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The unique Mesola red deer of Italy: taxonomic recognition (*Cervus elaphus italicus* nova ssp., Cervidae) would endorse conservation[#]

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Abstract
Most likely, the red deer *Cervus elaphus* Linnaeus, 1758 from the Bosco della Mesola Nature Reserve are the last autochthonous red deer in the Italian peninsula. In the 20th century, they nearly became extinct and have only recently recovered to higher numbers (at least *c.* 150 head in 2010). Apart from their historical relevance to the Italian fauna, they are also evolutionarily distinct at both the genetic and the morphological level. However, taxonomically, they are classified as part of the Central European red deer subspecies (*Cervus elaphus hippelaphus*), which encompasses most of the red deer from the European mainland. While we are fully aware of the high degree of arbitrariness of subspecific designations, it is also a fact that taxonomic recognition supports conservation, because subspecies are a legal category whereas other designations (such as evolutionarily significant units, ESUs) are not. We therefore argue that the Mesola red deer should be assigned to a subspecies of their own, and give an official description of *Cervus elaphus italicus* nova ssp., including the designation of a holo- and a paratype specimen. Given the evolutionary status of the Mesola red deer, subspecific recognition is certainly much better founded than is the case for many other so-called subspecies in present red deer taxonomy.

Keywords: Cervus elaphus*, conservation, Mesola, red deer, taxonomy*

Introduction

Taxonomy plays a vital role in conservation in that taxonomically recognised populations may also be granted legal status as protected species or subspecies. Assessment by the International Union for Conservation of Nature (IUCN), for instance, is only done for taxa with a name, i. e. species or subspecies. While the subspecies, just like supraspecific categories, is ultimately an arbitrary designation which can introduce a bias in or even severely skew quantitative approaches that use categories as proxies for biodiversity (e.g. Zachos 2011), it is obvious that many intraspecific units have benefited from their being labelled a subspecies of their own. If the subspecific status is supported by the occurrence of unique hereditary characters (be they molecular, physiological or phenological), then this taxonomic recognition will indeed represent a portion of the evolutionary legacy and potential at the intraspecific level. In this view, subspecies, rather than reflecting objective entities that differ from other intraspecific units that are not granted subspecific status, can be seen as a means to an end, namely emphasizing the intrinsic value of a (group of) population(s) for the conservation of species-wide diversity. Thus, if a species is subdivided into, say, three subspecies, this is not to say that these three subspecies are directly comparable to one another (let alone subspecies of other species!), but it means that research has come up with good arguments that the three groups deserve consideration and, if necessary, protection in their own right. It could be argued that the concept of evolutionarily significant units (ESUs, see Crandall et al. 2000 and references therein) has been introduced to guarantee the conservation of

intraspecific diversity without constructing an arbitrarily delimited taxon (Ryder 1986) and, indeed, the ESU concept owes its very existence to the shortcomings of the subspecies concept. For example, populations will doubtless be more likely to gain subspecific status if they differ from their conspecifics in conspicuous external traits (colour, size etc.) rather than less visible, but evolutionarily perhaps equally important, traits, simply because we as humans primarily rely on visual perception. This introduces a bias in what types of diversity are acknowledged and, consequently, protected. However, ESUs, apart from disagreements over how to define them, are not *named* (in a taxonomic sense), but it is names that guarantee legal protection and public perception. In the case of red deer (*Cervus elaphus*), this is exemplified by the Tyrrhenian red deer (*C. e. corsicanus*), endemic to Sardinia and Corsica, and by the North-African Barbary stag (*C. e. barbarus*), which are both acknowledged as subspecies and have therefore received legal status, including an official IUCN assessment and extensive conservation measures after recovery from the brink of extinction in the second half of the 20th century (Hmwe et al. 2006; Hajji et al. 2007, 2008; Zachos & Hartl 2011). These two subspecies combined make up one of three mitochondrial DNA lineages found in Europe; the other two are (i) a western lineage from Iberia through western and much of Central Europe to parts of eastern Europe; and (ii) a (south)eastern lineage that occurs from the Balkans to eastern and eastern Central Europe (Skog et al. 2009; Niedziałkowska et al. 2011; Fickel et al. 2012). Mesola red deer, on the other hand, are officially lumped, together with most European mainland red deer, into the subspecies *C. e. hippelaphus*, thus being of no particular concern taxonomically, although they possess a unique mitochondrial haplotype (whose position with respect to the western and eastern lineages is ambiguous, see Skog et al. 2009 and Niedziałkowska et al. 2011) and, most likely, they represent the last autochthonous red deer of the Italian peninsula (Ghigi 1911; Mattioli 1990; Mattioli et al. 2003). Their genetic diversity shows the typical depletion following a severe bottleneck and ranks among the lowest found in European red deer so far (Zachos et al. 2009; Zachos & Hartl 2011).

