Student Review by Rick Orozco, WFSC Undergraduate 2017

Hogan, K.M., M.C. Hedin, H.S. Koh, S.K. Davis, and I.F. Greenbaum. 1993. Systematic and taxonomic implications of karyotypic, electrophoretic, and mitochondrial – DNA variation in *Peromyscus* from the Pacific Northwest. *Journal of Mammalogy* Vol. 74, No. 4, pp. 819-831

In Hogan et al. (1993), two distinct groups of *Peromyscus* were recognized in northern Washington to southern Alaska area. One of these groups consists of *P. oreas, P. sitkensis,* and several subspecies of *P. maniculatus* that at that time included *P. m. hylaeus, P. m. keeni, P. m. macrorhinus,* and *P. m. prevostensis.* The second group consisted only of *P. m. austerus* (Allard and Greenbaum 1988). Hogan et al. (1993) examined the karyotypic, electrophoretic, and mitochondrial DNA variation of deer mice from the Queen Charlotte Islands and British Columbia mainland to better clarify the taxonomic and systematic affinities of *Peromyscus* from Washington north to southern Alaska and west of the Cascade and Coastal mountain ranges.

For the study, 284 deer mice were live-trapped from 14 insular and mainland localities in British Columbia and southeastern Alaska. The localities were chosen based on previous reports by Calhoun and Greenbaum (1991). Several techniques such as bone marrow collection and identification of non-differentiable stained C-banded and G-banded karyotypes were utilized to obtain different sets of data of chromosomal analysis. Observing karyotypes involves seeing what they look like under a microscope and involves paying close attention to their length, position of centromere, banding pattern, and to any differences in the sex chromosomes. For the mitochondrial DNA (mtDNA) analysis, mice that had chromosomal data available were used. Those samples were cut with 11 restriction endonucleases with six-base recognition sites. After that, the size from each mtDNA fragment was estimated and given a different numeric designation. The assumption was made that *Peromyscus* with the same numeric designations for the restriction sites were considered to have the same haplotype. The third method, electrophoretic analysis, involved the use of starch-gel electrophoresis to examine allozymic variation for 12 proteins encoded for 21 presumptive gene loci. Just like the localities, reference samples of *P. m. austerus* and *P. oreas* from Calhoun and Greenbaum (1991) were used to establish a direct comparison of allelic data generated from the Hogan et al. (1993) study.

After analyzing the chromosomal, mtDNA, and electrophoretic data, it was clear that deer mice from the Pacific Northwest represented two distinct evolutionary lineages. These lineages were separable by the range of fundamental numbers (FN) assigned to each of the 284 mice. According to Hogan et al. (1993), determining specific status is simple when the populations in questions are sympatric or continuously distributed. However, when populations are allopatric, designating species are focused on the congruence and cohesion of characters. The *Peromyscus* in the Pacific Northwest contained allopatric portions in their distribution which led to the conclusion that high-FN mice of *P. oreas, P. sitkensis, P. m. hylaeus, P. m. keeni, P. m. macrorhinus,* and *P. m. prevostensis* be formally recognized as *Peromyscus keeni*. As for the low-FN mice, due to their smaller size, shorter tail length, and being chromosomally diagnosable from the higher FN mice, they were recognized as *P. m. austerus.*

Just like every other study, this one created more questions than answers for me. Questions such as: is it possible that due to factors such as habitat loss, displacement, and others,

species of *Peromyscus* might go through some evolutionary change and remodel the order of the taxonomy? In my four years as a science major I have learned that every finding is a hypothesis to be tested. I see this study conducted by Hogan et al. (1993) as a test of Thomas (1973; who discovered that the genus *Peromyscus*) had specific karyotypic variation due to implications of evolution. I am not an expert in small mammal research but if I had any input on the continuation of this study I would suggest collecting samples every 5–7 years. Also, I am not too sure about the exact years but the focus would be to repeat every method to observe any similarities or differences of *Peromyscus* in each of the regions.

LITERATURE CITED

Allard, M. W., and I. F. Greenbaum. 1988. Morphological variation and taxonomy of chromosomally differentiated *Peromyscus* from the Pacific Northwest. Canadian Journal of Zoology 66: 2734–2739.

Calhoun, S. W., and I. F. Greenbaum. 1991. Evolutionary implications of genetic variation among insular populations of *Peromyscus maniculatus* and *Peromyscus oreas.* Journal of Mammalogy, 72: 248–262.

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