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The distributions of the six species constituting the smooth newt species complex (*Lissotriton vulgaris* sensu lato and *L. montandoni*) – an addition to the New Atlas of Amphibians and Reptiles of Europe

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Abstract. The ‘smooth newt’, the taxon traditionally referred to as *Lissotriton vulgaris*, consists of multiple morphologically distinct taxa. Given the uncertainty concerning the validity and rank of these taxa, *L. vulgaris* sensu lato has often been treated as a single, polytypic species. A recent study, driven by genetic data, proposed to recognize five species, *L. graecus*, *L. kosswigi*, *L. lantzi*, *L. schmidleri* and a more restricted *L. vulgaris*. The Carpathian newt *L. montandoni* was confirmed to be a closely related sister species. We propose to refer to this collective of six *Lissotriton* species as the smooth newt or *Lissotriton vulgaris* species complex. Guided by comprehensive genomic data from throughout the range of the smooth newt species complex we 1) delineate the distribution ranges, 2) provide a distribution database, and 3) produce distribution maps according to the format of the New Atlas of Amphibians and Reptiles of Europe, for the six constituent species. This allows us to 4) highlight regions where more research is needed to determine the position of contact zones.

Keywords: Amphibian, contact zone, hybridization, range map, taxonomy, UTM grid.

One of the aims of the recently published New Atlas of Amphibians and Reptiles of Europe (Sillero et al., 2014a) is to identify gaps in the currently available knowledge on species distributions. Such knowledge gaps are particularly prevalent where taxonomic progress has resulted in the splitting of one species into several species with as yet poorly understood mutual range boundaries. A good example is the ‘smooth newt’, *Lissotriton vulgaris* sensu lato, which is often treated as a single, polytypic species (Schmidler and Franzen, 2004) – as in the case of the New Atlas – but has been proposed to constitute multiple distinct species (Pabijan et al., 2017). The Carpathian newt, *L. montandoni*, is a close relative (Zavadil et al., 2003) and has its own map in the New Atlas. Because smooth and Carpathian newts are considerably more closely related to each other than to other *Lissotriton* species (Skorinov et al., 2008; Wiens et al., 2011; Pabijan et al., 2015; Pabijan et al., 2017), and because they have experienced periods of genetic exchange (Zieliński et al., 2013; Zieliński et al., 2016), we here support the proposal by Skorinov et al. (2011) to refer to the assemblage as a species complex: the smooth newt or *Lissotriton vulgaris* species complex. There has been disagreement in the literature concerning the validity and rank of the taxa comprising *L. vulgaris* sensu lato and the phylogenetic position of the Carpathian newt within the smooth newt species complex (Kalezić et al., 1987; Raxworthy, 1990; Krizmanić et al., 1997; Tuniyev, 1999; Dubois and Raffaëlli, 2009; Speybroeck et al., 2010; Frost, 2013; Wielstra et al., 2015). We briefly review previous

attempts to delineate taxa before discussing a new taxonomy reflecting the latest insights gained from genomic data. In the context of this new taxonomy we 1) delineate the distribution ranges, 2) provide a distribution database, and 3) produce distribution maps according to the New Atlas format for the constituent species of the smooth newt complex.

The taxa comprising the smooth newt species complex are distinguishable based on the male secondary sexual characters that develop during the annual aquatic breeding period (Zavadil et al., 2003; Schmidler and Franzen, 2004). Morphological differences pertain to the presence/absence and extent of dorsal crests and tail fins, toe flaps, a tail filament, dorso-lateral ridges and pigmentation patterns. Overall the morphological evidence points to narrow transition zones between some proposed taxa, while others show wider zones of intergradation (Schmidler and Schmidler, 1983; Krizmanić et al., 1997; Babik et al., 2003). Studies employing allozymes (Kalezić, 1984; Kalezić and Tucić, 1984; Kalezić et al., 1987; Rafiński et al., 2001; Skorinov et al., 2008) confirmed the genetic distinctiveness of some taxa but, due to the restricted geographical scope and difficulties in comparing allozyme results across studies, are of limited use to delineate taxa and their ranges at the scale of the entire species complex. The integration of DNA sequence data into smooth newt taxonomy has been hampered by the fact that the popular genetic marker mtDNA is highly misleading in this case. MtDNA shows extensive introgression between the different taxa and the original mtDNA of the Carpathian newt appears to have been completely replaced by smooth newt mtDNA (Babik et al., 2005; Nadachowska and Babik, 2009; Zieliński et al., 2013; Pabijan et al., 2015). Furthermore, not all mtDNA lineages correspond to morphologically defined taxa (Babik et al., 2005; Pabijan et al., 2015; Pabijan et al., 2017).

