

**NMOS 55th ANNUAL MEETING
ABSTRACTS**

ORAL PRESENTATIONS

(In Order of Presentation; Presenters Underlined)

**Natal Dispersal Distances of Golden Eagles in the Southwestern United States
Based On Satellite Telemetry**

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Knowledge of natal dispersal is vital to understanding avian population dynamics. Data on natal dispersal distances (NDDs) of Golden Eagles (*Aquila chrysaetos*) in North America are needed for defining local area populations to inform decisions authorizing take (i.e., injury, death, or disturbance) of individuals. Twelve Golden Eagles (four males, eight females) that we tagged with satellite transmitters as ~8-wk-old nestlings in the southwestern United States during 2010- 2013 dispersed an average of 49.8 km (SD = 32.6, median = 53.4) between their natal sites and sites they occupied when reaching adult age (4.75 yr \pm 1 mo) or where they first bred as subadults (3.75 yr \pm 1 mo). The median value corroborates that published earlier from band encounters. To the dataset we added NDDs from seven male and four female eagles tracked through subadult age but that did not breed, reasoning that some subadults on the study area bred and addition of this sample could provide tentative insight into sex-biased NDD. In the combined dataset (11 males, 12 females), male NDDs were shorter than those of females (mean = 40.6 km and 62.6 km, SD = 25.0 and 24.7, median = 34.5 and 65.6, respectively; one-tailed $t = 1.96$, $P = 0.03$, $df = 20$), corroborating findings from Europe of female-biased NDDs for the species and suggesting that decisions on take of Golden Eagles from local areas at least in the southwestern United States should be based on the more limiting distance (males).

Evolutionary Dynamics of Elevational Ranges in Andean Birds

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Andean uplift reorganized the South American climate since the mid-Miocene, creating steep environmental gradients and novel habitats. This period of geologic dynamism coincided with diversification into the Andes by many avian groups. Bird lineages that successfully colonized and persisted in the Andes are marked by physiological adaptations and restricted elevational ranges. Genera and families tend to have similar elevational ranges, suggesting constraints on evolutionary shifts in elevation. Here we used phylogenies and elevational range data for Andean birds to estimate the history of elevational transitions and elevational stasis. We asked three questions that have implications for evolutionary mechanisms: 1) Have the timing of elevational transitions indeed coincided with Andean uplift? 2) Do the rate and magnitude of elevational transitions vary according to their ancestral starting point, suggesting threshold effects? and 3) Do upward and downward shifts occur with equal probability? We present evidence that elevational ranges are continuing to shift in conjunction with recent diversification, that the rate of elevational shifts changes with elevation, and that downward shifts are less common than upward shifts during the history of Andean bird diversification.

Diversity and Host Specificity of Avian Blood Parasites in New Mexico and Peru: Towards A Genome-Wide Approach

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Avian haemosporidians (genera *Haemoproteus*, *Plasmodium*, and *Leucocytozoon*) are globally- distributed and highly diverse blood parasites that can significantly impact bird population demography, structure, and health. The propensity for haemosporidian parasites to switch hosts, and the potential consequences of infection for naïve bird communities, underscores the need to determine parasite species boundaries and host range limits. In the last decade, molecular studies have relied on a mitochondrial “barcode” to identify parasite lineages, which has likely underestimated diversity. Challenges in separating parasite DNA from bird host DNA have recently been overcome, providing the means to collect parasite genomic data from bird samples and greatly improve estimates of parasite diversity. We developed and tested a new genomic sequence capture approach in two well-characterized avian haemosporidian communities with similar levels of infection. Within New Mexico pine forests, 776 birds representing 61 species were screened, with 269 (34.7%) infected. Across elevational gradients in Peru, 3,983 birds representing 524 species were screened, with

1,554 (39.0%) infected. Focusing on *Haemoproteus* lineages, which exhibit high variation in host breadth, we tested our genomic approach on 51 samples. The most important predictor of sequencing success was parasitemia, providing clear parameters for successful implementation of this valuable tool. We successfully sequenced >100 loci from 12 parasite lineages (5 New Mexico, 7 Peru), including three lineages infecting multiple host species. Phylogenetic relationships among lineages were completely resolved using genomic data, much improved from mitochondrial data, and provide preliminary evidence of distinct host race formation in one of three lineages tested thus far.

