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MOLECULAR PHYLOGENY OF THE RODENT GENUS *LIOMYS*: EVIDENCE FROM THE MITOCHONDRIAL CYTOCHROME *B* GENE

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The number of species described in the world greatly underestimates its biodiversity, especially in some of the areas more rich in diversity such as Mexico. Once the biodiversity in a region is understood, the issues of management and conservation can be addressed. Spiny pocket mice of the genus *Liomys* are members of the rodent family Heteromyidae and are grouped with the genus *Heteromys* in the subfamily Heteromyinae. The genus *Liomys* has a rather broad geographic distribution that extends from Texas to Panama and consists of five recognized species: *L. irroratus*, *L. pictus*, *L. spectabilis*, *L. salvini*, and *L. adespersus*.

Previous research done on *Liomys* by Genoways (1973) who looked at morphological and chromosomal data proposed that these species were related as follows: *L. pictus* and *L. spectabilis* formed the *pictus* group, *L. salvini* and *L. adespersus* formed the *salvini* group, and *L. irroratus* formed the *irroratus* group. Rogers (1990) confirmed this relationship using data based on allozymes. He also noticed that *L. pictus*, as it was constituted, was paraphyletic which means that not all populations of *L. pictus* form a single (monophyletic) group relative to *L. spectabilis*. After further study of allozymes within the *pictus* species-group, Rogers and Engstrom (1992) determined that there was evidence to suggest that there was more than one distinct biological species within *L. pictus*.

Before this point, no DNA sequence data have been available to address the question of relationships among species in the genus *Liomys*. The purpose of my study was to test previous summaries of phylogenetic relationships using sequence data from the mitochondrial-DNA (mtDNA) cytochrome *b* (*cyt b*) gene for 70 specimens and from 15 localities. In addition, I tested the proposal of Rogers and Engstrom (1992), that there is more than one species in the *L. pictus* species group. My research focused on the following questions: how many candidate species exist within the genus *Liomys* and what are the relationships among these entities?

I extracted mtDNA from the liver of my specimens and through standard procedure isolated the *cyt b* gene and sequenced it. My analyses were done on the computer using a program called PAUP which analyzed the sequenced data based on maximum parsimony criteria and calculated the genetic distances (i.e. the amount of similarity) between populations. The results produced the tree of relationships seen in Figure 1. The average genetic distance within *L. salvini* is consistent with the values accepted for within subspecies comparisons. Within *L. irroratus*, however, the average genetic distances are greater than values usually observed within a single species and significantly higher values exist in *L. pictus* as well. This gives some indication of the possibility of candidate species within the currently recognized groupings.

Further indications of these candidate species can be seen by looking at the population from Jalcoctan which fell into two distinct groups (Fig 1). The genetic distance between the two Jalcoctan populations is, well above the values which normally indicate populations are within

