



## Genetic signature of the northward expansion of the Egyptian mongoose *Herpestes ichneumon* (Herpestidae) in the Iberian Peninsula

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In the last three decades, the range of the Egyptian mongoose (*Herpestes ichneumon*) has increased in the Iberian Peninsula. A panel of microsatellites was used to confront the patterns of genetic diversity of the species with the scenario of its recent northward expansion in its Iberian range. Evidence of substructure and significant genetic differentiation within the studied population were recorded, with a central-northern subpopulation (CNorth) and a southern subpopulation (S). Northward range expansion was supported by the observed allelic frequencies, diversity parameters, and observed heterozygosity of the studied loci, with S showing a higher allelic diversity and a higher number of private alleles than CNorth. Patterns of isolation-by-distance and isolation-by-barrier as a result of the Tagus River were demonstrated, suggesting that the river acted as a semi-permeable barrier, possibly leading to genetic differentiation of the studied population. The observed individuals from CNorth in southern locations and individuals from S in central/northern areas might comprise evidence for long-range dispersals across the studied range. A bottleneck event after population expansion was supported by a significant heterozygosity deficiency in CNorth, which is in agreement with a scenario of founder events occurring in recently colonized areas after the crossing of the Tagus River. © 2016 The Linnean Society of London, *Biological Journal of the Linnean Society*, 2016, 118, 686–697.

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### INTRODUCTION

The identification of the factors behind the limits of a species' range has been a central question in ecology and in evolutionary biology (Holt, 2003). Assessing the genetic structure of a population is critical for providing insights into the dynamics of the species' range and ecological attributes (Hanski & Gilpin, 1997). By unravelling such genetic patterns, one can infer the influence of dispersal, genetic drift, and

isolation on the genetic diversity of a population (Xu *et al.*, 2013), as well as identify the occurrence of bottlenecks and founder events (Dlugosch & Parker, 2008).

In wild populations, genetic patterns caused by range shifts may be influenced by intrinsic factors, such as the ability of a species to disperse (Clobert, Dhont & Nichols, 2001; Chambers & Garant, 2010). On the other hand, those patterns can also be greatly influenced by extrinsic features, such as physical barriers (Lowe, Harris & Ashton, 2004). In the light of the study of expanding species,

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