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mtDNA diversity in a rabbit population from Sicily (Italy)

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Abstract: The European rabbit *Oryctolagus cuniculus* (*O. c.*) is a small game species found in several parts of the world and represents an important resource for many predators. It has been classified as a Near-Threatened species on the Red List of Italian Vertebrates even though it is also considered to be an agricultural pest species in many areas. It is a polytypic species present as two known subspecies: *O. c. cuniculus* and *O. c. algirus*. The Italian geographical distribution of the two subspecies is known, but mostly based on morphological, biogeographic, and historical literature data. In Sicily, there is no complete genetic description of the actual existing subspecies; previous studies have only reported the differences in size of the Sicilian rabbit population. In this study, we analyzed genetic data within a phylogenetic framework through mitochondrial (mt) cytochrome *b* (cyt *b*) DNA from 13 rabbit samples collected from different sites in Sicily. We reconstructed the intraspecific phylogeny by comparing cyt *b* mtDNA sequences of 13 newly isolated *O. cuniculus* haplotypes from Sicily and 7 individuals from other areas (Canada, France, Mexico, North Italy, South Africa, Spain, Sweden). Our results show that the rabbit population from Sicily has a mitochondrial type (lineage B) previously shown to be associated with *O. c. cuniculus*, which is similar to sequences from rabbits in Northeast Spain, South France, Sweden, and South Africa.

Key words: Biodiversity, rabbit taxonomy, cyt b mitochondrial DNA, Oryctolagus cuniculus

1. Introduction

The European rabbit *Oryctolagus cuniculus* (*O. c.*) is traditionally one of the most important small game species in the Mediterranean Basin. It is also considered a multifunctional keystone species for natural and cultivated Mediterranean ecosystems (Delibes-Mateos et al., 2008). It is present in Europe, North Africa, South America, Australia, and New Zealand (Ferrand, 2008). Currently, the species has been classified and given the status of Near-Threatened at the international level (http://dx.doi. org/10.2305/IUCN.UK.2008.RLTS.T41291A10415170. en).

In Italy, the European rabbit has been classified as a Near-Threatened species on the Red List of Italian Vertebrates (IUCN, 2014; available at www.iucnredlist. org).

The European rabbit was quite common in central and southern Europe during the late Upper Pleistocene. At the end of the last glaciation the geographical distribution of this species was limited to the Iberian Peninsula (IP) and probably the south of France (SF) (Kaetzke et al., 2003; Lopez-Martinez, 2008), where there were likely two glacial refugia; thus, as a consequence, two divergent genetic lineages evolved. The signatures of this are evident throughout the genome and can be observed in the analysis of allozyme variation, mtDNA variation, the Y-chromosome, the X-chromosome, and autosomes (Branco et al., 2000; Geraldes et al., 2006, 2008; Ferrand and Branco, 2007; Carneiro et al., 2010, 2014a, 2014b). The European rabbit is recognized formally in two subspecies, *O. c. cuniculus* (L., 1758) and *O. c. algirus* (Loche, 1858), as described by Ferrand (2008).

The species later spread throughout almost all of the world as a result of human activity (Flux, 1994). Specifically, during the 2nd or 3rd centuries AD, the European rabbit was introduced onto the central Mediterranean islands, including Sicily (Flux and Fullagar, 1992; Flux, 1994; Kaetzke et al., 2003), probably by the Romans (Bodson,

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1978). After its introduction, the only evidence of the presence of the European rabbit in Sicily is represented by fossils found at the Brucato site during the Middle Ages (13th–14th centuries) (Barrett-Hamilton, 1912; Constable, 2003). At this site, archaeological research has revealed that about 40% of the animals hunted by humans consisted of rabbits (Bresc, 1980). Thanks to the income of "Venatio cuniculorum", of which there are different statements, it is known that rabbits abounded in many other places in Sicily. In the Mediterranean Basin, there is indication of the presence of the European rabbit from archaeological exploration on the islands of Nisida and Capri (Naples, Italy), and Zembra (Tunisia) (Flux and Fullagar, 1992; Flux, 1994; Kaetzke et al., 2003).

Today, in the Sicilian region of Italy, as well as in other European countries (Millán et al., 2012), the European rabbit is at the center of serious management and conservation problems. In fact, this lagomorph is very important for the conservation of the endangered Sicilian population of raptors such as Bonelli's eagle (*Hieraaetus fasciatus*), and also for very generalist species such as the common buzzard (*Buteo buteo*) and red fox (*Vulpes vulpes*) (Caruso and Siracusa, 2001; Moleón et al., 2012; Lopez-Lopez et al., 2012).

According to the Guidelines for the Release of Wildlife Species (INFS, 2007), the rabbit is considered to be a paraautochthonous species, as it was introduced before 1500 and is therefore now contextualized in the local fauna landscape (Lees and Bell, 2008). Nevertheless, in some areas of Sicily and on the nearest small islands, where there are no predators and in a nature reserve where hunting is prohibited, the European rabbit is a pest species inducing damage to the agroecosystem and a decrease in the plant population, and causing considerable irreversible ecological and economic damage (Lees and Bell, 2008; Cooke, 2012).

In Sicily, as well as in the rest of Europe, the reduction in the rabbit population was probably due to myxomatosis and rabbit haemorrhagic disease (reviewed by Abrantes et al., 2012) recorded in 1986. In this context, and mainly for hunting purposes, regional authorities have released about 10,000-15,000 captive-raised rabbits of uncertain origin every year. The population of European rabbit living in Sicily and on the nearest small islands seems to belong to the subspecies O. c. huxleyi (Haeckel 1874), which is synonymous for O. c. algirus, according to Toschi (1965). However, this statement is based only on the biometric analysis of the body size. Recently, Lo Valvo et al. (2014) examined 7 body variables and 23 cranial variables of 166 and 120 individuals, respectively, and compared the results with biometric data from other European populations. They showed that the European rabbit currently present in Sicily does not have a small body size, as assumed by Toschi (1965), but rather has a medium body size as in current populations living in northern Spain and southern France, which are referred to as *O. c. cuniculus* (Callou, 2002; Ferreira et al., 2015).

It is clear that the European rabbit population in Sicily has never been carefully managed, mainly because of very poor knowledge of its biology and ecoethology in the wild, and also because of a strong uncertainty about its genetic, morphometric, and biogeographic characteristics. To start filling these gaps, we worked on a research project on the European rabbit in Sicily, studying the genetics of the Sicilian O. c. by means of a marker gene, namely the mitochondrial DNA (mtDNA) of the cytochrome b (cyt b) gene, which is commonly used in phylogenetics to determine evolutionary relationships between organisms due to its DNA sequence divergence. It is considered one of the most useful genes in determining relationships within families and genera as demonstrated for mammals (Castresana, 2001; Tobe et al., 2010), and within subspecies, such as Lepus corsicanus (Pierpaoli et al., 1999). In the mitochondrion, the cyt b gene encodes for an integral membrane protein of approximately 400 amino acid residues; it is a component of the respiratory chain complex III, also known as the bc1 complex, involved in the electron transport of protons (Howell, 1989; Degli Esposti et al., 1993). Since it is possible to perform genetic studies about species evolutionary history, we used the mitochondrial cyt b gene known as a valid marker of intraand interspecific variation (Degli Esposti et al., 1993; Tobe et al., 2010).

mtDNA is a maternally inherited nonrecombinant molecule and therefore, in species that hybridize, only provides information on the ancestry of the female lineage. As an example, it was used to establish introgression cases for hares in the IP; in fact, a high frequency of *Lepus timidus* mtDNA is observed in individuals from native hares, but *Lepus timidus* itself no longer occurs in the IP (Melo-Ferreira et al., 2009).

In this study, we applied genetic analysis as a complement to the phenotypic descriptors of the *O. c.* Sicilian population investigated before. We present the results on Sicilian rabbit phylogeny by comparing cyt *b* mtDNA and protein sequences with homologs from European populations with the aim to better understand their taxonomic relationships and to specify which lineage (A or B) the Sicilian rabbit belongs to. The island of Sicily is at the border of the distribution of *O. c. cuniculus* in the area of the Italian Peninsula. Therefore, depending on the subspecies of the Sicilian population, the geographic ranges would be confirmed or modified.

