

Seascape-mediated patterns and processes of population differentiation in European seabass

Volckaert Filip¹, Hillen Jasmien¹, Hablützel Pascal^{1,2}, Maes Gregory³, Herten Koen³, Chaturvedi Anurag¹, Ogden Rob⁴, Taylor Martin⁵, Maroso Francesco⁶, Verheyden Dorothy¹, Cambiè Giulia⁷, Gkagkavouzis Konstantinos⁸, Triantafyllidis Alexander⁸, De Innocentiis Sabine⁹ and Coscia Ilaria¹

- ¹ Laboratory of Biodiversity and Evolutionary Genomics, University of Leuven, Ch. de Bériotstraat 32 box 2439, 3000 Leuven, Belgium
E-mail: filip.volckaert@kuleuven.be
- ² Flanders Marine Institute (VLIZ), Wandelaarkaai 7, 8400 Oostende, Belgium
- ³ Laboratory for Cytogenetics and Genome Research, Center for Human Genetics, Genomics Core, University of Leuven, Herestraat 49, 3000 Leuven, Belgium
- ⁴ TRACE Wildlife Forensics Network, PO Box 17477, Edinburgh EH12 1NY, United Kingdom
- ⁵ School of Biological Sciences, University of East Anglia, Norwich Research Park, Norwich NR4 7TJ, United Kingdom
- ⁶ Department of Compared Biomedicine and Food Science, University of Padova, Agripolis, Viale dell'Università 16, 35020 Legnaro, Italy
- ⁷ School of Ocean Sciences, Bangor University, Menai Bridge, Angelsey LL59 5AB, United Kingdom
- ⁸ Department of Genetics, Development and Molecular Biology, School of Biology, Aristotle University of Thessaloniki, University Campus, 54124 Thessaloniki, Greece
- ⁹ Italian National Institute for Environmental Protection and Research, Via Branconi 48, 00166 Roma, Italy

Identifying biologically relevant levels of population structure and demographically independent populations is imperative for sustainable fisheries management, but challenging because of high levels of gene flow and large population sizes leading to weak genetic structure. However, increasingly good access to genome-wide variation and architecture have facilitated accurate determination of fine scale genetic population structure. Here, we studied the population structure of European seabass (*Dicentrarchus labrax* L.), a commercially exploited and farmed fish with high dispersal capacity. In addition, we examined the influence of geographic distance and abiotic environmental variables on the observed genetic structure with a seascape genomics approach. Seabass showed a largely panmictic pattern within the Atlantic Ocean, whereas several genetic clusters were distinguished within the Mediterranean Sea based on 2,549 SNP markers genotyped using ddRAD sequencing. Introgression of Atlantic alleles was detected throughout the western Mediterranean Sea, but introgression of Mediterranean alleles was only found in a restricted area in the Atlantic Ocean off the Strait of Gibraltar. Seascape analysis suggested that genetic population structure is mediated by both dispersal limitation and environmental gradients, pointing to local adaptation. As such the study provides key information for fisheries and conservation management of European seabass.

Keywords: Atlantic Ocean; Mediterranean Sea; population genetics; seabass; seascape; SNP