

Supplemental Information for:**Phylogeography of a cryptic speciation continuum in Eurasian spadefoot toads
(*Pelobates*)**

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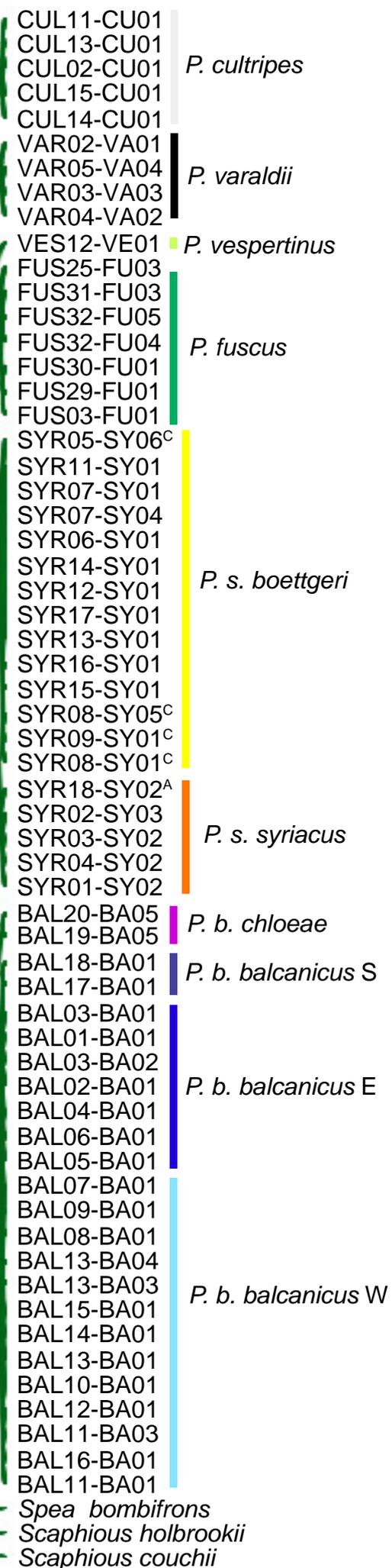


Fig. S1a: Sampled phylogenetic trees of concatenated *cyt-b* + 16S mitochondrial haplotypes.
^C: private *P. s. boettgeri* haplotypes from the Caucasus. ^A: private *P. s. syriacus* haplotype from Anatolia.

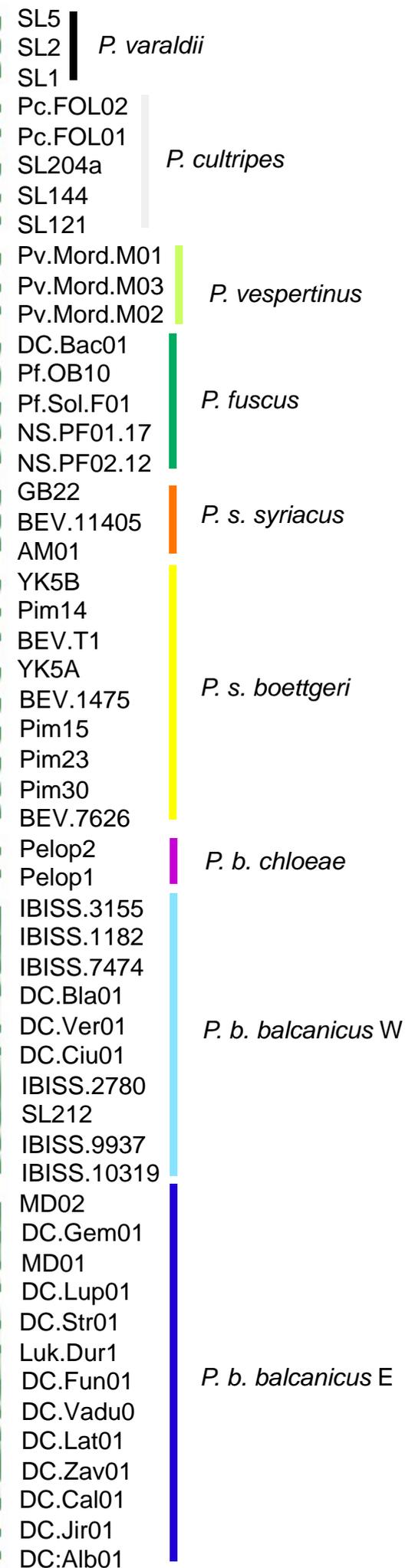


Fig. S1b: Sampled phylogenetic trees of concatenated nuclear RAD sequences.

