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Phylogeography of the *Lacerta viridis* complex: mitochondrial and nuclear markers provide taxonomic insights

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Abstract

Based on broad, nearly rangewide sampling, we reanalysed the phylogeography of the *Lacerta viridis* complex using the mitochondrial cytochrome *b* gene and the intron 7 of the nuclear *β*-fibrinogen gene. Using the mitochondrial marker, we identified in phylogenetic analyses 10 terminal clades clustering in four deeply divergent main lineages whose relationships are weakly resolved. These lineages correspond to *Lacerta bilineata*, *L. viridis*, the previously identified Adriatic or West Balkan lineage and a newly discovered fourth lineage from the Anatolian Black Sea coast and the south-eastern Balkan Peninsula. Except for the latter lineage, there is considerable phylogeographic structuring in each lineage, with higher diversity in the south of the distribution ranges. This pattern indicates the existence of two distinct microrefugia in the Italian Peninsula and Sicily and of up to seven microrefugia in the Balkan Peninsula, but of only one refugium along the Black Sea coast of Anatolia. We identified secondary contact zones of the main lineages and of terminal clades within these lineages. However, most of the formerly described putative contact zone of *L. bilineata* and *L. viridis* turned out to be a contact zone between the Adriatic lineage and *L. viridis*, but *L. bilineata* seems to be involved only marginally. Our nuclear marker could not unambiguously resolve whether there is gene flow in contact zones. Thus, further research is necessary to decide whether the four main lineages are conspecific or whether they represent distinct biological species. We restrict the name *L. v. meridionalis* to the newly identified genetic lineage from Turkey and south-eastern Europe, synonymize some previously recognized taxa and suggest a tentative nomenclature for the *L. viridis* complex.

Key words: Europe – glacial refugium – Lacertidae – Squamata – secondary contact zone – taxonomy

Introduction

Green lizards of the *Lacerta viridis* complex are brightly green-coloured medium-sized lizards with a snout–vent length of up to 13.6 cm and a tail length of up to approximately 40 cm (Nettmann and Rykena 1984). They are widely distributed in northern Spain, France, continental Italy and Sicily, across the Balkans and southern East Europe to western Ukraine and northern Turkey. Central Europe corresponds to a major distribution gap, with some isolated relict populations providing evidence for a formerly wider distribution range (Fig. 1; Nettmann and Rykena 1984; Nettmann 2001).

Green lizards (*Lacerta* sensu stricto) have experienced a confusing taxonomic history as reviewed in Nettmann (2001), and currently up to nine distinct species are recognized (Nettmann 2001; Arnold et al. 2007; Andres et al. 2014). Two of these species, *L. bilineata* Daudin, 1802 and *L. viridis* (Laurenti, 1768), constitute the *L. viridis* complex. For a long time, these two species have been regarded as conspecific. Based on captive breeding experiments, Rykena (1991) suggested that western (*L. bilineata*) and eastern green lizards (*L. viridis* sensu stricto) represent two distinct species. Using allozyme data, albeit of a limited data set, Amann et al. (1997) supported Rykena's (1991) conclusions and later on, many authors adopted the view that *L. bilineata* and *L. viridis* are distinct species. Morphologically, both taxa are difficult to tell apart, and only the coloration of hatchlings is a more or less reliable diagnostic character (Rykena 1991; Nettmann 2001). The contact zone between both species is thought to be located in north-eastern Italy and adjacent countries (Joger et al. 2001; Nettmann 2001). However, due to contradictory branching patterns using phylogenetic analyses of mitochondrial and nuclear DNA sequences and negligible sequence divergences, the species status of *L. bilineata* and *L. viridis* has repeatedly been challenged (Brückner et al. 2001; Mayer and Beyerlein 2001; Godinho et al. 2005; Böhme et al. 2007), and *L. bilineata* is not treated as a valid species by Arnold and Ovenden (2002).

Within *L. bilineata* and *L. viridis*, several subspecies have been recognized (Nettmann 2001; Rykena et al. 2001), some of which are also supported by molecular markers (Godinho et al. 2005; Böhme et al. 2007; Sagonas et al. 2014). However, a comprehensive investigation of the phylogeography of the *L. viridis* complex discovered, in addition to two main lineages corresponding to *L. bilineata* and *L. viridis*, an unexpected third main lineage, which is distributed along the west coast of the Balkan Peninsula (Böhme et al. 2007). The taxonomic allocation of this third lineage remains unclear. Another unresolved issue is the status of the populations of the *L. viridis* complex from northern Turkey, which are currently identified by some authors with three distinct subspecies (Fig. 1; Schmidtler 1986; Nettmann 2001). However, a thorough morphological study using samples from the whole Turkish distribution range concluded that all populations are morphologically indistinguishable and represent one

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*Our friend and colleague Werner Mayer deceased on 14 August 2015 after having approved the manuscript for submission. We dedicate this study to him, acknowledging his contributions to lacertid science and to commemorate him as a dear friend.

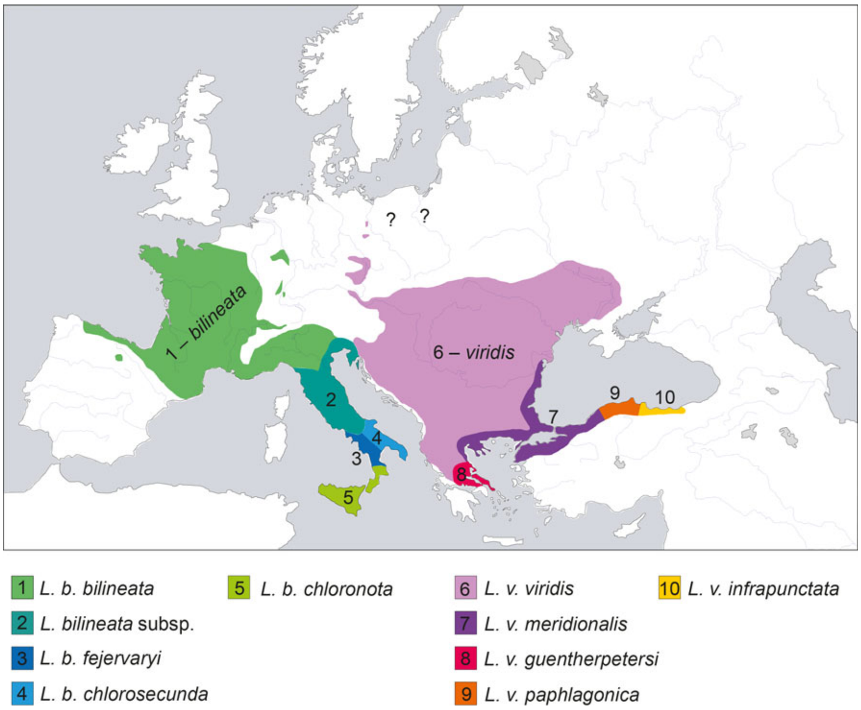

Fig. 1. Distribution of the subspecies of the *Lacerta viridis* complex (from Nettmann 2001). Question marks denote probably extinct populations of *L. v. viridis*.

and the same taxon (Kumlutaş 1996). This view was later reinforced by serological data (Arıkan et al. 1999). Moreover, based on allozyme data, the lizards from Turkey cluster among *L. viridis* from northern Greece and Euboea (Joger et al. 2001). Until now, these populations have never been examined using mitochondrial or nuclear DNA sequences.

Based on broad, nearly rangewide sampling and including for the first time representatives of the populations in northern Turkey, here we re-examine phylogeography and taxonomic differentiation within the *L. viridis* complex. For doing so, we apply a widely used mitochondrial marker, the cytochrome *b* gene (cyt *b*), and a nuclear marker, the intron 7 of the β-fibrinogen gene (β-fibint7). This intron is characterized by a pronounced length dimorphism (Godinho et al. 2005), which is promising for detecting gene flow between *L. bilineata* and *L. viridis*.

Assuming that distinct species represent largely distinct genetic lineages without extensive gene flow (‘biological species’, cf. Mayr 1963) and that subspecies are distinct genetic lineages that have not reached this stage yet, we aim at answering the following questions: (1) Do *L. bilineata* and *L. viridis* qualify as distinct species? (2) How is the general phylogeographic pattern of the *L. viridis* complex influenced by the inclusion of the populations from northern Turkey? (3) Are the currently recognized subspecies corroborated by genetic differentiation?

Materials and Methods

Sampling and laboratory procedures

We processed 394 samples from throughout the whole distribution range of the *Lacerta viridis* complex as listed in the Appendix. Total genomic DNA was extracted using the innuPREP DNA Mini Kit or the innuPREP Blood DNA Mini Kit (both Analytik Jena AG, Jena, Germany). The complete mitochondrial cyt *b* gene (1143 bp) of 359 samples was amplified using a newly designed primer pair (forward: 5′-GCC CCA AAA TAA GGA GAC GG-3′; reverse: 5′-TAG TGA TGG GGG ATT AGA GC-3′). PCR was carried out in a total volume of 25 µl containing 1 unit Top*Taq* DNA Polymerase with Q-Solution (Qiagen, Hilden, Germany), buffer as recommended by the supplier, 2 mM $MgCl_2$, 0.6 µM of each primer (Biomers, Ulm, Germany), 0.2 mM of each dNTP (Thermo-Scientific, St. Leon-Rot, Germany) and 10–30 ng of total DNA. Challenging samples were additionally treated with 7.5 µg BSA (Thermo-Scientific). PCR products were purified using the ExoSAP-IT enzymatic cleanup (USB Europe GmbH, Staufen, Germany; modified protocol: 30 min at 37°C; 15 min at 80°C). PCR products were sequenced on an ABI 3130xl Genetic Analyzer (Life Technologies, Darmstadt, Germany) using the same primers and the BigDye Terminator v3.1 Cycle Sequencing Kit (Life Technologies). Cycle sequencing reactions were purified by ethanol/sodium acetate precipitation or using Sephadex™ (GE Healthcare, München, Germany). After an initial denaturation step at 94°C for 5 min, 40 cycles were run with denaturation at 94°C for 45 s, annealing at 56°C for 45 s and elongation at 72°C for 2 min. The final elongation step lasted for 10 min. Resulting sequences were verified by manually checking electropherograms using BIOEDIT 7.1.3.0 (Hall 1999). Thirty-five additional samples were processed according to the procedures described in Pavlicev and Mayer (2009).

The β-fibint7 was analysed in a subsample ($n = 73$) representing all mitochondrial lineages (see Appendix). For amplification and sequencing, the primer pair FIB-B17U and FIB-B17L (Prychitko and Moore 1997) and the same PCR conditions were used as for cyt *b*, except that only 37 cycles were run, with initial denaturation at 94°C for 5 min, denaturation at 94°C for 30 s, annealing at 58°C for 30 s, elongation at 72°C for 1 min, and final elongation of 10 min. Since alleles of the β-fibint7 showed a pronounced length polymorphism (alleles differing by 380 bp) and direct sequencing of heterozygotes was not possible, a preparative gel electrophoresis and the peqGOLD Gel Extraction Kit (peqlab, Erlangen, Germany) was used. The short allele could then be sequenced directly using the PCR primers and the BigDye Terminator v3.1 Cycle Sequencing Kit, whereas the long allele had to be cloned for obtaining clean sequences. For this purpose, the TOPO TA Cloning Kit and pCR 2.1-TOPO Vector (Life Technologies) were applied. The maximally possible amount of DNA (10–30 ng) was used for ligation to facilitate successful insertion. One Shot Top10 Chemically Competent *E. coli* Cells (Life Technologies) were transformed by heat shock for 42 s and plated out on LB medium plates containing 50 mg/l ampicillin (Roth, Karlsruhe, Germany). To facilitate screening of successful cloning, the blue white approach was used and four white colonies were picked per sample, followed by PCR using the vector

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primer M13. Purified PCR products were sequenced as described for the short allele. Obtained sequences were up to 1074 bp long.

Alignment and sequence analyses

Additional cyt *b* sequences of the *Lacerta viridis* complex were downloaded from GenBank and aligned with our newly generated sequences using BIOEDIT 7.1.3.0. Sequences of *Lacerta agilis* Linnaeus, 1758, *L. media* Lantz and Cyrén, 1920, *L. schreiberi* Bedriaga, 1878, *L. strigata* Eichwald, 1831, *L. trilineata* Bedriaga, 1886, and *Timon lepidus* (Daudin, 1802) were included as outgroups, resulting in a data set of 475 cyt *b* sequences (see Appendix). All cyt *b* sequences aligned without any gaps, as expected for protein-coding DNA. Also *β*-fibint7 sequences aligned well using BIOEDIT, even though several gaps occurred, among them one corresponding to a pronounced length polymorphism as described below.

Phylogenetic relationships were inferred for cyt *b* sequences using Bayesian inference and the maximum-likelihood (ML) approach. For Bayesian analyses, the best evolutionary model (Tr2M+G) was determined using JMODELTEST 0.1.1 (Posada 2008) and the BIC. Then, phylogenetic trees were calculated with MRBAYES 3.2.4 (Ronquist et al. 2012) and the implemented Metropolis-coupled Markov chain Monte Carlo algorithm. Two parallel runs, each with one cold and three hot chains, were conducted. The chains ran for 15×10^6 generations, with every 500th generation sampled. For generating the final 50% majority rule consensus, a burn-in of 25% was used to sample only the most likely trees. In addition, phylogenetic ML trees were computed using RAxML 7.2.8 and the default GTR+G model (Stamatakis 2006). Five independent ML searches were run with different starting conditions and the fast bootstrap algorithm. The robustness of the branching patterns was examined by comparing the best trees. Subsequently, 1000 nonparametric thorough bootstrap replicates were calculated and the values plotted against the tree with the highest likelihood value. All analyses were run for a data set including all sequences listed in the Appendix and for another data set which excluded the 20 sequences from Sagonas et al. (2014).

