Abstract

A limited number of studies have focused on the population genetic structure of vampire bats (Desmodus rotundus) in America. This medium-sized bat is distributed in tropical areas of the continent with high prevalence in forested livestock areas. The aim of this work was to characterize the vampire population structure and their genetic differentiation. For this, we followed standard methods by which live vampires (caught by mist-netting) and preserved material from scientific collections, were obtained for a total of 15 different locations, ranging from Chihuahua (North) to Quintana Roo (Southeast). Tissue samples were obtained from both live and collected animals, and the genetic differentiation, within and among localities, was assessed by the use of seven microsatellite loci. Our results showed that all loci were polymorphic and no private alleles were detected. High levels of heterozygosis were detected when the proportion of alleles in each locus were compared. Pairwise $F_{ST}$ and $R_{ST}$ detected significant genetic differentiation among individuals from different localities. Our population structure results indicate the presence of eleven clusters, with a high percentage of assigned individuals to some specific collecting site. Rev. Biol. Trop. 62 (2): 659-669. Epub 2014 June 01.

Keywords

Key words, heterozygosity, México, microsatellite, population structure, vampire bats.