

# Assessing genetic variability in bat species of Emballonuridae, Phyllostomidae, Vespertilionidae and Molossidae families (Chiroptera) by RFLP-PCR

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**ABSTRACT.** A PCR-RFLP analysis of the restriction pattern in nuclear (RAG2) and mitochondrial (12S/16S) gene sequences of bat species from the Molossidae, Phyllostomidae, Vespertilionidae, and Emballonuridae families produced a large number of fragments: 107 for RAG2 and 155 for 12S/16S combined in 139 and 402 haplotypes, respectively. The values detected for gene variation

were low for both sequences (0.13 for RAG2 and 0.15 for 12S/16S) and reflected their conservative feature, reinforced by high values of inter- and intraspecies genetic identity (70-100%). The species with a high gene divergence were variable in the analyses of RAG2 (*Eumops perotis*, *Artibeus lituratus*, and *Carollia perspicillata*) and of 12S/16S (*Nyctinomops laticaudatus*, *C. perspicillata*, and *Cynomops abrasus*), and furthermore, one of them, *C. perspicillata*, also showed the highest intraspecific variation. The species that exhibited the lowest variation for both genes was *Molossus rufus*. In the families, the highest variation was observed in the Molossidae and this can be attributed to variation exhibited by *Eumops* and *Nyctinomops* species. The variations observed were interpreted as a natural variability within the species and genus that exhibited a conserved pattern in the two gene sequences in different species and family analyzed. Our data reinforce the idea that the analyses of mitochondrial and nuclear genes contribute to our knowledge of the diversity of New World bats. The genetic variability found in different taxa suggests that an additional diversity, unnoticed by other methods, can be revealed with the use of different molecular strategies.

**Key words:** Gene variation; RAG2 gene; 12S/16S gene; PCR-RFLP; Microchiroptera