



## One subspecies less for the European herpetofauna: the taxonomic and nomenclatural status of *Hemidactylus turcicus spinalis* (Reptilia: Gekkonidae)

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Reptile systematics is currently primarily supported by genetic evidence, which has brought numbers of cases of taxonomic reconsiderations within the last years. Genetic studies have resulted in taxonomic changes at the subspecific level with many subspecies being synonymized with species, lumped together, or elevated to a species status (see Torstrom *et al.* 2014 for a review). The reptile fauna of Europe ranks among the best studied in the world in terms of taxonomy, yet it still includes taxa whose original descriptions were based on insufficient morphological diagnoses and the status of which should be reassessed by integrating genetic methods. One such case is provided here.

*Hemidactylus turcicus* (Linnaeus) is a species distributed throughout the whole Mediterranean, most probably due to human-aided dispersal. Previous studies identified two widely distributed haplotype groups of *H. turcicus*—clade A and clade B (Moravec *et al.* 2011; Rato *et al.* 2011) with almost parapatric distribution ranges, roughly corresponding to northeastern and southwestern Mediterranean, respectively. The diversification between the clades A and B is nevertheless very shallow compared to genetic structure detected in other *Hemidactylus* species (Carranza & Arnold 2012; Šmíd *et al.* 2013). Regarding the taxonomy and nomenclature of *H. turcicus* we (Moravec *et al.* 2011) speculated about the phylogenetic position and taxonomic validity of the narrow-range and generally neglected subspecies *H. turcicus spinalis* Buchholz (type locality Isla Addaya Grande [Illa Gran d'Addaia] off the north coast of Menorca) and concluded that genetic examination of specimens from its type locality should precede any taxonomic decisions.

Buchholz (1954) based the description of *H. t. spinalis* on the distinct, longitudinally striped dorsal pattern of five specimens from Illa Gran d'Addaia (Fig. 1). Other morphological characters examined by him did not differ from those in other populations of *H. turcicus*. The subspecies was accepted in the influential compendium by Mertens & Wermuth (1960). Later on, despite the claim by Martínez-Rica (1974) that Buchholz's diagnostic characters were vague and unsatisfactory for a subspecies description, the taxon was considered valid by Salvador (1981), listed in the 1992 Red Book of Spanish Vertebrates as Rare (R) (Blanco *et al.* 1992) and in its updated 2002 version as Least Concern (LC) (Geniez 2002), and some authors continued to speculate on its validity (Salvador & Pleguezuelos 2002; Sindaco & Jeremčenko 2008; Rivera *et al.* 2011). Recently, van den Berg *et al.* (2013) pointed out that the dorsal colour pattern was not consistent among all specimens of *H. t. spinalis* on Illa Gran d'Addaia. The authors suggested rejecting the validity of this subspecies by arguing that the description was based on a limited number of specimens that may have been closely related and thus shared the unique morphological trait. Nevertheless, genetic data supporting this rejection were until now missing.

Here we provide the first genetic data of the *spinalis* morphotype from the type locality of *H. t. spinalis* and compare them with published sequences of *H. turcicus* from throughout its range (including Asiatic Turkey, its proposed type locality [Moravec *et al.* 2011]) to finally settle the debate concerning the validity of *H. t. spinalis*.

New material examined comprised four specimens of *Hemidactylus turcicus* from Illa Gran d'Addaia including the animal reported by van den Berg (2013; sample code JS323) and three voucher specimens from the collection of the National Museum, Prague (NMP6V 74986/1–3, sample codes M16–M18), some with very markedly developed dark dorsal stripe typical for the *spinalis* morphotype. Additionally, three individuals from the adjoining Menorcan city of Port d'Addaia (NMP6V 74984 [sample M05], NMP6V 74985/1–2 [M06–M07]) were examined. Photographs of all specimens together with all sequence alignments were deposited in MorphoBank (<http://www.morphobank.org>, Project 1236).