2. Materials and methods

2.1. Tissue sample collection

Between 1997 and 2006, European rabbit tissue specimens obtained from hunters were collected from different sites in the Sicilian provinces, including some small islands (such as Ustica in the province of Palermo and Vulcano in the province of Messina). The specimens were collected as representative samples from about 50 rabbits from diverse sites in different geographically distributed Sicilian provinces. Twenty samples were then amplified and sequenced, 13 of which were found to have different DNA sequences; for this reason, they were selected for the purpose of this study. The cyt *b* mtDNA partial sequence, 954 bp in length (out of the whole coding region of 1140 bp) was analyzed. In Table 1 and Figure 1A, the Sicilian sites are described in detail, together with the relative provinces of sampling, the geographic coordinates (UTM WGS84), and the size of the isolated DNA fragments. Two samples are smaller in size, probably due to a polymerase failure, being 921 and 927 nt long, from Isola delle Femmine (Palermo) and Oasi Scala (Caltanissetta), respectively.

Animals were treated in accordance with the guidelines of the local ethics committee.

2.2. mtDNA extraction and polymerase chain reaction (PCR) of the *cyt b* gene

The mtDNA was extracted from ear and muscle samples using the genomic DNA Purification Kit (Fermentas) according to the manufacturer's guidelines. An aliquot of DNA was amplified by using conventional PCR approaches. PCR was performed with Taq (Invitrogen) polymerase in 25-µL reactions under the following conditions: 1 cycle at 95 °C for 5 min; 30 cycles at 95 °C for 45 s (denaturation), 55 °C for 30 s (annealing), and 72 °C for 60 s (extension); and 7 min at 72 °C (final extension). Specific oligonucleotides used to amplify mtDNA were designed as follows: forward 5'-ATCCAACATCTCTGCTTGATG-3' and reverse 5'-GGTTGGCCTCCGATTCATGT -3'. The PCR reaction products were DNA fragments ranging from 921 to 954 nt that were purified by Exosap (BMR Genomics Service, Padua, Italy) and sequenced in both directions by MWG-Operon Sequencing Service (Germany). Sequences were deposited in GenBank and the comparison of sequences

Table 1. O. cuniculus individual names, A/B lineage assignment, geographical sites and coordinates, mtDNA length, and relative GenBank accession number.

Name	A/B ineage	Site	Sicilian province	UTMX	UTMY	DNA size (nt)	Accession number
1-Sicily	В	Cianciana	Agrigento	362000	4151400	954	HG810781.1
2-Sicily	В	OasiScala	Agrigento	395000	4156700	927	HG810791.1
3-Sicily	В	Realmonte	Agrigento	364300	4129500	954	HG810788.1
4-Sicily	В	Butera	Caltanissetta	428400	4120000	954	HG810780.1
5-Sicily	В	Terrasini	Palermo	330300	4223300	954	HG810785.1
6-Sicily	В	Giacalone	Palermo	345100	4211600	954	HG810782.1
7-Sicily	В	Nociazzi	Palermo	415800	4185100	954	HG810784.1
8-Sicily	В	Pizzo Inserra	Palermo	350500	4225000	954	HG810790.1
9-Sicily	В	Marsala	Trapani	280500	4185000	954	HG810783.1
10-Sicily	В	Segesta	Trapani	309300	4203100	954	HG810787.1
11-Sicily	В	Femmine Is.	Palermo	345600	4230600	921	HG810779.1
12-Sicily	В	Ustica Is.	Palermo	341100	4284600	954	HG810786.1
13-Sicily	В	Vulcano Is.	Messina	498500	4250000	954	HG810789.1
Lineage A (O. c. algirus)	А		Spain, south			954	AJ243096.1
Lineage B (O. c. cuniculus)	В		France			954	AJ243197.1
Italy	В		Italy			946	AF157467.1
Mexico	A		Mexico			954	HQ596486.1
Canada	В		Canada			954	U07566.1
Sweden	В		Sweden			954	AJ001588.1
South Africa	В		South Africa			954	AY292717.1
Lepus europaeus			Sweden			954	AJ421471.1
Lepus corsicanus			Italy			949	AF157463



Figure 1. A) Map of sampling sites in Sicilian provinces. Numbers correspond to sampling sites described in Table 1. B) Evolutionary relationships of taxa inferred by MEGA 5 program: neighbor-joining phylogenetic tree, derived from cyt *b* mtDNA multiple alignment shown in Figure S1, of *O. cuniculus* samples derived from the sites listed in Table 1. The percentages of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the maximum composite likelihood method (Tamura et al., 2004) and are in the units of the number of base substitutions per site. Bar = 0.02. Oc-cuniculus = *O. cuniculus*; Oc-algirus = *O. cuniculus algirus*.

was performed using the Blast program (Altschul et al., 1990). Restriction analysis was performed with the NEB Cutter 2.0 program (Vincze et al., 2003).

2.3. Phylogenetic analysis

DNA and protein alignments were performed using Clustal W2 software (Larkin et al., 2007). Shading of the multiple alignment of the selected sequences was obtained by using the Boxshade 3.21 program (http://www.ch.embnet.org/ software/BOX_form.html). On the basis of the alignment in supplementary Figure S1, we constructed a phylogenetic tree. L. corsicanus and L. europaeus were used as outgroups to root the tree. The evolutionary profile was determined using the MEGA 5 program (Tamura et al., 2011) and the neighbor-joining method (Saitou and Nei, 1987). The percentages of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein, 1985). The program DnaSP (Version 5.0) (Librado and Rozas, 2009) was used to sort haplotypes and analyze the number of variable sites (S), number of haplotypes (h), and haplotype diversity (Hd).

3. Results

The genetics of the Sicilian population of O. c. was studied using the cyt b mtDNA sequence, as described in Section 2. First, we compared the 13 isolated sequences with those of GenBank by using the Blast program, and we found that all the Sicilian sequences showed a high similarity (equal to 99%) to O. c. cuniculus (L., 1758), called lineage B by Branco et al. (2000). From our results, the reciprocal comparison between the cyt b nucleotidic sequences from the two annotated lineages, A (corresponding to O. c. algirus) and B (corresponding to O. c. cuniculus), showed 93% homology. Identity decreased to 85% when both sequences were compared with the Lepus species. The nucleotidic comparison between cyt *b* sequences from the Sicilian population and from other populations found in GenBank showed a high sequence identity (equal to 99%) with the sequences from France and South Africa, Canada, Sweden, and North Italy, and a lower sequence identity (equal to 93%) with sequences from Andalusia (South Spain) and Mexico.

We then compared the newly sequenced clones with a selected series of sequences found in GenBank from the two subspecies, *O. c. cuniculus* (L., 1758) and *O. c. algirus* (Loche, 1858), that for Branco et al. (2000) correspond to lineage A. In particular, the cyt *b* genes pertaining to both A and B lineages from other areas of the world such as Sweden, France, southern Spain, Mexico, southern Africa, Canada, and northern Italy were considered. The ClustalW2 multiple alignment of all 22 sequences analyzed here is shown in supplementary Figure S1. The results of the shading program in supplementary Figure S2 (where

the different nucleotides of Sicilian sequences with respect to lineage A are shaded) showed that there is intraspecific divergence for the mitochondrial cyt b gene. This divergence was higher between all the Sicilian nucleotidic sequences and lineage A with respect to lineage B.

The graphic phylogram (Figure 1B) shows that the main branch divides into two clades: one for lineage A and one for lineage B. Lineage B divides further into two branches: one giving rise to a group of 8 Sicilian sequences and another containing 5 Sicilian sequences besides those from France, South Africa, Canada, Sweden, and northern Italy. The higher bootstrap values indicate the accuracy of the data.

Polymorphic and haplotype analyses are shown in Table 2. A total of 75 variable sites were detected out of 954 total nucleotides. A total of 10 different haplotypes out of 15 analyzed sequences was sorted, indicating that individuals 10-Sicily/12-Sicily/13-Sicily/8-Sicily, 1-Sicily/6-Sicily, and 5-Sicily/9-Sicily were identical respectively, considering the mtDNA sequence analyzed here.