In this paper, we summarise the knowledge on the Mesola red deer and describe it as a new subspecies to further enhance the protection of this unique subgroup of *Cervus elaphus*.

History of the Mesola red deer

Toward the end of the early Middle Ages, the red deer was still a common species in almost all the Italian mainland (Mattioli 1990). During the late Middle Ages and the Renaissance, due to gradual deforestation and direct persecution, its distribution range shrank considerably. Red deer were forced to take refuge in some remote parts of the coast and in the mountains. Along the northern Adriatic coast, red deer survived in an almost continuous forest extending from the Po river delta southwards to the surroundings of the village Cervia near Ravenna, in an area comprising 90 km of sandy coast often bordered on the west by swamps, freshwater lagoons and other wetlands (Lovari & Nobili 2010). The northernmost forest tract, surrounded by a 12-km wall, was used by Duke Alfonso II Este as a hunting park from 1583 to 1597. In 1598, it was completely dismantled and all deer were killed. The contiguous forest tract, owned by the Pomposa Abbey and named Gran Bosco, originally covered 5000 hectares but was gradually reduced by the spread of flooded areas and deforestation, and only survived as the present Mesola Wood. Malaria-infested swamps on three sides and the sea in the east made the wood almost inaccessible for centuries, effectively protecting its red deer (Lovari & Nobili 2010). Another forest tract, named Bosco Eliceo, near the present village of San Giuseppe, was transformed into vineyards in 1675. The southernmost part of the coastal forest, known as the Pinewoods of Ravenna, has been partially preserved until today, but the last red deer were exterminated in the early 18th century. After the disappearance of red deer from the Alps and the Apennines at the beginning of the 20th century, the relict population of Mesola Wood must have remained as the only native red deer of the whole Italian peninsula (Ghigi 1911; Mattioli 1990; Lovari & Nobili 2010). In 1911, the population size of red deer was roughly estimated at about 200 animals, and it fluctuated between 160 and 300 between 1922 and 1938. Because the forest was managed as a hunting estate, every year, 25–40 red deer were harvested. From 1943 to 1947, the forest was heavily exploited and the red deer were on the brink of extinction with possibly only about 10 individuals remaining (Mattioli 1990; Lovari & Nobili 2010). In 1954, the National Forestry Service acquired the wood and began to actively protect its red deer. In 1970, their number was estimated at 40, increasing to 100 by 1980 after which the population declined again. In 1982, population size was about 90 animals, going down to a minimum of 54 in 1992. After that, red deer recovered again, particularly after the implementation of habitat amelioration measures (see below) and numbered 67 in 1999, 120 in 2006 and at least

c. 150 in 2010 (Mattioli et al. 2003; Lovari & Nobili 2010; Ferretti & Mattioli 2012).

Morphological characteristics of the Mesola red deer

A comparison between body weights, external somatic measures, craniometry and antler biometry of Mesola red deer and those of other European red deer showed that the former fall within the small-sized European populations (e.g. the Iberian *C. e. hispanicus* and the Tyrrhenian *C. e. corsicanus* red deer, of the Mediterranean habitats and the Scottish red deer of the food-restricted moorlands; Mattioli et al. 2003; Mattioli & Ferretti 2014). In 1981–1999, mean body weights of adult Mesola red deer were 108.7 kg (standard deviation = ± 15.5 kg, stags) and 76.2 kg (± 10.5 kg, hinds), i.e. 15–35% lower than those of other red deer from northern and central Europe (Mattioli & Ferretti 2014). Mean external linear dimensions of Mesola red deer are reduced by at least 8–15% compared with other European populations (Mattioli & Ferretti 2014). The Mesola red deer is also characterized by a low stature, because of its slight but significant shortening of the limbs (Mattioli & Ferretti 2014), similar to the Tyrrhenian red deer (Table I).