Problematic Pachycephalidae: A New Phylogenetic Hypothesis Using Ultraconserved Elements

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The utility of islands as natural laboratories of evolution is exemplified in the patterns of differentiation in widespread, phenotypically variable lineages. Pachycephalidae is one of the most complex avian radiations spanning the vast archipelagos of the Indo-Pacific, making it an ideal group to study the patterns and processes of diversification on islands. Here, we present a robust phylogenetic hypothesis for all five genera within Pachycephalidae, based on thousands of ultraconserved elements (UCEs) that we generated with a target-capture approach and high-throughput sequencing. Our dataset comprises 104 individuals and includes 50 species in the family. We sampled more densely within taxonomically recalcitrant clades, such as the *Pachycephala pectoralis* complex. We estimated a species tree for all whistlers within a multispecies coalescent framework and explored questions pertaining to the groups' systematics and biogeographical origins at multiple taxonomic levels within this clade (e.g., from the entire family to within species-complexes). This work further refines our understanding of one of the regions' most enigmatic bird lineages and adds to our growing knowledge about the patterns and processes of diversification on island systems.

Isolation and Gene Flow Affect the Diversification of a South Pacific Bird: The Foulehaio Honeyeater Complex

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Islands are natural barriers that prevent gene flow between populations and promote allopatric diversification. Birds in the South Pacific are an excellent model to explore the interplay between isolation and gene flow due to the region's extensive archipelagos and relatively well characterized avian communities. The Wattled Honeyeater complex (*Foulehaio* spp.) comprises three allopatric taxa that are widespread and common across Fiji, Tonga, Samoa, and Wallis and Futuna. Previous work using mitochondrial DNA found three well-differentiated lineages that are up to 8% diverged, but questions remain about what, if any, genetic structure exists within the nuclear genome of *Foulehaio*. Here, we explore patterns of gene flow within and between these lineages using a dataset of ultraconserved elements (UCEs). We sampled 134 individuals (132 ingroup plus two outgroup taxa: *Xanthotis provocator* and *Gymnomyza viridis*) from 21 islands across the entire range of *Foulehaio*. Our 95% complete datamatrix comprised 1,341 UCEs (mean contig length = 1,077 bp; total alignment = 1.4 Mb) from which we called SNPs. We used tree-based and population genetic approaches in a multispecies coalescent framework to study patterns of gene flow within *Foulehaio*. We found strong support for three lineages of *Foulehaio*, each pertaining to previously identified mitochondrial lineages (*F. carunculatus*, *F. procerior*, and *F. taviuensis*). There is minimal gene flow between these lineages, supporting treatment as three species; however, we detected interesting patterns of gene flow between populations of *F. carunculatus*, the most widespread taxon from Eastern Fiji to Samoa.

Lesser Prairie-Chicken Status and Conservation in New Mexico

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In 2017, Lesser Prairie-Chickens (LEPC) were surveyed audibly and visually along public roads and on State Game Commission-owned Prairie Chicken Areas (PCAs). Twenty-eight leks were detected on 18 of 52 (35%) roadside routes surveyed. Trend analysis of the total number of leks detected has shown a slight decrease from 1998–2017 along these routes, although not significant. Thirty Prairie Chicken Areas (PCAs) were also surveyed. Forty-seven leks were detected on or near PCAs, and 397 LEPC were observed on 33 of those leks. Average lek size was 9.79 birds/lek with an estimated minimum spring breeding population of approximately 4,230 birds. This is a 27% increase from 2016. Drought contributed to declines in LEPC populations in east-central New Mexico between 2011–2014, although populations have increased each year since 2014 with increased rainfall. In the southern periphery of the range,

restoration and reclamation efforts of previously developed areas and long-term planning efforts for re-establishing LEPC populations are on-going. Despite these conservation efforts, the current occupied range of LEPC in New Mexico is substantially reduced from the historical range. Given that LEPC numbers remain below historic averages, we recommend that continued emphasis and commitment be placed on habitat improvement projects in this area.