A genetic analysis of mitochondrial cyt b nucleotidic sequences conducted by analyzing the single cutter restriction enzyme analysis supported our investigations. Figure S1 highlights, in different colors, some of the most interesting and indicative single cutter restriction enzyme sites and their positions. Among the differences, a very interesting finding was the discovery that all Sicilian sequences contained an EcoRI restriction site at the same position (nucleotide 558 of the partial sequence considered here), a feature that was shared with lineage B, northern Italy, Canada, South Africa, and Sweden, but was in contrast to the sequences of lineage A and Mexico, which had no EcoRI site, as well as L. europaeus. The Sicilian sequences shared other typical restriction sites (HincII 148, AluI 806, DrdI 888) in an identical position with lineage B and were dissimilar to lineage A; the latter does not possess the DrdI site, and it possesses the other restriction sites in different positions (specifically, AluI 500 and HincII 439). The same Sicilian individuals did not contain a SalI restriction site, which is present only in Mexico and lineage A (at the same position of 437 of the partial sequence considered here) (see Figure S1).

4. Discussion

In this study, we applied genetic analysis as a complement to the previously defined phenotypic descriptors of the *O. c.* Sicilian population (Lo Valvo et al., 2014), by using the high variable region of cyt *b* mtDNA. In fact it rapidly accumulates nucleotidic substitutions, producing variants of mtDNA present in a single species, called haplotypes (Ingman et al., 2000). Cyt *b* mtDNA has been frequently used in mammals (Barome et al., 1998), including the wild rabbit from the IP (Branco et al. 2000), whereas this is the

Number of sequences	15
Number of sites	954
Number of polymorphic (segregating) sites	S: 75
Site positions	4 17 18 37 46 65 73 148 151 154 163 169 208 211 244 262 274 280 298 313 316 319 325 337 349 352 376 430 439 442 454 463 482 484 526 541 553 562 565 575 589 592 601 611 617 622 629 635 638 652 673 677 697 706 727 735 742 761 763 808 814 815 820 850 856 892 908 910
Number of haplotypes	h: 10
Haplotype diversity	Hd: 0.924
Hap_1:4	[10-Sicily 12-Sicily 13-Sicily 8-Sicily]
Hap_2: 1	[11-Sicily]
Hap_3: 2	[1-Sicily 6-Sicily]
Hap_4: 1	[2-Sicily]
Hap_5: 1	[3-Sicily]
Hap_6: 1	[4-Sicily]
Hap_7: 2	[5-Sicily 9-Sicily]
Hap_8: 1	[7-Sicily]
Hap_9: 1	[Lineage A O. c. algirus]
Hap_10: 1	[Lineage B O. c. cuniculus]
Standard deviation of haplotype diversity	0,053

Table 2. Genetic	c diversity estimate	es for Oryctolague	s cuniculus from	Sicily mtDNA
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first time it has been used for studying the taxonomy of the Sicilian *O. c.* population.

In addition to morphological data actually used to understand the phylogenetic characteristics of lagomorphs (Lo Valvo et al., 2014; Ge et al., 2015), the genetic and phylogenetic analyses have enabled variations in the genotypic traits to be identified. Here, genetics was useful to analyze the Sicilian *O. cuniculus* population and overall to distinguish which lineage this population belongs to out of the existing ones: lineage A (*O. c. algirus*) and lineage B (*O. c. cuniculus*), as described by Branco et al. (2000). Due to the possible intake of genetically different rabbits, which could cause a hybrid population with more health problems than the native Sicilian population that has evolved and already adapted itself to the environment, this new information can help to plan future strategies for the correct management and conservation of the Sicilian rabbit.

This study can also serve to stimulate further investigations of the genetic history of the rabbit in Sicily in order to reconstruct rabbit phylogeography in the Mediterranean, which has yet to be fully understood.

We conclude that the results related to the mtDNA analysis are consistent with the hypothesis that the Sicilian rabbit is more similar to *O. c. cuniculus*, in agreement with morphological data (Lo Valvo et al., 2014), and in disagreement with Toschi (1965), who ascribed the

Sicilian rabbit population to the O. c. algirus subspecies. Accordingly, Hardy et al. (1994) reported on rabbits from Zembra (Tunisia), a Mediterranean island near Sicily, belonging to the O. c. cuniculus subspecies. In a more recent study, rabbits from the island of Mallorca were identified as belonging to O. c. cuniculus, having origins from Iberian and French populations (Seixas et al., 2014). Instead, the IP population in the northeast was regarded as O. c. cuniculus, whereas populations in the southwest of the IP, North Africa, the Mediterranean islands (including Sicily), and the Portuguese Atlantic islands were considered as O. c. algirus (Branco et al., 2000; Esteves et al., 2004). All other introduced populations and domesticated varieties were considered to be descendants of the nominate subspecies (Monnerot et al., 1994; Branco et al., 2000; Branco and Ferrand, 2003).

Nevertheless, it is conceivable that an original form of *O. c. algirus* in Sicily has undergone a simple hybridization or a gene introgression after the introduction of *O. c. cuniculus* even if we have never found hybrids in Sicily. There has, moreover, not been sufficient time to determine whether *O. c. cuniculus* has been substituted by *O. c. algirus* because of the very recent intake of new rabbits on the island (in the 1980s). Thus, we hypothesize that the only species that has always lived in Sicily could be *O. c. cuniculus*.

Since mitochondrial DNA is inherited through the maternal line, given the large number of rabbits raised on Sicilian territory and the complex dynamics due to humanmediated introductions, only careful analysis conducted on genomic DNA can show whether the population of wild Sicilian rabbits belongs to a nominate subspecies or whether it is a hybrid population. If the second hypothesis were true, then this population would be a remarkable case study for evolutionary and conservation biology.

Furthermore, the Mediterranean-type ecosystem is characterized by hot, dry summers and mild, rainy winters. It is considered a very important center of biodiversity, after the tropics, and comprises the Italian Mediterranean Sea and the IP (Cowling et al., 1996), known as places of refuge for temperate species during past glaciations, as well as for rabbits (Taberlet et al., 1998).

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Consequently, examination of the ecological and economic importance of this lagomorph in Sicily, and the study of its genetic diversity compared to its geographical distribution, can help in designing adequate conservation and management strategies and in preserving ecosystems and biodiversity.

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CLUSTAL 2.1 multiple sequence alignment