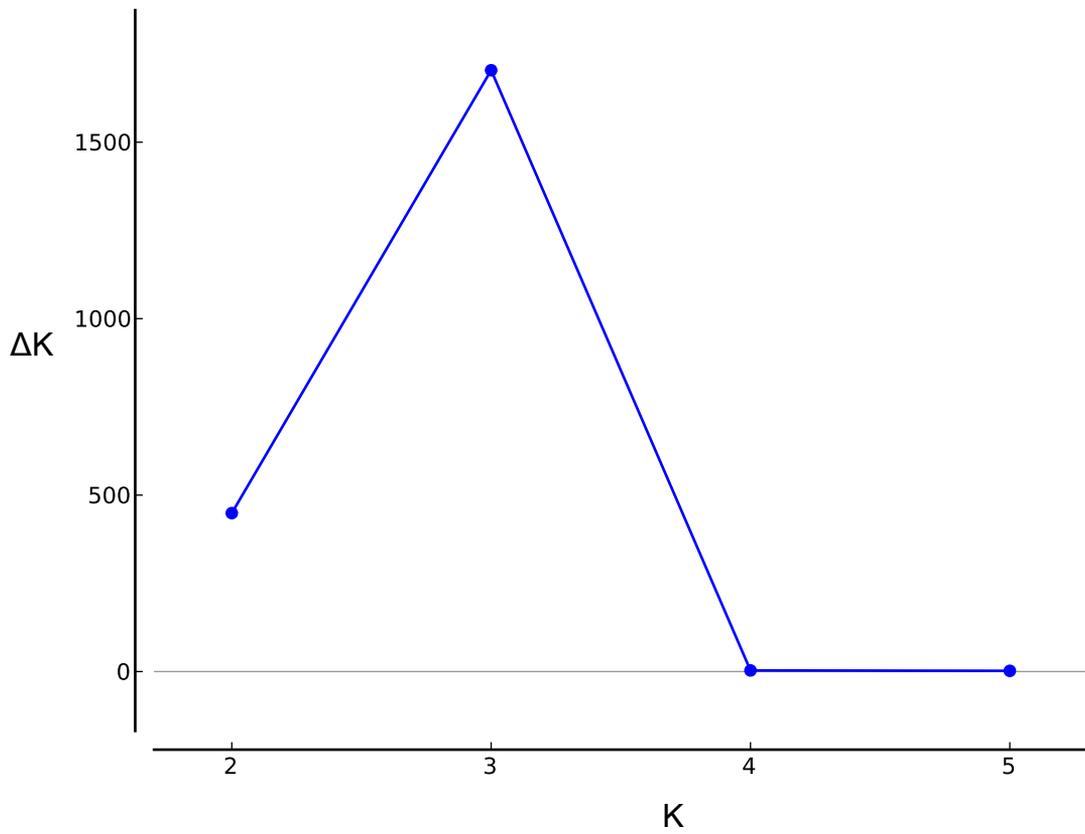
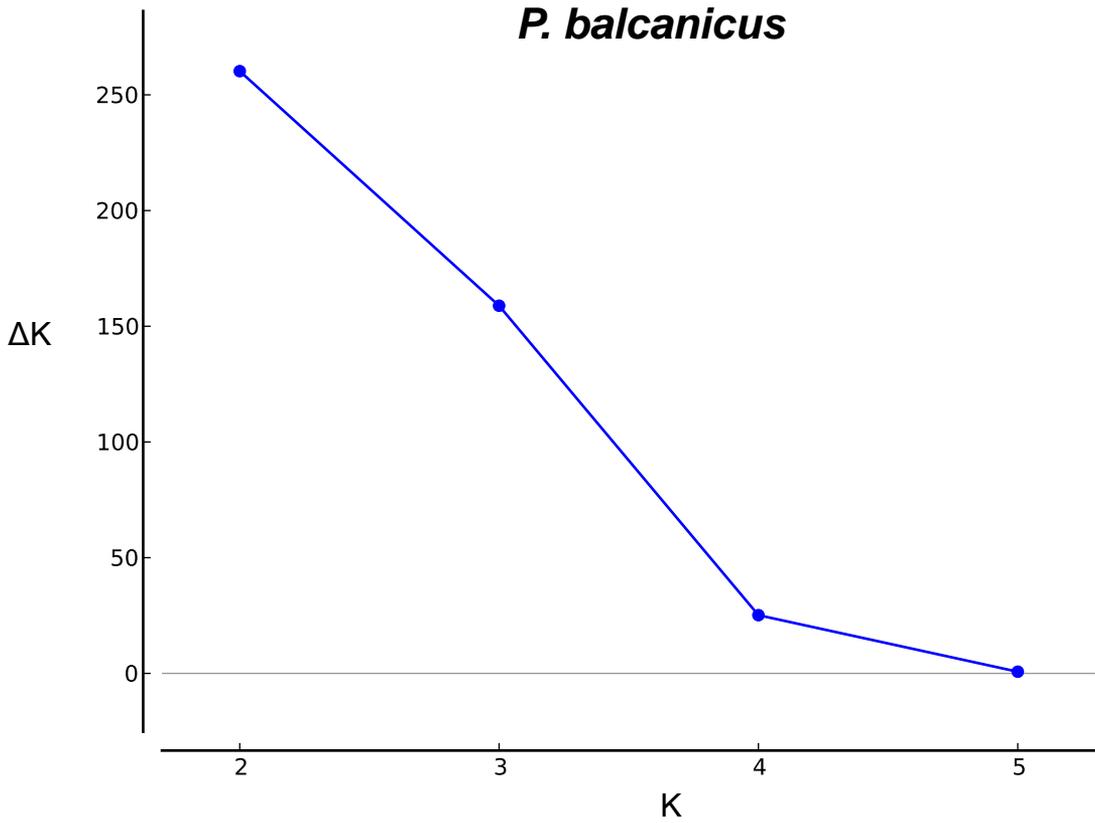
P. syriacus s. s.***P. balcanicus***

