Construction of high-density genetic map and mapping of sex-related loci in the yellow catfish (*Pelteobagrus fulvidraco*)

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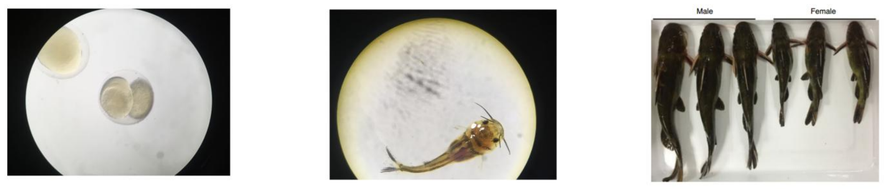
Abstract

The yellow catfish (*Pelteobagrus fulvidraco*) is a very important aquaculture species distributed in fresh water area of China. All-male yellow catfish is very popular in aquaculture because of their significant sex dimorphism phenomena. The males grow much faster than females in full sibling family. However, the sex dimorphism mechanisms is still unclear in yellow catfish. In order to better understand the genetic basis of yellow catfish sexual dimorphism, it is vital to map the sex related traits and localize the candidate genes across yellow catfish whole genome. Here, we constructed a high-density linkage map of yellow catfish using genotyping-by-sequencing (GBS) strategy. A total 5,705 single nucleotide polymorphism (SNP) markers were mapped to 26 different linkage groups (LGs) using 184 F1 offspring. The total genetic map length was 3,071.59 cM, with an average inter-locus distance of 0.54 cM. 11 significant sex-related QTLs in yellow catfish were identified. Six sex-related genes were identified from the region of reference genome near these QTLs including *amh, gnrhr, vasa, lnnr1, foxl2* and *bmp15*. The high-density genetic linkage map provides valuable resources for yellow catfish molecular assistant breeding, and elucidating sex differentiation process. Moreover, the comparative genomic study was analyzed among yellow catfish, channel catfish, and zebrafish. It revealed highly conserved chromosomal distribution between yellow catfish and channel catfish.

Keywords: Yellow catfish, genetic linkage map, sex-related genes, Quantitative trait locus

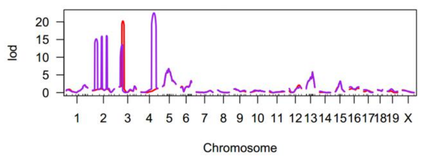
Materials and Methods



Mapping Population Construction and Genome Sequencing

SNPs Discovery and Genotyping

Linkage Map Construction



QTL Mapping Analysis and Association Study

Anchoring Scaffold and Comparative Genomics

184 full sib offspring were selected from the mapping family for subsequent genotyping and phenotype measure. The GBS libraries were constructed according to the standard workflow and sequenced on Illumina HiSeq2500 platform with 100-bp pair-end sequencing mode.Trimmed reads were mapped to the draft genome of the yellow catfish using BWA v0.7.17. The aligned bam files were sorted by coordinates using SAMTOOLS v1.9. The Genome Analysis Tool Kit (GATK) package v4.1.0 was used to further process bam files and SNP calling. Both female and male linkage maps were constructed using JoinMap 4.0 software. A sex-averaged map was established by integrating the sex-specific map through shared markers using the MergeMap Online. The QTLs were identified using MapQTL6 software package. Combining the results from QTL mapping, we identified sex-related SNP loci and further extracted candidate sex-related genes. Based on these anchored scaffolds and information of genetics map, a chromosome-level assembly were obtained. And then, comparative genomics was analyzed between the pseudo chromosomes of yellow catfish and genome of zebrafish (*Danio rerio*) and channel catfish (*Ictalurus punctatus*).

