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Katy Paul, Gwendal Restoux, Florence Phocas

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DETECTING SIGNATURES OF SELECTION BETWEEN THREE FRENCH DOMESTICATED AND ONE NORTH-AMERICAN WILD POPULATION OF RAINBOW TROUT

Paul, K.¹, Restoux, G.¹, Phocas, F.¹

1. Université Paris-Saclay, INRAE, AgroParisTech, GABI, 78350, Jouy-en-Josas, France

SUMMARY

Domestication and selection can often reduced genetic diversity in genomic region associated, it may induced a large homozygous haplotypic segments and a variety of genome prints. We analysed the haplotypes of 179 rainbow trout distributed in four populations : three domesticated french rainbow trout populations, genotyped using the HD Affymetrix 665k [3], including two commercial lines [1] (LB and LC), and one unselected experimentale line (SY). The latest population was one wild population from north-american area (Wild) sequenced by [2]. After basic filtering, 546,903 SNPs were in the final dataset. Genetic populations structure was studied using principal component analysis (PCA) and Fst. Signature of selection were studied using cross-population extended haplotype homozyosity method (XP-EHH). First, medium Fst value (0.10–0.12) were identified between french rainbow trout. And high Fst value were observed between domesticated and Wild populations (0.27 - 0.28). Secondly, at the local scale, the differences between populations calculated with XP-EHH analysis were exposed on figure1(SY vs Wild). For all XP-EHH analysis, between domesticated and wild populations, a highly significant differences at the genome scale ($p\text{-value} > 7$) were observed for two regions on Omy17 (from 18 to 20 Mb) containing 35 genes, and a larger region on Omy26 (from 39 to 48 Mb) with more than 100 genes. Moreover, other regions seems interesting : from 14 to 18Mb on Omy21 and from 12 to 14Mb on Omy18, where strong significant differences were observed between Wild and SY or LC populations. In the same way two regions from 13 to 14 Mb and from 52 to 62 Mb on Omy13 had high significant differences between Wild and SY or LB populations. A few small differences on chromosomal scale were identified between domesticated populations but the higher differences were still between domesticated and wild populations. The the gene composition study of these regions is essential to identify genes specific to some populations or linked to domestication or selection processes.

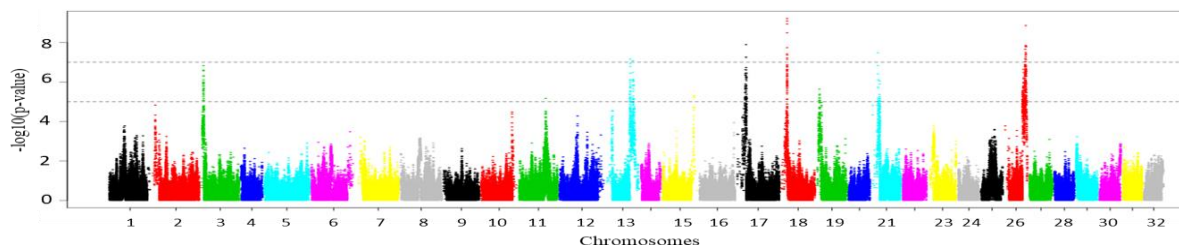


Figure 1. Manhattan plot of the log transformed XP-EHH values between Wild and SY populations. The y-axis shows the $-\log_{10}(P\text{-value})$ of XP-EHH values and x-axis shows chromosomal positions. The horizontal dotted lines represent the genome and chromosomal significant level.

References

[1] Hypotemp project, n° P FEA470019FA1000016. [2] Gao, G., Nome, T., Pearse, D. E., Moen, T., Naish, K. A., Thorgaard, G. H., ... & Palti, Y. (2018). A new single nucleotide polymorphism database for rainbow trout generated through whole genome resequencing. *Frontiers in Genetics*, 9, 147. [3] Bernard, M., Dehaullon, A., Gao, G., ... & Phocas, F. (...). Development of a high-density SNP array for rainbow trout genome-wide genotyping.