

## Short Note

# In “defense” of *Podarcis latastei*, an Italian insular endemic species (Squamata: Lacertidae)

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**Abstract.** Based on genetic and morphological evidence, Senczuk et al. (2019) formally raised the *Podarcis* populations from the Western Pontine Islands, previously classified as several subspecies of *P. siculus*, to species rank, i.e. *Podarcis latastei* (Bedriaga, 1879). This taxonomic change was not accepted in the checklist of the European herpetofauna by Speybroeck et al. (2020), recently published on Amphibia-Reptilia. In this note we respond to the reasons given by Speybroeck and colleagues and support the validity of *Podarcis latastei* as an endemic Italian species.

**Keywords:** island, Italian wall lizard, Lataste’s lizard, species delimitation, taxonomy.

In a recent review Speybroeck et al. (2020) provided an updated annotated species list of the European herpetofauna. This list leaves the species included in four previous checklists (Gasc et al., 1997, 2004; Sindaco and Jerecenko, 2008; Sindaco, Venchi and Grieco, 2013) unchanged, testing the validity of all new taxa proposed in the last years. In doing this, a conservative approach was applied since a series of recent taxonomic proposals have been rejected.

Following three recent detailed works based on genetics and morphology (Senczuk et al., 2018a, 2018b, 2019), Senczuk et al. (2019) formally raised the *Podarcis* populations from the

Western Pontine Islands, previously classified as several subspecies of *P. siculus*, to species rank, i.e., *Podarcis latastei* (Bedriaga, 1879), as ‘latastei’ was the oldest name available. However, Speybroeck et al. (2020) maintained in their checklist *P. latastei* as a subspecies of the Western Pontine Islands within the polytypic species *P. siculus* (Rafinesque, 1810).

Three points were given by Speybroeck et al. (2020, p. 21) for this decision:

1. “... the amount of divergence between the Western Pontine populations and the rest of the *P. siculus* complex in Senczuk et al. (2019) is only presented as a combined mtDNA and nuclear DNA tree, not allowing to check if nuclear data independently supports this species-level divergence or not”.

2. “More detailed results by Senczuk et al. (2017, 2018) display a much more complex situation, where the Western Pontine lineage appears as one of several deeply divergent lineages in *P. siculus*, and *latastei* and *siculus* are not reciprocally monophyletic”.

3. “While Senczuk et al. (2018) indicated differentiation in nuclear DNA between at least some of the main mtDNA lineages in *P. siculus*,

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no information on their level of reproductive isolation is yet available”.

Therefore Speybroeck et al. (2020) conclude that: “As a consequence, while the TC (... Taxonomic Committee ...) acknowledges that *P. siculus* as currently understood is possibly made up of several species, one of them corresponding to the Western Pontine islands populations, we consider adopting any formal taxonomic change premature”.

We have different arguments to answer to such criticisms, detailed below point by point, and we think that present evidence supports the recognition of the species rank for *P. latastei*:

1. In Senczuk et al. (2019) the results of mtDNA and nuDNA were presented combined in a single tree to corroborate the phylogenetic position of *P. latastei*. In fact, separate mtDNA and nuDNA analysis were already available in Senczuk et al. (2018b). In this last paper, mtDNA phylogeny is presented as a phylogenetic tree while, nuDNA relationships as two separate statistical parsimony networks (MC1R and B-FIB). These two networks showed a clear separation of *P. latastei* in respect to all other *P. siculus* populations. A certain level of haplotype sharing is present in the two species that therefore lack for a complete monophyly at these two markers. However, this situation is comparable with that observed among pairs of accepted species in *Podarcis* as, for example, in the Iberian and Nord African group of species (Pinho, Harris and Ferrand, 2008). In fact, in this group there is a complete lack of monophyly at nuclear markers of the mitochondrial-defined groups with many alleles that are even shared by distinct species (Pinho, Harris and Ferrand, 2008) and this is also true among very highly differentiated ones (Pinho, Harris and Ferrand, 2008; Salvi, Pinho and Harris, 2017). This situation has been interpreted by the authors as due to ancestral polymorphism and to

instances of introgression (Pinho et al., 2008).

