk, S.W., and Ostrander, E.A. 2002. Genetic diversity and fitness in black-footed ferrets before and during a bottleneck. Journal of Heredity 93:231-237.

Wisely, S.M.*, Ososky, J.J., and Buskirk, S.W. 2002. Morphological changes to black-footed ferrets resulting from captivity. Canadian Journal of Zoology. 80:1562-1568.

Publications in the Popular Press

Wisely, S.M. 2014. Facts about Wildlife Diseases: Pseudorabies. UF IFAS EDIS Document UW388.

Bankovich, B., Wisely, S.M., Boughton, E. March 2014. Quantifying forage loss following rooting by feral swine. The Florida Cattleman and Livestock Journal. Volume 78.

Publications in submission or revision:

Wisely, S.M.**, Ryder, O.A., Santymire, S.M., Engelhardt, J.F., Novak, B.J. In revision. Developing a Road Map for 21st Century Genetic Restoration: Gene Pool Enrichment of the Black-Footed Ferret. Journal of Heredity.

Publications in preparation:

Ganser, C., Gregory, A.J., Hunt, L., McNew, L.B., Sandercock, B.K., Wisely, S.M. Submitted. Fine-scale spatial epidemiology of avian malaria in a grassland ecosystem: disease hazard and risk to grassland birds. Journal of Wildlife Diseases.

Grants and Awards:

2011 – Top 150 Scientists in Kansas. I was named one of the top scientists, past or present, by the Ad Astra Science Council of Kansas

Current Grants

Cervidae Disease Research. $400,000. Samantha Wisely, P.I. September 2014-August 2016. Florida Legislative Budget Request.

Developing a rapid diagnostic tool for pseudorabies. $76,000. Samantha Wisely, P.I. September 2014-August 2015. USDA APHIS VS Cooperative Agreement.

US-Swaziland Planning Visit: Social and Ecological Drivers Impacting Biodiversity in Southern Africa. $34,754. Samantha Wisely, P.I, Rick Stepp, co-PI. October 2014 – September 2015. National Science Foundation.

Assessing diet in feral swine. $15,000. Samantha Wisely, P.I. June 2014 - May 2015. USDA APHIS WS Cooperative Agreement.

Assessing damage to rangelands by feral pigs in Florida. $145,000. Samantha Wisely, P.I. September 2012-August 2015. USDA APHIS WS Cooperative Agreement.

Pending Grants

Dept. of Defense, Strategic Enviornmental Resaerch and Development Program (SERDP). Understanding how host properties and environmental conditions contribute to current and future transmission and distribution of pathogens carried by invasive feral swine. PI: S. Wisely, co-PI's: R. Boughton, M. Farnsworth. $2,331,664.

Biodiversity Science and Technology Center: Cyber-Enabled Resources to Integrate Diverse Data for Research, Conservation and Education. $24 Million. PI: Pam Soltis, co-PIs: Kent Crippen, Jose Fortes, Doug Soltis, Samantha Wisely. National Science Foundation.

National Science Foundation. IRES: Changing Landscapes, Biodiversity, and Ecosystem Function in a Global Hotspot (in Africa). PI: Robert McCleery, co-PI's: Samantha Wisely, James Austin, Robert Fletcher.

National Science Foundation. CNH-S: Integrating human well-being and natural capital into a conservation land planning framework. $483,360. Samantha Wisely, PI, co-PIs: Robert McCleery, Greg Kiker, Grenville Barnes, J. Richard Stepp.

Previous Grants

Disease surveillance in Arctic-breeding shorebirds. $105,515. Richard Lanctot, P.I., Samantha Wisely, co-PI. June 2011- June 2014. U.S. Fish and Wildlife Service, Disease Surveillance Program.

Buccal sampling methods and preliminary assessment of pathogen diversity in feral swine. $75,000. Samantha Wisely, P.I. September 2012-August 2013. USDA APHIS WS Cooperative Agreement.

Patterns and Processes of Dispersal of Black-Tailed Prairie Dogs in a Heavily Managed Landscape of the Great Plains Landscape Conservation Cooperative. $98.008. Samantha Wisely, P.I., Jack Cully and Charles Lee, co-PI's. August 2011-September 2015. USFWS Great Plains Landscape Conservation Cooperative.

Biogeography of *Plasmodium* in Arctic-breeding shorebirds. $59,008. Samantha Wisely, P.I. July 2012-June 2013. U.S. Fish and Wildlife Service, Disease Surveillance Program.

URM: Undergraduate Research and Mentoring in Ecological Genomics. $781,567. Samantha Wisely, P.I. Ari Jumpponen, co-PI. January 2011- December 2016. National Science Foundation.

Development of regional planning tools to assess the impacts of climate and land use change on a sensitive grassland bird. $47,349. Samantha Wisely, P.I. Brett Sandercock, co-P.I. May 2010-September 2011. U.S. Fish and Wildlife Service.

Environmental impacts of wind power development on population biology of Greater Prairie-chickens. $299,998. Brett Sandercock and Samantha Wisely co-PI's. July 1, 2009 - June 30, 2011. 20% Wind by 2030: Overcoming the Challenges (Topic Area 3: Environmental Impacts). Department of Energy.

Environmental impacts of wind power development on population biology of Greater Prairie-chickens. $149,000. Brett Sandercock and Samantha Wisely co-PI's. July 1, 2009 - June 30, 2011. State Wildlife Grant. USFWS.

Assessing zoonotic disease threats overseas using a multimodal approach. Subcontract awarded to Samantha Wisely. Marty Vanier, P.I. July 2010-September 2010. $166,000. National Center for Medical Intelligence.

Effects of wind power on the demography and population genetics of the Greater Prairie Chicken. Brett Sandercock and Samantha Wisely co-PI's. March 2006 – December 2009. $731,000. National Wind Coordinating Committee.

Effects of Wind Power on Prairie Chickens. Samantha Wisely, PI. June 2007-May 2009. $149,546. National Fish and Wildlife Foundation.

Biogeography and molecular epidemiology of the PRNP gene in Kansas. $80,406. October 2007-September 2009.

National Fish and Wildlife Foundation. April 2005 – December 2006. $54,511. Biomedical survey of wild black-footed ferrets.

U.S. Forest Service, Northwest Pacific Research Station. April 2005 – December 2006. $60,090. Phylogeography and morphology of the red fox in North America.

LI-COR Biosciences Genomics Education Matching Fund Program. (PI Sue Brown Co-PI: Mark Ungerer, Sam Wisely). January – June 2006. $50,000.

Arizona Game and Fish Department. March – May 2005. $11,000. Biomedical survey of wild black-footed ferrets.

Phoenix Zoological Society. March – May 2005. $5,000. Biomedical survey of wild black-footed ferrets.

KSU - NSF - Long Term Ecological Research (Subcontract). March 2004 – April 2005. $8,000. Carnivore disease survey on Konza Prairie Biological Station.

KSU - Ecological Genomics in Kansas. August 2004 – June 2005. $20,000. Ecological, physiological and genomic consequences of environmental toxins.

KSU - Women and Minority in Science and Engineering Mentor Award. 2004-2005. $6,000. Conservation genetics of the fisher.

KSU - BRIEF. July 2005. $12,345. Microsatellite Development Workshop.

KSU - The Center for the Understanding of Origins. July 2005. $5,900. Microsatellite Development Workshop.

KSU-ADVANCE Seminar Series. 2004. $700. Invited speaker: Dr. Lisette Waits, University of Idaho.

National Fish and Wildlife Foundation. 2003-2004. $48,200. Biomedical surveys of wild black-footed ferrets. Funded. Administered by Friends of the National Zoo.

