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ESTIMATES OF GENETIC VARIABILITY AND INBREEDING IN SELECTED POPULATIONS OF EUROPEAN SEA BASS

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In recent years, the aquaculture industry has increasingly aimed at improving economically important traits, like growth, feed efficiency or resistance to infections, through artificial selection. It represents a great window of opportunity to significantly improve stocks. However, the pitfall of these procedures is that it may decrease genetic diversity and increase inbreeding. Therefore, it is important to monitor the level of inbreeding within a selected strain in order to ensure that genetic diversity remains acceptable throughout the selection process.

We have assessed the level of genetic variability over three generations of two populations of European sea bass (*Dicentrarchus labrax*) from an experimental farm located in France. The first strain originates from Atlantic wild broodstock, and was selected for growth over three generations. The second and third strain originate from Mediterranean wild broodstock and were selected for either high or low weight loss under a starvation regime (as an indirect predictor of feed efficiency) over two generations. We used a genomic approach (ddRADseq – double digest Restriction site Associated DNA sequencing) to screen 159 individuals. Using a suite of hundreds of genomic markers (single nucleotide polymorphisms – SNPs), we reliably estimate the inbreeding levels and genetic variability across generations for both strains. We also assess the relatedness of the individuals within each group and the number of effective breeders, in order to further determine the dynamics of reproduction. Finally, we calculate the genetic diversity within and between groups and generations. Our study is among the first using genomics to quantify inbreeding over generations of farmed sea bass selected for commercially relevant traits. The results provide a first insight on how such selection procedures affect inbreeding and genetic variability even within the short span of a few generations.

Keywords: inbreeding, selection, SNP, genetic

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