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Review

Species list of the European herpetofauna – 2020 update by the Taxonomic Committee of the Societas Europaea Herpetologica

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Abstract. The last species list of the European herpetofauna was published by Speybroeck, Beukema and Crochet (2010). In the meantime, ongoing research led to numerous taxonomic changes, including the discovery of new species-level lineages as well as reclassifications at genus level, requiring significant changes to this list. As of 2019, a new Taxonomic Committee was established as an official entity within the European Herpetological Society, Societas Europaea Herpetologica (SEH). Twelve members from nine European countries reviewed, discussed and voted on recent taxonomic research on a case-by-case basis. Accepted changes led to critical compilation of a new species list, which is hereby presented and discussed. According to our list, 301 species (95 amphibians, 15 chelonians, including six species of sea turtles, and 191 squamates) occur within our expanded geographical definition of Europe. The list includes 14 non-native species (three amphibians, one chelonian, and ten squamates).

Keywords: Amphibia, amphibians, Europe, reptiles, Reptilia, taxonomy, updated species list.

Introduction

Speybroeck, Beukema and Crochet (2010) (SBC2010, hereafter) provided an annotated species list for the European amphibians and non-avian reptiles. A decade later, a sizable amount of new research has been produced, fuelling the need for a contemporary update. Within the European Herpetological Society (Societas Europaea Herpetologica; SEH) and by invitation of the SEH Council, a newly composed Taxonomic Committee (SEH TC, or further TC) was formed in early 2019, and its chair was approved by SEH membership during the Ordinary General Meeting held in Milan,

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September 5th 2019 (SEH News, *Amphibia-Reptilia* **40**: 551-559).

We did not define our own limits for the geographical area considered here, but adopted the limits defined by previous projects. Our goal was to provide a taxonomic reference for the future mapping projects of the SEH. Therefore, we included all areas that were part of previous European atlas projects (cf. Gasc et al., 1997; Sillero et al., 2014). We also aimed at informing the taxonomic backbone of the Fauna Europaea initiative (<https://fauna-eu.org>), and therefore our geographical area also includes all territories that are covered by Fauna Europaea. As a result, we enlarged the geographical area considered by SBC2010 to encompass all areas covered by both Gasc et al. (1997) and Fauna Europaea. Areas included by Gasc et al. (1997), but not by Speybroeck, Crochet and Beukema (2010), include the northern versant of the Caucasus (including north-eastern Azerbaijan), all areas west of the Ural River (including westernmost Kazakhstan) and west of the Ural Mountains, and the Yekaterinburg Region. Areas included in Fauna Europaea, but not by Gasc et al. (1997) or SBC2010, are Macaronesia (without Cape Verde), the Greek Islands off the western Anatolian shore, and Cyprus. As such, our area exceeds that of the most recent European atlas (Sillero et al., 2014) by including Macaronesia, all Greek islands, and parts of Azerbaijan and Kazakhstan (fig. 1). A Google Earth .kml file with the limits of the area is provided in the supplementary material. For the rationale of these limits, we refer to Gasc et al. (1997) and <https://fauna-eu.org/data-handling>).

Upon enlarging the scope area and prior to discussing any taxonomic changes, a broader baseline list had to be set for species occurring outside the area considered by SBC2010. As such, in addition to SBC2010, we followed the taxonomy of Gasc et al. (1997, 2004, including the changes adopted by Dubois and Crochet in the 2004 reprint), and for species outside Europe (including Macaronesia and Cyprus), Sindaco and Jeremčenko (2008) and Sindaco,

Venchi and Grieco (2013). Together, these four sources led to a starting point species list. In the following, we only discuss taxonomic changes which deviate from this species list. We decided against using online databases as starting points, as they are changing constantly, with historical versions not remaining reliably and easily available.

The taxonomic decisions adopted here are not necessarily supported by all authors of this work. According to TC guidelines, a change to the starting list will only be adopted if widely supported among its members, specifically by a >75% majority. When a change is recommended by a large majority of the TC members, but different members favour different outcomes, the adopted solution may be supported by only a simple majority (>50%). Note that this process favours taxonomic stability, with changes requiring large support among TC members to become accepted.

TC members do not necessarily adhere to the same species concept. While many agree with the General Lineage Concept (GLC) of De Queiroz (2007), some prefer the general framework of the Biological Species Concept. However, all agree on using reproductive isolation as the primary operational criterion for the delimitation of species. The majority of TC members is of the opinion that, while every species is a lineage, not every lineage is a species. The common approach can be defined as either following the Biological Species Concept framework, or as applying a Biological Species Criterion under the GLC. More specifically, TC members adhere to a “soft” version of the reproductive isolation criterion. As such, we allow extensive introgression between recognised species, as long as there are intrinsic barriers to gene flow that prevent wide-reaching introgression beyond the contact zones. Even in the absence of geographical barriers, a sufficient level of reproductive isolation has to exist in order to ensure long-term persistence of the diverged lineages. Taxa connected by bimodal or trimodal hybrid zones (Gay et al., 2008) were unanimously treated as

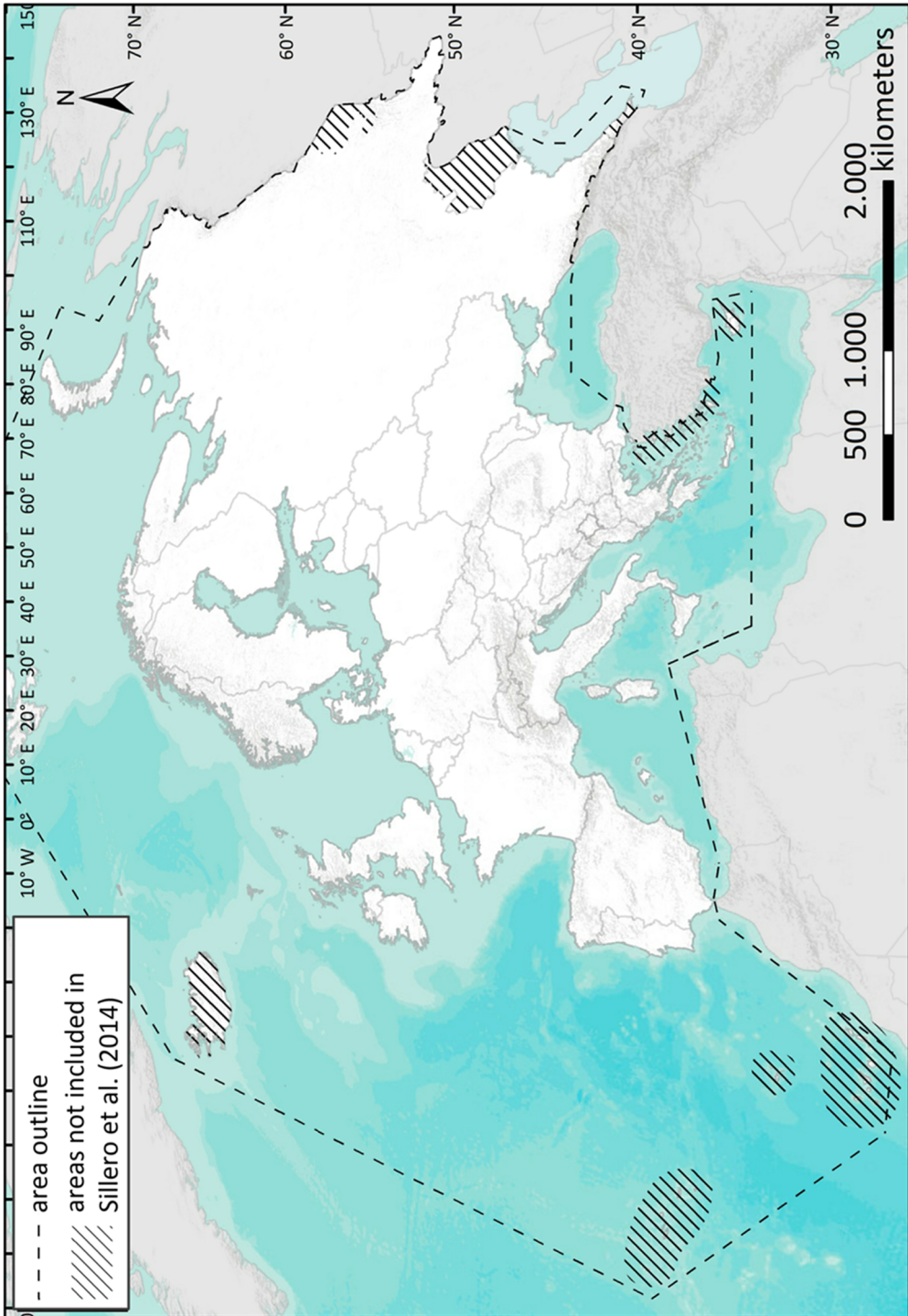


Figure 1. Extent of geographic area (Mollweide projection). Herpetofauna species within this area are dealt with. Shading indicates areas not included by Sillero et al. (2014).

valid species, but opinions often differed regarding how much introgression was “allowed” across unimodal hybrid zones, reflecting different opinions relative to where to cut the grey zone of speciation, how much reproductive isolation is necessary and when to treat incipient species as valid species. For allopatric taxa, or when contact zones were not studied, lineages that had divergence levels similar to closely related, unambiguously distinct species were accepted as species. As an auxiliary criterion, we sometimes use monophyly, even though we do not consider it as a necessary requirement for species status.

For supraspecific classification, the TC agreed to accept only monophyletic units. This causes issues regarding the class Reptilia, which in its traditional definition is paraphyletic through the exclusion of birds. All current hypotheses on the evolution of vertebrates agree that a group including squamates, turtles, *Sphenodon* and crocodiles, but not birds is paraphyletic (see e.g. Chiari et al., 2012a; Hasegawa, 2017). As a consequence, most current classifications of Vertebrata include Aves in the class Reptilia (see e.g. Modesto and Anderson, 2004; Ruggiero et al., 2015). To avoid confusion, we adopt the term ‘non-avian reptiles’ to refer to the components of the European fauna assigned to Testudines/Chelonii and Squamata.

For nomenclatural decisions, including spelling, we followed the International Code of Zoological Nomenclature (the Code hereafter, ICZN (1999 and subsequent changes), see <https://www.iczn.org/>). Such decisions were generally not submitted to voting, but they could be discussed, as many parts of the Code can be subject to interpretation, and many actual cases can be open to different decisions, even under the rules of the Code.

In the following, we review taxonomic and nomenclatural changes proposed since the publication of the four literature sources that we used to build our starting point, as well as other relevant new information pertaining the taxonomy of European amphibians and non-avian

reptiles. For each case, we provide the rationale underlying the respective decision of the TC, and conclude by providing an updated species list of the European herpetofauna.

Amphibia

Caudata/Urodela

A series of phylogenetic studies on mitochondrial DNA, allozymes, and nuclear DNA sequences of members of the family Salamandridae (Litvinchuk et al., 2005; Weisrock et al., 2006; Zhang et al., 2008; Kieren et al., 2018; Veith et al., 2018) confirmed that the newt genus *Triturus* sensu lato, as traditionally recognised, is not monophyletic. Litvinchuk et al. (2005) proposed the separation of *Triturus* into four genera, among which the new genus *Ommatotriton* contains (the former) *Triturus vittatus*. SBC2010 accepted this new arrangement, but did not explicitly acknowledge the need to recognise *Ommatotriton*, as the new genus does not occur in the area they considered. As we herein consider a wider area, we formally accept *Ommatotriton* as a separate genus.

Litvinchuk et al. (2005) also showed that morphology (number of trunk vertebrae, colour pattern), genome size, and allozymes (Nei’s genetic distances of 0.44-0.83) strongly differ between populations in the two widely disjoint areas inhabited by *Ommatotriton vittatus*, namely south-eastern Anatolia and the Levant (*O. v. vittatus*) versus the southern and eastern Black Sea and western Caucasus regions (*O. v. ophryticus*). This led them to elevate *ophryticus* to species level. A more comprehensive study also demonstrated restricted introgression between an eastern and a western taxon along the Black Sea coast of Turkey (van Riemsdijk et al., 2017). Consequently, we recommend to recognise three species in the genus *Ommatotriton*: *O. vittatus* (extralimital) in south-eastern Anatolia and the Levant, *O. ophryticus* in Russia, the Caucasus and northern Anatolia west to the region of Samsun, and *O. nesterovi* (extralimital)

in Anatolia from Samsun to the Sea of Marmara. The populations inhabiting the native *Ommatotriton* range in the European part of Russia belong to *O. ophryticus*, while the introduced (and persisting anno 2019; Speybroeck, pers. obs.) population in north-eastern Spain is of mixed ancestry, with genetic contribution from both *O. ophryticus* and *O. nesterovi* (van Riemsdijk et al., 2018).

In addition to mtDNA sequences, Vences et al. (2014) used sequences from thirteen nuclear loci to improve our understanding of the history of the genus *Salamandra*. Their nuclear data suggest that *Salamandra salamandra* contains several deeply divergent lineages whose monophyly relative to *S. algira* received weak support, although this requires confirmation. Based on mitochondrial data the subspecies *longirostris* is sister to all other *S. salamandra* lineages. However, nuclear genes place it with the subspecies *morenica*. The discordance between mtDNA and nuclear genes may result from past introgression and admixture processes. Furthermore, a clade comprising the subspecies *fastuosa*, *bernardezi* (including populations attributed to the subspecies *alfredschmidti*, whose validity was rejected, as it is phylogenetically nested within several subclades of *bernardezi*; Beukema et al., 2016) and *gigliolii* is recovered with strong support. While additional data are clearly needed, this suggests a high amount of evolutionary divergence within *S. salamandra*, and the existence of more than one species within *S. salamandra* cannot yet be fully ruled out.

SBC2010 recognised two species within the former *Triturus karelinii*: *T. arntzeni* from the Balkan Peninsula, and *T. karelinii*. Wielstra et al. (2013) suggested that the type specimens of *T. arntzeni* are in fact *T. macedonicus*, which led them to place *T. arntzeni* in the synonymy of *T. macedonicus*, and to create the name *ivanbureschi* for the taxon of the *karelinii* complex that occurs in the Balkans and in Western Anatolia. Later, Wielstra and Arntzen (2014) demonstrated that the types of *T. arntzeni* are in fact the

result of ancient admixture between *T. macedonicus* and *T. ivanbureschi*. We do not entirely agree with their interpretation of the Code. As they rightfully state, nomina based on genetically admixed individuals derived through several generations of backcrossing are indeed left in limbo in the Code. Yet, we do not agree that the Code should be interpreted as extending provisions of Art. 23.8 to nomina based on genetically admixed individuals, at least not without clear guidelines of what constitutes admixture in the sense of the Code. We do, however, agree with Wielstra and Arntzen (2014) that *arntzeni*, based on individuals that carry less than 50% of alleles derived from the *karelinii*-complex taxon, should not be used as the valid name for that taxon. We thus accept *T. ivanbureschi* as the valid nomen of the taxon of the *karelinii*-complex that occurs in Europe in the Balkans. With the extension of the geographic range of SBC2010, *T. karelinii* sensu stricto also occurs in our area in Russia, the Crimean Peninsula and the Caucasus region.

Using mitochondrial and nuclear DNA sequences, Sotiropoulos et al. (2007) and Recuero et al. (2014) investigated the phylogenetic structure of *Ichthyosaura alpestris*. They identified several deeply divergent lineages that largely correspond to currently recognised subspecies, except for the subspecies *alpestris*, which is further divided into a western and an eastern main lineage. Interestingly, nuclear sequences from two loci show a nearly complete lack of allele sharing between the eastern and western clades, suggesting reproductive isolation between them. However, no samples were collected close to their contact zones. As the eastern and western clades should meet in the Balkans and the southern Carpathian Mountains, we follow the recommendation of Recuero et al. (2014) and await more data on their level of reproductive isolation before making any taxonomic change. Thus, we do not follow Raffaëlli (2018) who (based on the genetic data presented in the aforementioned studies) elevated the subspecies *apuana*, *reiseri* and

veluchiensis to species level, and we note that such changes would make *I. alpestris* polyphyletic. We thus retain *I. alpestris* as a single species for now.

Pabijan et al. (2017) reconstructed phylogenetic relationships within the *Lissotriton vulgaris* species complex and inferred patterns of (historical) gene flow, using 74 nuclear DNA markers from one individual from each of 127 locations. Five highly divergent lineages were identified within our focal area: *Lissotriton montandoni* and four lineages corresponding to the *Lissotriton vulgaris* subspecies *graecus*, *lantzi*, *schmidtleri* and *vulgaris*. In spite of clear evidence of past historical introgression, their contemporary gene flow is restricted. Therefore, the authors proposed to treat the three former subspecies as species (Pabijan et al., 2017). Between *L. v. vulgaris* and the morphologically diverged *L. v. meridionalis* regular episodes of gene flow were identified, thus *meridionalis* was retained at subspecies level. While *L. v. graecus* is easily distinguished from other European populations by male nuptial characteristics, both *L. v. lantzi* and *L. v. schmidtleri* are morphologically cryptic in respect to *L. v. vulgaris* (Raxworthy, 1990). Rather than being confined to Anatolia, Pabijan et al. (2015, 2017) showed that *L. v. schmidtleri* also occurs in Greek and Turkish Thrace and on a number of Greek islands. Because the sampling gaps between several of the lineages remained wide, the TC has been reluctant to accept all systematic conclusions of Pabijan et al. (2017). The taxon *graecus* comes into close contact with *L. v. vulgaris* along the northern and eastern borders of its distribution. Although no dense sampling has been performed to delineate the contact zone in detail, and mitochondrial introgression from southern *L. v. vulgaris* into *graecus* occurs at its northern range border (Pabijan et al., 2017), nuclear gene pools of these two taxa appear to remain reciprocally distinct in relative close geographical proximity (Pabijan et al., 2017; Wielstra et al., 2018). We therefore accept *Lissotriton graecus* as a valid species. For *L. v.*

schmidtleri, its range limits and contact zones with other European lineages remain poorly known. Although data on the contact zone with *L. v. kosswigi* in Anatolia support a species-level divergence between *L. v. schmidtleri* and the *graecus-kosswigi* clade, areas of 100-300 km inhabited by *L. vulgaris* s.l. of unknown identity separate genotyped *L. v. schmidtleri* populations from those of *L. v. vulgaris* and *L. graecus* (Pabijan et al., 2017; Wielstra et al., 2018). The TC thus feels that more information on contact zones between *L. v. schmidtleri* and *L. v. vulgaris* is warranted before the species rank of *schmidtleri* can be accepted. Finally, *L. v. lantzi* is endemic to the Caucasus and shows an allopatric distribution (Wielstra et al., 2018). Mitochondrial data suggests that *L. v. lantzi* was the first to diverge from other lineages around 3.39 (1.42-5.37) Mya (Pabijan et al., 2015). Yet, nuclear data place *L. v. lantzi* as sister to *L. v. schmidtleri* and other eastern and central European *Lissotriton*, while suggesting that divergence within this group initiated with the split of the *graecus-kosswigi* clade (Pabijan et al., 2017). In conclusion, the TC recommends to treat *Lissotriton graecus* as a valid species, but, as awarding species status to *lantzi* but not to *schmidtleri* may render *L. vulgaris* paraphyletic, we prefer to maintain the other taxa, including *L. v. schmidtleri* and *L. v. lantzi*, as subspecies of *L. vulgaris* for the time being.

