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Mammal endemism in Italy: a review

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SUMMARY

Although there are various checklists of Italian mammals, there is not yet a synthesis of those mammals that are endemic to Italy. Therefore, we provide for the first time a detailed review on Italian mammal endemic species including endemic taxa deserving additional studies. This review is based on the most recent taxonomic revisions obtained using Scopus and Google Scholar databases. We also considered the age of endemic species. Some aspects of mammalian conservation are also provided and discussed.

INTRODUCTION

The terrestrial world was sub-divided into 14 biomes, and one of these corresponds to the “Mediterranean Forest, Woodlands and Shrub” (Olson et al. 2011) to which Italy belongs. A high proportion of Mediterranean animals are unique in this biome, with a quarter of mammal species being endemic (Cuttelod et al. 2008, Maiorano et al. 2013).

According to Bilton et al. (1998) Mediterranean peninsulas can be considered areas of endemism, in particular for small mammal populations, because they may represent long-term isolates undergoing allopatric speciation.

Italy is one of the European countries with the highest species richness and endemism (Minelli et al. 2006). In the past, different checklists of

species of Italian mammals have been published, which also included the endemic species (e.g. Amori et al. 1993, Amori et al. 1999). However, an exclusive work on endemic species has never been produced. Therefore, the aim of this work is to provide for the first time a detailed review on Italian mammal endemic species including endemic taxa deserving additional studies.

An updated checklist of the Italian endemic mammals seems necessary to incorporate some recent taxonomic revisions and also because previous lists include different numbers of endemic species (e.g., Amori et al. 1993: n = 4, Amori et al. 1999: n = 5, Carpaneto and Vigna Taglianti 2009: n = 9).

In particular, the most recent checklist of Italian mammals published by Gippoliti (2013) was produced by strictly applying a phylogenetic species

concept, i.e. by considering “good species” all the formerly described subspecies for which the genetic data (mainly mtDNA data) showed some level of divergence. For this reason, the number of endemic species in Gippoliti (2013)’s review results considerably higher than in other lists with 24 endemic/near endemic taxa reported.

METHODS

This review is based on peer reviewed literature data included in the Scopus and Google Scholar databases. Since almost all the recent taxonomic decision taken for European species of mammals arose from genetic information, the search criteria to query the database include different combinations of four keywords: “mtDNA”, “mammal”, “Italy”, “phylogeography”. We considered only mammal species whose taxonomic status is explicitly reported in the recent literature (search period from 2009, date of publication of the checklist of Carpaneto and Vigna Taglianti (2009), to November 2017). We adopted the following terminology for the different terms of endemism: “endemic species” as those species that are clearly settled within the Italian borders; “near-endemic species” as those species that have (or may have) a small portion of their range outside the Italian borders. Moreover, we reviewed also taxa that, considering the data at hand, could be considered good species but that deserve additional studies (“candidate endemic species”) and taxa historically considered problematic in terms of taxonomic definition (“cold cases”).

Species representing long evolutionary history are considered to deserve particular interest in conservation concern in comparison with species belonging to young lineages and thus representing shorter evolutionary history. In fact, the spatial extension of the range of endemic species alone (i.e. its size) ignores the substantial evolutionary and conservation implications that arise from the evolutionary distinctiveness of species (Mace et al. 2003; Redding and Moore 2006; Rosauer and Jetz 2015). Thus, we also extracted the age of endemic, near-endemic and candidate endemic species from published molecular phylogenetic/phylogeographic studies as the divergence time of the split between the endemic taxon and its sister species/group. We used phylogenies of single genera instead of multi-species supertrees (e.g. Bininda-Emonds et al. 2007) because many endemic species have been only

recently elevated to species rank and are not included in those supertrees.

RESULTS

Endemic species

Lepus corsicanus De Winton, 1898. This species is distributed in south-central Italy (the northern limit being marked by Elba Island on the Tyrrhenian coast and the province of Foggia on the Adriatic coast) and Sicily (Fig. 1). Sicilian populations show a genetic differentiation (mtDNA), probably due to isolation (Mengoni et al., 2015). It was also present in Corsica, where it was introduced by man in historical times (Scalera and Angelici 2002). This species shows a close genetic affinity (Alves et al. 2008, Melo-Ferreira et al. 2012) and niche similarities (Acevedo et al. 2014) with *L. castroviejoi* (Iberian peninsula). Thus, the conspecificity with this latter taxon has been suggested (Alves et al. 2008).