Sequence divergences between and within lineages identified by phylogenetic analyses were explored using uncorrected p distances. These values were obtained using MEGA6 (Tamura et al. 2013) and the pairwise deletion option. For uncorrected p distances, the data from Sagonas et al. (2014) were disregarded.

For the *β*-fibint7 sequences, parsimony networks were calculated using TCS 1.21 (Clement et al. 2000), with gaps treated as 5th character state. However, this intron shows a pronounced length dimorphism of 380 bp, causing a challenge for network building. To overcome this situation, we produced in a first step a network for the long sequences alone. Then, we computed a second network which included also the short sequences. Their 380-bp-long deletion was reduced for this purpose to an only 1-bp-long deletion; the corresponding nucleotides of the long alleles were also removed. This, however, resulted also in the loss of informative sites from the long sequences so that some haplotypes were collapsed. Therefore, a third network was constructed manually by linking the two haplotype clusters of short alleles from the second network to the respective haplotypes of the long alleles from the first network.

Results

Mitochondrial phylogeography

Both tree-building methods delivered largely congruent results which differed only with respect to the weakly resolved branching pattern of some deep nodes in the *Lacerta viridis* complex (Fig. 2). When the relatively short sequences (290–425 bp) from Sagonas et al. (2014) were included, bootstrap support for one terminal node decreased from 100 to 24 under ML and Bayesian analyses did no longer recover the respective clade. Moreover, most Sagonas sequences had long branches that were difficult to explain. Therefore, here we show the results (Fig. 2) of the calculations of the data set without the sequences from Sagonas et al. (2014), but present a RAxML tree including these sequences in the Supporting Information (Fig. S1).

Within the *L. viridis* complex, the sequences clustered in 10 well-supported terminal clades (Fig. 2). Their geographical distribution (Fig. 3), however, did not match with the ranges of the previously recognized subspecies of *L. bilineata* and *L. viridis* in most cases (Fig. 1). Some of the 10 clades were placed in well-supported, more inclusive clades whose sister-group relationships were badly resolved. In total, there were four suchlike ‘main lineages’, all having approximately the same hierarchical level. While Bayesian analyses placed them in an unresolved basal polytomy (Fig. 2), each had a very short branch in the RAxML tree (Fig. S1).

Only one of the main lineages (T) did not show phylogeographic substructure. This lineage contained all sequences from the Black Sea coast of Anatolia plus sequences of three green lizards from European Turkey and eastern mainland Greece (Fig. 3). Another of these main lineages contained the two clades B and B1, representing all sequences of *L. bilineata*. Clade B had a wide distribution, with sampled localities from Spain, France, western Germany and most of Italy, while clade B1 was only found in Calabria and Sicily. A further main lineage was comprised of three terminal clades (A, A1, A2) corresponding together to the Adriatic lineage of Böhme et al. (2007). Clade A showed a wide distribution from the border region of Italy, Slovenia and Croatia across the western Balkans southward to Lake Ohrid. In contrast, the other two clades, A1 and A2, being successive sister taxa of clade A, were sampled only from the border region of Albania and Greece. The last and most diverse main lineage consisted of four terminal clades (Fig. 2). One clade (G), constituting the sister taxon of the other three clades, was represented by samples from Euboea and adjacent mainland Greece (Fig. 3). Another clade (V) had a much wider distribution corresponding to most of the putative range of *L. v. viridis* (Figs 1 and 3). This clade V was the sister taxon of the remaining two clades V1 and V2. Clade V1 was found in the Former Yugoslav Republic Macedonia, central and eastern mainland Greece and south-eastern Bulgaria, whereas clade V2 was recorded only from few widely distant sites in Slovenia and Montenegro (Fig. 3). On Euboea and adjacent mainland Greece, haplotypes of clades V, V1 and G were found in close proximity. Further contact zones of haplotypes from distinct clades were revealed for the border region of Italy, Slovenia and Croatia (clades A, B, V, V2), Bosnia and Herzegovina (clades A, V), Montenegro (clades A, V, V2), the Former Yugoslav Republic of Macedonia and neighbouring Albania (clades A, V, V1), south-western Bulgaria (clades V, V1), and for western (clades A1, A2, V1) and eastern mainland Greece (clades V, V1, T).

The ten terminal clades of the *L. viridis* complex differed by uncorrected p distances ranging from 1.69% to 7.37% (Table 1). The weakest differentiation was found among the three clades of the Adriatic lineage (1.69–2.02%), while the two clades within *L. bilineata* (clades B and B1) differed by 2.97%. The divergences of the four clades representing together the fourth main lineage within the *L. viridis* complex (G, V, V1, V2) ranged from 2.61% to 5.63%, with the deepest divergences (5.02–5.63%) occurring between clade G and the remaining three clades. Within-group divergences ranged in the ten terminal clades of the *L. viridis* complex from 0.04% to 0.98%. If the terminal clades were lumped together, the four main lineages of the *L. viridis* complex (Table 2) differed by uncorrected p distances of 5.34–6.90%, with the smallest divergence observed between the lineage corresponding to *L. bilineata* (B + B1) and the Turkish lineage (T), and the largest divergence, between the Adriatic lineage (A + A1 + A2) and the Turkish lineage (T). The divergences among the four main

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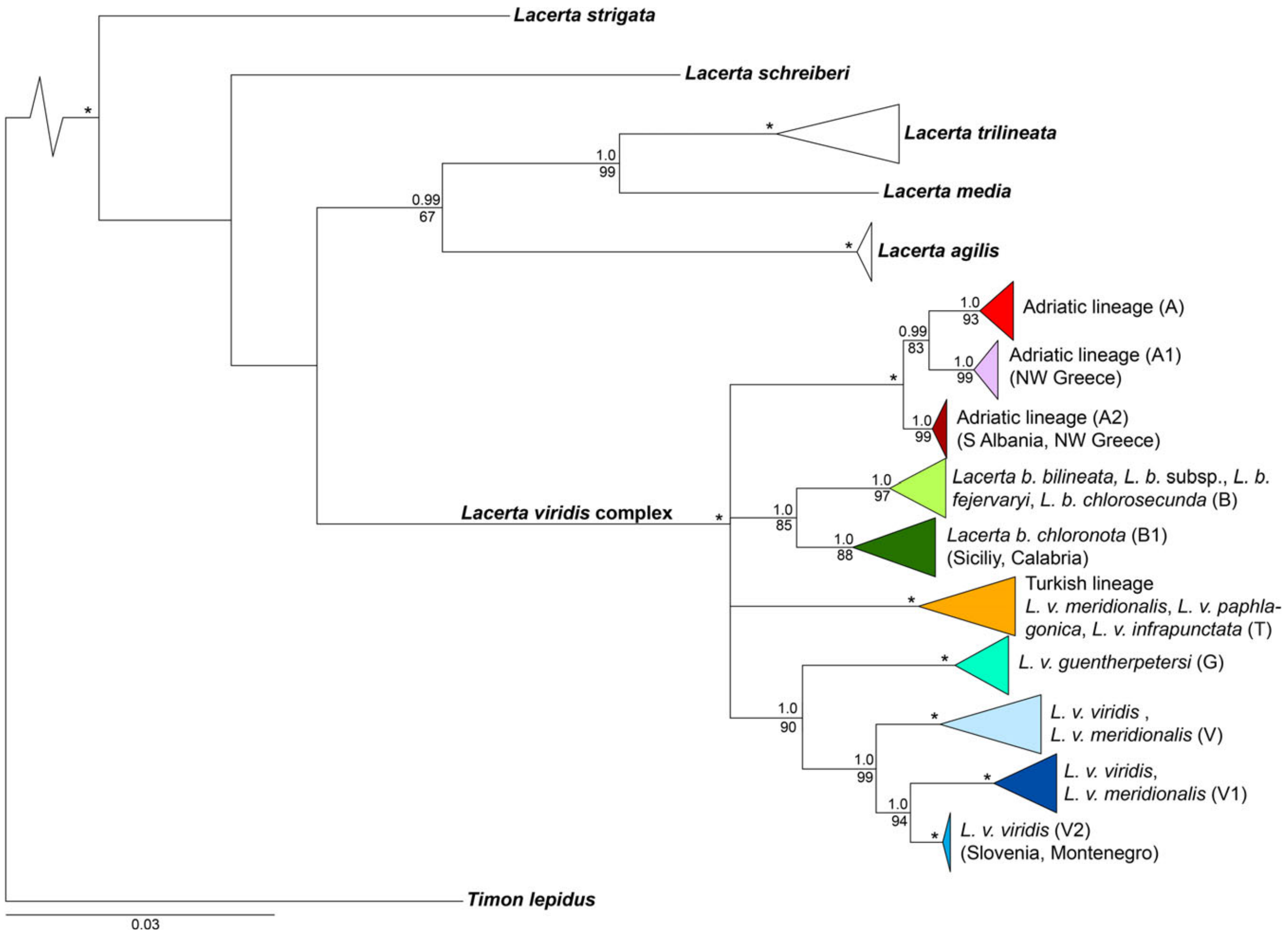

Fig. 2. Bayesian tree based on the mitochondrial cyt *b* gene of 454 green lizards (*Lacerta* sensu stricto), rooted with *Timon lepidus* (sequences from Sagonas et al. 2014 disregarded). Terminal clades collapsed to cartoons. Numbers along branches are posterior probabilities ≥ 0.95 and bootstrap support ≥ 50 obtained under maximum likelihood (ML). Asterisks indicate maximum support under both approaches. Root length shortened by 80%. ML analyses suggested a weakly supported sister-group relationship between T and G + [V + (V1 + V2)] and between (B + B1) and [A + (A1 + A2)], with short branch lengths and bootstrap values of 48 and 25, respectively. An ML tree showing all sequences including the data of Sagonas et al. (2014) is presented as Fig. S1 in the Supporting Information.

lineages of the *L. viridis* complex and the remaining species of *Lacerta* sensu stricto ranged from 7.95% to 15.63%, with the smallest divergence observed between *L. media* and *L. trilineata* and the largest divergence, between *L. media* and the lineage comprised of clades G, V, V1 and V2.

Evidence from the intron 7 of the *β*-fibrinogen gene

Among the 73 samples of green lizards studied for the *β*-fibint7 were 46 samples homozygous having variants of the long allele and 10 further samples were homozygous having variants of the short allele. The remaining 17 samples were heterozygous with respect to the length polymorphism of the *β*-fibint7. Our parsimony network analyses (Fig. 4) revealed that there are two highly distinct types of the short allele; both are characterized by the 380-bp-long deletion, but derived from different haplotypes of the long allele. One of the types of the short allele (s1) was linked in the network with the most frequent haplotype of the long allele of clades V, V1 and V2 (*Lacerta viridis*); this common haplotype of the long allele was shared with one individual of the Adriatic lineage (clade A) from Montenegro. The other type of the short allele (s2) was connected to a cluster of haplotypes of the long allele corresponding mainly to the Adriatic lineage (clades A, A1, A2). However, the most frequent haplotype in this cluster was shared with three samples representing clade V2, and another haplotype of this cluster, different by three mutational steps, represented clade V.

Variants of the long allele were found in lizards belonging to all studied mitochondrial clades. Generally, haplotypes of the main lineages corresponded in the network to different clusters which were, however, not perfectly mutually exclusive. Nonetheless, the variants of the long allele of most samples of *L. bilineata* (mitochondrial clades B, B1) and of a few samples of the Adriatic lineage (only clade A, from localities close to the distribution range of clade B) were quite distinct from the remaining samples.

With respect to the two types of short alleles, individuals of the Adriatic lineage had only one type (s2), while most samples of the main lineage corresponding to clades V, V1 and V2 (*L. v. viridis*, *L. v. meridionalis* from Europe) yielded the other type (s1). In addition, the s1 allele was also found in two *L. bilineata* (clade B), even though most studied samples of this species harboured variants of the long allele. Both types of short alleles (s1, s2) were recorded for clade G (*L. v. guentherpetersi*). For the Turkish lineage (clade T), no short alleles were found.

For samples representing the mitochondrial clades B, B1, G and T, only unique haplotypes were found, but in the network, these were located in very different positions and associated with haplotypes of other clades. Shared haplotypes were revealed only for the Adriatic lineage (clades A, A1, A2) and the main lineage

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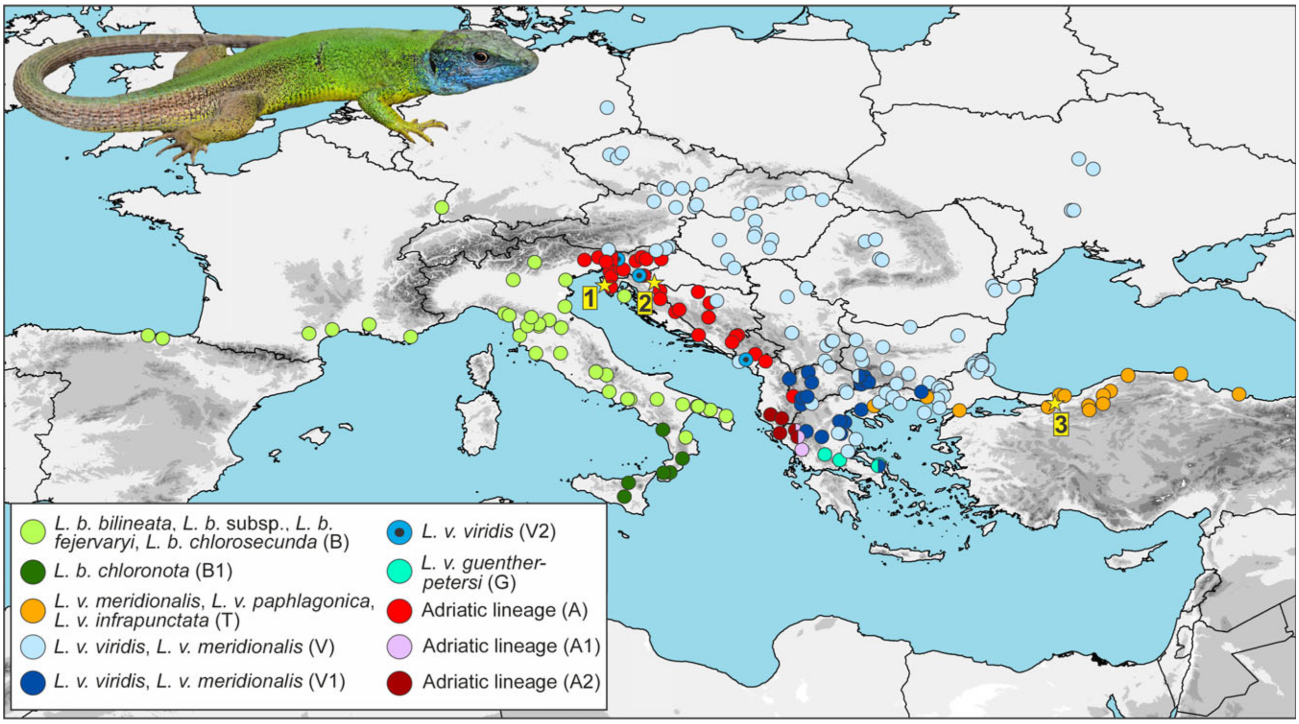

Fig. 3. Distribution of mitochondrial clades of the *Lacerta viridis* complex. Divided symbols represent syntopic occurrences or occurrences in close proximity. Stars indicate crucial type localities mentioned in the text: (1) Istria and Istrian islands, Croatia (type locality of *Lacerta viridis istriensis* Werner, 1897), (2) Ogulin, Croatia (type locality of *Lacerta viridis intermedia* Méhely, 1905), and (3) Adapazarı, Turkey (type locality of *Lacerta viridis meridionalis* Cyrén, 1933, restricted by Mertens and Müller 1940). Inset shows a green lizard of the '*meridionalis* morphotype' from Brodilovo, Bulgaria (male, clade V).