Invited Workshop

Tick-borne Disease Think Tank, Sponsored by UF Emerging Pathogen Institute and Tourism Crisis Management Institute.

Invited Professional Presentations:

Society for the Preservation of Natural History Collections. The utility of accessioned collections for conservation management of endangered species. S. M. Wisely, P.M. Marinari, O.A. Ryder. May 2015. Invited Speaker to Symposium: Specimens Full Circle: Collection to Digitization to Data Use.

University of Georgia, Warnell School of Forestry. Invasive mammals: Documenting distribution changes and assessing impacts in the 21st Century, January 2015.

Symposium on Genomics in Wildlife Research at The Annual Meeting of The Wildlife Society, October 2014. Using Genomic Approaches to Understand Wildlife Diseases. Katherine Sayler, Samantha Wisley, Toni Piaggio.

Infectious Disease Seminar Series, Centers for Disease Control, Colorado State University, and the National Wildlife Research Center, January 2014. The Biogeography of Infectious Wildlife Diseases.

Oxford Round Table on Critical Issues of Sustainability, Harris Manchester College, Oxford University, July 2013. The complex relationship of biodiversity and disease emergence on the agro-ecological landscape.

Biology Department, University of Florida, November 2012. The effect of late Quaternary history on the extinction risk and conservation value of Holarctic species.

Geography Department, University of Florida, September 2012. The effect of late Quaternary history on the extinction risk and conservation value of Holarctic species.

Dept. of Environmental and Global Health, University of Florida, June 2012. Deforestation and cattle ranching drive the emergence of zoonotic pathogens.

JW Jones Ecological Research Center, May 2012. Deforestation and cattle ranching drive the emergence of zoonotic pathogens.

Archbold Biological Field Station, January 2012. Intrinsic and extrinsic factors drive the emergence of rabies.

International Grassland Symposium, September 2011. Drivers of disease dynamics in grassland ecosystems.

One Health Kansas. Professional Development Seminar for Public Health Professionals. Zoonotic Diseases of Kansas. July 2011.

University of Montana. Ecology of Infectious Disease, Scholar in Residence Program. Landscape epizootiology. November 2010.

Kansas State University College of Veterinary Medicine. Department of Pathobiology. Deforestation and cattle ranching drive the emergence of zoonotic pathogens. October 2010.

Central Plains Society of Mammalogists. Keynote address. What fossil remains and DNA evidence tell us about mesocarnivores: foxes, ferrets and skunks. October 2010.

Keynote address, Black-footed Ferret Recovery in Kansas. 46th Conservation Achievement Program Awards Banquet, Kansas Wildlife Federation, Manhattan, Kansas. February 2010.

Missouri State University. Biology Department. Contrasting epidemiology of evolutionarily independent strains of rabies in a common host species. December 2009.

Kansas Association of Zoological Parks. Black-footed Ferret Recovery in Kansas. March 2009.

University of Nevada at Reno. Ecology, Evolution and Conservation Biology Colloquium. Contrasting epidemiology of evolutionarily independent strains of rabies in a common host species. April 2009.

Kansas State University College of Veterinary Medicine. Department of Pathobiology. Contrasting epidemiology of evolutionarily independent strains of rabies in a common host species. October 2007.

University of Wyoming, Dept. of Zoology and Physiology. Quaternary history affects the risk of extinction and conservation value of Holarctic fauna. April 2007.

University of Missouri, Division of Biological Sciences. Quaternary history affects the risk of extinction and conservation value of Holarctic fauna. April 2007.

U.S. Geological Survey, National Conservation Genetics Laboratory. Conservation genetics of the black-footed ferret captive breeding program. October 2006.

University of Denver, Dept. of Biology. Quaternary history affects the risk of extinction and conservation value of Holarctic fauna. October 2006.

Emporia State University, Dept. of Biological Sciences. Conservation breeding of the endangered black-footed ferret. April 2006.

Michigan Technical University, Dept. of Natural Resources. Conservation genetics of the Pacific fisher. April 2005.

Colby College, Biology Department. Conservation biology of the black-footed ferret. April 2005.

US Fish and Wildlife Service, Executive Committee of the Black-Footed Ferret Recovery Team. Biomedical survey of wild black-footed ferrets. 2004.

US Geological Survey, Midcontinent Research Laboratory, Black-Footed Ferret Symposium, Genetic diversity in the black-footed ferret: Past, present and future. 2004.

US Fish and Wildlife Service, Conservation Subcommittee of the Black-Footed Ferret Recovery Team. Biomedical survey of the black-footed ferret. 2004.

Professional Presentations (Presenter underlined. *Undergraduate author)

University of Florida Emerging Pathogens Institute Research Day, Gainesville, Florida, February 26, 2015. Environment and demography influence seroprevalence of pseudorabies in feral swine populations of Florida. Carr AN, Hernandez F, Milleson MP, Wisely SM.

The Florida Chapter of The Wildlife Society 2015 Spring Meeting, Jacksonville, Florida, March 31-April 2, 2015. Environment and demography predict seroprevalence of pseudorabies in feral swine populations of Florida. Carr AN, Hernandez F, Milleson MP, Wisely SM.

Southeastern Association of Fish and Wildlife Agencies, Destin, Florida, October 22-23, 2014. Epizootiology of pseudorabies virus infection in the Florida panther. Cunningham, MW, Conley, K., Mead DG, Onorato D, Terrell SP, Shindle DS, Wisely SM, Jansen D, Clemons BC, Caudil GE, Maes RM, Kiupel M.

Student Conference on Conservation Science New York. American Museum of Natural History, New York City, New York, October 9-11, 2013. Microbes and host physiology – an understanding of health at multiple biological levels. Hernandez, F., Wisely, S. and Beasley, J.

University of Florida Emerging Pathogen Institute Research Day Mapping the Landscape of Evolving Science. UF Campus at the Emerging Pathogens Institute, Gainesville, Florida, February 14th, 2013. Fecal and Bloodborne Pathogen Community Assemblage of an Invasive Alien Species: Feral Swine in the Southeastern U.S.A. Satterlee, S.A., Bankovich, B., Boughton, R., Campbell, T.B., Hernandez, F., Jiang, C.J., Milleson, M.P., Slezak, T., Tillman, E.A. and Wisely, S.M.

Society of Wetland Scientists South Atlantic Chapter/Florida Association of Environmental Soil Scientists/South West Chapter of the Florida Association of Environmental Professionals. 2013 Short-term trajectories of Carolina Redroot Following Rooting Disturbance by Feral Swine in South Florida. Bankovich, B., Boughton, E., and Wisely, S.M.

5th Western Hemisphere Shorebird Group Meeting. 2013 Avian malaria of Arctic-breeding shorebirds and their global transmission patterns. Ganser, C., and Wisely, S.M.

62nd International Conference of the Wildlife Disease Association. 2013. Biogeography of transmission dynamics for vector-borne pathogens recently found in Artic-breeding shorebirds. Ganser, C., and Wisely, S.M.

Joint Meeting of the American Ornithologists' Union (131st), and the Cooper Ornithological Society (83rd), Chicago, Illinois. August 2013. Demographic effects of wind power development on Greater Prairie-Chickens. Sandercock, B.K., V.L. Winder, L.B. McNew, A.J. Gregory, and S.M. Wisely.

Joint Meeting of the American Ornithologists' Union (131st), and the Cooper Ornithological Society (83rd), Chicago, Illinois. August 2013. Quantifying Greater Prairie-Chicken spatial ecology in response to wind energy development in north-central Kansas. Winder, V.L., L.B. McNew, A.J. Gregory, L.M. Hunt, S.M. Wisely, and B.K. Sandercock.

