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Transcriptome analysis of the Yesso scallop, *Patinopecten yessoensis* gills in response to water temperature fluctuations

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ABSTRACT: Water temperature fluctuations are considered to be a major factor affecting the immune functions and metabolic processes of scallops. To better understand the immune defense mechanisms of Yesso scallop, *Patinopecten yessoensis* following exposure to water temperature fluctuations, transcriptomic profiles in the gills from high-frequency fluctuations (HF_G), low-frequency fluctuations (LF_G), and no fluctuations (NF_G) groups were obtained using HiSeq™ 2500 (Illumina). For HF_G, scallops were transferred directly between 18 and 8°C every 4 h and for 10 fluctuations, while scallops in LF_G were transferred between 18 and 13°C every 12 h, for a total of 4 fluctuations. A total of 442,922,590 clean reads were generated in 9 libraries and then assembled into 210,780 unigenes with an average length of 705 bp and an N50 of 1253 bp. Based on sequence similarity, 54,529 unigenes (25.87%) were annotated in at least one database. Comparative analysis revealed that 696 unigenes differentially expressed in temperature stressed groups compared with the control, including 229 unigenes between HF_G and NF_G, and 548 unigenes between LF_G and NF_G, respectively. Additionally, among these differentially expressed genes (DEGs), there were 41 immune-related unigenes and 16 protein metabolism-related unigenes. These results provide fundamental information on the molecular defense mechanisms in the Yesso scallop gills after exposure to water temperature fluctuations.

Key words: Transcriptome, *Patinopecten yessoensis*, water temperature fluctuations

1. Introduction

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