

The complete mitochondrial genome of freshwater crab *Sinopotamon xiushuiense* (Decapoda: brachyura: Potamoidea)

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ABSTRACT

We report for the first time the complete mitochondrial genome of *Sinopotamon xiushuiense*, which is found to be 18,460 bp in length, and contains 13 protein-coding genes (PCGs), 2 ribosomal RNA (rRNA) genes, 22 transfer RNA (tRNA), and 1 non-coding region known as the D-loop. In addition, the mitogenome has 18 intergenic regions ranging from 1 to 1221 bp in length. The complete mitogenome of *S. xiushuiense* is the longest among brachyurans reported in GenBank before November 2015, and its AT content is slightly lower than that in *Geothelphusa dehaani*. The mitogenome data provides a basis for further studies on population genetics and phylogenetics.

ARTICLE HISTORY

Received 20 June 2016
Accepted 30 June 2016

KEYWORDS

Brachyuran; complete mitochondrial genome; phylogenetic; *Sinopotamon xiushuiense*

The genus *Sinopotamon* (Bott 1970) (Crustacea: Malacostraca: Decapoda: Brachyura: Potamidae) is endemic to mainland China. Due to geographical restrictions by mountain ranges, river basins, and other natural regions (Dai 1999), there is a high degree of species diversity. To understand the mechanism of the wide geographical distribution of this genus, it is important to know the genetic basis underlying the morphological variations. However, the complete mitogenome of *Sinopotamon* has not been reported. In this study, we report for the first time the complete sequence of mitochondrial genome for *S. xiushuiense*, providing the data for species identification, as well as for future studies on phylogeny and species conservation.

A male adult specimen of *S. xiushuiense* (catalogue number JX20140910) was collected from the mountain stream in Sanzhualun, Jing'an, Jiangxi Province, China in 2014 (N 29°04'32.454", E 115°13'08.736"). The sample was fixed in ethanol and then stored at -20 °C before sequence analyses. Genomic DNA extraction, sequencing, gene annotation, and phylogenetic analyses were performed according to the method described by Plazzi et al. (2013). The Bayesian Inference (BI) method was performed using MrBayes vers. 3.2 (Ronquist et al. 2012), with best model GTR+I+G selected by jModelTest vers. 2.1.7. The maximum-likelihood (ML) method was performed using MEGA 6.

There are 18,460 base pairs (bp) in the complete mitogenome of *S. xiushuiense* (GenBank accession no. KU042041). The genome is rich in AT (74.5% AT content). All genes of

the standard metazoan mitogenome are found, including 13 protein-coding genes (PCGs), 2 ribosomal RNA (rRNA) genes, 22 transfer RNA (tRNA, one for each amino acid, and two for serine and leucine), and 1 non-coding region known as the D-loop. The initiation codon of *S. xiushuiense* is the typical ATN codons, with the most common being ATG and another being ATA (*atp6*, *nd3*, *nd6*, and *nd1*). The most frequent complete termination codon is TAA (found in nine genes. *atp8* is terminated with codon TAG. Of the remaining genes, *cox2*, *nd5*, and *cytb* are terminated with the abbreviated stop codon T. The 16S and 12S rRNA are 1310 bp (76.1% AT content) and 828 bp (78.4% AT content) in length, respectively. The 22 tRNA genes of *S. xiushuiense* vary from 61 to 73 bp. The complete mitogenome of *S. xiushuiense* has 18 intergenic regions. The longest region (1221 bp with 81.3% AT content) is between *rrnL* and tRNA^{leu}. There are seven shorter intergenic regions (37–350 bp), with 76.7%–87.4% of AT content. The remaining intergenic regions range from 1 to 8 bp in length. The mitogenome of *S. xiushuiense* is the longest compared to those in other brachyuran species that GenBank has reported before November 2015, and its AT content is slightly lower than that in *Geothelphusa dehaani* (74.9% AT content) (Segawa & Aotsuka 2005; Liu et al. 2015).

The phylogenetic position of *S. xiushuiense* is mitogenome relative to other brachyuran mitogenomes is determined by applying the BI and ML methods on 11 PCGs (Figure 1). Only two mitogenomes of freshwater crabs have reported previously in GenBank, *G. dehaani* (complete

