



# Characterization of the complete mitochondrial genome and phylogenetic relationships of the three-spot swimming crab (*Portunus sanguinolentus*)

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**ABSTRACT.** In this study, we determined the whole mitochondrial genome profile of the three-spot swimming crab (*Portunus sanguinolentus*) and elucidated phylogenetic relationships between representative species in the order Decapoda. The mitochondrial genome was 16,024 bp in length and consisted of 13 protein-coding genes, 22 transfer RNA genes, two ribosomal RNA genes, and a putative control region. Of the 37 genes, 23 were encoded by the heavy strand while 14 were encoded by the light strand. Four types of start codons were identified; ATG initiated nine genes, ATT initiated two genes, and

ATC and GTG each started one gene. Nine protein-coding genes ended with a complete TAA or TAG stop codon, and four genes ended with an incomplete T or TA codon. Fourteen non-coding regions were found, which ranged from 1 to 34 bp in length. Nine overlaps were observed, with lengths between 1 and 7 bp. Phylogenetic analysis suggested that *P. sanguinolentus* is genetically closest to *P. trituberculatus* and *P. pelagicus*. *Charybdis feriata*, *C. japonica*, and *Thalamita crenata* formed a single cluster, and were close to the genera *Callinectes* and *Portunus*. Therefore, the genera *Charybdis* and *Thalamita* should be classified into the subfamily Portuninae.

**Key words:** *Portunus sanguinolentus*; Mitochondrion; Gene order; Phylogenetic relationship