

Heterospecific interactions play an important role in shaping avian communities. Cooperative or competitive, associations across species can alter foraging, vigilance, patterns of habitat use, and nest site choice. These behaviors can be influenced by information eavesdropped from the broader heterospecific community or through direct interactions such as mixed species foraging flocks which may allow birds to expand their foraging niche or territorial disputes which result in competitive exclusion. In this introduction to the symposium, I discuss examples of heterospecific associations and discuss broadly how such associations may impact avian behavior and evolution. How are long-term heterospecific associations mediated? How do patterns of habitat use and recruitment in one population impact another? How do heterospecific social interactions differ from conspecific associations? I also discuss briefly how the field is advancing, touching on new techniques such as social network analysis and new hypotheses that are helping us to clarify why heterospecific associations occur and with whom.

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#### **Traveling as a Newbie: Migratory Strategies Linked to Survivorship in Juvenile Shorebirds in Peru**

Eveling A Tavera, David B Lank, Mark C Drever, Viviana V Gutierrez-Ruiz

Selection of non-breeding sites by long-distance birds should involve a balance between local survival rate, the relative costs of migration, and the effects on other components of life history strategies. We use Western and Semipalmated Sandpipers at Paracas, Peru, as models to test survival differences among populations with different migration distances to travel between breeding and non-breeding grounds. Westerns breed in Alaska, whereas Semipalmated populations at Paracas are a mixture of short-billed birds from western Arctic breeding sites 11,000km from Paracas, plus long-billed birds from eastern sites, migrating 8000km. Western sandpiper juveniles confirmed the overwintering strategy of more southerly non-breeding populations, with no individuals preparing for northward migration in their first year. These non-migrants had significantly higher annual survival than adults (Juveniles: 0.93 0.06 (SE) to 0.760.04 (SE)/Adults: 0.86 0.09 (SE) to 0.600.04 (SE)). The high survivorship of non-migrants highlights the the life history advantage of missing a first potential breeding season and provides an estimate of the survival cost of migration and breeding attempts. On the other hand, Semipalmated juveniles showed a bimodality strategy. Long-billed eastern birds showed a higher propensity to migrate north in the first year of

life. However, these long-billed birds had a significant lower survival than short-billed ones (-0.0590.02 (SE) per mm), thus explaining why only a lower proportion (31%) attempt to perform this migration as a juvenile. Our results help us explain how these birds may offset the real cost of migration by selecting the best migratory strategy with no life experience at all.

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#### **Genomic Signatures of Pleistocene Dry Forest Connections in a Widespread South American Songbird**

Eamon C Corbett, Gustavo A Bravo, Fábio Schunck, Luciano N Naka, Luís F Silveira, Scott V Edwards

South American dry forests are an important and understudied biome, with a complex and poorly understood biogeographic history. Based on the fragmented distribution of many Neotropical dry forest species, Prado and Gibbs (1993) suggested that this habitat was more widely distributed under drier climate conditions in the Late Pleistocene. But this “Pleistocene Arc Hypothesis” has rarely been tested genetically, much less with genome-wide data. We used ddRADseq in combination with mtDNA sequencing to sample 7,167 genome-wide single-nucleotide polymorphisms from 74 individuals across the range of the Rufous-fronted Thornbird (*Phacellodomus rufifrons*), a widespread dry forest bird with a disjunct distribution closely matching that of the biome itself. We found low genetic differentiation across two prominent geographic breaks including, most strikingly, a 1,000 km gap between populations in Bolivia and Northern Peru. Using demographic analyses of the joint site frequency spectrum, we also found evidence of recent divergence without subsequent gene flow across those breaks. This pattern is highly consistent with the idea that currently disjunct patches of dry forest were more connected in the recent past, likely during the Middle and Late Pleistocene. This scenario was also supported by paleoclimate species distribution modeling. By contrast, we found a deep genetic break with recent introgression between morphologically distinct parapatric populations in Brazil, suggesting that there may be a previously unrecognized hybrid zone between them. Our results support the major predictions of the Pleistocene Arc Hypothesis and illustrate the importance of genome-wide sampling of widespread species for examining biogeographic and evolutionary questions.

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#### **Application of a Novel Nest Density Estimator: An Example Using Sagebrush-Steppe Songbirds**