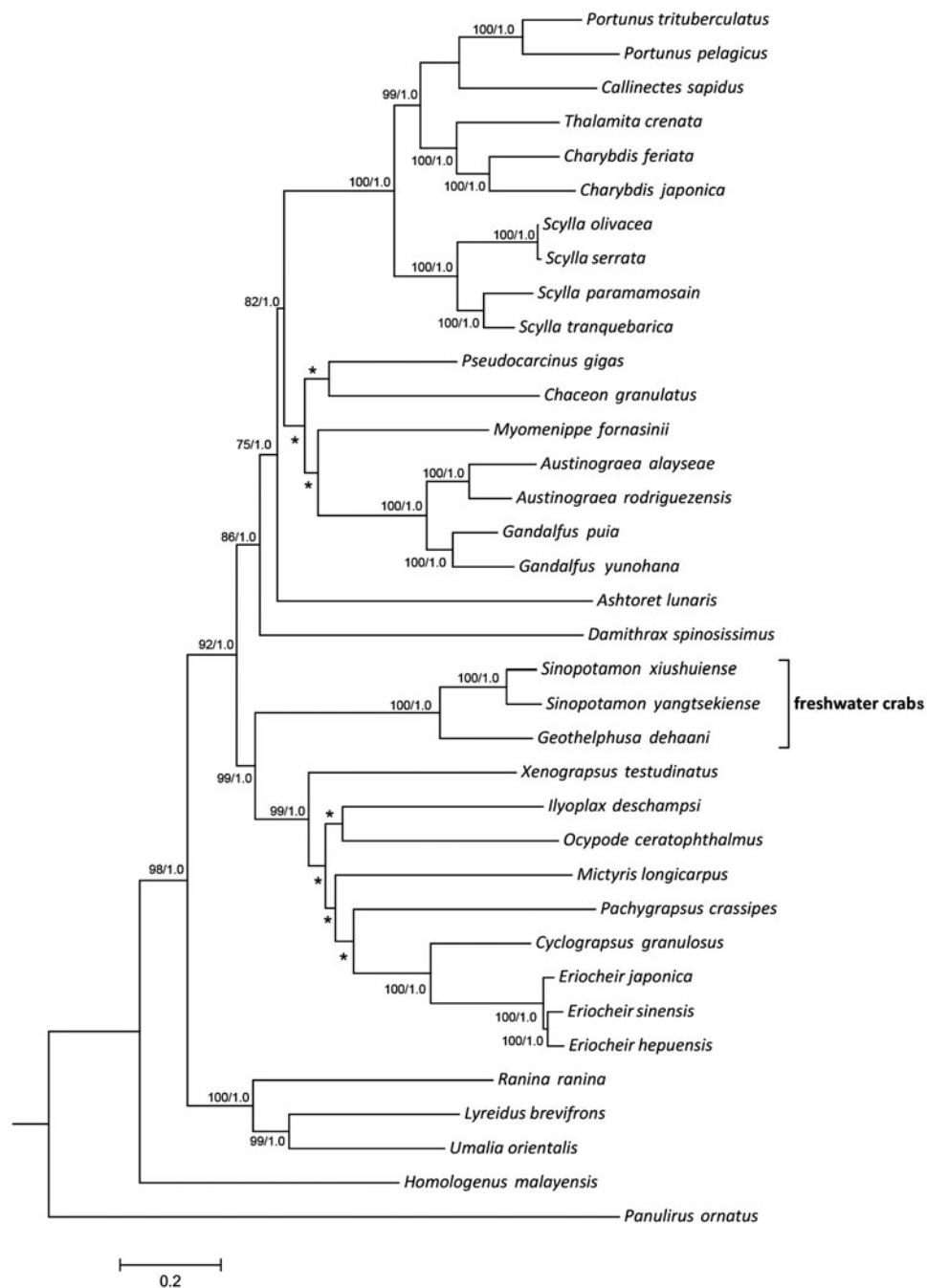


Figure 1. Phylogenetic maximum-likelihood (ML) tree of *Sinopotamon xiushuiense* and other related brachyurans based on 11 PCGs in mitogenomes. *Panulirus ornatus* is served as an outgroup. Numbers on internodes are ML bootstrap proportions and the BI posterior proportions. The differences of phylogenetic trees between ML and BI are indicated by '*'. The accession nos. of brachyuran crabs are *Portunus pelagicus* (KR153996), *Portunus trituberculatus* (AB093006), *Callinectes sapidus* (AY363392), *Charybdis feriata* (KF386147), *Charybdis japonica* (FJ460517), *Thalamita crenata* (LK391945), *Scylla olivacea* (FJ827760), *Scylla paramamosain* (JX457150), *Scylla serrata* (HM590866), *Scylla tranquebarica* (FJ827759), *Chaceon granulatus* (AB769383), *Pseudocarcinus gigas* (AY562127), *Myomenippe fornasinii* (LK391943), *Ashtoret lunaris* (LK391941), *Austinograea alayseae* (KC851803), *Austinograea rodriguezensis* (JQ035658), *Gandalfus puia* (KR002727), *Gandalfus yunohana* (EU647222), *Damithrax spinosissimus* (KM405516), *Ranina ranina* (AB752308), *Lyreidus brevifrons* (KM983394), *Umalia orientalis* (KM365084), *Homologenus malayensis* (KJ612407), *Sinopotamon yangtsekiense* (JF909980), *Geothelphusa dehaani* (AB187570), *Mictyris longicarpus* (LN611670), *Eriocheir hepuensis* (FJ455506), *Eriocheir japonica* (FJ455505), *Eriocheir sinensis* (KP126617), *Cyclograpsus granulatus* (LN624373), *Ilyoplax deschampsii* (JF909979), *Pachygrapsus crassipes* (KC878511), *Ocypode ceratophthalmus* (LN611669), *Xenograpsus testudinatus* (EU727203), and *Panulirus ornatus* (GQ223286).

mitogenome, contains 13 PCGs) and *S. yangtsekiense* (partial mitogenome, contains 11 PCGs). Our result shows that the freshwater crabs form a clade in brachyurans. *Sinopotamon xiushuiense* is the sister group of *S. yangtsekiense*, and they are sisters to *G. dehaani*. This result is consistent with morphological classification and other molecular analyses. (Dai 1999; Tsang et al. 2014).

Acknowledgements

We thank Dr Bin Li for reviewing the manuscript.

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the article.

Funding

This work was supported by National Natural Foundation of People's Republic of China [Nos 31460156, 81260257, 81160207 and 31560179] and Natural Science Foundation of Jiangxi, China [20132BAB205059]

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