LineA Oc-algirus	ATCCAACATCTCTGCTTGATGAAACTTTGGCTCTCTGCTAGGCCTATGCCTTATAATTCA	60
Mexicol		60
NexTCOA		60
12-SICILY	ATCAAACATCTCTGCCTGATGAAACTTTGGCTCTCTACTAGGCCTGTGCCTTATAATTCA	60
2-Sicily	ATCAAACATCTCTGCCTGATGAAACTTTGGCTCTCTACTAGGCCTGTGCCTTATAATTCA	60
10-Sicily	ATCAAACATCTCTGCCTGATGAAACTTTGGCTCTCTACTAGGCCTGTGCCTTATAATTCA	60
13-Sicily	ATCAAACATCTCTGCCTGATGAAACTTTGGCTCTCTACTAGGCCTGTGCCTTATAATTCA	60
8-Sicily	ATCAAACATCTCTGCCTGATGAAACTTTGGCTCTCTACTAGGCCTGTGCCTTATAATTCA	60
3-Sicily	ATCAAACATCTCTGCCTGATGAAACTTTGGCTCTCTACTAGGCCTGTGCCTTATAATTCA	60
7-Sicily	ATCAAACATCTCCACCTGATGAAACTTTGGCTCTCTACTAGGCCTGTGCCTTATAATTCA	60
A-Sicily		60
4 DICITY		00
LINEB_OC-CUNICUIUS_		60
CanadaB	ATCAAACATCTCTGCCTGATGAAACTTTTGGCTCTCTACTAGGCCTGTGCCTTATAATTCA	60
South.AfricaB	ATCAAACATCTCTGCCTGATGAAACTTTGGCTCTCTACTAGGCCTGTGCCTTATAATTCA	60
ItalyB	TCTCTGCCTGATGAAACTTTGGCTCTCTACTAGGCCTGTGCCTTATAATTCA	52
SwedenB	ATCAAACATCTCTGCCTGATGAAACTTTGGCTCTCTACTAGGCCTGTGCCTTATAATTCA	60
1-Sicily	ATCAAACATCTCTGCCTGATGAAACTTTGGCTCTCTACTAGGCCTGTGCCTTATAATTCA	60
6-Sicily	ATCAAACATCTCTGCCTGATGAAACTTTGGCTCTCTACTAGGCCTGTGCCTTATAATTCA	60
9-Sicily	ATCAAACATCTCCACCTGATGAAACTTTGGCTCTCTACTAGGCCTGTGCCTTATAATTCA	60
5-Sicily	ATCAAACATCTCCACCTGATGAAACTTTGGCTCTCTACTAGGCCTGTGCCTTATAATTCA	60
11-Sicily	ΔΨCΔΔΔCΔΨCΨCΨCCΨGΔΨGΔΔΔCΨΨΨGGCΨCΨCΨΔCΦΔCΦΔGCCCΨGΨGCCΨΨΔΨΔΔΨΨCΔ	60
Lenus europaeus		60
Lepus.europaeus		EE
Lepus.corsicanus	ACATTICAGCCIGAIGAAACIIIGGCICCCIAIIAGGACIAIGCCIAAIAAICCA * ** * ******** **** ** * * * * * ***** ****	55
Time 2 On all simula		100
LineA_OC-aigirus_	AATTUTUACTGGTUTATTUTTAGCUATACACTACACCTUTGACACAACAACAGCATTCTC	120
MexicoA	AATTCTCACTGGTCTATTCTTAGCCATACACTACACCTCTGACACAACAACAGCATTCTC	120
12-Sicily	AATTTTCACTGGCCTATTCTTAGCCATACACTACACCTCTGACACAACAACAGCATTCTC	120
2-Sicily	AATTTTCACTGGCCTATTCTTAGCCATACACTACACCTCTGACACAACAACAGCATTCTC	120
10-Sicily	AATTTTCACTGGCCTATTCTTAGCCATACACTACACCTCTGACACAACAACAGCATTCTC	120
13-Sicily	AATTTTCACTGGCCTATTCTTAGCCATACACTACACCTCTGACACAACAACAGCATTCTC	120
8-Sicily	AATTTTCACTGGCCTATTCTTAGCCATACACTACACCTCTGACACAACAACAGCATTCTC	120
3-Sicily	ΔΑͲͲͲͲϹΆϹͲGGCCͲΆͲͲϹͲͲΆGCCΆͲΆCΆCΤΑCΆCCͲCͲGΆCΆCΆΔCΆCΆCΑ	120
7-Sicily		120
/ Sicily		120
4-SICILY		100
LineB_OC=Cuniculus_	AATTTTCACTGGCCTATTCTTAGCCATACACTACACCTCTGACACAACAACAGCATTCTC	120
CanadaB	AATTTTCACTGGCCTATTCTTAGCCATACACTACACCTCTGACACAACAACAGCATTCTC	120
South.AfricaB	AATTTTCACTGGCCTATTCTTAGCCATACACTACACCTCTGACACAACAACAGCATTCTC	120
ItalyB	AATTTTCACTGGCCTATTCTTAGCCATACACTACACCTCTGACACAACAACAGCATTCTC	112
SwedenB	AATTTTCACTGGCCTATTCTTAGCCATACACTACACCTCTGACACAACAACAGCATTCTC	120
1-Sicily	AATTTTCACTGGCCTATTCTTAGCCATACACTACACCTCTGACACAACAACAGCATTCTC	120
6-Sicily	AATTTTCACTGGCCTATTCTTAGCCATACACTACACCTCTGACACAACAACAGCATTCTC	120
9-Sicily	AATTTTCACTGGCCTATTCTTAGCCATACACTACACCTCTGACACAACAACAGCATTCTC	120
5-Sicily		120
11_Sigily		120
11-51C119		120
Lepus europaeus		115
Lepus.corsicanus	AATCCTAACTGGCCTGTTCCTAGCTATACACTACACATCAGCAACAGCATTTTC	115
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	HincII	
LineA_Oc-algirus_	ATCAGTAACCCATATTTGCCGAGATGTAAATTACGGCTGACTCATCCGGTACCTCCACGC	180
MexicoA	ATCAGTAACCCATATTTGCCGAGATGTAAATTACGGCTGACTCATCCGGTACCTCCACGC	180
12-Sicily	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC	180
2-Sicilv	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC	180
10-Sicily		
10 010111	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC	180
13-Sicily	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC	180
13-Sicily	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGACAGTGTTAACTATGGCTGACTTATCCGATACCTCCACGC	180 180
13-Sicily 8-Sicily	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC	180 180 180
13-Sicily 8-Sicily 3-Sicily	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC	180 180 180 180
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13-Sicily 8-Sicily 3-Sicily 7-Sicily 4-Sicily	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC	180 180 180 180 180 180
13-Sicily 8-Sicily 3-Sicily 7-Sicily 4-Sicily LineB_Oc-cuniculus_	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC	180 180 180 180 180 180 180
13-Sicily 8-Sicily 3-Sicily 7-Sicily 4-Sicily LineB_Oc-cuniculus_ CanadaB	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC	180 180 180 180 180 180 180 180
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13-Sicily 8-Sicily 3-Sicily 4-Sicily LineB_Oc-cuniculus_ CanadaB South.AfricaB ItalyB SwedenB	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC	180 180 180 180 180 180 180 180 180 172 180
13-Sicily 8-Sicily 3-Sicily 7-Sicily 4-Sicily LineB_Oc-cuniculus_ CanadaB South.AfricaB ItalyB SwedenB 1-Sicily	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC	180 180 180 180 180 180 180 180 180 172 180 180
13-Sicily 8-Sicily 3-Sicily 4-Sicily LineB_Oc-cuniculus_ CanadaB South.AfricaB ItalyB SwedenB 1-Sicily 6-Sicily	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC	180 180 180 180 180 180 180 180 172 180 180 180
13-Sicily 8-Sicily 3-Sicily 7-Sicily 4-Sicily LineB_Oc-cuniculus_ CanadaB South.AfricaB ItalyB SwedenB 1-Sicily 6-Sicily 9-Sicily	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC	180 180 180 180 180 180 180 180 172 180 180 180
13-Sicily 8-Sicily 3-Sicily 7-Sicily 4-Sicily LineB_Oc-cuniculus_ CanadaB South.AfricaB ItalyB SwedenB 1-Sicily 6-Sicily 9-Sicily 5-Sicily	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC	180 180 180 180 180 180 180 180 172 180 180 180 180
13-Sicily 8-Sicily 7-Sicily 4-Sicily LineB_Oc-cuniculus_ CanadaB South.AfricaB ItalyB SwedenB 1-Sicily 6-Sicily 9-Sicily 5-Sicily	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC	180 180 180 180 180 180 180 180 172 180 180 180 180 180
13-Sicily 8-Sicily 3-Sicily 7-Sicily 4-Sicily LineB_Oc-cuniculus_ CanadaB South.AfricaB ItalyB SwedenB 1-Sicily 6-Sicily 9-Sicily 5-Sicily 11-Sicily	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC	180 180 180 180 180 180 180 180 180 180
13-Sicily 8-Sicily 7-Sicily 4-Sicily LineB_Oc-cuniculus_ CanadaB South.AfricaB ItalyB SwedenB 1-Sicily 6-Sicily 9-Sicily 5-Sicily 11-Sicily Lepus.europaeus	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC CCCAGTTACCACATATTTGCCGAGATGTTAACTATAGGCTGACTTATCCGATACCTCCACGC	180 180 180 180 180 180 180 180 180 180
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13-Sicily 8-Sicily 3-Sicily 7-Sicily 4-Sicily LineB_Oc-cuniculus_ CanadaB South.AfricaB ItalyB SwedenB 1-Sicily 6-Sicily 9-Sicily 11-Sicily Lepus.europaeus Lepus.corsicanus	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC CTCAGTAACCCATATTTGCCGAGATGTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTAACTATGGCTGACTTATCCGATACCTCCACGC TTCAGTCACACATATTTGCCGAGATGTAACTATGGCTGACTCATTGCTAACCTCCACGC TTCAGTCACACATATTTGCCGAGATGTAACTATGGCTGACTCATTGCTACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTAACTACGGCTGACTCATTGCTACCCACGC TTCAGTCACACATATTTGCCGAGATGTAACTATGGCTGACTCATTGCTACCTAC	1800 1800 1800 1800 1800 1800 1800 1800
13-Sicily 8-Sicily 3-Sicily 7-Sicily 4-Sicily LineB_Oc-cuniculus_ CanadaB South.AfricaB ItalyB SwedenB 1-Sicily 6-Sicily 9-Sicily 11-Sicily Lepus.europaeus Lepus.corsicanus	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC TTCAGTAACCCATATTTGCCGAGATGTAACTATGGCTGACTTATCCGATACCTCCACGC TTCAGTAACCCATATTTGCCGAGATGTAACTATGGCTGACTTATCCGATACCTCCACGC TTCAGTAACCCATATTTGCCGAGATGTAACTATGGCTGACTTATCCGATACCTCCACGC TTCAGTACACATATTTGCCGAGATGTAACTATGGCTGACTTATCCGATACCTCCACGC TTCAGTCACACATATTTGCCGAGATGTAACTATGGCTGACTTATCCGATACTCCACGC TTCAGTCACACATATTTGCCGAGATGTAACTACGGCTGACTCACTGCTACCCACGC TTCAGTCACACATATTTGCCGAGATGTAACTACGGCTGACTTATCCGATACTCCCACGC TTCAGTCACACATATTTGCCGAGATGTAACTACGGCTGACTTATTCGGTACCTCCACGC TTCAGTCACACATATTTGCCGAGACGTAAACCACGGCGCGCGC	1800 1800 1800 1800 1800 1800 1800 1800
13-Sicily 8-Sicily 3-Sicily 7-Sicily 4-Sicily LineB_Oc-cuniculus_ CanadaB South.AfricaB ItalyB SwedenB 1-Sicily 6-Sicily 9-Sicily 5-Sicily 11-Sicily Lepus.europaeus Lepus.corsicanus LineA_Oc-algirus_ MexicoA	ATCAGTAACCCATATTTGCCGAGATGTTAACTATGGCTGACTTATCCGATACCTCCACGC CTCAGTAACCCATATTTGCCGAGATGTAACTATGGCTGACTTATCCGATACCTCCACGC ATCAGTAACCCATATTTGCCGAGATGTAACTATGGCTGACTTATCCGATACCTCCACGC CTCAGTAACCCATATTTGCCGAGATGTAACTATATGGCTGACTTATCCGATACCTCCACGC TTCAGTAACCCATATTTGCCGAGATGTAACTATATGGCTGACTTATCCGATACTCCACGC CTCAGTAACCCATATTTGCCGAGATGTAACTATATGGCTGACTTATCCGATACTCCACGC TTACACACACATATTTGCCGAGATGTAACTATATGGCTGACTTATCCGATACTCCACGC ATCAGTAACCCATATTTGCCGAGATGTAACTATATGGCTGACTTATCCGATACTCCACGC TTCAGTACACCATATTTGCCGAGATGTAACTATACGGCGCGCGGAATCTACTA TAACGGAGCATCTATATTCTTTATTTGTCTTTACATACACGTAGCGCGCGGGAATCTACTA	1800 1800 1800 1800 1800 1800 1800 1800

