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Management of Wild Ungulate Populations in Italy: Captive-Breeding, Hybridisation and Genetic Consequences of Translocations

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ABSTRACT

Captive-reproduced stocks of some species of ungulates (Artiodactyla), and particularly the red deer (*Cervus elaphus*), fallow deer (*Dama dama*), roe deer (*Capreolus capreolus*) and the wildboar (*Sus scrofa*) are more or less extensively translocated in Italy, mainly for local reintroductions or restocking of exploited wild populations. However, captive breeding often involves the reproduction of non-indigenous individuals or the production of artificial hybrids. Consequently, translocations of captive-reproduced ungulates are of concern for the conservation of indigenous populations and gene pools. The impact of translocations should be evaluated within the background of the growing knowledge on population genetic and phylogeographic structure of ungulates. Molecular genetic markers are being used to map geographic genetic diversity, and reconstruct the phylogeographic history of natural populations (i.e., in the roe deer). Molecular makers are also used to detect the consequences of domestication and identify hybrids between wild and domesticated populations (i.e., in the wildboar), or to detect inter-specific hybridisation (i.e., between the red deer and wapiti). Hybridisation of wild and domestic pigs, and diffusion of hybrids in nature is widespread in Italy. Admixture of indigenous and non-indigenous roe deer stocks is also widespread. Therefore, conservation and management of indigenous ungulates calls for careful evaluation of captive-reproduced stocks.

Keywords: captive-breeding, genetics, hybridisation, translocations, wild ungulates

INTRODUCTION

Many wild populations of ungulates strongly declined during the last few centuries in several European countries, mainly in consequence of deforestation and over-hunting. Species which were widespread and probably distributed continuously in the past, were locally eradicated and, after the second World War (WWII), survived in patches of fragmented populations. For instance, the roe deer (*Capreolus capreolus*) was extirpated from most of its historical range in Portugal, Spain and Greece, it was totally eradicated from the western Alps and most of the Apennines in Italy. Also species that are now widespread showed strong demographic declines in the past, at the continental scale (i.e., the wildboar, *Sus scrofa*), or locally (i.e., the red deer, *Cervus elaphus*, which was completely eradicated in Italy). At the end of nineteenth century mountain ungulates were on the verge of extinction in Italy. The ibex (*Capra ibex*) and the endemic Apennine chamois (*Rupicapra pyrenaica ornata*) suffered dramatic population and genetic bottlenecks, and survived only thanks to active protection and translocations after WWII. Different is the history of the fallow deer (*Dama dama*), which went most probably extinct before the Holocene in Europe for natural causes, that is in consequence of climate changes during the last glaciation. All extant fallow deer populations in Italy and Europe originated from historical reintroductions of fallows surviving in the Near East. Also different is the history of the muflon (*Ovis musimon*) and the Montecristo goat *(Capra aegagrus*), domesticated populations of sheep and goat ancestors, which were anciently introduced in Sardinia and Montecristo where they became feral (Spagnesi and De Marinis, 2002).

The decline of exploited populations has been contrasted with reintroduction and restocking projects, which sometime used captive-reproduced individuals. Some species of ungulates are reproduced in captivity, and captive-reproduced stocks, particularly red deer, fallow deer, roe deer and wildboar, are more or less extensively used for local reintroductions or restocking of wild populations. However, captive breeding often involves the reproduction of non-indigenous individuals or the production of artificial hybrids. For instance, red deer stocks that are farmed in Italy and in other European countries might be hybridised with sika or wapiti deer. It is well known that the diffusion of wildboar and domestic pig hybrids is widespread in Italy. Admixture of indigenous and non-indigenous roe deer stocks is also widespread in central and southern Apennines. Consequently, translocations of captive-reproduced ungulates are of concern for the conservation of indigenous ungulate populations and gene pools.

Molecular genetics offer the possibility to develop and apply diagnostic markers which can be used to assess the genetic status of captive-reproduced stocks and evaluate the impact of translocations on wild populations of ungulates. The impact of translocations should be evaluated within the background of the population genetic and phylogeographic structure of ungulates. Molecular genetic markers can be used to map geographic genetic diversity, and reconstruct the phylogeographic history of natural populations, to detect inter-specific hybridisation, or the consequences of domestication and identify hybrids between wild and domesticated populations (Avise and Hamrick, 1996). I will summarize results from two case studies, the first one involving the consequences of translocating non-indigenous roe deer in the Italian Apennines; the second one showing the consequences of restocking natural populations with captive-reared wildboars.

