



Short Communication

Managing Spanish European mink populations: Moving from a precautionary approach towards knowledge-based management



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ABSTRACT

Understanding the phylogenetic history, genetic variation and ecological requirements of a species is fundamental to the design of effective strategies for its conservation and management. Where such knowledge is lacking, it is particularly important that newly acquired information be incorporated into conservation programs immediately, following a protocol of adaptive management. However, given the inertia of conservation projects, this information is often not incorporated into the decision-making process in a timely fashion. Herein, I present an example in which molecular techniques and distribution trends shed light on the conservation value of one of the three populations of a globally threatened species: the European mink (*Mustela lutreola*). This note suggests that conservation programs for this population should be reviewed in depth, and reoriented appropriately.

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Introduction

Although the poor conservation status of many threatened species often justifies the urgent implementation of conservation actions, long-term conservation plans should always be accompanied by research that informs the future directions of conservation strategies. However, the dissemination of scientific knowledge is often slow in reaching decision-makers in the field (Sutherland, Pullin, Dolman, & Knight, 2004 for general view). Moreover, different populations of a species may fall into different risk categories, face different threats, or exhibit different histories and population trends. Therefore, focusing on the appropriate scale of an endangered population can help to direct and guide conservation actions.

Herein, this study aims to present the case of the European mink (*Mustela lutreola*), which is globally considered one of the most endangered mustelids and Critically Endangered by IUCN (Maran et al., 2011). Today, their population is restricted to isolated areas of north-eastern Europe (mainly Russia), south-eastern Europe (the Danube and Dniester deltas in Romania and Ukraine) and the apparently more recently established western Europe (south-western France and northern Spain). Here, this study examines the

appropriateness of conservation measures that are currently being implemented in the westernmost part of their range in the Iberian Peninsula.

Current conservation actions for the western European mink

The presence of this endangered species in France and Spain has encouraged the implementation of specific conservation programs, which have provided an opportunity for protecting both European mink populations and their habitats. The main actions involved are (i) restoring the freshwater ecosystems upon which the species depends; (ii) protecting the rivers that support European mink populations, by including them in the Natura 2000 network (a European Union-wide network of nature reserves); and (iii) controlling the growing population of American mink (*Neovison vison*), an alien species that may outcompete European mink where the two are sympatric. Many of these conservation measures have been supported by projects of the LIFE program, the major European Union funding body for environmental and nature conservation. Conservation efforts have been accompanied by legal protection measures, which resulted in the protection of the European mink both in France in 1981 (MEDAD, 2007) and Spain in 1990 (MMARM, 2009a). In both countries and over the last decade, the inclusion of the species on red lists motivated the development of

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national and regional strategies for the conservation of the species in the wild and the development of ex situ conservation programs (Maran et al., 2011). These plans involve a captive breeding program that aims to maintain the genetic diversity of the western population and reinforce their wild population by supplementing it with captive-bred animals (MMARM, 2009b).

The origin and current status of western European minks

The European mink was once widespread in central and eastern Europe. The species' presence in France was first reported in 1831 (de Bellefroid, 1999), and since then it has gradually expanded southwards, while at the same time disappearing from industrialized middle Europe (Youngman, 1982). During the 20th century, its range shrank to a few fragmented and largely disconnected areas (see Amstislavsky, Lindeberg, Aalto, & Kennedy, 2008 for a review of threats). It was first recorded in the Iberian Peninsula in 1951 (Rodríguez de Oндarra, 1955), having entered Spain from France through the Western Pyrenees from where it extended its range southwards in a slow but steady expansion (Fig. 1; Palazón et al., 2003; Zabala, Zuberogoitia, & Martínez-Climet, 2004). Local disappearances have also occurred, leading some authors to voice concerns about the danger of extinction of the European mink in the Iberian Peninsula (MMARM, 2009a; Palazón & Ceña, 2007). The Iberian range of European mink has expanded over the last half-century but with large fluctuations. For example, in Bizkaia (a 2217 km² area in the northwest of the European mink distribution in Spain) during the last two decades (1990–2013), the European mink spread quickly and again declined later (Zuberogoitia & Pérez de Ana, 2014). These fluctuations may be due to different regression factors, including deaths on roads and competition with American minks, which seem to be the key threats (Palazón et al., 2012; and a regional comprehensive review in Zuberogoitia & Pérez de Ana, 2014).