Table 1. Uncorrected p distances (percentages) of the cyt *b* gene (1143 bp) of the terminal clades of the *Lacerta viridis* complex and outgroups. Between-group divergences below diagonal; within-group divergences on the diagonal in boldface; *n* = number of sequences

	n	A	A1	A2	B	B1	G	T	V	V1	V2	*agilis*	*media*	*schrei*	*striga*	*trilin*	*Timon*
A	52	**0.19**															
A1	4	2.02	**0.56**														
A2	6	1.69	1.89	**0.76**													
B	51	6.54	6.33	6.28	**0.41**												
B1	10	6.38	6.65	5.97	2.97	**0.88**											
G	6	6.58	6.33	6.60	5.99	5.51	**0.42**										
T	21	6.84	7.37	7.04	5.34	5.36	6.36	**0.63**									
V	264	6.81	6.57	6.83	6.19	6.12	5.63	6.66	**0.36**								
V1	24	7.17	6.90	7.33	5.40	5.59	5.26	6.25	3.97	**0.98**							
V2	4	6.44	6.16	6.40	5.39	5.43	5.02	5.67	2.83	2.61	**0.04**						
agilis	3	14.67	14.36	15.11	13.77	13.72	14.39	15.10	14.25	14.61	14.28	**0.29**					
media	1	15.21	15.17	15.51	14.60	13.76	15.19	15.34	15.69	15.16	14.98	13.52	—				
schreiberi	1	15.48	15.79	15.57	15.06	14.74	15.37	15.16	15.49	15.96	15.22	14.79	14.44	—			
strigata	1	15.54	15.24	15.74	14.17	13.90	15.20	15.60	15.17	15.17	15.51	14.67	14.09	14.26	—		
trilineata	6	14.13	14.61	14.31	14.17	13.59	14.29	14.60	14.82	14.30	14.25	11.48	7.95	13.32	13.88	**1.49**	
Timon	1	19.65	19.42	19.07	18.50	18.21	19.24	20.30	19.32	19.73	19.09	19.45	17.85	18.90	18.72	17.79	—

embracing *L. v. viridis* and European *L. v. meridionalis* (clades V, V1, V2), and only for lizards collected in contact zones or regions close to contact zones. A similar picture emerged for heterozygous lizards with the short allele s2 combined with the long allele. Most of the respective samples originated from contact zones or regions close to contact zones (see Appendix).

Discussion

In our phylogenetic analyses of the mitochondrial cyt *b* gene, most data generated by Sagonas et al. (2014) diverged from the majority of other sequences, resulting in long branches and, in part, weaker clade support, even though the general phylogeographic pattern remained unchanged (Fig. S1). Basically, there are two explanations for this divergence: low sequence quality or the involvement of numts, that is of nuclear copies of mitochondrial DNA. If numts were responsible, it should be expected that such sequences show rather less variation than authentic mitochondrial DNA because of the repair mechanisms in the nucleus, causing a slower evolutionary rate (Brown et al. 1982; Zhang and Hewitt 1996). Also non-synonymous mutations, indels, frameshift mutations and the presence of unexpected stop codons are characteristic for numts (Zhang and Hewitt 1996; Bensasson et al. 2001; Song et al. 2008). This is all not the case, but this does not necessarily exclude that the sequences in question are numts (Bertheau et al. 2011). Yet, numts are often indicated by double peaks in the electropherograms because authentic mitochondrial DNA and numt are

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Table 2. Uncorrected p distances (percentages) of the cyt *b* gene (1143 bp) of the four main lineages of the *Lacerta viridis* complex and outgroups. For further explanation, see Table 1.

	n	1	2	3	4	*agilis*	*media*	*schrei*	*striga*	*trilin*	*Timon*
1 (A + A1 + A2)	62	**0.67**									
2 (B + B1)	61	6.48	**1.13**								
3 (G + V + V1 + V2)	298	6.82	6.10	**1.14**							
4 (T)	21	6.90	5.34	6.60	**0.63**						
agilis	3	14.69	13.77	14.28	15.10	**0.29**					
media	1	15.23	14.46	15.63	15.31	13.52	—				
schreiberi	1	15.51	15.00	15.52	15.15	14.79	14.44	—			
strigata	1	15.54	14.12	15.18	15.60	14.67	14.09	14.26	—		
trilineata	6	14.18	14.08	14.76	14.59	11.48	7.95	13.32	13.88	**1.49**	
Timon	1	19.58	18.45	19.35	20.29	19.45	17.85	18.90	18.72	17.79	—

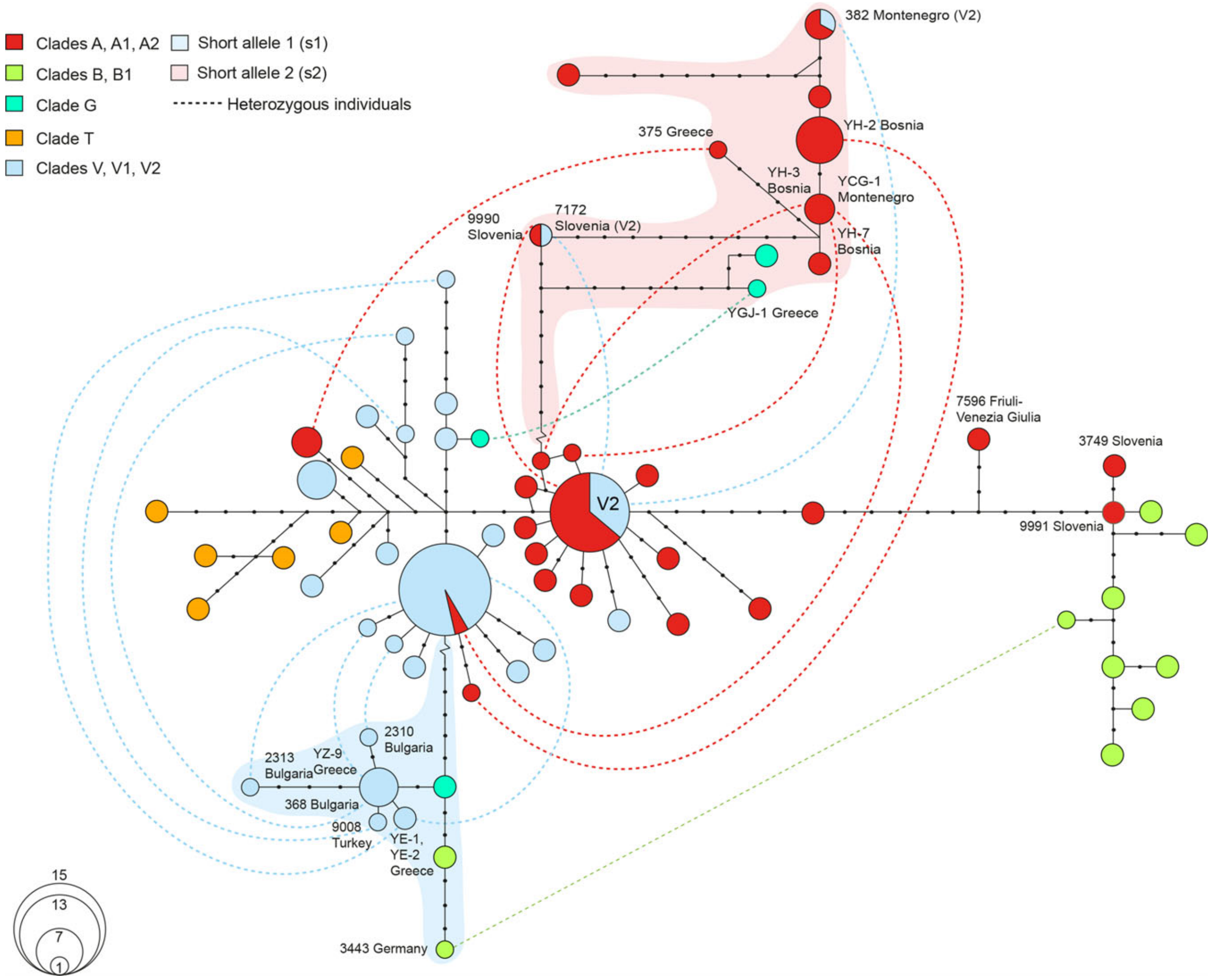

Fig. 4. Parsimony network for the intron 7 of the *β*-fibrinogen gene (*β*-fibint7), based on 73 samples. Symbol size reflects haplotype frequency. Missing haplotypes are represented by small black circles. Lines connecting two haplotypes correspond to one mutational step. Flexed connections of short alleles indicate that the length polymorphism was reduced for network building (see text). Sequences of individuals heterozygous for the length polymorphism are connected by broken lines (for their sample codes, see Appendix). Samples of clade V2 mentioned in the text are highlighted.

amplified together. Unfortunately, the electropherograms of the Sagonas sequences are not accessible. Thus, we cannot exclude completely that these short sequences (290–425 bp) are numts. However, we believe that low sequence quality is more likely because the Sagonas sequences contain many singletons, suggestive of base-calling errors or *Taq* errors during amplification. In addition, these sequences cluster in the same clades as the clean mitochondrial sequences produced for the present study and previous papers (Brückner et al. 2001; Böhme et al. 2007), whereas a different phylogenetic placement would be expected for numts (Zhang and Hewitt 1996; Bensasson et al. 2001; Fritz et al. 2010).

In any case, compared to previous studies (Brückner et al. 2001; Joger et al. 2001; Mayer and Beyerlein 2001; Godinho et al. 2005; Böhme et al. 2007; Sagonas et al. 2014) we found in the present investigation a more complex phylogeographic pat-

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tern for the *Lacerta viridis* complex. Based on the cyt *b* gene, we identified four deeply divergent main lineages (Fig. 2). Hitherto, only three of these lineages were known, and Böhme et al. (2007) believed that their newly discovered 'West Balkan lineage' (i.e. the Adriatic lineage) is closely related to and conspecific with *L. bilineata*. However, if the phylogenetic tree of Böhme et al. (2007) is scrutinized, it turns out that this assumption is based on a weakly supported sister-group relationship with a very short common branch. Thus, *L. bilineata* and the Adriatic lineage are better understood as basal lineages having approximately the same hierarchical level as the lineage comprising the clades of *L. viridis*. This is in accord with our results.

We found, in addition to the three previously known lineages (Adriatic lineage, *L. bilineata*, *L. viridis*), a fourth main lineage (T), which is largely confined to the Black Sea coast of Anatolia (Fig. 3), that is from within the ranges of the morphologically defined subspecies *L. v. meridionalis*, *L. v. paphlagonica* and *L. v. infrapunctata* (Schmidtler 1986). The Turkish lineage was also discovered at three sites in eastern mainland Greece and European Turkey, in close proximity to records of clades V and V1.

Except for the Turkish lineage, we found for all main lineages considerable substructuring. The greatest genetic diversity occurs then in the south of the distribution ranges, according to the well-known paradigm of 'southern richness' and 'northern purity' (Hewitt 2000). This pattern reflects the relatively large genetic diversity of populations in former southern glacial refugia. Typically, not all of these refugia contributed to the Holocene colonization of more northerly parts of the current distribution ranges of Western Palaearctic animals and plants, and during the rapid range expansions, further genetic diversity was lost due to founder effects and drift. Accordingly, the more northerly parts of the distribution range of the Adriatic lineage are occupied only by clade A, whereas two additional clades (A1, A2) occur in the very south (Fig. 3). These three clades (A, A1, A2) show largely parapatric distributions, arguing for the existence of three distinct microrefugia in the south. Moreover, distinct clades (V, V1, G) of the main lineage corresponding to *L. viridis* occur in close proximity to A, A1 and A2, again with largely parapatric distribution ranges. This suggests the existence of additional microrefugia in the southern Balkans. Obviously, only one of these clades of *L. viridis* (V) was capable to expand its range with the Holocene warming considerably, and it spreads all over what is now the northern distribution range of *L. viridis*. A similar differentiation pattern suggestive of several microrefugia in the southern Balkan Peninsula has also been found in the European pond turtle (*Emys orbicularis*; Fritz et al. 2007), the grass snake (*Natrix natrix*; Kindler et al. 2013), the common wall lizard (*Podarcis muralis*; Salvi et al. 2013), in slow worms (*Anguis* spp.; Gvoždík et al. 2013) and in the smooth newt (*Lissotriton vulgaris*; Pabijan et al. 2015), supporting a common phylogeographic pattern. However, within *L. viridis,* there is yet another clade (V2), which is known only from three sites in Slovenia and Montenegro (Fig. 3), but not from the southernmost part of the species' range. This distribution is surprising and incomplete sampling, ancestral polymorphism or translocation by humans have to be considered as possible explanations. Also another more northerly microrefugium in the Balkan Peninsula seems possible, even though it cannot explain the widely disjunct records of clade V2.