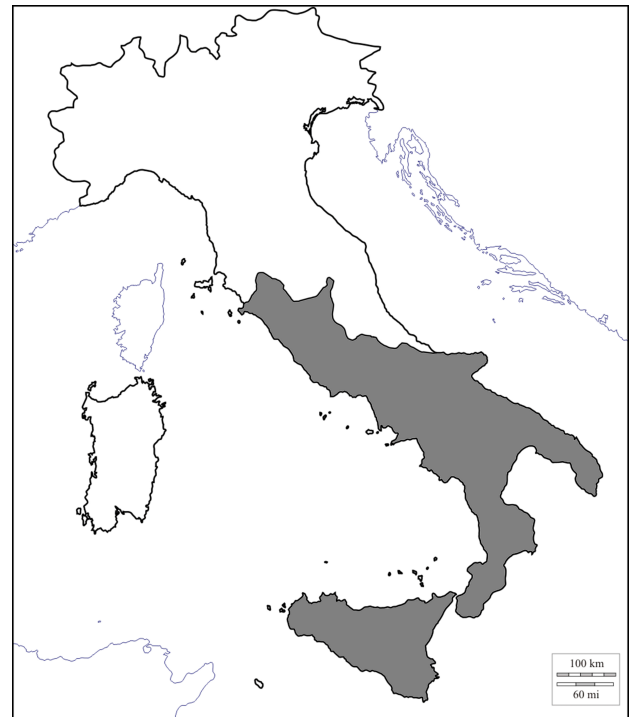


Figure 1. Distribution map of *Lepus corsicanus* (redrawn from Angelici and Spagnesi 2008).

Microtus nebrodensis (Mina-Palumbo, 1868). It is a Sicilian endemic, widespread across the entire island (Fig. 2) and locally considered a pest (Ranchelli et al. 2016). It seems to be missing from the slopes of Etna. Castiglia et al. (2008)

suggested a possible specific status of the Sicilian *Microtus*, then they confirmed this in further papers based on molecular genetics, karyotypic and morphological studies (Gornung et al. 2011, Bezerra et al. 2016). The split of this species with the other species of the complex, *M. savii* and *M. brachycercus*, dated about 1.81 million years ago (MYA) (Tougaard 2017).

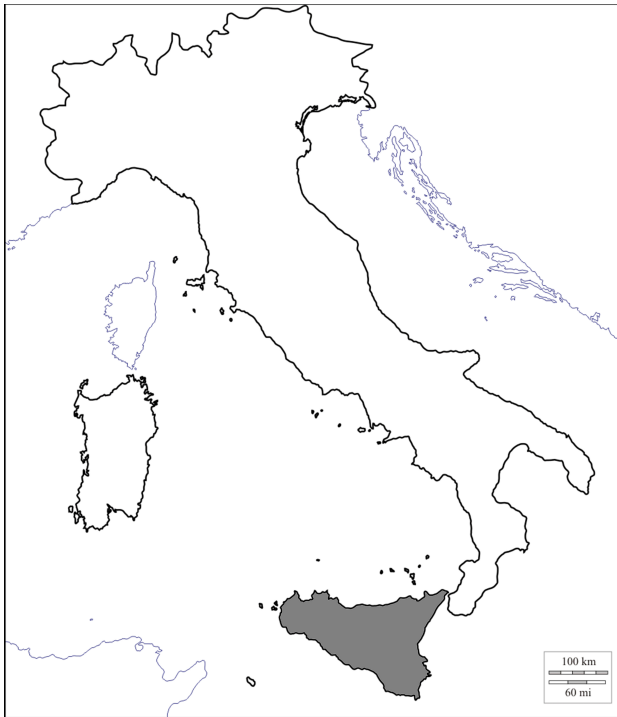


Figure 2. Distribution map of *Microtus nebrodensis* (redrawn from Bezerra et al. 2016).

Microtus brachycercus (von Lehmann, 1961). This species was formerly believed to occur only in the Calabrian Peninsula. However, mtDNA hapotypes belonging to this species showed that its northernmost limit is much further to the north in central Italy (Fig. 3) (Castiglia et al. 2008, Bezerra et al. 2016). Its species status is supported by chromosomal and hybridological data (Galleni et al. 1994). Genetic divergence with the sister species, *M. savii*, dated about 1.03 MYA (Tougaard 2017).

Sciurus meridionalis Lucifero, 1907. On the basis of genetic and morphological data, the subspecies *Sciurus vulgaris meridionalis* was elevated to the rank of species (Wauters et al. 2017). The range of this taxon is restricted to Calabria and Basilicata regions (Fig. 4). Middle Pleistocene (0.7 MYA) is the divergent time since its separation from *Sciurus vulgaris* (Grill et al. 2009).

