Research on sex determination mechanism and sex chromosome of *Fenneropenaeus chinensis*

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Introduction

Fenneropenaeus chinensis is a commercially cultured shrimp in China. *F. chinensis* adults show significant sexual dimorphism; the females are larger than the males. However, sex determination *of F. chinensis* has not yet been elucidated.

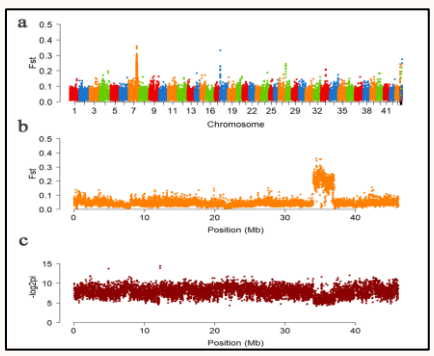
Materials and Methods

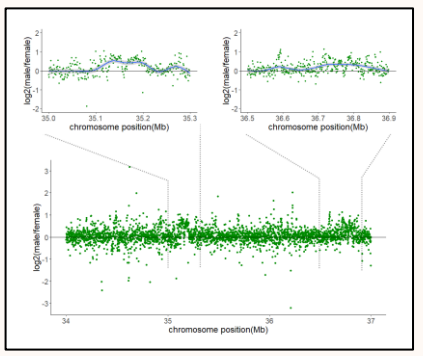
We randomly selected 10 female and 11 male *F. chinensis* ‘Huanghai No.1’ shrimps at 4 months old. The fixation index (F_{ST}) and nucleic acid polymorphism (π) were calculated to detect the genetic differentiation of the 2 sexes of *F. chinensis* on the basis of resequencing data. We assembled female-specific sequences basing on the resequencing data, and analyzed the RNA-seq data to profile the expression of two sexes of shrimps.

Results

Increased F_{ST} was observed on Chr7, spanning a region of approximately 3 Mb, from 34 to 37. In female, nucleotide diversity (π) increased in the same interval, as expected in a system of female heterogamety. There are 60 genes located on this 3 Mb interval according to the genomic annotation file.

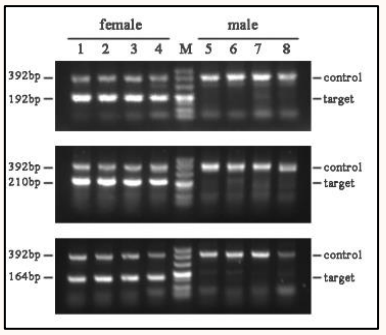
The mapping depth was estimated across Chr7. More reads aligned to the 34 - 37 Mb interval in the males than in the females, and the ratio of male to female coverage in some zones was close to 2:1.

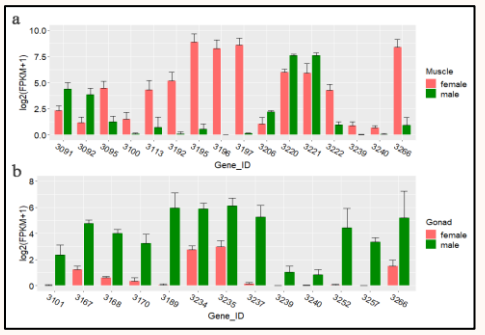




In total, we obtained 103.25 Mb of fragments, consisting 435,866 contigs, with 70 contigs longer than 2,000 bp. After further screening, we obtained 363 candidate female-specific contigs.

We selected 16 of the longest candidate female-specific contigs for validation. Sequences from three contigs amplified only with female DNA pools. Further validation was performed using individual DNA templates .



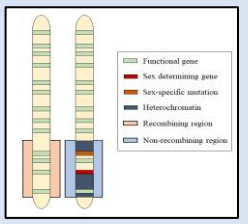


We detected abundant differentially expressed genes (DEGs). DEGs in the gonad showed a higher proportion of male-biased expression on Chr7 than other chromosomes.

In the 34–37 Mb interval of Chr7, we found the expression of all 13 DEGs in gonad was male-biased; even expression of the adjacent genes was male-biased.

Discussion

The Chr7 was regarded as candidate sex chromosome in this study. In the differentiation region, the higher read mapping depth in males and the increased π in females suggest that the sex determination system of *F. chinensis* is ZW/ZZ.



However, the sex chromosome formation of this species may only stay a primary stage.

All the DEGs in and near the candidate Z-linked region exhibited male-biased expression, suggesting that many mutations causing male-biased expression have accumulated. These DEGs may be related to sex development and sexual dimorphism or reproduction.

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