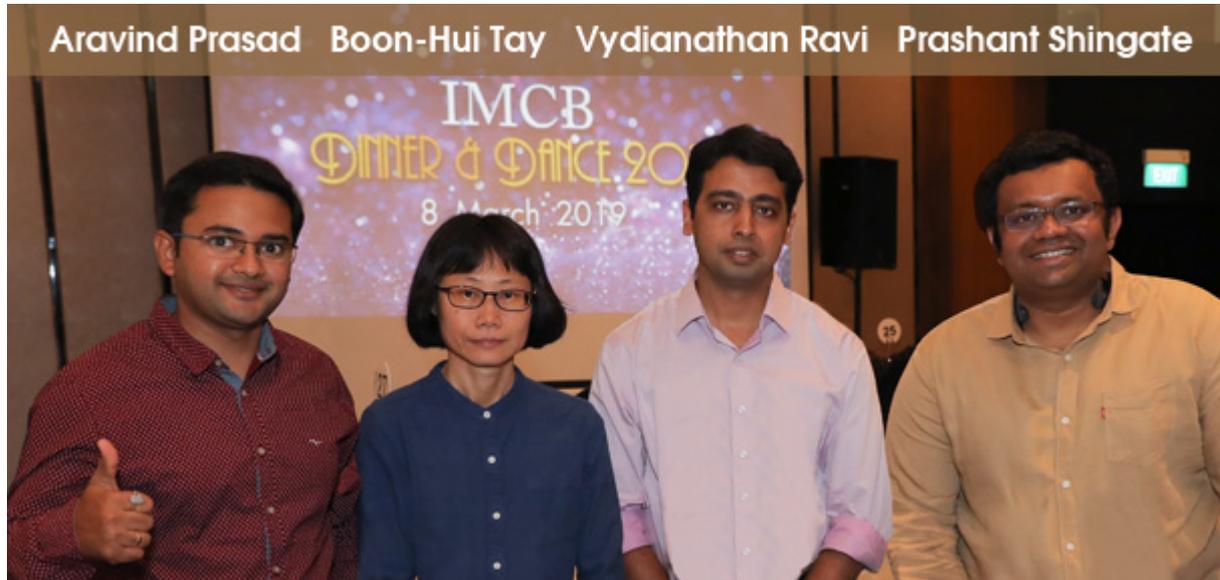


Chromosome-level assembly of the horseshoe crab genome provides insights into its genome evolution

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Abstract

Horseshoe crabs, popularly known as “living-fossils”, have existed for over 500 million years, yet are represented by only four living species. Singapore is home to two (mangrove horseshoe crab and coastal horseshoe crab) of the four species. However, their populations are under threat due to coastal developments, habitat destruction and irresponsible fishing. Thus, there is an urgent need to understand their genetic diversity and population structure, and to develop strategies for conserving their populations. Here we report a chromosome-level genome assembly for the mangrove horseshoe crab (*Carcinoscorpius rotundicauda*) using PacBio reads and Hi-C data. The assembly spans 1.67 Gb and 98% of the genome assigned to 16 chromosomes. Reconstruction of the population history showed that the mangrove horseshoe crabs experienced a drastic decline in their population ~60,000 years ago. Unexpectedly, detailed analysis of the genome provided evidence that suggests three rounds of whole-genome duplication (WGD) in the horseshoe crab lineage. The presence of only four species of horseshoe crabs in spite of three WGD events challenges the generally held view that WGD triggers species diversity and radiation. Several gene families, particularly those involved in innate immunity, have undergone extensive tandem duplication in the horseshoe crab genome. These expanded gene families may be important components of the innate immune system of horseshoe crabs, whose amebocyte lysate is a sensitive agent for detecting endotoxin contamination.

Figure

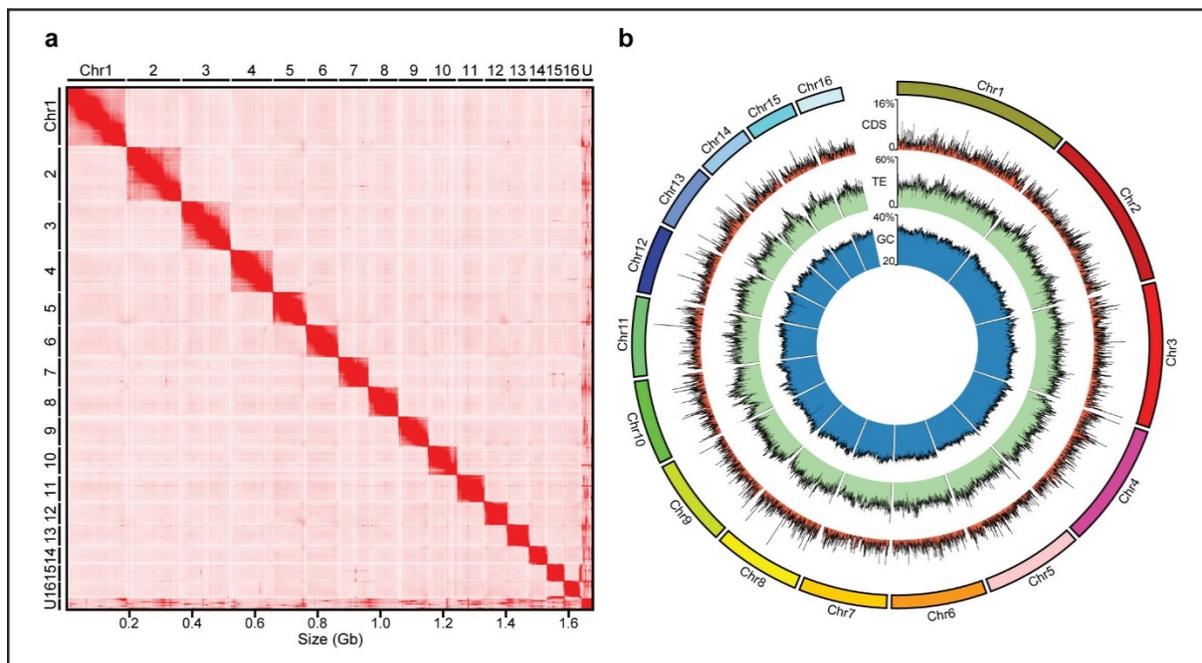


Figure Legend

Mangrove horseshoe crab genome assembly. (a) Hi-C contact map of the mangrove horseshoe crab genome assembly. U, unplaced scaffolds. (b) CIRCOS plot showing the distribution of GC content, transposable elements (TE) and coding sequences (CDS) in the genome.

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