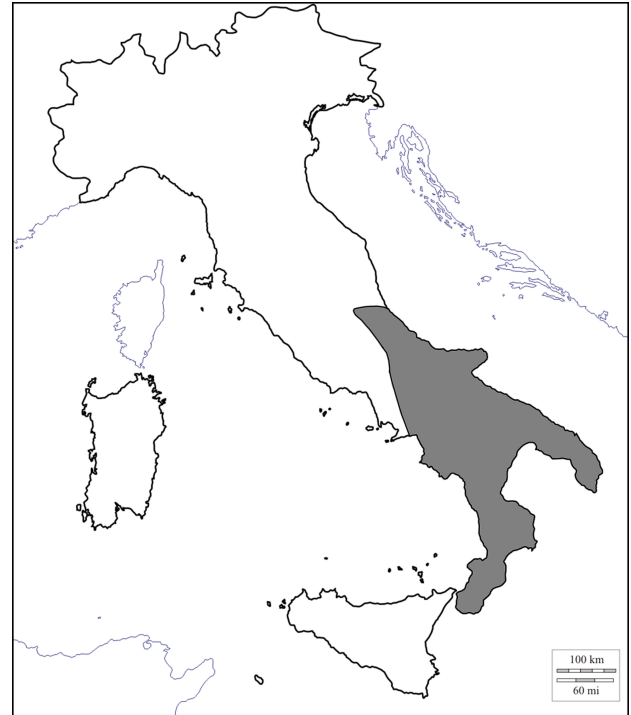


Figure 3. Distribution map of *Microtus brachycercus* (redrawn from Bezerra et al. 2016).

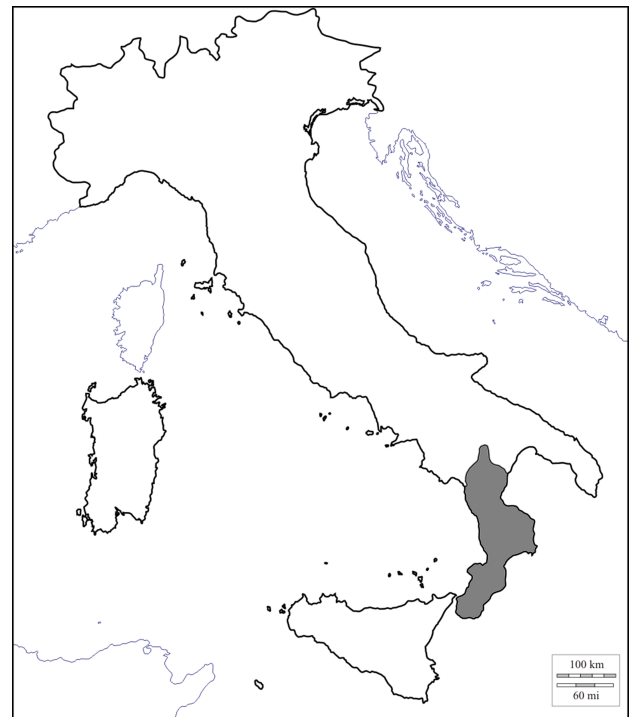


Figure 4. Distribution map of *Sciurus meridionalis* (redrawn from Wauters et al. 2017).

Dryomys aspromontis Von Lehmann, 1964. Previous studies did not show substantial cytogenetic and morphometric differences between the disjoined population of Calabria with those of the Alps (Civitelli et al. 1995, Filippucci et al. 1995). Recent molecular studies (Bisconti et al. 2017) have shown that the subspecies of Calabria *D. nitedula aspromontis* (see distribution in Fig. 5) is a deeply divergent evolutionary lineage representing a new endemic taxon to Italy. The high genetic divergence is not limited to mtDNA but extends to four nuclear loci. Moreover, the Calabrian taxon is characterized by a distinct fur colour. Therefore, the authors suggest this Calabrian subspecies may be elevated to species level *Dryomys aspromontis*. The amount of sequence divergence suggested a divergence time between the Calabrian and north Italian population around one million years ago (i.e. the Early Pleistocene) (Bisconti et al. 2017).

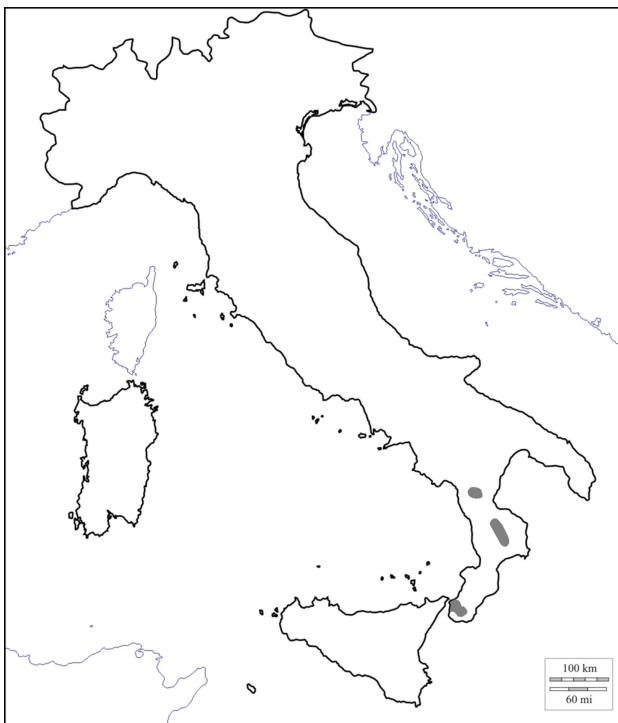


Figure 5. Distribution map of *Dryomys aspromontis* (redrawn from Capizzi and Filippucci 2008).

