

Genetic discrimination of wild versus farmed gilthead sea bream



Farm escapees and their offspring impose a significant impact on the environment and may therefore alter the future evolutionary trajectories of wild populations. To date, there is no management plan in place in Mediterranean countries to prevent fish escapes. Here, we investigate microsatellite length variations in three candidate genes, including prolactin (PRL), growth hormone (GH), and the receptor activity modifying protein 3 gene (RAMP3), to study the genetic structure of the main fish species farmed in the Mediterranean, gilthead seabream (*Sparus aurata*). We also evaluate the performance of microsatellites in discriminating fish origin (wild or farmed). Results from 298 individuals, including farmed, wild adult and juvenile fish were compared with results from 19 neutral markers used in a previous study. All loci were polymorphic, selectively neutral, and had the statistical power to detect significant population differentiation. Global F_{ST} was similar to that estimated using 19 loci (0.019 and 0.023, respectively), while pairwise comparisons identified farmed populations as the main drivers of genetic divergence, with a much higher magnitude of overall genetic differentiation within farmed populations (0.076) than that estimated using the 19 neutral microsatellite loci (0.041). Bayesian structural analysis showed that the PRL, GH, and RAMP3 markers were able to distinguish farmed from wild populations, but were not able to distinguish different wild groups as 19 neutral microsatellite markers did. Farmed populations of different origins were assigned to a separate cluster with a high individual assignment score (>88%). It appears that the candidate markers are more influenced by artificial selection compared to neutral markers. Further validation of their efficiency in discriminating wild, farmed, and mixed fish origins using a more robust sample size is needed to ensure their potential use in an escaped fish monitoring programme.

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