

The formation of species boundaries is a complex, and often non-linear process that can span a continuum from divergence in allele frequencies, to the development of reproductive barriers (Coyne and Orr 2004). Examining the underlying evolutionary forces that lead to genetic divergence and reproductive isolation is key to understanding the process of speciation and the generation of biodiversity. While these characteristics are often difficult to assess due to the non-linear nature of speciation, hybrid zones provide unique opportunities to study the maintenance of species boundaries, and the evolutionary outcomes of genetic exchange between divergent lineages.

The House Wren (*Troglodytes aedon*) is an incredibly diverse species, with 32 identified subspecies and the largest breeding range of any songbird in the New World (Clements et al. 2019). Across the continental United States, there are two distinct House Wren mitochondrial clades, the eastern and western forms. Preliminary data suggest these two forms are about 4% divergent in the mtDNA. This degree of mtDNA divergence is comparable to other species-level pairs (e.g. Black-capped and Carolina Chickadees, 5% divergent, Reudink et al. 2007). Preliminary data also suggest that the western form of the House Wren in the United States is most closely related to a clade within the West Mexican mountains, while the Eastern form is most closely related to a form from Central America, indicating these divergence lineages are not sister taxa. Broadly, these results highlight there is a deep divergence within House Wrens (Chavez et al. in revision). While these two forms are divergent in mtDNA, they form a contact zone along mountain/prairie transition zones extending from the Black Hills of South Dakota to the Front Range of Colorado, similar to many other east/west species pairs (e.g. Warbling Vireos, the Northern Oriole complex; Walsh et. al. 2020). Despite deep genetic divergence in mtDNA, it remains unclear the extent to which this divergence is reflected in the nuclear genome, or the degree to which gene flow in this contact zone is homogenizing genomic variation. We propose genomic sequencing of the House Wrens along the front range to better characterize hybridization and quantify population structure and gene flow between the two North American lineages.

Hybrid zones are often described as windows into the evolutionary process, and provide a unique opportunity to understand the generation, or maintenance, of reproductive barriers. By generating individuals with a mix of genomic backgrounds, hybrid zones can be used to quantify the consequences of gene flow across divergent lineages: the extent of hybrid formation can reveal negative or neutral costs to hybridization and can highlight genomic regions that are resistant to gene flow that may play an important role in the maintenance of species boundaries, especially when species diversity is cryptic and difficult to characterize visually. Using whole genome data to explore the House Wren contact zone will uncover the evolutionary processes responsible for generating divergence between these lineages and will illuminate the genomic context in which divergence and subsequent speciation can occur. An understanding of the hybrid zone will also allow for more informed characterization of species limits, including examinations of their separate ecologies. Phenotypic variation in House Wrens is much less conspicuous than many other bird species pairs that meet at the Rocky Mountains. As a result, this system has remained understudied. The examination of this system using a genomics framework may reveal cryptic diversity that is important for characterizing the divergence of these taxa, and will fill a considerable knowledge gap with respect to House Wrens and North America avifauna more generally.