

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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Supplementary material

Text S1.

Additional genomic data to delineate species ranges

We extend the sampling of Pabijan et al. (2017) by including a large number of new localities (1-3 individuals from 329 localities, 379 individuals in total; Supplementary Table S1) focusing in particular on geographical regions previously poorly covered. As genetic markers we use single nucleotide polymorphisms (SNPs), derived from resequencing of protein coding genes using molecular inversion probes (MIP), following the protocol of Niedzicka et al. (2016). Per gene the single most informative (highest minor allele frequency) SNP was used giving a total of 1138 SNPs (Supplementary Material S1). To allocate individuals to nine evolutionary lineages delimited by Pabijan et al. (2017) we analysed the data with ADMIXTURE 1.3.0 (Alexander et al., 2009), assuming $K = 9$ genetic clusters (which was also considered the best supported K value over a 1-20 range in the present analysis based on cross-validation results and logLikelihoods). As in Pabijan et al. (2017), four intraspecific groups showing extensive genetic admixture were identified in *L. vulgaris*. We collapsed these intraspecific groups into *L. vulgaris* and used a threshold of cluster membership 0.8 to allocate individuals, which we equate with populations, to species; otherwise populations were considered genetically admixed (Supplementary Fig. S1; Supplementary Table S1). A detailed analysis of the SNP data will be published elsewhere.

Compiling a distribution database

The core of our database consists of localities obtained during our own fieldwork and from the Batrachological collection of the Institute for Biological Research “Siniša Stanković”, University of Belgrade (Džukić et al., 2015). Furthermore, we include records from the literature (e.g. Skorinov et al., 2008; Denoël et al., 2009; Skorinov et al., 2014; Wielstra et al., 2015; see Supplementary Table S2 for a full list of references). For the Czech Republic we consulted an online database (AOPK ČR, Nálevková databáze ochrany přírody; portal.nature.cz, accessed 19 September 2016) and as the available smooth data was far denser than required for our purposes (containing more localities than all our other

records combined) we randomly selected 5% of localities. Similarly, for the Romanian atlas (Cogălniceanu et al., 2013) we reduced density by taking a single data point per 10x10km UTM grid, while up to four were available. We considered the Ukrainian part of the range of the Carpathian newt as presented in the New Atlas (the only member of the smooth newt species complex treated separately) to be overestimated. To delineate the range here we use the locality database presented in Pisanets et al. (2005), but excluded records based on larvae alone, as larvae of the Carpathian and northern smooth newt cannot be reliably distinguished based on morphology (Szymura, 1974; Juszczuk, 1987).

We augment our database for the vast range of *L. vulgaris* away from the contact zones with other species with data from the New Atlas, using the centre of occupied 50 x 50 km UTM grid cells, as follows. For a subset of countries we fully relied on data from the New Atlas: Belarus, Belgium, Denmark, Estonia, Finland, Ireland, Latvia, Lithuania, Luxembourg, Moldova, the Netherlands, Norway, Sweden, and Switzerland. For other countries we only included grid cells for which we did not have localities of our own: Austria, Bosnia and Herzegovina, Croatia, France, Germany, Hungary, Italy, Poland, Russia, Slovenia, Romania, Serbia (including Kosovo), the Ukraine and the United Kingdom. For the remaining countries, namely Bulgaria, the Czech Republic, Kazakhstan, Montenegro, and Slovakia, we purely relied on our own data. For *L. graecus* we incorporated several grid cells from Greece that were not covered by our own data, while for Albania, Bosnia and Herzegovina, Bulgaria, Croatia, Macedonia, and Montenegro we only used our own data. For *L. lantzi* (covering Armenia, Azerbaijan, Georgia, Russia, and Turkey), *L. kosswigi* (distributed in Turkey outside of the area covered by the New Atlas), *L. schmidtleri* (found in Bulgaria, Greece and Turkey, partially outside of the area covered by the New Atlas) and *L. montandoni* (occurring in the Czech Republic, Poland, Romania, Slovakia, and the Ukraine) we did not include any New Atlas data. We left localities from around Balkan contact zones for which no genetic or morphological data could be consulted unidentified to species. This mostly concerns the transition between *L. vulgaris* and *L. schmidtleri*. Localities with considerable genetic admixture were highlighted as such. The database is available as Supplementary Table S2. We obtained a digital elevation model from the CGIAR Consortium for Spatial Information website (<http://srtm.csi.cgiar.org/>) and extracted elevation for the localities in our distribution database (Table S2) in ArcGIS 10 (www.esri.com).

