

Chromosome-level genome assembly of *Scapharca kagoshimensis* reveals the expanded molecular basis of heme biosynthesis in ark shell

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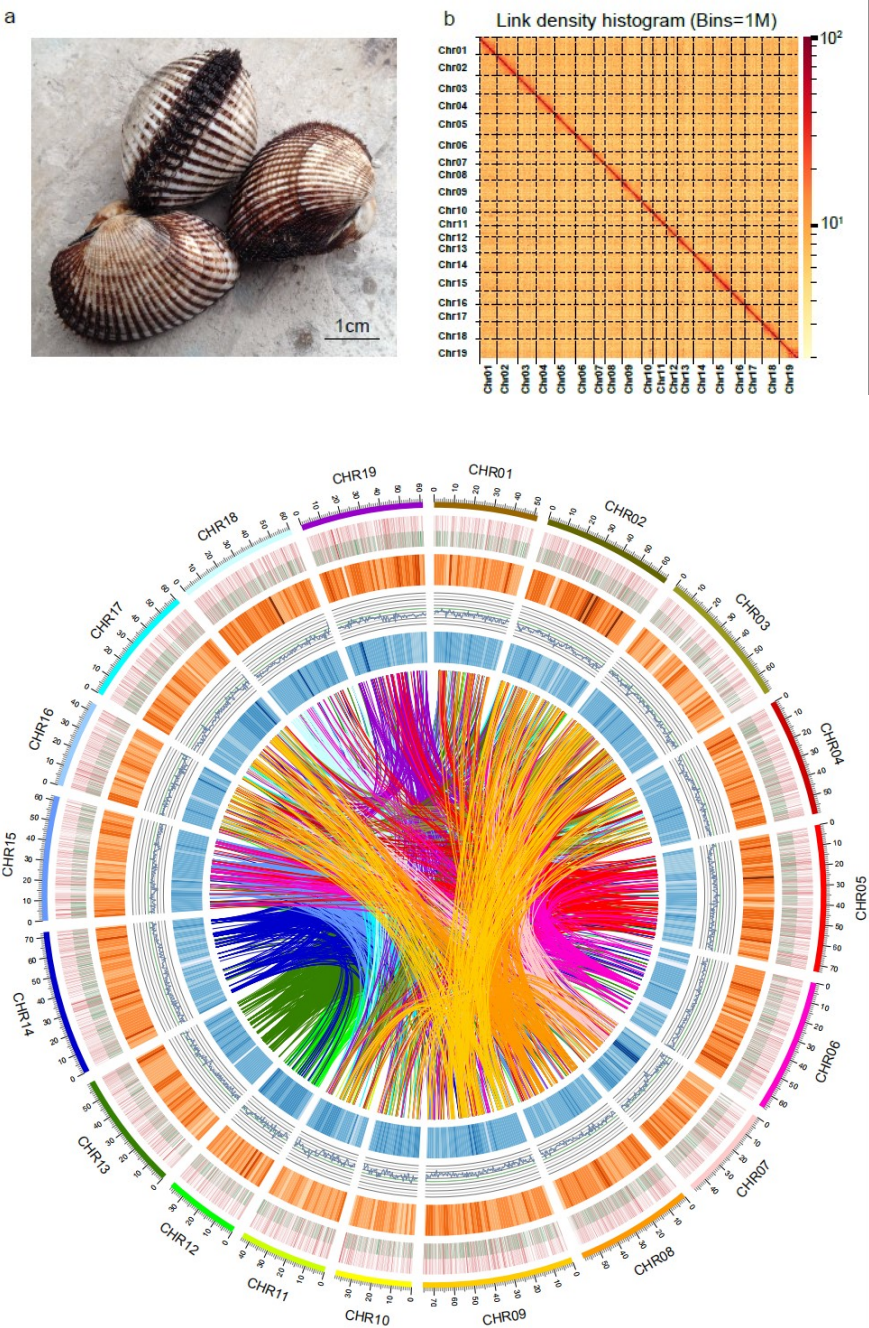
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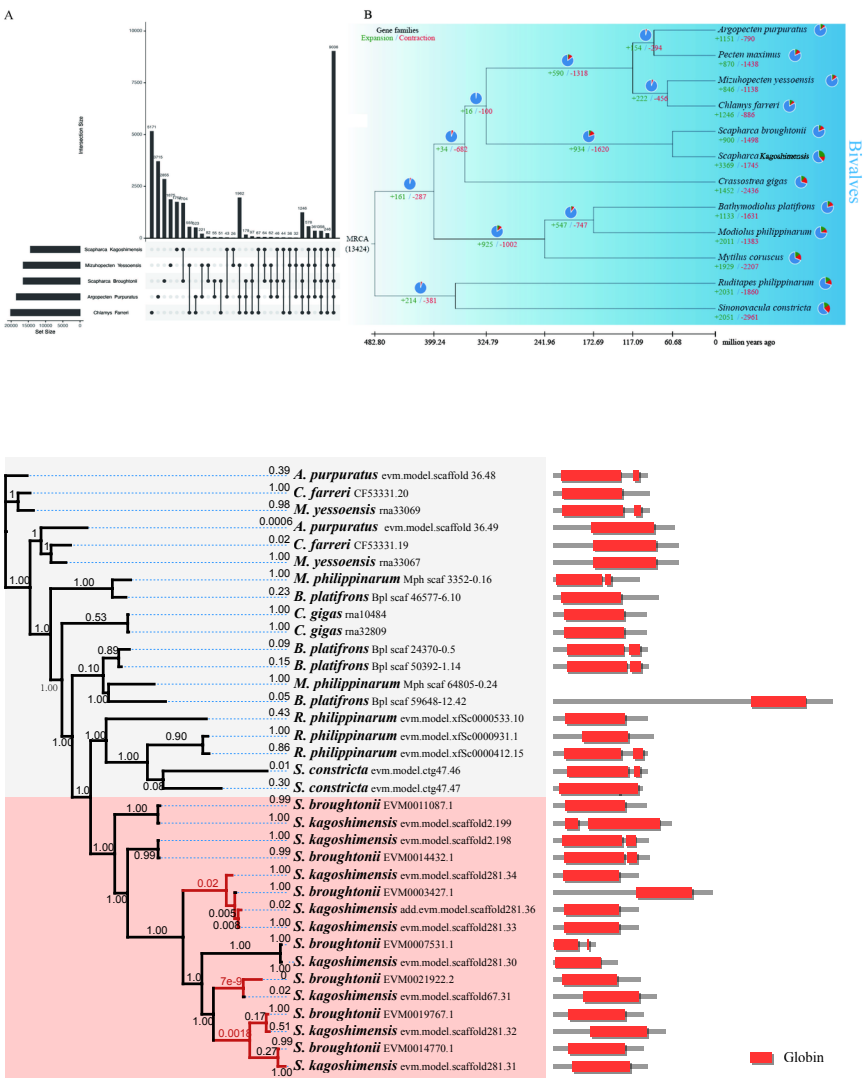
Abstract

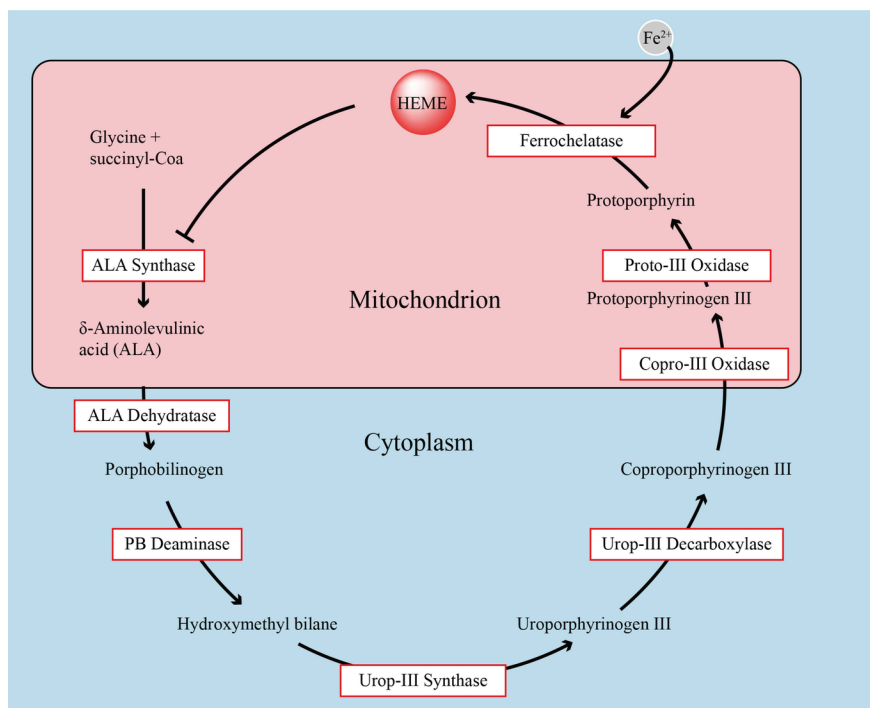
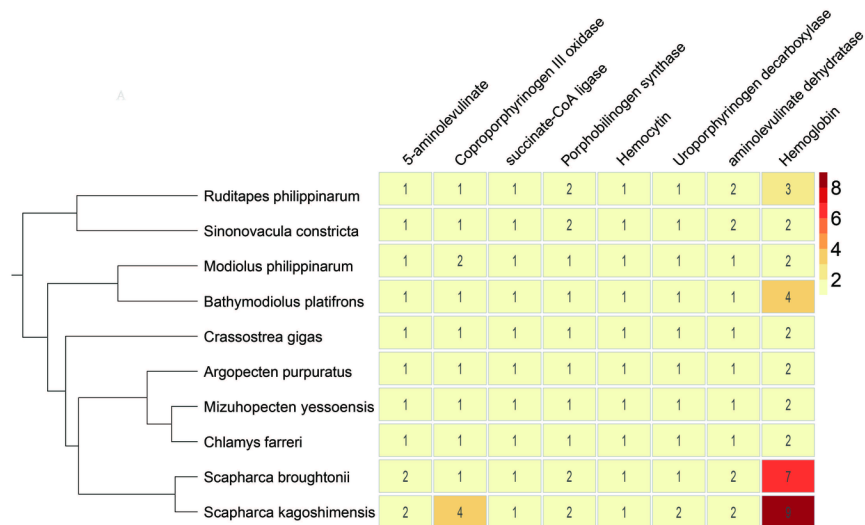
Ark shells are commercially important clam species that inhabit in muddy sediments of shallow coasts in East Asia. For a long time, the lack of genome resources has hindered scientific research of ark shells. Here, we reported a high-quality chromosome-level genome assembly of *Scapharca kagoshimensis*, with an aim to unravel the molecular basis of heme biosynthesis, and develop genomic resources for genetic breeding and population genetics in ark shells. Nineteen scaffolds corresponding to 19 chromosomes were constructed from 938 contigs (contig N50=2.01 Mb) to produce a final high-quality assembly with a total length of 1.11 Gb and scaffold N50 around 60.64 Mb. The genome assembly represents 93.4% completeness via matching 303 eukaryota core conserved genes. A total of 24,908 protein-coding genes were predicted and 24,551 genes (98.56%) of which were functionally annotated. The enrichment analyses suggested that genes in heme biosynthesis pathways were expanded and positive selection of the hemoglobin genes was also found in the genome of *S. kagoshimensis*, which gives important insights into the molecular mechanisms and evolution of the heme biosynthesis in mollusca. The valuable genome assembly of *S. kagoshimensis* would provide a solid foundation for investigating the molecular mechanisms that underlie the diverse biological functions and evolutionary adaptations of *S. kagoshimensis*.

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