Lesser Prairie-Chicken Space Use in Varying Densities of Energy Development

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The level at which oil and gas infrastructure begins to adversely affect lesser prairie-chicken (*Tympanuchus pallidicinctus*) habitat selection is poorly understood. Our objectives were to provide a quantitative measure of the space use response of lesser prairie-chickens to varying densities of structures associated with oil and gas development in eastern New Mexico. In three field seasons, we captured 70 females and 128 males and fitted them with VHF radio collars or PTTs to monitor their movements. Oil and gas structures (well pads, roads, utility poles, etc.) were used as covariates in a conditional logistic regression analysis to determine the probability of use for a given area by lesser prairie-chickens. Data were subset into two sampling periods (spring and summer) to investigate potential differences in space use that may be a result of seasonally-varying behavioral thresholds to disturbance. Of the structures examined, we found that the presence of utility poles best explained space use for both seasons, although a negative relationship was observed for several other covariates. The strength of the relationship between probability of use and infrastructure presence was noticeably weaker in the spring when compared to the summer months, suggesting that reproductively motivated individuals are more tolerant of disturbance. By understanding the effects of oil and gas infrastructure on lesser prairie-chicken habitat selection, we may better plan the distribution and density of such development, thereby increasing the likelihood of population persistence.

The Value of Undergraduate Researchers: A Long-Term Study of Gray Vireos in Central New Mexico

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The Sevilleta National Wildlife Refuge, located in central New Mexico, contains about 25,000 acres of Juniper woodland and savanna. Much of this woodland provides breeding habitat for the Gray Vireo (*Vireo vicinior*), a little-known southwestern songbird listed as threatened within the state of New Mexico. For the last six of seven years, I have investigated various aspects of their breeding biology, cowbird parasitism and habitat characteristics. I have conducted the field work using undergraduate students from the UNM Research Experience for Undergraduates program. Each summer I had two different undergraduates conducting the research. They conducted point surveys using a playback protocol, searched for nests, monitored nest success, collected nest site and area habitat measurements, and characterized defended territories in three locations within Los Piños Mountains on the eastern portion of the refuge. One year included a prescribed fire in a portion of one of the study areas, and I compared pre-fire and post fire vireo numbers and territory locations. Over the 6 years, we located a total of 68 nests, 21 of which fledged at least one young (31%), and 11 of which were parasitized by Brown-headed Cowbirds (*Molothrus ater*) and failed (16%). This presentation summarizes the habitat used on the refuge, characterizes nest trees, and reports on the size of defended territories. It also examines cowbird parasitism in relation to distance from cattle grazing, and discusses pinyon-juniper management in the range of the Gray Vireo. I include discussion on the pros and cons of using undergraduate researchers to conduct the research.

Beyond The Nest: The Post-Fledging Period in Gray Vireos

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Gray Vireos (*Vireo vicinior*) are short-distance migratory songbirds that breed primarily in piñon (*Pinus* spp.) –juniper (*Juniperus* spp.) systems in the southwestern United States and northwestern Mexico. Compared to many songbirds in North America, Gray Vireos are understudied throughout their range, making it challenging to develop and implement meaningful conservation plans. Additionally, most studies of Gray Vireo demography focus on the nesting stage (i.e., nesting success as a measure of productivity). However, incorporating data from the post-fledging period is essential to determine full-season productivity and habitat associations. We monitored nests ($n=36$ in 2016; $n=51$ in 2017) at Sevilleta National Wildlife Refuge in central New Mexico, USA. Nest success was 24% and 25% in 2016 and 2017, respectively. Brown-headed Cowbirds (*Molothrus ater*) parasitized 38% and 43% of Gray Vireo nests in those years, respectively. In 2017, we used radio telemetry to track the daily movements of 32 fledglings to determine post-fledging space use, survival, and habitat features associated

with those parameters. Fledgling survival was 66% during the dependent stage (i.e., between nest departure and independence from adult care). The mean distance between daily movements was 241.1 m (\pm 235.4 SD), and the maximum observed daily distance was 1.4 km. These movements increased with age. Like other fledgling studies, the majority of mortality occurred during the first week post-fledgling. Our study highlights the importance of monitoring fledgling songbirds when considering full-season productivity and management decisions.

