This project tests predictions of divergence with gene flow (DwGF) in empirical and simulated systems and builds collaboration between the PIs labs. The *in vivo* system will focus on the chipmunk radiation in the genus *Tamias*, a promising model for DwGF, and continue funding an RA for student Brice Sarver at UofI and the simulations are being conducted by an RA at UT, Emily McTavish. This interdisciplinary approach is synergistic and will provide preliminary data for a larger NSF proposal, to be submitted in 2013.

**Goals:** Divergence with gene flow has predominantly been examined in simple sister-species pairs, primarily (although not exclusively; Danley et al., 2000) with respect to speciation of model organisms (e.g., *Drosophila* - Coyne et al. 2005; *Mus* – Payseur et al. 2004; *Homo* – Green et al. 2010). Here, we are using genome wide data to test DwGF across a range of species pair relationships in the *Tamias* chipmunk radiation.

This project has two **intellectual-merit goals**. *First*, we are testing genomic predictions of DwGF models of speciation in the chipmunk radiation. We’ve begun to generate comparative genomic data from several introgressing chipmunk complexes to examine differential introgression between reproductive protein genes (e.g., acr, zna, and zp-1, zp-2, & zp-3; Reid et al. 2011), versus thousands of randomly sequenced genes. We now have ca. 9,000 contigs (from 200-2000 bp). These data are allowing us to test a central tenet of DwGF, that genes involved in reproductive divergence are refractory to introgression even in the face of substantial hybridization. To date, preliminary analyses of genomic data for *T. ruficaudus* and *T. amoenus canicaudus* indicate support the conclusions from 1st-gen data that these taxa represent Phase 4 of Wu’s (2001) conceptualization of DwGF; 92% of SNPs (7820) support the species tree whereas the remaining 8% are split evenly between the other possible gene trees. More introgressing complexes (e.g.,*T. umbrinus*, *T. dorsalis*) will be assessed this spring.

*Second*, we are conducting geographically explicit computer simulations to parameterize genomic expectations for alternative drivers of introgressions. We are modeling these processes using DimSum (Brown et al. 2010) and splatche2 (Currat et al. 2004), which allows us to leverage both the spatial data about species pair’s ranges and dispersal distributions, and to explore complex linkage and recombination scenarios. Stochastic simulations allow us to paramterize realistically complex scenarios. Comparing the genomic data generated by this project to these expectations will determine whether observed patterns are consistent with neutral introgression or selection. We will extend our simulations to examine patterns of nuclear divergence and introgression across all sampled *Tamias* taxon pairs, which will allow us to assess whether the same processes are driving genomic patterns of introgression between groups across a range of divergence times. By combining genomic data and computational tools we will can understand divergence with gene flow as it is currently happening in the wild, capturing evolution in action.

We have two **broader-impact goals.** The *first* is to provide interdisciplinary training to two graduate students (Brice Sarver at UofI and Emily Jane McTavish at UT). *Second*, we’re collecting preliminary data for a more expansive NSF proposal integrating genomic and computational studies of DwGF models of speciation. Specifically, for DwGF to lead to speciation, resistance to introgression must spread from the targets of selection (i.e., the divergence genes) throughout the genome; the hypothesized mechanism for this spread is hitchhiking of closely linked genes (which itself is related to the size of syntenic groups) accompanied by coadaptation of interacting genes. Thus, the size of syntenic groups is predicted to increase with time since lineage divergence. These issues can be best addressed via computational studies that are guided by information gleaned from naturally evolved systems such as the *Tamias* radiation.

Brown, J, K. Savidge, and E. J. McTavish, 2010. DIM SUM: Demography and Individual Migration Simulated Using a Markov chain. Molecular Ecology Resources 11:358-363

Currat, M, N. Ray and L. Excoffier, 2004. splatche: a program to simulate genetic diversity taking into account environmental heterogeneity. Molecular Ecology Notes 4:139-142