Among the clades of *L. viridis*, clade G (*L. v. guentherpetersi*) is deeply divergent. It differs from the other three clades (V, V1, V2) by uncorrected p distances (5.02–5.63%) resembling the divergences among the four main lineages (5.34–6.90%; Tables 1 and 2). This implies that *L. v. guentherpetersi* harbours an old and well-differentiated mitochondrial lineage. However, our records of clades V and V1 in close proximity (Euboea, mainland Greece; Fig. 3; Appendix) indicate secondary contact, perhaps during Holocene range shifts.

Also with respect to *L. bilineata*, a pronounced phylogeographic break is only observed in the southern part of the range. Samples from Sicily and Calabria represent the distinct clade B1, whereas the samples from more northern parts of the range belong to clade B, with a putative contact zone of the two clades in Calabria and Campania. Thus, the observed variation suggests the existence of two distinct refugia in the southern Italian Peninsula and Sicily, and the more northern parts of the species' range were colonized only from one refugium. The phylogeographic distinctness of Sicily and its close link to Calabria is well-known and observed in many other species, see the recent review in Kindler et al. (2013).

According to our results, there are several secondary contact zones between distinct mitochondrial clades and main lineages of the *L. viridis* complex (Fig. 3). Previous studies focused mainly on the putative contact zone of *L. bilineata* and *L. viridis* in the border region of Italy, Slovenia and Croatia (e.g. Brückner et al. 2001; Joger et al. 2001; Böhme et al. 2007). However, the only records of *L. bilineata* in this region are known from the island of Cres, Croatia (Brückner et al. 2001; Böhme et al. 2007; this study). Except for Cres, the very most samples from the putative contact zone of *L. bilineata* and *L. viridis* turned out to represent the Adriatic lineage (clade A), and only few records refer to *L. viridis* (clades V, V2; Fig. 3). Thus, this region represents a secondary contact zone of three lineages, and not two as previously assumed, and the exact location of the break line between the Adriatic lineage and *L. bilineata* remains unknown. In any case, except for the enigmatic record of *L. bilineata* for Cres, the contact zone seems to be further westward than previously thought.

We identified previously unknown, additional contact zones between the Adriatic lineage and *L. viridis* for Bosnia and Herzegovina, Montenegro, the Lake Ohrid region and western mainland Greece (Fig. 3). In eastern Greece (and most likely adjacent European Turkey), there is another contact zone between *L. viridis* and the Turkish lineage (T), and within the southern parts of the distribution ranges of *L. bilineata* and *L. viridis*, there are further contact zones between the individual clades of these lineages. It seems likely that all of these secondary contact zones established during Holocene range expansions.

Of paramount interest for the taxonomic interpretation of the observed distribution pattern of mitochondrial lineages is the question of whether there is gene flow in secondary contact zones, and if yes, to what extent. Our original approach was to tackle this question using the nuclear β-fibint7. Unfortunately, the interpretation of this marker is not straightforward. Godinho et al. (2005) thought that the long allele 'is only present in some individuals of *L. viridis* within a well-defined geographical area but [. . .] in all the *L. bilineata* individuals analysed throughout the distribution range of this species'. Godinho et al. (2005) found heterozygous lizards 'in a transect between southern Croatia, western Greece (*L. v. viridis*) and the Aegean Greek islands (*L. v. guentherpetersi*)', suggestive of gene flow. However, the original interpretation of Godinho et al. (2005) was based on the erroneous identification of the Adriatic lineage with *L. viridis* (Böhme et al. 2007). Moreover, according to our results, there are two distinct types of short alleles of the β-fibint7 (see below) and not only one, as thought by Godinho et al. (2005).

Even though our data are at first glance complicated, they allow some insights. Variants of the long allele were widely distributed and occurred in green lizards of all studied mitochondrial clades. The haplotypes of the long allele showed some

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geographical structuring (Fig. 4) and we found no shared haplotypes for lizards corresponding to the mitochondrial clades B, B1, G and T. Most differentiated were the haplotypes of *L. bilineata* (clades B, B1). This cluster included also two Slovenian lizards of the Adriatic lineage (clade A). An Italian lizard of clade A from Friuli-Venezia Giulia, a region close to the distribution range of *L. bilineata*, had a somewhat more remote position in the network, being intermediate between the haplotypes of *L. bilineata* and most haplotypes of the Adriatic lineage. Most studied lizards of clades B and B1 had only haplotypes of the long allele, a finding resembling the observations of Godinho et al. (2005), although two of our *L. bilineata* samples harboured haplotypes of the short allele s1.

For short *β*-fibint7 sequences, we identified in our network analyses two distinct clusters of haplotypes (Fig. 4). Godinho et al. (2005) were not aware of these two types because they determined in many samples allele lengths only by PCR. One allele type (s1) occurred mainly in lizards of clades V, V1 and V2 (corresponding to *L. v. viridis* and *L. v. meridionalis* from Europe), the other type (s2) was largely restricted to the Adriatic lineage (clades A, A1, A2). However, there were also two haplotypes of s2 which were shared between representatives of the Adriatic lineage and clade V2, and these lizards were from contact zones of the respective mitochondrial clades. Also shared haplotypes of the long allele and heterozygous lizards having the short allele s2 combined with the long allele (Fig. 4) originated mainly from contact zones or regions close to contact zones (Fig. 4; Appendix). This suggests gene flow between the Adriatic lineage and *L. viridis* (clades V, V1, V2). However, an alternative explanation could be incomplete lineage sorting (ancestral polymorphism). That incomplete lineage sorting plays a role is suggested by the presence of the short allele s1 in two *L. bilineata* from south-western France and south-western Germany (see Appendix), two sites far away from any contact zone, and by the occurrence of both short allele types (s1, s2) and the long allele in *L. v. guentherpetersi* (clade G). Thus, the described patterns of haplotype sharing and heterozygosity cannot be understood as hard evidence for gene flow.

Conclusions and taxonomic recommendations

The mitochondrial phylogeography of the *Lacerta viridis* complex corresponds to a general pattern for thermophilic taxa in the Western Palaearctic, with several glacial refugia located in the southern European peninsulas and Anatolia (cf. Hewitt 2000; Joger et al. 2007; Schmitt 2007). In the *L. viridis* complex, two distinct refugia can be identified for the Italian Peninsula and Sicily, and one for Anatolia. The situation in the southern Balkan Peninsula is intricate, with seven distinct terminal clades, each of which could correspond to a distinct refugium. The Adriatic lineage as a whole, comprised of three distinct clades (A, A1, A2), and clade G (*L. v. guentherpetersi*) are most differentiated and we hypothesize that they represent old genetic lineages that diverged more than one glacial cycle ago.

The mitochondrial phylogeography of the *L. viridis* complex reflects the radiation of four main lineages which are approximately of the same hierarchical level. Our nuclear marker delivered no unambiguous results with respect to gene flow among these lineages. Hybridization experiments (Rykena 1991, 2001) and allozyme studies (Amann et al. 1997; Joger et al. 2001) suggested that *L. bilineata* and *L. viridis* should be recognized as distinct species. According to the allozyme studies, gene flow between both taxa was thought to be largely unidirectional from *viridis* into *bilineata*, and restricted to a small contact zone in the border region of Italy and Slovenia (Amann et al. 1997; Joger et al. 2001). However, according to our results, *L. bilineata* is not present in this region, and the green lizards there belong mostly to the Adriatic lineage and, to a lesser extent, to *L. viridis*, challenging the previous conclusions.

Thus, we could not answer one of our original questions, whether *L. bilineata* and *L. viridis* represent distinct species without extensive gene flow. This calls for further research, with denser sampling farer westwards to locate the proper eastern range boundary of *L. bilineata*, which must be in eastern Italy. In this context, also the enigmatic record of *L. bilineata* for the island of Cres (Croatia) needs to be re-examined. According to the present state of the knowledge, this population is completely isolated.

For assessing the species status of *L. bilineata* and *L. viridis*, but also of the two other main lineages of the *L. viridis* complex, the application of sensitive nuclear markers, such as polymorphic microsatellite loci or SNPs, is recommended to detect possible gene flow across contact zones. All four main lineages show approximately the same degree of mitochondrial differentiation and, thus, if *L. bilineata* and *L. viridis* should turn out as distinct species, the same could be true also for the other two lineages.

With respect to the previously postulated subspecies of the *L. viridis* complex (Fig. 1; Table 3), our genetic data confirmed for *L. bilineata* the distinctiveness of only two subspecies. The taxon endemic to Sicily and Calabria had already been previously identified with *L. b. chloronota* Rafinesque, 1810 (Nettmann 2001), and its distribution range agrees well with our clade

Table 3. Tentative nomenclature for the *Lacerta viridis* complex and correspondence of taxa to mitochondrial clades. Except for names that could refer to the Adriatic lineage are only synonyms shown which have been used in recent studies as valid taxa (cf. Nettmann 2001). The putative subspecies of *L. bilineata* from central peninsular Italy (Nettmann 2001) is included in *L. b. bilineata*. Note that most European populations formerly included in *L. v. meridionalis* are now assigned to L. *v. viridis*.

Taxon	Synonym(s)	Mitochondrial clade(s)
‘Adriatic lineage’	‘West Balkan lineage’ *Lacerta viridis istriensis* Werner, 1897? *Lacerta viridis intermedia* Méhely, 1905?	A, A1, A2
Lacerta bilineata bilineata Daudin, 1802	*Lacerta bilineata fejervaryi* Vasvary, 1926 *Lacerta bilineata chlorosecunda* Taddei, 1950	B
Lacerta bilineata chloronota Rafinesque, 1810	–	B1
Lacerta viridis viridis (Laurenti, 1768)	–	V, V1, V2
Lacerta viridis guentherpetersi Rykena, Nettmann and Mayer, 2001	–	G
Lacerta viridis meridionalis Cyrén, 1933	*Lacerta viridis infrapunctata* Schmidtler, 1986 *Lacerta viridis paphlagonica* Schmidtler, 1986	T

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B1 (Figs 1 and 3). From the more northerly regions from Italy, up to four putative subspecies have been distinguished (Nettmann 2001; Fig. 1). However, our results suggest that all should be lumped together under the oldest available name *L. b. bilineata* Daudin, 1802 (Fig. 3; Table 3).

Among the currently recognized subspecies of *L. viridis* (Fig. 1; Table 3), our data confirmed the distinctiveness of *L. v. guentherpetersi* Rykena, Nettmann and Mayer, 2001. The situation is different with respect to *L. v. meridionalis* Cyrén, 1933. It has morphologically been diagnosed by brownish legs and brownish tail coloration in adults (Arnold and Ovenden 2002), characters which are perhaps best understood as pedomorphic or clinal variation without taxonomic relevance. According to our mitochondrial data, *L. v. meridionalis* is composed of three distinct mitochondrial clades (Fig. 2, clades T, V, V1) and needs to be redefined. Its restricted type locality Adapazarı (Mertens and Müller 1940) lies in Anatolia (Fig. 3), making clear that our Turkish lineage (clade T) has to be identified with this taxon. However, the two other Anatolian subspecies, *L. v. paphlagonica* Schmidtler, 1986 and *L. v. infrapunctata* Schmidtler, 1986, are not supported and should be regarded as junior synonyms of *L. v. meridionalis* Cyrén, 1933 (Table 3). Our results are in line with the findings of Kumlutaş (1996) and Arıkan et al. (1999), who concluded that *L. v. paphlagonica* and *L. v. infrapunctata* are morphologically and serologically indistinguishable from Turkish *L. v. meridionalis* and should be synonymized.

The genetic lineage of *L. v. meridionalis* extends into southeastern Europe (Fig. 3), but the green lizards in most of the European range currently attributed to this subspecies (Fig. 1) harbour haplotypes identical with or very similar to those found within the distribution range of *L. v. viridis* (Laurenti, 1768) (clade V). However, within the putative European range of *L. v. meridionalis*, and in the southern part of the range of *L. v. viridis*, also another clade (V1) occurs whose status needs to be reinvestigated using additional markers. The same is true for the enigmatic clade V2, which is currently only known from Slovenia and Montenegro. Provisionally, we suggest lumping together the clades V, V1 and V2 under *L. v. viridis*.

As already pointed out by Böhme et al. (2007), the Adriatic lineage (clades A, A1, A2) undoubtedly represents a distinct taxon. However, our new data reveal that this lineage could correspond to up to three closely related taxa (Figs 2 and 3). It could be that the names *L. v. istriensis* Werner, 1897 (type locality: Istria, Istrian islands) and *L. v. intermedia* Méhely, 1905 (type locality: Ogulin, Croatia) refer to the Adriatic lineage. Böhme et al. (2007) were reluctant to identify *L. v. intermedia* with this lineage because in the region of Ogulin could also other genetic lineages be expected. Indeed, we recorded from localities close to Ogulin green lizards representing clades A and V2, and a similar situation is true for Istria (Fig. 3). The question of whether *L. v. istriensis* and *L. v. intermedia* represent clade A or not, can only be resolved by studying several individuals from the type localities. For the time being, we recommend to continue using 'Adriatic lineage' or 'West Balkan lineage' for these lizards, pending further study. Table 3 summarizes our tentative nomenclature for the *L. viridis* complex.

