

# GENOME SEQUENCING AND ASSEMBLY STRATEGIES AND A COMPARATIVE ANALYSIS OF THE GENOMIC CHARACTERISTICS IN PENAEID SHRIMP SPECIES

Jianbo Yuan\*, Xiaojun Zhang, Fuhua Li and Jianhai Xiang

CAS and Shandong Province Key Laboratory of Experimental Marine Biology  
Center for Ocean Mega-Science, Institute of Oceanology  
Chinese Academy of Sciences, 7, Nanhai Road  
Qingdao 266071, China  
yuanjb@qdio.ac.cn

Penaeid shrimp (family Penaeidae) represents one of the most economically and ecologically important groups of crustaceans. However, their genome sequencing and assembly have encountered extreme difficulties during the last twenty years.

In this study, based on our previous genomic data, we investigated the genomic characteristics of four penaeid shrimp species, and identified potential factors resulting in their poor genome assembly, including heterozygosity, polyploidization and repeats.

Genome sequencing and comparison of somatic cells (diploid) of four shrimp species and a single sperm cell (haploid) of *Litopenaeus vannamei* identified a common bimodal distribution of K-mer depths, suggesting either high heterozygosity or abundant homo-duplicated sequences present in their genomes. However, penaeids have not undergone whole genome duplication as indicated by a series of approaches. Besides, the remarkable expansion of simple sequence repeats was another outstanding character of penaeid genomes, which also made the genome assembly highly fragmented. Due to this situation, we tried to assemble the genome of penaeid shrimp using various genome sequencing and assembly strategies and compared the quality. Therefore, this study provides new insights about the genomic characteristics of penaeid shrimps, while also improving their genome assemblies.