



Original Investigation

Mitochondrial demographic history of the Egyptian mongoose (*Herpestes ichneumon*), an expanding carnivore in the Iberian Peninsula



Tânia Barros^{a,*}, Philippe Gaubert^b, Rita G. Rocha^a, Victor Bandeira^a, Luis Souto^a, António Mira^c, Carlos Fonseca^a

^a Departamento de Biologia & CESAM, Universidade de Aveiro, Portugal

^b Institut des Sciences de l'Evolution de Montpellier (ISEM) – UM2-CNRS-IRD-CIRAD-EPHE, Université de Montpellier, Place Eugène Bataillon – CC 64, 34095 Montpellier cedex 05, France

^c Unidade de Biologia da Conservação, Universidade de Évora, Portugal

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ABSTRACT

Describing the genetic patterns and the demographic history of expanding species is essential for providing insights into the processes linked with range dynamics. We analysed the mitochondrial diversity of the Egyptian mongoose (*Herpestes ichneumon*) across the Iberian Peninsula, where the species is currently expanding north-west. A total of 242 individuals were analysed, together with nine representatives from the North African dispersal source. Haplotype segregation and strong differentiation between Iberian and North African populations confirmed the long-term presence of the species in the Iberian Peninsula. The distribution of mitochondrial diversity fitted the pattern of a historically diversified population in southern Iberia, from which the recent dispersals into northern areas may have occurred. Higher levels of haplotype and nucleotide diversities in the northern areas, together with the heterogeneous distribution of pairwise population differentiations and the weak signal for isolation-by-distance suggest the existence of long-dispersal migrants across the Iberian Peninsula. Sudden and spatial expansion scenarios of *H. ichneumon* in the Iberian Peninsula were supported by mismatch analysis and marginally supported by neutrality tests. However, the precise time of occurrence of the detected expansion remains unclear. Future studies should incorporate additional markers in order to further clarify the population dynamics of the Egyptian mongoose in its Iberian range.

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Introduction

The genetic structure of a species can be substantially influenced by historical and environmental factors (e.g. Schwartz et al. 2003; Mora et al. 2007). Such dynamics cause a diversity of specific responses that can result in population stability or range shifts, which in turn produce signatures in the species' demographic history (Slatkin 1993; Ramírez-Soriano et al. 2008; Excoffier et al. 2009). Genetic patterns of colonizing populations are dependent on the size of the founding group and the timeframe of the colonization event (Arenas et al. 2012; Szűcs et al. 2014). Species under geographic expansion usually show a gradient of genetic

diversity across their range, with a tendency of presenting a lower genetic diversity in newly colonized areas in comparison with areas where the species is long-established (Frankham and Ralls 1998). Notwithstanding some exceptions exist, in which high genetic diversity is found in newly colonized areas (e.g. Zalewski et al. 2011; Gaubert et al. 2011).

The majority of studies concerning the genetic structure of expanding populations have focused on invasive and exotic species (e.g. Zalewski et al. 2009; Estoup and Guillemaud 2010). This is notably the case for introduced carnivores in the Iberian Peninsula (e.g. Lecis et al. 2008; Gaubert et al. 2009, 2015; Alda et al. 2013). These studies are of extreme importance for improving knowledge on the dynamics of introduced populations and for providing appropriate management guidelines. Nevertheless, it is also crucial to investigate the genetic patterns of naturally expanding species (e.g. Lubina and Levin 1988; Swenson et al. 1998) to improve our knowledge on dispersal/colonization processes.

* Corresponding author at: Departamento de Biologia/CESAM, Universidade de Aveiro, Campus Universitário Santiago, 3810-193 Aveiro, Portugal.
E-mail address: taniabarro@ua.pt (T. Barros).