A phylogeographic study based on two mtDNA markers by Martínez-Solano et al. (2006) revealed two major mitochondrial lineages of Miocene origin in *Lissotriton boscai*. One of them is restricted to central and southwestern coastal Portugal, while the other occupies the remainder of the species range, including the type locality of *L. boscai*. Martínez-Solano et al. (2006) acknowledged that the two lineages might represent cryptic species, but called for additional morphological and molecular studies, including data on variation in nuclear DNA markers. Dubois and Raffaelli (2009) resurrected the nomen *Triton maltzani* Boettger, 1879 for the southwestern lineage in

the new combination *Lissotriton maltzani*. According to these authors, *L. maltzani* can be distinguished from *L. boscai* by its smaller size and by its paler dorsal coloration, especially in females, with less distinct dark spots. Teixeira et al. (2015) used DNA sequences of one nuclear gene and found overall congruence with mtDNA genes in terms of sequence divergence and geographic structure. They, however, also revealed wide areas of admixture and evidence for recombination, suggesting a lack of complete reproductive isolation and the presence of incomplete speciation. In a recent study, Sequeira et al. (2020) used ten microsatellites, one mtDNA gene and two single copy nuclear DNA markers in a cline analysis framework to investigate one of the hybrid zones between *L. boscai* and *L. maltzani*. The results show evidence for partial reproductive isolation between *L. boscai* and *L. maltzani*, with narrow clines (3–28 km) consistent with selection against hybrids. We thus recognise *L. maltzani* as a separate species.

Wake (2012) addressed the taxonomy of the Plethodontidae, advocating to treat *Atylodes* (comprising *Speleomantes genei*) and *Speleomantes* (comprising the other European plethodontid species) as subgenera of a single, cross-Atlantic genus *Hydromantes*. Addressing the genus name confusion, Wake (2013) compared five potential arrangements, missing however the arrangement of SBC2010 (i.e. two genera without subgenera). Comparing with other plethodontid genera, he argued in favour of an arrangement of a single genus with three subgenera. However, the arguments of SBC2010 still stand: the position of *Atylodes* remains unresolved, and the European species form a well-defined monophyletic group with a large genetic distance from the five Californian species *Hydromantes brunus*, *H. platycephalus*, *H. samweli*, *H. shastae*, and *H. wintu* (Nascetti et al., 1996; Pyron and Wiens, 2011; Chiari et al., 2012b; Bingham, Papenfuss and Wake, 2018). Thus, no change seems in order, and we maintain the European species for the time being in a single taxon, the genus *Speleomantes*.

Vörös, Ursenbacher and Jelić (2019) used 10 microsatellite loci to investigate patterns of differentiation between four Croatian cave populations of *Proteus anguinus*. They uncovered long-lasting isolation between caves belonging to different hydrogeographic systems, with the most ancient divergence being older than 7 Mya. This suggests that some of the evolutionary lineages within this species might constitute cryptic taxa, possibly of species rank (Vörös, Ursenbacher and Jelić, 2019).

Anura

Alytes obstetricans is composed of four subspecies: *A. o. obstetricans*, *A. o. pertinax*, *A. o. boscai* and *A. o. almogavarii*. The latter taxon is endemic to Catalonia and adjacent areas in north-eastern Spain and southern France, and it is highly differentiated in allozyme (Arntzen and García-París, 1995; García-París, 1995), mitochondrial (Gonçalves et al., 2007, 2015) and microsatellite markers (Maia-Carvalho et al., 2018), and features peculiar osteological (Martínez-Solano et al., 2004) and bioacoustics characters (Márquez and Bosch, 1995). Possibly due to ancestral hybridisation or incomplete lineage sorting (Gonçalves et al., 2007; Maia-Carvalho et al., 2014), the nuclear phylogeny, based on intron sequences, is not well resolved. Using microsatellites, Maia-Carvalho et al. (2018) identified a distinct cluster corresponding to all *A. o. almogavarii* populations, suggesting that the lack of monophyly in mtDNA data is due to cyto-nuclear discordance. This cluster extends as far west as the southern slopes of the Pyrenees in the north-westernmost parts of Aragon. These authors also found restricted genetic admixture between *A. o. almogavarii* and neighbouring subspecies (*A. o. pertinax*, *A. o. obstetricans*). Following up on this study, Dufresnes and Martínez-Solano (2020) targeted the hybrid zone between *A. o. almogavarii* and *A. o. pertinax* with genomic analyses using RADseq-derived markers along a fine-scale transect in Catalonia. They documented a very narrow mitochondrial (cline width ca.

13 km) and nuclear (cline width ca. 16 km) transition, and detected portions of the genome that were completely impermeable to gene flow. Given the absence of barriers to dispersal in the contact zone, the authors concluded that these lineages exhibit substantial (even if incomplete) reproductive isolation. We adopt their recommendation and treat *Alytes algomavarii* as a distinct species.

Pabijan et al. (2012) found a lack of reciprocal monophyly in nuclear data of Iberian painted frogs (*Discoglossus* spp.), while Dufresnes et al. (2020a) found numerous introgressed individuals in their RAD datasets and a broad hybrid zone (average cline width of nuclear markers >136 km). These results indicate weak (or no) restriction to gene flow and confirm that *D. g. galganoi* and *D. g. jeanneae* are better treated as conspecific, as previously advocated by SBC2010.

Borkin et al. (2001) reported differences in genome size between the morphologically similar eastern and western populations of *Pelobates fuscus*, with a transition between both groups in north-eastern Ukraine and adjacent parts of Russia. The name *Rana vespertina* Pallas, 1771 is available for the eastern taxon. Subsequently, analyses using mtDNA data across the entire species range confirmed the existence of two major mitochondrial lineages (Crottini et al., 2007). Litvinchuk et al. (2013) confirmed that these two lineages differ in their nuclear genomes, with Nei's genetic distance based on allozymes being similar to the divergence between *Pelobates syriacus syriacus* and *P. s. balcanicus* (see below), and with a restricted introgression zone. Based on its independent evolutionary history, they thus proposed to treat *vespertinus* as a species. More recently, based on RADseq data, Dufresnes et al. (2019a) reported narrow clines between *fuscus* and *vespertinus* (average nuclear cline width: 16 km). On the basis of the narrow hybrid zone, indicating strong (albeit incomplete) reproductive isolation, and in spite of the relatively recent divergence of this taxon (between 2 and 3 Mya, see Dufresnes

et al., 2019a, b), we accept the specific rank of *Pelobates vespertinus*.

Dufresnes et al. (2019a) also demonstrated complete reproductive isolation between *Pelobates syriacus syriacus* and *P. s. balcanicus*, warranting elevation of European populations, except those from south-eastern Bulgaria, parts of European Turkey and a number of eastern Greek islands (including Limnos and Lesbos), to species level as *Pelobates balcanicus*, with an estimated Mio-Pliocene divergence (>5 Mya) between both taxa. Deep intraspecific divergence within each species further leads to recognise the subspecies *P. balcanicus chloae* (Peloponnese) and *P. syriacus boettgeri* (all European parts of the distribution of *Pelobates syriacus*).

The complex pattern of genetic variation within Iberian *Pelodytes* has been known for several years (e.g., van de Vliet et al., 2012). It was taxonomically formalised by Díaz-Rodríguez et al. (2017), who described two new species: *Pelodytes atlanticus* from Portugal and *P. hespericus* from central eastern Spain, in addition to the previously established species, *P. ibericus* and *P. punctatus*. The two new lineages show no consistent morphological or bioacoustics differences, are only weakly differentiated in mtDNA (<2% in the 16S rRNA gene, <7% in COI), but show limited sharing of nuclear alleles. Díaz-Rodríguez et al. (2017) recognised that this was a disputable case, in which, for the time being, “species status for all four western lineages of *Pelodytes* [was] the hypothesis best fitting the available data”. A new study by Dufresnes et al. (2020a), based on RADseq-derived loci from spatially dense sampling, found that *P. atlanticus* and *P. ibericus* are separated by a narrow hybrid zone, featuring little introgression, whereas the contact zone of *P. hespericus* and *P. punctatus* has a considerably more flattened cline, with an introgression zone possibly extending up to 200-300 km. There is no known contact zone between *P. atlanticus* and *P. hespericus*. While the position of *P. atlanticus* (sister to *ibericus* or to *hespericus*) remains unresolved, its genetic divergence

from *hespericus* and *punctatus* is quite large. We thus follow the suggestion of Dufresnes et al. (2020a) to accept *P. atlanticus* as separate species, while retaining *hespericus* at subspecies level as *P. punctatus hespericus*.

Despite growing support for recognition of various clades in the family Bufonidae as separate genera (Stöck et al., 2006; Van Bocxlaer et al., 2009), several authors advocated retaining *Bufo* for all species from the Western Palaearctic and Central Asia, at least as an ad interim solution (Dubois and Bour, 2010; SBC2010). Formal taxonomic action was further hampered by nomenclatural confusion, such as the use of either *Pseudepidalea* or *Bufotes* as the valid generic nomen for the green toad group (Frost et al., 2006; Dubois and Bour, 2010). Dubois and Bour (2010) demonstrated that *Pseudepidalea* is a junior objective synonym of *Bufotes*, thereby giving priority to the latter. However, based on the presence of hybridisation between representatives of these clades, and the restricted sampling size of previous studies, Dubois and Bour (2010) listed these nomina as subgenera, rather than genera. According to Van Bocxlaer et al. (2010), Pyron and Wiens (2011), and Beukema et al. (2013), which together provide a dense sampling of bufonid species, most genera currently recognised by Frost (2019) represent well-supported monophyletic units. Moreover, time-calibrated analyses showed *Bufo*, *Bufotes* and *Epidalea* to be of similar age as or older than most other recognised bufonid genera (Beukema et al., 2013). Considering these results, we accept *Bufo*, *Bufotes* and *Epidalea* at genus level.

Recuero et al. (2012) published a multilocus mitochondrial and nuclear DNA sequence data set for *Bufo bufo* and associated species, covering the entire documented range and providing extensive genetic data. The study yields a fully resolved phylogeny, with the recently described *Bufo eichwaldi* from the Talysh Mountains of southern Azerbaijan and northern Iran as the sister taxon of a clade including three deeply diverged lineages: i) north African, Iberian,

and most French populations of *Bufo bufo* (for which the name *Bufo spinosus* is available), and a clade composed of two lineages, representing ii) *verrucosissimus* from the Caucasus and iii) *bufo* from northern France to Russia, while populations from Greece, southern Italy and Sicily and most of Anatolia carried *bufo* mtDNA but grouped with *verrucosissimus* in nuclear DNA. Estimations of divergence times indicated a long evolutionary history of the group, starting with the split from *eichwaldi* at about 12 Mya, and the divergence of *spinosus* taking place around 6 Mya. The deep level of genetic divergence observed between the western and eastern groups of common toads indicated that these groups may be different species. However, Garcia-Porta et al. (2012) found extensive admixture of mitochondrial lineages between the eastern and western clades in the Languedoc area of southern France (as also reported by Arntzen et al., 2017 for the Provence area of southern France), and detected signs of ancient introgression of *bufo* allozyme alleles into *spinosus*. They thus suggested to treat *B. b. spinosus* and *B. b. bufo* as conspecific pending studies of the contact zones. Detailed analysis of the amount of reproductive isolation in two geographically distant contact zones on the basis of mtDNA, morphology and nuclear markers have subsequently been published by Arntzen et al. (2016, 2017). Both studies documented an extensive amount of hybridisation and introgression in the contact zone, but also the presence of narrow and concordant clines for most nuclear markers, resulting in a unimodal, yet narrow hybrid zone of ca. 30 km wide, and indicating intrinsic barriers to gene flow in spite of incomplete reproductive isolation. Karyological analysis (albeit based on only four males and a single female) identified heteromorphic sex chromosomes in *spinosus*, but not in *bufo* (Skorinov et al., 2018). The combined available evidence justifies treating *Bufo spinosus* as a distinct species.

Based on differences in morphology and karyotype and a study suggesting lowered fertility of F1 hybrids (summary in Kuzmin, 1999), the Caucasian populations of the complex are sometimes also treated as a distinct species as *Bufo verrucosissimus*. Recent genetic studies paint a more complex picture. Firstly, based on nuclear markers, the Anatolian populations, traditionally excluded from *B. b. verrucosissimus* on the basis of morphology, are in fact genetically closer to this group than to *B. b. bufo* or *B. spinosus*, even if they carry *B. b. bufo* mtDNA (Garcia-Porta et al., 2012; Arntzen et al., 2013). Secondly, mtDNA divergence between Caucasian (*B. b. verrucosissimus*) and Eastern European (*B. b. bufo*) populations is much lower than between *B. b. bufo* and *B. spinosus*. Indeed, divergence in mtDNA and allozymes between the Caucasian and Eastern European lineages is even lower than between the subclades of *B. spinosus* (Garcia-Porta et al., 2012). Most importantly, based on frequencies of allozyme alleles, populations of *B. b. bufo* from Greece and north-western Turkey appear intermediate between Caucasian and European populations (Garcia-Porta et al., 2012) or group with Caucasian populations in nuclear trees (Recuero et al., 2012), suggesting extensive introgression between *B. b. verrucosissimus* and *B. b. bufo* in north-western Turkey and the southern Balkans (but see Arntzen et al., 2013). In our opinion, the specific status of *B. b. verrucosissimus* is currently insufficiently supported by the available evidence, and we maintain it as conspecific with *Bufo bufo* for the time being.

Stöck et al. (2006) elevated a number of mitochondrial lineages of green toads (now *Bufo*) to species level (for Europe: *B. variabilis* and *B. balearicus*, in addition to *B. viridis*) and subsequently described a new species from Sicily based on the same lines of evidence. SBC2010 argued against accepting these species on the basis of mitochondrial DNA alone. Colliard et al. (2010) documented a contact zone in Sicily between the taxa *siculus* and *balearicus* (sensu

Stöck et al., 2006) and demonstrated strong reproductive isolation between them. As these two taxa belong to the two most divergent lineages (North African and Eurasian), a two-species split of the green toad complex is clearly warranted. The Sicilian taxon *siculus* is closely related to the North African taxon *boulengeri*, which has priority over *siculus*. Subsequently, nuclear data were added to the picture (microsatellites – Dufresnes et al., 2018a; Gerchen, Dufresnes and Stöck, 2018, and RADseq markers – Dufresnes et al., 2019c). Although cytonuclear discordance was present in large areas of Europe where populations of *viridis* carry the *variabilis* mtDNA lineage, these studies confirmed that overall the previously identified mtDNA lineages correspond to distinct evolutionary units. Dufresnes et al. (2019c) also discovered that the type locality of *variabilis* is inhabited by the western lineage, rendering *variabilis* a junior synonym of *viridis*, and that the valid name for the Anatolian lineage is *sitibundus*. These two lineages (*B. v. sitibundus* and *B. v. viridis*) widely admix over a very large geographic area in Anatolia and Russia (Dufresnes et al., 2019c), suggesting that they are best treated as subspecies. The contact zone between *B. v. viridis* and *B. v. balearicus* is narrower (63 km), but still extensive if compared with other contact zones between taxa that are here treated as different species (Gerchen, Dufresnes and Stöck, 2018). In addition, raising *B. v. balearicus* but not *B. v. sitibundus* to species rank would make *B. v. viridis* paraphyletic (see Dufresnes et al., 2019c). The TC therefore preferred to treat *B. v. sitibundus* and *B. v. balearicus* (and the extralimital *B. v. perrini*) as subspecies of *B. viridis*.