In Mesola red deer, the relative production of antler bone tissue does not appear to be different from that of other European red deer (Mattioli & Ferretti 2014). Antlers are small (adult stags, mean main beam length: 70.2 cm; mean beam weight: 643.6 g), scarcely branched (mean number of tines/adult antler pair: 6.2 ± 1.7), with short trez tines and a modest spread (Mattioli et al. 2003; Mattioli & Ferretti 2014). Bez tine and crown are rare and present almost exclusively in fully mature stags (2.2% and 3.6% of antler beams of adult stags, respectively, Mattioli & Ferretti 2014). The rudimentary crown can be cup-like, the most frequent configuration in Europe, or fan-like, with three short transverse tines medially arising from different points of the main beam, which is a peculiar shape (Figure 1;

Table I). In 1996, environmental improvements (culling of fallow deer, recurrent mowing and reseeding of pastures and supplementary feeding during winter) were introduced to the Bosco della Mesola Nature Reserve, leading to favourable effects on physical condition and population dynamics of red deer (Mattioli et al. 2003; Ferretti & Mattioli 2012). After the introduction of these habitat improvement measures, despite the infrequent re-occurrence of bez tines and crowns after decades, the architecture of antlers continued to be rather simplified and scarcely variable (e.g. the mean number of tines/antler pair, in adults, increased from 5.4 to only 6.7; Mattioli & Ferretti 2014).

The colour pattern of the rump patch of Mesola red deer is similar to that of the central European populations. However, in Mesola red deer, the summer coat of both sexes has a slight but clearly visible spotting in every age class (Figure 2; Table I). This spotting is rarely present in adult individuals of other European red deer populations (e.g. *c.* 10% of individuals in an area of eastern Germany; Wagenknecht 1986). Conversely, it is frequent in the Caucasian and Iranian *C. e. maral* and in yearlings and subadults of the North African *C. e. barbarus* (Meyer

Figure 1. Mesola stag with antlers showing the peculiar fan-like crown shape. Picture by Stefano Mattioli.

Table I. Morphological and genetic comparison among the three subspecies of red deer occurring in Italy.

Trait		*Cervus elaphus hippelaphus*	*C. e. corsicanus*	*C. e. italicus* nova ssp.
Genetics	Genetic lineage	Lineages A and C	Sardinian/African lineage B	Intermediate between western and eastern lineages A and C
Morphology	Summer coat	Reddish brown	Dark reddish brown	Reddish brown with yellowish spots
	Height at withers	Normal	Proportionally low	Proportionally low
	Antler crown	Common, typically cup-like and well branched	Rare, three-pointed and cup-like, sometimes with a small palmation	Rare, three-pointed, cup-like or fan-like

Figure 2. Hind group with a calf. Note the summer coat with spots. Picture by Norino Canovi.

1972; Dolan 1988). Spotting is generally absent in *C. e. corsicanus* (S. Mattioli, pers. obs.).

Reduced sexual size dimorphism, slow body growth and delay in antler initiation of stags are typical traits of resource-restricted deer populations ("maintenance phenotypes", e.g. Tyrrhenian, Iberian, North African and Scottish populations, Geist 1987, 1998). It remains to be determined to just what extent the body size of Mesola red deer is genetically fixed as opposed to environmentally dependent phenotypic plasticity. High nutrition plane experiments will permit us to fully test the potential of this population in terms of body size and growth. The study of vocal characteristics of roars and the comparison with other European populations could help to further elucidate its taxonomic status, as tested in the Tyrrhenian and Iberian red deer (Kidjo et al. 2008; Frey et al. 2012; Passilongo et al. 2013), although the phenology of animal vocalisations is also influenced by the habitat where they have lived.

Genetic distinctness of the Mesola red deer

The red deer of Mesola Wood are probably the only red deer native to mainland Italy, since all other extant populations were founded either by immigrants from the neighbouring countries (central and eastern Alps), or by animals reintroduced artificially (western Alps and Apennines) (Mattioli et al. 2001). Nevertheless, the current Mesola population is facing a serious extinction risk due to small size (a minimum of 148 individuals in 2010, Ferretti & Mattioli 2012) and geographical isolation. Strategies for the conservation and management of this deer have been developed since the end of the 1990s, with the purpose of increasing the chances for population long-term survival (Mattioli et al. 2003). In this

respect, assessing the genetic diversity of the population was immediately regarded as a priority for the action plans in progress. A first genetic investigation was conducted at the biochemical level (Lorenzini et al. 1998), aiming at evaluating the population's genetic variability, as well as the differentiation between Mesola and other red deer populations from Italy. Polymorphisms at 43 protein loci revealed low genetic variation, along with an excess of homozygosity indicative of inbreeding, and suggested that lack of gene flow and small effective population size were the main causes of genetic depletion. Prolonged geographical isolation, repeated bottlenecks and slow recoveries, following habitat loss and overhunting, have marked the demographic history of this red deer over the last centuries, with a clear impact on the population genetic structure.