Sorex samniticus Altobello, 1926. This species is distributed along the Apennine chain down to Calabria (Fig. 6). It is morphologically very similar to the sympatric *S. antinorii* with which it was believed to be conspecific (Brünner et al. 2002). Its species status was first supported by a

different karyotype respect to the one found in *Sorex antinorii* (Graf et al., 1979). Moreover, molecular phylogenetic analysis demonstrated its phylogenetic distinctiveness respect to all the other *Sorex* species (Yannic et al. 2008). Divergence time was calculated as 3.1 MYA (Fumagalli et al. 1999).

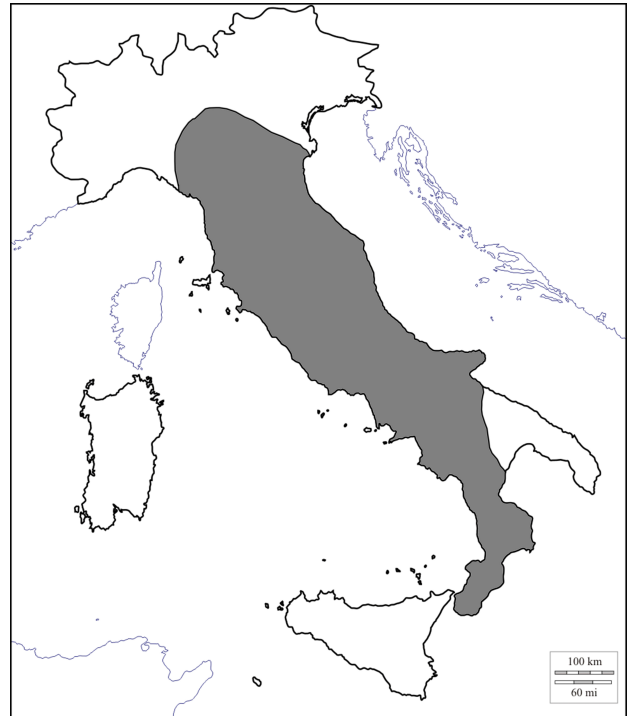


Figure 6. Distribution map of *Sorex samniticus* (redrawn from Nappi and Aloise 2008).

Sorex arunchi Lapini and Testone, 1998 (invalidated). This species was described by Lapini and Testone (1998) on the basis of morphological differences. However, mtDNA studies (Yannic et al., 2012) did not support a genetic distinction with *S. antinorii* and pointed out that the two taxa are conspecific.

Talpa romana Thomas, 1902. This species is distributed in southern and central Italy (Fig. 7), where it co-occurs with *T. europaea*. Divergence time with the sister species, *T. caeca*, dated back 3.75 MYA (Colangelo et al. 2010).

Plecotus sardus Mucedda et al. 2002. This is the only bat species endemic to Italy (Mucedda et al. 2002). Its specific distinction was supported by morphology and high mtDNA divergence (Mucedda et al. 2002). It is found only in few localities in Sardinia (Fig. 8). The time of divergence of the split with *P. auritus* dates back to 2.68 MYA (Kiefer 2007).

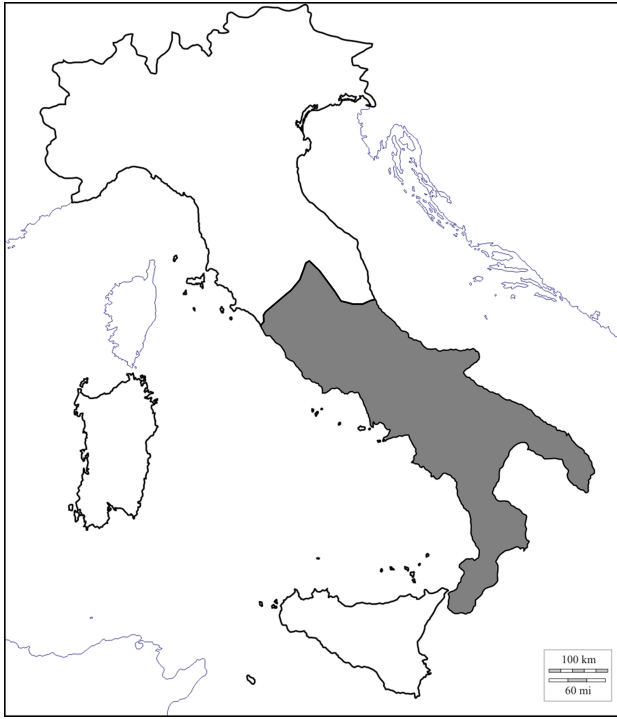


Figure 7. Distribution map of *Talpa romana* (redrawn from Loy 2008)