Dufresnes et al.'s (2019c) range-wide sampling of all known taxa of the *Bufo viridis* complex identified a total of eight diploid genetic clusters, including a new lineage endemic to Cyprus, which they describe as *Bufo cypriensis*. Estimated to be of Messinian origin (5.3 Mya), this insular taxon is as old as or older than many species of anuran amphibians

from the Western Palearctic. Yet, all ten individuals from four localities carry mtDNA haplotypes of *B. v. sitibundus*. Secondary contact and hybridisation with the Anatolian mainland lineage during the Pleistocene would explain this mitochondrial capture, as well as the remnants of nuclear introgression that were detected as well. In addition to this deep genomic divergence, the genome of *B. cypriensis* is also significantly larger than that of all other Western Palearctic *Bufo* taxa. Morphologically, the Cyprus green toads are smaller than those from mainland populations, as previously reported by Stugren and Tassoula (1987). The combination of an old divergence and a larger genome size led the TC to accept the species status of *B. cypriensis*. Adriatic populations could represent a valid subspecies of *B. viridis* (for which the nomen *longipes* Fitzinger in Bonaparte, 1840 might be available), while green toads from Naxos (Cyclades) and Crete differ genetically from other populations and deserve genomic investigations (Dufresnes et al., 2019c). In summary, for Europe, we accept (1) *Bufo viridis*, including the widespread *B. v. viridis*, *B. v. balearicus* (Italian Peninsula, Corsica, Sardinia, Sicily, Balearic islands) and *B. v. sitibundus* (within Europe restricted to a number of eastern Greek islands), (2) the Sicilian *Bufo boulengeri siculus* and (3) *Bufo cypriensis*. We note that the availability of the nomen *siculus* remains unclear, given that the corresponding description (Stöck et al., 2008) was only issued electronically and prior to 2011 (see Article 8.5 of the Code): whether “numerous identical and durable copies” (Article 8.1) were registered by the authors in parallel is yet to be addressed (see also Dubois et al., 2013).

Based on a high level of divergence in mitochondrial DNA sequences of *Hyla* tree frogs, Stöck et al. (2008) have suggested to recognise the Iberian taxon *molleri* and the eastern European taxon *orientalis* as species distinct from *Hyla arborea*. However, given the lack

of other supporting characters (weak acoustic divergence: see Schneider, 1974; no well-supported morphological characters), SBC2010 refrained from formally accepting this systematic treatment, as it would have rested solely on mitochondrial DNA data. Several more recent studies offer a better understanding of the phylogeny of this group and of the patterns of gene flow across contact zones. Firstly, Dufresnes et al. (2015, 2016) investigated the *arborea-orientalis* contact zones in Poland and in the Balkans with microsatellite markers. In Poland, they found evidence of admixture over a 200 km wide zone, with mosaic contacts and interspersed hybrid populations, but with strongly restricted introgression at sex-linked loci and many populations of seemingly pure ancestry in close contact to each other (Dufresnes et al., 2016). In the Balkans, Dufresnes et al. (2015) found narrow clines (30 and 32 km of average cline width in Serbia and Greece respectively). In line with our treatment of taxa connected by unimodal hybrid zones with narrow clines, we recommend affording species status to *Hyla orientalis*. Secondly, the phylogenomic tree in Dufresnes et al. (2018b) unambiguously groups *orientalis* and *molleri* as sister taxa, with *arborea* splitting from a node basal to the *molleri* – *orientalis* divergence. Therefore, we accept *molleri* at species rank as well. Although the close relationships between *molleri* and *orientalis* could justify to treat them as conspecific, we refrain for the time being from this arrangement. We thus treat *Hyla molleri* and *Hyla orientalis* as valid species.

Supported by mtDNA and genomic data, two major cryptic lineages reside within *Hyla intermedia* (Canestrelli, Verardi and Nascetti, 2007; Stöck et al., 2008; Dufresnes et al., 2018b). They are not known to differ in any diagnostic morphological or acoustic character, even if they differ in the averages of one acoustic and some morphometric traits. The northern lineage occupies the Po Plain and adjacent regions (including Ticino in Switzerland), with

the northern Apennines acting as the biogeographical barrier separating it from the southern lineage. As the name *intermedia* applies to the southern lineage, Dufresnes et al. (2018b, c) coined a new name, *Hyla perrini*, for the northern lineage. Note that, as its registration in the Official Register of Zoological Nomenclature (ZooBank) occurred later than the publication of Dufresnes et al. (2018b), the name *perrini* is not made available by Dufresnes et al. (2018b), but by Dufresnes et al. (2018c), who met all conditions of nomenclatural availability. Detailed analyses of the contact zone based on genomic (RADseq) data by Dufresnes et al. (2018b) revealed broad clines (96 km of average cline width) for nuclear markers and detectable admixture over approximately 130 km. Despite a relatively high *cyt b* distance of around 9%, and even though Dufresnes et al. (2018b) argued that the extent of the contact zone would be even larger without some form of selection against hybrids, the TC felt that the observed extent of introgression and thus the lack of strong reproductive barriers did not unambiguously allow treatment of *perrini* at species rank. We thus recommend to treat the northern lineage as *Hyla intermedia perrini*.

The authorship of the family Ranidae has been clarified by Dubois and Bour (2011), attributing it to Batsch, 1796.

Based on allozyme data (Arano, Esteban and Herrero, 1993; Veith et al., 2002, 2012), two genetically distinct groups have been recognised within *Rana temporaria* populations of northern Spain. The first was assigned to the subspecies *R. t. parvipalmata* and is restricted to the westernmost edges of the Iberian distribution (Galicia and Asturias). Frogs from western Galicia feature reduced feet webbing, smaller size and lower number of pulses per call (Vences, 1992). The second group corresponds to the nominal taxon *R. t. temporaria*, which extends throughout Europe. Mitochondrial data suggested a more complex picture, with four deeply differentiated lineages in the same area (Vences et al.,

2013b, 2017). In a phylogeographic survey using genome-wide data, Dufresnes et al. (2020b) found one of these mitochondrial groups to be a “ghost lineage”, not differentiated in the nuclear genome. The two main lineages are strongly differentiated and are estimated to have diverged around 4 Mya. Despite the absence of geographic or ecological barriers to dispersal, they form a narrow hybrid zone (25 km) in the eastern Cantabrian Mountains. Because partial reproductive isolation is thus likely to prevent these two taxa from merging, we follow the recommendation of Dufresnes et al. (2020b) to treat *R. parvipalmata* as a distinct species.

Using allozymes and mtDNA, a detailed analysis of gene flow patterns across the contact zone of the northern Anatolian lineage and the Balkan lineage of the *Pelophylax ridibundus* – *bedriagae* complex in northern Greece revealed the existence of a wide hybrid zone, with introgression detectable over more than 200 km (Hotz et al., 2013). This suggests that the European and Anatolian lineages are conspecific (contra SBC2010). Since the European lineage splits from a node basal to the diversification of Anatolian lineages with respect to mtDNA according to Plötner et al. (2012), it further suggests that most lineages of this complex are conspecific, with the possible exception of the populations from Syria and Jordan (possibly the ‘true’ *bedriagae*, see Plötner et al., 2012). On the other hand, Plötner et al. (2010) suggested hybrid breakdown between some of these lineages, indicating incipient speciation. While undoubtedly the last word on this subject has not been written, the TC felt that it was premature to suggest taxonomic changes, especially as a large taxonomic paper based on genomic variation patterns is in preparation (G. Mazepa, pers. comm.). The same applies to the newly proposed *P. cypriensis*, which was found to be placed between the European and the Anatolian lineages in mtDNA, but grouped with *P.*

cretensis (albeit with very low support) in nuclear DNA (Plötner et al., 2012). For the moment, we thus suggest no change to the taxonomy adopted in SBC2010 for European *Pelodytes*.

Reptilia

Testudines/Chelonii

Based on nuclear genomic ISSR fingerprints and mtDNA sequences, Fritz et al. (2005) described *Emys trinacris* as a distinct species endemic to Sicily and Calabria, albeit the record from Calabria was later questioned (Vamberger et al., 2015). A phylogenetic study using seven nuclear genes (Spinks and Shaffer, 2009) found *E. orbicularis* to be paraphyletic with respect to *trinacris*: *E. o. hellenica* was sister to a clade containing *trinacris* and the remaining lineages of *E. orbicularis*. This led SBC2010 to conclude that *trinacris* should not be recognised as a species, which has been criticised by Vamberger and Fritz (2018). While *trinacris* is the most basal lineage in mtDNA trees (Fritz et al., 2005, 2007), this position is weakly supported, and the level of mtDNA divergence between *trinacris* and the other lineages is not clearly larger than that between some lineages of *E. orbicularis*. A first combined analysis of genetic differentiation at eight microsatellite loci and mtDNA sequences found concordant patterns for both markers: no evidence for admixture between Sicilian pond terrapins and the remaining lineages was found, while extensive admixture was found between some other lineages of *E. orbicularis* (Pedall et al., 2011). Using 15 microsatellite loci and mtDNA sequences, Vamberger et al. (2015) found evidence for limited admixture between the two taxa in one Sicilian population. In addition, Vamberger et al. (2015) reported concordant clines for both markers, with cline centres matching the Strait of Messina. Vamberger et al. (2015) argue that the coincidence of the cline centres with the Strait of Messina

cannot be explained by a geographic barrier effect of this narrow sea strait, because in *E. orbicularis* recent gene flow occurred across the Strait of Gibraltar (Velo-Antón et al., 2015), and possibly across the Adriatic Sea between southern Italy and the Balkans (Vamberger et al., 2015). In contrast, Pereira, Teixeira and Velo-Antón (2018), using seven microsatellite loci, concluded that the Strait of Gibraltar currently impedes gene flow between Iberian and North African pond turtles. However, they show that the break between the two clusters corresponds to the Central Iberian Mountains and not the sea strait. Clines of microsatellites for the *trinacris* – *orbicularis* contact zone across the Strait of Messina were inferred to be very wide (247 km) in Vamberger et al. (2015), although the significance of this estimate is hampered by a substantial (150 km) sampling gap between the two taxa. The TC takes therefore a conservative stance and treats *trinacris* as a subspecies of *E. orbicularis*, waiting for further studies resolving the complicated relationships of this complex. In this context, we note that Pöschel et al. (2018) reported a sharp transition between *occidentalis* and *orbicularis* + *galloitalica* in north-eastern Spain, matching that of distinct species recognised here, suggesting that the *E. orbicularis* complex could comprise several species. In the meantime, we recommend to maintain the Sicilian lineage as *Emys orbicularis trinacris*.

Squamata

The family Agamidae is sometimes credited to Fitzinger, 1826 or Gray, 1827 (see e.g. Melville and Smith, 1987). In fact the nomen was first published by Spix in 1825 as “Familia Agamae”. Even if Spix did not use the correct suffix ‘-idae’, Article 11.7.1.3 of the Code states that “a family-group name of which the family-group name suffix is incorrect is available with its original authorship and date, but with a corrected suffix”. Other conditions of availability all seem to be fulfilled in Spix (1825), who is thus the author of the nomen.

Macey et al. (2000a) sequenced a 1685-1778 bp long segment of mtDNA (including the ND1, ND2 and COI genes) to assess phylogenetic relationships of acrodont lizards. Their results suggested that the agamid genus *Laudakia* is paraphyletic, yet, low bootstrap support prevented definite conclusions. Subsequent studies based on mitochondrial and nuclear genes (ND2, RAG1) by Melville et al. (2009) and Edwards and Melville (2011) recovered *Laudakia* as monophyletic with high support. Baig et al. (2012) summarised the results of the aforementioned studies in a morphology-based revision of *Laudakia*. Despite failing to find distinct morphological variation within the genus, and acknowledging that Melville et al. (2009) and Edwards and Melville (2011) recovered *Laudakia* as monophyletic, Baig et al. (2012) partitioned *Laudakia* into three genera acknowledging its potential paraphyly (Macey et al., 2000a). This taxonomic act was subsequently criticised by Pylon, Burbrink and Wiens (2013), who confirmed the monophyly of *Laudakia* using a supermatrix approach. Within our focal area, the classification proposed by Baig et al. (2012) would affect *Laudakia stellio* and *L. caucasia*, as these authors placed the former species in the newly erected genus *Stellagama*, and the latter into *Paralaudakia*. While these genera were rapidly adopted by the wider herpetological community, we do not follow the split of *Laudakia*, pending substantial evidence to reject its monophyly, and therefore retain *L. stellio* and *L. caucasia* in *Laudakia*.

The family Chamaeleonidae is sometimes credited to Gray, 1825 (e.g. Glaw, 2015). However, Rafinesque (1815) published the name “Famille CAMÆLONIA”, based on the genus “*Camæleo* Daud.”, which is an incorrect subsequent spelling of the available genus *Chamaeleo* Laurenti, 1768. The Code is somewhat ambiguous regarding the availability of family-group nomina based on an incorrect subsequent spelling of an available genus. Article 19.1 of the Code states that an incorrect subsequent

spelling is not an available name. If one follows this and Art. 11.7.1.1 (“a family-group name when first published must [...] be a noun in the nominative plural formed from the stem of an available generic name”), a family-group name based on an incorrect subsequent spelling of an available genus name is not available. Yet, the Code also states that “a family-group name is an incorrect original spelling and must be corrected if it is formed from an incorrect subsequent spelling of a generic name” (Art. 32.5.3.3) and that “a family-group name based upon [...] an incorrect spelling of the name of the type genus must be corrected” (Art. 35.4.1). It is thus clear that the Code has no intention to make a family-group name unavailable based on an incorrect spelling of the name of the type genus (see also Dubois, 2010). In conclusion, the family-group name *Camaelonina* is available as published by Rafinesque (1815), but its spelling needs to be corrected. The nowadays prevailing spelling *Chamaeleonidae* should be preserved (Art. 29.5), with its authorship attributed to Rafinesque (1815) instead of Gray (1825).

SBC2010 adopted the inclusion of *Cyrtopodion kotschy* in the well-supported monophyletic genus *Mediodactylus*, as proposed by Macey et al. (2000b), Červenka, Frynta and Kratochvíl (2008) and Bauer et al. (2013). By enlarging the focal area of SBC2010, we hereby also include the former *C. russowi*, now *Mediodactylus russowii*. Another species occurring in the area considered by Gasc et al. (1997) but not in that of SBC2010 is the former *Cyrtopodion caspium*. We follow Bauer et al. (2013) in recognising the well-resolved genus *Tenuidactylus* and list this species as *Tenuidactylus caspius*. Furthermore, an introduced, well-established population of *Tenuidactylus fedtschenkoi* has recently been reported from the city of Odessa (Ukraine). The native range of *T. fedtschenkoi* lies in central Asia (western Pamiro-Altay mountains), and it was probably transported passively to Odessa (Duz', Kukushkin and Nazarov, 2012). Not long

after the record from Odessa, a revision of the genus *Tenuidactylus* led to the description of a new species from Uzbekistan and Turkmenistan, which was split from *T. fedtschenkoi* and named *T. bogdanovi* (Nazarov and Poyarkov, 2013). Krasylenko and Kukushkin (2017) provided an update on the status of the non-native Odessa population and assigned it to *T. bogdanovi*.

Within *Mediodactylus kotschyi*, many subspecies have traditionally been recognised. As indicated by Kasapidis et al. (2005), the genetic substructure of *Mediodactylus kotschyi* shows a high degree of divergence, suggesting that *M. kotschyi* represents a species complex. Nearly range-wide data (with limited areas in eastern and northern Anatolia excluded) of three mtDNA and three nuclear DNA fragments allowed unravelling the evolutionary history of *Mediodactylus kotschyi* (Kotsakiozi et al., 2018). Divergence dates back to 15 Mya, and several of the main lineages show overlapping distribution areas. Divergence in mtDNA is known to be often quite large in geckos (e.g. Nagy et al., 2012). However, distances between the main lineages are particularly large in this case (>10% 16S and >15% cyt *b* and COI *p*-distances). In addition, nuclear data groups specimens in concordance with their mtDNA lineage, and not with their geographical origin, which suggests a high level of reproductive isolation between them. The proposed splits also largely agree with morphological data (Štěpánek, 1937, 1939; Szczerbak and Golubev, 1996). The narrow contact between *M. orientalis* and *M. danilewskii* in the Western Taurus Mountains, identified by Kotsakiozi et al. (2018), corresponds to a lack of morphological intergrades (despite the narrow gap between the subspecies *danilewskii* and *ciliciensis* in the same area, see Rösler, Schmidler and Moravec, 2012), while these new species are very close to the *M. kotschyi* groups defined by Beutler (1981). Five species were recognised, for all of which previously existing names are available (Kotsakiozi et al., 2018). While the

delimitation of the ranges and contact zones of these new species requires further investigation (e.g. *M. danilewskii* and *M. orientalis*), we accept these species here. The following species are thus recognised in our area: *M. kotschyi* (mainland Balkans, most of Aegean islands, and Italy (Apulia)), *M. bartoni* (Crete and nearby islets), *M. danilewskii* (Black Sea region and south-western Anatolia), *M. oertzeni* (southern Dodecanese Islands), and *M. orientalis* (Levant, Cyprus, southern Anatolia, and south-eastern Aegean islands).

The endemic gecko from the Selvagens Islands has variously been treated as the valid species *Tarentola bischoffi* (e.g. Rebelo, 2008; Sindaco and Jeremčenko, 2008; Uetz, Freed and Hošek, 2019), or as a subspecies of the Canarian *T. boettgeri* as *T. boettgeri bischoffi* (e.g. Carranza et al., 2000; Pleguezuelos, Márquez and Lizana, 2002; Gübitz, Thorpe and Malhotra, 2005; Sá-Sousa et al., 2009). Its phylogenetic affinities were examined by Carranza et al. (2000, 2002) and Gübitz, Thorpe and Malhotra (2005). The genetic data available (albeit based only on mtDNA) show that the mitochondrial lineages of *bischoffi* are closely related to those of *T. boettgeri*, especially to the subspecies *T. b. hierrensis* from El Hierro, and are in fact nested inside the mitochondrial diversity of *T. b. boettgeri* from Gran Canaria, suggesting that the Selvagens Islands were recently colonised from El Hierro or Gran Canaria (Carranza et al., 2000, 2002; Gübitz, Thorpe and Malhotra, 2005). Treating *bischoffi* as a valid species, while retaining *hierrensis* as a subspecies of *boettgeri* (as done by the above authors who rank *bischoffi* as a species), is thus likely to render *Tarentola boettgeri* paraphyletic. The amount of mitochondrial divergence between *hierrensis* and *bischoffi* is also smaller than within the populations of *T. delalandii* from Tenerife or between the populations of *T. angustimentalis* from Fuerteventura and Lanzarote. Based on the available data, we thus recommend to treat the geckos from the

Selvagens Islands as conspecific with the populations from El Hierro and Gran Canaria, as *Tarentola boettgeri bischoffi*.