American Society of Mammalogy, June 2013. Broad-scale patterns of connectivity among black-tailed prairie dog colonies in a heavily managed landscape. Rachel Pigg, Samantha Wisely, Charlie Lee, and Jack Cully, Jr.

Western Section of the Wildlife Society; Sacramento, CA, USA. February 2013. Stable mitochondrial variation in a declining population: a 135-year genetic survey of Buff-breasted Sandpipers. Zachary T. Lounsberry, Juliana B. Almeida, Richard B. Lanctot, Joe Liebezeit, Brett K. Sandercock, Khara M. Strum, Steve Zack, and Samantha M. Wisely.

Society for Rangeland Management Meeting, February 2013. Effects of rangeland management and wind power on greater prairie-chickens in eastern Kansas. Brett K. Sandercock, Virginia L. Winder, Lyla M. Hunt, Lance B. McNew, Andrew J. Gregory, and Samantha M. Wisely.

6th Biennial Conference of International Society of Biogeography, January 2013. The Biogeography of Pathogen Community Assemblage in the Southeastern United States. Samantha M. Wisely, S. Andrew Satterlee, Tyler B. Campbell, Michael P. Milleson, Brittany Bankovich, Felipe Hernandez

6th Biennial Conference of International Society of Biogeography, January 2013. Biogeography of avian malaria in the Great Plains. Ganser, C. and Wisely, S.M. ***Claudia won best student presentation!**

North American Ornithological Conference (5th), Vancouver, British Columbia. August 2012. Greater Prairie-Chicken nest survival within a fragmented grassland landscape in northcentral Kansas. Hunt, L.M., L.B. McNew, A.J. Gregory, S.M. Wisely, and B.K. Sandercock.

North American Ornithological Conference (5th), Vancouver, British Columbia. August 2012. Lounsberry, Z., J. Almeida, R.B. Lanctot, B.K. Sandercock, K. Strum, and S.M. Wisely. Conservation status of Buff-breasted Sandpipers (Tryngites subruficollis): a conservation genetics approach.

Wind Wildlife Research Meeting, November 2012. Effects of Wind Power Development on Greater Prairie-Chickens in Kansas. Sandercock, B.K., Hunt, L.M., Gregory, A.J., McNew, L.B., Wisely, S.M.

International Conference on Emerging Infectious Diseases. March 2012. Using host population to structure to forecast the spread of rabies in Northern Ohio. Wisely, S.M., Berensten, A.R., Fitzpatrick, C.E., Dunbar, M.R., and Gregory, A.J.

Kansas Natural Resources Conference (5th), Wichita, Kansas. January 2012. Greater Prairie-Chicken nest survival in relation to habitat characteristics and anthropogenic disturbance in north central Kansas. Hunt, L.M., L.B. McNew, A.J. Gregory, S.M. Wisely, and B.K. Sandercock

Kansas Natural Resources Conference (5th), Wichita, Kansas. January 2012. Responses of a grassland rodent community to patch-burn grazing in the northern Flint Hills of Kansas. Ricketts, A.M., B.K. Sandercock, and S.M. Wisely.

Rabies in the Americas Meeting. October 2011. Using host population to structure to forecast the spread of rabies in Northern Ohio. Wisely, S.M., Berensten, A.R., Fitzpatrick, C.E., Dunbar, M.R., and Gregory, A.J.

Annual Meeting of the American Society of Mammalogy, June 2011. Phylogeography of striped skunks, (*Mephitis mephitis*) in North America: Pleistocene dispersal and contemporary population structure. Wisely, S.M. and H.D. Barton.

International Biogeography Society, January 2011. Assessing the threat of zoonotic disease in the face of deforestation in Paraguay. Wisely, S.M., Campos Krauer, J.M.

International Biogeography Society, January 2011. Forecasting habitat suitability for a grassland specialist as a function of changes in land use and climate across the Central Great Plains. Gregory, A.J., S.M. Wisely, B.K. Sandercock.

International Society for EcoHealth. August 2010. Assessing the threat of zoonotic disease in the face of deforestation in Paraguay. Wisely, S.M., Campos Krauer, J.M.

Global Land Conference. 2010. Exurbanization, landscape fragmentation, and changes in habitat connectivity in the Flint Hills of Kansas. Harrington J., Prebyl, T.*, Wisely, S.M.

European Conference on Rabies. September 2010. Genetic Relatedness of Raccoons in Northeastern Ohio, USA: Implications for Rabies Spread. Berensten, A.R., Wisely, S.M., Dunbar, M.R., Fitzpatrick, G.E.

Kansas Natural Resource Conference, Wichita, Kansas. February 2010. Estimating population size of white-tailed deer on Konza Prairie Biolgical Station. Siders, A.*, Wisely, S.M.

Annual Meeting of the Society for Northwestern Vertebrate Biology, Medford, Oregon. February 2010. Phylogeography of the North American red fox: vicariance in Pleistocene forest refugia. Aubry, K.B., M.J. Statham, B.N. Sacks, J.D. Perrine, and S.M. Wisely.

Annual Meeting of the Society for Northwestern Vertebrate Biology, Medford, Oregon. February 2010. The origin of putative non-native red foxes in the contiguous United States: translocations or natural range expansions? Statham, M.J., B.N. Sacks, K.B. Aubry, J.D. Perrine, S.M. Wisely.

Annual Meeting of the Society for Northwestern Vertebrate Biology, Medford, Oregon. February 2010. North American montane red foxes: expansion, fragmentation, and the origin of the Sacramento Valley red fox. Sacks, B.N., M.J. Statham, K.B. Aubry, J.D. Perrine, S.M. Wisely, H. Wittmer, M. Moore.

Carnivores 2009. November 2009. Landscape genetics meets phylogeography: evolutionary relationships, recent history, connectivity, and the trajectory of southwestern red fox populations. Sacks, B.N., M. Moore, M. Statham, S. Brown, H. Wittmer, K. Aubry, S. Wisely, J. Perrine.

Carnivores 2009. November 2009. The origin of putative nonnative red foxes in the contiguous United States: Translocations or natural range expansions? Statham, M.J., B.N. Sacks, K.B. Aubry, J.D. Perrine, S. M. Wisely.

Carnivores 2009. November 2009. Phylogeography of the North American red fox: vicariance in Pleistocene forest refugia. Aubry, K.B., M.J. Statham, B.N. Sacks, J.D. Perrine, S. M. Wisely.

Prairie Grouse Technical Council Meeting (28th), Portales, New Mexico. October 2009. The use of population genetics to inform prairie-chicken management. Gregory, A.J., S.M. Wisely, L.B. McNew, and B.K. Sandercock.

Prairie Grouse Technical Council Meeting (28th), Portales, New Mexico. October 2009. Location of greater prairie-chicken nests in relation to wind power development in Kansas. McNew, L.B., A.J. Gregory, S.M. Wisely, and B.K. Sandercock.

International Conference on Rabies in the Americas. October 2009. Landscape epidemiology in a changing environment: Forecasting the influence of exurbanization on the emergence of rabies. Wisely, S.M., S. Bowe, A. Sydney, P. Schumm*, C. Scoglio.

Central Plains Society of Mammalogists. October 2009. Reintroduction of Black-footed Ferrets into Northwest Kansas. Mulhern, D. and S. Wisely

International Wader Study Group (Annual Conference 2009), Den Burg, Texel, Netherlands. September 2009. Sexual differences in parental care of Upland Sandpipers. Sandercock, B.K., J.E. Mendoza*, A.E. Casey, and S.M. Wisely.

The Wildlife Society Annual Conference. September 2009. Population Density and Distribution of White Tailed Deer (*Odocoileus virginianus*) on Konza Prairie Biological Station, Kansas. Gugler, R.C.*, A.C. Siders*, S.M.Wisely, The Wildlife Society Student Chapter.