Systematics of the Avian Order Coraciiformes

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The avian order Coraciiformes comprises 177 species in six families with diverse ecologies and morphological characteristics, but their collective evolutionary history has not been adequately explored. Apart from kingfishers, the remaining five coraciiform families are understudied by molecular systematists. Indeed, motmots and rollers have no published molecular phylogeny. Here, we present the first species-level phylogeny of Coraciiformes using ultraconserved elements (UCEs) and high-throughput sequencing. Ultraconserved elements are short genomic regions with a conserved core and variable ends that are scattered throughout the genome and are conserved across the tetrapod tree of life. Our dataset comprised every species currently recognized by the current IOC checklist (v 7.1), with less than 20% of samples derived from museum skins. We recovered well-supported species trees using RAxML, SVDquartets, and ASTRAL. This is the first phylogenetic analysis of all coraciiforms and includes 18 species whose relationships weren't previously known. We discuss general systematics of the order and novel species-level relationships uncovered in our analysis.

Metabolic and Evaporative Limits to Avian Activity in the Heat

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Speakman and Król (2010a,b) have hypothesized that heat dissipation limits (HDL) are responsible for constraints on activity rates and energy expenditure in endotherms and developed a model for heat loss in mammals and birds. Interestingly, the clearly stated assumptions of the heat dissipation model require that animals are not heat stressed: that air temperatures (T_{air}) remain below upper critical temperature (T_{uc}), solar

radiation is negligible, and internal surfaces do not participate in heat exchange with the environment as “heat is normally conserved in the process of conserving water” (Speakman and Król, 2010a, p. 730). As diurnal endotherms, desert birds are often exposed to intense solar radiation and high T_{air} that leads them to experience environmental temperatures above T_{uc} and normothermic T_b . Although birds typically reduce activity levels and seek shaded microsites during the heat of the day, operative environmental temperatures exceeding T_b result in the evaporation of large quantities of water for heat dissipation. As a consequence, for desert endotherms, during a large part of their annual cycle, the assumption of the HDL model that evaporative water loss is unimportant to heat balance is not valid. Our data on birds indicate that they may dissipate more than two times their metabolic heat loads evaporatively and thus water loss rates may in fact constrain performance and behavior. Therefore, we propose that the HDL model be modified to account for evaporative heat loss in endotherms and in desert birds specifically.

Improving Models of Nest-Site Selection to Better Inform Pinyon Jay Habitat Management

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The ability to delineate animal habitat is critical to managers when making on-the-ground decisions. These delineations may be transferable across the distributional range of some species, while other species may have local adaptations to available habitat. In these more locally adapted species, a single definition of habitat may perform poorly across their distributional range, resulting in potentially detrimental management actions. We used nest-site selection models for the Pinyon Jay (*Gymnorhinus cyanocephalus*) in four areas along a 400-km transect to test the transferability of habitat models and the potential losses of nesting habitat if the resulting management prescriptions from one nesting area are inappropriately applied to another area. Using tree diameter and canopy cover in generalized linear mixed models, we found the transfer of models from one area to other areas resulted in the potential loss of up to 79% of nesting habitat in some locations, while a single model incorporating all nesting areas still resulted in a potential 64% loss. Transferability was greatly improved when a single model adjusting for local conditions was applied; the greatest potential loss was reduced to 26% of habitat. The assumption that a single habitat management prescription is appropriate across multiple nesting sites can result in loss of suitable habitat. However, constructing habitat models and management prescriptions for individual nesting areas may not be feasible. A single model adjusting for local conditions may provide the best of both approaches.