When molecular studies were conducted to evaluate the level of mitochondrial (mt) DNA variation, the genetic results remained unchanged. One single mtDNA haplotype was obtained from both the analysis of restriction fragment length polymorphisms of four mitochondrial segments (Lorenzini et al. 2005) and sequencing of 531 base pairs of the control region (Hmwe et al. 2006), disclosing no mitochondrial variability for the Mesola red deer. A comprehensive picture of the population genetic make-up was obtained using nuclear microsatellite loci (Hmwe et al. 2006; Zachos et al. 2009). This class of highly polymorphic, single-locus markers is routinely used to assess levels of genetic variability in small, endangered populations. Because of their high mutation rates, microsatellites are excellent markers to study genetically depauperate populations which harbour little or no variation at allozyme loci or mtDNA. The analysis of up to 20 microsatellites revealed an extremely low extent of genetic variation also at the nuclear level compared to the rest of the European populations. Thus, biochemical and genetic (both mitochondrial and nuclear) data converge towards the same alarming scenario, emphasising that the genetic potential of the current population of Mesola red deer is very limited, and the capability to cope with environmental changes could be greatly reduced.

Evidence for the genetic uniqueness of the Mesola population is demonstrated by the presence of a mitochondrial haplotype which is not shared with any other European population of red deer studied so far (Lorenzini et al. 2005; Hmwe et al. 2006; Zachos et al. 2009; Table I). As to the phylogeography, recent studies investigated the genetic relationships of this private haplotype with respect to the western and eastern lineages observed for red deer

in Europe, but safe conclusions regarding its placement on the phylogenetic trees were not reached (Lorenzini et al. 2005; Skog et al. 2009; Niedziałkowska et al. 2011). It remains unclear if the Mesola haplotype belongs to one of the two lineages or, alternatively, if it may represent a remnant refugial lineage which was formerly widespread in the Italian peninsula prior to the fragmentation and, ultimately, the extinction of populations caused by human activities.

Some (sub)species of medium/large mammals from the central-southern areas of Italy differ substantially from their northern counterparts, showing high genetic divergence, e.g. the roe deer *Capreolus capreolus italicus* (Lorenzini et al. 2002), the Apennine chamois *Rupicapra pyrenaica ornata* (Nascetti et al. 1985; Pérez et al. 2013), the red fox *Vulpes vulpes* (Frati et al. 1998), and the Italian hare *Lepus corsicanus* (Pierpaoli et al. 1999). A primary role in the differentiation of these taxa was probably played by the refuge areas of the Mediterranean basin during the Quaternary (cf. Bilton et al. 1998; Frati et al. 1998; Hewitt 2000). Similarly, the Mesola red deer may represent one such relevant endemism, present at the northern edge of central-southern Italy, which differs genetically from both the Alpine and central European populations. Further research, based on the alignment of longer mitochondrial sequences and coding genes and the analysis of ancient DNA from (sub)fossil Italian red deer might eventually solve the enigma of the phylogeographic status and origin of this population.

Taxonomic accounts

Taxonomic recognition of the Mesola red deer as a new subspecies

Based on the morphological, genetic, geographical and historical uniqueness outlined above and in light of the need for conservation actions, we propose to grant taxonomic status to the Mesola red deer and assign it a subspecific name (see also Table I):

Cervus elaphus italicus, *new subspecies*

Holotype. Adult male skull with eight-pointed antlers, deposited in the Mammal Collection of the Natural History Museum Vienna in Austria (collection number NMW 68166, Figure 3a). Collected in September 2012, donated to the Natural History Museum Vienna by Giovanni Nobili from the Corpo Forestale dello Stato, Ufficio Territoriale per la Biodiversità di Punta Marina (Ravenna).

Figure 3. (**a**) Holotype of *Cervus elaphus italicus* (skull with antlers of a Mesola stag, NMW 68166 of the Mammal Collection of the Natural History Museum Vienna). (**b**) Paratype of *Cervus elaphus italicus* (skull of a Mesola hind, NMW 68167 of the Mammal Collection of the Natural History Museum Vienna; mandibles not shown).

Description of holotype. Age around 14 years. Condylobasal length 354.3 mm; ecto-orbital width 159.1 mm. Antler beam length 87.6 cm (left), 84.7 cm (right).

Paratype. Adult female skull, deposited in the Mammal Collection of the Natural History Museum Vienna in Austria (collection number NMW 68167, Figure 3b). Collected in March 2013 and donated to the Natural History Museum by Giovanni Nobili from the Corpo Forestale dello Stato, Ufficio Territoriale per la Biodiversità di Punta Marina (Ravenna).

