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Innovation & Investment

A novel chromosome-level genome assembly of the Pacific white shrimp

22 January 2024

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Significant expansion of gene families was observed in the genome related to locomotion, vision and neural transmission

This study details the generation of a high-quality de novo assembly of the *L. vannamei* genome, addressing the limitations of previous fragmented assemblies. It provides a more accurate representation of the *L. vannamei* genome but also offers new avenues for functional genomics, breeding programs, and comparative evolutionary studies in this economically significant species. Photo by Darryl Jory.

A genome is all the genetic information of an organism. A high-quality reference genome is crucial for genetic improvement of species and the exploration of the molecular mechanisms underlying important biological processes. However, shrimp genomes contain numerous repetitive sequences, rendering assembly a challenge. Recently developed **third-generation sequencing technologies** (https://doi.org/10.1111/1755-0998.13463) have helped alleviate assembly difficulties caused by heterozygosity and repetitive sequences in genomes.

The genomes of several shrimp species of commercial importance – including black tiger shrimp (*Penaeus monodon*), Chinese white shrimp (*Fenneropenaeus chinensis*), Kuruma shrimp (*Marsupenaeus japonicus*) and others – have recently been assembled using these newer third-generation sequencing technologies. However, compared to other species, the availability of shrimp genomes is still limited.

A draft genome of *L. vannamei* has been previously generated, although it is highly fragmented and is not constructed at the **chromosomal level** (https://doi.org/10.1038/s41467-018-08197-4). The lack of a high-quality genome impedes further genetic research on *L. vannamei*.

This article – summarized from the **original publication** (https://doi.org/10.1016/j.aqrep.2023.101859) (Peng, M. et al. 2023. A high-quality genome assembly of the Pacific white shrimp (*Litopenaeus vannamei*) provides insights into its evolution and adaptation. *Aquaculture Reports* Volume 33, December 2023, 101859) – reports on a study to generate a high-quality genome assembly of *L. vannamei* and provide critical new genomic information for shrimp breeding and investigations of this shrimp species.

(https://cvent.me/m23mdm)

Study setup

A de novo assembly refers to the genome assembly of a novel genome from scratch without the aid of reference genomic data. For sequencing and assembly of the genome, *L. vannamei* samples were obtained from the Shrimp Genetic Breeding Center at the Guangxi Academy of Fisheries Sciences (Nanning, China). Genomic DNA was extracted from muscle tissue and genomic libraries using a commercial kit (SMRTbell kit, PacBio, USA) according to the manufacturer's protocol and sequenced on the PacBio Sequel platform. This DNA was then processed and analyzed in detail.

For detailed information on the sequencing and assembly of the *L. vannamei* genome; gene annotation; repeat sequence annotation; transcriptomic sequencing of various tissues; and evolutionary analysis, refer to the original publication.

Results and discussion

L. vannamei has received widespread research attention due to its enormous economic value. A draft genome of this species was previously published, although this earlier genome assembly remains relatively fragmented and incomplete, limiting its applicability as a reference for breeding and research.

To obtain a resolved genome of *L. vannamei*, we used novel technologies in this study to generate a high-quality de novo assembly of the genome, with a total length of 1869 megabases (Mbp; megabases or millions of base pairs, is one of the ways used to measure the size of a genome) and other improved characteristics. These metrics considerably improve on the previously published incomplete genome assembly.

