

Abstract

Population structure, biogeography and phylogenetic relationships of the fruit bat genus *Rousettus* have been studied in Africa and adjacent regions. The current population patterns of rousettine fruit bats in the Old World are influenced by several environmental attributes, namely the topography, climate and land cover. These variables are mirrored in fruit bat plesiomorphies related to the ecological niche of tropical flying frugivore, as well as apomorphies of rousettines including echolocation ability, roosting in caves and dispersal capacity in open landscapes with discontinuous tree cover. Phylogenetic relationships among species and subspecies of the genus have been indicated and confronted with the existing colonization scenarios. Insular populations (including habitat islands within desert oases) show frequent genetic differentiation from their mainland relatives suggesting successful founder events after traversing stretches of unsuitable habitats. Genetic differentiation evolving in less distant islands suggests involving behavioural mechanisms maintaining cohesion of isolated demes as site fidelity and natal habitat-biased dispersal. In sub-Saharan mainland Africa within the large range reaching from the southern border of Sahara to Cape Peninsula, *Rousettus* populations share a homogeneous nuclear pool but form two mitochondrial haplogroups that occur partly in sympatry. The observed pattern is attributed to the Plio- / Pleistocene climatic oscillations and differentiation within hypothetical forest refugia in the Congo basin and/or Upper Guinea and in eastern Africa. The current distribution of both haplogroups implies different modes of dispersal from particular refugia and the possibility of adaptive traits associated with mitochondrial DNA. A contrasting situation was uncovered on the northern border of the genus' distribution, in the Middle East. A complex geomorphology of the region together with founder effects and a later colonization have caused fine-scale population diversification, isolation by distance and frequent insular effects. The observed patterns have been discovered by means of mitochondrial and fast evolving nuclear markers. A detailed study of a contact zone between Mediterranean and desert habitats in the Levantine region confirmed a steep gradient in both genetic and morphological traits of the local fruit bats, concordant with isolation by environment and isolation by adaptation and indicating the presence of ecotypic variation. Human activities including horticulture have increased the amount of roosting and foraging sites, thus affecting movement ecology of both ecotypes, however, the impact of anthropogenic changes in the environment on the admixture was not proved. Since fruit bats play a crucial role in pollination and seed dispersal of a large number of plants and trees, they represent a keystone species of respective forest ecosystems. Unfortunately, especially small populations of fruit bats are threatened by increasing land-use, agriculture, their conflicting status as pests, their hunting for bushmeat and controversial role as vectors of viruses (Ebola, Marburg, etc.). For these reasons and due to the importance of rousettine bats for forest recovery and their ability to pioneer dry and distant habitats, they are proper object in the fields of conservation biology and restoration ecology.