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## Heterogeneity of genetic diversity throughout the genome in rainbow trout populations.

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The genetic variability of farmed fish can decrease due to high selection intensity, jeopardizing the long-term genetic progress and the adaptation capacities of populations to environmental changes. Variation throughout the genome in the density of selection sites and in the rates of recombination can modulate the intensity of genetic drift and therefore generate heterogeneity of genetic diversity across the genome.

As information on genome-wide diversity accumulates, we lack information for farmed fish. Recent access to the genome sequence of rainbow trout and a 57K SNP chip made possible to describe the genome landscape of genetic diversity in rainbow trout populations. Our aim was to quantify the genetic diversity for French rainbow trout populations, focusing on comparing of the genomic estimates between the chromosomes. The linkage disequilibrium (LD) and the average inbreeding (F) derived from runs of homozygosity were measured per chromosome and individual within population.

Four commercial strains (SA, SB, SC, SD) as well as the INRA synthetic line (SY) and the INRA Suave line (SU) were considered. The SY line was managed to maintain a large genetic variability since the 1980s and the SU line was selected for adaptation to a 100% plant-based diet. The Axiom<sup>TM</sup> Trout Genotyping Array was used to genotype 290 females: 32-49 fish with low kinship coefficients within strain. After quality control, 31,190-34,723 SNP with MAF greater than 5% within population were kept in the analysis.

Results showed high F (8-12%) and LD at long distance (> 1 Mb) compared to livestock species. There was strong evidence for important heterogeneity of genetic diversity along the genome. Average LD between adjacent SNPs ranged 0.23 (chromosome 22) to 0.38 (chromosome 5). This variation did not fully correlated with F values. Mean F ranged 5% (chromosome 13) to 17% (chromosome 5). For some chromosomes (for instance 23), there was a large discrepancy in F between the unselected line SY (F=5%) and selected strains as SA (F=25%). Currently, SNP information is predominantly used in selection programs to predict breeding values. But, it could also be used to manage the local inbreeding rate in the genome of livestock populations.

*Keywords: fish, linkage disequilibrium, inbreeding coefficient, runs of homozygosity, selection*  
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