*H. lemurinus*, *H. mindiae*) published in previous studies (Carranza & Arnold 2006; Gamble *et al.* 2011; Moravec *et al.* 2011; Rato *et al.* 2011; Šmíd *et al.* 2013) into a single dataset. Two specimens of *H. flaviviridis* were used as outgroup (samples JS111 and JS119 from Šmíd *et al.* 2013). Assembly of contigs, sequence alignment, substitution model selection, and maximum likelihood (ML) analysis of the two mtDNA gene fragments concatenated were performed as described in details by Šmíd *et al.* (2013). The best nucleotide substitution models were as follows: *12S*, *cytb*—GTR + G; *cmos*, *rag2*—JC; *mc1r*—HKY. Only unique haplotypes were included in the ML analysis. Haplotype identification was done in DnaSP 5.1 (Rozas *et al.* 2003), which recognized 68 unique haplotypes. To infer genealogical relationships within *H. turcicus* for each nuclear gene we phased the alignments and reconstructed haplotype networks following Rato *et al.* (2011), with the only difference that the *p* threshold was set to 0.7. Because Rato *et al.* (2011) and Šmíd *et al.* (2013) sequenced different *rag2* fragments that overlap only partially (334 bp) the alignment was trimmed to include only this overlapping region.

All samples of *H. t. spinalis* shared identical haplotypes in all genes but *rag2* in which the sample JS323 differed in two nucleotide positions along the 334 bp long alignment. All phylogenetic analyses were congruent in that *H. t. spinalis* is nested within the *H. turcicus* clade B (Fig. 1). Sequences of all gene fragments were identical to those of *H. turcicus* already deposited in GenBank: *12S*—KC818741, DQ120299–300 shared with samples from Turkey, Cyprus, Jordan, Greece, Croatia, Italy, France, Tunisia, Spain, Morocco, Portugal, and USA; *cytb*—DQ120146–47, HQ675989, HQ676016, HQ833728–29 shared with samples from Tunisia, Spain, and Morocco; *cmos*—JQ957162 shared with samples from Turkey, Lebanon, Egypt, Albania, and Spain; *mc1r* - JQ957301 shared with samples from Egypt and Spain; *rag2*—e.g. HQ676055–56 (M16–M18) and JQ957423, JQ957440–42 (JS323) shared with samples of *H. turcicus* from Turkey, Israel, Egypt, and Spain and even with other *Hemidactylus* species (*H. dawudazraqi*, *H. lemurinus*, *H. mindiae*). Because all these genes have identical haplotypes deposited in Genbank we do not submit the data there.

The three NMP specimens from Illa Gran d'Addaia have the following morphological characters: supralabials 8–9; infralabials 6–8; rows of dorsal tubercles 12–14; lamellae under 1<sup>st</sup> toe 6–7; lamellae under 4<sup>th</sup> toe 10; preanal pores 6–7; SVL 42.6–52.4 mm. All morphological characters of the specimens from Illa Gran d'Addaia, including the type series of *H. t. spinalis*, fall within the known range of *H. turcicus* intraspecific variability (Moravec *et al.* 2011) (although from the numbers of lamellae under fingers given by Buchholz (1954) we assume he probably confused the 1<sup>st</sup> and 5<sup>th</sup> finger). Examination of the dorsal pattern of seven specimens of *H. turcicus* from Illa Gran d'Addaia (van den Berg *et al.* 2013, NMP collection) revealed a wide variation in the dorsal pattern ranging continuously from spotted to striped forms (Fig. 1).

Therefore, as there are no consistent morphological characters delimiting the Illa Gran d'Addaia population of *H. turcicus* from other Mediterranean populations and all the specimens from Illa Gran d'Addaia are in all examined molecular markers indistinguishable from other *H. turcicus* samples from the Mediterranean (including its designated type locality in Asiatic Turkey), we definitively reject the subspecific status of this population and synonymize the name *Hemidactylus turcicus spinalis* Buchholz, 1954 with the name *Hemidactylus turcicus* (Linnaeus, 1758).

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