Sánchez-Vialas et al. (2018) re-examined the description of *Algyroides hidalgoi* Boscá, 1916, a nomen for which the holotype has been lost, to settle its position in the synonymy of the genus *Algyroides*. They argued that the characters of the holotype, said to originate from the Sierra de Guadarrama and described by Boscá, fall within the morphological variability of *Algyroides marchi* Valverde, 1958, and designated a specimen of *A. marchi* as neotype of *A. hidalgoi*. This would make *A. marchi* a junior subjective synonym of *A. hidalgoi*. Because the conditions for automated reversal of precedence are not met (Art. 23.9.1 of the Code), *A. hidalgoi* would become the valid nomen of the Spanish *Algyroides*. Several TC members felt, however, that the interpretation of the description of Boscá (1916) by Sánchez-Vialas et al. (2018) left room for doubt, and that Boscá may not have described a specimen of Spanish *Algyroides* when he created the name *Algyroides hidalgoi*. If so, this could affect the validity of the neotype designation, respective to Art. 75.3.5 of the Code, and result in the unnecessary change of the well-established and widely used name *A. marchi*. Although opinions in the TC were divided about this, we recommend to maintain for the time being the use of *A. marchi*, in anticipation of an upcoming application to the Commission, which would maintain *marchi* in use until the Commission has ruled on the case.

Morphological and molecular (mtDNA and nuclear) data support the split of *Psammodromus hispanicus* into three distinct lineages (Fitze et al., 2011, 2012; Mendes et al., 2017). While not all areas of potential contact have been sampled (despite a recent distribution update by Molina et al., in press), the available data seem to warrant accepting these lineages as distinct species. Age estimates, lineage allopatry, the lack of mitochondrial and nuclear haplotype sharing between lineages, bioclimatic niche divergence, and the current biogeographic

distribution, indicate that the three lineages correspond to three independent species. The name of the eastern species is often spelled *P. edwardsianus*. As shown by Crochet (2015), this is an incorrect subsequent emendation that does not meet the requirements of the Code. As a consequence, the valid spelling of the eastern species is *Psammodromus edwardsianus*. Thus, we add *Psammodromus edwardsianus* and *P. occidentalis* to the list of the European herpetofauna species.

A 9 Mya split marks the divergence of *Timon lepidus nevadensis* from the nominal subspecies *T. l. lepidus* (Miraldo et al., 2013). After studies on genetic (Paulo et al., 2008; Miraldo et al., 2011, 2013) and morphological differentiation (Mateo and Castroviejo, 1990; Mateo, López-Jurado and Guillaume, 1996), mtDNA and microsatellites were used to investigate gene flow patterns in a zone of secondary contact (Miraldo et al., 2013). While hybridisation and introgression were observed, gene flow was shown to be restricted. The cline width for nuclear markers was estimated at around 10 km (although with a sampling gap of around 20 km, it may actually be less). Furthermore, mostly pure populations are present on either side of the sampling gap. Considering this together with the aforementioned old genetic divergence, we accept the proposal of Miraldo et al. (2013) and treat *T. nevadensis* as a valid species.

Lacking range-wide sampling and adequate molecular analysis, the taxonomy of the *Lacerta trilineata-pamphylica* complex has remained unresolved, until mitochondrial phylogenies showed the eastern Anatolian species *L. pamphylica* to be nested within *trilineata* (Godinho et al., 2005; Ahmadzadeh et al., 2013; Sagonas et al., 2014). Remarkably, Sagonas et al. (2014) found evidence that central Aegean populations (*L. t. citrovittata*) are closely related to *L. pamphylica*. Yet, this was poorly supported across analyses and the biogeographically surprising relationship between *L. t. citrovittata* and *L. pamphylica* could reflect a methodological artefact (long branch attraction). Thus, the

monophyly of *L. trilineata* could not be rejected. More recently, analyses of SNPs and mitochondrial sequences by Kornilios et al. (2019, 2020) found a sister-group relationship between *pamphylica* and eastern Aegean populations of *trilineata*. This led to the identification of four species-level units: *L. trilineata* (eastern Adriatic Coast, Greece except northeast and including Milos archipelago and Crete, south-eastern Bulgaria and North Macedonia), *L. pamphylica* (southern Anatolia east of Antalya), *L. citrovittata* (central Aegean islands, including among others Naxos, Tinos, Andros, Syros, Mykonos, Paros), and *L. diplochondrodes* (north-eastern Greece, Romania, Bulgaria except southeast, Turkey, eastern Aegean Greek islands). All evidence (morphology, blood biochemistry, immunoserology, congruence between highly divergent mtDNA and nuclear genomics, bioclimatic niche differences, no signs of admixture) suggests that *L. pamphylica* deserves species status. As the eastern Aegean populations of the complex are the sister taxon of *L. pamphylica*, maintaining monophyly implies also treating them as a species, *L. diplochondrodes*. The latter taxon does not show a lot of contact, nor signs of introgression with any of the other three clades. Concerning the population west of the Aegean Barrier, the conclusion may seem less straightforward. However, genomic analyses offer stronger support for the species status of *L. citrovittata* than for that of *L. pamphylica*. The former equally corresponds to one of the major mtDNA lineages of Kornilios et al. (2019). Given its allopatry, there is no evidence of admixture. While the (potential) contact zone between *L. diplochondrodes* and *L. trilineata* in north-eastern Greece and its wider surroundings requires more comprehensive sampling, we suggest to accept the new four species arrangement and to recognise *Lacerta trilineata*, *L. diplochondrodes*, *L. citrovittata*, as well as the extralimital *L. pamphylica*.

Using one mitochondrial and one nuclear gene, Marzahn et al. (2016) investigated the

phylogeography of the *Lacerta viridis* complex. Four main mtDNA lineages, whose phylogenetic relationships were weakly resolved, emerged from the data: (i) *Lacerta bilineata*, (ii) *Lacerta viridis* s.s., (iii) an Adriatic and western Balkan lineage, and (iv) a newly discovered lineage from the south-eastern Balkans as well as the Turkish Black Sea Coast. A previously supposed (Amann et al., 1997) contact zone between *L. bilineata* and *L. viridis* in north-eastern Italy was found to be in fact a contact zone between the Adriatic and western Balkan lineage and *L. bilineata*. Another contact zone between the Adriatic and western Balkan lineage and *L. viridis* s.s. lies further east in Slovenia and adjacent Croatia. As a consequence, there is no known geographical contact zone between *L. viridis* s.s. and *L. bilineata*. Several other contact zones between mitochondrial lineages were identified across the distribution range. However, the nuclear data were insufficient to examine gene flow among lineages. Consequently, no species-level changes were suggested. The previously reported occurrence of *L. bilineata* on Cres, Croatia (Brückner et al., 2001), was confirmed. However, this record is isolated from the remaining distribution range and lies among surrounding records of the Adriatic and western Balkan lineage (Marzahn et al., 2016), suggestive of an introduced population.

Speybroeck and Crochet (2007) and SBC2010 adopted the split of the former genus *Lacerta* s.l., accepting all genus names recognised by Arnold, Arribas and Carranza (2007), as far as they pertained to taxa occurring within their considered area. As we have adopted a broader area definition here, we additionally formally accept the genera *Anatololacerta* and *Phoenicolacerta*. The latter only has a single representative within our area, the Cypriot *P. troodica*. Within our area, the genus *Anatololacerta* can be found on several Greek islands, including Ikaria, Samos, Rhodes, Pentanisos and Kastellorizo. Based on morphology, Eiselt and

Schmidtler (1986) treated *A. anatolica* (including the subspecies *aegaea* from Samos), *A. danfordi* and *A. oertzeni* (including the subspecies *A. o. pelasgiana* on Rhodes, Symi and Pentanisos and the nominotypical subspecies on Ikaria) as valid species. However, because the biochemical differentiation (based on albumins) between them was deemed to be too small, Sindaco and Jermenčenko (2008) maintained all populations within *Anatololacerta danfordi*, following Mayer and Lutz (1989). Bellati et al. (2015) combined multi-locus species tree approaches with species delimitation methods to suggest the recognition of four distinct species in this group. Some of these species are closely related and were inferred to have diverged as recently as 500,000 years ago, i.e. a remarkably young age for speciation events within Lacertidae. Yet, there seems to be evidence of reproductive isolation between some of these species, as shown by the patterns of allele sharing in some nuclear markers. While more detailed analyses of patterns of gene flow in contact zones would be desirable, we tentatively accept the four-species taxonomy (*A. anatolica*, *A. budaki*, *A. danfordi* and *A. pelasgiana*) of Bellati et al. (2015). In our area, *A. anatolica* is present on Ikaria and Samos, and *A. pelasgiana* on Symi, Pentanisos and Rhodes. In addition, *A. pelasgiana* was also found (although presumed introduced in both cases) on Kasos (Kornilios and Thanou, 2016) and Kastellorizo (Kalaentzis et al., 2018), while *A. budaki* was found on the (nearby) islet Psomi (Kalaentzis et al., 2018).

As pointed out by Busack et al. (2016), the microfiche publication of Arribas's (1997) thesis does not meet the criteria of publication for valid zoological nomenclature, neither under the current version of the Code nor under the previous (and then relevant) version. As a consequence, the names *Iberolacerta* and *Darevskia* were not made available in Arribas (1997). For *Iberolacerta*, this has no major nomenclatural consequences, as

the next available nomen is *Iberolacerta* Arribas, 1999. However, because *Darevskia* Arribas, 1999 is a junior synonym of *Caucasilacerta* Harris, Arnold and Thomas, 1998, Busack et al. (2016) conclude that *Caucasilacerta* must replace *Darevskia* as the valid nomen for the genus of the Caucasian Rock Lizards. The conclusions drawn by Busack et al. (2016) prompted a number of responses (Arribas, 2016; Arribas et al., 2017), advocating that *Caucasilacerta* is a nomen nudum and hence is unavailable. Subsequently, Arribas et al. (2018) appealed to the ICZN (under Articles 78.1 and 81 of the Code) to accept Arribas (1997) as published in the sense of the Code and preserve *Darevskia* Arribas, 1997 and *Iberolacerta* Arribas, 1997. While we regard *Caucasilacerta* as available, we support the current application to preserve *Darevskia*. We note that, while the case is under consideration by the Commission, the prevailing usage of *Darevskia* and *Iberolacerta* with their authorship as Arribas, 1997 is to be maintained (Article 82).

Based on morphological variation, Stugren (1961) advocated the recognition of three subspecies of *Darevskia praticola*: the nominotypical subspecies in the east of the distribution (central and eastern Caucasus, northern and south-eastern Georgia, northern Armenia, southern Azerbaijan, and north-eastern Iran), the subspecies *pontica* in the west of the Caucasus and in western Georgia, and *D. p. hungarica* in Europe (north-eastern Serbia, southern Romania, north-eastern Greece, eastern and western Bulgaria). Later, he recommended to treat *D. p. hungarica* as a synonym of *D. p. pontica*, resulting in a two-subspecies classification (Stugren, 1984). On the basis of multivariate analysis of morphological, meristic and qualitative characters of Balkan and Caucasus populations, Ljubisavljevic et al. (2006) confirmed the validity of the two subspecies *D. p. praticola* and *D. p. pontica*. Tuniyev et al. (2011) presented a detailed morphological study for the populations of the Caucasian Isthmus. They confirmed two morphological clusters in the Caucasus and

Transcaucasia (western Caucasus: *D. p. pontica*; eastern Caucasus + Transcaucasia: *D. p. praticola*), and described a new subspecies from the Talysh Mountains (the extralimital *D. p. hyrcanica*). On the basis of morphological differentiation and unpublished genetic data, they also advocated species status for *D. p. pontica*. Later, Freitas et al. (2016) provided a phylogeographic study of the species, based on comprehensive sampling covering most of the range (although the central and eastern Caucasus parts of the range were missing). They recovered two clades in the Caucasus and in Transcaucasia, one in the western Caucasus (corresponding with the Caucasian range of the *D. p. pontica* subspecies) and one in Transcaucasia (Armenia) and the Talysh Mountains, corresponding with the extralimital subspecies *D. p. hyrcanica* and Tuniyev's et al. (2013) *D. p. loriensis*. Samples of the nominotypical subspecies were not included, although their morphology suggests that they would presumably group with the Transcaucasian samples (see Tuniyev et al., 2011, 2013). Freitas et al.'s (2016) results thus seem to support the divergence of two lineages in the Caucasus, corresponding to Caucasian populations of *pontica* on the one hand, and populations of the *praticola* phenotype (including *loriensis* and *hyrcanica*) on the other hand. However, genetic analyses of samples of *praticola* from the eastern Caucasus would be needed to confirm this. More surprisingly, Freitas et al. (2016) also uncovered a deep split within populations traditionally classified as *pontica*, with the European samples from the Balkans forming a deeply divergent lineage in both mtDNA and nuclear DNA that splits from a node basal to the clade grouping the Caucasian and Transcaucasian samples. They estimated the divergence between the European and Caucasian + Transcaucasian clades at around 2.5 Mya, with a much younger split of the Transcaucasian lineage around 650,000 year ago. As pointed out by Ljubisavljevic et al. (2006), the name *D. p. hungarica* (Sobolevsky, 1930), with type locality in the Transylvanian Alps (which at the time

was part of the Kingdom of Hungary, including parts of today's Romania), should be applied to the Balkan lineage. Given the incomplete geographic coverage of Freitas et al. (2016) and the somewhat borderline level of genetic divergence between the Balkans and Caucasian + Transcaucasian lineages, we refrain from recommending species status for the time being, and thus suggest to treat the Balkan populations as *Darevskia praticola hungarica*. We further disagree with the conclusion of Freitas et al. (2016) to treat *D. p. pontica* as a synonym of *D. p. praticola*, as all their samples correspond with the range of *D. p. pontica* according to Tuniyev et al. (2011), and they have therefore not analysed any sample from the range of *D. p. praticola*. Conclusively, we maintain the morphologically well-supported subspecies *D. p. pontica* and *D. p. praticola* for the Caucasian populations occurring in our area, while the Balkan populations are referred to as the subspecies *D. p. hungarica*.

Genetic relationships based on a mtDNA (cyt *b*) fragment suggest that *Darevskia brauneri szczerbaki* is sister to *D. saxicola* rather than grouping with other lineages of *D. brauneri* (Doronin, Tuniyev and Kukushkin, 2013; Tarkhnishvili et al., 2016). Based on this and on analysis of morphological variation coupled with differences in ecology, Tuniyev and Tuniyev (2012) and Doronin, Tuniyev and Kukushkin (2013) suggested to treat *szczerbaki* as a valid, monotypic species. However, this hypothesis is in conflict with the results of MacCulloch et al. (2000), who found a lack of fixed differences in 15 polymorphic allozyme loci between *D. b. brauneri*, *D. b. darevskii* and *D. b. szczerbaki*, and concluded that these three taxa are conspecific. The high incidence of hybridisation within Caucasian *Darevskia* makes mtDNA relationships potentially unreliable. In addition, because of the low level of cyt *b* divergence (2.4% between *D. saxicola* and *D. b. szczerbaki*, and 4.8-5.6% of both *D. saxicola* and *D. b. szczerbaki* towards other *D. brauneri* sequences) and the conflict with allozyme data,

we consider this species complex to be currently too poorly studied to recognise additional species without extensive evidence from nuclear genes and/or strong morphological differentiation in sympatry or close parapatry. As both of these lines of evidence are still lacking in this case, we maintain *D. b. szczyrbaki* at subspecies rank for the time being.

Two parthenogenetic *Darevskia* species which are not native to our area have been introduced near Zhytomyr, Ukraine (Nekrasova and Kostiusyn, 2016). *Darevskia armeniaca* occurs naturally in north-western Armenia, western Azerbaijan, southern Georgia and north-eastern Turkey, and is believed to have been introduced in 1963, whereas *D. dahli*, known from northern Armenia and southern Georgia, was discovered more recently (1980) within the introduced *armeniaca* population. A third species, *D. mixta*, was also introduced in 1968, but its contemporary presence could not be confirmed (Nekrasova and Kostiusyn, 2016).

Mayer et al. (2000) described the oviparous *Zootoca vivipara* populations of Carinthia (Austria), Slovenia, Friuli and isolated sites across the Po Plain (Italy) as the distinct and allopatric subspecies *Z. v. carniolica*. Additional molecular analysis confirmed its validity (Surget-Groba et al., 2001, 2002). More recently, this taxon was shown to inhabit a wider range than previously known, not only occupying parts of southern Austria, Slovenia, northern Croatia and north-eastern Italy, but actually extending west as far as the central southern Italian Alps (Cornetti et al., 2015a). Lindtke, Mayer and Böhme (2010) documented a narrow contact zone in Carinthia (Austria), and detected two natural hybrids (identified by clutch features) in a sample of 36 specimens. As they did not use genetic markers, they could not investigate the level of introgression. More recently, two studies by Cornetti et al. (2015a, b) demonstrated complete reproductive isolation between *carniolica* and *vivipara*, in spite of widespread close parapatry between these two taxa. Cornetti et al. (2015a) focused on the contact zone with local syntopy

in northern Italy, and did not detect any hybrid or admixed genotype out of around 30 individuals (genotyped with 13 microsatellites). Cornetti et al. (2015b) genotyped many more individuals from several regions in the northern Italian Alps where the two taxa come in close parapatry, and found a similar lack of admixture. Thus, *carniolica* and *vivipara* appear to represent two different species, and we accept *Zootoca carniolica* at species level.

