Gene regulatory variation in Atlantic salmon in multiple tissues

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INTRODUCTION

Atlantic salmon is the largest group in foreign culture, and the data of Atlantic salmon in fish species is relatively large and has a lot of DNA data, RNA data and other genetic data. However, relatively perfect collation and meta-analysis are not available. If the molQTL map is constructed for Atlantic salmon and the conservation of regulatory variation is explored, it will provide a basis for the mining and identification of major genes of economic traits in Atlantic salmon.With eQTL analysis, researchers can identify which genotypic variants (typically single nucleotide polymorphisms, SNPS) are associated with changes in gene expression levels. cis-eQTL can directly reflect the regulatory expression information of the target gene itself, while trans-eQTL analyzes the relationship between the genetic variation of other genes and the expression level of the target gene, and is often used to construct gene regulatory networks in combination with other methods. At present, eQTL technology has important applications in human disease, animal disease resistance growth and other important traits.This analysis helps to reveal gene regulatory mechanisms and the genetic basis of complex traits.

METHODS

Through the collection and filtering of public data of Atlantic salmon, 647 highly sequenced DNA data and 5200 qualified RNA sequencing data from 21 tissues were obtained. The DNA data were genotyped according to the standard procedure and the reference group was constructed. The RNA data were also genotyped, and the DNA typing results were used as the reference group to fill in, and then eqtl sqtl 3aqtl analysis was performed on the 21 tissue typing, and then tissue specific analysis was performed, and finally multi-tissue expression panoramas were constructed, in order to provide data support for subsequent breeding and selection of Atlantic salmon

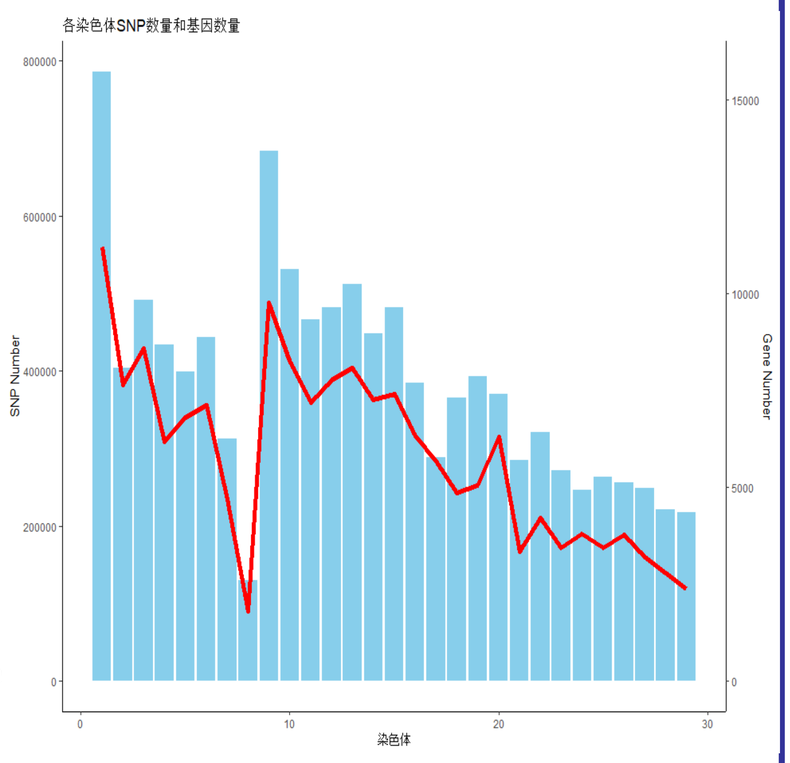

Fig.1. Each chromosome's SNP count and gene count

RESULTS

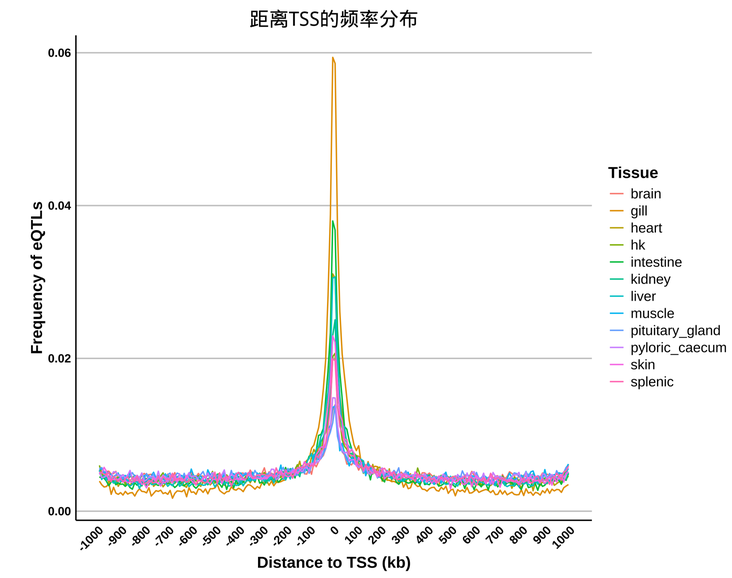

Fig. 2. Proportions of TSS distances for eGene loci in eQTLs across different tissues

