

PEROMYSCUS GENETIC LINKAGE COMPARISONS WITH RATTUS AND MUS

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In all of North American mammalogy no genus has been studied as thoroughly as the genus *Peromyscus*. However, little large scale work has explored the genomics of this wide ranging and abundant genus until recently. A medium-density genomic map can be used to find 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. To advance this goal, efforts are underway to develop a medium-density genomic map with markers located every 5-10cM. These efforts include the use of hundreds of 1) Type I markers (protein coding genes) generated from ~7000 Expressed Sequence Tags from two cDNA libraries, one from placental and another from testis tissues, and 2) Type II markers (microsatellites), which are highly polymorphic and will be used for QTL analysis. These markers are being screened on an interspecific backcross panel between the sister species *P. maniculatus bairdii* and *P. polionotus*, and in regions of suspected chromosomal inversions, markers are screened on a 5000 rad whole-genome radiation hybrid cell panel. Combined results from both panels have indicated a high degree of gene order conservation of the telomeric 64 cM of *Mus* Chr 11 in the deer mouse genome. The remaining centromeric portion also shows gene order conservation with the deer mouse but as a separate linkage group. This indicates a translocation of that portion of *Mus* Chr 11 in *P. maniculatus* and is consistent with rearrangement breakpoints observed between *Mus* and other mammalian genomes, particularly the rat (*Rattus norvegicus*) genome. Furthermore, this separate linkage group is likely to reside in a chromosomal region of inversion polymorphism between *P. maniculatus* and *P. polionotus*.