



## Mitochondrial DNA Part B Resources

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## The European anchovy, a genetically highly diverse species displays null within-sample haplotype diversity on a single study?

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### ABSTRACT

The European anchovy has been the focus of numerous population genetic studies, most of which exposing high levels of haplotype diversity. However, Keskin and Atar (2012) revealed rather singular results of null haplotype diversities. We therefore call for caution when considering these findings.

### ARTICLE HISTORY

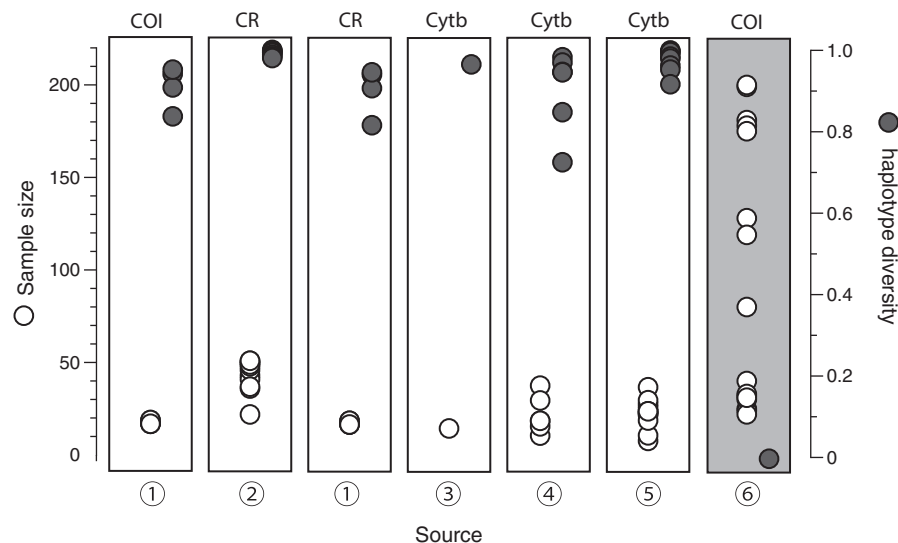
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### KEYWORDS

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Keskin and Atar (2012) study “Genetic structuring of European anchovy (*Engraulis encrasicolus*) populations through mitochondrial DNA sequences” report a singular finding for this species: 16 sampled locations have null haplotype diversity, independently from sampling size, which varies from 24 to 202 fishes. Additionally, some locations share the same haplotype (see Keskin & Atar 2012; Table 1). The European anchovy, a highly mobile small pelagic fish, has been subjected to

numerous population genetic studies involving three mitochondrial markers (cytochrome oxidase subunit I, cytochrome b and control region) and, to the best of our knowledge, no single paper on this species has reported null haplotype diversity values (Pappalardo et al., 2015, Vi4nas et al., 2013, Grant & Bowen, 2006, Borrell et al., 2012, Silva et al., 2014). In fact, the opposite is the rule with sampling locations displaying high haplotype diversities even with modest sampling sizes



**Figure 1.** Comparative results of cytochrome oxidase subunit I (COI), Control Region (CR) and Cytochrome b (Cytb) from different sources: (1) Pappalardo et al. (2015), (2) Vi4nas et al. (2013), (3) Grant & Bowen (2006), (4) Borrell et al. (2012), (5) Silva et al. (2014); (6) Keskin and Atar (2012).

(Figure 1). The unlikely results from Keskin and Atar (2012) should have warranted a thorough explanation in the light of previously known reports (Bembo et al. 1995; Grant et al. 2005; Grant & Bowen 2006; Magoulas et al. 2006; Zarraonaindia et al. 2012) cited in the paper in question. However, no clarification for the null haplotype diversity on each location is produced and we cannot propose any plausible explanation for Keskin and Atar (2012) results. Therefore, we advise extreme caution when dealing with these findings.

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