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Supporting Information

Additional Supporting Information may be found in the online version of this article:

Fig. S1. Maximum Likelihood tree for the complete data set of 475 cyt *b* sequences, including the data from Sagonas et al. (2014).

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Appendix. Used samples, GenBank sequences and their accession numbers. For homozygous individuals, only one accession number is given for β-fibint7. Nomenclature of taxa follows recommendations of the present study.

		Coordinates				GenBank accession numbers			
Taxon	Collecting site	N	E	Clade	Sample	Cyt *b*	β-fibint7 short allele	β-fibint7 long allele	Reference
Adriatic lineage	Albania: Boge	42.40	19.65	A	NMWWG-4	LN834625	LN835032 (s2)	—	Present study
Adriatic lineage	Albania: Cajupit pass	40.19	20.17	A2	MTDT12936	LN834626			Present study
Adriatic lineage	Albania: Cajupit pass	40.19	20.17	A2	MTDT12937	LN834627			Present study
Adriatic lineage	Albania: Griba Mts.	40.37	19.78	A2	MTDT12938	LN834628			Present study
Adriatic lineage	Albania: Lin	41.06	20.61	A	MTDT12941	LN834629			Present study
Adriatic lineage	Albania: Vagalat	39.74	20.13	A2	MTDT11610	LN834630			Present study
Adriatic lineage	Bosnia and Herzegovina: Gornje Peulje	44.13	16.51	A	MTDT10857	LN834631			Present study
Adriatic lineage	Bosnia and Herzegovina: Gornji Podgradci, Kozara Mts.	45.03	17.00	A	MTDT10856	LN834632			Present study
Adriatic lineage	Bosnia and Herzegovina: Korita	43.05	18.50	A	NMWYH-3	LN834633	LN835033 (s2)	LN835065	Present study
Adriatic lineage	Bosnia and Herzegovina: Gračanica	44.00	17.48	A	MTDT10858	LN834634			Present study
Adriatic lineage	Bosnia and Herzegovina: Sirovac	44.57	17.57	A	NMWYCG-1	LN834635	LN835034 (s2)	LN835066	Present study
Adriatic lineage	Bosnia and Herzegovina: Tjentište	43.31	18.67	A	MTDT10859	LN834636			Present study
Adriatic lineage	Bosnia and Herzegovina: Tjentište	43.37	18.71	A	NMWYH-2	LN834637	LN835035 (s2)	LN835067	Present study
Adriatic lineage	Croatia: Biokovo	43.38	17.07	A	NMWYH-1	LN834638	LN835036 (s2)	—	Present study
Adriatic lineage	Croatia: Dinara	44.07	16.39	A	NMWYH-6	LN834639	—	LN835068	Present study
Adriatic lineage	Croatia: Sveti Petar u Šumi (Istria)	45.18	13.87	A	MTDT13248	LN834640			Present study
Adriatic lineage	Croatia: Krbavica	44.72	15.62	A	NMWYH-7	LN834641	LN835037 (s2)	LN835069	Present study
Adriatic lineage	Croatia: Slunj	45.11	15.59	A	MTDT11607	LN834642			Present study
Adriatic lineage	Greece: Arta	39.16	20.99	A1	—	AF233423			Brückner et al. (2001)
Adriatic lineage	Greece: Arta	39.16	20.99	A1	—	KJ940311			Sagonas et al. (2014)
Adriatic lineage	Greece: Arta	39.16	20.99	A1	NMWYAR-5	AM292971			Böhme et al. (2007)
Adriatic lineage	Greece: Arta	39.16	20.99	A1	NMWYAR-7	LN834643	LN835038 (s2)	—	Present study
Adriatic lineage	Greece: Ioannina	39.66	20.85	A2	—	KJ940310			Sagonas et al. (2014)
Adriatic lineage	Greece: Ioannina	39.66	20.85	A1	—	KJ940309			Sagonas et al. (2014)
Adriatic lineage	Greece: Zagoria	39.91	20.77	A2	ZSL374	AM292972			Böhme et al. (2007)
Adriatic lineage	Greece: Zagoria	39.91	20.77	A2	ZSL375	LN834644	LN835039 (s2)	LN835070	Present study
Adriatic lineage	Greece: Zagoria	39.91	20.77	A1	ZSL376	AM292974	—	LN835071	Böhme et al. (2007)
Adriatic lineage	Italy: Friuli-Venezia Giulia: Pordenone: Travesio	46.20	12.87	A	MTDT7596	LN834645	—	LN835072	Present study
Adriatic lineage	Italy: Friuli-Venezia Giulia: Pordenone: Travesio	46.20	12.87	A	MTDT7597	LN834646	—	LN835073	Present study
Adriatic lineage	Italy: Friuli-Venezia Giulia: Udine: Musi	46.31	13.27	A	NMWYF-1	AM292993	—	LN835074	Böhme et al. (2007)
Adriatic lineage	Montenegro: N Podgorica	42.58	19.30	A	ZSL379	AM292975			Böhme et al. (2007)
Adriatic lineage	Montenegro: N Podgorica	42.58	19.30	A	ZSL380	LN834647	—	LN835075	Present study
Adriatic lineage	Montenegro: N Podgorica	42.58	19.30	A	ZSL383	LN834648	LN835041 (s2)	—	Present study
Adriatic lineage	Slovenia: Bilpa ob Kolpi	45.49	15.08	A	MTDT10073	LN834649			Present study
Adriatic lineage	Slovenia: Bohinj	46.31	13.96	A	MTDT3748	LN834650			Present study
Adriatic lineage	Slovenia: Bohinj	46.31	13.96	A	MTDT3749	LN834651	—	LN835076	Present study
Adriatic lineage	Slovenia: Bohinj	46.31	13.96	A	MTDT3750	LN834652	—	LN835077	Present study
Adriatic lineage	Slovenia: Bohinj	46.31	13.96	A	MTDT3752	LN834653	—	LN835078	Present study
Adriatic lineage	Slovenia: Bohinj	46.31	13.96	A	MTDT3753	LN834654	—	LN835079	Present study

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Appendix *(continued)*

		Coordinates				GenBank accession numbers			
Taxon	Collecting site	N	E	Clade	Sample	Cyt *b*	β-fibint7 short allele	β-fibint7 long allele	Reference
Adriatic lineage	Slovenia: Bohinj	46.31	13.96	A	MTDT7167	LN834655			Present study
Adriatic lineage	Slovenia: Bohinj	46.31	13.96	A	MTDT7173	LN834656	—	LN835080	Present study
Adriatic lineage	Slovenia: Bohinj	46.31	13.96	A	MTDT7175	LN834657	—	LN835081	Present study
Adriatic lineage	Slovenia: Bohinj Lake	46.29	13.85	A	ZSL369	LN834658			Present study
Adriatic lineage	Slovenia: Bohinj Lake	46.29	13.85	A	ZSL370	LN834659			Present study
Adriatic lineage	Slovenia: Bohinj Lake	46.29	13.85	A	ZSL371	LN834660			Present study
Adriatic lineage	Slovenia: Borjana	46.26	13.47	A	MTDT13550	LN834661			Present study
Adriatic lineage	Slovenia: Borjana	46.25	13.46	A	MTDT13551	LN834662			Present study
Adriatic lineage	Slovenia: Cerknica	45.81	14.36	A	MTDT10076	LN834663	—	LN835082	Present study
Adriatic lineage	Slovenia: Grgelj ob Kolpi	45.52	14.95	A	MTDT10078	LN834664	LN835042 (s2)	—	Present study
Adriatic lineage	Slovenia: Kamenče	46.27	15.04	A	ZSL372	AM292976			Böhme et al. (2007)
Adriatic lineage	Slovenia: Kopriva	46.24	13.45	A	MTDT13554	LN834665			Present study
Adriatic lineage	Slovenia: Kopriva	45.80	13.84	A	MTDT13555	LN834666			Present study
Adriatic lineage	Slovenia: Laško	46.15	15.24	A	MTDT10472	LN834667			Present study
Adriatic lineage	Slovenia: Moravče, Gabrje pod Limbarsko Goro	46.15	14.77	A	MTDT9990	LN834668	LN835043 (s2)	LN835083	Present study
Adriatic lineage	Slovenia: Planina, Ravbarjev stolp	45.83	14.25	A	MTDT10077	LN834669	—	LN835084	Present study
Adriatic lineage	Slovenia: Podbela	46.25	13.44	A	MTDT13553	LN834670			Present study
Adriatic lineage	Slovenia: Rogaška Slatina, Donačka gora	46.26	15.72	A	MTDT9984	LN834671	—	LN835085	Present study
Adriatic lineage	Slovenia: Rogaška Slatina, Donačka gora	46.26	15.72	A	MTDT9985	LN834672	—	LN835086	Present study
Adriatic lineage	Slovenia: Socerb	45.59	13.86	A	MTDT11220	LN834673			Present study
Adriatic lineage	Slovenia: Socerb	45.59	13.86	A	MTDT11221	LN834674			Present study
Adriatic lineage	Slovenia: Sočerga, Sveti Kirik	45.47	13.89	A	MTDT9987	LN834675			Present study
Adriatic lineage	Slovenia: Stari trg ob Kolpi, Dol	45.49	15.08	A	MTDT10072	LN834676	LN835044 (s2)	—	Present study
Adriatic lineage	Slovenia: Sveti Anton, Galantiči	45.50	13.88	A	MTDT9989	LN834677	—	LN835087	Present study
Adriatic lineage	Slovenia: Tolmin, Javarca	46.19	13.73	A	MTDT9986	LN834678			Present study
Adriatic lineage	Slovenia: Tomačevica	45.82	13.77	A	MTDT9991	LN834679	—	LN835088	Present study
Lacerta bilineata bilineata	Croatia: Cres	44.96	14.41	B	—	AF233422			Brückner et al. (2001)
Lacerta bilineata bilineata	Croatia: Cres	44.96	14.41	B	NMWYCR-1	AM292989			Böhme et al. (2007)
Lacerta bilineata bilineata	Croatia: Cres	44.96	14.41	B	NMWYCR-2	LN834680	—	LN835057	Present study
Lacerta bilineata bilineata	Croatia: Cres	44.96	14.41	B	NMWYCR-3	LN834681	—	LN835058	Present study
Lacerta bilineata bilineata	France: Bouches-du-Rhône: Eyguières	43.70	5.03	B	MTDT2543	AM292987	—	LN835059	Böhme et al. (2007)
Lacerta bilineata bilineata	France: Hérault: Aigues Vives	43.34	2.82	B	MTDT2544	AM292986	—	LN835060	Böhme et al. (2007)
Lacerta bilineata bilineata	France: Hérault: Cournonterral	43.56	3.72	B	MTDT2546	AM292985	LN835030 (s1)	—	Böhme et al. (2007)
Lacerta bilineata bilineata	France: Var: Plan de la Tour	43.34	6.55	B	MTDT2548	AM292984			Böhme et al. (2007)
Lacerta bilineata bilineata	Germany: Baden-Württemberg: Kaiserstuhl	48.10	7.67	B	MTDT3443	LN834682	LN835031 (s1)	LN835061	Present study
Lacerta bilineata bilineata	Italy: Abruzzo: L’Aquila: Villa San Sebastiano	42.03	13.31	B	MTDT11504	LN834683			Present study
Lacerta bilineata bilineata	Italy: Abruzzo: L’Aquila: Villa San Sebastiano	42.03	13.31	B	MTDT11505	LN834684			Present study
Lacerta bilineata bilineata	Italy: Abruzzo: National Park of Abruzzo	41.81	13.79	B	MTDT11507	LN834685			Present study
Lacerta bilineata bilineata	Italy: Abruzzo: National Park of Abruzzo	41.81	13.79	B	MTDT11508	LN834686			Present study
Lacerta bilineata bilineata	Italy: Abruzzo: National Park of Abruzzo	41.81	13.79	B	MTDT11512	LN834687			Present study
Lacerta bilineata bilineata	Italy: Apulia: Bari: Altamura	40.83	16.55	B	MTDT11511	LN834688			Present study
Lacerta bilineata bilineata	Italy: Apulia: Ceglie Messapica	40.65	17.52	B	NMWYJ-2	LN834705	—	LN835062	Present study
Lacerta bilineata bilineata	Italy: Apulia: Lecce: San Cataldo	40.39	18.30	B	MTDT11500	LN834689			Present study
Lacerta bilineata bilineata	Italy: Apulia: Lecce: San Cataldo	40.39	18.30	B	MTDT11501	LN834690			Present study
Lacerta bilineata bilineata	Italy: Apulia: Lecce: San Cataldo	40.39	18.30	B	MTDT11502	LN834691			Present study
Lacerta bilineata bilineata	Italy: Apulia: Lecce: San Cataldo	40.39	18.30	B	MTDT11503	LN834692			Present study

