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Possible genetic isolation between different sympatric morphs of Dolly Varden (*Salvelinus malma*) from Kronotskoe lake

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Motivation and Aim: Arctic chars (Salvelinus alpinus) and Dolly Varden (Salvelinus malma) are wide-spead circumpolar specia of Salmonids. They produce many sympatric and allopatric morphs with unclear taxonomic status and even sometimes considered one species. Dolly Warden inhabits rivers and lakes of Pacific basin, and were so we can speak about fish from Kronotskoe Lake as Dolly Varden, taking into account data on mtDNA [1]. Kronotskoe lake is inhabited by multiple sympatric morphs of Dolly Varden, some authors define to 8 [2]. In this study we make an attempt to solve the problem of genetic isolation between sympatric Dolly Varden morphs in Kronotskoe lake using morph transcriptomic data.

Methods and Algorithms: Sampes of muscle tissue were taken from fish, caught in Kronotskoe lake in 2013. Samples were stored in RNAlater solution and transported to University of Southern California, then libraries were prepared and Illumina sequencing was performed. 150-bp pair end reads were obtained for each fish and trimmed by Trimmomatic. Then reads were aligned with reference genome of *Salvelinus* sp., putative hybrid between *S. alpinus* and *S. malma* [3]. Assembly ASM291031v2, RefSeq GCF_002910315.2) with hisat2 (Kim et al., 2019; RRID:SCR_015530 [4]). The bam files for each fish were generated with samtools and polymorphisms were searched by bcftools. Annotation of SNP was made with snpEff и snpSift.

Results: Transcriptomic reads were successfully mapped on reference genome (average 89.29 % reads mapped) 1697 SNP were found and annotated, most of them were modifiers (84.5 %) and silent (82.78 %). The most abundant locations were downstream (38.18 %) and upstream (33.33 %) variants. Most SNP were silent (82.7 %), less abundant were missense (16 %) and nonsense (0.566 %) mutations. PCA analysis of all SNPs revealed low portion of variance explained by first two components. PC1 for the whole list of SNPs was 5.32 %, PC2 – 13.50 %. Taken together PC1 and PC2 explain 28.82 % of variance. For mitDNA PC1 explains 27.82 % of variance, PC2 – 20.37 %, taken together PC1 and PC2 explain 48.19 %. For moprh-specific SNPs were determined GO. Dwarfs had the highest proportion of unique SNPs among all morphs and the highes percent of SNPs with high and low impact on affected gene (0.791 and 20.261 %). Also dwarf morph has the lowest percent of missense mutations and highest of silent (27.916 and 71.409 %). Fst analysis revealed no significant genetic distance between mophs, we can speak only of mild reproductive isolation between dwarf morph and other (Fst = 0.1 between dwarf and long-head morphs).

Conclusion: We found no evidence of reproductive isolation between different Dolly Varden morphs in Kronotskoe lake. Only mild traces of genetic isolation can be found in the dwarf morph, probably due to its longer history. We can suppose than dwarf morph

was lake-spawning non-migrating population before Kronotskoe was locked by volcanic eruption.

References

1. Weinstein S.Y., Gallagher C.P., Hale M.C. et al. An updated review of the post-glacial history, ecology, and diversity of Arctic char (Salvelinus alpinus) and Dolly Varden (S. malma). *Environ Biol Fish*. 2024;107:121-154. doi 10.1007/s10641-023-01492-0
2. Esin E.V., Markevich G.N. Evolution of the charrs, genus Salvelinus (Salmonidae). 1. Origins and Expansion of the Species. *J Ichthyol.* 2018;58(2):187-203. doi 10.1134/S003294521802005
3. Christensen K.A., Rondeau E.B., Minkley D.R. et al. The Arctic charr (Salvelinus alpinus) genome and transcriptome assembly. *Plos One.* 2018;13(9):e0204076. doi 10.1371/journal.pone.0204076
4. Kim D., Paggi J.M., Park C. et al. Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype. *Nat Biotechnol.* 2019;37:907-915. doi.org/10.1038/s41587-019-0201-4