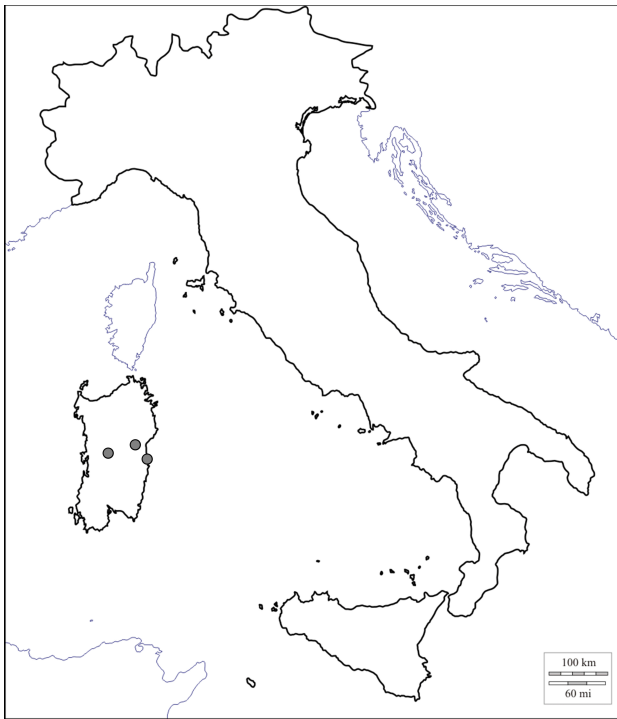


Figure 8. Distribution map of *Plecotus sardus* (data from Mucedda et al. 2002).

Near-endemic species

Crocidura sicula Miller, 1901. This species is endemic to Sicily, surrounding islands (Ustica, Gozo, and the Egadi islands) (Fig. 9) and Malta. However, it may be extinct on the island of Malta, where it is known only from subfossil remains (Vogel 1999). Recently this species was recorded in the Comino Island (Maltese Archipelago) (Aloise et al. 2011). Divergence time between *C. sicula* and the sister species *C. canariensis* was estimated to be 5 MYA (Vogel et al. 2003).

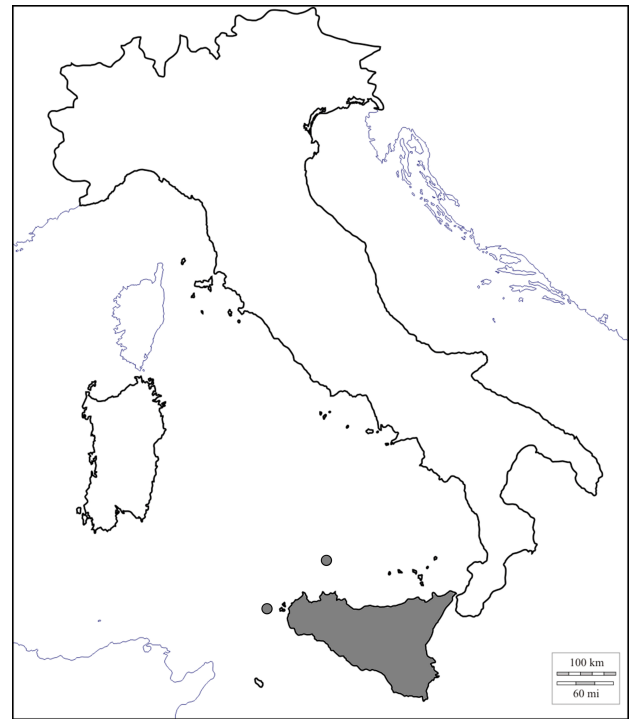


Figure 9. Distribution map of *Crocidura sicula* (redrawn from Sarà 2008).

Sorex antinorii Bonaparte, 1840. This species occurs in northern, central, southern Italy (Fig. 10), and marginally in southern Switzerland and western France (Brünner et al. 2002), even if during the Last Glacial Maximum *S. antinorii* was apparently restricted to the Italian Peninsula (Yannic et al., 2012). *Sorex antinorii* was previously considered a chromosomal race of *Sorex araneus*. Then, species status was suggested following a detailed analysis of the hybrid zone with *S. araneus* (Brünner et al. 2002). The events that separated *S. antinorii* and *S. araneus* would have occurred around 0.27 MYA in the middle Pleistocene (Yannic et al. 2008).

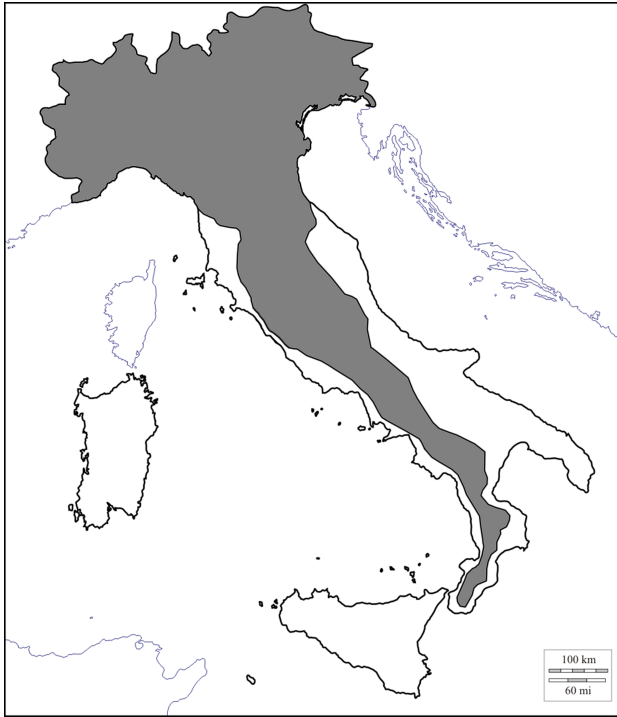


Figure 10. Distribution map of *Sorex antinorii* (redrawn from Aloise and Nappi 2008).

