

Abstract

Genetic Diversity of Barbary Macaques (*Macaca sylvanus*) and Its Implications in Conservation Management of the Species †

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Abstract: Barbary macaques (*Macaca sylvanus*) are critically endangered primates. They are unique within their genus, as the only African macaque. By the late Miocene, their habitat extended across Northern Africa and in Southern Europe. Aside from an introduced population in Gibraltar, their current distribution is reduced to disjointed forests in Algeria and Morocco. Our knowledge of the phylogeographic history and intra-specific diversity of this highly endangered species is also fragmented. In this study we aimed to improve our understanding of the phylogeographic history and genetic diversity of the Barbary macaque by expanding the genetic data available on the Algerian populations. Moreover, we investigated captive populations of Barbary macaques for comparison to wild populations. The mtDNA hypervariable control region I was sequenced using DNA extracts from faecal and hair samples from wild and captive populations. The newly produced data (N = 157), from both Algerian and Moroccan populations, were combined with previously published data (N = 212) and used to characterize genetic variability and reconstruct phylogenetic relationships among wild and captive populations. We found that Algerian populations exhibit an increased genetic diversity relative to Moroccan populations. Phylogenetic relationships suggest that the Moroccan populations diversified after being isolated from the Algerian populations. Captive populations were found to be not fully representative of the genetic diversity exhibited in the species, but rather only of Moroccan populations. Findings in this study suggest that the fragmented Algerian populations should be managed to increase gene flow between them by increasing habitat connectivity where it is feasible.

Keywords: conservation genetics; genetic diversity; phylogeography; Barbary macaques; population fragmentation; mtDNA

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