

Coding and long noncoding transcriptomic responses of *Emiliania huxleyi* to viral infection

ENQUAN ZHANG, WEICONG CAI, AND JINGWEN LIU*

College of Food and Bioengineering, Jimei University, Xiamen 361021, China (* correspondence: ljwsbch@163.com)

Methods and results

We analyzed the global transcriptome changes of marine phytoplankton *Emiliania huxleyi* in response to its specific virus (EhV). As a result, a total of 14695 mRNAs and 4294 lncRNAs were differentially expressed at 6 h and 45 h post-infection. KEGG enrichment analysis of DE lncRNAs showed that some metabolic pathways were regulated by lncRNAs, including fatty acid metabolism, steroid metabolism, terpenoid backbone biosynthesis and so on. These pathways were shown in the figure below.

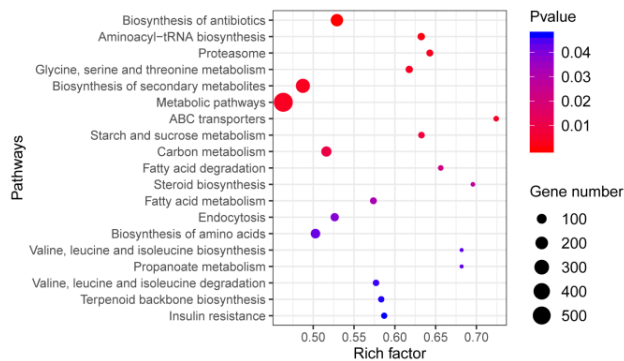


Figure 1: Pathway enrichment analysis of DE lncRNAs.

Discussion of results

Our transcriptomic results showed that there was a deep remodeling of transcripts associated with lipid metabolism under the condition of viral infection, indicating that lipids might be the key materials in the process of viral infection. This result was consistent with previous studies [1, 2]. We identify a multitude of novel lncRNAs specifically responsive to viral infection, suggesting putative regulatory roles in the regulation of EhV infection. Twenty of these lncRNAs were validated by reverse transcription qPCR. Moreover, part of the DE mRNAs linked with lipid metabolism were predicted to be the target mRNAs of lncRNAs (correlation coefficient cutoff was 0.95), so we speculated that these mRNAs might be regulated by lncRNAs.

[1] Zeng *et al.* (2019) *Sci Total Environ* **688**, 521-528. [2] Rosenwasser *et al.* (2014) *Plant Cell* **26**, 2689-2707.