Figure S1. Multiple sequence alignment of *Oryctolagus cuniculus* cyt *b* mtDNA from different individuals. GenBank accession numbers are indicated in Table 1. The single enzyme restriction sites are highlighted in colors/gray.

2-Sicily TAACGGAGCATCTATATTCTTTATTTGCCTCTACATACACGTAGGCCGCGGAATCTACTA 240 10-Sicily TAACGGAGCATCTATATTCTTTATTTGCCTCTACATACACGTAGGCCGCGGAATCTACTA 240 13-Sicily ΤΑΑCGCAGCATCTATATTCTTTTTCCCTCTACATACACGTAGGCCGCGCAATCTACTA 240 TAACGGAGCATCTATATTCTTTATTTGCCTCTACATACACGTAGGCCGCGGAATCTACTA 240 8-Sicily TAACGGAGCATCTATATTCTTTATTTGCCTCTACATACACGTAGGCCGCGGAATCTACTA 240 3-Sicily 7-Sicily TAACGGAGCATCTATATTCTTTATTTGCCTCTACATACACGTAGGCCGCGGAATCTACTA 240 4-Sicily TAACGGAGCATCTATATTCTTTATTTGCCTCTACATACACGTAGGCCGCGGAATCTACTA 240 LineB Oc-cuniculus TAACGGAGCATCTATATTCTTTATTTGCCTCTACATACACGTAGGCCGCGGAATCTACTA 240 CanadaB TAACGGAGCATCTATATTCTTTATTTGCCTCTACATACACGTAGGCCGCGGAATCTACTA 240 South.AfricaB TAACGGAGCATCTATATTCTTTATTTGCCTCTACATACACGTAGGCCGCGGAATCTACTA 240 TAACGGAGCATCTATATTCTTTATTTGCCTCTACATACACGTAGGCCGCGGAATCTACTA 232 ItalyB SwedenB TAACGGAGCATCTATATTCTTTATTTGCCTCTACATACACGTAGGCCGCGGAATCTACTA 240 TAACGGAGCATCTATATTCTTTATTTGCCTCTACATACACGTAGGCCGCGGAATCTACTA 240 1-Sicilv 6-Sicily TAACGGAGCATCTATATTCTTTATTTGCCTCTACATACACGTAGGCCGCGGAATCTACTA 240 TAACGGAGCATCTATATTCTTTATTTGCCTCTACATACACGTAGGCCGCGGAATCTACTA 240 9-Sicily 5-Sicily TAACGGAGCATCTATATTCTTTATTTGCCTCTACATACACGTAGGCCGCGGAATCTACTA 240 TAACGGAGCATCTATATTCTTTATTTGCCTCTACATACACGTAGGCCGCGGAATCTACTA 240 11-Sicily TAATGGAGCATCAATATTCTTTATTTGCTTATATATACATGTAGGCCGTGGAATCTACTA 240 Lepus.europaeus Lepus.corsicanus ** ******* ***** ***** * ** ***** ***** ** **** LineA Oc-algirus TGGGTCATACACATACCTAGAAACCTGAAACATCGGCATTATCCTCCTATTCGCAGTGAT 300 MexicoA TGGGTCATACACATACCTAGAAACCTGAAACATCGGCATTATCCTCCTATTCGCAGTGAT 300 TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT 300 12-Sicily TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT 300 2-Sicily TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT 10-Sicily 13-Sicily TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT 8-Sicily TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT 300 3-Sicilv 7-Sicilv TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT 4-Sicily TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT 300 LineB Oc-cuniculus TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT 300 CanadaB TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT 300 TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT 300 South.AfricaB TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT 292 ItalyB TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT 300 SwedenB TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT 1-Sicilv TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT 300 6-Sicily 9-Sicily TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT 300 5-Sicily TGGATCATACACATACCTAGAGACCTGAAACATTGGCATCATCCTCCTATTCGCAGTAAT 300 11-Sicily CGGCTCATATACTTACCTAGAAACCTGAAACATTGGCATTATTCTACTATTCGCAGTAAT 300 Lepus.europaeus Lepus.corsicanus TGGCTCATATACTTACCTAGAAACCTGGAATATTGGCATTATTCTTCTATTTGCAGTAAT 295 **** ** ** ***** ** * * * * * * * * LineA Oc-algirus_ AGCCACAGCATTCANGGGATATGTTCTCCCCATGAGGTCAAATATCATTTTGAGGAGCAAC 360 AGCCACAGCATTCATGGGATATGTTCTCCCATGAGGTCAAATATCATTTTGAGGAGCAAC 360 MexicoA AGCCACAGCATTTATGGGTTATGTCCTCCCATGAGGACAAATATCATTTTGGGGAGCAAC 12-Sicily AGCCACAGCATTTATGGGTTATGTCCTCCCATGAGGACAAATATCATTTTGGGGAGCAAC 2-Sicilv 10-Sicily AGCCACAGCATTTATGGGTTATGTCCTCCCATGAGGACAAATATCATTTTGGGGAGCAAC 13-Sicily AGCCACAGCATTTATGGGTTATGTCCTCCCATGAGGACAAATATCATTTTGGGGAGCAAC 360 8-Sicily AGCCACAGCATTTATGGGTTATGTCCTCCCATGAGGACAAATATCATTTTGGGGAGCAAC 360 3-Sicily AGCCACAGCATTTATGGGTTATGTCCTCCCATGAGGACAAATATCATTTTGGGGAGCAAC 360 7-Sicily AGCCACAGCATTTATGGGTTATGTCCTCCCATGAGGACAAATATCATTTTGGGGAGCAAC 360 4-Sicily AGCCACAGCATTTATGGGTTATGTCCTCCCATGAGGACAAATATCATTTTGGGGAGCAAC 360 AGCCACAGCATTTATCGGTTATGTCCTCCCATGAGGACAAATATCATTATGGGGAGCAAC LineB Oc-cuniculus AGCCACAGCATTTATCGGTTATGTCCTCCCATGAGGACAAATATCATTATGGGGAGCAAC CanadaB South.AfricaB AGCCACAGCATTTATCGGTTATGTCCTCCCATGAGGACAAATATCATTATGGGGAGCAAC AGCCACAGCATTTATGGGTTATGTCCTCCCATGAGGACAAATATCATTTTGGGGAGCAAC ItalyB AGCCACAGCATTTATGGGTTATGTCCTCCCATGAGGACAAATATCATTTTGGGGAGCAAC SwedenB 1-Sicily AGCCACAGCATTTATGGGTTATGTCCTCCCATGAGGACAAATATCATTTTGGGGAGCAAC 6-Sicily AGCCACAGCATTTATGGGTTATGTCCTCCCATGAGGACAAATATCATTTTGGGGAGCAAC 360 9-Sicily AGCCACAGCATTTATGGGTTATGTCCTCCCATGAGGACAAATATCATTTTGGGGAGCAAC 360 5-Sicily AGCCACAGCATTTATGGGTTATGTCCTCCCATGAGGACAAATATCATTTTGGGGAGCAAC 360 AGCCACAGCATTTATGGGTTATGTCCTCCCATGAGGACAAATATCATTTTGGGGAGCAAC 360 11-Sicily GGCTACAGCATTCATAGGCTACGTCCTCCCATGAGGACAAATATCATTCTGAGGGGGCTAC Lepus.europaeus AGCCACAGCATTTATAGGCTATGTCCTCCCATGAGGACAAATATCATTCTGAGGCGCTAC Lepus.corsicanus ** ********* ********** LineA Oc-algirus MexicoA 12-Sicily 2-Sicily 10-Sicily 13-Sicily 8-Sicily