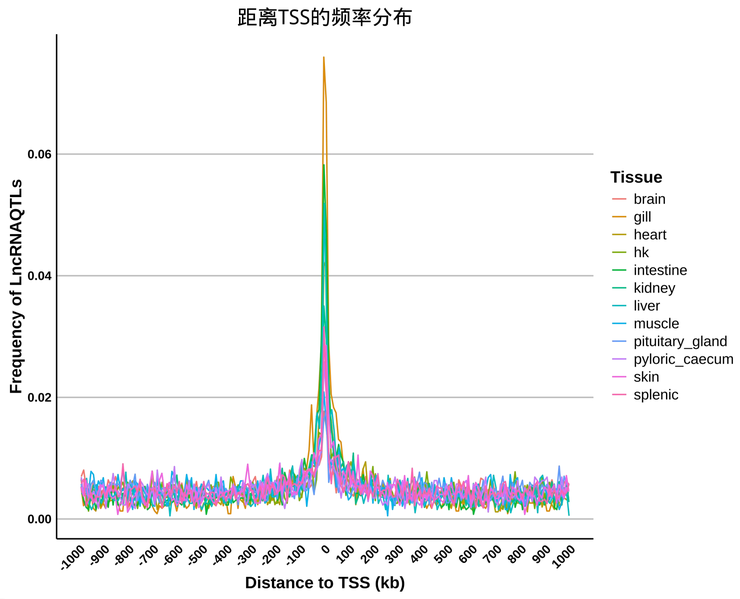

Fig.3. Proportions of TSS distances for eGene loci in LncQTLs across different tissues