Fig. S2: ΔK statistics for intraspecific STRUCTURE analyses of *P. syriacus s. s.* and *P. balcanicus*.

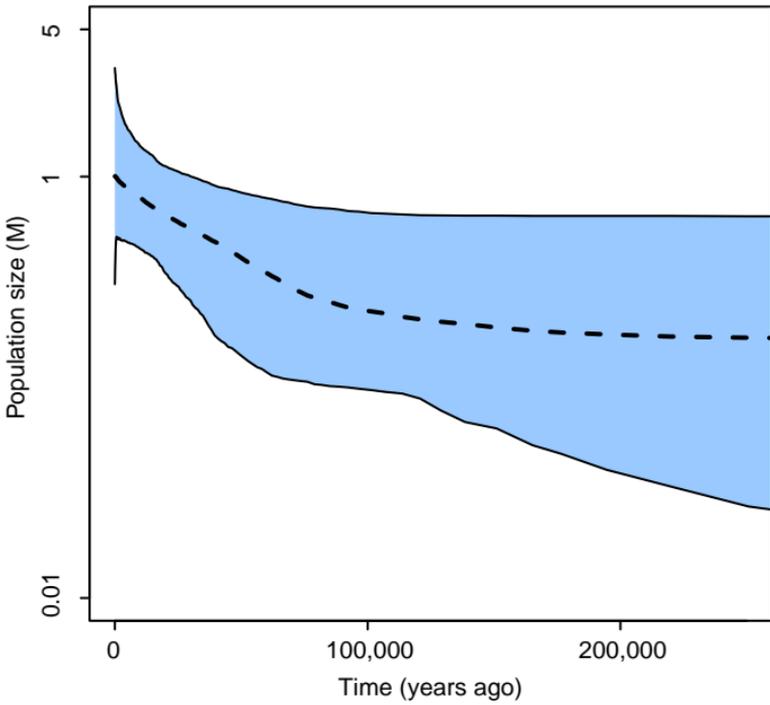
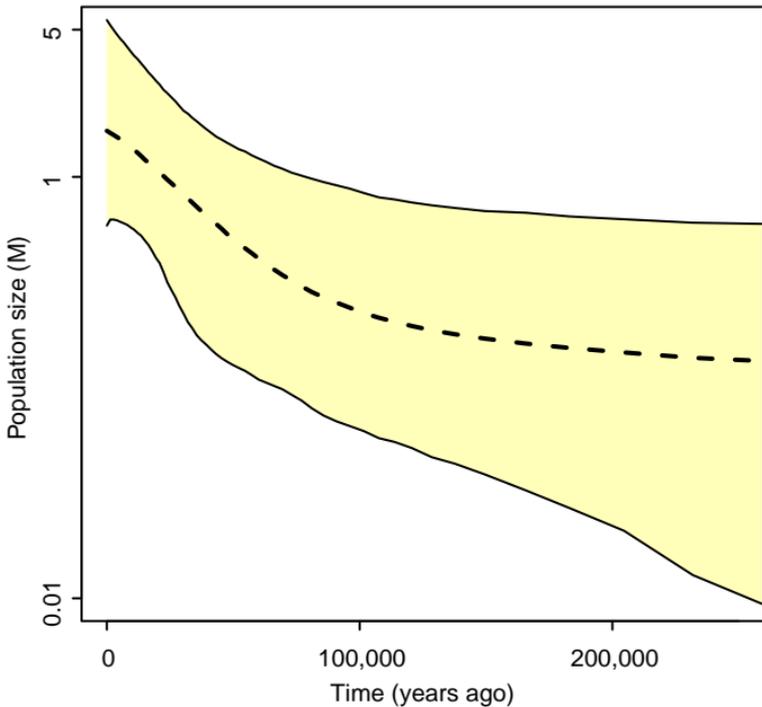
P. balcanicus balcanicus***P. syriacus boettgeri***