PHYLOGEOGRAPHY AND CONSERVATION OF THE ROE DEER

The roe deer includes two species, the smaller European *C. capreolus* (distributed in western Europe), and the larger Siberian *C. pygargus* (distributed in Asia and eastern Europe) roe deer (Randi *et al.*, 1998). The European roe deer is widespread across the continent, with populations distributed in former Mediterranean glacial refuges (Sierra de Cadiz in southern Spain, southern Apennines in Italy, southern Balkans), and in northern regions (Scandinavia) or mountain ranges (the Alps and Pyrenees) that were glaciated until the Holocene (ca. 10 000 years ago). Roe deer are highly adaptable, living in broadleaved forests, ecotonal strips and agricultural areas, in mountains or in lowland regions. Deforestation and over-hunting led to decline and eradication of local roe deer populations, particularly in central and south Iberia, in the western Italian Alps and Apennines, and in

Greece. After WWII some populations began to expand naturally, following the expansion of forests in mountains, or colonising agricultural lowlands. Population decline was successfully hindered by reintroductions, which were often carried out using non-indigenous roe deer. All extant populations in the western Italian Alps and many populations in the northern Apennines were reintroduced or restocked in the last few decades. Subspecies distinction in roe deer is uncertain. Two subspecies were described in the past: the Italian roe deer *C. c. italicus* (Festa, 1925), distributed in southern Italy, and the Spanish roe deer *C. c. garganta* (Meunier, 1983), from central-southern Spain. The identity of the Spanish subspecies is doubtful. Populations of *C. c. italicus* showed unique mtDNA haplotypes (Randi *et al.*, 1998), distinctive microsatellites genotypes (Randi *et al.*, 2004), and skull morphometry (Montanaro *et al.*, 2003). Patterns of geographic diversification in roe deer have been investigated using mitochondrial DNA (mtDNA) and microsatellite markers, aimed to identify extant population genetic units; and infer the consequences of natural and anthropogenic factors in shaping current population structure. Phylogenetic mtDNA trees identify three main mtDNA groups, which could have originated in Iberia (clade West and Central) or in the Balkans (clade East). Microsatellite data confirmed these population subdivisions. Clade West apparently contributed little to the current genetic diversity in central Europe, which is mainly due to the widespread distributions of clade East and Central. Some clade West mtDNA types (haplotypes) were sampled in the Italian Alps, suggesting a postglacial colonization route from Iberia towards the Mediterranean coasts, or the presence of ancestral haplotypes in the Alps. The restricted distribution of clade East haplotypes supports the existence of an eastern glacial refuge, from which, however, roe deer did not disperse extensively westward. In contrast, the widespread distribution of clade Central haplotypes in the Balkans, central and north Europe, Apennines, Alps (although some haplotypes could have been translocated in the western Alps), and Iberia, supports the existence of distinct refugial populations that contributed extensively to the recolonization of Europe. These findings indicate that roe deer dispersed in Europe from multiple refuges. A distinct subclade joined all the haplotypes from populations of *C. c. italicus* (Castelporziano, Gargano and Orsomarso), as well as other samples collected from neighbouring central and southern Apennine localities. The origin of this clade is the likely consequence of population isolation/expansion in a southern Italian refuge during the Last Glacial Maximum (LGM)/early Holocene. These vicariant populations evolved distinctive diagnostic traits, which support the validity of subspecies *C. c. italicus*. However, mtDNA haplotypes of *C. c. italicus* were detected also in roe deer sampled in north Tuscany and Emilia-Romagna, north of the putative distribution limits of the Italian subspecies, where they are admixed with roe deer bearing haplotypes belonging to clade Central. The original distribution of *C. c. italicus* is unknown, because roe deer in the Apennines were already largely eradicated before WWII. Molecular and morphometric data now suggest that populations of *C. c. italicus* persisted not only in the protected areas of Castelporziano, Gargano and Orsomarso, but also in southern Tuscany, and probably in small remnant populations along the ridge of the Apennines, in Tuscany and Emilia-Romagna. Alternatively, or concomitantly, roe deer bearing *C. c. italicus* mtDNA haplotypes might have recently expanded their range towards northern Tuscany and Emilia-Romagna. In these areas, roe deer populations are currently admixing, also in consequences of reintroduction and restocking operations, which are threatening the integrity of *C. c. italicus*.