The Wildlife Society Annual Conference. September 2009. The origin of low-elevation red foxes in the contiguous United States: Translocations or natural range expansions? Statham, M.J., B.N. Sacks, K.B. Aubry, J. D. Perrine, S. M. Wisely

The Wildlife Society Annual Conference. September 2009. Landscape epidemiology in a changing environment: The influence of land use and virulence on the emergence of rabies. Wisely, S.M., S. Bowe, A. Sydney, P. Schumm*, C. Scoglio.

The Wildlife Society Annual Conference. September 2009. Life history strategies across a gradient of human landscape alteration: Comparative demography of Greater Prairie-chicken populations in Kansas. McNew, L.B., A.J. Gregory, B.K. Sandercock, and S.M. Wisely.

The Wildlife Society Annual Conference. September 2009. Conservation genetics and breeding biology of the Rock Ptarmigan. Gregory, A., McNew, L., B.K. Sandercock, S.M. Wisely.

The Wildlife Society Annual Conference. September 2009. Winter denning habits of striped skunks informs the disease ecology of rabies. Shields, P.*, S. Bowe, and S. Wisely.

All Scientists Meeting, National Science Foundation Long Term Ecological Research Program. 13-17 September 2009. A Call for Collaborators: Developing a One Health Initiative across the LTER Network. Wisely, S.M., D. van der Merwe, B. Montelone, K. Harkin, L. Freeman.

International Conference of the Wildlife Disease Association. August 2009. Landscape epidemiology in a changing environment: The influence of land use patterns and viral properties on the emergence of rabies. Wisely, S.M., S. Bowe, A. Sydney, P. Schumm*, C. Scoglio.

International Conference of the Wildlife Disease Association. August 2009. Molecular epidemiology of rabies in the central Great Plains: Do host ecology and landscape influence viral emergence? Barton, H.D., S. M. Wisely, R. Davis, C. Hanlon.

International Conference of the Wildlife Disease Association. August 2009. Key players in human rabies exposure from case data, 1998-2008, and the implications for public health. Ganser, C.*, H.D. Barton, S.M. Wisely, S. Moore, C. A. Hanlon.

International Society of Biogeography. January 2009. Phylogeography of the North American red fox. Statham, M.J., K.B. Aubry, B.N. Sacks, J.D. Perrine, S.M. Wisely.

International Society of Biogeography. January 2009. The use of population genetics to evaluate landscape permeability. Gregory, A., L. McNew, B.K. Sandercock, S.M. Wisely. ***Andy won best student presentation!**

International Society of Biogeography. January 2009. Rabies epidemiology in the Midwestern United States: Construction of contact networks to predict the influence of host ecology and landscape heterogeneity on disease spread. Bowe, S., S.M. Wisely, A. Sydney, P. Schumm*, C. Scoglio.

International Society of Biogeography. January 2009. Does landscape influence viral emergence in the central Great Plains? Barton, H.D., S.M. Wisely, R. Davis.

International Society of Biogeography. January 2009. Biogeography of capybara (*Hydrochaeris hydrochaeris*) in the Chaco region of Paraguay. Campos, J.M. and S.M. Wisely.

The Wildlife Society. November 2008. Prevalence and biogeography of genetic susceptibility to Chronic Wasting Disease in white-tailed deer from Kansas. Wisely, S.M., M. Statham, A. Mattox*, L. Fox, J. Cully.

The Wildlife Society. November 2008. Rabies host ecology of the striped skunk (*Mephitis mephitis*): Modeling disease spread and exposure risk in the Flint Hills. Bowe, S.E., S. M. Wisely, A. Sydney, P. Schumm, and C. Scoglio

Centers for Disease Control-Rabies in the Americas. October 2008. The role of landscape barriers, pathogen evolution and host ecology in rabies emergence. Wisely, S.M., R. Davies, H. Barton.

European Wildlife Disease Association. October 2008. Evaluating barriers and corridors to raccoon (*Procyon lotor*) strain rabies movement in Cleveland, Ohio, USA: research update. Berentsen,A., M. Dunbar, C. Fitzpatrick, S. Wisely.

International Grouse Symposium (11th), Whitehorse, Yukon Territory. September 2008. The link between Greater Prairie-chicken genetic structure and landscape configuration. Gregory, A.J., L.B. McNew, B.K. Sandercock, and S.M. Wisely.

International Grouse Symposium (11th), Whitehorse, Yukon Territory. September 2008. Demography of Greater Prairie-chickens at the core of their range: regional variation in population dynamics and vital rate contributions. McNew, L.B., A.J. Gregory, B.K. Sandercock, and S.M. Wisely.

International Grouse Symposium. September 2008. Demography and genetics of a reintroduced population of Evermann's Rock Ptarmigan in the Aleutian Islands. Sandercock, B.K., Kaler, R.S.A., Ebbert, S.E., Braun, C.E., Gregory, A.J., Prebyl, T.J.*, Wisely, S.M.

Joint meeting of the American Ornithologists' Union (126th), Cooper Ornithological Society (78th), and the Society of Canadian Ornithologists (28th), Portland, Oregon. August 8, 2008 Molecular analysis of the breeding system in the Upland Sandpiper. Casey, A.E., B.K. Sandercock, and S.M. Wisely.

Joint meeting of the American Ornithologists' Union (126th), Cooper Ornithological Society (78th), and the Society of Canadian Ornithologists (28th), Portland, Oregon. August 8, 2008 (symposium). Effects of wind power development on the ecology of prairie grouse. Hagen, C.A., L.B. McNew, A.J. Gregory, B.K. Sandercock, and S.M. Wisely.

American Society of Mammalogy. June 2008. The role of landscape barriers, pathogen evolution, and host ecology in rabies emergence. Wisely, S.M., H.D. Barton, R. Davis.

American Society of Mammalogy. June 2008. Landscape ecology of capybara in the Chaco region of Paraguay. Campos, J.M., S.M. Wisely, D. Merritt.

International Conference on Emerging Infectious Diseases. March 2008. Landscape barriers, pathogen evolution and host ecology contribute to rabies emergence in the Midwest. Wisely, S.M., H.D. Barton, R. Davis.

International Conference on Emerging Infectious Diseases. March 2008. Landscape Genetics of Genetic Susceptibility of White-Tailed Deer to Chronic Wasting Disease: Implications for CWD Emergence Across Kansas. Statham, M.J., S.M. Wisely, A. Mattox*, L. Fox, J. Cully.

International Conference on Emerging Infectious Diseases. March 2008. Molecular epidemiology of cross-species transmission of rabies in the Central Great Plains. H.D. Barton, S.M. Wisely, and R.Davis.

International Conference on Emerging Infectious Diseases. March 2008. Striped Skunk (*Mephitis mephitis*) Host Ecology in Urban and Rural Habitats: Modeling Exposure Risk to Rabies in the Midwest. Bowe, S.E., S.M. Wisely, C. Scoglio, P. Schumm*, and A. Sydney.

Kansas Natural Resource Conference. February 2008. Landscape connectivity of the Flint Hills for Greater Prairie Chickens. Prebyl, T.J.*, A. J. Gregory, S.M. Wisely.

Kansas Natural Resource Conference. February 2008. Population Monitoring of White-tailed Deer on Konza Prairie Biological Station Lantz, B*, T. Prebyl*, S.M. Wisely, KSU Student Chapter of The Wildlife Society.

Kansas Natural Resource Conference. February 2008. Association with humans and urban sprawl as driving forces of woody encroachment on Kansas prairies. Gregory, A.J., D. Goodin, S. M. Wisely.

