Hird and colleagues (2010) showed that along the contact zone of the subspecies *Tamias ruficaudus ruficaudus* and *Tamias ruficaudus simulans* in Idaho there is discrepancy between inter-specific introgression of mitochondrial DNA (mtDNA) and nuclear DNA. This discrepancy appears to be due to biased mtDNA introgression from *T r. ruficaudus* into *T. r. simulans*. This bias may be driven by either neutral gene flow or selection. For example, neutral demographic processes can drive introgression. Rare alleles can become common along a range expansion front (Klopstein et al 2006). Alternatively, selection for the introgressed *T. r. ruficaudus* mtDNA in *T. r. simulans* may be driving the observed imbalance.

We are using geographically explicit simulations to parameterize genomic expectations for patterns of introgressions between these taxa. We are modelling these processes using DimSum (Brown et al. 2010) and splatche2 (Currat et al. 2004), which allows us to leverage both the spatial data we have about these species’ ranges and dispersal distributions and explore complex linkage and recombination scenarios. Comparing the genomic data generated in this project to these expectations will determine whether observed patterns are consistent with neutral introgression, or selection for inter-specific mtDNA. Understanding the processes that have led to the patterns we see in the *T. r. ruficadus/simulans* pair will provide insight into how speciation and reproductive isolation occurs in the face of gene flow. We will then extend our simulations from this well-characterized hybrid zone to examine patterns of nuclear and mitochondrial divergence and introgression across all sampled *Tamias* taxon pairs, which will allow us to assess whether these same processes are driving patterns of introgression between groups across a range of divergence times.

This project builds on EJM’s previous work using genomic data to study ongoing evolution of New World cattle via hybridization between subspecies. In this collaboration we are combining computational approaches with analyses of empirical data to understand speciation as it is currently happening in the wild, capturing evolution in action. This work will improve understanding of a key evolutionary process, that of divergence between populations in the face of gene flow.

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