

Transcriptome profile of sex-related gene expression and effects of cyp19a1 Sirna-silencing on sex differentiation and determination in yellow perch

ABSTRACT

In this study, we first sequenced the whole genome of the yellow perch (YP, *Perca flavescens*) and screened transcripts of brain, liver, and gonadal tissues from fish of different sexes. By comparing known female sex-related genes in fish such as *cyp19a1* and *dmrt1* with YP genome, we obtained full-length sequences through genomic homology analysis. Then an experiment was conducted to evaluate the effects of *cyp19a1*-siRNA interference on gonadal development and sex differentiation and determination in YP. Transcriptome analysis revealed that the gonadal tissue of female YP exhibited predominantly and differentially up-regulated expression of genes than males, and *cyp19a1* was predominantly expressed in the gonads while *cyp19a2* showed predominant expression in the brain. KEGG pathway enrichment analysis illustrated the metabolic pathways of the top 25 enriched genes and confirmed CYP19 (P450) pathway in YP. For the *cyp19a1*-siRNA interference experiment, four intermittent in vivo injections of siRNA were administered to interfere with *cyp19a1* gene expression in an all-female group of YP. The results collected at 180 dph revealed that the siRNA interference resulted in an incomplete masculinization and hermaphroditism of all-female monosex YP, displaying the presence of male spermatocytes along with female oocytes. In contrast, tissues from the blank control and negative control groups only contained oocytes. The appearance of the gonads in the experimental group appeared more irregular, lacking the smooth surface and typical histoarchitecture observed in the blank control and negative control groups. In addition, the *cyp19a1*-siRNA treatment group had significantly ($P < 0.05$) lower body weight than the control groups, indicating that the interference with *cyp19a1* might have affected the expression of estrogen, leading to a trend similar to the growth of males; similarly, the gonad weight and GSIs of the *cyp19a1* group were significantly ($P < 0.05$) lower than those in the control groups, suggesting that the *cyp19a1*-siRNA interference might have led to a trend of male type of gonadal development. Meanwhile, the treatment group had significantly ($P < 0.05$) higher HSI and VSI levels compared to control groups, indicating that stimulation of external siRNA might have resulted in more vigorous liver metabolism processes. Furthermore, the expression level of the *dmrt1* in the treatment group was significantly ($P < 0.05$) upregulated compared to the control groups, suggesting the correlation roles between these two genes in the regulation of sex development. The findings provide valuable insights for future research

into the underlying mechanisms involved and hold significant promise for sex control in aquaculture