Biodiversity Genomics of *Dryobates* Woodpeckers

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Woodpeckers in the genus *Dryobates* (formerly part of *Picooides*) are found worldwide in the northern hemisphere, with three representatives in North America: Ladder-backed Woodpecker (*D. scalaris*), Nuttall's Woodpecker (*D. nuttallii*), and Downy Woodpecker (*D. pubescens*). Ladder-backed and Nuttall's Woodpeckers are sister species and occasionally hybridize, and both are sister to the Downy Woodpecker. With somewhat sporadic hybridization in the species group, it is unclear if there is widespread genomic introgression between species. We used several genetic datasets, including mitochondrial DNA, reduced representation genomic sequencing, and whole genomes to characterize the evolutionary history of North American *Dryobates*. We found strong genetic differentiation and little introgression between species, suggesting that these woodpeckers evolved in isolation with low levels of gene flows in contact zones. Hybridization between *Dryobates* species appears to be infrequent or an evolutionary dead-end, with little genetic material passing between species.

POSTER PRESENTATION (PRESENTERS UNDERLINED)

The Paradoxical Giant Hummingbird: Comparison of Andean and Coastal Subspecies With Respect To Blood, Migration, and Genes

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The Giant Hummingbird (*Patagona gigas*) is twice as large as the next largest hummingbird species and has long been considered paradoxical with respect to flight biomechanics. It is also an extreme outlier in other respects. For example, it is the only hummingbird species that breeds above 4,000 m elevation and also along the beaches of the Pacific Ocean. The high Andean populations of Giant Hummingbird (*P. g. peruviana*) that we have studied previously have a beta-hemoglobin genotype (serine at beta-hemoglobin A positions 13 and 83) that is characterized by high O₂-affinity and is only shared with four unrelated hummingbird taxa that are also restricted to extreme high altitudes. Here we report that lowland-breeding populations of Giant Hummingbird (*P. g. gigas*) are genetically highly similar to their high-elevation

counterparts; they even share the same beta-hemoglobin genotype, a unique characteristic among lowland hummingbirds. We found that hemoglobin concentration is lower and red blood cell volume is higher in the lowland *P. g. gigas* compared to their high Andean relatives. Complicating this comparison is the possibility that coastal *P. g. gigas* may be a seasonal elevational migrant, but neither the geographic range nor elevation of non-breeding *P. g. gigas* are known at present. We describe our efforts to describe its migratory behavior using geolocators.

Comparisons among Haemosporidian Parasite Communities of Three New Mexico Mountain Ranges

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Birds and their haemosporidian parasites (Haemoproteus, Plasmodium, and Leucocytozoon) comprise a diverse multi-host, multi-parasite system that is uniquely suited for studying evolutionary dynamics of hosts-parasite relationships. However, because of the challenges of surveying entire bird communities for parasites, only a few studies to date have been able to ask about parasite diversity, rates of species-turnover, and geographic variation in host-parasite relationships. We conducted community-level surveys of haemosporidians within a narrow elevational zone (2100–2500 m) in three adjacent mountain ranges in New Mexico. We screened 776 bird specimens of 61 species using an mtDNA 'barcode' (cytb), as well as microscopy. We used phylogenies of parasite and host lineages, respectively, to evaluate the uniformity of community composition and host-parasite relationships among the three mountain ranges. We found 269 infections (34.7% of birds) representing 99 distinct lineages. The majority were Haemoproteus (50.0%), followed by Leucocytozoon (38.7%), and Plasmodium (24.2%). Compared to previously published sequences, 60% were novel. We found conserved host-specificity at the avian clade and species level, but host-range varied strikingly by parasite genus. Host-switching by haemosporidian lineages was common, and more frequent between closely related hosts. Infection rates were highly variable among host species and clades; for example, vireos and nuthatches exhibited nearly universal infection and non-infection, respectively. Haemosporidian species turnover among mountain ranges was higher than expected by chance, and much higher than bird species turnover. Haemosporidian parasite diversity is higher than bird diversity in New Mexico due to geographic variation in community composition.

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