Genome-wide nuclear genetic data have the potential to provide an objective measure of species identity and a more reliable estimate of phylogeny. Recently, Pabijan et al. (2017) used sequences of 74 nuclear DNA markers (obtained with the protocol of Zieliński et al., 2014b) for species delimitation, phylogenetic reconstruction, and inference of historical gene flow throughout the range of the smooth newt species complex. The authors recognize five *L. vulgaris* sensu lato species, for which vernacular names are proposed here: Greek smooth newt *L. graecus* (Wolterstorff, 1906), Kosswig's smooth newt *L. kosswigi* (Freitag, 1955), Caucasian smooth newt *L. lantzi* (Wolterstorff, 1914), Schmidler's smooth newt *L. schmidleri* (Raxworthy, 1988), and (a more strictly defined) northern smooth newt *L. vulgaris* (Linnaeus, 1758). Furthermore, Pabijan et al. (2017) confirm that the Carpathian newt *L. montandoni* (Boulenger, 1880) is not clustered within, but is the sister species of, the other members of the smooth newt species complex. Considering the extensive geographical and genomic sampling

by Pabijan et al. (2017), we presume this taxonomical treatment reflects current knowledge based on multiple lines of evidence and is likely to be stable.

The geographical distribution of the six species constituting the smooth newt species complex is well understood in a broad sense (Zavadil et al., 2003; Schmidler and Franzen, 2004). While the species *L. kosswigi* and *L. lantzi* are allopatrically distributed, the species *L. graecus*, *L. schmidleri* and *L. vulgaris* meet in parapatry on the Balkan Peninsula. In the Carpathians the range of *L. montandoni* is fully enclosed by that of *L. vulgaris* and the two generally exclude each other by altitude (with *L. montandoni* taking over at higher elevations). Where the four species with parapatric ranges meet in nature, hybridization occurs to a smaller or greater extent, but the narrowness of the transition zones suggests substantial reproductive isolation (Babik et al., 2003; Babik et al., 2005; Nadachowska-Brzyska et al., 2012; Zieliński et al., 2014a; Pabijan et al., 2015; Pabijan et al., 2017). Pabijan et al. (2017) homed in on the contact zones between species and we here extend their sampling, filling in geographical regions previously poorly covered. We allocate population to species based on maximum likelihood estimation of individual ancestry, employing single nucleotide polymorphisms (SNPs), obtained with the protocol of Niedzicka et al. (2016), using the program ADMIXTURE 1.3.0 (Alexander et al., 2009). For further background and input and output files, see Supplementary Text S1; Supplementary Fig. S1; Supplementary Table S1; and Supplementary Material S1.

Our understanding of the mutual range borders of the members of the smooth newt species complex has increased to such an extent that we feel confident in delineating the ranges for the individual species. We compose a distribution database for each individual species, focusing particularly on the regions where the different species come into contact: the Balkan Peninsula and the Carpathians. The vast range of *L. vulgaris* away from the contact zones with other species is already well covered by the New Atlas. The core of our database consists of localities, generally available at a high resolution, from 1) our own fieldwork, 2) museum collections, 3) the literature, and 4) online databases, and we augment our database with coarse-grained (50×50 km) data from the New Atlas (see Supplementary Text S1 for further details). Our distribution database (5741 data points in total, 4177 newly collected and 1564 taken from the New Atlas) is visualized in Fig. 1 and is available online as Supplementary Table S2.