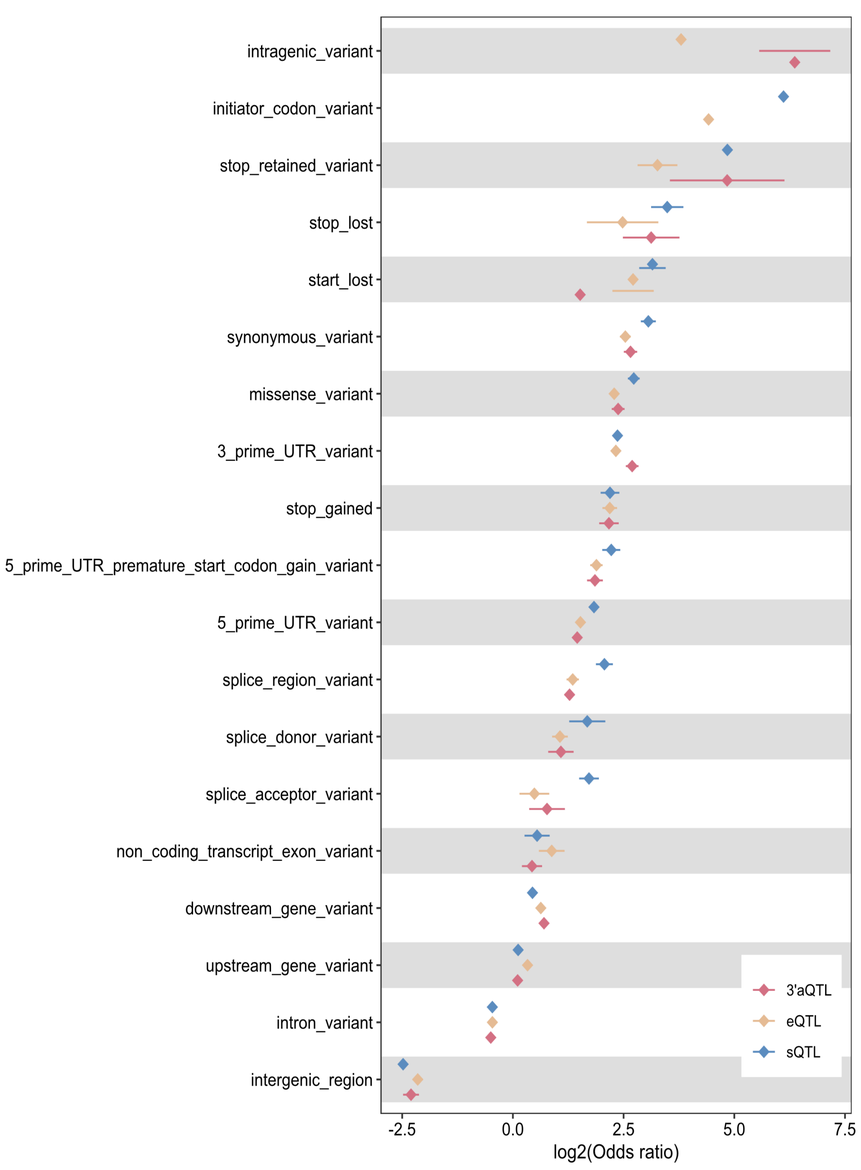

Fig.6. Enrichment of variant types

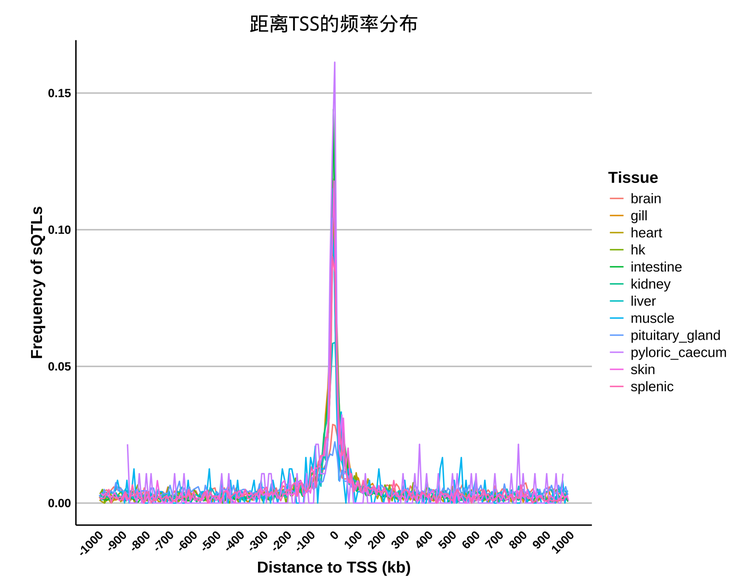

Fig.4. Proportions of TSS distances for eGene loci in sQTLs across different tissues

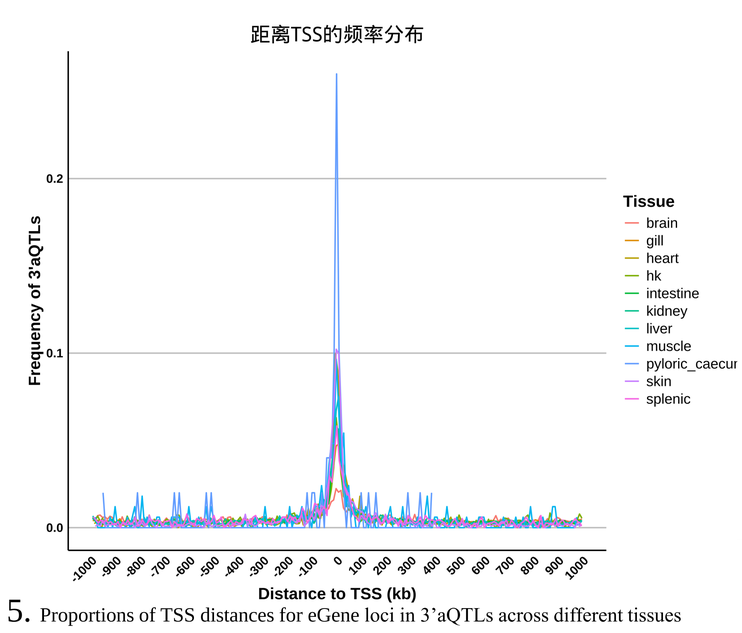

Fig. 5. Proportions of TSS distances for eGene loci in 3’aQTLs across different tissues

CONCLUSION

We explored the distance distribution of SNPS in eGene from transcription start sites in various tissues. It was found that the closer to the transcription start site, the higher the proportion of eGene, and the same trend was found in all twelve tissues. In addition, the results of Cis-eQTL, Cis-sQTL, and Cis-3 'aQTL were enriched by variation annotation types. We found that Cis-eQTL was mainly enriched in some variation regions such as intra gene, start codon deletion, terminon deletion, and stop codon retention. Cis-sQTL is mainly enriched in the start codon retention and stop codon retention regions, and Cis-3 'aQTL is mainly enriched in the mutation regions of the gene, stop codon retention and stop codon deletion regions

FUNDING

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