Kansas Natural Resource Conference. February 2008. Comparing host-pathogen population structures: Implications for rabies management in striped skunks. Barton, H.D., S.M. Wisely, and R.Davis.

Kansas Natural Resource Conference. February 2008. Rabies host ecology on a tall-grass prairie: The role of trees in striped skunk (Mephitis mephitis) habitat selection Bowe, S.E., S.M. Wisely.

Western Section of the Wildlife Society. February 2008. Quaternary zoogeography of a North American boreal carnivore: evolution of the montane red foxes. Aubry, K.B., M.J. Statham, B.N. Sacks, J.D. Perrine, S.M. Wisely.

Ecological Genomics Symposium. November 2007.Hybrid molecules result from small deletions on the CHD-Z intron, but cause big errors in avian sexing analyses Casey, A.E.*, B.K. Sandercock, K.L. Jones & S.M. Wisely

The Wildlife Society National Meeting. September 2007. The Role of Host Ecology in the Genomic Epidemiology of Rabies in the Central Great Plains, Wisely, S.M., H. D. Barton, R.Davis.

The Wildlife Society National Meeting. September 2007. Male Greater Prairie-Chicken (*Tympanuchus cupido*) Reproductive Success is Linked to Genetic Diversity. Gregory, A.J. J. Nooker, B. Sandercock and S. Wisely.

Long-Term Ecological Research Grant Renewal Workshop. September 2007. Risk assessment of rabies in the face of changing land use practices, Bowe, S.E., S. M. Wisely, J. Harrington.

National Wildlife Federation National Meeting. September 2007. The effect of reintroduction history on the genetic health of elk, Conard, J., P. Gipson, S.M. Wisely.

Rabies in the Americas Conference. September 2007. The Role of Host Ecology in the Genomic Epidemiology of Rabies in the Central Great Plains, R. Davis, H.D. Barton, and S.M. Wisely.

Midwestern Furbearers Conference. September 2007. Biogeography of red fox in North America. Statham, M.J., K. Aubry, B. Sacks, S.M. Wisely.

Midwestern Furbearers Conference. September 2007. Population Dynamics of Rabies and its Host Species, the Striped Skunk Barton, H.D., S. M. Wisely, and R. Davis.

Center for Disease Control International Rabies Day. September 2007. The Role of Host Ecology in the Genomic Epidemiology of Rabies in the Central Great Plains, R. Davis, H. D. Barton, and S. M. Wisely.

Merck-Merial National Veterinary Scholar Symposium. August 2007. Ecotoxicogenomics of Fecal Bacteria of Deer Mice (*Peromyscus maniculatus*) in a Former Mining Community. Lambo, C. G. Peterson, S. Narayanan, S. Wisely.

American Ornithological Union, National Meeting. August 2007. Male Greater Prairie-Chicken (*Tympanuchus cupido*) Reproductive Success is Linked to Genetic Diversity. Gregory, A.J., J. Nooker, B. Sandercock and S. Wisely.

American Ornithological Union, National Meeting. August 2007. Multiple alleles cause sexing errors in a monomorphic shorebird, Casey, A.*, B. Sandercock, K. Jones and S. Wisely.

Kansas Department of Wildlife and Parks Chronic Wasting Disease Workshop. July 2007. Landscape Genetics of White-Tailed Deer and the Implications for the Spread of Chronic Wasting Disease Across Kansas, Wisely, S.M., M. Statham, A. Mattox*, L. Fox, J. Cully.

Kansas State University, Division of Biology, Graduate Student Research Forum. April 2007. Population Genetics of Striped Skunks: Implications for Rabies Dynamics. Barton, H.D., Wisely, S.M., and Davis, R.

Kansas State University, Student Research Symposium. April 2007. Genetic diversity lost and gained: conservation genetics of the black-footed ferret. Mueting, S.A.*, Wisely, S.M., Van Pelt, W. ***Sara won best undergraduate student presentation!**

Kansas Chapter of the Wildlife Society Spring Meeting. February 2007. The potential for habitat fragmentation to alter Prairie Chicken genetic structure in Kansas. Gregory, A., Wisely, S.M., Sandercock, B.K., McNew, L.B.

Kansas Chapter of the Wildlife Society Spring Meeting. February 2007. Population Genetics of Striped Skunks: Implications for Rabies Dynamics, Barton, H.D., Wisely, S.M., and Davis, R. **Heather won best graduate student presentation!**

Kansas Chapter of the Wildlife Society Spring Meeting. February 2007. Are Midwestern red fox native? Phylogeography of red fox in North America. Statham, M.J., Wisely, S.M., Aubry, K., Sacks, B.N.

Kansas Chapter of the Wildlife Society Spring Meeting. February 2007. The microevolution of Interleukin-6 in an immunocompromised species, the black-footed ferret. Mueting, S.A., Brown, S.J., Wisely, S.M.

Kansas Chapter of the Wildlife Society Spring Meeting. February 2007. Estimates of adult apparent survival for a native grassland shorebird. Casey, A.E.*, B.K. Sandercock and S. M. Wisely.

Kansas Chapter of the Wildlife Society Spring Meeting. February 2007. Evolutionary consequences of heavy metal contamination to deer mice and their intestinal microbial community. Wisely, S.M., Narayanan, S., With, K.A., Brown, S.J.

International Symposium on Altered Landscapes. February 2007. Evolutionary consequences of heavy metal contamination to deer mice and their intestinal microbial community. Wisely, S.M., Narayanan, S., With, K.A., Brown, S.J.

Ecological Genomics Symposium. November 2006. The role of host ecology in the microevolution of rabies virus. Barton, H.D., Wisely, S.M., Davis, R.

Ecological Genomics Symposium. November 2006. The characterization of CHD-Z polymorphism and associated fitness costs in the Upland Sandpiper. Casey, A.E.*, Statham, M.J., Sandercock, B.K., Wisely, S.M.

Ecological Genomics Symposium. November 2006. Differential gene expression in small mammals exposed to heavy metals. Delamaide, J., Crawford, L., Narayanan, S., Wisely, S.M., Jones, K.L., Coolon, J.D., Brown, S.J.

Ecological Genomics Symposium. November 2006. Microbial diversity in intestine of small mammals and soil of the Tri-State Mining District. Crawford, L., Delamaide, J., Narayanan, S., Wisely, S.M., Jones, K.L., Coolon, J.D., Brown, S.J.

Ecological Genomics Symposium. November 2006. The microevolution of interleukin-6 in an immunocompromised species, the black-footed ferret. Mueting, S.A.*, Wisely, S.M., Brown, S.J., Howard, J.G., Statham, M.J., Phillips, T.M.

Ecological Genomics Symposium. November 2006. Adaptive divergence, genetic drift, and incipient speciation in the grasshopper, *Hesperotettix viridis*. Apple, J.L., Joern, A., Sword, G., Wisely, S.M.

Carnivore Conference, Defenders of Wildlife. November 2006. The role of host ecology in the microevolution of rabies virus. Barton, H.D., Wisely, S.M., Davis, R.

Carnivore Conference, Defenders of Wildlife. November 2006. Genetic diversity lost and gained: conservation genetics of the black-footed ferret. Wisely, S.M., Mueting, S.A.*, Santymire, R.M., Livieri, T.M., Howard, J.G., Van Pelt, W.

National Wind Coordinating Committee, Wildlife working Group Conference. November 2006. The Genetic Consequences of Wind Power Development on Greater Prairie Chicken Leks of Eastern Kansas. Gregory, A.J., Wisely, S.M., Sandercock, B.K.