After being placed into the genus *Lacerta*, *Teira dugesii* and *Scelarcis perspicillata* were transferred to the subgenus *Teira* and the genus *Podarcis*, respectively, based on morphology (Richter, 1980). Subsequently, *Teira* was elevated to genus level by Mayer and Bischoff (1996). Yet, the generic allocation of *S. perspicillata* and *T. dugesii* remained a matter of confusion, with several authors attributing both species to the genus *Lacerta* until quite recently (e.g. Brehm et al., 2003; Perera et al., 2007). Even though Pavlicev and Mayer (2009) suggested treating *Scelarcis* as a junior synonym of *Teira* and placing both species into the genus *Teira*, SBC2010 adopted the genus arrangement of Arnold, Arribas and Carranza (2007) and assigned the Moroccan Rock Lizard to *Scelarcis* as *Scelarcis perspicillata*. However, a recent study using data from anchored phylogenomics and a fossil-dated time tree by Garcia-Porta et al. (2019) confirmed that *Teira* and *Scelarcis* are sister taxa and that their divergence is at a similar level or even lower than among species of many well-established genera. According to this study, *Teira* and *Scelarcis* diverged from each other in the mid-Miocene, coinciding with or even post-dating intrageneric splits in many other lacertid genera such as *Algyroides*, *Gallotia*, *Iberolacerta*, *Lacerta*, *Podarcis*, *Psammotromus*, *Takydromus*, and *Timon*. Mendes et al. (2016) argued to maintain *Scelarcis* mainly because of nomenclatural stability. We follow this approach and maintain *Teira* and *Scelarcis* as valid genera, awaiting additional evidence.

Psonis et al. (2017, 2018) examined species delimitation in the *Podarcis tauricus* group (including *P. tauricus*, *P. milensis*, *P. gaigeae* and *P. melisellensis*) using mitochondrial and nuclear DNA sequences, microsatellites and RADseq data. Their most complete phylogenomic analysis offered a fully resolved species level phylogeny, and confirmed the existence of extensive genetic structuring within *P. tauricus*. Two main clades correspond with the western and eastern part of the distribution of the species on either side of the Pindos Mountains. The level of divergence between them is comparable with their divergence from the well-established species *P. melisellensis*, *P. milensis* and *P. gaigeae*, and extensive admixture is not apparent from the available data. They differ quite obviously in coloration of adult males. Even if no information on the nature of the contact zones is available, the data at hand support the split of *P. tauricus* into an eastern species (retaining the name *P. tauricus* and including the subspecies *P. t. thasopulae*) and a western species, for which the oldest available name is *P. ionicus* (Psonis et al., 2017, 2018). Several of the subclades within *P. ionicus*, supported by mitochondrial and genomic data, are as divergent as other species pairs in the genus *Podarcis* and probably warrant species status as well, but formal recognition as separate species is still lacking. On the basis of published information, we accept the split of *Podarcis tauricus* into two species: *P. tauricus* and *P. ionicus*.

Using published data on three mitochondrial and three nuclear genes, Senczuk et al. (2019) examined the phylogeny of the genus *Podarcis* to address the systematic status of the *Podarcis siculus* populations from the Western Pontine Islands, off the Italian west coast. They estimated that the Western Pontine lineage diverged from all other *P. siculus* lineages around 4 Mya, and showed that this genetic divergence is similar to or greater than that between many other species pairs of *Podarcis* lizards. Hence, they formally raised the Western Pontine

populations, currently classified as several subspecies of *P. siculus*, to species rank as *Podarcis latastei*, as *latastei* is the oldest name available for this lineage. At this stage we are reluctant to follow this decision for two reasons. Firstly, 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. As multiple examples of deep mtDNA divergence that are not reflected in genomic divergence are known, we feel that compelling evidence of nuclear DNA divergence is needed before adopting this new species. Secondly, Senczuk et al. (2019) presented a simplified picture of the patterns of genetic divergence in *P. siculus*. 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. While Senczuk et al. (2018) indicated differentiation in nuclear DNA between at least some of the main mtDNA lineages in *P. siculus*, no information on their level of reproductive isolation is yet available. As a consequence, while the TC 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.

Michels and Bauer (2004) provided a list of what they argued to be justified emendations (citing Article 31.1.2 of the Code) of non-avian reptile and amphibian scientific names which the authors identified as inappropriate original constructions of patronyms or matronyms. Among the listed species was *Podarcis raffonei* (as *Lacerta sicula raffonei* Mertens, 1952). Because this taxon was named in honour of the collectors' wife, Michels and Bauer (2004) concluded that *raffonei* should be changed into *raffoneae*. However, Article 31.1.2 simply states

how species-group names should originally be formed. The article does not provide grounds for subsequent changes to the name. Furthermore, justified emendations can only be made to ‘spellings that must be corrected’ (Article 32.5, see also 33.2.2), in which these cases are not included. Even though Michels and Bauer (2004) are linguistically correct (Arribas, 2017), amending *raffonei* to *raffoneae* is unjustified (Article 33.2.3), making the latter an unjustified emendation and hence a junior objective synonym of the former (see also Dubois, 2007). We thus recommend to maintain the original spelling *P. raffonei*. As a side note, we highlight that the results of Senczuk et al. (2019) also cast serious doubts on the validity of the species status of *P. raffonei*, but we refrain here from advocating any change for now.

Investigating the species group comprising *Podarcis cretensis*, *P. levendis* and *P. peloponnesiacus*, Spilani et al. (2019) found well-supported differentiation within the latter species. Based on 17 microsatellites, the eastern populations diverged 1.86 Mya. Most noteworthy, the eastern and western lineages occur in actual or near syntopy without any apparent sign of admixture. The observed level of divergence, together with evidence of reproductive isolation, warrant a species-level split within *P. peloponnesiacus*. However, Spilani et al. (2019) refrain from making any taxonomic change. The TC follows this position, as we await a forthcoming morphological study, prior to proposing a formal change.

From a long line of studies on the Iberian *Podarcis* species, the acceptance of *Podarcis liolepis* and the redefinition of *Podarcis hispanicus* sensu stricto were the most recent steps that were adopted by SBC2010. At the time, two additional species were sufficiently substantiated, genetically as well as morphologically. Awaiting formal naming, they were listed as *Podarcis hispanicus* type 1 (north-western Iberian Peninsula and central Iberian mountain chains) and type 2 (parts of central and south-western Iberian Peninsula). Geniez et al.

(2014) provided additional morphological analyses, and formally named them as *Podarcis guadarramae* (former type 1) and *P. virescens* (former type 2). Morphological and molecular differentiation within *Podarcis guadarramae* resulted in the description of the subspecies *P. g. lusitanicus* from northern Portugal and north-western Spain. We accept *P. guadarramae* and *P. virescens* as valid species, while the status of *lusitanicus* will be the focus of a forthcoming study (G. Dias and C. Pinho, pers. comm.).

Although sometimes credited to Gray, 1825 (e.g. Sindaco and Jeremčenko, 2008), the family name Scincidae must be credited to Oppel (1811), as adopted by Hedges (2014) and others. Oppel (1811) created the name as “Familia. Scincoides”. Article 11.7.3 of the Code (see family Agamidae above) makes it clear that the nomen is made available by its publication in Oppel (1811), even if the suffix must be corrected.

A split of the Scincidae into seven families would affect the systematics of the European genera, with *Ablepharus* being placed into Eugongylidae, *Heremites* into Mabuyidae and the remaining genera *Chalcides*, *Ophiomorus* and *Eumeces* remaining in Scincidae s.s. (Hedges and Conn, 2012; Hedges, 2014). This was neither adopted in the large-scale squamate phylogeny of Zheng and Wiens (2016), nor in the online Reptile Database (Uetz, Freed and Hošek, 2019). As most skinks are readily recognisable as belonging to this group, and the monophyly of Scincidae sensu lato is well established, we follow the argument of the ‘phenotypic diagnosability’ taxon naming criterion of Vences et al. (2013a) for the time being, keeping all species (even if there are many) within a single family. Distinction of subfamilies, however, certainly makes sense as it provides more manageable units for taxonomic revision and other purposes.

For a long time, the skink genus *Mabuya* included numerous species from South America, Africa and Asia. A series of phylogenetic works (e.g. Mausfeld et al., 2000, 2002; Carranza and

Arnold, 2003; Mausfeld and Schmitz, 2003; Whiting et al., 2006) confirmed the monophyly of the genus, but also uncovered deep evolutionary divergence between its main radiations, which also differ consistently in several morphological and life-history traits. The initial divergence within the group is estimated to date back to the Eocene, between 40 and 50 million years ago (Karin et al., 2016). Mausfeld et al. (2002) were the first to suggest a split of the genus *Mabuya* to reflect the long evolutionary divergence of its main lineages, a proposal that has been universally adopted since. The Middle Eastern *Mabuya* species (*M. aurata*, *M. septemtaeniata* and *M. vittata*) form a well-supported monophyletic group in all phylogenies. They have been classified with the African species in the genus *Trachylepis* for several years but, even if their phylogenetic position within the radiation of the former *Mabuya* is still poorly resolved, they are not part of the radiation of African species in the genus *Trachylepis* (Karin et al., 2016). Their origin is quite ancient (estimated around the late Oligocene, more than 30 million years ago) and their clade is thus now afforded genus rank by all recent works on the subject, a position that we follow here. The valid genus-group nomen of the Middle-East clade is *Heremites* Gray, 1845 (masculine, see Karin et al., 2016). We thus recommend calling the Middle East species *Heremites auratus*, *H. vittatus* and the extralimital *H. septemtaeniatus*.

The phylogeography of *Ophiomorus punctatissimus* was examined by Poulakakis et al. (2008) using three mitochondrial fragments. On the basis of divergence rates of mitochondrial genes calibrated in other groups of squamates, they uncovered a deep divergence between the Asian (Anatolian) and European populations of the species, estimated to have occurred around 10 Mya. This date fits nicely with the opening of the mid-Aegean trench, estimated from geological information to have started around 12 Mya and being completed around 9 Mya. More recently, Kornilios et al. (2018) used mtDNA and nuclear DNA data

(three nuclear genes) for single-locus and multilocus coalescent-based species delimitation. The established COI *p*-distance is substantial (12.7%). No allele sharing was found, and the Asian and European lineages appeared reciprocally monophyletic for all three nuclear genes, confirming their long-term isolation. Even if suboptimal preservation of specimens and/or morphological conservatism in these fossorial species did not allow identifying any morphological differentiation between the two allopatric *Ophiomorus* lineages, the authors advocated recognition of the eastern lineage from Anatolia as a new species, which they described as *O. kardesi*. The status of several mitochondrial lineages recovered within *O. punctatissimus* awaits further study. Based on the divergence time and level of genetic divergence between these two cryptic species, we accept the species status of *O. kardesi*. In our area, the new species occurs on the Greek island of Kastellorizo (Kornilios et al., 2018).

Phylogenetic analysis based on mitochondrial and nuclear markers (Skourtanioti et al., 2016) showed strong divergence, supporting the independent history of a clade of snake-eyed skinks (*Ablepharus*) from Kastellorizo and southwestern Turkey. The samples of this clade originate from an area where the only taxon known to occur according to Schmidtler (1997) is *Ablepharus budaki anatolicus*. As a consequence, Skourtanioti et al. (2016) suggested that the name *anatolicus* is available for this new species-level lineage, which splits from a more basal node than all other but one (*A. pannonicus* from Iran) species of the genus, and whose divergence was estimated to date back to the mid-Miocene. As the genetic differentiation and deep phylogenetic divergence of the new species was confirmed by independent analyses of both mitochondrial and nuclear genes, we agree that the genetic data strongly support the recognition of an additional *Ablepharus* species from SW Turkey (including Kastellorizo and hence entering our area). However, we refrain from formally accepting a new species here and

prefer to wait until genetic data confirm that animals from the type locality of *anatolicus* indeed represent this new lineage.

Sindaco and Jeremčenko (2008), who provided the starting point of our taxonomy for areas not covered by SBC2010 or Gasc et al. (1997), follow Pasteur, Keymar and Perret (1988) in treating the Gran Canaria skinks as two species, *Chalcides bistrriatus* in the north-east of the island and *C. sexlineatus* in the south-west. This classification was based on a sharp geographic transition in morphology and (especially) colour pattern between the skinks inhabiting the mesic and xeric habitats on Gran Canaria (see Brown and Thorpe, 1991a, b, although these authors rejected the hypothesis of speciation between these morphotypes). Studies on the evolutionary history of these populations using allozymes (Mayer and Tiedemann, 1991) or a combination of mtDNA and microsatellites (Suárez, Pestano and Brown, 2014) established that this differentiation has a genetic basis, originating from allopatric diversification within Gran Canaria. This divergence is linked to volcanic activity 1.5-3 Mya and is currently maintained by strong selection on coloration, in spite of considerable introgression and gene flow between the two morphs. While the deepest divergence between the mtDNA clades within Gran Canaria is dated to 1.5 Mya, the divergence between the two morphs was dated to 260,000 years ago. This discrepancy could reflect real differences between coalescence time of mtDNA lineages versus divergence time of populations, or analytical issues with one of the methods. Either way, the available data suggest a young divergence of *C. s. sexlineatus* and *C. s. bistrriatus*, together with a lack of reproductive isolation. We thus recommend to treat these taxa as conspecific as *C. s. sexlineatus* and *C. s. bistrriatus*, as adopted by Mayer and Tiedemann (1991), Carranza et al. (2008) and Salvador and Brown (2015).

Mitochondrial DNA data of the Canarian skinks establish with a very high support that the *Chalcides* from Tenerife (*C. v. viridanus*)

and La Gomera and El Hierro (*C. v. coeruleopunctatus*) are not each other's closest relative, with *coeruleopunctatus* being more closely related to the taxa from Gran Canaria (*sexlineatus* and *bistrriatus*) than to *viridanus* (Brown and Pestano, 1998; Carranza et al., 2008). These relationships rule out maintaining *coeruleopunctatus* as a subspecies of *viridanus*, as was traditionally the case based on their morphological similarity. In addition, the amount of divergence between *C. sexlineatus*, *C. viridanus* and *C. coeruleopunctatus* is typical of interspecific divergences in the genus *Chalcides* (Carranza et al., 2008). We thus accept the conclusion of Carranza et al. (2008) and treat the animals from La Gomera and El Hierro as *Chalcides coeruleopunctatus*.

The publication dates of the works of Daudin have been worked out by Harper (1940). The volume 4 of "Histoire Naturelle des Reptiles", containing the description of *Eumeces schneiderii*, was published in August 1802. The specific epithet is often spelled *schneideri*, even if both *schneideri* and *schneiderii* are in use. The original spelling is *schneiderii* (see Daudin, 1802), with *schneideri* as an incorrect subsequent spelling. The only reason to use this spelling rather than the original spelling would be if the incorrect subsequent spelling *schneideri* was in prevailing usage (see Art. 33.3.1 of the Code). Prevailing usage is defined by the Code as "that usage of the name which is adopted by at least a substantial majority of the most recent authors concerned with the relevant taxon". We checked the number of publications using either spelling after 2000 using the electronic version of the Zoological Record and found that 17 works published after 2000 used *schneiderii* while 28 used *schneideri*. We interpret this as a lack of clear support for a prevailing usage of the incorrect subsequent spelling and thus adopt the original spelling *E. schneiderii*.

Considerable divergence within the genus *Anguis* has been revealed by means of genetic

and morphological analyses (Cabela and Gril-litsch, 1989; Gvoždík et al., 2010). This led to the recognition of *A. graeca* and *A. colchica*, resulting in the acceptance of at least four *Anguis* species in Europe by Gvoždík et al. (2010) and, subsequently, SBC2010. Although no Italian specimens were incorporated in previous analyses, *Anguis fragilis* was hitherto presumed to inhabit much of western, central and eastern Europe, including the Italian Peninsula (Gvoždík et al., 2010). More recently, Gvoždík et al. (2013) showed Italian *Anguis* to represent a deeply differentiated mtDNA clade, which presumably diverged during or shortly after the basal radiation within the genus. Genetic distances between the Italian clade and all recognised species are larger than the interspecific distances among *A. fragilis*, *A. graeca* and *A. colchica*. Hence, Gvoždík et al. (2013) proposed to recognise the populations from Italy and adjacent extreme south-eastern France as *Anguis veronensis*. Two specimens (one from NE Italy and one from Slovenia) were heterozygous for the most common *A. fragilis* and *A. veronensis* PRLR haplotypes and carried *A. fragilis* mtDNA, indicating hybridisation. While morphological differentiation between *A. veronensis* and *A. fragilis* is significant, the ranges of all studied characters overlap. In light of the earlier accepted splits among the European *Anguis* by SBC2010, the divergence during the basal radiation of the genus, and the genetic and morphological evidence presented by Gvoždík et al. (2013), we recognise the Italian and south-eastern French populations as *A. veronensis*.

Albert and Fernández (2009) partitioned the Iberian Worm Lizard *Blanus cinereus* into two species, attributing southwestern Iberian populations to the cryptic *Blanus mariae* and designating a lectotype for *B. cinereus*. Their lectotype designation was, however, found to be invalid, due to the lack of explicitly stated taxonomic purpose, while they did not establish whether the original type series consists of one holotype or several syntypes, nor examined the status of other, older nomina in the synonymy of

Iberian *Blanus* (SBC2010). These issues were tackled by Ceriaco and Bauer (2018), who argued that the type locality of *Amphisbaena cinerea* Vandelli, 1797 falls within the range of populations attributed to *B. mariae* by Albert and Fernández (2009). To further strengthen their interpretation, they made a valid neotype designation for *B. cinereus*, selecting a neotype belonging to the south-western Iberian species. This effectively places *B. mariae* in the synonymy of *B. cinereus*, which becomes the valid name for the south-western Iberian *Blanus* species. In agreement with Sampaio et al. (2015), who confirmed that the two Iberian *Blanus* clades show high levels of mitochondrial differentiation and no signs of nuclear haplotype sharing, Ceriaco and Bauer (2018) accepted the existence of two Iberian *Blanus* species. However, they deemed no name to be valid for the Central Iberian species. Yet, two older names, *Amphisbaena oxyura* Wagler, 1824 and *Amphisbaena rufa* Hemprich, 1820, are available and relate to *Blanus* from Spain. The type specimen of *A. oxyura* is lost, while its type locality ('Spain', according to Wagler, 1830) makes it impossible to link this name to either of the two Spanish *Blanus* species. The name *A. rufa* was based on a holotype that is still present in the Zoological Museum in Berlin (ZMB), but the catalogue entry for this specimen shows that it originates from southern Spain, where both *Blanus* clades occur. As morphological identification of the two Spanish *Blanus* species is currently impossible, robust attribution of *A. rufa* to either clade requires molecular data. Yet, this is problematic with the currently available methods (Ceriaco and Bauer, 2018). Ceriaco and Bauer (2018) thus treated these two names as nomina dubia and created the new nomen *Blanus vandellii*. SBC2010 had already recognised the two Iberian *Blanus* clades at species level. We follow this arrangement, and accept that *B. mariae* is a junior synonym of *B. cinereus*, with the latter being the valid name for the southwestern *Blanus* clade (Ceriaco and Bauer, 2018).