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Appendix *(continued)*

Taxon	Collecting site	Coordinates N	Coordinates E	Clade	Sample	GenBank accession numbers Cyt *b*	GenBank accession numbers β-fibint7 short allele	GenBank accession numbers β-fibint7 long allele	Reference
Lacerta bilineata bilineata	Italy: Apulia: Noci	40.80	17.12	B	—	AF233420			Brückner et al. (2001)
Lacerta bilineata bilineata	Italy: Apulia: Noci	40.79	17.13	B	IÖE-A8	AM292991			Böhme et al. (2007)
Lacerta bilineata bilineata	Italy: Basilicata: Melfi	41.00	15.64	B	IÖE-M10	AM292990			Böhme et al. (2007)
Lacerta bilineata bilineata	Italy: Basilicata: Melfi	40.99	15.65	B	—	AF233419			Brückner et al. (2001)
Lacerta bilineata bilineata	Italy: Calabria: Cosenza: Cropalati	39.52	16.72	B	MTDT11509	LN834696			Present study
Lacerta bilineata bilineata	Italy: Calabria: Cosenza: Cropalati	39.52	16.72	B	MTDT11510	LN834697			Present study
Lacerta bilineata bilineata	Italy: Campania: Avellino: Avella	40.96	14.60	B	MTDT11519	LN834701			Present study
Lacerta bilineata bilineata	Italy: Campania: Avellino: Avella	40.96	14.60	B	MTDT11520	LN834702			Present study
Lacerta bilineata bilineata	Italy: Campania: Avellino: Avella	40.96	14.60	B	MTDT11521	LN834703			Present study
Lacerta bilineata bilineata	Italy: Campania: Naples: Roccarainola	40.97	14.56	B	MTDT11518	LN834704			Present study
Lacerta bilineata bilineata	Italy: Campania: Sessa Aurunca	41.24	13.93	B	—	AF233418			Brückner et al. (2001)
Lacerta bilineata bilineata	Italy: Emilia Romagna: Ravenna	44.42	12.20	B	MTDT11487	LN834706			Present study
Lacerta bilineata bilineata	Italy: Emilia Romagna: Ravenna	44.42	12.20	B	MTDT11488	LN834707			Present study
Lacerta bilineata bilineata	Italy: Emilia Romagna: Ravenna	44.42	12.20	B	MTDT11489	LN834708			Present study
Lacerta bilineata bilineata	Italy: Trentino: Terlago	46.10	11.06	B	MTDT10862	LN834712			Present study
Lacerta bilineata bilineata	Italy: Tuscany: Anghiari	43.54	12.05	B	—	AF233416			Brückner et al. (2001)
Lacerta bilineata bilineata	Italy: Tuscany: Florence: Londa	43.86	11.57	B	MTDT11491	LN834713			Present study
Lacerta bilineata bilineata	Italy: Tuscany: Florence: Padule di Fucecchio	43.73	10.81	B	MTDT11506	LN834709			Present study
Lacerta bilineata bilineata	Italy: Tuscany: Florence: Peretola	43.81	11.20	B	MTDT11522	LN834714			Present study
Lacerta bilineata bilineata	Italy: Tuscany: Florence: Scandicci	43.75	11.19	B	MTDT11493	LN834715			Present study
Lacerta bilineata bilineata	Italy: Tuscany: Grosseto: Alberese	42.67	11.11	B	MTDT11496	LN834716			Present study
Lacerta bilineata bilineata	Italy: Tuscany: Livorno	45.55	10.31	B	—	AF233415			Brückner et al. (2001)
Lacerta bilineata bilineata	Italy: Tuscany: Massa Carrara: Pian della Fioba	44.06	10.20	B	MTDT11495	LN834717			Present study
Lacerta bilineata bilineata	Italy: Tuscany: Massa Carrara: Pulica	44.14	10.04	B	MTDT11490	LN834718			Present study
Lacerta bilineata bilineata	Italy: Tuscany: near Livorno: Bibbona	43.27	10.60	B	MTDT11494	LN834719			Present study
Lacerta bilineata bilineata	Italy: Tuscany: Pistoia: Piteccio	44.01	10.90	B	MTDT11492	LN834720			Present study
Lacerta bilineata bilineata	Italy: Umbria: Orvieto	42.72	12.11	B	—	AF233417			Brückner et al. (2001)
Lacerta bilineata bilineata	Italy: Venezia	45.44	12.33	B	—	AF233414			Brückner et al. (2001)
Lacerta bilineata bilineata	Spain: Bilbao	43.26	−2.92	B	NMWYBJ-1	AM292988	—	LN835064	Böhme et al. (2007)
Lacerta bilineata bilineata	Spain: Cantabria: Oriñon	43.40	−3.33	B	MTDT11656	LN834721			Present study
Lacerta bilineata bilineata	Spain: Cantabria: Oriñon	43.40	−3.33	B	MTDT11659	LN834722			Present study
Lacerta bilineata chloronota	Italy: Calabria: Aspromonte	38.17	16.00	B1	IÖE-C46	AM292992			Böhme et al. (2007)
Lacerta bilineata chloronota	Italy: Calabria: Aspromonte	38.17	15.84	B1	—	AF233421			Brückner et al. (2001)
Lacerta bilineata chloronota	Italy: Calabria: Catanzaro: Novalba	38.65	16.39	B1	MTDT11514	LN834693			Present study
Lacerta bilineata chloronota	Italy: Calabria: Catanzaro: Novalba	38.65	16.39	B1	MTDT11515	LN834694			Present study
Lacerta bilineata chloronota	Italy: Calabria: Catanzaro: Novalba	38.65	16.39	B1	MTDT11516	LN834695			Present study
Lacerta bilineata chloronota	Italy: Calabria: Cosenza: Scalea	39.81	15.79	B1	MTDT11497	LN834698			Present study
Lacerta bilineata chloronota	Italy: Calabria: Cosenza: Scalea	39.81	15.79	B1	MTDT11498	LN834699			Present study
Lacerta bilineata chloronota	Italy: Calabria: Cosenza: Scalea	39.81	15.79	B1	MTDT11499	LN834700			Present study
Lacerta bilineata chloronota	Italy: Sicily	37.40	14.39	B1	NMWYJ-3	LN834710	—	LN835063	Present study
Lacerta bilineata chloronota	Italy: Sicily: Monti Nebrodi	37.90	14.59	B1	MTDT11513	LN834711			Present study
Lacerta viridis guentherpetersi	Greece: Dirfis	38.61	23.85	G	NMWYD-4	LN834723	LN835045 (s2)	—	Present study
Lacerta viridis guentherpetersi	Greece: Evvia	38.52	23.86	G	—	AF233424			Brückner et al. (2001)

Appendix *(continued)*

		Coordinates				GenBank accession numbers			
Taxon	Collecting site	N	E	Clade	Sample	Cyt *b*	*β*-fibint7 short allele	*β*-fibint7 long allele	Reference
Lacerta viridis guentherpetersi	Greece: Iti	38.74	22.40	G	NMWYGJ-1	AM292969	LN835047 (s2)	LN835104	Böhme et al. (2007)
Lacerta viridis guentherpetersi	Greece: Iti	38.74	22.40	G	NMWYGJ-2	AM292970	LN835048 (s1)	—	Böhme et al. (2007)
Lacerta viridis guentherpetersi	Greece: Timfristos	38.91	21.92	G	NMWYTF-1	LN834724			Present study
Lacerta viridis guentherpetersi	Greece: Timfristos	38.91	21.92	G	NMWYTF-2	LN834725			Present study
Lacerta viridis meridionalis	Greece: Rospoli	41.08	25.73	T	MTDT3715	LN834726			Present study
Lacerta viridis meridionalis	Greece: Stavros	40.67	23.71	T	MTDT3727	LN834727	—	LN835089	Present study
Lacerta viridis meridionalis	Turkey: Bolu	41.06	32.06	T	MTDT9003	LN834728	—	LN835090	Present study
Lacerta viridis meridionalis	Turkey: Bolu	40.54	31.65	T	MTDT9007	LN834729	—	LN835091	Present study
Lacerta viridis meridionalis	Turkey: Bolu	40.74	31.61	T	NMWYET-1	LN834730	—	LN835092	Present study
Lacerta viridis meridionalis	Turkey: Bolu: Yeniçağa	40.77	32.03	T	MTDT3728	LN834731			Present study
Lacerta viridis meridionalis	Turkey: Karabük: Yenice	41.21	32.36	T	MTDT9004	LN834732			Present study
Lacerta viridis meridionalis	Turkey: Karabük: Yenice	41.21	32.36	T	MTDT9005	LN834733			Present study
Lacerta viridis meridionalis	Turkey: Karabük: Yenice	41.21	32.36	T	MTDT9006	LN834734	—	LN835093	Present study
Lacerta viridis meridionalis	Turkey: Kastamonou: Cide	41.89	33.01	T	MTDT3740	LN834735			Present study
Lacerta viridis meridionalis	Turkey: Ordu: Ünye	41.15	37.29	T	MTDT3729	LN834736			Present study
Lacerta viridis meridionalis	Turkey: Sakarya: Karasu	41.10	30.70	T	MTDT3730	LN834737			Present study
Lacerta viridis meridionalis	Turkey: Sakarya: Karasu	41.10	30.70	T	MTDT3733	LN834738			Present study
Lacerta viridis meridionalis	Turkey: Sakarya: Karasu	41.10	30.70	T	MTDT3734	LN834739			Present study
Lacerta viridis meridionalis	Turkey: Sakarya: Kocaali	41.06	30.85	T	MTDT3731	LN834740			Present study
Lacerta viridis meridionalis	Turkey: Sakarya: Sapanca	40.69	30.26	T	MTDT3736	LN834741			Present study
Lacerta viridis meridionalis	Turkey: Sinop	42.02	35.15	T	MTDT3732	LN834742	—	LN835094	Present study
Lacerta viridis meridionalis	Turkey: Sinop	42.02	35.15	T	NMWYET-2	LN834743			Present study
Lacerta viridis meridionalis	Turkey: Tekirdağ: Sarköy	40.62	27.12	T	MTDT3735	LN834744			Present study
Lacerta viridis meridionalis	Turkey: Tekirdağ: Sarköy	40.62	27.12	T	MTDT3738	LN834745			Present study
Lacerta viridis meridionalis	Turkey: Tekirdağ: Sarköy	40.62	27.12	T	MTDT3741	LN834746			Present study
Lacerta viridis viridis	Austria: Arnoldstein	46.55	13.70	V	NMWYKA-1	LN834747	—	LN835095	Present study
Lacerta viridis viridis	Austria: Gumpoldskirchen	48.05	16.28	V	ZSL329	LN834748			Present study
Lacerta viridis viridis	Austria: Gumpoldskirchen	48.05	16.28	V	ZSL330	LN834749			Present study
Lacerta viridis viridis	Austria: Hundsheim	48.12	16.94	V	NMWYN-1	LN834750			Present study
Lacerta viridis viridis	Austria: Thayatal	48.84	15.88	V	NMWYN-12	LN834751	—	LN835096	Present study
Lacerta viridis viridis	Austria: Weißenkirchen	48.39	15.47	V	ZSL327	LN834752			Present study
Lacerta viridis viridis	Austria: Weißenkirchen	48.39	15.47	V	ZSL328	AM292929			Böhme et al. (2007)
Lacerta viridis viridis	Bosnia and Herzegovina: near Teslič	44.64	17.89	V	MTDT10860	LN834753			Present study
Lacerta viridis viridis	Bulgaria: Ahtopol	42.08	27.95	V	MTDT10968	LN834754			Present study
Lacerta viridis viridis	Bulgaria: Arkutino	42.33	27.73	V	MTDT10965	LN834755			Present study
Lacerta viridis viridis	Bulgaria: Asenovgrad: Asenovitza river	41.98	24.87	V	MTDT10960	LN834756			Present study
Lacerta viridis viridis	Bulgaria: Bladoevgrad: Kresna Gorge	41.80	23.10	V	ZSL363	AM292958			Böhme et al. (2007)
Lacerta viridis viridis	Bulgaria: Bladoevgrad: Kresna Gorge	41.80	23.10	V	ZSL366	LN834757			Present study
Lacerta viridis viridis	Bulgaria: Bladoevgrad: Kresna Gorge	41.80	23.17	V1	ZSL364	LN834758			Present study
Lacerta viridis viridis	Bulgaria: Bladoevgrad: Kresna Gorge	41.80	23.17	V1	ZSL365	LN834759			Present study
Lacerta viridis viridis	Bulgaria: Brodilovo	42.11	27.83	V	MTDT10970	LN834760			Present study
Lacerta viridis viridis	Bulgaria: Burgas: Ropotamo Reserve	42.30	27.68	V	ZSL362	LN834761	—	LN835097	Present study

