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INVESTIGATING THE GENETICS OF SEX DETERMINATION IN EUROPEAN SEA BASS (Dicentrarchus labrax) USING RAD-SEQ

Palaiokostas C.[1], Bekaert M.B.[1], Taggart J.B.[1], Gharbi K.[2], McAndrew B.J.[1], Chatain B.[3], Penman D.J.[1#], Vandeputte M.[3,4]

[1] Institute of Aquaculture, School of Natural Sciences, University of Stirling, Stirling FK9 4LA, Scotland, United Kingdom
[2] Edinburgh Genomics, Ashworth Laboratories, King's Buildings, University of Edinburgh, Edinburgh EH9 3JT, Scotland, United Kingdom
[3] *Ifremer, Chemin de Maguelone, 34250 Palavas-les-Flots, France*
[4] INRA, UMR1313 Génétique animale et Biologie intégrative, 78350 Jouy-en-Josas, France

European sea bass (*Dicentrarchus labrax*) is one of the most important farmed species for Mediterranean aquaculture. The observed sexual growth and maturity dimorphism in favour of females adds additional value to deciphering its sex-determining system. Current knowledge indicates the existence of a polygenic sex-determining system interacting with temperature. Restriction-site Associated DNA (RAD) sequencing was used in a test panel of 175 offspring originating from a F2 factorial cross between two dams and four sires from one F1 family between parents with contrasted sex tendencies. In total, 1,156,659,542 raw reads (100 bases long) were produced (578,329,771 paired-end reads). After removing low quality sequences (quality score under 30), ambiguous barcodes and orphaned paired-end reads, 76.7% of the raw reads were retained (886,927,866 reads) from which 56,696 unique RAD-tags were retrieved. In order to maximise the number of informative markers and minimise the amount of missing or erroneous data, we used RAD-tags retrieved in at least 75% of the samples, and carrying one or two single nucleotide polymorphisms (SNPs). The family structure was identified *a posteriori* using R/hsphase and Vitassign with the SNP markers from the offspring and parents. A consensus SNP-based linkage map was constructed, consisting of 5,097 SNPs grouped into 24 linkage groups. Indications for putative sex-determining QTL are provided in linkage groups 13, 19 and 21. A preliminary study was conducted testing whether breeding values, estimated by including the additive SNP effects, could be used as a predictive measure of phenotypic sex. Prediction of phenotypic sex within each of the eight full-sib families, using genomic models (MCMC-BLUP, BayesCPi), consistently outperformed pedigree BLUP. The advantage of using genomic models was particularly evident in dam half-sib family 2, where one of the sex-determining QTLs had been detected. Altogether, our results further support the polygenic hypothesis for sex determination in sea bass, while they also highlight the potential use of within-family genomic selection to rank individuals within families for their estimated breeding value for sex tendency.

Keywords: RAD-seq, Dicentrarchus labrax, QTL, Genomic Selection

[§] Corresponding author. Tel.: + 44 (0)1786 467901; Fax: + 44 (0)1786 472133
E-mail address: d.j.penman@stir.ac.uk