However, instead of introducing a new name in the form of *B. vandellii*, we promote the use of the oldest available name, *Blanus rufus*, as the valid name for the central clade until information on the identity of the *A. rufa* holotype can be obtained. Rather than discarding the old name until proven to apply, we advocate that when an available name exists, it should be used until proven not to apply to the relevant taxon. We thus list the two Iberian species as *B. cinereus* (south-western species) and *B. rufus* (north-eastern species).

Hedges et al. (2014) present molecular and morphological data to clarify the phylogeny of the Typhlopidae and split the large genus *Typhlops* into a number of well-defined new genera. As a consequence, the European blind snake species is now referred to as *Xerotyphlops vermicularis*. Additionally, according to Hedges et al. (2014), the non-native Flowerpot Snake, recently introduced to Italy and Spain (Zamora-Camacho, 2017; Paolino, Scotti and Grano, 2019), is now called *Indotyphlops braminus*.

The name of *Hierophis viridiflavus* has been involved in nomenclatural debate over the last few decades, but are now solved (ICZN Opinions 1463 and 1686). In 1833, Charles-Lucien Bonaparte (the nephew of Napoleon) described *Coluber viridi-flavus carbonarius* for the eastern Italian populations that are completely or almost completely black. The subspecies *H. v. carbonarius* was considered valid, until Schätti and Vanni (1986) placed it in the synonymy of the nominal form. A series of phylogeographic studies based on mtDNA and nuclear DNA confirmed that *viridiflavus* and *carbonarius* are distinct evolutionary lineages which form reciprocally monophyletic clades in mtDNA (Nagy et al., 2001; Rato et al., 2009; Mezzasalma et al., 2015; Avella, Castiglia and Senczuk, 2017). These two lineages differ in the morphology of their W chromosomes (submetacentric in the E clade and telocentric in the W clade – Mezzasalma et al., 2015). As a consequence, they have been treated as valid subspecies since Nagy et al. (2001). In 2015, Mezzasalma et al. (2015)

proposed to treat *H. viridiflavus* and *H. carbonarius* as different species on the basis of (i) different morphology of the W sex chromosome, (ii) reciprocal monophyly in mtDNA with a genetic divergence of 4% in both *cyt b* and ND4, and (iii) morphological differentiation consistent with mtDNA differentiation. However, Rato et al. (2009) found a lack of general agreement between colour pattern and mtDNA clade in Italy, and no differences in the nuclear intron beta-fibrinogen intron 7 between the two lineages. The amount of divergence in mtDNA between *H. v. carbonarius* and *H. v. viridiflavus* is much lower than between *H. gemonensis* and *H. viridiflavus*, while the amount of divergence in PRLR between them resembles the divergence within *H. gemonensis*. The sample size for the chromosomes is quite low as well. The split of *H. v. carbonarius* from *H. v. viridiflavus* did not reach broad support in the TC, as several members felt the evidence is still insufficient, and they prefer to wait for information on genetic variation near the contact zones. We thus recommend to maintain *Hierophis viridiflavus carbonarius* as a subspecies for the time being.

Jablonski et al. (2019) applied phylogenetic and morphological analyses to range-wide sampled data, aiming to better understand the intraspecific relationships and biogeography of *Elaphe sauromates*, and subsequently revised its taxonomy. Known from the Balkans, Anatolia, the Caucasus, the Ponto-Caspian steppes, and the Levant, this species has been suspected to be composed of two or more genetically diverse populations (Lenk, Joger and Wink, 2001). Sequences from 63 specimens and morphological data from 95 specimens were analysed. The authors found two distinct evolutionary lineages, one of which represents a new species, *Elaphe urartica*. The new species is distributed in eastern Turkey, Georgia, Armenia, Azerbaijan, Nagorno-Karabakh, Iran, and Russia (Dagestan). The mtDNA genetic distances between *E. sauromates* and *E. urartica* (6-8%

in COI and ND4) were interpreted as indicating a split at the Miocene-Pliocene boundary (5-8 Mya; see Kornilios et al., 2014), thus they presumably separated not very long after their common ancestors separated from *E. quatuorlineata*. Two out of four analysed nuclear genes were also clearly differentiated, though closely related, between *E. urartica* and *E. sauromates*, while the remaining two showed signs of incomplete lineage sorting. Both lineages are also moderately morphologically differentiated and, while none of the characters are exclusively diagnostic, their combination can be used for confident lineage identification. Conclusively, we accept *Elaphe urartica* as a separate species.

The ladder snake *Rhinechis scalaris* is characterised by a backward-oriented rostral scale that is wedged between the internasal scales. Apart from this striking feature, external morphology of *R. scalaris* has long been acknowledged to closely match that of *Zamenis* rat snakes (Salvi et al., 2018). Multiple recent phylogenetic assessments have revealed that *Rhinechis* (with the sole member *R. scalaris*) and *Zamenis* are closely related (Burbrink and Lawson, 2007; Pyron et al., 2011; Pyron, Burbrink and Wiens, 2013; Zheng and Wiens, 2016). Some of these studies found *Zamenis* to be paraphyletic in respect to *Rhinechis*, while others placed *Rhinechis* as sister to all *Zamenis* species, albeit with low support (reviewed by Salvi et al., 2018). The latter authors argue that this phylogenetic uncertainty reflects an evolutionary scenario in which early cladogenetic events took place at the same time or within a short time frame, making it hard to disentangle which (if any) lineage branched off first. Using two mitochondrial and five nuclear genes, Salvi et al. (2018) then inferred phylogenetic relationships between *Zamenis* and *Rhinechis*. They recovered a strongly supported clade consisting of *Rhinechis scalaris* and *Zamenis*, while the monophyly of *Zamenis* without *scalaris* remained poorly supported. As a result, these authors proposed to include *scalaris* in *Zamenis*. In agreement with the ‘clade stability’ taxon

naming criterion of Vences et al. (2013a) and as a named genus of uncontroversial monophyly is obtained, we here follow this.

The California Kingsnake *Lampropeltis getula californiae* has been introduced to Gran Canaria, where it turned into a problematic invasive species (Monzón-Argüello et al., 2015; Fisher et al., 2019). Based on mtDNA data and morphological variation, Pyron and Burbrink (2009) elevated *L. g. californiae* and four other subspecies to species status. While the basal division in their phylogeny has *L. g. getula* and *L. g. nigra* in the one main branch and *L. g. holbrooki*, *L. g. splendida* and *L. g. californiae* in the other, the division between *L. g. splendida* and *L. g. californiae* is retrieved as the most recent one. Pending the publication of a multilocus analysis or a detailed study of the various contact zones, we maintain *L. g. californiae* as a subspecies of the Common Kingsnake *Lampropeltis getula* for the time being.

The groundwork of contemporary elucidation of the *Natrix natrix* complex was initiated by the mitochondrial phylogeography of Kindler et al. (2013), leading to rejection of *Natrix megalcephala* and the identification of multiple contact zones, three of which were further investigated more recently (see below). Subsequently, a virtual lack of gene flow between *N. natrix helvetica* and *N. natrix astreptophora* and the differentiation between both taxa established on multiple sources of evidence, such as microsatellites, mtDNA, osteology and external morphology, led to suggesting species status for *Natrix astreptophora* (Pokrant et al., 2016). Within central Europe, Kindler et al. (2017) investigated two macro-scale transects across *Natrix* transition zones. The eastern contact zone between two lineages identified by Kindler et al. (2013) as running from Central Europe to the southern Balkans displayed wide-reaching introgression. In contrast, the western contact zone between the traditional subspecies *N. n. natrix* and *N. n. helvetica* in western Germany was shown to be narrow (microsatellite cline width of about 40 km), with a deficit of admixed

individuals generating a bimodal hybrid zone, indicative of strongly restricted gene flow. We therefore accept *N. astreptophora* and *N. helvetica* as valid species in addition to *N. natrix*.

Ferchaud et al. (2012) provided a well-resolved mitochondrial phylogeny of the *Vipera ursinii* complex, which indicates that the *renardi* clade, the *ursinii* clade and the *graeca* clade diverged approximately 3–4 Mya. The divergence between these three clades is of the same magnitude as between the two widely accepted species *V. berus* and *V. seoanei*. The *renardi* and *ursinii* clades do not seem to share haplotypes, although they inhabit similar habitats along the north-western Black Sea coast where *Vipera ursinii moldavica* occurs. Given the level of genetic divergence, lack of haplotype sharing, marked morphological divergence and lack of well supported morphological intergradation, it seems more adequate to treat *V. renardi* as specifically distinct from *V. ursinii*. Given its well-supported position at the base of a *renardi* + *ursinii* clade and although we verified a very low genetic distance between *ursinii* and *graeca* in *cyt b* (3.2%), this arrangement makes it necessary to treat *V. graeca* as a distinct species as well. Additional morphological and mtDNA and nuclear DNA data support the distinct position of the *graeca* clade (Mizsei et al., 2017). Several other taxa from the Caucasus and the Middle East have been put forward as valid species, two of which occur in our area: the Caucasian *lotievi* and the recently described *shemakhensis* (Tuniyev et al., 2013) from north-eastern Azerbaijan. A recent phylogenomic (RADseq data) analysis of multiple specimens of *renardi* and *lotievi* by Zinenko et al. (2016) showed a lack of genetic differentiation at the genome scale between specimens collected in the lowlands (*renardi*) and Caucasian uplands (*lotievi*). There is no genetic information for *shemakhensis*, which is, however, very similar to *lotievi* morphologically. In conclusion, we consider three European species within the *Vipera ursinii* complex: *V. graeca*, *V. renardi* and *V. ursinii*, and recommend treating

V. r. lotievi and *V. r. shemakhensis* as conspecific with *V. renardi*.

Tuniyev and Ostrovskikh (2001) described *Vipera orlovi* and *V. magnifica*, two viper species from the Russian Caucasus that are related to *Vipera kaznakovi*. *Vipera orlovi* inhabits both slopes of the northwesternmost Caucasus, while *V. magnifica* is described from the Malaja Laba river valley and restricted to Krasnodar territory. As no molecular data was provided, and it was later shown that both taxa share mtDNA haplotypes with *V. kaznakovi* (Zinenko et al., 2015), further enquiry was needed. Zinenko et al. (2016) used genomic methods to demonstrate the hybrid origin of these taxa, with parapatric *V. kaznakovi* and *V. renardi* as likely parental species. Low admixture and limited genetic differentiation led these authors to treat *V. magnifica* as a synonym of *V. kaznakovi*. The authors build a case for not revoking the species status of *V. orlovi* by advocating caution with regards to its conservation status. While we do not reject species of hybrid origin per se, the 2016 data does not suggest reproductive isolation or strong genetic differentiation of either taxon in relation to *V. kaznakovi*. Thus, we do not treat *V. magnifica* or *V. orlovi* as valid species. As they are more closely related to *V. kaznakovi* than to *V. renardi*, we treat both as conspecific with *V. kaznakovi*. In addition, we disagree with Zinenko et al. (2016) that the Code does not allow the recognition of taxa with hybrid ancestry. The Code rules nomenclature, not systematics, and nothing in the Code precludes treating taxa of admixed ancestry as valid. As both *orlovi* and *magnifica* were described on the base of distinct phenotypic features, we tentatively maintain them as subspecies of *V. kaznakovi* (*V. k. orlovi* and *V. k. magnifica*) until a detailed examination of morphological variation might show them not to be morphologically distinct.

A new viper species, named *Vipera walser*, was described from northern Piedmont, Italy (Ghielmi et al., 2016) based on mtDNA, nuclear DNA and morphological discriminant analyses. Remarkably, while morphologically very

similar to north Italian *V. berus*, mtDNA data showed the new taxon to be nested with geographically distant taxa of the *ursinii-kaznakovi* complex. For two protein-coding nuclear genes (BACH2 and RAG1), *V. walser* does not share haplotypes with *V. berus*. However, only single individuals of both species have so far been sequenced. Moreover, for RAG1, the new species is similar to *V. berus*, while no sequences of the *ursinii* complex exist for this gene. Therefore, the existence of cytonuclear discordance cannot be discarded. Until additional nuclear DNA data confirms the distinct nature of the *walser* population, we consider acceptance of the new species to be premature, and tentatively regard it as a population of *V. berus* with distinct, perhaps introgressed, mtDNA. Morphologically, *V. walser* does not differ much from the *V. berus* populations inhabiting the Italian Alps (the Italian clade of *V. berus* in Ursenbacher et al., 2006) but it is easily distinguishable from the Central and Northern European populations of *V. berus*. Thus, the Italian Alps populations of *V. berus* could be treated as a subspecies under the name *V. b. walser*. However, we refrain from making formal recommendations here, pending a detailed analysis of morphological variation between populations of *V. berus* from the Italian Alps (including the populations described as *V. walser*) and the rest of the *V. berus* populations.

The populations of mostly black adders inhabiting the forest-steppe zone of the south and south-eastern parts of the East European Plain have been described as *Vipera nikolskii* Vedmederya, Grubant and Rudaeva, 1986. The distribution and morphological characters of *nikolskii* compared to *berus* have been reviewed by Bakiev, Böhme and Joger (2005), Milto and Zinenko (2005) and Zinenko, Țurcanu and Strugariu (2010, who showed that populations of *nikolskii* from the western parts of its range can be mostly composed of non-melanistic specimens). According to Milto and Zinenko (2005), several older names created by Pallas for black adders from southern Russia

were based on populations resulting from intergradation between *berus* and *nikolskii* and cannot apply to the later taxon, leaving *nikolskii* as the valid nomen for this taxon. While it was first described at species rank, *nikolskii* is now variously treated as a full species (e.g. Bakiev, Böhme and Joger, 2005; Uetz, Freed and Hošek, 2019) or as a subspecies of *Vipera berus* (e.g. SBC2010; Zinenko, Țurcanu and Strugariu, 2010; Mizsei et al., 2017; Crnobrnja Isailovic et al., 2019 by implication). Depending on their geographical origin, specimens of *nikolskii* either carry *berus* mtDNA haplotypes, or haplotypes grouping (within the diversity of the *berus* group) close to *V. b. barani* (Joger et al., 1997; Kalyabina-Hauf et al., 2004). A multilocus phylogeny places *nikolskii* within *V. berus* (Mizsei et al., 2017). Detailed morphological studies show extensive introgression in the contact zones with *V. b. berus* (Zinenko, 2004; Milto and Zinenko, 2005; Zinenko, Țurcanu and Strugariu, 2010). We thus maintain the treatment of SBC2010 and consider *nikolskii* as conspecific with *V. berus*, supporting its recognition as *V. b. nikolskii* to acknowledge its morphological and ecological peculiarities.

The correct spelling of the specific epithet of the Lataste's viper has been a matter of long lasting debates because Boscá (1878) used the spelling "*Vipera Latasti*" in the text and "*Vipera latastei*" in the caption for the accompanying plate, with both spellings in current use in the literature (see Alonso-Zarazaga, 2013 and Salvador et al., 2014 for summaries). Following an application to the International Commission on Zoological Nomenclature (ICZN) by Salvador et al. (2014), the ICZN (2017) confirmed that *Vipera latastei* Boscá, 1878 is the correct original spelling of the specific name.

Frétey (2019) provided compelling argumentation of why the capitalised epithet *Lebetinus* in *Coluber Lebetinus* Linnaeus, 1758 is a noun in apposition and must be treated as invariable. We agree with his interpretation, and accept that the Blunt-nosed Viper should be called *Macrovipera lebetinus*.

Based on morphology, Nilson and Andr n (1988) elevated *Macrovipera lebetinus schweizeri* to species rank. St mpel (2012), however, found that the mtDNA haplotypes found in *M. schweizeri* are not limited to the Milos archipelago, but are also present near Mersin on the Turkish mainland. This author thus pointed out that treating *M. schweizeri* as a valid species might render *M. lebetinus* paraphyletic. Furthermore, they showed that in their mtDNA trees *schweizeri* is neither basal to the rest of the *M. lebetinus* haplotypes, nor highly divergent. Yet, while St mpel's dissertation is available, and a (brief) sentence in St mpel and Joger (2009) refers to these results, these findings have not yet been properly published in a peer-reviewed journal, and the relevant *Macrovipera* sequences are not yet available in GenBank either. As a consequence, many TC members felt that a formal taxonomic decision on this case would be premature, and, while it is likely that *schweizeri* is best treated as a subspecies, the decision can only be taken after the evidence has been properly published, or the data has been made publicly available. Conclusively, we maintain *Macrovipera schweizeri* at species level for now.

