

DEVELOPMENT OF *PEROMYSCUS* GENOMICS

Julie L Weston¹, Clifton M Ramsdell¹, Stephanie C Napier¹, Rebecca Bullard-Dillard², Chantal Braithwaite², Hermes Exeter², Travis C Glenn³, and Michael J Dewey¹.

¹*Peromyscus* Genetic Stock Center, U of S Carolina, Columbia, SC 29208; ²Dept Biol, Claflin U, Orangeburg, SC 29115; ³Savannah River Ecology Lab, Drawer E, Aiken SC 29802.

Aptly called “The *Drosophila* of North American Mammalogy”, peromyscines are considered to be an ideal genetic model for studying 1) the genes responsible for reproductive isolation and speciation, and 2) the genes enabling the physiological and behavioral adaptation to changing environmental conditions, adaptation to other species, adaptation to each other, and adaptation to microbial and other parasites. Full exploitation of the research potential of *Peromyscus* depends on the ability to define and analyze the genes involved in these processes. Therefore, our goal is to develop a linkage map with PCR-based markers of *P maniculatus* that will allow identification of candidate genes affecting particular traits of interest. Markers are being developed and mapped at sufficient density, ~5-10 cM, to permit identification of major genomic segments syntenic with the reference species, *Mus musculus*. Such markers consist of 1) Type I (protein coding genes), important for synteny identification, and 2) Type II (microsatellites), which are highly polymorphic and will ultimately be used for QTL analysis. Thus far, for Type I markers, about 1500 Expressed Sequence Tags (ESTs) from a placental cDNA library have been characterized

(www.biol.sc.edu/~dewey/Peromyscus/EST.html) and over 100 microsatellites are available for the project. The linkage analysis panel was selected for maximizing utilizable polymorphism and is composed of interspecific meiotic segregants of crosses between the sister species *P m bairdii* and *P polionotus*. Results thus far have established substantial synteny between *Mus* chr11 and *Peromyscus* chr13. Furthermore, loci have been tentatively identified that reside in the region of chr13 inverted between *P m bairdii* and *P polionotus*.

(Supported in part by SC EPSCoR-BRIN, 8-PORR16461A; NIH RR14279; NSF DBI0130348)