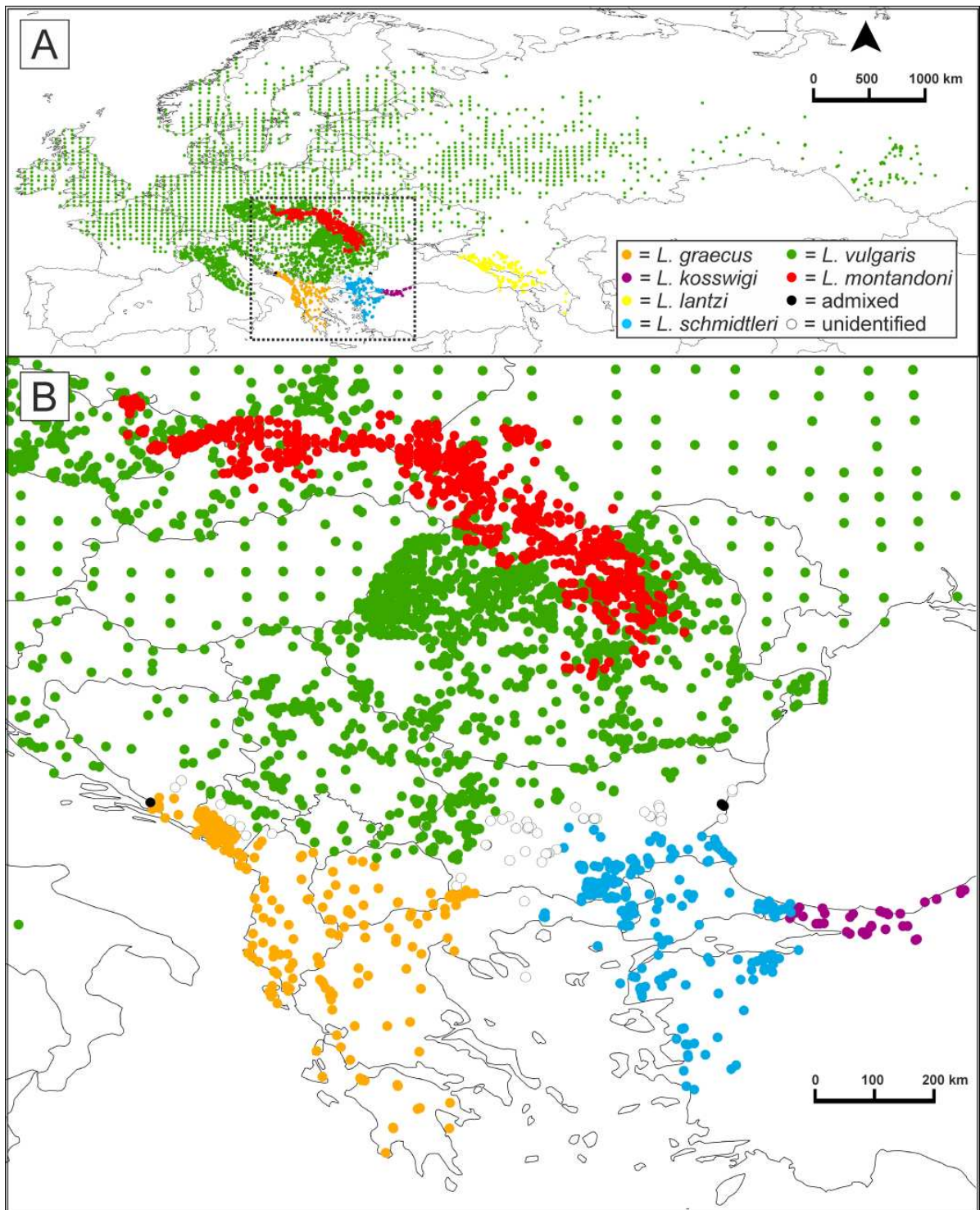


Figure 1. Distribution database for the six species constituting the smooth newt species complex (*Lissotriton vulgaris* sensu lato and *L. montandoni*). Raw data are provided in Supplementary Table S2. Data points are colour coded according to species (note that many *L. vulgaris* sensu stricto are obscured by *L. montandoni* dots). We highlight populations showing considerable genetic admixture. Populations for which no genetic or morphological data could be consulted were not identified to species. The boxed area in panel A is shown in more detail in panel B.

