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MOLECULAR INBREEDING AND GENETIC LOAD FOR FEMALE REPRODUCTION TRAITS IN A RAINBOW TROUT SELECTED LINE

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Introduction

Selection for production traits in closed and small broodstock populations of rainbow trout (*Oncorhynchus mykiss*) over the last 30 years have induced significant levels of inbreeding [1]. Molecular inbreeding can be derived from the identification of homozygous genomic segments, named ROH for run of homozygosity [2]. ROH allow to identify the regions responsible for inbreeding depression along the genome [3]. The aim of the study was to identify through ROHs the main chromosomes that contribute to inbreeding depression for female reproduction traits in a rainbow trout selected line.

Materials and Methods

To answer this question, we analyzed the performance of 1,366 females under linear animal models including the fixed effects of the cohort and spawn week within cohort and the animal additive and dominance genetic effects. A first model fitted a single covariate accounting for the individual inbreeding coefficient (F) derived at the all genome scale. A second model fitted 30 covariates accounting for the distinct inbreeding effects (Fi) of the 30 chromosomes. The traits studied were the female post-spawning weight (PW), the female fork length (FL), the spawning date (SD), the spawn weight (SW), the cœlomic fluid weight (CF), the egg number (EN) and the egg average weight (EW).

Results

The dominance variance explained about 4 to almost 19% of the phenotypic variance of each trait under the second model, the largest effect being estimated for SW and the lowest ones for CF and FL. At the genome scale, a significant effect of inbreeding was only observed for SD and EW, with +10% in F level leading to variations of +12.3% and -3.8% of SD and EW performance, respectively (Figure 1). However, at the chromosome scale, we observed some positive or negative significant effects (ranging from -3.9 to +4.6%) of the Fi for all the traits studied (Figure 2). For example, we estimated positive effects of inbreeding on Omy5 for SD, EW and SW, but negative effects on Omy23 for the three traits. On Omy10, we saw a positive effect of inbreeding for SD while effects were negative for EW and SW.

Discussion and conclusion

We estimated higher dominance ratios for reproduction traits (particularly for SW and EN) in comparison to size traits. It may correspond to a higher number of loci with overdominant alleles playing a role on female fecundity. As expected, we estimated rather unfavorable effects of genome-wide inbreeding on female size and reproduction traits. However, we observed very variable inbreeding effects along the genome, with some favorable or unfavorable effects of local inbreeding. These results suggest that local inbreeding can strongly impact the performance despite the fact that no effect is associated to the total inbreeding coefficient F. To conclude, this work helps

identify genomic areas whose genetic diversity is essential for good female reproduction performance and provide tools for a better management of genetic diversity in breeding programs.

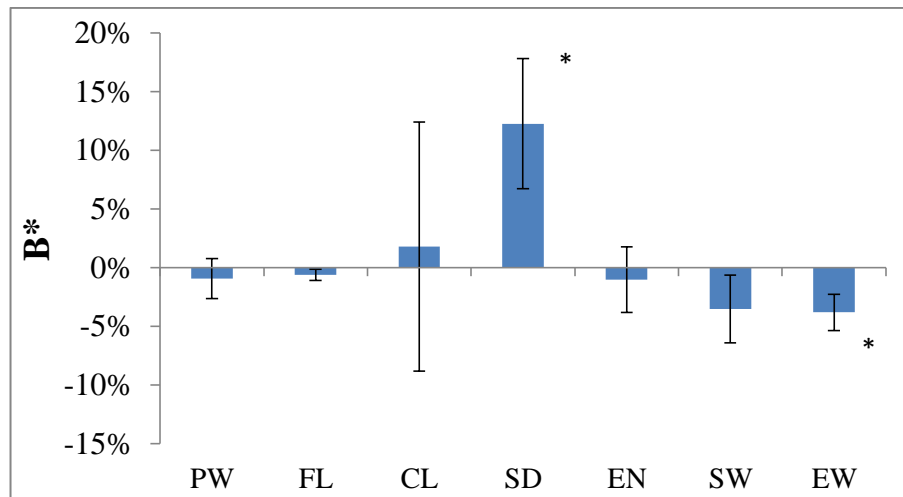


Figure 1. Performance variations expressed in proportion of trait mean for an increase of 10% of total inbreeding coefficient F (e.g. standardized genetic load B*)

*Significant effect of inbreeding at the all genome scale.

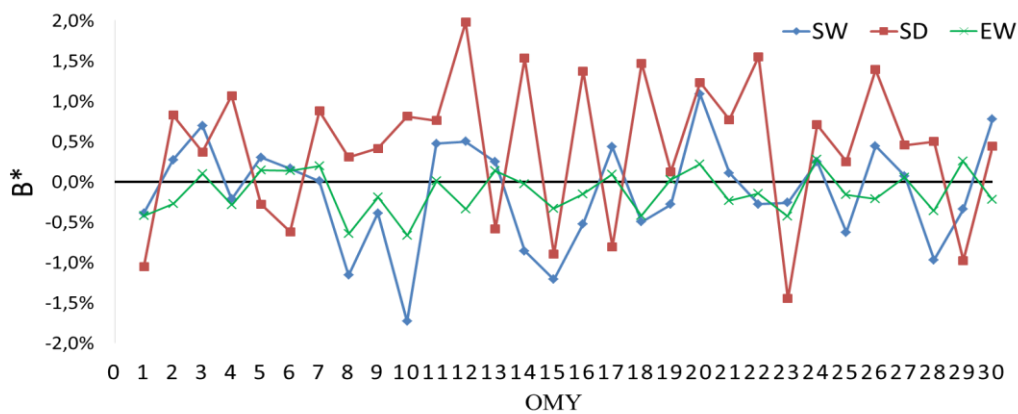


Figure 2. Representation of the standardized genetic load for EW (egg average weight), SW (spawn weight) and SD (spawning date) traits along the chromosomes Omy1 to Omy30.

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