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4-Sicily LineB Oc-cuniculus CanadaB South.AfricaB ItalvB SwedenB 1-Sicilv 6-Sicily 9-Sicilv 5-Sicily 11-Sicily Lepus.europaeus Lepus.corsicanus LineA Oc-algirus MexicoA 12-Sicily 2-Sicily 10-Sicily 13-Sicily 8-Sicily 3-Sicilv 7-Sicily 4-Sicily LineB Oc-cuniculus CanadaB South.AfricaB ItalyB SwedenB 1-Sicily 6-Sicily 9-Sicily 5-Sicilv 11-Sicily Lepus, europaeus Lepus.corsicanus LineA Oc-algirus MexicoA 12-Sicily 2-Sicilv 10-Sicily 13-Sicily 8-Sicily 3-Sicily 7-Sicily 4-Sicily LineB Oc-cuniculus CanadaB South.AfricaB ItalyB SwedenB 1-Sicily 6-Sicily 9-Sicily 5-Sicily 11-Sicily Lepus.europaeus Lepus.corsicanus LineA Oc-algirus MexicoA 12-Sicily 2-Sicily 10-Sicily 13-Sicily 8-Sicilv 3-Sicily 7-Sicily 4-Sicily LineB Oc-cuniculus CanadaB South.AfricaB ItalvB SwedenB

***** ** ** ** ** ********* **** ***** ** Sall /<u>HinclI</u> CTGAGGAGGGTTTTCA<mark>GTCGAC</mark>AAAGCCACTCTAACCCGATTTTTCGCTTTTCACTTCAT 480 CTGAGGAGGGTTTTCAGTCGACAAAGCCACTCTAACCCGATTTTTCGCTTTTCACTTCAT 480 CTGAGGAGGATTTTCAGTTGATAAAGCTACTCTTACCCGATTCTTCGCTTTTCACTTCAT 480 CTGAGGAGGATTTTCAGTTGATAAAGCCACTCTTACCCGATTCTTCGCTTTTCACTTCAT 480 CTGAGGAGGATTTTCAGTTGATAAAGCCACTCTTACCCGATTCTTCGCTTTTCACTTCAT 480 CTGAGGAGGATTTTCAGTTGATAAAGCCACTCTTACCCGATTCTTCGCTTTTCACTTCAT 480 CTGAGGAGGATTTTCAGTTGATAAAGCCACTCTTACCCGATTCTTCGCTTTTCACTTCAT 480 CTGAGGAGGATTTTCAGTTGATAAAGCCACTCTTACCCGATTCTTCGCTTTTCACTTCAT 472 CTGAGGAGGATTTTCAGTTGATAAAGCCACTCTTACCCGATTCTTCGCTTTTCACTTCAT 480 CTGAGGAGGATTTTCAGTTGATAAAGCCACTCTTACCCGATTCTTCGCTTTTCACTTCAT 480 CTGAGGAGGATTTTCAGTTGATAAAGCCACTCTTACCCGATTCTTCGCTTTTCACTTCAT 480 CTGAGGAGGATTTTCAGTTGATAAAGCCACTCTTACCCGATTCTTCGCTTTTCACTTCAT 480 CTGAGGAGGATTTTCAGTTGATAAAGCCACTCTTACCCCGATTCTTCGCTTTTCACTTCAT 480 CTGAGGAGGATTTTCAGTTGATAAAGCCACTCTTACCCGATTCTTCGCTTTTCACTTCAT 480 CTGAGGAGGATTTTCAGTCGATAAAGCCACACTTACCCGATTTTTCGCTTTTCACTTTAT 480 TTGAGGAGGGTTCTCAGTCGACAAAGCTACACTCACCCGATTCTTCGCTTTCCACTTCAT 475 ***** **** AluI CCTACCATTTATCATTGCAGCTTTAGTCTTAATTCACCTCCTCCTACATGAAACTGG 540 CCTACCATTTATCATTGCAGCTTTAGTCTTAATTCACCTCCTCCTACATGAAACTGG 540 CTTGCCATTTATCATTGCAGCTTTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG 540 CTTGCCATTTATCATTGCAGCTTTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG 540 ${\tt CTTGCCATTTATCATTGC} {\tt AGCT} {\tt TTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG} {\tt 540}$ CTTGCCATTTATCATTGCAGCTTTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG 540 CTTGCCATTTATCATTGCAGCTTTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG 540 CTTGCCATTTATCATTGCAGCTTTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG 540 CTTGCCATTTATCATTGCAGCTTTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG 540 CTTGCCATTTATCATTGCAGCTTTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG 540 CTTGCCATTTATCATTGCAACTTTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG 540 CTTGCCATTTATCATTGCAACTTTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG 540 CTTGCCATTTATCATTGCAACTTTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG 540 CTTGCCATTTATCATTGCAACTTTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG 532 CTTGCCATTTATCATTGCAACTTTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG 540 CTTGCCATTTATCATTGCAACTTTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG 540 CTTGCCATTTATCATTGCAACTTTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG 540 CTTGCCATTTATCATTGCAACTTTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG 540 CTTGCCATTTATCATTGCAACTTTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG 540 CTTGCCATTTATCATTGCAACTTTAGTCTTAATTCACCTCCTCTTTCTACATGAAACTGG 540 TCTCCCATTCATCATCGCAGCACTAGTGATGATTCACCTACTTTTCCTCCATGAAACTGG 535 * ***** ** ** *** * * * * * * ***** * ** ** EcoRI TTCCAACAACCCCACAGGAATCCCCTCAAACTCAGATAAAATCCCTTTTCATCCCTACTA 600 TTCCAACAACCCCACAGGAATCCCCTCAAACTCAGATAAAATCCCTTTTCATCCCTACTA 600 CTCCAACAACCCCACAGGAATTCCTTCAAACTCAGATAAAATCCCTTTCCACCCCTACTA 600 CTCCAACAACCCCACAG<mark>GAATTC</mark>CTTCAAACTCACATAAAATCCCTTTCCACCCCTACTA 600 CTCCAACAACCCCACAGGAATTCCTTCAAACTCAGATAAAATCCCTTTCCACCCCTACTA 600 CTCCAACAACCCCACAG<mark>GAATTC</mark>CTTCAAACTCAGATAAAATCCCTTTCCACCCCTACTA 600 CTCCAACAACCCCACAG<mark>GAATTC</mark>CTTCAAACTCAGATAAAATCCCTTTCCACCCCTACTA 600 CTCCAACAACCCCACAG<mark>GAATTC</mark>CTTCAAACTCAGATAAAATCCCTTTCCACCCCTACTA 600 CTCCAACAACCCCACAG<mark>GAATTC</mark>CTTCAAACTCAGATAAAATCCCTTTCCACCCCTACTA 600 CTCCAACAACCCCACAG<mark>GAATTC</mark>CTTCAAACTCAGATAAAATCCCTTTCCACCCCTACTA 600 CTCCAACAACCCAACAGGAATTCCTTCAAACTCAGATAAAATCCCTTTCCACCCCTACTA 600 CTCCAACAACCCAACAGGAATTCCTTCAAACTCAGATAAAATCCCTTTCCACCCCTACTA 600 CTCCAACAACCCAACAG<mark>GAATTC</mark>CTTCAAACTCAGATAAAATCCCTTTCCACCCCTACTA 600 CTCCAACAACCCCACAGGAATTCCTTCAAACTCAGATAAAATCCCTTTCCACCCCTACTA 592 CTCCAACAACCCCACAGGAATTCCTTCAAACTCAGATAAAATCCCTTTCCACCCCTACTA 600