Western Sandpiper Workshop, Burnaby, British Columbia. December 2006. Polymorphic introns lead to sexing errors in a monomorphic wader. Sandercock, B.K., A.E. Casey*, and S.M. Wisely. (b)

International Wader Study Group (Annual Conference 2006), Höllviken, Sweden. October 2006. Polymorphic introns lead to sexing errors in a monomorphic wader. Sandercock, B.K., A.E. Casey*, and S.M. Wisely.

Natural Resources Symposium of the Sacramento-Shasta Chapter of the Wildlife Society. October 2006. Is the Sacramento Valley red fox an overlooked native population? Sacks, B., Aubry, K., Perrine, J., Pollinger J., Statham, M., Wayne, R., Wisely, S.

American Genetics Association, Genetics of Speciation Symposium. June 2006. Adaptive divergence, genetic drift, and incipient speciation in the grasshopper, *Hesperotettix viridis*. Apple, J.L., Joern, A., Sword, G., Wisely, S.M.

American Association of Zoo Veterinarians. June 2006. Biomedical survey of wild black-footed ferrets (*Mustela nigripes*). Howard, J.G., S.M. Wisely, R. M. Santymire, T.M. Livieri, S. A. Williams, J.S. Kreeger, P.E. Marinari, D.E. Wildt, and E. S. Williams.

Undergraduate Research Symposium. April 2006. Genetic diversity lost and gained: conservation genetics of the black-footed ferret. Mueting, S.*, S. Wisely, R. Santymire, T. Livieri, J.G. Howard.

Undergraduate Research Symposium. April 2006. Conservation genetics of Northern Bobwhite Quail in southeastern Kansas. Fredrickson, C.*, S. Wisely, T. Strakosh, B. Flock, P. Gipson, and R. Applegate.

Undergraduate Research Symposium. April 2006. Optimization of molecular methods for sexing shorebirds. Casey, A.*, K. Kiefer*, S. Wisely, B. Sandercock.

Undergraduate Research Symposium. April 2006. Phylogeography of red fox in North America. Maddox, A.*, M. Statham, K. Aubry, S. Wisely.

Kansas Chapter of The Wildlife Society. March 2006. Genetic diversity lost and gained: conservation genetics of the black-footed ferret. MuetingS.*, S. Wisely, R. Santymire, T. Livieri, J.G. Howard.
***Sara won best undergraduate presentation at the meeting!**

North American Shorebird Conference. March 2006. Optimization of molecular methods for sexing shorebirds. Casey, A.*, K. Kiefer*, S. Wisely, B. Sandercock.

Genes in Ecology, Ecology in Genes, Overland Park, KS. November 2005. Ecotoxicogenomics of a small mammal community exposed to heavy metals. Wisely, S.M., S. Brown, D. Gasper, C. Patricola-Simpson*, S. Narayanan.

Central Plains Society for Mammalogists, Kirksville, MO, October 2005. Conservation genetics of the black-footed ferret: genetic diversity lost and gained. Mueting, S.* and S. Wisely.

Central Plains Society for Mammalogists, Kirksville, MO, October 2005. Winter densities of white-tailed deer at Konza Prairie. Brinkley, P.*, S. Wisely, K. Kiefer*, T. Mong, B. Sandercock.

Central Plains Society for Mammalogists, Kirksville, MO, October 2005. A new technique of capturing and monitoring animal movement of capybara in South America. Campos, J.M., S. Wisely, I. Rivera, R. Golightly and A. Mutlow.

Central Plains Society for Mammalogists, Kirksville, MO, October 2005. Ecotoxicogenomics of a small mammal community exposed to heavy metals. Patricola-Simpson, C.*, S. Wisely, S. Brown, D. Gasper, S. Narayanan.

Kansas Chapter of The Wildlife Society, Emporia, KS, March 2005. Reintroduction history affects genetic diversity and morphology of the black-footed ferret. Wisely, S.M., R.M. Santymire, T.M. Livieri, and J.G. Howard.

Defenders of Wildlife Conference, Santa Fe, NM, November 2004. Biomedical Survey of Wild Black-Footed Ferrets. Howard, J.G., S.M. Wisely, R. M. Santymire, T. M. Livieri, J. S. Kreeger, P.E. Marinari, D.E. Wildt and E.S. Williams.

Defenders of Wildlife Conference, Santa Fe, NM, November 2004. Reintroduction History Affects Genetic Diversity and Morphology of the Black-Footed Ferret. Wisely, S.M., R. M. Santymire, T. M. Livieri, and J.G. Howard.

Defenders of Wildlife Conference, Santa Fe, NM, November 2004. Seminal Characteristics of Wild Black-Footed Ferrets. Santymire, R.M., J.G. Howard, S. M. Wisely, T. M. Livieri, J. S. Kreeger, P. E. Marinari And D. E. Wildt.

Genes in Ecology, Ecology in Genes, Overland Park, KS October 2004. Reintroduction History Affects Genetic Diversity and Morphology of the Black-Footed Ferret. Wisely, S.M., R.M. Santymire, T. M. Livieri, and J.G. Howard.

4th Annual International Symposium on *Martes*. Lisbon, Portugal. July 2004. Conservation genetics of the fisher: consequences to natural resource management. Wisely, S.M., S. W. Buskirk, G. Russell, K. Aubry, and W. Zielinski.

American Society of Mammalogy, Arcata, California. June 2004. From captivity to the wild: further changes in black-footed ferret morphology. Wisely, S.M., R.M. Santymire, J.G. Howard, T.M. Livieri, J.S. Kreeger, P.E. Marinari And D.E. Wildt.

American Society of Mammalogy, Arcata, California. June 2004. Historical changes to black-footed ferret morphology. Wisely, S.M., J.J. Ososky, S.W. Buskirk.

American Society of Mammalogy, Arcata, California. June 2004. Phylogeography and genetic structure of the Pacific fisher. Wisely, S.M., S.W. Buskirk, G. Russell, K. Aubry, and W. Zielinski.

Black-Footed Ferret Symposium, Ft. Collins, CO. January 2004. Genetic diversity in the black-footed ferret: Past, present and future. Wisely, S.M. and R.C. Fleischer.

Black-Footed Ferret Symposium, Ft. Collins, CO. January 2004. Biomedical Survey of Wild Black-Footed Ferrets. Howard, J.G., S.M. Wisely, R.M. Santymire, T.M. Livieri, J. S. Kreeger, P.E. Marinari, D.E. Wildt and E.S. Williams.

Public Presentations for Outreach:

Natural history tour of OSBS for Field Camp for 6th graders, Florida Museum of Natural History, 26 July 2012.

The role of NEON in education and outreach at Ordway-Swisher Biological Station, Florida Wildlife and Fisheries Research Cooperative, Cooperators meeting, 9 May, 2012.

Science Café for Citizen Science, Manhattan, KS. Zombie skunks, killer cats, and ninja bats: why rabies is still a threat in the Midwest. February 2011.

Science Pioneers' Saturday Science Seminar program in Union Station, Kansas City, Missouri. Zombie skunks, killer cats, and ninja bats: why rabies is still a threat in the Midwest. 6 November 2010.

Lunch and Learn for Employees and Members, Rolling Hills Zoo, Salina, Kansas. Black-footed Ferret Recovery in Kansas, 13 May 2010.

Lectureships:

Wildlife and Fisheries Conservation – Kansas State University. Co-taught this junior level class. Enrollment ~75. 2005-2010.

Organismic Biology – KSU. Co-taught this freshman level class. Enrollment ~175. 2005-2011.

Population Biology – KSU. Developed this senior level class. Enrollment ~25. 2007-2008.

Microsatellite Markers – KSU. Developed this graduate class. Enrollment =15. 2005.

Field Ecology – University of Wyoming. Developed this senior level class. Enrollment ~10. 1998-2000.