Appendix *(continued)*

Taxon	Collecting site	Coordinates		Clade	Sample	GenBank accession numbers			Reference
		N	E			Cyt *b*	*β*-fibint7 short allele	*β*-fibint7 long allele	
Lacerta viridis viridis	Bulgaria: Byala Voda	42.18	27.46	V	MTDT10978	LN834762			Present study
Lacerta viridis viridis	Bulgaria: Damyanica: Nožva	41.50	23.28	V1	MTDT10957	LN834763			Present study
Lacerta viridis viridis	Bulgaria: Dupnitica: Saparevo	42.29	23.27	V	ZSL351	LN834764			Present study
Lacerta viridis viridis	Bulgaria: Dupnitica: Smočevo	42.28	23.27	V	ZSL352	LN834765			Present study
Lacerta viridis viridis	Bulgaria: Etropole: Lopian	42.83	24.00	V	ZSL353	LN834766			Present study
Lacerta viridis viridis	Bulgaria: Godeč	43.03	23.05	V	NMWYE-6	LN834767	—	LN835098	Present study
Lacerta viridis viridis	Bulgaria: Gramatikovo	42.03	27.62	V	MTDT10973	LN834768			Present study
Lacerta viridis viridis	Bulgaria: Izgrev	42.12	27.78	V	MTDT10972	LN834769			Present study
Lacerta viridis viridis	Bulgaria: Jasna Poljana	42.27	27.61	V	MTDT10980	LN834770			Present study
Lacerta viridis viridis	Bulgaria: Kašina	41.55	23.48	V1	MTDT2310	LN834771	LN835052 (s1)	LN835111	Present study
Lacerta viridis viridis	Bulgaria: Kašina	41.55	21.37	V1	MTDT2340	LN834772	—	LN835112	Present study
Lacerta viridis viridis	Bulgaria: Lilyanovo	41.61	23.31	V1	MTDT10959	LN834773			Present study
Lacerta viridis viridis	Bulgaria: Lilyanovo	41.61	23.31	V1	MTDT12912	LN834774			Present study
Lacerta viridis viridis	Bulgaria: Malko Tarnovo	41.95	27.57	V	MTDT10975	LN834775			Present study
Lacerta viridis viridis	Bulgaria: near Arkutino	42.35	27.71	V	MTDT10961	LN834776			Present study
Lacerta viridis viridis	Bulgaria: near Arkutino	42.35	27.71	V	MTDT10962	LN834777			Present study
Lacerta viridis viridis	Bulgaria: near Burgas: Otmanli Park	42.43	27.54	V	MTDT10981	LN834778			Present study
Lacerta viridis viridis	Bulgaria: near Ivailovgrad: Meden Buk	41.38	26.04	V	ZSL368	LN834779	LN835046 (s1)	LN835099	Present study
Lacerta viridis viridis	Bulgaria: near Kardzhali: Studen Kladenets	41.61	25.64	V	ZSL367	LN834780			Present study
Lacerta viridis viridis	Bulgaria: near Pleven: Muselievo	43.63	24.85	V	ZSL350	LN834781			Present study
Lacerta viridis viridis	Bulgaria: Pass to Slivarovo	41.99	27.58	V	MTDT10974	LN834782			Present study
Lacerta viridis viridis	Bulgaria: Petrova Niva	42.07	27.52	V	MTDT10977	LN834783			Present study
Lacerta viridis viridis	Bulgaria: Pirin	41.76	23.40	V1	MTDT2311	LN834784	—	LN835113	Present study
Lacerta viridis viridis	Bulgaria: Pirin	41.76	23.40	V1	MTDT2312	LN834785			Present study
Lacerta viridis viridis	Bulgaria: Pirin	41.76	23.40	V1	MTDT2313	LN834786	LN835053 (s1)	LN835114	Present study
Lacerta viridis viridis	Bulgaria: Pismenovo	42.20	27.66	V	MTDT10979	LN834787			Present study
Lacerta viridis viridis	Bulgaria: Primorsko	42.29	27.75	V	MTDT10964	LN834788			Present study
Lacerta viridis viridis	Bulgaria: Primorsko	42.29	27.75	V	MTDT10966	LN834789			Present study
Lacerta viridis viridis	Bulgaria: Primorsko	42.29	27.75	V	MTDT10967	LN834790			Present study
Lacerta viridis viridis	Bulgaria: Rezovo	41.99	28.02	V	MTDT10969	LN834791			Present study
Lacerta viridis viridis	Bulgaria: Ropotamo	42.30	27.73	V	MTDT10963	LN834792			Present study
Lacerta viridis viridis	Bulgaria: Shumen	43.26	26.89	V	MTDT10624	LN834793			Present study
Lacerta viridis viridis	Bulgaria: Sofia: Vladaya	42.63	23.20	V	ZSL354	LN834794			Present study
Lacerta viridis viridis	Bulgaria: Sozopol	42.40	27.69	V	MTDT12913	LN834795			Present study
Lacerta viridis viridis	Bulgaria: Sozopol	42.40	27.69	V	MTDT12939	LN834796			Present study
Lacerta viridis viridis	Bulgaria: Varvara	42.15	24.14	V	MTDT10958	LN834797			Present study
Lacerta viridis viridis	Bulgaria: Zhelezino	41.48	25.95	V	MTDT2339	LN834798			Present study
Lacerta viridis viridis	Bulgaria: Zvezdets	42.11	27.41	V	MTDT10976	LN834799			Present study
Lacerta viridis viridis	Czech Republic: Bohemia: Karlík	49.94	14.26	V	ZSL320	LN834800			Present study
Lacerta viridis viridis	Czech Republic: Bohemia: Křivoklát	50.04	13.87	V	ZSL318	AM087299			Böhme et al. (2007)
Lacerta viridis viridis	Czech Republic: Bohemia: Křivoklát	50.04	13.87	V	ZSL319	LN834801			Present study
Lacerta viridis viridis	Czech Republic: Bohemia: Praha-Roztoky	50.15	14.37	V	MTDT11608	LN834806			Present study
Lacerta viridis viridis	Czech Republic: Moravia: Bzenec	48.97	17.27	V	ZSL325	LN834802			Present study
Lacerta viridis viridis	Czech Republic: Moravia: Bzenec	48.97	17.27	V	ZSL326	LN834803			Present study
Lacerta viridis viridis	Czech Republic: Moravia: Pavlovské kopce	48.87	16.66	V	ZSL321	AM087308			Böhme et al. (2007)
Lacerta viridis viridis	Czech Republic: Moravia: Pavlovské kopce	48.87	16.66	V	ZSL322	LN834805			Present study

Appendix *(continued)*

Taxon	Collecting site	Coordinates N	Coordinates E	Clade	Sample	GenBank accession numbers Cyt *b*	GenBank accession numbers β-fibint7 short allele	GenBank accession numbers β-fibint7 long allele	Reference
Lacerta viridis viridis	Czech Republic: Moravia: Podyjí National Park	48.83	15.98	V	ZSL323	LN834804			Present study
Lacerta viridis viridis	Czech Republic: Moravia: Podyjí National Park	48.83	15.98	V	ZSL324	AM087326			Böhme et al. (2007)
Lacerta viridis viridis	FYROM: Dojran Lake	42.15	22.03	V	ZSL346	LN834807			Present study
Lacerta viridis viridis	FYROM: Dojran Lake	42.15	22.03	V	ZSL347	LN834808			Present study
Lacerta viridis viridis	FYROM: Dojran Lake	42.15	22.03	V	ZSL348	LN834809			Present study
Lacerta viridis viridis	FYROM: Matka	41.96	21.30	V1	MTDT12933	LN834810			Present study
Lacerta viridis viridis	FYROM: Matka	41.96	21.30	V1	MTDT12927	LN834812			Present study
Lacerta viridis viridis	FYROM: Matka	41.96	21.30	V1	MTDT12928	LN834813			Present study
Lacerta viridis viridis	FYROM: Nikolič	41.25	22.74	V	MTDT12922	LN834814			Present study
Lacerta viridis viridis	FYROM: Nikolič	41.25	22.74	V	MTDT12923	LN834815			Present study
Lacerta viridis viridis	FYROM: Prespansko jezero, Gorno Perovo	41.03	20.99	V1	MTDT12924	LN834811			Present study
Lacerta viridis viridis	FYROM: Prespansko jezero, Stenje	40.95	20.90	V1	MTDT12925	LN834818			Present study
Lacerta viridis viridis	FYROM: Ribnica	41.72	20.60	V1	MTDT12934	LN834816			Present study
Lacerta viridis viridis	FYROM: Rotino	41.06	21.21	V1	MTDT12940	LN834817			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lausitz	—	—	V	—	AF233426			Brückner et al. (2001)
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6880	LN834819			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6882	LN834820			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6884	LN834821			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6885	LN834822			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6886	LN834823			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6888	LN834824			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6889	LN834825			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6890	LN834826			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6891	LN834827			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6892	LN834828			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6893	LN834829			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6894	LN834830			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6895	LN834831			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6896	LN834832			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6898	LN834833			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6899	LN834834			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6900	LN834835			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6901	LN834836			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6902	LN834837			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6905	LN834838			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6906	LN834839			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6910	LN834840			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6911	LN834841			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6912	LN834842			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6915	LN834843			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6916	LN834844			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6919	LN834845			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6920	LN834846			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6925	LN834847			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6926	LN834848			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6927	LN834849			Present study

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Appendix *(continued)*

		Coordinates				GenBank accession numbers			
Taxon	Collecting site	N	E	Clade	Sample	Cyt *b*	β-fibint7 short allele	β-fibint7 long allele	Reference
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6931	LN834850			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6934	LN834851			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6942	LN834852			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6943	LN834853			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6944	LN834854			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT6945	LN834855			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT9992	LN834856			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT9993	LN834857			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT9994	LN834858			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT9995	LN834859			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT9996	LN834860			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT9997	LN834861			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT9998	LN834862			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT9999	LN834863			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10000	LN834864			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10001	LN834865			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10002	LN834866			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10004	LN834867			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10005	LN834868			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10006	LN834869			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10007	LN834870			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10009	LN834871			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10010	LN834872			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10011	LN834873			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10012	LN834874			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10013	LN834875			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10014	LN834876			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10015	LN834877			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10016	LN834878			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10017	LN834879			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10018	LN834880			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10019	LN834881			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10020	LN834882			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10021	LN834883			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10022	LN834884			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10023	LN834885			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10024	LN834886			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10027	LN834887			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10028	LN834888			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10029	LN834889			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10030	LN834890			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10031	LN834891			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10032	LN834892			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10033	LN834893			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10034	LN834894			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10035	LN834895			Present study

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Appendix *(continued)*

		Coordinates				GenBank accession numbers			
Taxon	Collecting site	N	E	Clade	Sample	Cyt *b*	β-fibint7 short allele	β-fibint7 long allele	Reference
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10036	LN834896			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10037	LN834897			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10038	LN834898			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10040	LN834899			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10041	LN834900			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10042	LN834901			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10043	LN834902	—	LN835101	Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10044	LN834903			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10045	LN834904			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10046	LN834905			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10047	LN834906			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10048	LN834907			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10049	LN834908	—	LN835102	Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10050	LN834909			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10051	LN834910			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10052	LN834911			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10053	LN834912			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10054	LN834913			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10055	LN834914			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10056	LN834915			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10057	LN834916			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10058	LN834917			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10059	LN834918			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10060	LN834919			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10061	LN834920			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10062	LN834921			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10063	LN834922			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	MTDT10064	LN834923			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	ZSL310	AM087289			Böhme et al. (2007)
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	ZSL311	LN834924			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	ZSL312	AM87297			Böhme et al. (2007)
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	ZSL313	LN834925			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	ZSL314	AM087294			Böhme et al. (2007)
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	ZSL316	LN834926			Present study
Lacerta viridis viridis	Germany: Brandenburg: Lübbenau	51.86	13.95	V	ZSL317	LN834927			Present study
Lacerta viridis viridis	Greece: 50 km NW Alexandroupoli	41.25	25.55	V1	MTDT3724	LN834928	—	LN835107	Present study
Lacerta viridis viridis	Greece: Amfipoli: Strimonas river	40.82	23.84	V	MTDT10852	LN834929			Present study
Lacerta viridis viridis	Greece: Dadia	41.14	26.26	V	MTDT10622	LN834930			Present study
Lacerta viridis viridis	Greece: Doirani	41.18	22.76	V	NMWYZ-10	LN834931	—	LN835103	Present study
Lacerta viridis viridis	Greece: Drama (Makedonia)	41.15	24.15	V	—	KJ940322			Sagonas et al. (2014)
Lacerta viridis viridis	Greece: Drama (Makedonia)	41.15	24.15	V	—	KJ940321			Sagonas et al. (2014)
Lacerta viridis viridis	Greece: Drama (Makedonia)	41.15	24.15	V	—	KJ940320			Sagonas et al. (2014)
Lacerta viridis viridis	Greece: Drama (Makedonia)	41.15	24.15	V	—	KJ940319			Sagonas et al. (2014)
Lacerta viridis viridis	Greece: Drama (Makedonia)	41.15	24.15	V	—	KJ940318			Sagonas et al. (2014)
Lacerta viridis viridis	Greece: Euboea	38.50	24.00	V1	MTDT3717	LN834932			Present study
Lacerta viridis viridis	Greece: Evros (Thrace)	41.00	26.00	V	—	KJ940312			Sagonas et al. (2014)