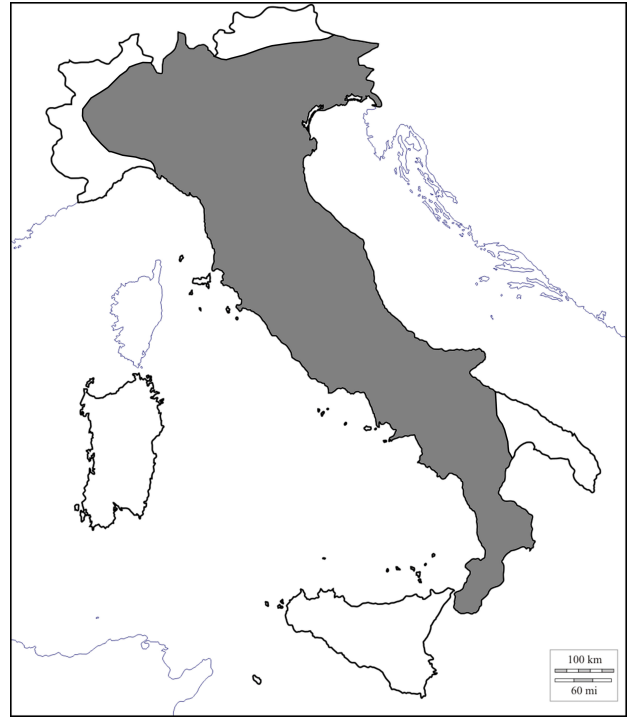


Figure 12. Distribution map of *Arvicola italicus* (redrawn from Cagnin 2008).



Figure 11. Distribution map of *Microtus savii* (redrawn from Bezerra et al. 2016).

Microtus savii (de Selys Longchamps 1838). This species is found throughout northern and central Italy (with the exception of the extreme north-east) (Fig. 11) and it occurs marginally in southern Switzerland. The southernmost distribution limits required additional studies because the species may be replaced in central Italy by *M. brachycercus* (Castiglia et al. 2008, Ranchelli et al. 2016). This species resulted karyotypically different from *M. brachycercus* and male hybrids between the two species are sterile (see account for the sister species *M. brachycercus*). The divergence time with its sister species *M. brachycercus* is 1.03 MYA (Tougaard 2017).

Arvicola italicus Savi, 1838 The genus *Arvicola* recently underwent molecular studies that have highlighted the inadequacy of the current taxonomy (Krystufek et al. 2015, Castiglia et al. 2016). These studies agreed that *A. amphibius* s.l. includes three distinct mitochondrial lineages. One of these lineages is settled along all the Italian peninsula and includes aquatic and fossorial forms (previously considered belonging to *A. scherman*) (Fig. 12). Given the high mtDNA divergence and the results of previous investigations on allozymes and hybrid fertility (reviewed in Castiglia et al. 2016) it was suggested that the Italian water voles

belong to a distinct species, *Arvicola italicus* Savi, 1838. The species range would be also outside the Italian political borders. In fact, an mtDNA haplotype belonging to this Italian lineage was found in southern Switzerland (Brace et al. 2016). Thus, this species should be considered as near-endemic.

Candidate endemic species

Myodes glareolus. Recent molecular data strongly support that the Calabrian populations of *M. glareolus* may represent a distinct species (Colangelo et al. 2012a). This interpretation is supported by its phylogenetic position and mitochondrial DNA distinctiveness respect to all the other *M. glareolus* populations distributed in Europe and central and northern Italy (Colangelo et al. 2012a, Filipi et al. 2015). The available name for the Calabrian population would be *Myodes hallucalis* (Thomas, 1906) (Gippoliti, 2013). Molecular clock suggests a divergence of the Calabrian lineage that can be set around 0.79 MYA (Colangelo et al. 2012a).

Talpa caeca. Recent genetic molecular studies found that *T. caeca* has segregated into an Italian and a Balkan lineage (Bannikova et al. 2015). The taxonomic status of these lineages deserves additional studies considering the observed chromosomal difference relative to the general conservation of karyotype in the genus (Gornung et al. 2008). The time of divergence between the two *T. caeca* lineages (about 1 MYA) is close to the maximum limit of intraspecific divergence in the genus *Talpa* (Bannikova et al. 2015).