1-Sicily CTCCAACAACCCCACAGGAATTCCTTCAAACTCAGATAAAATCCCTTTCCACCCCTACTA 600 6-Sicily CTCCAACAACCCCACAG<mark>GAATTC</mark>CTTCAAACTCAGATAAAATCCCTTTCCACCCCTACTA 600 9-Sicily 5-Sicily CTCCAACAACCCCACAG<mark>GAATTC</mark>CTTCAAACTCAGATAAAATCCCTTTCCACCCCTACTA 600 CTCCAACAACCCCACAGGAATTCCTTCAAACTCAGATAAAATCCCTTTCCACCCCTACTA 600 11-Sicily Lenus, europaeus CTCCAATAACCCATCAGGCATCCCATCAAACTCTGATAAAATTCCATTCCACCCCTACTA 600 Lepus.corsicanus CTCCAATAATCCATCAGGTATCCCATCAGACTCTGATAAGATTCCATTCCACCCCTATTA 595 ++++ ++ ++ +++ **** **** 44 44 LineA Oc-algirus TACAATCAAAGACACCTTAGGATTCCTTATAGCCGTTATTCTCCTCCTTATCTTAGTCCT 660 TACAATCAAAGACACCTTAGGATTCCTTATAGCCGTTATTCTCCTCCTTATCTTAGTCCT 660 MexicoA 12-Sicily CACAATCAAAGACACCCTAGGTTTCCTTGTAGCCATTCTTCTCCTCCTTATTTTAGTCCT 660 2-Sicily CACAATCAAAGACACCCTAGGTTTCCTTGTAGCCATTCTTCTCCTCCTTATTTTAGTCCT 660 CACAATCAAAGACACCCTAGGTTTCCTTGTAGCCATTCTTCTCCTCCTTATTTTAGTCCT 660 10-Sicily CACAATCAAAGACACCCTAGGTTTCCTTGTAGCCATTCTTCTCCCCCCTTATTTTAGTCCT 660 13-Sicily 8-Sicily 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Lepus.corsicanus LineA Oc-algirus MexicoA 12-Sicily 2-Sicily 10-Sicily 13-Sicily 8-Sicily 3-Sicily 7-Sicily 4-Sicily LineB Oc-cuniculus CanadaB South.AfricaB ItalyB SwedenB 1-Sicily 6-Sicily 9-Sicily 5-Sicily 11-Sicily Lepus.europaeus Lepus.corsicanus LineA Oc-algirus MexicoA 12-Sicilv 2-Sicily 10-Sicilv 13-Sicily 8-Sicily 3-Sicily 7-Sicily 4-Sicily LineB Oc-cuniculus CanadaB South.AfricaB ItalyB SwedenB 1-Sicilv 6-Sicily 9-Sicily 5-Sicily 11-Sicily Lepus.europaeus Lepus.corsicanus LineA Oc-algirus MexicoA 12-Sicily 2-Sicily 10-Sicily 13-Sicily 8-Sicily 3-Sicily 7-Sicily 4-Sicily LineB Oc-cuniculus CanadaB South.AfricaB ItalyB SwedenB 1-Sicily 6-Sicily 9-Sicily 5-Sicily 11-Sicily Lepus.europaeus Lepus.corsicanus

CCCTCCCCATATCAAACCTGAATGGTATTTTCTATTTGCCTACGCCATTTTACGCTCCAT 775 **** ** ** AluI CCCTAATAAACTAGGTGGTGTTCTAGCCCTAGTTATATCAATTCTTATCCTAGCAATTAT 840 CCCTAACAAACTAGGAGGCGTTCTAGCCCTAGTTATGTCAATTCTCATCCTAGCAATTAT 835 ***** DrdI CCCATTCCTCCATATATCTAAACAACGTANCATGATATTCCGACCCATTAGCCAAGTCCT 900 CCCATTCCTTCATATATCTAAACAACGTAGCATGATATTCCGACCCATCAGCCAAGTCCT 900 CCCATTCCTTCATATGTCTAAACAACGTAGCATGATATTCCGACCCATTAGTCAAGTCCT 892 CCCATTCCTTCATATGTCTAAACAACGTAGCATGATATTCCGACCCATTAGTCAAGTCCT 900 CCCATTCCTTCATATGTCTAAACAACGTAGCATGATATTCCGACCCATTAGTCAAGTCCT 900 CCCATTCCTTCATATGTCTAAACAACGTAGCATGATATTCCGACCCATTAGTCAAGTCCT 900 CCCATTCCTTCATATGTCTAAACAACGTAGCATGATATTCCGACCCATTAGTCAAGTCCT 900 CCCATTCCTTCATATGTCTAAACAACGTAGCATGATATTCCGACCCATTAGTCAAGTCCT 900 CCCATTCCTTCATATGTCTAAACAACGTAGCATGATATTCCGACCCATTAGTCAAGTCCT 900 CCCCTTCCTTCATATATCCAAACAACGTAGCATAATATTCCGCCCCATTAGCCAAGTCCT 900 CCCCTTCCTCCACATATCCAAACAACGCAGCATAGTATTCCGACCCATTAGCCAAGTCCT 895 *** ***** ** ** ** ******* ****** ***** ** EcoRI ATTCTGAATCCTCGTCGCAGATCTTCTGACACTGACATGAATCGGGGGGTCAGCC 954 ATTCTGAATCCTCGTCGCAGATCTTCTGACACTGACATGAATCGGGGGTCAGCC 954 ATTCTGAGTTCTCGTCGCAGATCTTCTCACACTCACATGAATCGGAGGCCAACC 954 ATTCTGAGTTCTCGTCGCAGATCTTCT----- 927 ATTCTGAGTTCTCGTCGCAGATCTTCTCACACTCACATGAATCGGAGGCCAACC 954 ATTCTGAGTTCTCGTCGCAGATCTTCTCACACTCACATGAATCGGAGGCCAACC 954 ATTCTGAGTTCTCGTCGCAGATCTTCTCACACTCACATGAATCGGAGGCCAACC 954 ATTCTGAGTTCTCGCCGCAGATCTTCTCACACTCACATGAATCGGAGGCCAACC 954 ATTCTGAGTTCTCGTCGCAGATCTTCTCACACTCACATGAATCGGAGGCCAACC 954 ATTCTGAGTTCTCGTCGCAGATCTTCTCACACTCACATGAATCGGAGGCCAACC 954 ATTCTGAGTTCTCGTCGCAGATCTTCTCACACTCACATGAATCGGAGGCCAACC 954 ATTCTGAGTTCTCGTCGCAGATCTTCTCACACTCACATGAATCGGAGGCCAACC 954 ATTCTGAGTTCTCGTCGCAGATCTTCTCACACTCACATGAATCGGAGGCCAACC 954 ATTCTGAGTTCTCGTCGCAGATCTTCTCACACTCACATGAATCGGAGGCCAACC 946 ATTCTGAGTTCTCGTCGCAGATCTTCTCACACTCACATGAATCGGAGGCCAACC 954 ATTCTGAGTTCTCGTCGCAGATCTTCTCACACTCACATGAATCGGAGGCCAACC 954 ATTCTGAGTTCTCGTCGCAGATCTTCTCACACTCACATGAATCGGAGGCCAACC 954 ATTCTGAGTTCTCGTCGCAGATCTTCTCACACTCACATGAATCGGAGGCCAACC 954 ATTCTGAGTTCTCGTCGCAGATCTTCTCACACTCACATGAATCGGAGGCCAACC 954 ATTCTGAGTTCTCGTCGCAGA----- 921 TTTCTGAATCCTTGTCGCAGACCTTCTTACACTCACATGAATTGGAGGACAACC 954 CTTCTGAATTCTCGTTGCAGACCTTCTGACACTCACATGGATTGGAGGACAACC 949 والمرابقة المرابق المرابق