Appendix *(continued)*

		Coordinates				GenBank accession numbers			
Taxon	Collecting site	N	E	Clade	Sample	Cyt *b*	*β*-fibint7 short allele	*β*-fibint7 long allele	Reference
Lacerta viridis viridis	Greece: Florina	40.78	21.41	V	MTDT11218	LN834933			Present study
Lacerta viridis viridis	Greece: Florina	40.78	21.41	V	MTDT11219	LN834934			Present study
Lacerta viridis viridis	Greece: Giannouli	39.67	22.39	V	NMWYE-1	AM087228	LN835040 (s1)	LN835105	Böhme et al. (2007)
Lacerta viridis viridis	Greece: Giannouli	39.67	22.39	V	NMWYE-2	AM292962	LN835049 (s1)	LN835106	Böhme et al. (2007)
Lacerta viridis viridis	Greece: Giannouli	39.67	22.39	V	NMWYE-3	LN834935			Present study
Lacerta viridis viridis	Greece: Kavala (Makedonia)	40.94	24.41	V	—	KJ940317			Sagonas et al. (2014)
Lacerta viridis viridis	Greece: Kavala (Makedonia)	40.94	24.41	V	—	KJ940316			Sagonas et al. (2014)
Lacerta viridis viridis	Greece: Larissa (Thessaly)	39.64	22.42	V1	—	KJ940328			Sagonas et al. (2014)
Lacerta viridis viridis	Greece: Larissa (Thessaly)	39.64	22.42	V1	—	KJ940327			Sagonas et al. (2014)
Lacerta viridis viridis	Greece: Metsovo	39.77	21.18	V1	NMWYME-1	LN834936			Present study
Lacerta viridis viridis	Greece: Mikri Prespa	40.76	21.07	V1	NMWXMP-1	LN834937	—	LN835115	Present study
Lacerta viridis viridis	Greece: Mikri Prespa	40.76	21.07	V1	NMWYP-1	LN834938	—	LN835116	Present study
Lacerta viridis viridis	Greece: Mt. Olympus	40.11	22.36	V1	NMWOY-18	LN834939			Present study
Lacerta viridis viridis	Greece: Othris	39.08	22.71	V	NMWYOT-1	LN834940			Present study
Lacerta viridis viridis	Greece: Pierias (Makedonia)	40.10	22.50	V1	—	KJ940323			Sagonas et al. (2014)
Lacerta viridis viridis	Greece: Pilio	39.44	23.05	V	NMWYPL-1	LN834941			Present study
Lacerta viridis viridis	Greece: Rodopi (Thrace)	41.50	24.50	V	—	KJ940313			Sagonas et al. (2014)
Lacerta viridis viridis	Greece: Samothraki	40.47	25.53	V	NMWYA-6	LN834942			Present study
Lacerta viridis viridis	Greece: Samothraki island	40.47	25.53	V	—	KJ940315			Sagonas et al. (2014)
Lacerta viridis viridis	Greece: Samothraki island	40.47	25.53	V	—	KJ940314			Sagonas et al. (2014)
Lacerta viridis viridis	Greece: Thasos	40.78	24.71	V	NMWYS-11	LN834943			Present study
Lacerta viridis viridis	Greece: Trikala (Thessaly)	39.56	21.77	V1	—	KJ940326			Sagonas et al. (2014)
Lacerta viridis viridis	Greece: Trikala (Thessaly)	39.56	21.77	V1	—	KJ940325			Sagonas et al. (2014)
Lacerta viridis viridis	Greece: Trikala (Thessaly)	39.56	21.77	V1	—	KJ940324			Sagonas et al. (2014)
Lacerta viridis viridis	Greece: Zagkliveri	40.57	23.29	V1	NMWYZ-9	AM292965	LN835054 (s1)	LN835117	Böhme et al. (2007)
Lacerta viridis viridis	Hungary: Balaton, Tihany	46.91	17.87	V	ZSL335	AM292937			Böhme et al. (2007)
Lacerta viridis viridis	Hungary: Bugac Puszta	46.67	19.63	V	ZSL336	AM087314			Böhme et al. (2007)
Lacerta viridis viridis	Hungary: Bugac Puszta	46.67	19.63	V	ZSL338	AM292939			Böhme et al. (2007)
Lacerta viridis viridis	Hungary: Dabas	47.18	19.30	V	MTDT12935	LN834944			Present study
Lacerta viridis viridis	Hungary: Gödöllő	47.60	19.35	V	ZSL332	AM087321			Böhme et al. (2007)
Lacerta viridis viridis	Hungary: Gödöllő	47.60	19.35	V	ZSL333	LN834945			Present study
Lacerta viridis viridis	Hungary: Gödöllő	47.60	19.35	V	ZSL334	AM087302			Böhme et al. (2007)
Lacerta viridis viridis	Hungary: Kecskemét	46.91	19.68	V	—	AF233425			Brückner et al. (2001)
Lacerta viridis viridis	Hungary: Kunpeszér	47.07	19.26	V	MTDT11606	LN834946			Present study
Lacerta viridis viridis	Hungary: Pécs	46.07	18.23	V	ZSL339	LN834947			Present study
Lacerta viridis viridis	Hungary: Villány	45.87	18.46	V	MTDT7579	LN834948			Present study
Lacerta viridis viridis	Hungary: Villány	45.87	18.46	V	MTDT7580	LN834949			Present study
Lacerta viridis viridis	Hungary: Villány	45.87	18.46	V	MTDT7581	LN834950			Present study
Lacerta viridis viridis	Hungary: Villány	45.87	18.46	V	MTDT7583	LN834951			Present study
Lacerta viridis viridis	Hungary: Villány	45.87	18.46	V	MTDT7587	LN834952			Present study
Lacerta viridis viridis	Hungary: Villány	45.87	18.46	V	MTDT7589	LN834953			Present study
Lacerta viridis viridis	Hungary: Villány	45.87	18.46	V	MTDT7590	LN834954			Present study
Lacerta viridis viridis	Hungary: Villány	45.87	18.46	V	MTDT7591	LN834955			Present study
Lacerta viridis viridis	Hungary: Villány	45.87	18.46	V	NMWYB-2	LN834956	—	LN835108	Present study
Lacerta viridis viridis	Montenegro: Ćeklići	42.45	18.87	V2	ZSL381	LN834957			Present study
Lacerta viridis viridis	Montenegro: Ćeklići	42.45	18.87	V2	ZSL382	LN834958	LN835055 (s2)	LN835118	Present study

Appendix (*continued*)

		Coordinates				GenBank accession numbers			
Taxon	Collecting site	N	E	Clade	Sample	Cyt *b*	β-fibint7 short allele	β-fibint7 long allele	Reference
Lacerta viridis viridis	Montenegro: Radovići	42.39	18.67	V	ZSL349	LN834959			Present study
Lacerta viridis viridis	Romania: between Ciuguzel and Cicărd	46.27	23.90	V	MTDT10861	LN834960			Present study
Lacerta viridis viridis	Romania: Căpușu Mare	46.79	23.32	V	MTDT10621	LN834961			Present study
Lacerta viridis viridis	Romania: Cluj-Napoca	46.81	23.62	V	MTDT10620	LN834962			Present study
Lacerta viridis viridis	Romania: Lopadea Nouă	46.29	23.84	V	MTDT10623	LN834963			Present study
Lacerta viridis viridis	Romania: Măcin	45.25	28.14	V	NMWYRT-2	LN834964			Present study
Lacerta viridis viridis	Romania: Tulcea	45.18	28.81	V	NMWYRT-3	LN834965	—	LN835109	Present study
Lacerta viridis viridis	Romania: Turcoaia	45.10	28.18	V	NMWXR-2	LN834966	LN835050 (s1)	—	Present study
Lacerta viridis viridis	Serbia: Baljevac	43.39	20.63	V	ZSL343	LN834967			Present study
Lacerta viridis viridis	Serbia: Baljevac	43.39	20.63	V	ZSL344	LN834968			Present study
Lacerta viridis viridis	Serbia: Donji Dušnik	43.16	22.10	V	MTDT12930	LN834969			Present study
Lacerta viridis viridis	Serbia: Leskovac	43.00	21.95	V	ZSL345	LN834970			Present study
Lacerta viridis viridis	Serbia: Prohor	42.32	21.90	V	MTDT12914	LN834971			Present study
Lacerta viridis viridis	Serbia: Prohor	42.32	21.90	V	MTDT12915	LN834972			Present study
Lacerta viridis viridis	Serbia: Prohor	42.32	21.90	V	MTDT12916	LN834973			Present study
Lacerta viridis viridis	Serbia: Prohor	42.32	21.90	V	MTDT12917	LN834974			Present study
Lacerta viridis viridis	Serbia: Prohor	42.32	21.90	V	MTDT12918	LN834975			Present study
Lacerta viridis viridis	Serbia: Prohor	42.32	21.90	V	MTDT12919	LN834976			Present study
Lacerta viridis viridis	Serbia: Prohor	42.32	21.90	V	MTDT12920	LN834977			Present study
Lacerta viridis viridis	Serbia: Prohor	42.32	21.90	V	MTDT12921	LN834978			Present study
Lacerta viridis viridis	Serbia: Sopotnica	43.16	22.13	V	MTDT12931	LN834979			Present study
Lacerta viridis viridis	Serbia: Sopotnica	43.16	22.13	V	MTDT12932	LN834980			Present study
Lacerta viridis viridis	Serbia: Višnjica	44.83	20.55	V	MTDT6908	LN834981			Present study
Lacerta viridis viridis	Serbia: Višnjica	44.83	20.55	V	MTDT6913	LN834982			Present study
Lacerta viridis viridis	Serbia: Višnjica	44.83	20.55	V	MTDT6914	LN834983			Present study
Lacerta viridis viridis	Serbia: Višnjica	44.83	20.55	V	MTDT6928	LN834984			Present study
Lacerta viridis viridis	Serbia: Višnjica	44.83	20.55	V	MTDT6933	LN834985			Present study
Lacerta viridis viridis	Serbia: Višnjica	44.83	20.55	V	MTDT6939	LN834986			Present study
Lacerta viridis viridis	Serbia: Vrsacki breg	45.13	21.36	V	ZSL340	LN834987			Present study
Lacerta viridis viridis	Serbia: Vrsacki breg	45.13	21.36	V	ZSL341	AM292934			Böhme et al. (2007)
Lacerta viridis viridis	Serbia: Vrsacki breg	45.13	21.36	V	ZSL342	LN834988			Present study
Lacerta viridis viridis	Slovakia: Bratislava, Devínska Kobyla	48.19	16.99	V	MTDT10956	LN834989			Present study
Lacerta viridis viridis	Slovakia: Čabrad’	48.25	19.11	V	ZSL306	LN834990			Present study
Lacerta viridis viridis	Slovakia: Čabrad’	48.25	19.11	V	ZSL307	LN834991			Present study
Lacerta viridis viridis	Slovakia: Kamenica nad Hronom	47.83	18.74	V	MTDT10619	LN834992			Present study
Lacerta viridis viridis	Slovakia: Slovenský kras	48.58	20.58	V	ZSL304	LN834993			Present study
Lacerta viridis viridis	Slovakia: Slovenský kras	48.58	20.58	V	ZSL305	LN834994			Present study
Lacerta viridis viridis	Slovakia: Slovenský kras National Park: Zádiel	48.62	20.84	V	MTDT10618	LN834997			Present study
Lacerta viridis viridis	Slovakia: Streda nad Bodrogom: Tajba	48.39	21.77	V	ZSL308	LN834995			Present study
Lacerta viridis viridis	Slovakia: Streda nad Bodrogom: Tajba	48.39	21.77	V	ZSL309	LN834996			Present study
Lacerta viridis viridis	Slovenia: Bodonci	46.75	16.12	V	MTDT10475	LN834998			Present study
Lacerta viridis viridis	Slovenia: Bodonci	46.75	16.12	V	MTDT10476	LN834999			Present study
Lacerta viridis viridis	Slovenia: Bohinj	46.31	13.96	V2	MTDT7172	LN835000	LN835056 (s2)	LN835119	Present study
Lacerta viridis viridis	Slovenia: Kostel, Sveti Štefan	45.51	14.91	V2	MTDT10075	LN835001	—	LN835120	Present study
Lacerta viridis viridis	Slovenia: Lastomerci	46.64	15.95	V	MTDT10074	LN835002			Present study
Lacerta viridis viridis	Slovenia: Maribor	46.58	15.65	V	MTDT3756	LN835003			Present study

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Appendix *(continued)*

Taxon	Collecting site	Coordinates N	Coordinates E	Clade	Sample	GenBank accession numbers Cyt *b*	GenBank accession numbers β-fibint7 short allele	GenBank accession numbers β-fibint7 long allele	Reference
Lacerta viridis viridis	Slovenia: Maribor	46.58	15.65	V	MTDT3758	LN835004			Present study
Lacerta viridis viridis	Slovenia: Maribor	46.58	15.65	V	ZSL331	AM292954			Böhme et al. (2007)
Lacerta viridis viridis	Turkey: Edirne: Enez	40.72	26.08	V	MTDT9008	LN835005	LN835051 (s1)	LN835110	Present study
Lacerta viridis viridis	Ukraine: 70 km SE Kiev along Dnieper	50.01	30.98	V	ZSL361	LN835006			Present study
Lacerta viridis viridis	Ukraine: Kaniv	49.75	31.48	V	ZSL358	LN835007			Present study
Lacerta viridis viridis	Ukraine: Kaniv	49.75	31.48	V	ZSL359	LN835008			Present study
Lacerta viridis viridis	Ukraine: Kaniv	49.75	31.48	V	ZSL360	LN835009			Present study
Lacerta viridis viridis	Ukraine: near Myhiya	48.04	30.95	V	MTDT2349	LN835010			Present study
Lacerta viridis viridis	Ukraine: near Myhiya	48.04	30.95	V	MTDT2350	LN835011			Present study
Lacerta viridis viridis	Ukraine: near Myhiya	48.04	30.95	V	MTDT2351	LN835012			Present study
Lacerta viridis viridis	Ukraine: near Myhiya	48.04	30.95	V	MTDT2352	LN835013			Present study
Lacerta viridis viridis	Ukraine: near Myhiya	48.04	30.95	V	MTDT2353	LN835014			Present study
Lacerta viridis viridis	Ukraine: near Myhiya	48.04	30.95	V	MTDT2354	LN835015			Present study
Lacerta viridis viridis	Ukraine: Pervomays'k	48.04	30.86	V	ZSL355	LN835016			Present study
Lacerta viridis viridis	Ukraine: Pervomays'k	48.04	30.86	V	ZSL356	LN835017			Present study
Lacerta viridis viridis	Ukraine: Pervomays'k	48.04	30.86	V	ZSL357	LN835018			Present study
Outgroups									
Lacerta agilis	Austria: Weitra	48.70	14.89	—	NMWWT-1	LN835019			Present study
Lacerta agilis	Czech Republic: Bohemia: Praha-Roztoky	50.16	14.39	—	MTDT12929	LN835020			Present study
Lacerta agilis	Germany: Saxony-Anhalt: Bernburg	51.80	11.73	—	ZSL378	AM292994			Böhme et al. (2007)
Lacerta media	Turkey: Kahramanmaraş	37.58	36.93	—	NMWXKM-1	LN835021			Present study
Lacerta schreiberi	Spain: Covadonga	43.31	−5.05	—	NMWES-2	LN835023			Present study
Lacerta strigata	Georgia: Tbilisi	41.71	44.79	—	NMWGT-3	LN835024			Present study
Lacerta trilineata	Albania: Vagalat	39.74	20.13		MTDT11611	LN835025			Present study
Lacerta trilineata	Albania: Vagalat	39.74	20.13		MTDT11612	LN835026			Present study
Lacerta trilineata	Albania: Vagalat	39.74	20.13		MTDT11613	LN835027			Present study
Lacerta trilineata	Croatia: Krk	45.09	14.61		—	AF233427			Brückner et al. (2001)
Lacerta trilineata	Greece: Immitos	37.96	23.81		NMWXH-1	LN835028			Present study
Lacerta trilineata	Greece: Gialova (Peloponnese)	36.95	21.70		MTDT10851	LN835029			Present study
Timon lepidus	Spain: Alicante	38.36	−0.49		—	GQ142119			Pavlicev and Mayer (2009)

Sample codes: IÖE – Institut für Ökologie und Evolutionsbiologie, Universität Bremen; MTDT – Museum of Zoology, Senckenberg Dresden; NMW – Naturhistorisches Museum Wien; ZSL – Institut of Biology (Molecular Evolution/Animal Systematics), Leipzig University.

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