2. Speybroeck et al. (2020) suggested that the elevation of *P. latastei* to species level would led to a non-monophyletic condition in *P. siculus* because in Senczuk et al. (2018b) *P. latastei* results as sister of a subclade of *P. siculus*. To this criticism we answer that even if the tree topologies in Senczuk et al. (2018b) suggested paraphyly of *P. siculus*, the relationships between *P. latastei* and the lineages of *P. siculus* are uncertain as the confidence value of the node supporting the position of *P. latastei* is very low (0.65). When nuclear and mitochondrial genes are combined as in Senczuk et al. (2019), the topology of the phylogeny changes with *P. siculus* being monophyletic but still with uncertainty given by the low support value at the nodes (0.70). Finally, the species monophyly is not a necessary requirement for species status even in the rules given by Speybroeck et al. (2020, p. 4). As also pointed out by Speybroeck et al. (2020) ‘*Podarcis siculus*’ is possibly a species complex awaiting a complete revision that at the end will probably identify a number of monophyletic clades.
3. The last point raised by Speybroeck et al. (2020) is that since there is no information on reproductive isolation of the mainland lineages of *P. siculus*, then a specific status of the insular lineage cannot be assessed. This sentence, implicitly, considers the lineages in the mainland of the same taxonomic rank as the one present on Western Pontine. Probably, but not explicitly explained by Speybroeck et al. (2020), because some of these lineages have a divergence time comparable to that observed for *P. latastei*. We disagree with this line of thinking. Instead, we think that the insularity itself of *P. latastei* is very important in order to affirm its specific status. In fact, it is widely recognized that

islands represent a set of particular conditions for which evolution is accelerated with a large number of studies focusing on lizards (e.g., Herrel et al., 2008; Raia et al., 2010; Senczuk et al., 2014; de Amorim et al., 2017; Anderson and Poe, 2019; Zhu et al., 2020). The time of isolation of *P. latastei*, has been estimated around 4 million years (Senczuk et al., 2019), in agreement with the genesis and geological evolution of these islands (Cadoux et al., 2005). This large time span allowed *P. latastei* to evolve more markedly than the mainland lineages of *P. siculus*. In fact, we observed a greater distinction of the two studied nuclear markers compared to the distinction observed among the lineages present on the mainland (Senczuk et al., 2018b). Moreover, and more significantly, the distinction of *P. latastei* respect to mainland populations is showed by the recently published geometric morphometry work on variation in head shape (Senczuk et al., 2018a). This study, overlooked and not cited by Speybroeck et al. (2020), showed that the populations of the Western Pontine Islands are significantly different from those of the mainland as well as those on the eastern Pontine Islands. This result enforces the morphological uniqueness of the Western Pontine Archipelago respect to other populations. Moreover, our study has also highlighted another important aspect. The populations of the Western Pontine morphologically overlap with those once present on the Island of Santo Stefano (Eastern Pontine). The latter became extinct in historical times, probably due to the invasion of *P. siculus* currently the only lacertids on the island. It is therefore not to be excluded that *P. latastei* had a wider distribution that included also Eastern Pontine in the past.

An additional aspect that we should consider is that not even a single mitochondrial haplotype belonging to the continental lineages of

*P. siculus* has been found on the western Pontine Archipelago. Since that *P. siculus* has colonized in recent times by long distance passive transport several islands of the Mediterranean Sea (Silva-Rocha et al., 2014; Santos et al., 2019), including for example the Tremiti Islands and the Eastern Pontine (Senczuk et al., 2017), it seems very strange to us that this has not happened for the Western Pontine. Although there are signs of sporadic introgression of some nuclear haplotypes (Senczuk et al., 2018b), the absence of mitochondrial haplotypes indicates some type of “blocking” of invasive lizards belonging to the mainland. This phenomenon may include “density blocking”, local adaptation or competitive exclusions (Waters et al., 2013) and suggests a certain level of reproductive isolation that would be interesting to study in depth (Nosil et al., 2005).

We understand that the criterium adopted by Speybroeck et al. (2020) in their checklist is a prudential one that gives value to taxonomic stability. However regrettably, there is no guarantee that such approach is more error-free than the alternative ones (e.g., Robuchon et al., 2019). Artificial taxonomic stability may have negative consequences for the future of hidden endemic taxa, as in the case reported here of *P. latastei* (Melville et al., 2019), and this may be particularly dangerous in Europe due to an excessively rigid list of endangered species that govern biodiversity policies in the continent (Gippoliti et al., 2017).

Furthermore, we understand all the difficulties that Speybroeck et al. (2020) faced in drawing up their checklist and the need to find compromises. However, their decision to only consider recent taxonomic changes while leaving the previous species unchanged has nothing to do with “Taxonomy” and even “Biology”. In fact, this procedure risks not considering as valid species taxa which, on the other hand, are much more differentiated than those currently present in the list.

For all the above reasons we will continue to use the species rank for the *Podarcis* population

inhabiting the Western Pontine Islands. This species represents a new undescribed taxon, as also highlighted by Speybroeck et al. (2020), and it is not a simple elevation of a subspecies to the rank of species. In fact, only thanks to molecular phylogenetics analyzes emerged the real evolutionary unit, with its distribution and its evolutionary history hinged on the archipelago for millions of years.

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