

Molecular analysis of recently introduced populations of the Italian wall lizard (*Podarcis siculus*)

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SUPPLEMENTARY MATERIAL

Table S1. Molecular diversity indices based on *cytb* for *Podarcis siculus* and its clades including the introduction sample size (n_{In}), the general sample size (n), the number of haplotypes (H), haplotype diversity (h), and nucleotide diversity (π).

	n_{In}	n	H	h	π
Clade S1	0	17	3	0.974	0.021
Clade S2	2	7	7	0.951	0.006
Clade S3	14	154	54	0.985	0.021
Clade A1	0	5	3	0.932	0.028
Clade A2	13	71	16	0.953	0.007
Clade A3	0	10	3	0.982	0.009
Clade T	28	66	20	0.934	0.020
Total	57	330	106	0.961	0.025

Table S2. Uncorrected genetic distances (p-distances) between seven clades of *Podarcis siculus* media based on *cytb* marker.

	Clade S1	Clade S2	Clade S3	Clade A1	Clade A2	Clade A3	Clade T
Clade S1							
Clade S2	0.0515						
Clade S3	0.0574	0.0515					
Clade A1	0.0791	0.0674	0.0782				
Clade A2	0.0850	0.0703	0.0820	0.0146			
Clade A3	0.0821	0.0733	0.0812	0.0381	0.0351		
Clade T	0.0977	0.0821	0.0791	0.0558	0.0569	0.0645	

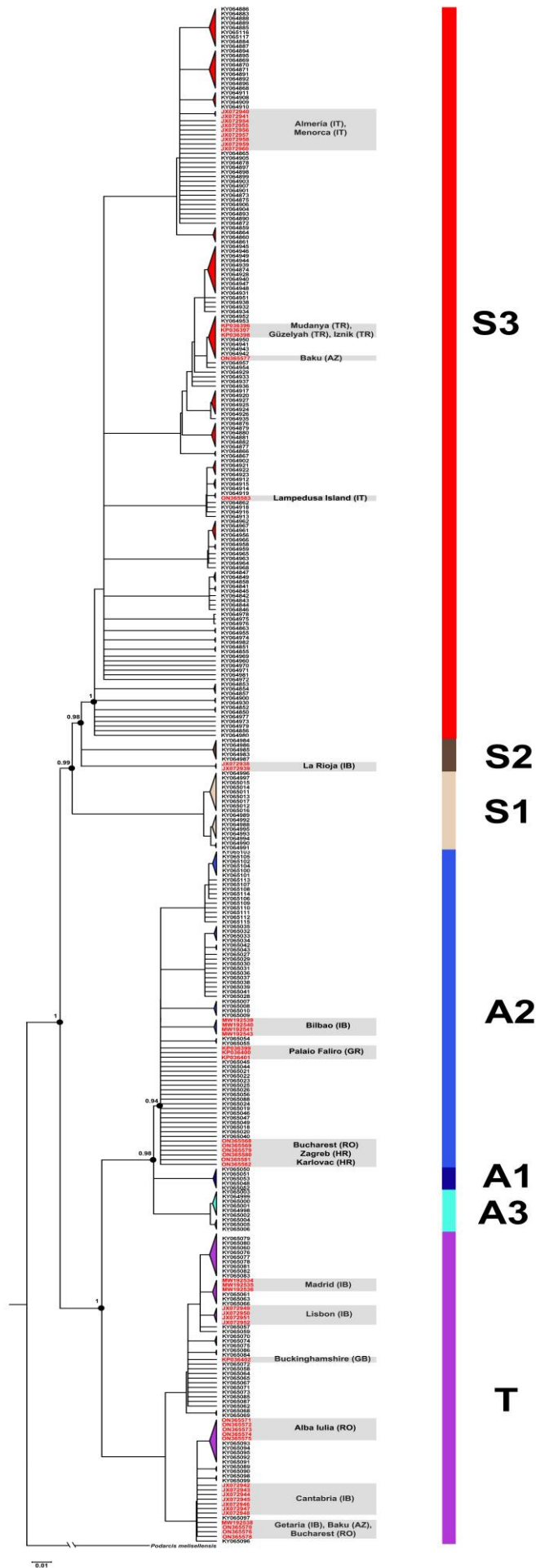


Figure S1. Phylogenetic tree of the *cytb* data of *Podarcis siculus* set obtained with MrBayes. The seven clade such as its nested haplogroups are depicted with different colors according to Senczuk et al. (2017). GenBank numbers of introduced populations are marked in red. Location names are highlighted in gray rectangle; Abbreviation: AZ – Azerbaijan, GB - Great Britain, GR – Greece, HR – Croatia, IB - Iberian Peninsula, IT –Italy, RO – Romania.