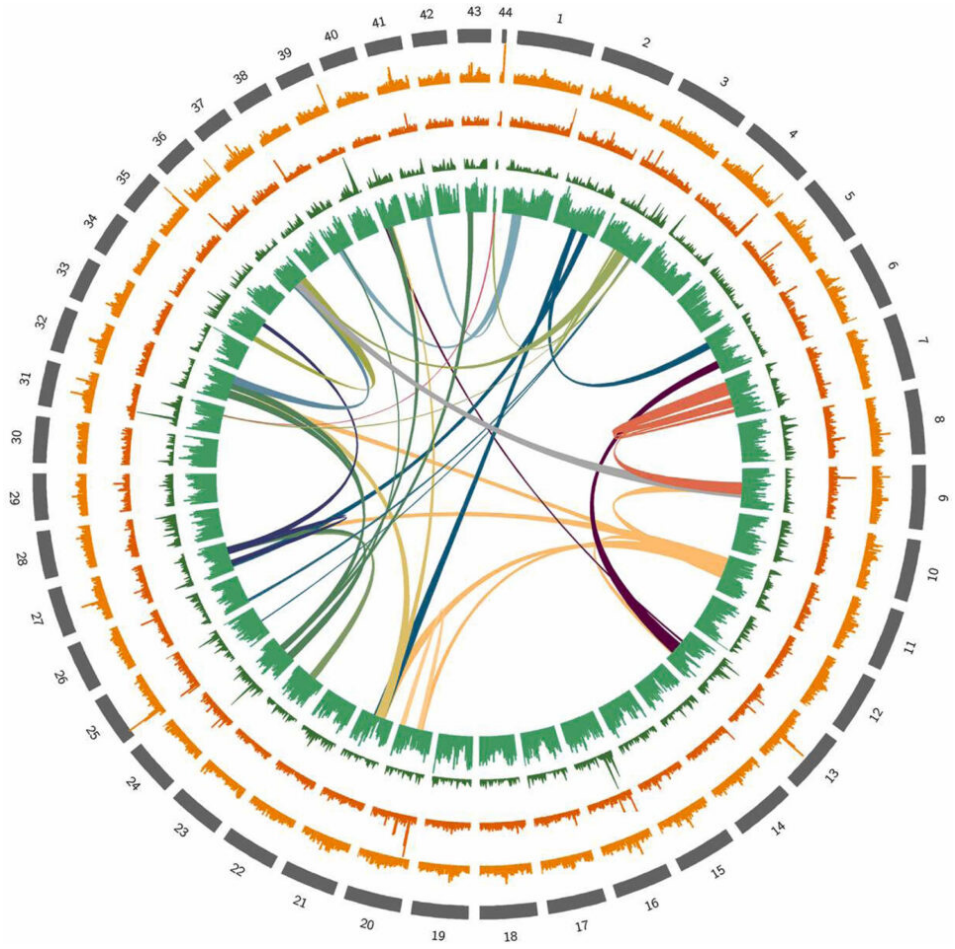


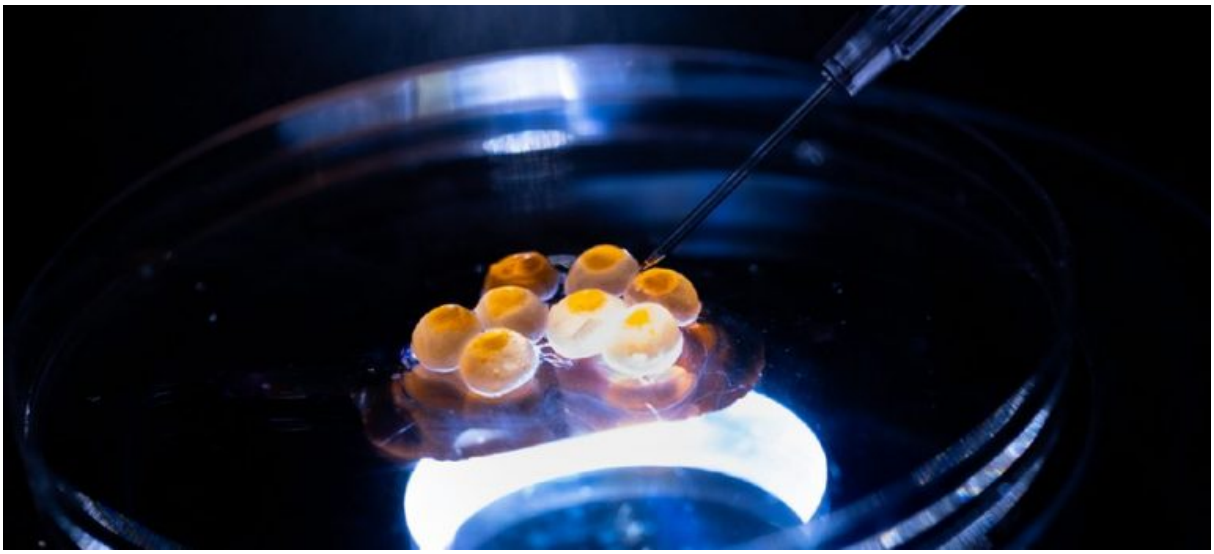
Fig. 1: Circos plot (visualization tool that facilitates the identification and analysis of similarities and differences arising from comparisons of genomes) showing *L. vannamei* genome characteristics. Track 1 (from the outermost ring inwards) shows the individual chromosomes of the genome. Adapted from the original.