The occurrence of the genus *Gloydius* inside the area covered by this list is unclear. The only European area where the occurrence of the genus has been reported is north of the Caspian Sea, between the Volga and Ural valleys. As explained by Conant (1982) and Dirksen and B hme (2005), all records supported by specimens in museum collections are either on the east side of the Ural River, hence outside our area (Induski Hills = Indersky Mountains), or cannot be precisely localised (one specimen from "Gur'jev", now Atyrau, which lies at the mouth of the Ural River on both sides of the river). Attempts to locate *Gloydius* west of the Ural River have failed (Conant, 1982; Bakiev, Ratnikov and Zinenko, 2007; Sarayev and Pestov, 2010; Simonov, pers. comm.). Thus, no modern records of the presence of the genus in Europe exist, and no record is supported by

a collected specimen. The possible occurrence of *Gloydius* within Europe is based on several ancient sources that report the genus between the Volga and Ural rivers in the dry steppes or deserts east of Astrakhan (see Conant, 1982 and Bour, 1993 for details). They all seem to originate from just two original sources: Gmelin (1789), who mentions the arid deserts of Astrakhan for *Coluber halys*, and Pallas (1799), who, in his book devoted to his second journey to the southern areas of Russia, mentions (on p. 112) the species "*Berus*" and "*Halys*" were seen in an area called "Saltan-Murat" and located east of the Volga River, in an area of dry steppes close to Astrakhan (more precisely north-east of present-day Krasnyy Yar, see Conant, 1982 and Bour, 1993). All subsequent references are based on these two sources. It is even unclear if the mention of the deserts of Astrakhan in J.F. Gmelin's book is based on original information he received from his uncle J.G. Gmelin, who also travelled widely in Russia including the Caspian Sea area, from Pallas himself, or from any other source. J.F. Gmelin never visited these areas himself. We may never know how reliable these old records are. However, the other venomous species mentioned by Pallas (1799) from the same area, *Vipera berus*, is currently absent from the dry areas between the Ural and Volga Rivers. This casts doubt on the reliability of these observations. In summary, the presence of the genus *Gloydius* west of the Ural River entirely rests on unsubstantiated records that cannot be verified. We thus believe the species should be formally removed from the list of European species. In addition, we note that the systematics and nomenclature of the *Gloydius halys* complex (for a brief review, see Wagner et al., 2016) remain problematical. One of the contentious issues is the type locality of *Coluber halys* Pallas 1776, which determines the valid name of the *Gloydius* taxon occurring close to Europe in western Kazakhstan, but this question might need to be settled by an application to the Commission.

Species list

Within the area considered for our species list, a number of non-native species have been introduced and/or have become established, and are reproducing. As far as they were not yet listed in the starting point species lists mentioned in the introduction, we add these naturalised species here. More precisely, these are *Tenuidactylus bogdanovi* (see above), *Darevskia dahli* (see above), *Indotyphlops braminus* (see above), *Elaphe schrenckii* (introduced and persisting in the Netherlands, see Van de Koppel et al., 2012), and *Lampropeltis getula* (see above).

While no objective standards exist to choose vernacular names, to improve user-friendliness of the list, we added English species names, most of which were adopted from Speybroeck et al. (2016). Others were added to harmonise as much as possible with those of Speybroeck et al. (2016) and Arnold and Ovenden (2002), or with suggestions in the respective species description, or they are newly proposed here.

Changes, as discussed in the text, are marked in bold. Non-native species are marked with an asterisk. Taxa above genus level are listed in traditional order, genera and species arranged alphabetically. For the Class Reptilia, we restrict ourselves to non-avian reptiles and disregard the Subclass Aves.

Class Amphibia Linnaeus, 1758

Order Caudata Scopoli, 1777 or Urodela
Duméril, 1805

Family Hynobiidae Cope, 1859 (1856)

Salamandrella Dybowski, 1870

Salamandrella keyserlingii Dybowski,
1870 – Siberian Salamander

Family Salamandridae Goldfuss, 1820

Calotriton Gray, 1858

Calotriton arnoldi Carranza and Amat,
2005 – Montseny Brook Newt

Calotriton asper (Dugès, 1852) – Pyre-
nean Brook Newt

Chioglossa Bocage, 1864

Chioglossa lusitanica Bocage, 1864 –
Golden-striped Salamander

Euproctus Gené, 1839

Euproctus montanus (Savi, 1838) – Corsi-
can Brook Newt

Euproctus platycephalus (Gravenhorst,
1829) – Sardinian Brook Newt

Ichthyosaura Sonnini and Latreille, 1801

Ichthyosaura alpestris (Laurenti, 1768) –
Alpine Newt

Lissotriton Bell, 1839

Lissotriton boscai (Lataste in Tourneville,
1879) – Bosca's Newt

***Lissotriton graecus* (Wolterstorff,
1906) – Greek Smooth Newt**

Lissotriton helveticus (Razoumowsky,
1789) – Palmate Newt

Lissotriton italicus (Peracca, 1898) – Ital-
ian Newt

***Lissotriton maltzani* (Boettger, 1879) –
Maltzan's Newt**

Lissotriton montandoni (Boulenger,
1880) – Montandon's Newt

Lissotriton vulgaris (Linnaeus, 1758) –
Smooth Newt

Lyciasalamandra Veith and Steinfartz, 2004

Lyciasalamandra helverseni (Pieper,
1963) – Karpathos Salamander

Lyciasalamandra luschani (Steindachner,
1891) – Luschan's Salamander

Pleurodeles Michahelles, 1830

Pleurodeles waltl Michahelles, 1830 –
Sharp-ribbed Newt

Salamandra Garsault, 1764

Salamandra atra (Laurenti, 1768) – Alpine
Salamander

Salamandra corsica (Savi, 1838) – Corsi-
can Fire Salamander

Salamandra lanzai (Nascetti, Andreone,
Capula and Bullini, 1988) – Lanza's
Salamander

Salamandra salamandra (Linnaeus,
1758) – Fire Salamander

Salamandrina Fitzinger, 1826

Salamandrina perspicillata (Savi, 1821) –
Northern Spectacled Salamander

Salamandrina terdigitata (Bonnaterre, 1789) – Southern Spectacled Salamander

Triturus Rafinesque, 1815

Triturus carnifex (Laurenti, 1768) – Italian Crested Newt

Triturus cristatus (Laurenti, 1768) – Great Crested Newt

Triturus dobrogicus (Kiritzescu, 1903) – Danube Crested Newt

***Triturus ivanbureschi* Arntzen and Wielstra, 2013 – Buresch's Crested Newt**

Triturus karelinii (Strauch, 1870) – Karelin's Crested Newt

Triturus macedonicus (Karaman, 1922) – Macedonian Crested Newt

Triturus marmoratus (Latreille, 1800) – Marbled Newt

Triturus pygmaeus (Wolterstorff, 1905) – Southern Marbled Newt

***Ommatotriton* Gray, 1850**

***Ommatotriton ophryticus* (Litvinchuk, Zuiderwijk, Borkin and Rosanov, 2005) – Northern Banded Newt**

Family Plethodontidae Gray, 1850

Speleomantes Dubois, 1984

Speleomantes ambrosii (Lanza, 1955) – Ambrosi's Cave Salamander

Speleomantes flavus (Stefani, 1969) – Monte Albo Cave Salamander

Speleomantes genei (Temminck and Schlegel, 1838) – Gené's Cave Salamander

Speleomantes imperialis (Stefani, 1969) – Imperial Cave Salamander

Speleomantes italicus (Dunn, 1923) – Italian Cave Salamander

Speleomantes sarrabusensis Lanza, Leo, Forti, Cimmaruta, Caputo and Nascetti, 2001 – Sette Fratelli Cave Salamander

Speleomantes strinati (Aellen, 1958) – Strinati's Cave Salamander

Speleomantes supramontis (Lanza, Nascetti and Bullini, 1986) – Supramonte Cave Salamander

Family Proteidae Gray, 1825

Proteus Laurenti, 1768

Proteus anguinus Laurenti, 1768 – Olm

Order Anura Duméril, 1805

Family Alytidae Fitzinger, 1843

Alytes Wagler, 1829

***Alytes almogavarii* Arntzen and García-París, 1995 – Catalan Midwife Toad**

Alytes cisternasii Boscá, 1879 – Iberian Midwife Toad

Alytes dickhilleni Arntzen and García-París, 1995 – Betic Midwife Toad

Alytes muletensis (Sanchiz and Adrover, 1979) – Mallorcan Midwife Toad

Alytes obstetricans (Laurenti, 1768) – Common Midwife Toad

Discoglossus Otth, 1837

Discoglossus galganoi Capula, Nascetti, Lanza, Bullini and Crespo, 1985 – Iberian Painted Frog

Discoglossus montalentii Lanza, Nascetti, Capula and Bullini, 1984 – Corsican Painted Frog

Discoglossus pictus Otth, 1837 – Painted Frog

Discoglossus sardus Tschudi in Otth, 1837 – Tyrrhenian Painted Frog

Family Bombinatoridae Gray, 1825

Bombina Oken, 1816

Bombina bombina (Linnaeus, 1761) – Fire-bellied Toad

Bombina variegata (Linnaeus, 1758) – Yellow-bellied Toad

Family Pipidae Gray, 1825

Xenopus Wagler, 1827

**Xenopus laevis* (Daudin, 1802) – African Clawed Toad

Family Pelobatidae Bonaparte, 1850

Pelobates Wagler, 1830

***Pelobates balcanicus* Karaman, 1928 – Balkan Spadefoot Toad**

Pelobates cultripes (Cuvier, 1829) – Western Spadefoot Toad

Pelobates fuscus (Laurenti, 1768) – Common Spadefoot Toad

- Pelobates syriacus* Boettger, 1889 – Eastern Spadefoot Toad
- Pelobates vespertinus* (Pallas, 1771) – Pallas's Spadefoot Toad**
- Family Pelodytidae Bonaparte, 1850
- Pelodytes* Bonaparte, 1838
- Pelodytes atlanticus* Díaz-Rodríguez, Gehara, Márquez, Vences, Gonçalves, Sequeira, Martínez-Solano and Tejedo, 2017 – Portuguese Parsley Frog**
- Pelodytes caucasicus* Boulenger, 1896 – Caucasian Parsley Frog
- Pelodytes ibericus* Sánchez-Herráiz, Barbadillo, Machordom and Sanchiz, 2000 – Iberian Parsley Frog
- Pelodytes punctatus* (Daudin, 1802) – Parsley Frog
- Family Bufonidae Gray, 1825
- Bufo* Garsault, 1764
- Bufo bufo* (Linnaeus, 1758) – Common Toad
- Bufo spinosus* Daudin, 1803 – Spiny Toad**
- Bufotes Rafinesque, 1815***
- Bufotes boulengeri* (Lataste, 1879) – African Green Toad**
- Bufotes cypriensis* Litvinchuk, Mazepa, Jablonski and Dufresnes in Dufresnes et al., 2019 – Cyprus Green Toad**
- Bufotes viridis* (Laurenti, 1768) – Green Toad**
- Epidalea* Cope, 1864**
- Epidalea calamita* (Laurenti, 1768) – Natterjack Toad**
- Family Hylidae Rafinesque, 1815
- Hyla* Laurenti, 1768
- Hyla arborea* (Linnaeus, 1758) – Common Tree Frog
- Hyla intermedia* Boulenger, 1882 – Italian Tree Frog
- **Hyla meridionalis* Boettger, 1874 – Stripeless Tree Frog
- Hyla molleri* Bedriaga, 1889 – Iberian Tree Frog
- Hyla orientalis* Bedriaga, 1890 – Eastern Tree Frog
- Hyla sarda* (de Betta, 1857) – Tyrrhenian Tree Frog
- Hyla savignyi* Audouin, 1827 – Savigny's Tree Frog
- Family Ranidae Batsch, 1796
- Pelophylax* Fitzinger, 1843
- Pelophylax bedriagae* (Camerano, 1882) – Levant Water Frog
- Pelophylax cretensis* (Beerli, Hotz, Tunner, Heppich and Uzzell, 1994) – Cretan Water Frog
- Pelophylax epeiroticus* (Schneider, Sofianidou and Kyriakopoulou-Sklavounou, 1984) – Epirus Water Frog
- Pelophylax* kl. *esculentus* (Linnaeus, 1758) – Edible Frog
- Pelophylax* kl. *grafi* (Crochet, Dubois, Ohler and Tunner, 1995) – Graf's Hybrid Frog
- Pelophylax lessonae* (Camerano, 1882) – Pool Frog
- Pelophylax perezi* (Seoane, 1885) – Iberian Water Frog
- Pelophylax ridibundus* (Pallas, 1771) – Marsh Frog
- Pelophylax shqipericus* (Hotz, Uzzell, Günther, Tunner and Heppich, 1987) – Albanian Pool Frog
- Lithobates* Fitzinger, 1843
- **Lithobates catesbeianus* (Shaw, 1802) – American Bullfrog
- Rana* Linnaeus, 1758
- Rana arvalis* Nilsson, 1842 – Moor Frog
- Rana dalmatina* Fitzinger in Bonaparte, 1838 – Agile Frog
- Rana graeca* Boulenger, 1891 – Greek Stream Frog
- Rana iberica* Boulenger, 1879 – Iberian Stream Frog
- Rana italica* Dubois, 1987 – Italian Stream Frog
- Rana latastei* Boulenger, 1879 – Italian Agile Frog

- Rana macrocnemis* Boulenger, 1885 – Caucasian Frog
- Rana parvipalmata* Seoane, 1885 – Galician Common Frog**
- Rana pyrenaica* Serra-Cobo, 1993 – Pyrenean Stream Frog
- Rana temporaria* Linnaeus, 1758 – Common Frog
- Class Reptilia Laurenti, 1768
- Order Testudines Linnaeus, 1758 or Chelonii Brongniart, 1800
- Family Cheloniidae Opperl, 1811
- Caretta* Rafinesque-Schmaltz, 1814
- Caretta caretta* (Linnaeus, 1758) – Loggerhead Turtle
- Chelonia* Brongniart, 1800
- Chelonia mydas* (Linnaeus, 1758) – Green Turtle
- Eretmochelys* Fitzinger, 1843
- Eretmochelys imbricata* (Linnaeus, 1766) – Hawksbill Turtle
- Lepidochelys* Fitzinger, 1843
- Lepidochelys kempii* (Garman, 1880) – Kemp's Ridley
- Lepidochelys olivacea* (Eschscholtz, 1829) – Olive Ridley
- Family Dermochelyidae Fitzinger, 1843 (1825)
- Dermochelys* de Blainville, 1816
- Dermochelys coriacea* (Vandelli, 1761) – Leatherback Turtle
- Family Testudinidae Batsch, 1788
- Testudo* Linnaeus, 1758
- Testudo graeca* Linnaeus, 1758 – Spur-thighed Tortoise
- Testudo hermanni* Gmelin, 1789 – Hermann's Tortoise
- Testudo marginata* Schoepff, 1792 – Marginated Tortoise
- Family Geoemydidae Theobald, 1868
- Mauremys* Gray, 1869
- Mauremys caspica* (Gmelin, 1774) – Caspian Terrapin
- Mauremys leprosa* (Schweigger, 1812) – Spanish Terrapin
- Mauremys rivulata* (Valenciennes, 1833) – Balkan Terrapin
- Family Emydidae Rafinesque, 1815
- Emys* Duméril, 1805
- Emys orbicularis* (Linnaeus, 1758) – European Pond Terrapin
- Trachemys* Agassiz, 1857
- **Trachemys scripta* (Thunberg in Schoepff, 1792) – Pond Slider (Red-eared Slider for ssp. *elegans*)
- Family Trionychidae Fitzinger, 1826
- Trionyx* Geoffroy, 1827
- Trionyx triunguis* (Forskål, 1775) – Nile Soft-shelled Turtle
- Order Squamata Opperl, 1811
- Family Agamidae Spix, 1825
- Laudakia* Gray, 1845
- Laudakia caucasia* (Eichwald, 1831) – Caucasian Agama
- Laudakia stellio* (Linnaeus, 1758) – Starred Agama
- Phrynocephalus* Kaup, 1825
- Phrynocephalus guttatus* (Gmelin, 1789) – Toad-headed Agama
- Phrynocephalus helioscopus* (Pallas, 1771) – Sunwatcher Toad-headed Agama
- Phrynocephalus mystaceus* (Pallas, 1776) – Secretive Toad-headed Agama
- Trapelus* Cuvier, 1817
- Trapelus agilis* (Olivier, 1804) – Brilliant Ground Agama
- Family Chamaeleonidae Rafinesque, 1815
- Chamaeleo* Laurenti, 1768
- **Chamaeleo africanus* Laurenti, 1768 – African Chameleon
- Chamaeleo chamaeleon* (Linnaeus, 1758) – Mediterranean Chameleon
- Family Sphaerodactylidae Underwood, 1954
- Euleptes* Fitzinger, 1843
- Euleptes europaea* (Gené, 1839) – European Leaf-toed Gecko
- Family Gekkonidae Opperl, 1811
- Alsophylax* Fitzinger, 1843
- Alsophylax pipiens* (Pallas, 1827) – Caspian Even-fingered Gecko