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Figure S1. Results of the ADMIXTURE analysis for the smooth newt species complex (*Lissotriton vulgaris sensu lato* and *L. montandoni*), plotted on a map. This analysis is based on 1138 SNPs genotyped for 379 individuals from 329 populations. Pie slices reflect ancestry (the fraction of alleles derived from each parental species at the level of the population) and are colour coded. Raw scores are in Supplementary Table S1. The boxed area in panel A is shown in more detail in panel B. Grey shading in panel B reflects elevation.

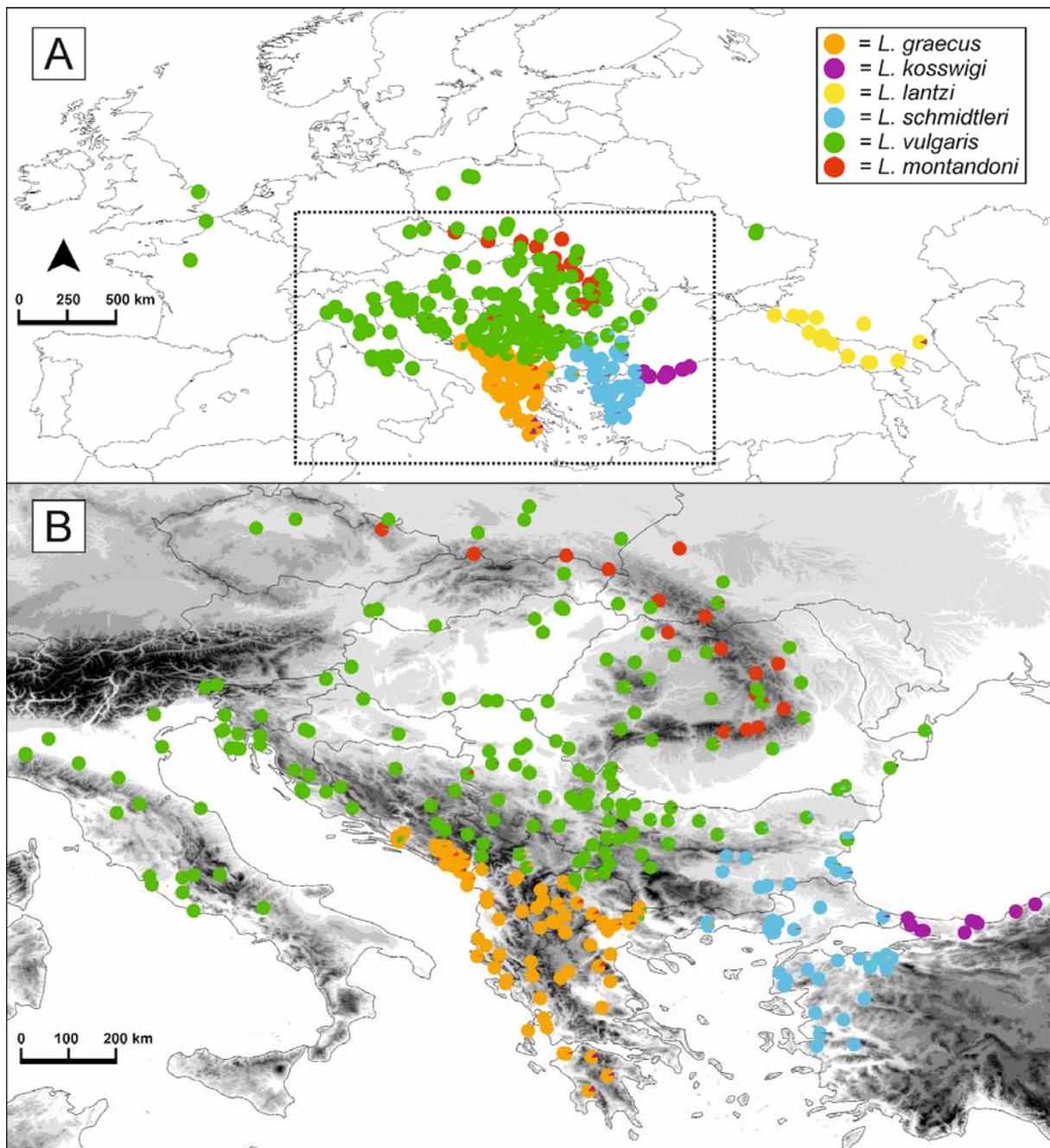
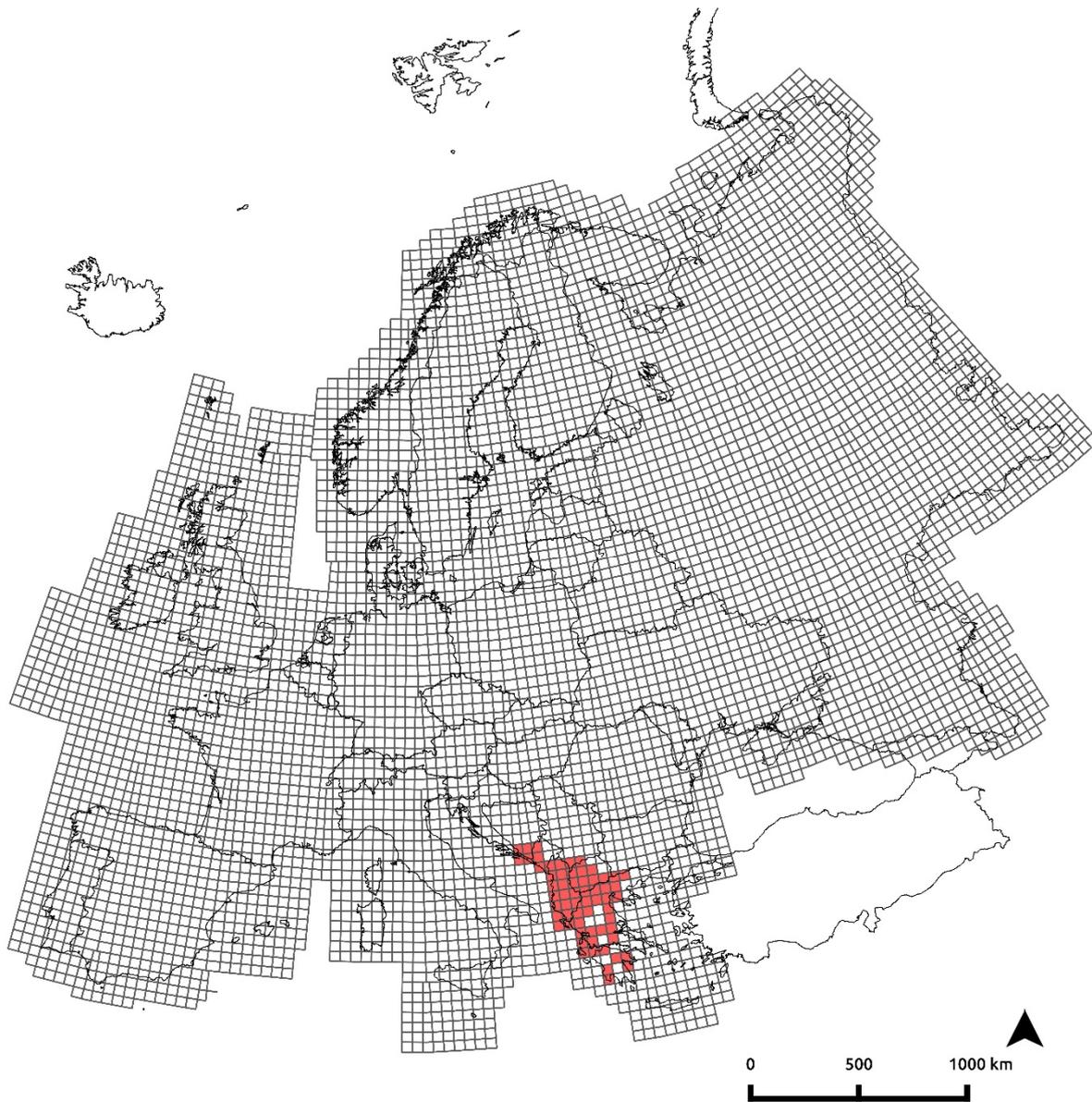
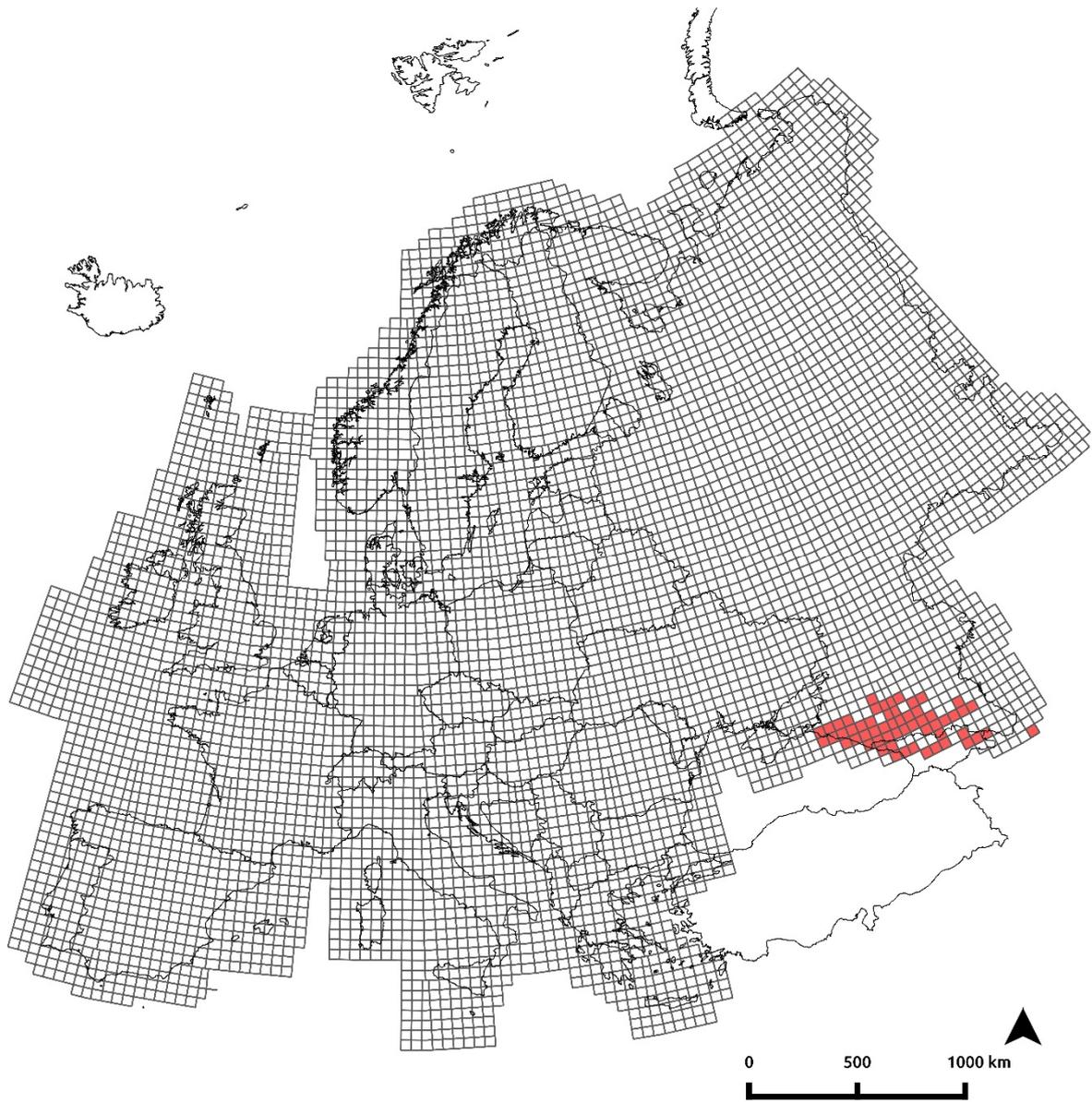