Guest Lectureships:

University of St. George's College of Veterinary Medicine, Grenada. Conservation Medicine in Carnivores. November 2013.

Kansas State University College of Veterinary Medicine (KSUCVM). Dept. of Pathology. Emerging Diseases. I lectured on Disease Ecology. 2007-2011.

KSUCVM. Pathways to Public Health. Undergraduate Summer Research Experience. I lectured on the role of zoonotic disease in public health. 2010-2011.

Current Advisees:

Postdoctoral Fellows:

Katherine Sayler, Ecology of hemorrhagic disease in Cervidae.

Graduate Students:

Claudia Ganser, M.S. student, Avian malaria in Arctic-breeding Shorebirds
Felipe Hernández, Ph.D. Student, Effects of contaminants on pathogen communities of feral swine
Thomas McVay, Ph.D. student, Community ecology of southern African mammalian scavengers
Sieara Claytor, Ph.D. student, The influence of global change on amphibian diseases

Undergraduate Students:

Andraya Mendez, Mark-recapture analysis of genets in Swaziland
Jamie Nicholson, Avian malaria in shorebirds

Past Advisees:

Postdoctoral Researchers:
Mark Statham, Phylogeography of red fox in North America.
Michael Westphal, (co-advised with Ted Morgan) Genetic architecture of adaptive melanism in a grassland snake species. Biologist for BLM.
Jennifer Apple, Host race formation in *Hesperotettix viridis*. Currently Asst. Professor at SUNY Geneseo.
Graduate Students:
Claudia Ganser, M.S., Vector ecology in the Great Plains
Zachary Lounsberry, M.S., Conservation genetics of Buff-breasted Sandpiper
Andrew Gregory, Doctoral Candidate Defended. Graduation May 2011. Landscape genetics of the Greater Prairie-chicken. Asst. Professor at Bowling Green State University.
Heather Barton, Ph.D., Phylogeography of rabies and its host, the striped skunk. Asst. Professor at Grove City College.
Juan Campos, Ph.D., Biogeography of capybara in Paraguay. Director of CCCI, a Paraguayan conservation NGO.
Sarah Bowe, M.S., Risk assessment of rabies exposure in the Midwest.
Ashley Casey*, M.S., Breeding biology and mating system of Upland Sandpiper
*co-advised with Brett Sandercock

Other Graduate Students Contributing to My Lab:
Rachel Pigg, Ph.D. student, Landscape genetics of Black-tailed Prairie Dog
Emilie Blevins, M.S. Landscape genetics of collared lizards in the Flint Hills.
Tony Grace, Ph.D., Host race formation in the grasshopper, *Hesperotettix viridis*.
Page Klug, Ph.D., Landscape genetics of Yellow-bellied Racers
Jonathan Conard, Ph.D., Landscape genetics of an elk herd on Ft. Riley Army Base
Khara Strum, M.S., Molecular sexing of Buff-breasted Sandpipers
Ron Van Nimmwiggen, Ph.D. Landscape genetics of the grasshopper mouse

Veterinary Student Research:
Kelsey Schroeder. Surveillance of mosquitos for avian malaria.
Lauren Bodenhamer. Environmental variation in mosquito community dynamics.
Caitlin Burrell. Pathology of Greater Prairie-chicken.
Anne-Catrin Geuthner. Pathology of the striped skunk.
Colleen Lambo. Ecotoxicogenomics of small mammals.
Joy Delamaide, Ecotoxicogenomics of small mammals.
Lindsey McKinsey, Ecotoxicogenomics of small mammals. (coadvised with S.J. Brown).
David Gasper, Ecotoxicogenomics of small mammals. Pathology residency program, UC Davis.

Undergraduates:
Samantha Gamble. Avian malaria in shorebirds.
Paige Berry. Landscape genetics of Greater Prairie chicken.
Cody Simmons. Prevalence of avian malaria in Greater Prairie-chickens
Jasmine Sharp. Biogeography of Buff-breasted sandpiper.
Alexia Sampson. Natural history of mosquito communities in Kansas.
Hailey Peterson. Landscape genetics of Greater Prairie chicken. K-INBRE Scholar.
Jorge Mendoza. Evaluating application requirements for graduate schools.
Adam Siders. Density estimates of white-tailed deer on Konza Prairie Biological Station
Claudia Ganser. Rate of human exposure to rabies in Kansas, 1998-2008. Cancer Center Scholar, K-INBRE Scholar

Alyssa Maddox. Landscape genetics of white-tailed deer. Howard Hughes Medical Institute Scholar 2006. NASA Scholar 2006.
Tom Prebyl. Landscape genetics of Greater Prairie-chicken. Mark Enloe Memorial Scholarship winner.
Taryn Cipra. Conservation genetics of Kansas elk.
Ashley Casey. Molecular sexing of Upland Sandpiper.
Sarah Mueting. Conservation genetics of black-footed ferret. Cancer Center Scholar
Carissa Fredrickson. Conservation genetics of Bobwhite Quail.
Katrina Kiefer. Howard Hughes Medical Institute Undergraduate Scholar. Molecular sexing of Upland Sandpipers. (Coadvised with Brett Sandercock). Currently a veterinary student at KSU.
Charity Patricola-Simpson. Ecotoxicogenomics of a small mammal community.
Jeremy Thornbrough. Research Experience for Undergraduates. Spotlight surveys of carnivores on Konza Prairie Biological Station.
Ben Neely. Presence and distribution of mesocarnivores on Konza Prairie Biological Station. Currently a M.S. student at U. Nebraska.

***Professional Service*:**

National Science Foundation, National Ecological Observatory Network.

- Board of Directors, 2015-2017
- Member, NEON Workshop Committee.
- Workshop Organizer, NEON Member meeting, Integrating Site-based Science questions with regional and continental scale data.
- Member Representative for University of Florida
- External Compliance Evaluator – Institutional Animal Care and Use Committee for the National Ecological Observatory Network, 2013
- Representative, Climate Science Day on Capitol Hill, 2012
- Member, Domain 6 Science and Education Coordination Committee, 2009-2011

USDA APHIS WS National Wildlife Research Center

- Panelist – Employee Research Grade Evaluation
- Panelist – 10 Year Institutional Review, 2014

External Reviewer for Promotion and Tenure

- University of Georgia Odum School of Ecology, 2013
- University of Wisconsin, Milwaukee, 2012
- University of The United Arab Emirates, 2013

Organization of Biological Field Stations

- Representative for Congressional Meetings Day on Capitol Hill, Washington, D.C., April 11, 2013.
- Member of Diversity Committee

Zoonotic Disease and Health Advisor

- Member – Florida Interagency Zoonotic Disease Working Group, 2012-present
- Member – Florida Dept. of Public Health, Florida Rabies Advisory Committee, 2012-present
- Ad hoc Advisor – New Mexico Department of Public Health, Rabies Outbreak Task Force, 2012

Wildlife Conservation Advisor

- ***Member – Genetics Advisory Board for USFWS Black-footed Ferret Recovery Team, 2014-present***
- ***Member - Kansas Black-Footed Ferret Reintroduction Team, 2006-2011.***
- ***Member – Advisory Committee to The Nature Conservancy's Prairie Dog Management Plan, 2007-2011.***

Panel Reviewer:

- NSF, DEB, Population and Community Ecology Panel, 2013, 2014.
- National Science Center, Republic of Poland. Ad Hoc Reviewer for research proposal. 2012.
- NSF, DEB, DDIG Panel. 2010.
- NSF, DEB, Population Ecology and Evolution Panel, 2007, 2008.
- EPA Star Grants 2004-2005.
- University of California at Davis, College of Veterinary Medicine, Wildlife Health Center Grants Program 2005.