CAPTIVE BREEDING AND HYBRIDIZATION OF WILD AND DOMESTIC PIGS

The Eurasian wild boar (*Sus scrofa*) is one of the most widely distributed terrestrial mammals, with an uncertain number of poorly described subspecies. The wild boar is an economically very important species, which played crucial roles in the development of prehistoric hunting and agricultural societies. Nowadays, the wild boar is still a primary food resource for indigenous human communities in South East Asia, and it is a prominent sport hunting species throughout the world (Oliver, 1993). Agriculture and human-induced habitat transformations, game management practices and translocations deeply affected the recent demographic trends and the genetic composition of wild boar populations in Europe. Domesticated pigs have been introduced in the USA, Australia, New Zealand, New Guinea and on many oceanic islands, where often they originated feral pest populations, which damage crops and threaten indigenous plant and animal species. In South East Asia and Europe, and particularly in the Mediterranean Basin (central Italy, Sardinia, Corsica), wild and domestic pigs are crossed, either if intentionally or by traditional rearing in semi-wild conditions, thus originating hybrid stocks that might pollute the genetic integrity of indigenous wild boar populations. Genetic data concordantly suggested the existence of a main phylogeographic splitting between Asian and European wild boar populations (Randi, 1995). Mitochondrial DNA studies showed that haplotypes in domestic breeds were assigned to both Asian and European groups, suggesting multiple domestication, with cases of subsequent hybridisation, from genetically distinct wild boar populations (Giuffra *et al.*, 2000). Giuffra *et al.* (2000), using partial mtDNA sequences, identified three distinct mtDNA clades, which were distributed mainly in Asian (clade A1), or in European wild and domestic pigs (clades E1 and E2). Haplotypes in clades A1 and E1 were geographically widespread respectively in South East Asia and western Europe, while haplotypes in clade E2 were found only in some wild boars collected in central Italy. These E2 haplotypes were described for the first time in Italian wild boars (Randi *et al.*, 1996) sampled in Tuscany and Lazio, that is within the distribution range of the endemic Maremma wild boar subspecies (*S. s. majori*). New mtDNA data allowed us describing the geographical distribution of the unique wild boar mtDNA haplotypes that were detected only in Italy (Tabarroni *et al.*, in prep.). Wild boars sampled in Europe were split into two deeply divergent clades: clade E1 included all the wild boars sampled in EU and in Israel, while clade E2 included exclusively wild boars sampled in Italy, thus confirming the presence of private mtDNA haplotypes in Italian wild boars. Nowadays, haplotypes in the Italian clade E2 are always distributed in populations showing also haplotypes belonging to the widespread EU clade E1. We assume that wild boar populations went fragmented and diversified in allopatry during the last glaciation, and that expanded after the LGM. The restricted geographic distribution of the Italian clade E2 suggests that wild boar populations survived the LGM in a southern refuge in peninsular Italy, and that they did not cross the Alps during postglacial population expansion. E2 haplotypes might be not present in the gene pool of modern domestic pigs. The widespread occurrence of haplotypes of clade E1 in Italy suggested ancient mtDNA polymorphisms, postglacial colonization of wild boars from central Europe across the Alps, or recent artificial translocations and restocking that might have led to population admixture in Italy. A scenario of artificial admixture of formerly allopatric populations seems more plausible. Haplotypes of the Italian clade E2 were not found in the three most meridional populations (Puglia, Calabria and Sardegna). Wild boar populations in the Adriatic side of southern Italy were eradicated between 1930 and 1950, and were recently reintroduced using non-indigenous individuals. Wild boars in Sardegna were introduced by humans a few thousands of years ago, probably using stocks from the Near East or North Africa (note that mtDNA haplotypes found in wild boars sampled from Israel clustered within clade E1). Therefore, it seems likely that surviving indigenous wild boars (subspecies *S. s. majori*) expanded recently from refuge areas, colonizing most of central and northern Italian Apennines and parts of the western Italian Alps. Expanding Italian wild boars could have admixed with central European wild boars expanding from France into the western Alps, or with non-indigenous wild boars in central Italy. In this case, unwise management of wild boar populations (over-hunting, restocking using non-indigenous wild boars, cross-breeding in captivity with domestic pigs and non-indigenous wild boars, release of captive-reared admixed stocks, translocations of wild boars from different regions) might have lead to widespread genetic pollution of the local populations and of the endemic Italian subspecies. Additional genetic analyses with nuclear markers (microsatellites) and population admixture analyses, could contribute to further elucidate the recent history and current population structure of wild boars in Italy.

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