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4-Sicily	1A
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LineB_Oc-cuniculus_ CanadaB South.AfricaB ItalyB SwedenB	T. C. T. T. A. T. C. T. T. A. T. C. T. T. A. T. C. T. A.
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ItalyB	CC
SwedenB	CC
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Lepus corsi capus	
Lepus.corsteanus	C
LineA_Oc-algirus_	TGGGTCATACACATACCTAGAAACCTGAAACATCGGCATTATCCTCCTATTCGCAGTGAT
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LINEB_OC-CUNICULUS_	····A·································
CanadaB	A
South AfricaB	A
ItalyB	AC
SwedenB	ACC
1-Sicily	AC
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9-Sicily	AC
5-Sicily	AC
11-Sicily	AC
Lepus.europaeus	CCTTA
Lepus.corsicanus	CTT
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LineA Oc-algirus	AGCCACAGCATTCANGGGATATGTTCTCCCATGAGGTCAAATATCATTTTGAGGAGCAAC
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LineB_Oc-cuniculus_	A
CanadaB	A
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SwedenB	
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Lepus, europaeus	G. T TA C C C
Lepus corsicerus	
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LineA_Oc-algirus_	CGTAATCACTAACCTTCTATCAGCAATCCCATATATCGGAACAACCTTAGTTGAATGAA
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LineB_Oc-cuniculus_	CC
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11-Sicily	C
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Lepus carojanna	
Lepus.corsicanus	1
LineA_Oc-algirus_	CTGAGGAGGGTTTTCAGTCGACAAAGCCACTCTAACCCGATTTTTCGCTTTTCACTTCAT
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LineB_Oc-cuniculus_	ATT
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Lepus.europaeus	A
Lepus.corsicanus	TCCTACCC.
LineA Oc-algirus	CCTACCATTTATCATTGCAGCTTTAGTCTTAATTCACCTCCTCTTCCTACATGAAACTGG
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IU-SICILY	.T.GT.
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LineB Oc-cuniculus	T.G.
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Lepus.europaeus	СТСGAТ.АТ.АТ.
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xo. cororoundo	

LineA_Oc-algirus_	TTCCAACAACCCCACAGGAATCCCCTCAAACTCAGATAAAATCCCTTTTCATCCCTACTA
MexicoA	
12-Sicily	СТ.Т.ТСССС.
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LineB_Oc-cuniculus_	CATTCCC
CanadaB	CATTCCC
South.AfricaB	САТ.Т.ТССС
ItalyB	СССТТ
SwedenB	ССС
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11-Sicily	CCCCC
Lepus.europaeus	CTATCATTACC.
Lepus.corsicanus	CTTATTAGTGTACCT
LineA Oc-algirus	TACAATCAAAGACACCTTAGGATTCCTTATAGCCGTTATTCTCCTCCTTATCTTAGTCCT
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7-Sicily	ССТGАС
4-Sicily	C
LineB Oc-cuniculus	ССТАСТТ
CanadaB	
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South.AfricaB	CCTGACT
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South.AfricaB ItalyB SwedenB 1-Sicily 6-Sicily 9-Sicily 5-Sicily 11-Sicily Lepus.europaeus Lecus.corsicanus	C
South.AfricaB ItalyB SwedenB 1-Sicily 6-Sicily 9-Sicily 5-Sicily 11-Sicily Lepus.europaeus Lepus.corsicanus	C. C. T. G. A. C. T. C. . C. T. G. A. C. T. C. . A. C. T. G. A. C. T. C. . A. C. T. C. T. C. T. C. . A. C. T. C. T. C. C. .
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South.AfricaB ItalyB SwedenB 1-Sicily 6-Sicily 9-Sicily 5-Sicily 11-Sicily Lepus.europaeus Lepus.corsicanus	C. C. T. G. A. C. T. C. A. C. T. G. A. C. T. C. A. C. T. G. A. C. T. C. C. T. G. G. A. C. T. C. T. C. T. G. T. C. G. A. C. T. C. </td
South.AfricaB ItalyB SwedenB 1-Sicily 6-Sicily 9-Sicily 5-Sicily 11-Sicily Lepus.europaeus Lepus.corsicanus LineA_Oc-algirus_ MexicoA	C.
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LineA_Oc-algirus_	CCCTCCTCATATCAAACCAGAGTGATACTTTCTATTTGCCTATGCTATCCTACGCTCTAT
MexicoA	A
12-Sicily	C
2-Sicily	C
10-Sicily	C
13-Sicily	C
8-sicily	C
3-Sicily	C
7-Sicily	C
4-sicily	
LipeB Oc-cupiculus	С Л С
CanadaB	C 7 C
Canadab Couth AfricaD	······
South.AfricaB	·····C································
ItalyB	C
SwedenB	C
1-Sicily	C
6-Sicily	C
9-Sicily	C
5-Sicily	C
11-Sicily	C
Lenus europaeus	
Lepus corgi conug	
Lepus.corsicanus	······
LineA Oc-algirus	TCCAAATAAACTCGGAGGAGTCCTAGCACTAGTTTTATCTATC
MexicoA	
12-Sicily	GG
2-Sicily	G T CC C
10-Sicily	
12-Sicily	
0 disile	
8-SICILY	
3-Sicily	G
7-Sicily	GG
4-Sicily	GG
LineB Oc-cuniculus	CCC
CanadaB	C
South.AfricaB	Сс
ItalvB	. Т
SwedenB	
1-Sicily	т сс с
	······
6-SICILY	T
9-Sicily	·····CC····C·····
5-Sicily	CC.
11-Sicily	CC
Lepus.europaeus	CTATTTTCAATA.CAA.T
Lepus.corsicanus	CTCACTCA.GATCA.CAA.T
LineA Oc-algirus	CCCATTCCTCCATATATCTAAACAACGTANCATGATATTCCGACCCATTAGCCAAGTCCT
MexicoA	
12-Sicily	т с с т
2_Sicily	т с с т
10 Cicily	
10-SICILY	
13-Sicily	······
8-Sicily	TGG
3-Sicily	TGGG
7-Sicily	TGG
4-Sicily	TGG
LineB Oc-cuniculus	TGG
CanadaB	TG
South AfricaB	
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T-STOTTÀ	
o-sicily	······.T·····T·····T······T···········
9-Sicily	fG
5-Sicily	TGG
11-Sicily	$\cdots \cdots \mathbb{T} \cdots \mathbb{G} \cdots G$
Lepus.europaeus	CTCGAC
Lepus.corsicanus	C

LineA_Oc-algirus_	ATTCTGAATCCTCGTCGCAGATCTTCTGACACTGACATGAATCGGGGGTCAGCC 95	54
MexicoA		54
12-Sicily	G.T	54
2-Sicily	G.T	27
10-Sicily	G.T	54
13-Sicily	G.TAC	54
8-Sicily	G.T	54
3-Sicily	G.T	54
7-Sicily	G.T	54
4-Sicily	G.T	54
LineB Oc-cuniculus	G.T	54
CanadaB	G.T	54
South.AfricaB	G.T	54
ItalyB	G.T	16
SwedenB	G.T	54
1-Sicily	G.T	54
6-Sicily	G.T	54
9-Sicily	G.T	54
5-Sicily	G.T	54
11-Sicily	G.T	21
Lepus.europaeus	ТТСТСТАА95	54
Lepus.corsicanus	CTTCCGTAA94	19