Description of paratype. Age around 8 years. Condylobasal length 302.4 mm; ecto-orbital width 135.8 mm.

Diagnosis. Small-sized red deer, with adult stags averaging about 110 kg and adult hinds about 75 kg (Mattioli 1990; Mattioli et al. 2003; Mattioli & Ferretti 2014). The stature is low, with the mean height at withers and the hind-foot length being, respectively, 57–58% and 26–27% of the head-trunk length, against a standard of about 62–64% and 29–30% (Mattioli et al. 2003; Mattioli & Ferretti 2014). Antlers are relatively small and scarcely branched (Mattioli 1990, 1993; Mattioli et al. 2003; Mattioli & Ferretti 2014). In adult stags the mean beam length is about 70 cm, and the mean number of tines per antler pair is around six. The trez tine is relatively short, and the bez tine and crown are rare. The crown can be fan-like, with three short tines arising from different points of the upper part of the antler beam. The summer coat is characterised by yellowish spots. Genetically, *C. e. italicus* is also unique in that it harbours a single exclusive mitochondrial control region DNA haplotype whose phylogenetic position is somewhat unclear but it seems to be intermediate between the two major mtDNA haplogroups (western and eastern, usually abbreviated A and C, respectively) of European red deer. Genetic diversity is very low in *C. e. italicus* when compared with other European red deer populations. Observed and expected heterozygosities averaged over 20 nuclear microsatellite loci were 0.50 and 0.61, respectively, in a sample of 25 specimens (Zachos et al. 2009).

Distribution. Restricted to the Nature Reserve "Bosco della Mesola" in the province of Ferrara, Italy, at the southern edge of the Po river delta.

Conservation plans and future perspectives

The Mesola red deer have a notable relevance from a zoogeographical, ecological and historical point of view. Nevertheless, the population is highly endangered, and this calls for immediate conservation actions. Recently, a Population Viability Analysis (PVA) was conducted (Zachos et al. 2009) to test for susceptibility to extinction of this population, given the actual demographic, genetic and biological data. The results showed that the population is highly vulnerable to environmental stochasticity and particularly prone to inbreeding depression due to its narrow distribution, small size and genetic depletion. However, the simulations revealed that appropriate conservation measures would prevent further, critical decay of genetic variability and could considerably limit the extinction risk. Some management actions (for example habitat ameliorations and reduction of competition with fallow deer that live

in the same area) have already been implemented in the last two decades, with positive consequences on the population (Mattioli et al. 2003). When the data pertaining to these measures were included in the PVA simulations, the population viability increased significantly, as did the probability of survival (Zachos et al. 2009). Thus, the adoption of relevant conservation measures positively affects the long-term chances of survival and can save this important population from ultimate extinction.

As suggested by the PVA simulations, one of the most effective conservation measures for the Mesola red deer is the establishment of at least one newly founded population, in addition to the main population. Subpopulations should be established in suitable areas, i.e. coastal woods or lowland forests, and managed as a metapopulation. This could significantly counteract the detrimental effects that any catastrophic event, for example an epidemic, would have on one single population. Genetically selected founders should be translocated into the new subpopulations and gene flow among them should be maintained through the exchange of animals, with the aim of counteracting genetic drift, preventing further loss of genetic diversity, and minimising the detrimental effects of inbreeding. A genetic monitoring of both the main population and its derived nuclei should be performed to survey genetic variability in future generations. In addition to genetic data, morphological data should also be collected as it has been shown that malformations may be an easily visible sign of inbreeding depression in red deer (Zachos et al. 2007).

Recently, a National Conservation Plan for the conservation of the Mesola red deer has been developed by the Italian Ministry of Environment in cooperation with the National Forestry Service (Lovari & Nobili 2010). The available information on the history, biology and ecology of this deer has been collected and evaluated in order to assess the threats to the population and to suggest main conservation measures. Taxonomic recognition of the Mesola red deer was regarded by the Action Plan as one important step to focus the attention of the relevant agencies which potentially play an active role in the preservation of this important population through public awareness and funding. Notwithstanding the above-mentioned theoretical shortcomings of the subspecies concept in general, we therefore suggest to introduce to the literature an official taxonomic name for the Mesola red deer: *Cervus elaphus italicus*. By this, we hope that this unique population will receive the attention it deserves and, given its morphological as well as genetic distinctness, this subspecific designation is doubtless in much more

accordance with the evolutionary history of the red deer than many, if not most, of the huge number of suggested subspecies (see Grubb 2005) within this species.

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