Myotis nattereri. A central and southern Italian population of this species comprises a highly divergent mtDNA lineage which may represent an additional undescribed species (Galimberti et al. 2012). Divergence with other populations settled in northern Italy, Spain and France dates back to 0.43 MYA (Middle Pleistocene) (Salicini et al. 2013).

Apodemus sylvaticus (Sicily). On the basis of genetic analyses (Michaux et al. 2003), the Sicilian population of *Apodemus sylvaticus* represents an old lineage that could have survived elsewhere in southern Italy and entered in Sicily during the last glaciation, 70 000 years ago where it remained isolated without contact with other continental populations. Therefore, the Sicilian population of *A. sylvaticus* appears to be genetically very differentiated (but not cytogenetically,

Gornung et al. 2009) and highly variable respect to other populations of this species.

Muscardinus avellanarius. Mouton et al. (2017) identified two highly divergent lineages of *Muscardinus avellanarius* respectively distributed in western and central-eastern Europe and Anatolia. Moreover adopting several species definitions and methods the number of species can be between one and 10 (Mouton et al. 2017). One of this putative species is an Italian endemic diverging 3.5 MYA from western European populations. If confirmed, the subspecies *Muscardinus avellanarius speciosus* Dehene, 1855 described for central and southern Italy and Sicily could be elevated to species rank.

Sorex minutus. According to Vega et al. (2010) the peninsular Italian populations of *Sorex minutus* are genetically different from European ones, with a divergence time around 0.8 MYA. Moreover, the most southern populations also show a differentiation in the form of the jaw. These populations were in the past assigned to a different subspecies, *S. minutus lucanius* Miller 1909. These data suggest that Italian pygmy shrew forms, at least, a different ESU (Evolutionary Significant Unit) (Moritz, 1994) distinct from the European *S. minutus minutus*.

Glis glis. Hürner et al. (2010) identified three main haplogroups of *Glis glis* using mtDNA. One corresponding to the western, central and eastern European populations and two in the Italian peninsula namely in Calabria region and Sicily. Lo Brutto et al. (2011) studied in more detail the Italian populations confirming the substructure of the southern and Sicilian populations, aiming further studies especially for the island populations. We believe that no taxonomic decision can be made before additional studies based on nuclear loci and morphometry will be available.

Cold cases

Here, we discussed the “cold cases”, as television series about crime, those species with unresolved taxonomy but that there is suspicion that they could be (or not) endemic taxa.

Ursus arctos marsicanus Altobello, 1921. This Apennine endemic subspecies appears to be deeply distinct from the other European populations from a morphological point of view (Colangelo et al. 2012b), while showing a genetic affinity between the remnant and isolated population of the other southern European populations (Swenson et al., 2011). However, Benazzo et al. (2017) on the basis

of genomic analyzes have indicated a separation of the Apennine bears, from the rest of the other bear populations, of about 1500 years. The authors conclude that Apennines bear population represents a divergent evolutionary lineage.

Rupicapra pyrenaica ornata Neumann, 1899. *Rupicapra pyrenaica* is divided into three subspecies, *R. pyrenaica pyrenaica* (Pyneeres, Spain), *R. pyrenaica ornata* (Apennines, Italy), *R. pyrenaica parva* (Cantabrians, Spain). A subspecies status of the Apennine population is reported in recent literature (e.g. Rodriguez et al. 2010) and also by Italian researches (Corlatti et al. 2011). Only Groves and Leslie (2011) consider all the subspecies at the species rank then reporting *Rupicapra ornata* as a monotypic, endemic species to the Abruzzi Apennines.

Cervus elaphus corsicanus Erxleben, 1777. The Sardinian population of *Cervus elaphus*, described as the subspecies *Cervus elaphus corsicanus*, has been considered as a good species by Groves and Grubb (2011). In a recent paper Doan et al. (2017) identifies a unique lineage now extinct for the Italian peninsula, but that was introduced in historical times in Sardinia (Vigne, 1992). The same Italian lineage was found by Doan et al. (2017) also in Switzerland, Hungary and Bulgaria probably as evidence of a wider distribution of this lineage or due to translocations of game animals. Doan et al. (2017) found that also the population of Mesola is genetically distinct and hence hypothesized two native lineages for Italy.

Capra aegagrus Erxleben, 1777. Even if some authors recognize some morphological peculiarities of *Capra aegagrus* of the Montecristo Island (cf. Masseti 2016), according to Weinberg et al. (2008) this population should be considered introduced by humans from feral populations of ancient domestic stocks, as well as for the other Mediterranean populations.

DISCUSSION

The presented checklist of Italian endemic species of mammals includes twelve endemic/near-endemic species. This number of species is higher than previous available checklists, with the exception of Gippoliti (2013) who listed 24 Italian endemic/near-endemic species by applying a phylogenetic species concept. Even when Gippoliti's (2013) list has the merit of representing a starting point for future studies, here we preferred to apply a more conservative approach considering as valid only

those species that have been explicitly reported and published in peer-reviewed articles.