This improved genome assembly provides a more comprehensive and accurate representation of the *L. vannamei* genome, enabling deeper insights into its genetic composition and regulatory mechanisms. It also opens up new opportunities for research and applications. Researchers can now explore the gene content, evolution and functional aspects of *L. vannamei* in greater detail, including investigations into key traits such as growth, reproduction, disease resistance and environmental adaptation.

Additionally, this high-quality genome assembly serves as an invaluable reference for future studies on *L. vannamei* genomics, allowing the identification and annotation of previously unknown genes and regulatory elements and facilitating comparative genomics studies to understand evolutionary relationships and the genetic basis of phenotypic diversification within the shrimp family.

While previous research has suggested that the haploid (single set) chromosome count of *L. vannamei* is 44, more research may be necessary to precisely determine the exact number of chromosomes in this species.

Regarding the annotation of repetitive sequences (short or long patterns of nucleic acids – DNA or RNA – that occur in multiple copies throughout the genome), our results showed a lower proportion compared to a previous study. This variation could stem from the utilization of improved genome assembly techniques in our research or the possibility of missing repeats in our assembly.



With tools like CRISPR, can genome editing deliver more resilience for aquaculture?

Research in Japan shows genome editing can improve muscle growth in farmed fish, resulting in less feed and boosting disease resistance.

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Repetitive sequences play a crucial role in genome structure and function, as they are known to regulate gene expression in *F. chinensis* and *L. vannamei*, driving adaptive evolution, such as the variable osmoregulatory capacity of these shrimps under low salinity stress. Future studies should focus on addressing the limitations in our assembly to enhance our understanding of the repetitive content within the *L. vannamei* genome.

Expansion or contraction of gene families are key mechanisms in organismal adaptive evolution. We observed significant expansion of some gene families in the *L. vannamei* genome. Expanded gene families included some that are primarily involved in movement functions, in addition to other gene families involved in visual and neural transmission functions. The significant expansion of these gene families could lead to enhanced visual, neural speed, and movement capabilities *of L. vannamei*, perhaps enabling their adaptation to escape predation in dark benthic habitats. The abundant gene repertoire in the *L. vannamei* genome related to visual, neural transmission and movement may explain their benthic adaptations.

We also constructed a phylogenetic tree involving *L. vannamei* and 11 other arthropod species. Our findings suggest that *L. vannamei* is closely related to other crustaceans like the marbled crayfish (*Procambarus virginalis)* and the giant freshwater prawn (*Macrobrachium rosenbergii*) and supporting previous studies. However, it is noteworthy that the water flea (*Daphnia pulex*), another crustacean, did not cluster with *L. vannamei*, and this may be due to its small genome size of only 200 Mbp, resulting in significant genetic differences compared to *L. vannamei* with a much larger genome size. This result contradicts the results of previous research and further investigation is required in future studies.

Fig. 2: Comparison of gene families in the genomes of *L. vannamei* and 11 other arthropods. (A) Petal plot visualization showing gene family clusters among the 12 species. The number in the central circle is the number of gene families common to all species and the petals show the numbers of gene families unique to each species. (B) The top 20 enriched KEGG (the Kyoto Encyclopedia of Genes and Genomes is a collection of databases dealing with genomes, biological pathways, diseases, drugs and chemical substances. KEGG is utilized for bioinformatics research and education, including data analysis in genomics, metagenomics, metabolomics and other omics studies, modeling and simulation in systems biology and translational research in drug development) pathways for species-specific genes. Adapted from the original.

Perspectives

This study documented the generation of a high-quality de novo assembly of the *L. vannamei* genome, addressing the limitations of previous fragmented assemblies. Our refined product not only provides a more accurate representation of the *L. vannamei* genome but also offers new avenues for functional genomics, breeding programs and comparative evolutionary studies in this economically significant species.

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