Fig. S3: Demographic reconstructions with the Extended Bayesian Skyline Plot (EBS) for the widely distributed *P. b. balcanicus* (loc. 24-64, top panel) and *P. s. boettgeri* (loc. 10-23, bottom panel). The former is based on 38 samples sequenced for 1.3Mb of nuclear RAD tags and 166 samples sequenced for 1.2kb of mtDNA. The latter is based on 20 samples sequenced for 1.9kb of nuclear RAD tags and 39 samples for 1.2kb of mtDNA.

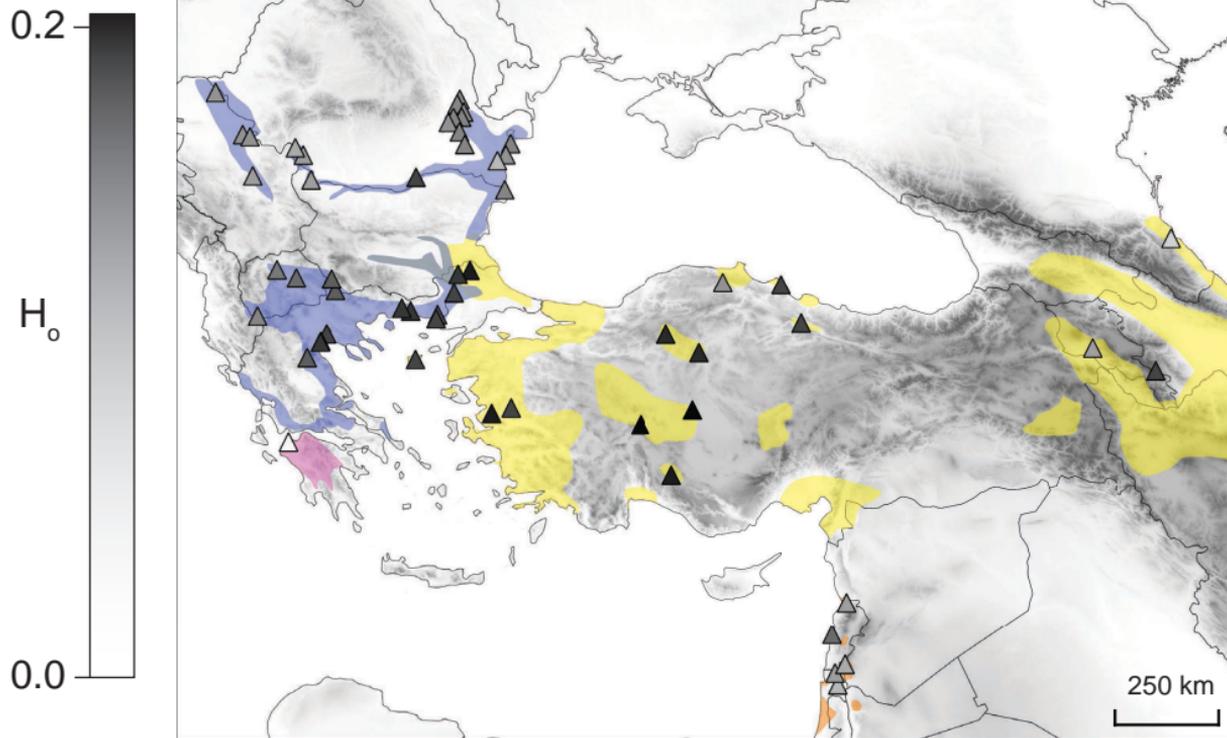


Fig. S4: Distribution of the nuclear genetic diversity (observed heterozygosity H_o) of *P. balcanicus* (blue / purple) and *P. syriacus* s. s. (orange / yellow).