Editorial Reviewer:

- Book Editor Board, Emergent Enviornmental Observatories, Springer Books
- Associate Editor, Journal of Mammalogy. 2009-2013.
- Ad Hoc Reviewer: Biological Journal of Linnean Society, Proceedings of the 4th *Martes* Symposium, Prairie Naturalist, Conservation Genetics, Molecular Ecology, Journal of Mammalogy, Journal of Evolutionary Biology, Annales Zoologici, Genetics and Molecular Biology, Journal of Wildlife Management, Biological Conservation, Genetica, Journal of Heredity, Revista Mexicana e Biodiversidad, International Journal of Artificial Life Research, Southwestern Naturalist, Animal Conservation, Environmental Conservation

Departmental Service Activities:

UF IFAS – Environmental Health Sciences Building Planning Committee
UF Dept. of Wildlife Ecology and Conservation – Dept. seminar co-coordinator, Fall 14.
UF Dept. of Wildlife Ecology and Conservation – WEC-FWC Steering Committee
UF Dept. of Wildlife Ecology and Conservation – Search Committee for Coop Unit Leader, 2015.
UF Dept. of Wildlife Ecology and Conservation – Search Committee for WEC Chair, 2013.
UF Dept. of Wildlife Ecology and Conservation – Search Committee for Ona Range Scientist, 2013.
UF Dept. of Wildlife Ecology and Conservation – Graduate Programming Committee, 2012-present.
KSU Division of Biology Faculty Search Committee - USGS Coop Unit Leader 2010
USGS Coop Assistant Fisheries Leader 2010
Physiological Ecologist 2007
KSU Division of Biology Graduate Affairs Committee, 2010
KSU Ecological Genomics Institute, Workshop Committee Member. 2005-2007
KSU Ecological Genomics Institute, Visiting Scholars Committee Member. 2005-2007
KSU Division of Biology Fish and Wildlife Biology Curriculum Committee. 2005 – 2005.
KSU Division of Biology Graduate Student Symposium Judge. 2004, 2006, 2008
KSU Center for the Understanding of Origins. Member.
NSF - Girls Researching Our World, GROW. Instructor. 2004-present.
Faculty Advisor to the Student Chapter of The Wildlife Society. 2005-present.
Seminar Coordinator, KSU Division of Biology, Ecology and Evolutionary Biology Section, 2004-2005, 2008-2009.

Professional Training:

Basic Certified Wildland Fire Training, National Wildfire Coordinating Group (NWCG) Certified Courses (I-100, S-130, S-190, L-180). August 2012.

Society Memberships:

American Society of Mammalogists - Life Member
- Member, Conservation Awards Committee
The Wildlife Society - Faculty Sponsor of the KSU Student Chapter, 2004-2011.

International Biogeography Society
Wildlife Disease Association

APPENDIX E

Comment Response Matrix

California Gnatcatcher Facilitated Science Panel Workshop

U.S. Fish & Wildlife Service

Comment Response Matrix

Draft Summary Report, Coastal California Gnatcatcher Science Panel

Comment #	*The comment refers to the following location in the document:*		Comment	Office of Reviewer	Action Taken to Address the Comment
	Section	Page			
1	Cover		Change name to "California Gnatcatcher Facilitated Science Panel Workshop"	USFWS CFWO	Completed
2	ExSum		Text revisions for clarification	USFWS CFWO	Completed
3	1		Text revisions for clarification	USFWS CFWO	Completed
4	2		Text revisions for clarification	USFWS CFWO	Completed
5	2.0		Do we need to say WHY this communication was limited?	USFWS CFWO	added "to ensure the independence of the panelists."
6	2.2		This is a little unclear (facilitation via email, purpose of facilitation?). Can you please describe this better?	USFWS CFWO	Sentence revised to "The PM relayed questions and answers between the Service and the panelists regarding the discussion questions and the materials provided. "
7	2.2 and B		These 4 pdf files should be included in Appendix B.	USFWS CFWO	The 4 summaries are included in Appendix B.
8	2.3		Paragraph added to clarify purpose of the Workshop	USFWS CFWO	Completed
9	Throughout		Capitalize Workshop	USFWS CFWO	Completed
10	Throughout		Change presentations to document or summary	USFWS CFWO	Completed
11	2.3		Please make sure that all documents that were transmitted are included or at least identified in the Appendix.	USFWS CFWO	Verified
12	2.4		Might want to clarify this. Was this part of their discussion on Day 2? See also comment below (section 4.0)	USFWS CFWO	added "This was confirmed by the Service on Day 2 of the Workshop (see summary below)."
13	3		Text revisions for clarification	USFWS CFWO	Completed
14	4		Text revisions for clarification	USFWS CFWO	Completed
15	4	4	Day 1: Was this a discussion topic? Maybe reword “Each panel member stated that morphology is an important…..”	USFWS CFWO	Added "Panel discussion about the role of morphology data and its importance as a data type for subspecies definition."
16	4	5	Day 1: Bullet below were edited to indicate that these were topics of discussion. Please check with your notes from Workshop.	USFWS CFWO	Edits reviewed and are in agreement with my notes. Minor edits were made to clarify as necessary.
17	4	5	Day 1: As written, this was not clear. Please check this edit and add any other discussion points, as needed.	USFWS CFWO	Revised and confirmed edits provided.
18	4	5	Day 1: Can you provide some point of reference here? Threshold related to?	USFWS CFWO	Deleted "but where is threshold ?" and added "How much neutral genetic data and what type is informative? How much weight should it have relative to the phenotypic data?"
19	4		Day 1: Or do you mean each of the panelists concluded?	USFWS CFWO	The revisions provided by you were correct.
20	4		Day 2: I think this Q&A was not at the very beginning, but please check your notes.	USFWS CFWO	There was some organizational discussion prior to the Q&A but not much.

Comment #	*The comment refers to the following location in the document:*		Comment	Office of Reviewer	Action Taken to Address the Comment
	Section	Page			
21	4		Day 2: Just to clarify this discussion: Two Service personnel were asked to answer a few clarifying questions and invited to meet the panel members. The panelists asked about our previous review of morphological data and specifically about the analysis presented in Skalski et al. 2008. We told them that we responded to this issue most recently in our 2011 90-day finding. We relayed that they should look at the best available information to address the 5 questions that were provided to them. After this discussion, the panel members determined it was unnecessary to reexamine data that had been reviewed repeatedly and there was also no new morphology data to modify those original datasets. The panel also asked about DPS criteria, particularly significance and discreteness, and we referred the panelists our summary document on this topic, also previously provided to them. The session was approximately 20 minutes.	USFWS CFWO	Paragraph revised significantly.
22	4		Day 2: This is not clear. Was this a discussion by each panelist for each of the Questions?	USFWS CFWO	Revised paragraph. It was a round table where each panelist summarized their basic opinion (as they stood at that point) for each question.
23	5		Text revisions for clarification	USFWS CFWO	Completed
24	6		Text revisions for clarification	USFWS CFWO	Completed
25	6		Is this summary based on the written memos or oral discussion at the Workshop?	USFWS CFWO	Both since the individual memos reflect the same opinions expressed in the workshop. Did make some additional revisions to make that clear and consistent throughout this summary.
26	6		In all samples, or samples reviewed by Zink?	USFWS CFWO	Those used in Zink et al. 2013. Revisions made for clarification.
27	6		This should be more explicit.	USFWS CFWO	Added "Different panelists performed different analyses (as presented in their individual memoranda), in addition to those presented in McCormack and Maley (2015), but generally found indications that specific loci showed breaks between populations." If i provide more details, it opens a floodgate of details, that are all presented in the memos.
28	7		Added reference USFWS 2014	USFWS CFWO	Completed