Results

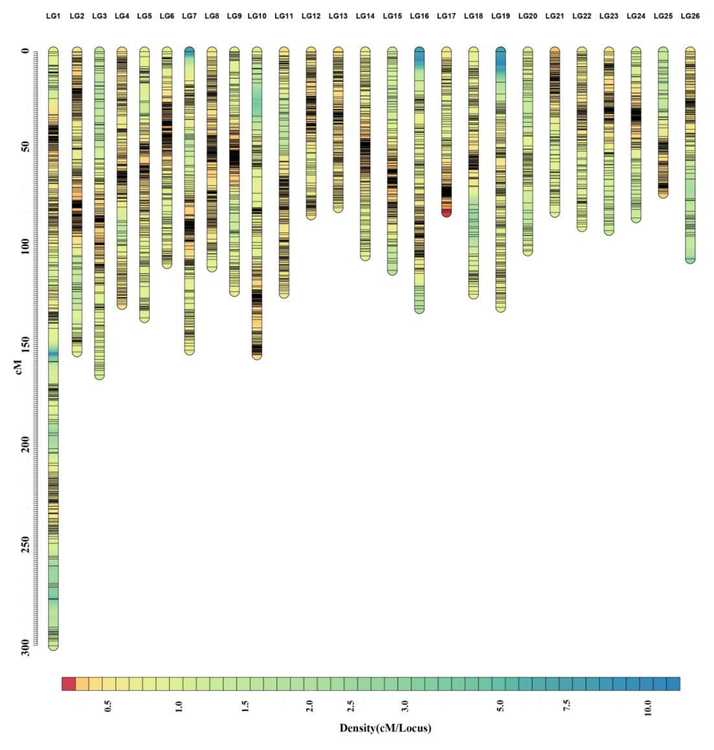


Figure 1 | Linkage group lengths and maker distributions of the high-resolution linkage map of the yellow catfish. A black bar represents a SNP marker. The scaleplate on the left represents genetic distance (centiMorgan as unit). The color represents the density of position/marker, the position with lower density will be colored with red suggests that there are more markers cluster at a narrow range.

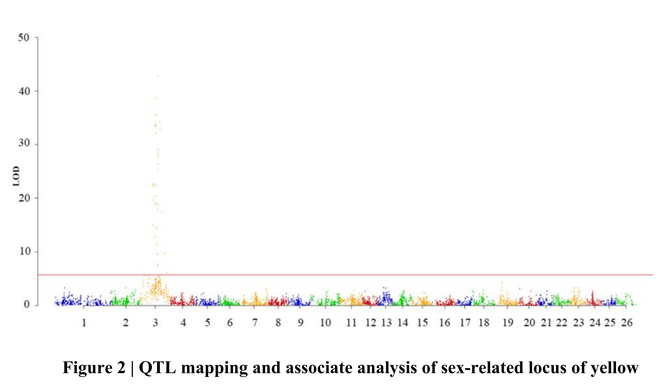


Figure 2 | QTL mapping and associate analysis of sex-related locus of yellow catfish. Threshold for genome-wide significance is denoted with red line.

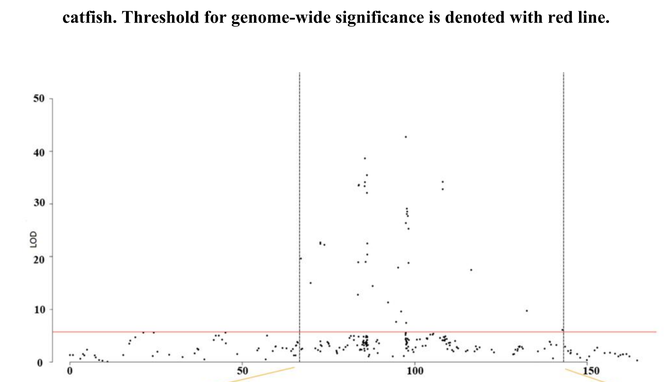


Figure 3 | QTL region and sex-related genes identified from QTL mapping of yellow catfish. Genes are extracted in the ± 50,000 bp genome regions around the significant SNPs. Blue blocks represent the sex-related genes.

