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The morphological paradox of the Maltese Wall Lizard *Podarcis filfolensis* (Bedriaga, 1876)

A short note on reevaluating taxonomic classifications

Arnold Sciberras, June 2025

Abstract

The Maltese Wall Lizard *Podarcis filfolensis* has long fascinated biologists due to its remarkable phenotypic plasticity and island-specific traits. Historically, the species was divided into multiple subspecies based on morphology, a framework that persisted unchallenged for most of the 20th century. However, contemporary genetic studies undermine the subspecies model, instead revealing two major clades across the Maltese and Pelagian Islands. This paper reviews historical and modern taxonomic interpretations, presents detailed morphological field observations, and critiques the persistent misuse of outdated subspecies nomenclature in both academic and public discourse. We advocate for the recognition of island morphs within a single species model and call for institutional leadership in taxonomic modernization.

Keywords: Maltese Wall Lizard *Podarcis filfolensis*, Island Morphology, Maltese Islands.

Introduction

Island biogeography offers unique insights into speciation, isolation, and evolutionary adaptation. The Maltese and Pelagian Islands, situated centrally in the Mediterranean, are home to a single endemic lacertid species: the Maltese Wall Lizard, *Podarcis filfolensis* (Bedriaga, 1876). For nearly a century, five subspecies were recognized based on phenotypic variation correlated with geographic origin (Sciberras 2007, Savona-Ventura 2001). These included the forms from mainland Malta, Gozo, Comino, Filfla, and the now-extinct Selmunett population.

However, until the mid 2010s, these classifications remained largely unchallenged, despite growing awareness of the limitations of morphology-based taxonomy. Renewed attention emerged with the advent of molecular techniques. A pivotal decade-old genetic study by Salvi et al. (2014) involving 16 lizard populations (including the extinct Selmunett) revealed the absence of subspecies and the presence of two distinct clades: the Gozitan clade (Gozo, Comino, associated islets, and Pelagian Islands) and the Maltese clade (Malta and its satellites). The Filfla population, though part of the Maltese group, exhibited a unique genetic divergence. These revelations call into question the continued use of outdated taxonomy in modern publications, government documents, websites, and educational materials. The retention of subspecies names where no taxonomic justification exists undermines both scientific clarity and conservation priorities.

Historical context of subspecies designations

The traditional classification into five subspecies was based entirely on morphological traits such as dorsal patterns, body size, scale arrangement, and coloration. These features, however, are influenced by micro-environmental conditions, predator regimes, and island size parameters that can mislead taxonomic decisions when considered in isolation. Savona-Ventura (2001) advanced the field by proposing four degrees of melanism, relating these to Pleistocene sea-level fluctuations and island isolation events. His work was critical in highlighting the morphological diversity of *P. filfolensis* across Malta and the Pelagian islands, and set a precedent for understanding biogeographic patterns in the region. Despite the significance of such early efforts, they lacked genetic context. As we now know from mitochondrial and nuclear DNA studies, morphological variation is not always mirrored by significant phylogenetic divergence (Salvi et al. 2014).

Morphological trends across the Archipelago

Malta

Mainland Malta presents the highest degree of intra-island variation. Observations indicate that urban populations such as in Fgura, Paola, and Tarxien resemble the extinct Selmunett form in both body shape and dorsal markings. Coastal lizards from Sliema, Gżira, St. Julian's, and Buġibba to Qawra typically show lighter colored pigmentation yet thicker dorsal pattern and a smoother scale texture compared to inland specimens. When it comes to size, it was noted that coastal specimens vary, being somewhat larger than inland ones. However, there remains a striking biogeographic anomaly: lizards are absent along the first 2 km inland on the western coast of Malta, suggesting strong environmental or geological constraints (Sciberras 2006a, 2006b, 2007a). Places like Ghajn Tuffieha, Bajja tal-Mixquqa, Ghadira and Anchor Bay are exceptional and have small introduced populations from the 1990s.

Gozo and Comino

Gozo maintains a more uniform population, generally marked by vivid dorsal coloration and a darker net-back pattern. The population of Dwejra area looks like an intermediate between Gozo and Fungus Rock specimens (Sciberras 2007b). Comino, by contrast, supports a dull-colored population, with light undersides and low dorsal contrast, traits aligning with typical coastal phenotypes.

Isolated Islet Populations

The satellite islets are morphologically distinctive. Cominotto, Pigeon Rock, Halfa Rock, Battery Rock, and Tac- Cawl Rock each host highly localized morphs. Cheirolophus Rock supports the most melanistic form recorded to date. Filfla's population is more robust (being the largest) variable focusing on the melanistic side and largest overall, comprising at least three subpopulations showing morphological isolation. The Fungus Rock's form, dorsally, closely resembles the melanistic populations of the Pelagian Islands (excluding that the underbelly is bright red), Linosa and Lampione, indicating a convergent evolution. These variations underline how island microecology and historical isolation shape morphology without necessarily affecting phylogenetic relationships.

Genetic realignment of taxonomy

The 2014 study by Salvi et al. marked a watershed moment for Maltese herpetology. Mitochondrial and nuclear DNA from all known populations confirmed a lack of genetic differentiation sufficient to support subspecies designations. Instead, two broad clades were identified:

Gozitan Clade: Gozo, Comino, surrounding islets, extinct Selmunett, and Pelagian Islands.

Maltese Clade: Mainland Malta and associated satellite islets.

Filfla, while genetically part of the Maltese clade, showed modest divergence likely resulting from extreme isolation and founder effects.

Furthermore, a 2025 whole-genome sequence of a female Filfla specimen confirmed the pattern observed by Salvi et al. (2014), supporting species-level unity despite unique localized adaptations (Feiner et al. 2025). With the latest study we are also aware of the affinity with other species.

Taxonomic stagnation and scientific responsibility

Despite the overwhelming genetic evidence, many academic and public-facing publications continue to use the outdated subspecies taxonomy. This inconsistency has broader implications. Why do we resist updating *P. filfolensis* taxonomy when other Mediterranean herpetofauna have undergone timely revisions? We propose that this inertia is institutional and systemic. Taxonomic modernization must begin with national authorities, conservation agencies, and academic bodies. Only then can accurate knowledge cascade down to educators, journalists, and enthusiasts. Importantly, shedding the subspecies label does not devalue the endemic nature of these populations. On the contrary, it elevates them through recognition of ecological specialization within a unified evolutionary framework.

Evolutionary considerations and island biogeography

The *Podarcis* genus itself diverged from *Lacerta* in the late Miocene, distinguished by skeletal and hemipenial morphology and now comprising 27 species and over 200 subspecies. During the Messinian salinity crisis (~5.96–5.33 Ma), extensive island colonization, divergence, and hybridization occurred (Oliverio et al. 2000). In Malta, observed morphological diversity fits the classic island biogeography model (MacArthur & Wilson 1967): larger islands promote greater morphological variation, while smaller islets exhibit homogenized traits due to founder effects and ecological constraints.

Conclusion

The *Podarcis filfolensis* case study illustrates the critical role of integrative taxonomy, melding morphology, genetics, and ecology. While morphological differences across the Maltese archipelago are real and ecologically significant, they do not justify subspecies designation in the absence of genetic support. To ensure scientific integrity and conservation efficacy, stakeholders must retire outdated nomenclature and adopt a morph-based population model grounded in modern genetic evidence. Let us not delay this update any longer; science evolves and our language and classifications must too.

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