- Hemidactylus* Oken, 1817
Hemidactylus turcicus (Linnaeus, 1758) – Turkish Gecko
- Mediodactylus* Szczerbak and Golubev, 1977
Mediodactylus bartoni (Štěpánek, 1934) – Cretan Bent-toed Gecko
Mediodactylus danilewskii (Strauch, 1887) – Bulgarian Bent-toed Gecko
Mediodactylus kotschyi (Steindachner, 1870) – Kotschy's Bent-toed Gecko
Mediodactylus oertzeni (Boettger, 1888) – Oertzen's Bent-toed Gecko
Mediodactylus orientalis (Štěpánek, 1937) – Eastern Bent-toed Gecko
Mediodactylus russowii (Strauch, 1887) – Russow's Bent-toed Gecko
- Tenuidactylus* Szczerbak and Golubev, 1984
 **Tenuidactylus bogdanovi* Nazarov and Poyarkov, 2013 – Bogdanov's Bent-toed Gecko
Tenuidactylus caspius (Eichwald, 1831) – Caspian Bent-toed Gecko
- Family Phyllodactylidae Gamble, Bauer, Greenbaum and Jackman, 2008
Tarentola Gray, 1825
Tarentola angustimentalis Steindachner, 1891 – East Canary Gecko
Tarentola boettgeri Steindachner, 1891 – Gran Canaria Gecko
Tarentola delalandii Duméril and Bibron, 1836 – Tenerife Gecko
Tarentola gomerensis Joger and Bischoff, 1983 – La Gomera Gecko
Tarentola mauritanica (Linnaeus, 1758) – Moorish Gecko
- Family Lacertidae Batsch, 1788
Acanthodactylus Wiegmann, 1834
Acanthodactylus erythrurus (Schinz, 1833) – Spiny-footed Lizard
Acanthodactylus schreiberi Boulenger, 1918 – Schreiber's Spiny-footed Lizard
- Algyroides* Bibron and Bory de Saint-Vincent, 1833
Algyroides fitzingeri (Wiegmann, 1834) – Pygmy Algyroides
Algyroides marchi Valverde, 1958 – Spanish Algyroides
Algyroides moreoticus Bibron and Bory de Saint-Vincent, 1833 – Greek Algyroides
Algyroides nigropunctatus (Duméril and Bibron, 1839) – Dalmatian Algyroides
- Anatololacerta* Arnold, Arribas and Carranza, 2007
Anatololacerta anatolica (Werner, 1900) – Anatolian Rock Lizard
Anatololacerta budaki (Eiselt and Schmidler, 1986) – Budak's Rock Lizard
Anatololacerta pelasgiana (Mertens, 1959) – Pelasgian Rock Lizard
- Archaeolacerta* Mertens, 1921
Archaeolacerta bedriagae (Camerano, 1885) – Tyrrhenian Rock Lizard
- Dalmatolacerta* Arnold, Arribas and Carranza, 2007
Dalmatolacerta oxycephala Duméril and Bibron, 1839 – Sharp-snouted Rock Lizard
- Darevskia* Arribas, 1997
Darevskia alpina (Darevsky, 1967) – Alpine Rock Lizard
 **Darevskia armeniaca* (Méhely, 1909) – Armenian Rock Lizard
Darevskia brauneri (Méhely, 1909) – Brauner's Rock Lizard
Darevskia caucasica (Méhely, 1909) – Caucasus Rock Lizard
Darevskia daghestanica (Darevsky, 1967) – Dagestan Rock Lizard
 **Darevskia dahli* (Darevsky, 1957) – Dahl's Rock Lizard
Darevskia derjugini (Nikolsky, 1898) – Derjugin's Rock Lizard
Darevskia lindholmi (Lantz and Cyrén, 1936) – Crimean Rock Lizard
Darevskia praticola (Eversmann, 1834) – Meadow Lizard
Darevskia rudis (Bedriaga, 1886) – Rough-tailed Rock Lizard
Darevskia saxicola (Eversmann, 1834) – North-western Caucasus Rock Lizard

- Dinarolacerta* Arnold, Arribas and Carranza, 2007
- Dinarolacerta montenegrina* Ljubisavljević, Arribas, Džukić and Carranza, 2007 – Prokletije Rock Lizard
- Dinarolacerta mosorensis* Kolombatović, 1886 – Mosor Rock Lizard
- Eremias* Fitzinger in Wiegmann, 1834
- Eremias arguta* (Pallas, 1773) – Steppe Runner
- Eremias velox* (Pallas, 1771) – Rapid Steppe Runner
- Gallotia* Boulenger, 1916
- Gallotia atlantica* (Peters and Doria, 1882) – Atlantic Lizard
- Gallotia bravoana* Hutterer, 1985 – La Gomera Giant Lizard
- Gallotia caesaris* (Lehrs, 1914) – Boettger's Lizard
- Gallotia galloti* (Oudart in Webb and Berthelot, 1939) – Tenerife Lizard
- Gallotia intermedia* Hernández, Nogales and Martín, 2000 – Tenerife Speckled Lizard
- Gallotia simonyi* (Steindachner, 1889) – El Hierro Giant Lizard
- Gallotia stehlini* (Schenkel, 1901) – Gran Canaria Giant Lizard
- Hellenolacerta* Arnold, Arribas and Carranza, 2007
- Hellenolacerta graeca* Bedriaga, 1886 – Greek Rock Lizard
- Iberolacerta* Arribas, 1997
- Iberolacerta aranica* (Arribas, 1993) – Aran Rock Lizard
- Iberolacerta aurelioi* (Arribas, 1994) – Aurelio's Rock Lizard
- Iberolacerta bonnali* (Lantz, 1927) – Pyrenean Rock Lizard
- Iberolacerta cyreni* (Müller and Hellmich, 1937) – Cyren's Rock Lizard
- Iberolacerta galani* Arribas, Carranza and Odierna, 2006 – Galan's Rock Lizard
- Iberolacerta horvathi* (Méhely, 1904) – Horvath's Rock Lizard
- Iberolacerta martinezricai* (Arribas, 1996) – Peña de Francia Rock Lizard
- Iberolacerta monticola* (Boulenger, 1905) – West Iberian Rock Lizard
- Lacerta* Linnaeus, 1758
- Lacerta agilis* Linnaeus, 1758 – Sand Lizard
- Lacerta bilineata* Daudin, 1802 – Western Green Lizard
- Lacerta citrovittata* Werner, 1935 – Cyclades Green Lizard**
- Lacerta diplochondrodes* Wettstein, 1952 – Eastern Balkan Green Lizard**
- Lacerta media* (Lantz and Cyrén, 1920) – Middle East Green Lizard
- Lacerta schreiberi* Bedriaga, 1878 – Schreiber's Green Lizard
- Lacerta strigata* (Eichwald, 1831) – Caspian Green Lizard
- Lacerta trilineata* Bedriaga, 1886 – Balkan Green Lizard
- Lacerta viridis* (Laurenti, 1768) – Eastern Green Lizard
- Ophisops* Ménétries, 1832
- Ophisops elegans* Ménétries, 1832 – Snake-eyed Lacertid
- Parvilacerta* Arnold, Arribas and Carranza, 2007
- Parvilacerta parva* (Boulenger, 1887) – Dwarf Lizard
- Phoenicolacerta* Arnold, Arribas and Carranza, 2007
- Phoenicolacerta troodica* (Werner, 1936) – Troodos Rock Lizard
- Podarcis* Wagler, 1830
- Podarcis bocagei* (Seoane, 1884) – Bocage's Wall Lizard
- Podarcis carbonelli* Pérez-Mellado, 1981 – Carbonell's Wall Lizard
- Podarcis cretensis* (Wettstein, 1952) – Cretan Wall Lizard
- Podarcis erhardii* (Bedriaga, 1876) – Erhard's Wall Lizard
- Podarcis filfolensis* (Bedriaga, 1876) – Maltese Wall Lizard

- Podarcis gaigeae* (Werner, 1930) – Skyros Wall Lizard
- Podarcis guadarramae* (Boscá, 1916) – Guadarrama Wall Lizard**
- Podarcis hispanicus* (Steindachner, 1870) – Spanish Wall Lizard
- Podarcis ionicus* (Lehrs, 1902) – Ionian Wall Lizard**
- Podarcis lewendis* Lymberakis, Poulakakis, Kaliontzopoulou, Valakos and Mylonas, 2008 – Pori Wall Lizard
- Podarcis lilfordi* (Günther, 1874) – Lilford's Wall Lizard
- Podarcis liolepis* (Boulenger, 1905) – Catalanian Wall Lizard
- Podarcis melisellensis* (Braun, 1877) – Dalmatian Wall Lizard
- Podarcis milensis* (Bedriaga, 1882) – Milos Wall Lizard
- Podarcis muralis* (Laurenti, 1768) – Common Wall Lizard
- Podarcis peloponnesiacus* (Bibron and Bory de Saint-Vincent, 1833) – Peloponnese Wall Lizard
- Podarcis pityusensis* (Boscá, 1883) – Ibiza Wall Lizard
- Podarcis raffonei* (Mertens, 1952) – Aeolian Wall Lizard
- Podarcis siculus* (Rafinesque-Schmaltz, 1810) – Italian Wall Lizard
- Podarcis tauricus* (Pallas, 1814) – Balkan Wall Lizard
- Podarcis tiliguerta* (Gmelin, 1789) – Tyrrhenian Wall Lizard
- Podarcis vaucheri* (Boulenger, 1905) – Vaucher's Wall Lizard
- Podarcis virescens* Geniez, Sá-Sousa, Guillaume, Cluchier and Crochet, 2014 – Geniez's Wall Lizard**
- Podarcis waglerianus* Gistel, 1868 – Sicilian Wall Lizard
- Psammodromus* Fitzinger, 1826
- Psammodromus algirus* (Linnaeus, 1758) – Large *Psammodromus*
- Psammodromus hispanicus* Fitzinger, 1826 – Spanish *Psammodromus*
- Psammodromus edwardsianus* (Dugès, 1829) – Edwards's *Psammodromus***
- Psammodromus occidentalis* Fitzze, Gonzalez-Jimena, San-Jose, San Mauro and Zardoya, 2012 – Western *Psammodromus***
- Scelarcis* Fitzinger, 1843
- Scelarcis perspicillata* (Duméril and Bibron, 1839) – Moroccan Rock Lizard
- Teira* Gray, 1838
- Teira dugesii* (Milne-Edwards, 1829) – Madeira Rock Lizard
- Timon* Tschudi, 1836
- Timon lepidus* (Daudin, 1802) – Ocellated Lizard
- Timon nevadensis* (Buchholz, 1963) – Sierra Nevada Ocellated Lizard**
- Zootoca* Wagler, 1830
- Zootoca carniolica* Mayer, Böhme, Tiedemann and Bischoff, 2000 – Carniolian Lizard**
- Zootoca vivipara* (Jacquin, 1787) – Viviparous Lizard
- Family Scincidae Oppel, 1811
- Ablepharus* Fitzinger in Eversmann, 1823
- Ablepharus kitaibelii* Bibron and Bory de Saint-Vincent, 1833 – Snake-eyed Skink
- Ablepharus budaki* Göcmen, Kumlutas and Tosunoglu, 1996 – Budak's Snake-eyed Skink
- Chalcides* Laurenti, 1768
- Chalcides bedriagai* (Boscá, 1880) – Bedriaga's Skink
- Chalcides chalcides* (Linnaeus, 1758) – Italian Three-toed Skink
- Chalcides coeruleopunctatus* Salvador, 1975 – La Gomera Skink**
- Chalcides ocellatus* (Forskål, 1775) – Ocellated Skink
- Chalcides sexlineatus* Steindachner, 1891 – Gran Canaria Skink
- Chalcides simonyi* Steindachner, 1891 – East Canary Skink
- Chalcides striatus* (Cuvier, 1829) – Iberian Three-toed Skink

- Chalcides viridanus* (Gravenhorst, 1851) – West Canary Skink
- Eumeces* Wiegmann, 1834
- Eumeces schneiderii* (Daudin, 1802) – Schneider's Skink
- Heremites Gray, 1845**
- Heremites auratus* (Linnaeus, 1758) – Levant Skink**
- Heremites vittatus* (Olivier, 1804) – Bridled Skink**
- Ophiomorus* Duméril and Bibron, 1839
- Ophiomorus kardesi* Kornilios, Kumlutaş, Lymberakis and Ilgaz, 2017 – Anatolian Limbless Skink**
- Ophiomorus punctatissimus* (Bibron and Bory de Saint-Vincent, 1833) – Limbless Skink
- Family Anguidae Gray, 1825
- Anguis* Linnaeus, 1758
- Anguis cephalonica* Werner, 1894 – Peloponnese Slow Worm
- Anguis colchica* (Nordmann, 1840) – Eastern Slow Worm
- Anguis fragilis* Linnaeus, 1758 – Slow Worm
- Anguis graeca* Bedriaga, 1881 – Greek Slow Worm
- Anguis veronensis* Pollini, 1818 – Italian Slow Worm**
- Pseudopus* Merrem, 1820
- Pseudopus apodus* (Pallas, 1775) – Glass Lizard
- Family Blanidae Kearney, 2003
- Blanus* Wagler, 1830
- Blanus cinereus* (Vandelli, 1797) – Iberian Worm Lizard
- Blanus rufus* (Hemprich, 1820) – Central Iberian Worm Lizard**
- Blanus strauchi* (Bedriaga, 1884) – Anatolian Worm Lizard
- Family Typhlopidae Merrem, 1820
- Indotyphlops* Hedges, Marion, Lipp, Marin and Vidal, 2014**
- **Indotyphlops braminus* (Daudin, 1803) – Flowerpot Snake**
- Xerotyphlops* Hedges, Marion, Lipp, Marin and Vidal, 2014**
- Xerotyphlops vermicularis* (Merrem, 1820) – Worm Snake**
- Family Erycidae Bonaparte, 1840
- Eryx* Daudin, 1803
- Eryx jaculus* (Linnaeus, 1758) – Sand Boa
- Eryx miliaris* (Pallas, 1773) – Dwarf Sand Boa
- Family Psammophiidae Boie, 1827
- Malpolon* Fitzinger, 1826
- Malpolon insignitus* (Geoffroy Saint-Hilaire, 1827) – Eastern Montpellier Snake
- Malpolon monspessulanus* (Hermann, 1804) – Western Montpellier Snake
- Family Natricidae Bonaparte, 1840
- Natrix* Laurenti, 1768
- Natrix astreptophora* (Seoane, 1884) – Iberian Grass Snake**
- Natrix helvetica* (Lacépède, 1789) – Barred Grass Snake**
- Natrix maura* (Linnaeus, 1758) – Viperine Snake
- Natrix natrix* (Linnaeus, 1758) – Grass Snake
- Natrix tessellata* (Laurenti, 1768) – Dice Snake
- Family Colubridae Oppel, 1811
- Coronella* Laurenti, 1768
- Coronella austriaca* Laurenti, 1768 – Smooth Snake
- Coronella girondica* (Daudin, 1803) – Southern Smooth Snake
- Dolichophis* Gistel, 1868
- Dolichophis caspius* (Gmelin, 1789) – Caspian Whip Snake
- Dolichophis jugularis* (Linnaeus, 1758) – Black Whip Snake
- Dolichophis schmidtii* (Nikolsky, 1909) – Schmidt's Whip Snake
- Eirenis* Jan, 1863
- Eirenis collaris* (Ménétries, 1832) – Collared Dwarf Snake
- Eirenis levantinus* Schmidtler, 1993 – Levant Dwarf Snake

- Eirenis modestus* (Martin, 1838) – Masked Dwarf Snake
- Elaphe* Fitzinger, 1833
- Elaphe dione* (Pallas, 1773) – Steppe Snake
- Elaphe quatuorlineata* (Bonaterre, 1790) – Four-lined Snake
- Elaphe sauromates* (Pallas, 1814) – Blotched Snake
- **Elaphe schrenckii* Strauch, 1876 – Amur Rat Snake
- Elaphe urartica* Jablonski, Kukushkin, Avci, Bunyatova, Ilgaz, Tuniyev and Jandzik in Jablonski et al., 2019**
- Hemorrhois* Boie, 1826
- **Hemorrhois algirus* (Jan, 1863) – Algerian Whip Snake
- Hemorrhois hippocrepis* (Linnaeus, 1758) – Horseshoe Whip Snake
- Hemorrhois nummifer* (Reuss, 1834) – Coin-marked Snake
- Hemorrhois ravergieri* (Ménétries, 1832) – Spotted Whip Snake
- Hierophis* Fitzinger in Bonaparte, 1834
- Hierophis gemonensis* (Laurenti, 1768) – Balkan Whip Snake
- Hierophis viridiflavus* (Lacépède, 1789) – Western Whip Snake
- Hierophis cypriensis* (Schätti, 1985) – Cyprus Whip Snake
- Lampropeltis* Fitzinger, 1843
- **Lampropeltis getula* (Linnaeus, 1766) – Common Kingsnake
- Macroprotodon* Guichenot, 1850
- Macroprotodon brevis* (Günther, 1862) – Iberian False Smooth Snake
- **Macroprotodon cucullatus* (Geoffroy Saint-Hilaire, 1827) – Algerian False Smooth Snake
- Platyceps* Blyth, 1860
- Platyceps collaris* (Müller, 1878) – Reddish Whip Snake
- Platyceps najadum* (Eichwald, 1831) – Dahl's Whip Snake
- Telescopus* Wagler, 1830
- Telescopus fallax* (Fleischmann, 1831) – Cat Snake
- Zamenis* Wagler, 1830
- Zamenis hohenackeri* (Strauch, 1873) – Transcaucasian Rat Snake
- Zamenis lineatus* (Camerano, 1891) – Italian Aesculapian Snake
- Zamenis longissimus* (Laurenti, 1768) – Aesculapian Snake
- Zamenis scalaris* (Schinz, 1822) – Ladder Snake**
- Zamenis situla* (Linnaeus, 1758) – Leopard Snake
- Family Viperidae Opperl, 1811
- Macrovipera* Reuss, 1927
- Macrovipera lebetinus* (Linnaeus, 1758) – Blunt-nosed Viper**
- Macrovipera schweizeri* (Werner, 1935) – Milos Viper
- Montivipera* Nilson, Tuniyev, Andrén, Orlov, Joger and Herrmann, 1999
- Montivipera xanthina* (Gray, 1849) – Ottoman Viper
- Vipera* Garsault, 1764
- Vipera ammodytes* (Linnaeus, 1758) – Nose-horned Viper
- Vipera aspis* (Linnaeus, 1758) – Asp Viper
- Vipera berus* (Linnaeus, 1758) – Adder
- Vipera dinniki* (Nikolsky, 1913) – Dinnik's Viper
- Vipera graeca* Nilson and Andrén, 1988 – Greek Meadow Viper**
- Vipera kaznakovi* (Nikolsky, 1909) – Caucasus Viper
- Vipera latastei* (Boscá, 1878) – Lataste's Viper
- Vipera renardi* (Christoph, 1861) – Steppe Viper
- Vipera seoanei* (Lataste, 1879) – Seoane's Viper
- Vipera ursinii* (Bonaparte, 1835) – Meadow Viper

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