

GENOMIC ESTIMATES OF DIVERSITY BETWEEN AND WITHIN FRENCH RAINBOW TROUT POPULATIONS

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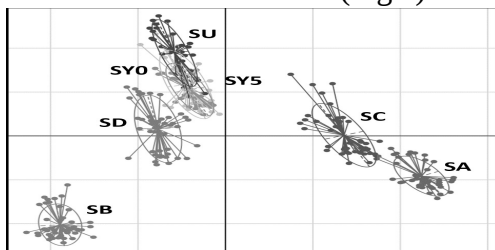
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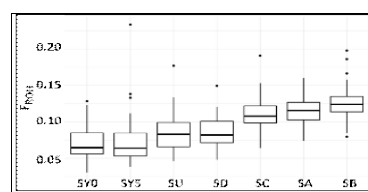
Recent access to the genome sequence of rainbow trout and a medium-throughput genotyping chip of 57,501 Single Nucleotide Polymorphism (SNP) markers open up new perspectives for the design of efficient breeding programs. However, the genetic variability of farmed fish can decrease significantly due to high selection intensity, jeopardizing the long-term genetic progress as well as the adaptation capacities of populations at the onset of a change in the environment. The aim of the study was therefore to evaluate the impact of selection practices through molecular estimates of genetic diversity between or within population. The analysis of linkage disequilibrium (LD) was used to estimate effective population sizes (N_e) across the last 5-10 generations for each strain. Average inbreeding (F_{ROH}) was derived from runs of homozygosity measured in each individual within population. This work was funded by the European Maritime and Fisheries Fund (EMFF) and French Government via the national public body in charge of agriculture products and seafood FranceAgrimer (n°2015-0638).

Four commercial strains of French breeding companies, hereafter SA, SB, SC and SD, as well as two INRA experimental lines, SY and SU, were considered. The synthetic line SY was developed by intercrossing several domesticated strains during the 1980s to create a population with a large genetic variability. The line has since been managed without any selective breeding. The SY cohort from birth year 2006 was the founder generation (SY0) for a new strain (SU) selected its ability to survive and grow with a complete plant-based diet. The 5th generation of SU line was analyzed, jointly with the corresponding generation of the unselected SY line (SY5). The Axiom™ Trout Genotyping Array was used to genotype 290 females comprising 32 to 49 fish with low kinship coefficients within strain. After quality control, only 38,351 SNP were kept for the analysis of genetic diversity between strains. For the within strain analysis, we kept subsets of 31,191 to 34,724 SNP with minor allele frequency greater to 5% in each population.

Our results showed a moderate genetic differentiation between strains (Fig.1). F_{ST} values ranged from 0.02 (SY0-SU) to 0.15 (SA-SB). Within population, LD declined rapidly over the first 100 kb (mean r^2 decreased from 0.34 at 10 kb to 0.23 at 100 kb), but then stayed quite high at long distance compared to other livestock species (mean r^2 was still 0.16 at 1 Mb). Estimates of N_e in the last generation were low (< 25) for all strains. Average F_{ROH} ranged from 7% for SY0 to 8.5-12.5% for the selected strains (Fig.2). Molecular inbreeding was high compared to values in



other livestock populations. Our study gave the



breeding companies a better understanding the genetic

of

diversity of their strains to implement effective genomic breeding programs.