Even using our more conservative approach, the presented list includes more species than previous ones and also in comparison with the red list of the IUCN in which there are 6 endemic mammal species only (1 rodent, 3 soricids and 2 bats) (Rondinini et al. 2013).

The difference between our list and others is mainly due to the inclusion of species derived from the recent elevation at the species rank of populations formerly considered subspecies (*Microtus nebrodensis*, *Sciurus meridionalis*, *Arvicola italicus*).

The locations of the individual ranges of the identified endemic/near endemic species have different characteristics. Only three endemic species can be found in northern Italy while the largest number of endemic species (eight) occurs in central/southern Italy. Therefore, this latter region represents an important area of endemism for mammals in the country. This is an expected result considering the well-known role of southern Italy as refugial areas for many terrestrial vertebrates (Vega et al. 2010).

Despite the general uncertainties in the estimation of divergence time from molecular based phylogenies, it results by our literature review that the origin of the endemic and near endemic species can be safely dated back to the Middle Pleistocene and Pliocene (Tab. 1). Older species result to be the soricomorph *Sorex samniticus* and *Talpa romana*, and the two insular endemics: the bat *Plecotus sardus* and the soricomorph *Crocidura sicula*. It should be considered that the southernmost part of Italy, including Sicily and Sardinia, constitute for some xerophilic species a particular favorable area not only during interglacials but even during glacial maxima when a strong sea level decrease occurred (as much as 120–135 m) leading to the increase of the Mediterranean coastal plains and favoring the formation of new suitable habitats with consequent population expansions (Bisconti et al. 2011; Senczuk et al. 2017). This could have allowed the survival of some old mammal endemic species as well as for other paleoendemic vertebrates across different climatic oscillations in those southern areas of the country.

Candidate endemic species of mammals are of more recent origin than strict Italian endemics, being all originated during the Early to Middle Pleistocene. One exception is constituted by the

Italian lineage of *Muscardinus avallanarius* whose divergence time dates back to the Pliocene.

Holocene endemic extinct species and the future of Italian endemic mammals

The list of the Italian endemic species that went extinct during the Holocene (Turvey 2009) can be found in Table 2. It is evident from this list that the species belonging to the orders Rodentia, Primates, and Artiodactyla were more prone to becoming extinct in comparison with those belonging to the orders Chiroptera and Carnivora, which were less so (Amori et al. 2014).

In Italy, endemic species that have become extinct during the Holocene belong almost exclusively to Rodentia and Soricomorpha island species (Turvey 2009). This pattern is also found in

the Mediterranean basin where extinctions involve almost always island small mammals. One exception is Cyprus islands where two large mammals went extinct *Elephas cypriotes* (Proboscidea) and *Phanourios minor* (Artiodactyla) (Turvey 2009).

More generally, the majority of mammalian extinctions, from the last 400 years to those occurring during the last few decades, are of small-bodied species (cf. Krystufek et al. 2009). This urges us to pay more attention to the endemic species of small body size because they are more prone to extinction. This is particularly important because, among mammals, the small body species are the ones that receive less attention in conservation actions (Amori and Gippoliti 2000).

Table 1. Distribution and origin of the endemic and near endemic species to the Middle Pleistocene and Pliocene based on phylogenetic studies applying a molecular clock.

Species	Northern Italy	Central Italy	Southern Italy	Sicily	Sardinia	Time (MYA) - Epoch
Endemic						
<i>Lepus corsicanus</i>		X	X	X		-
<i>Microtus nebrodensis</i>				X		1.81 - Early Pleistocene
<i>Microtus brachycerchus</i>		X	X			1.03 - Early Pleistocene
<i>Sciurus meridionalis</i>			X			0.7 - Middle Pleistocene
<i>Dromomys aspromontis</i>			X			1.0 - Early Pleistocene
<i>Sorex samniticus</i>	X	X	X			3.1 - Pliocene
<i>Talpa romana</i>		X	X			3.75 - Pliocene
<i>Plecotus sardus</i>					X	2.68 - Pliocene
Near-endemic						
<i>Crocidura sicula</i>				X		5 - Pliocene or older
<i>Sorex antinorii</i>	X	X	X			0.27 - Middle Pleistocene
<i>Microtus savii</i>	X	X				1.03 - Early Pleistocene
<i>Arvicola italicus</i>	X	X	X			not reported

Table 2. Extinct endemic species during Holocene in Italy (from Turvey 2009).

Species	Order	Family	Locality	Notes
<i>Asoriculus similis</i>	Soricomorpha	Soricidae	Sardinia	
<i>Prolagus sardus</i>	Lagomorpha	Ochotonidae/Prolagidae	Sardinia	Historical record 1774
<i>Tyrrhenicola henseli</i>	Rodentia	Arvicolidae	Sardinia - Corsica	
<i>Rhagamys orthodon</i>	Rodentia	Muridae	Sardinia - Corsica	
<i>Meriones malatestae</i>	Rodentia	Gerbillidae	Lampedusa	
<i>Praemegaceros cazioti</i>	Cetartiodactyla	Cervidae	Sardinia - Corsica	

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