

**OPEN** **Publisher Correction:****Reconstructing hotspots of genetic diversity from glacial refugia and subsequent dispersal in Italian common toads (*Bufo bufo*)**

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The original version of this Article contained an error in Figure 1 and Figure 3 where parts of the figures were incorrectly captured. The original Figure 1 and Figure 3 and accompanying legends appear below.

The original Article has been corrected.

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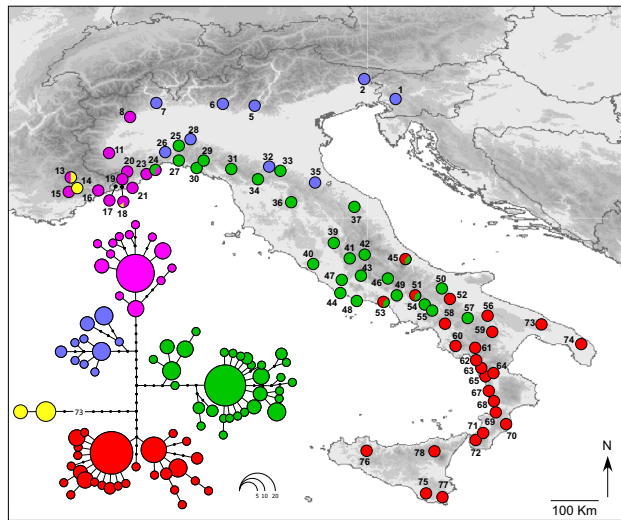


Figure 1. Maximum likelihood phylogenetic network of the *Bufo bufo* mitochondrial haplotypes found in Italy, and geographic distribution of the main haplotype groups. Circle sizes are proportional to haplotype frequency, and black dots represents missing intermediate haplotypes. Populations are numbered as in Table 1. The map was drawn using the software Canvas 11 (ACD Systems of America, Inc.).

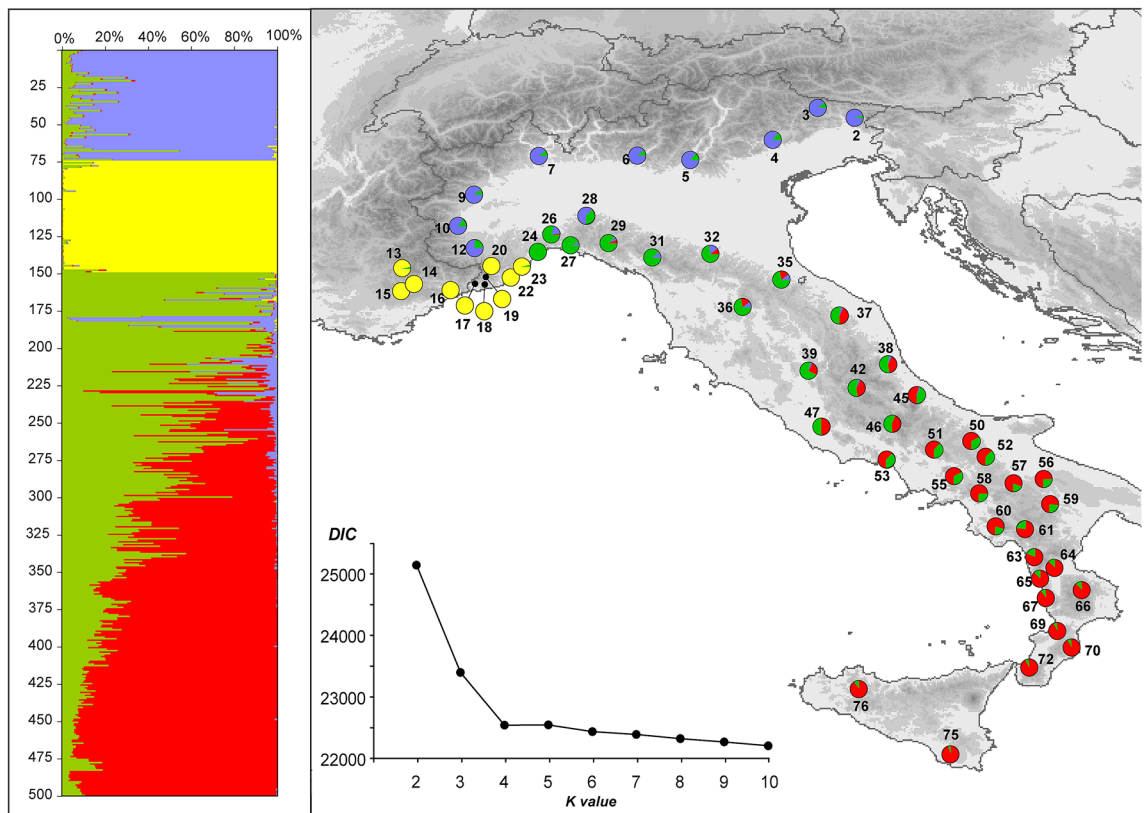


Figure 3. Genetic structure of the Italian *Bufo bufo* populations, as inferred by the Bayesian clustering analysis implemented in TESS based on eight microsatellite loci. The bar plot on the left shows the admixture proportions of each individual for the four genetic clusters identified; the pie diagrams on the maps show the frequency of each cluster within the studied populations. Populations are numbered as in Table 1. The line chart shows values of the deviance information criterion (DIC) statistics estimated for models with the number of genetic clusters (K) ranging from 2 to 10. The map was drawn using the software Canvas 11 (ACD Systems of America, Inc.).



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