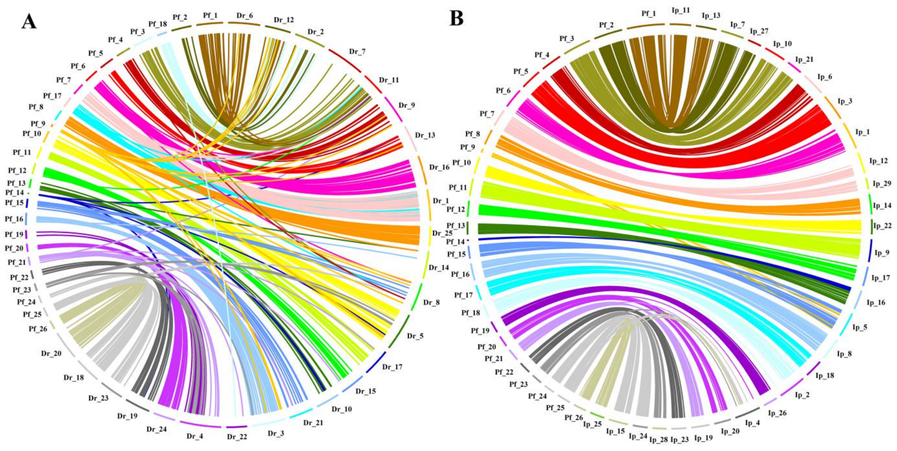


Figure 4 | Genomic comparison between yellow catfish (left semi-circle) and zebrafish (right semi-circle) was shown in (a) and the similarly comparison between yellow catfish (left semi-circle) and channel catfish (right semi-circle) was shown in (b).

Finnaly, 561 million of trimmed reads were aligned on genome and 5,705 SNP markers were selected for further linkage analysis and mapping.The resulting sex-averaged map was consisted with 26 linkage groups (LGs) in total (Figure1). And the sex-averaged map length was 3,071.59 cM, with an average interlocus distance of 0.54cM. In this study, eleven significant QTLs were detected on LG3 (Figure 2). Six sex-related genes were identified from QTL mapping of the high-density map based on the yellow catfish gene annotation (Figure 3), such as anti Mullerian hormone (*amh*), ATP-dependent RNA helicase (*vasa*) and forkhead box L2 (*foxl2*). Comparative genomic studies presented an expected high level of overall syntenic relationship for corresponding chromosomes between yellow catfish and channel catfish compare with the syntenic relationship between yellow catfish and Zebrafish. In detail, we observed the good correspondence of chromosomes/chromosomes and chromosome-chromosome relationship betweenyellow catfish and channel catfish. For example, the alignment blocks of Pf_1 (chromosome 1 of *P. fulyidraco*) corresponds with Ip_11 and Ip_13 (chromosome 11 and chromosome 13 of *I. punctatus*) separately.

Disscusion and Conclusion

In our study, eleven sex-related QTLs were found at LG3 suggested that the sex of the yellow catfish may be primarily associated with this linkage group. To get further proofs for this inference, we screened the region near the significant markers and identified 6 sex-related genes. For instance, *amh*, during the period of sexual differentiation of zebrafish, has a male-specific expression indicates that an involvement of amh in male sex differentiation.

Moreover, the high-density linkage map is useful to analyze the genetic relationships between model species and related non-model species. Here, we performed the comparisons among the yellow catfish, zebrafish (model fish species) and channel catfish (related species). The results providedevidence that the yellow catfish is more closely related to the channel catfish genome than the genome of zebrafish. Interestingly, extensive syntenic blocks were quite obviously observed in comparison between the yellow catfish and channel catfish though they are in different taxonomic families (*Bagridae* and *Ictaluridae* respectively).

In conclusion, this is the first time to report the high-density genetic map of yellow catfish. And the high-resolution genetic linkage map offered usefulresources of molecular breeding of complex traits and will facilitate production and economic value of yellow catfish.