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

Rita Castilho[a] and Gonçalo Silva[b]

[a]CCMAR, Centro de Ciências do Mar, Universidade do Algarve, Campus de Gambelas, Faro, Portugal; [b]MARE – Marine and Environmental Sciences Centre, ISPA – Instituto Universitário, Departamento de Biociências, R. Jardim do Tabaco, Lisboa, Portugal

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.

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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, Viñas 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

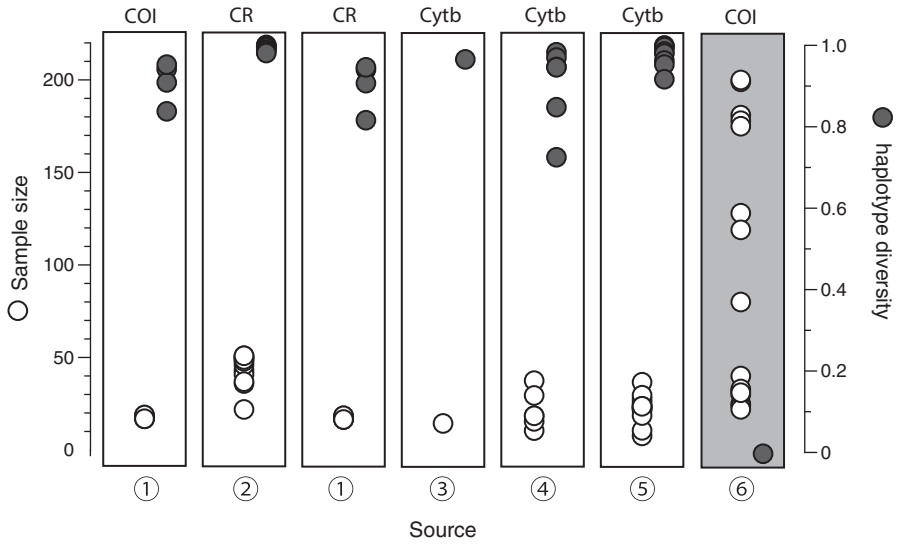

Figure 1. Comparative results of cytochrome oxidase subunit I (COI), Control Region (CR) and Cytochrome b (Cytb) from different sources: (1) Pappalardo et al. (2015), (2) Viñas et al. (2013), (3) Grant & Bowen (2006), (4) Borrell et al. (2012), (5) Silva et al. (2014); (6) Keskin and Atar (2012).

CONTACT Rita Castilho rcastil@ualg.pt CCMAR, Centro de Ciências do Mar, Universidade do Algarve, Campus de Gambelas, 8005-139 Faro, Portugal

(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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