Along with the protection measures that have been implemented, research efforts have increased our knowledge of the ecology, behaviour and phylogeography of the western population of European mink. One important recent scientific advance concerns the origin of this population as either a long-term member of the local fauna overlooked until recently, or a recent colonizer from populations to the east with two alternative hypotheses, a natural colonization event or human-assisted arrival (Youngman, 1982). Despite sampling bias and difficulties identifying fragmentary fossil material (Davison et al., 2000), the lack of historical data and fossil records exclude the hypothesis of ancient European mink populations existing in Western Europe (Palazón et al., 2003; Youngman, 1982; Zabala et al., 2004). Therefore, the European mink in Western Europe can be considered a cryptogenic species; that is, a species that has neither demonstrably occurred naturally nor was introduced (Carlton, 1996). Nevertheless, both Youngman (1982) and Maran (2007) proposed the westward expansion of central European populations as the most likely scenario, without regard to human-assisted arrival.

At the end of the 20th century, molecular techniques for the study of wild populations boosted the study of the historical biogeography of the European mink. Since the first analyses of the genetic background of the species, various studies have used increasingly precise approaches that have provided significant insights into the evolutionary history of mink populations. In the latest and most comprehensive studies, Michaux et al. (2005) and Cabria (2009) analyzed the genetic structure of the three extant populations of the European mink, aiming to provide data to aid in developing the best strategies for their conservation. They concluded that the three European mink populations can be regarded as a single population that recently became fragmented, and that

they therefore should not be considered as “distinct population segments” (see USFWS, 1996). More precisely, they found that genetic variation is not geographically structured among the three European mink populations, and that there is no reason to believe that such populations have undergone long periods of independent evolutionary history. Regarding the status of western mink populations, an analysis of mitochondrial DNA variation (using control region sequences) found only one haplotype in western Europe, which was not shared with eastern populations and only differed from several eastern haplotypes by a single nucleotide out of 731 (Michaux et al., 2005). The northeastern population was much more diverse, with thirteen different mtDNA haplotypes (Cabria, 2009), while the southeastern population showed an intermediate level of genetic variation between the two (with four haplotypes). Microsatellite markers (Cabria, 2009; Michaux et al., 2005) also showed lower diversity in the western population (total number of alleles $N_A=32$, number of private alleles $P_A=3$, allelic diversity $A=2.91$ and observed heterozygosity $H_O=0.336 \pm 0.161$) than in the southeastern and northeastern populations ($N_A=35$, $P_A=2$, $A=3.18$ and $H_O=0.464 \pm 0.17$ and $N_A=59$, $P_A=20$, $A=5.36$ and $H_O=0.559 \pm 0.15$, respectively), which led the authors to conclude that this population was most likely recently founded by a few colonizers and ‘possibly a human introduction’ (Michaux et al., 2005). However, the data were not definitive regarding whether colonization occurred naturally or was human-assisted.

Genetic considerations of western European mink

Isolated populations may lose genetic diversity owing to stochastic effects of genetic drift after population bottlenecks. Those circumstances force individuals to breed with close relatives and this may jeopardize population viability due to inbreeding depression (Crnokrak & Roff, 1999; Reed & Frankham, 2003). Although the western European mink population has reduced genetic diversity, its range in Spain is expanding. Hence, there is currently no evidence to suggest that they have low fitness through inbreeding, although inbreeding effects on population dynamics may be masked by environmental and demographic processes (Caro & Laurenson, 1994; Frankham, 2010a; Lande, 1988). Much evidence to date suggests that losses of quantitative variation in expanding introduced populations may be minimal compared with losses of molecular variation (Dlugosch & Parker, 2008).

Refocusing Iberian conservation strategies

The combined insights into the distribution and phylogeography of the European mink suggest that it is a new addition to Iberian fauna and that the species is expanding its range in Spain. The genetic diversity of the western population has a signal consistent with a recent founder effect (low mtDNA and nDNA diversity) from a few individual founders. This perspective on the status of the species should prompt careful consideration of whether ongoing actions and plans for the separate conservation of this species in southwestern Europe are appropriate. In particular, the genetic data and expanding border range raise two important questions. First, are ex situ conservation programs appropriately designed? A captive breeding program aimed at preserving the western stock of European mink (MMARM, 2009a) is questionable for two reasons: the idea that this population may be considered an evolutionarily significant unit or distinct population segment has been refuted by molecular data, and it is characterized by lower neutral marker diversity than European minks from other regions, as is typical of recently founded populations (see Dlugosch & Parker, 2008). If the ex situ conservation program aims to maintain the genetic variability of the species as a whole, it seems inappropriate to develop

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