Figure S2. Distribution maps for the five members of the smooth newt species complex (*Lissotriton vulgaris sensu lato* and *L. montandoni*) distributed (partially) in Europe, in the format of the New Atlas of Amphibians and Reptiles of Europe.

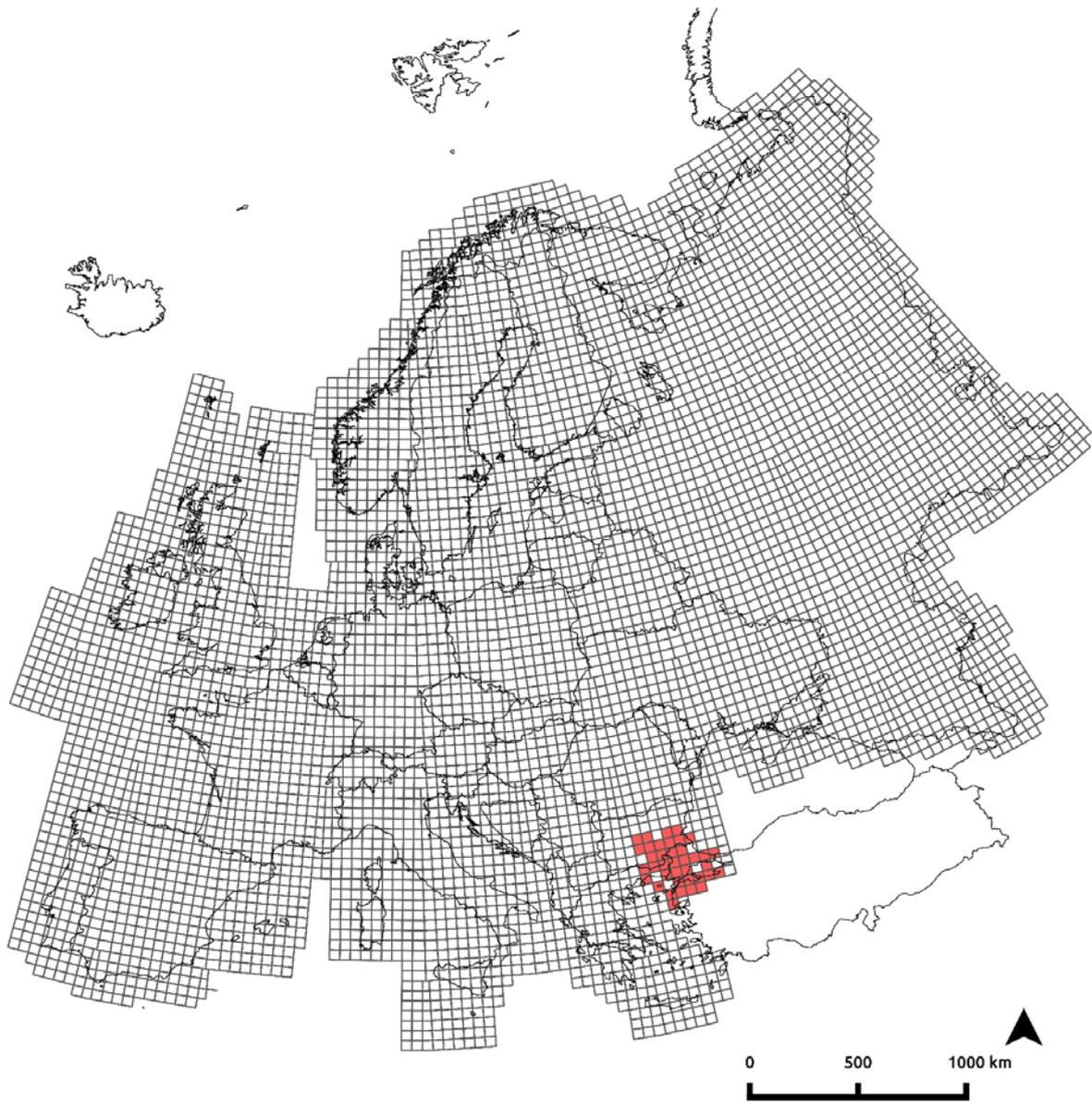
Lissotriton graecus:



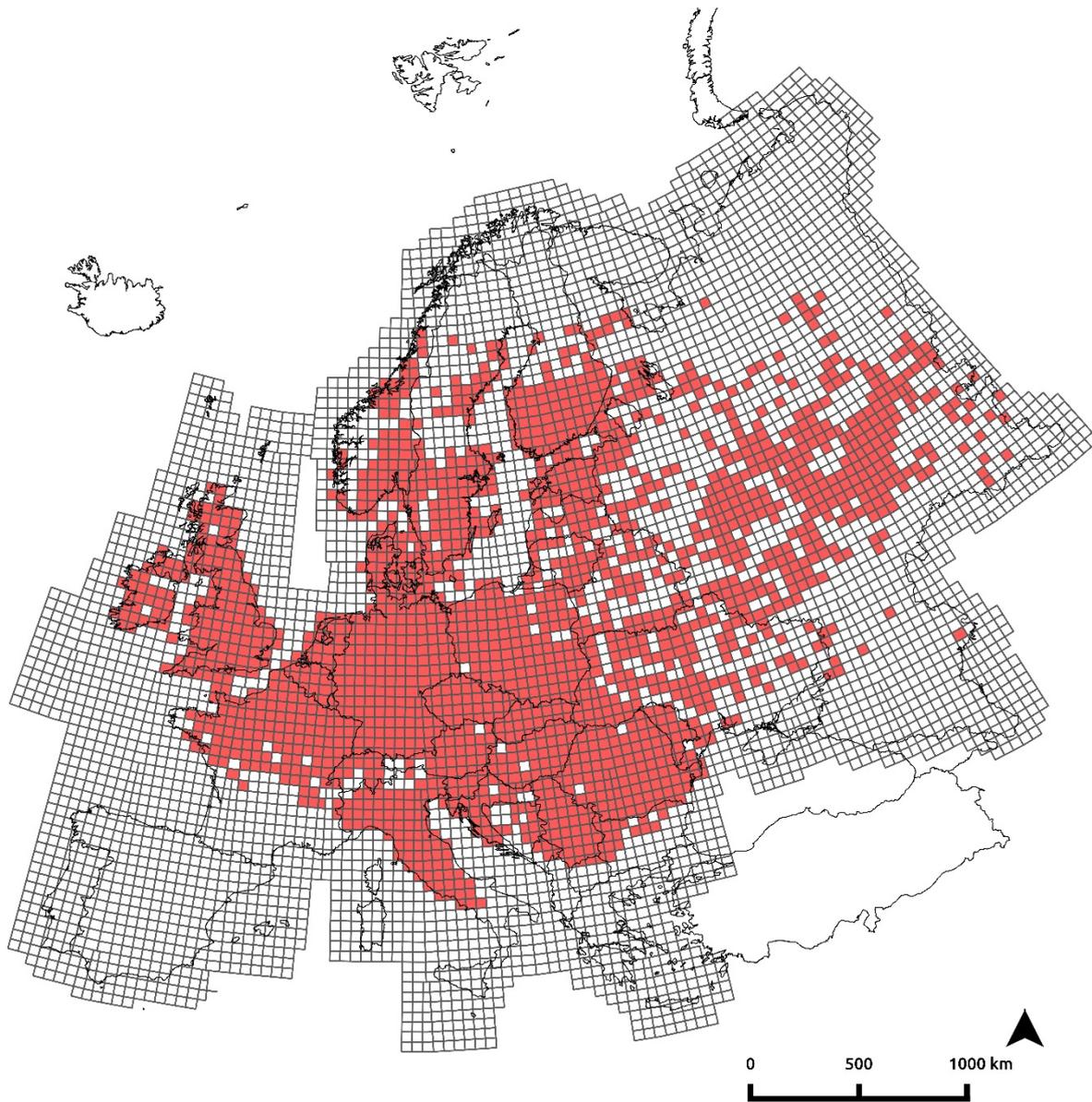
Lissotriton lantzi:



Lissotriton schmidleri:



Lissotriton vulgaris:



Lissostriton montandoni:

