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ERRATUM

Erratum to: Population genetics of pike, genus *Esox* (Actinopterygii, Esocidae), in Northern Italy: evidence for mosaic distribution of native, exotic and introgressed populations

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Due to an unfortunate mistake during the production process of the original publication, Fig. 5 became distorted causing illegible legends in the subfigures b, c1, d1, e1 and e2. The correct image and its caption is published here and should be treated as definitive by the reader.

The online version of the original article can be found under doi:10.1007/s10750-016-3083-1.

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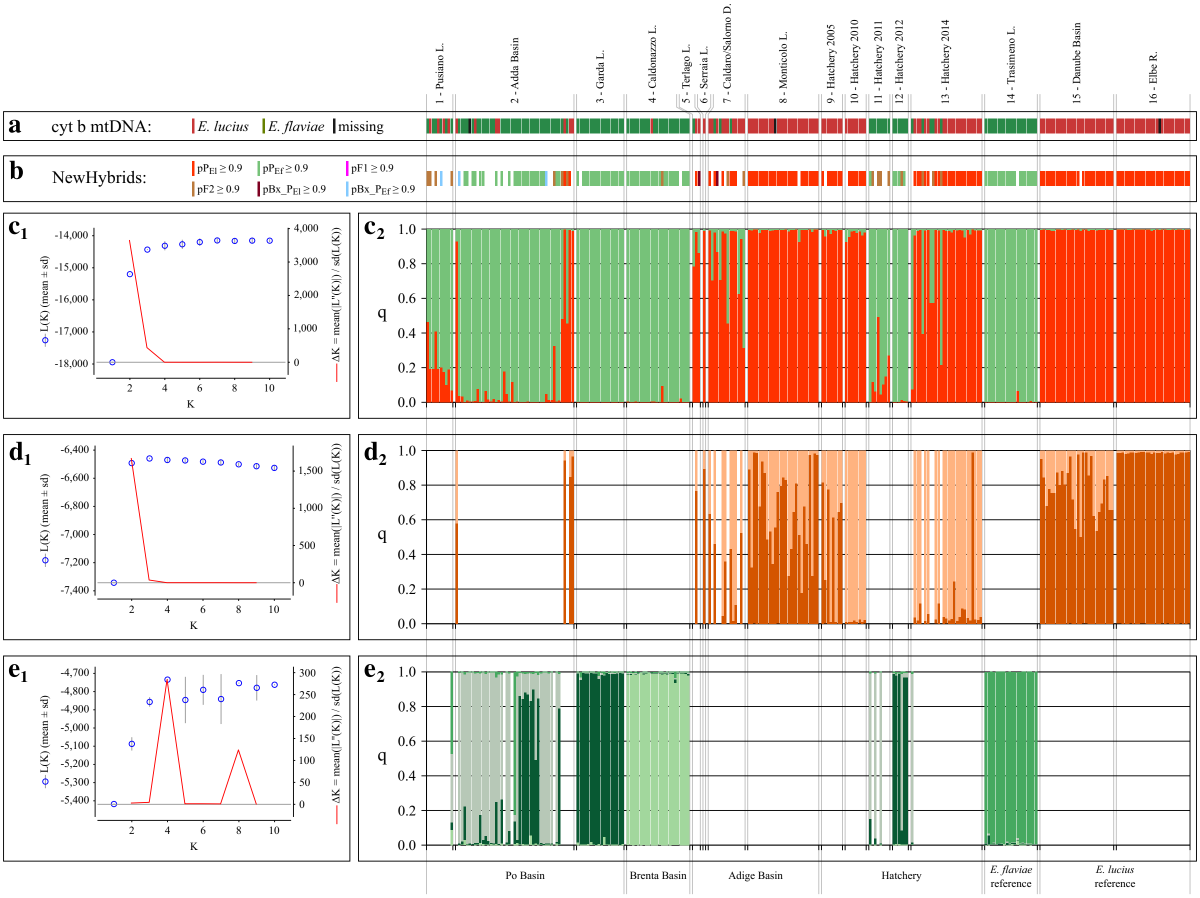

Fig. 5 **a** Cytochrome b mtDNA haplogroup membership is presented for each individual. **b** Results of NewHybrids analysis: each individual having assignment posterior probability to one of the pure/hybrid classes $P \geq 0.90$ is represented in a *different colour*, depending on the assignment class. **c1**–**e2** Results of hierarchical Bayesian clustering analyses by Structure: mean of the estimated ln probability of data (±SD) and ΔK statistics (Evanno et al., 2005) as a function of the different tested number of genetic clusters (K) including (**c1**) the entire dataset (first level of hierarchical analysis), **d1** only individuals with a q value $\geq$ 0.90 for the European cluster retrieved by the first-level analysis (second level of hierarchical analysis) or (**e1**) only individuals with a q value $\geq$ 0.90 for the Italian cluster retrieved by the first-level analysis (second level of hierarchical analysis); *barplots* representing the proportional membership of each individual to one of the K genetic clusters identified by Structure (**c2**) in the entire dataset, (**d2**) in the European cluster or (**e2**) in the Italian cluster