

## **Iso-seq and RNA-seq profiling of *Fenneropenaeus penicillatus*: Unravelling the signaling pathway and genes involved in the ovarian development**

### **ABSTRACT**

The impediment of inadequate shrimp gonad development has adversely affected their production in the aquaculture sector. One promising strategy to enhance the quality and timing of offspring for commercial purposes is the regulation of their reproductive activity. Nevertheless, the availability of information pertaining to ovarian development in *Fenneropenaeus penicillatus* remains limited. To address this knowledge gap, our study employed a multi-faceted approach, integrating cutting-edge technologies such as Iso-seq, RNA-seq, RT-qPCR, histological and morphological observations. The Iso-seq generating 81,964,598 subreads with an average length of 1600 bp. This effort yielded 926,713 CCS reads and 557,043 FLNC reads, culminating in a robust set of 16,587 non-redundant full-length transcripts. This study utilized CPC, CPAT, PLEK, and pfam, to predict the numbers of long non-coding RNAs (lncRNAs). The outcomes were as follows: 5204, 4478, 7055, and 8175 lncRNAs, respectively. Our findings unveiled the intricate molecular underpinnings of ovarian development, encompassing pivotal pathways such as oocyte meiosis, insulin signaling pathway, oxytocin signaling pathway, progesterone-mediated oocyte maturation, estrogen signaling pathway, and GnRH signaling pathway. Notably, we identified specific genes—including Vtg, VgR, Sxl4, UCH, Hsp70, PP1, CDK2, Rheb, MKK3, and CDC42—that exhibited dynamic expression patterns during ovarian development. This study has produced a comprehensive dataset of full-length transcripts that holds significant potential as a genomic reference for future research on *F. penicillatus*. Furthermore, these insights may substantially contribute to the advancement of artificial breeding techniques and the ongoing development of sustainable aquaculture practices for *F. penicillatus*.