

# Dynamics of Genes in a European Mouse Hybrid Zone

## Undergraduate Research Opportunities in the Tucker Lab

Department of Ecology and Evolutionary Biology and Museum of Zoology, University of Michigan

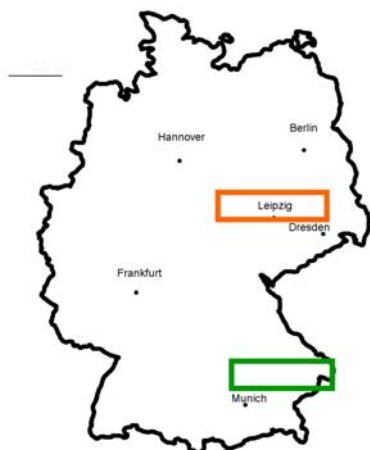
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Current research in the Tucker lab involves investigating the genetic basis of speciation between the European house mouse species *Mus musculus* and *Mus domesticus*. We are studying a naturally-occurring hybrid zone between these two species in central Europe. This work is a collaboration with Kate Teeter, a Ph.D. student in the Dept. of Ecology and Evolutionary Biology and Dr. Michael Nachman at the University of Arizona.

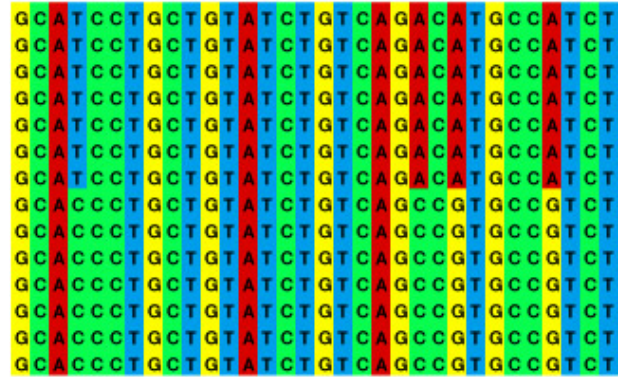
The genetic basis of speciation is a central problem in evolutionary biology. Because reproductive isolation delineates the point at which emerging species will no longer freely exchange genes, considerable speciation research has focused on the genetics of reproductive isolation. Historically, there have been two major approaches to this problem. The first approach relies on crosses in the laboratory between species that display partial reproductive isolation. The second approach, one we are using, involves investigations of naturally-occurring hybrid populations to make inferences about the genetics of reproductive isolation. The underlying assumption for this type of study is that differential movement (introgression) of alleles across a hybrid zone reflects fitness differences of specific alleles or alleles at closely linked loci when placed on a hybrid background. In cases where markers have been genetically mapped, it is possible to evaluate the entire genome and identify specific chromosomal blocks that contain genes involved in hybrid sterility or inviability.

To date, studies of laboratory crosses and hybrid zones indicate that reproductive isolation often arises through multiple substitutions at different, interacting loci and that sex chromosomes appear to be preferentially involved in the evolution of hybrid incompatibilities. However, there is still much we do not know. First, most of the work has only been done in *Drosophila*. Thus, these conclusions need to be corroborated in other species to see if they are general. More importantly, many of the details of the genetics of speciation are completely unknown. For example, how many genes are typically involved in reproductive isolation and how are they distributed in the genome? Are there a few genes of major effect or many genes of more equal effect? What kinds of genes are involved? Are changes primarily due to changes in protein structure or to changes in gene regulation? The long-term goals of this research are to address these and related issues in house mice belonging to the genus *Mus*.

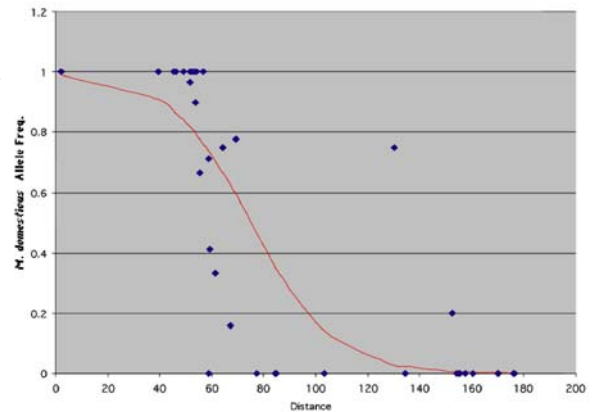
We are conducting a genome-wide study of introgression using genetic markers from across the genome. Preliminary analyses suggests differential introgression among genome regions with some regions exhibiting limited introgression and others extensive introgression.



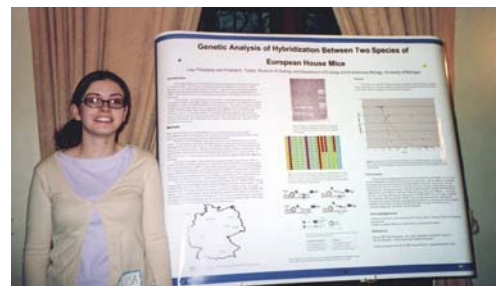
Map of Germany. The orange box shows the location of the Saxony hybrid zone transect and the green box shows the location of the Bavarian hybrid zone transect.



Partial DNA sequences of one genetic marker for fourteen individual mice. Each row represents a different mouse, the top seven rows contain *M. musculus* mice and the bottom seven are *M. domesticus*. This part of the marker sequence highlights the 4 nucleotide sites at which there is a difference between the two species.



Cline analysis for one genetic marker showing the frequency of *M. domesticus* alleles versus the distance in kilometers from the most western locality along a transect across the hybrid zone. The blue points show the actual frequencies for barn populations of mice collected. The red line is the cline shape using logistic regression.



Lisa Thibodeau, an undergraduate researcher in our lab, presenting her data at a symposium.