

MITOGENOME ANNOUNCEMENT



The complete mitochondrial genome of the true limpet *Scurria scurra* (Lottiidae)

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ABSTRACT

The complete mitochondrial DNA sequence of the scurrinid limpet *Scurria scurra* (Lesson 1830) is reported here. This mitogenome is 18,482 bp long and includes two rRNA genes, 13 protein-coding genes, and 24 tRNAs. The genus *Scurria* is a nascent model group for marine ecological studies. This mitogenome will help to gain a better understanding of the phylogenetic relationships within Patellogastropoda, the most primitive group of extant gastropods.

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KEYWORDS

Scurria scurra; mitochondrial genome; Patellogastropoda; South Eastern Pacific

Scurria scurra is one of several species of the genus *Scurria*, one of the eight genera of Lottiidae, the most diverse family of Patellogastropoda. The genus *Scurria* is characterized by having conic shells with a complex prismatic external layer, and is restricted to the Southeastern Pacific coast (SEP) (Espoz et al. 2004). *S. scurra* is distributed from 24°S to 42°S (Espoz et al. 2004). *S. scurra* is found exclusively on two macroalgae (*Lessonia nigrescens* and *Durvillaea antarctica*) (Muñoz and Santelices 1989), an adaptation that is uncommon within true limpets. Most of these animals live on rocks and feed by scraping the microalgae film covering these surfaces. Scurrinid limpets are not commercially important species but play vital roles in the dynamics of intertidal communities of the SEP (Aguilera et al. 2013; Broitman et al. 2018). These organisms are a nascent model group for marine ecological studies, yet their phylogenetic relationships and evolutionary history remain poorly studied.

DNA was extracted using a commercial kit from one gonad sample of one individual captured in Calfuco, Chile (latitude −39.780325 and longitude −73.393157). The sample was collected under permit REx N 2036, 2019 from the Subsecretaría de Pesca y Acuicultura (SUBPESCA) of the Chilean government, and following policies and procedures of the Universidad Austral de Chile bioethical committee. The specimen was deposited at the Instituto de Ciencias Ambientales y Evolutivas, Facultad de Ciencias, Universidad Austral de Chile (voucher ID: ICAEV/N1/2020, contact: pablo.saenz@uach.cl). DNA was sequenced using PacBio sequel II. Reads were assembled using Wtdbg2 (Ruan and Li 2020). MITOs WebServer (Bernt et al. 2013) and Geneious prime v2021.1.1 (Biomatters Ltd., Auckland, New Zealand) were used for annotation.

The mitochondrial genome of *S. scurria* is 18,482 bp long and was deposited in GenBank (accession number

MZ196208). It includes 13 protein-coding genes, two ribosomal RNA genes, and 24 tRNA genes. The overall base composition was 31.3% A, 19.3% C, 22.4% G, and 27.1% T. A Bayesian phylogenetic tree was built using the concatenated amino acid sequences of the 13 protein-coding genes of *S. scurra* and 11 species within Patellogastropoda and one species of the order Heterobranchia (*Elysia cornigera*) as an out-group. Mitogenome sequences for all species are available in GenBank (Figure 1).

The phylogenetic relationships of all species are coherent with the most recent phylogeny generated using whole mitochondrial genomes (Feng et al. 2020) and placed *S. scurra* as sister species of *Lottia goshimai* and *Lottia digitalis*. Therefore, this new mitochondrial genome will be useful for further phylogenetic and population genetic studies of these gastropods.

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Authors contributions

PS-A conceived and designed the study, analyzed and interpreted the data, wrote the paper and approved the final version to be published. PS-A agrees to be accountable for all aspects of the work.

Disclosure statement

No conflicts of interest to declare.

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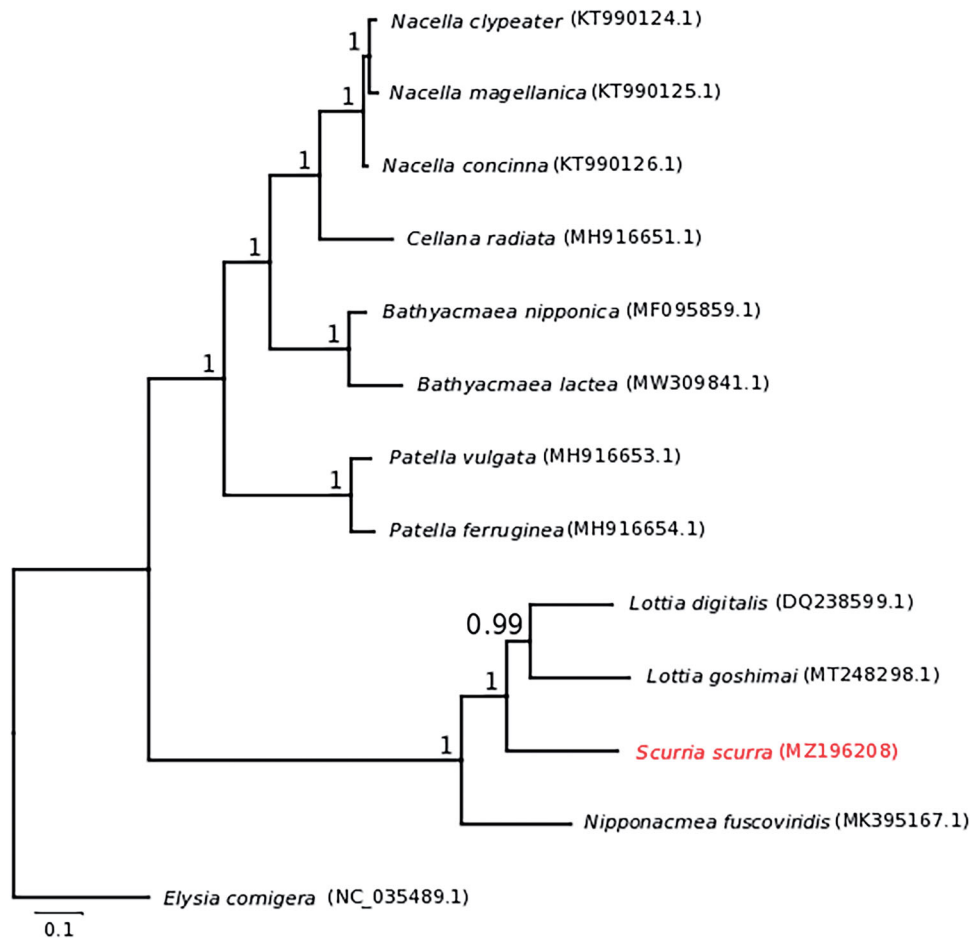


Figure 1. Bayesian inference tree based on 3606 amino acids of protein-coding genes, reconstructed using MrBayes (Huelsenbeck and Ronquist 2001), using a Poisson rate matrix and Gamma variation, burn-in of 100,000 and four 1,000,000 steps heated chains. Posterior probability values are indicated for each node.

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Data availability statement

The genome sequence data supporting this study's findings are openly available in GenBank of NCBI (<https://www.ncbi.nlm.nih.gov/>) and is available under accession number MZ196208. Biosample: SAMN24607335 and Bioproject: PRJNA794077.

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