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## IN-DEPTH GENOMIC CHARACTERIZATION OF A UNIQUE COLLECTION OF RAINBOW TROUT ISOGENIC LINES

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A unique collection of 17 isogenic homozygous rainbow trout lines has been established and maintained in INRA fish experimental facilities. These lines exhibit a wide range of phenotypes for most of the traits screened for. Such isogenic lines have many advantages in experimental approaches, including homozygosity, within-line genetic homogeneity, the availability of the same 'individual' genetic background at different places and times or the possibility to carry out investigations at different levels (cell, tissue, whole individual) for a given genetic background. In particular, these lines are being used to investigate the molecular bases of complex traits: lines with contrasted phenotypes are used for functional and genetic analyses (such as transcriptomics or QTL mapping).

Genomic characterization of isogenic lines is pivotal to realize the whole benefit of this material in integrative approaches aimed at dissecting complex traits. Having access to the genomic variability among lines is essential in expression or QTL studies in order to identify polymorphism(s) responsible for the phenotypes of interest. So far, the main information has come from RAD-tag genotyping, resulting in no more than a few thousand SNPs per line, which limits the accuracy of investigations at whole genome level or in targeted areas.

The objective of this study was to carry out in-depth genomic characterization of the trout isogenic lines, by investigating both small genomic variations (SNPs and InDels) and structural variants (SVs). SVs are defined as genomic alterations that affect large DNA segments  $\geq 50$  nucleotides, thereby causing modifications in either DNA quantity (insertions, deletions and duplications) or DNA structure (inversions). Although SVs have received increasing interest in many species and were shown to be associated with several diseases and phenotypes, they are poorly documented in fish.

All isogenic lines (one or two individuals per line) have been resequenced at a depth of coverage ranging from 10X to 32X, on an Illumina HiSeq X-Ten platform, in paired-end 2x150 bp configuration. Analysis of small genomic variants was performed according to the GATK Best Practices. The identification and characterization of SVs was done by using 4 different tools corresponding to three distinct but complementary approaches: i) Pindel and Delly (split-read approach); ii) BreakDancer (paired-end approach); iii) CNVnator (depth of coverage approach). After SVs annotation, a subset of SVs with potential relevant biological effects will be validated experimentally.

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