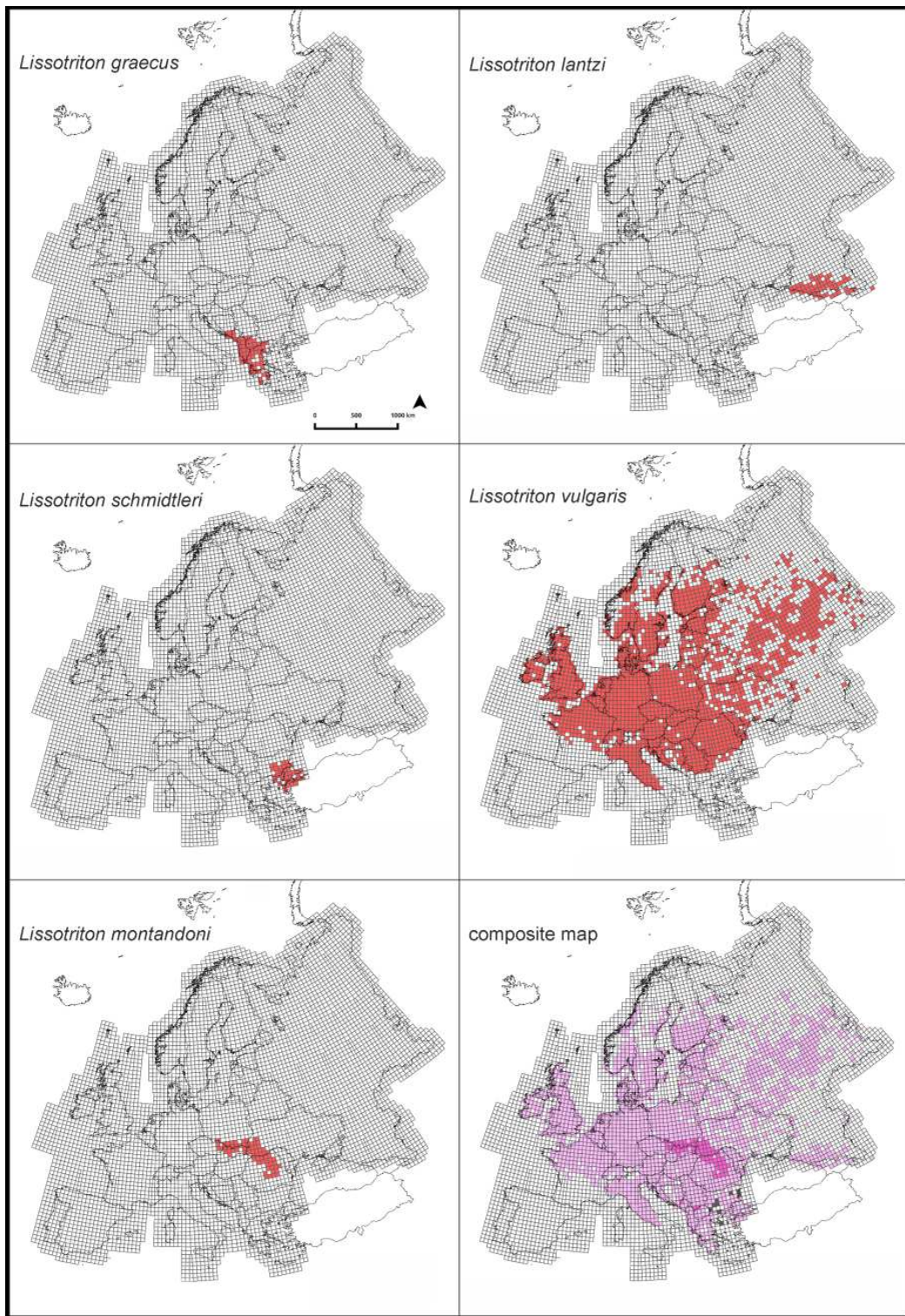


Figure 2. Distribution maps for the five members of the smooth newt species complex (*Lissotriton vulgaris* sensu lato and *L. montandoni*) in Europe, in the format of the New Atlas of Amphibians and Reptiles of Europe. The composite map shows how many species are present per grid cell, light filled grid cells reflecting the presence of a single and intermediate filled ones the presence of two species. Dark filled grid cells only contain smooth newt localities not identified to species. Higher resolution versions of the individual maps can be found in Supplementary Fig. S2 and shape files are available as Supplementary Material S2.

We follow Sillero et al. (2014a) and, based on our distribution database, produce atlas maps at a 50×50 km UTM grid resolution for the five members of the smooth newt species complex occurring in the territory covered by the New Atlas (hence excluding *L. kosswigi*). Note that we completely remake the map for the Carpathian newt (the only member of the smooth newt species complex treated separately in the New Atlas). Compared to the New Atlas, we added 107 smooth newt grid cells and these were particularly positioned in the Balkans. An overview of the atlas maps is provided in Fig. 2, detailed maps can be found as Supplementary Fig. S2 and shape files are included as Supplementary Material S2. Based on our dataset, we manage to present the latest insights on smooth newt distribution and identify key areas where more fieldwork is required. For instance, distribution limits between *L. graecus* and *L. vulgaris* are now much better understood, but the contact zone in central Montenegro (if any) requires further study. A particularly glaring gap in knowledge concerns the region where the ranges of *L. vulgaris* and *L. graecus* approach that of *L. schmidtleri* in Bulgaria and Greece.

In light of the taxonomic revision of the smooth newt species complex and the up to date distribution information collected here, we suggest that the IUCN status for the five species currently subsumed in *L. vulgaris* sensu lato should be revised (Arntzen et al., 2009). Inclusive taxa are likely to be more vulnerable than *L. vulgaris* sensu lato itself because of their considerably smaller distribution ranges. For example, *L. kosswigi* occurs in a densely populated area and has a very restricted distribution range (Wielstra et al., 2015), *L. lantzi* appears to have gone extinct in Turkey, Azerbaijan and Armenia (Skorinov et al., 2014), and *L. graecus* has been negatively affected by fish introductions, particularly in Montenegro (Denoël et al., 2009). A particular advantage of the open access of the New Atlas and the underlying data is that herpetologists can easily produce up to date atlas maps for the taxa they are working on (e.g. Wielstra et al., 2014). To facilitate future European mapping efforts, providing clear taxonomic justification, accurate estimates of distribution ranges and high-resolution distribution data is essential. For instance, the NA2RE project (Sillero et al., 2014b) aims at automatically centralizing data from local providers, whose effort will benefit from the availability of such information.

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