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A NEW 665K SNP ARRAY USED FOR DETECTING SIGNATURES OF POSITIVE SELECTION IN RAINBOW TROUT (ONCORHYNCHUS MYKISS)

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Native from North America, rainbow trout has been domesticated since the 1870s and introduced on all continents. Domestication and selective breeding have led to genetic changes due to inbreeding, genetic drift and selection. To address evolutionary biology questions, we used variant databases from USDA and INRAE to develop a 665K SNP array* (HD chip) for rainbow trout from a subset of the 32,372,492 SNPs. We prioritized the most variable SNPs in both databases with homogenous repartition over the genome. Of the 664,531 HD chip SNPs, 65% and 61% passed quality control and were polymorphic in samples of 288 and 175 genotyped fish from two commercial French lines (LB and LC respectively). Then, a subset of 72 LB and 67 LC genotypes of weakly related fish was pooled with the HD genotypes of 14 fish from the INRAE synthetic line (SY) and of 20 fish coming from rivers of the North West of USA (HA). These genotypes were used to reveal regions of the genome with low genetic diversity among various populations, likely to involve genes positively selected during either domestication or selection. The three French lines were moderately differentiated ($F_{st} \sim 0.10-0.12$), but strongly differed from the HA population ($F_{st} \sim 0.27-0.29$). A run of homozygosity (ROH) study revealed homozygous regions shared by all populations on Omy2, Omy12 and Omy15. These ROH islands included 26 annotated genes related to key roles in reproduction, embryonic development, genome stability and immunity.

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