



Data Article

Genome statistics and phylogenetic reconstructions for Southern Hemisphere helms (Gastropoda: Buccinidae)

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ABSTRACT

This data article provides genome statistics, phylogenetic networks and trees for a phylogenetic study of Southern Hemisphere Buccinidae marine snails [1]. We present alternative phylogenetic reconstructions using mitochondrial genomic and 45S nuclear ribosomal cassette DNA sequence data, as well as trees based on

Specifications Table

Subject area	Biolog
More specific subject area	Phylogenetics; Genetics; Evolutionary Biology
Type of data	Table, text file, graph, figure
How data was acquired	High-throughput and Sanger DNA sequencing
Data format	Text file format for DNA sequence alignments and phylogenetic trees is .nexus and .tree respectively.
Experimental factors	Total DNA was extracted from specimens using CTAB buffer. DNA was paired-end sequenced using the high-throughput Illumina HiSeq, 2500 platform. Short-length DNA sequences were amplified via PCR and Sanger sequenced.
Experimental features	

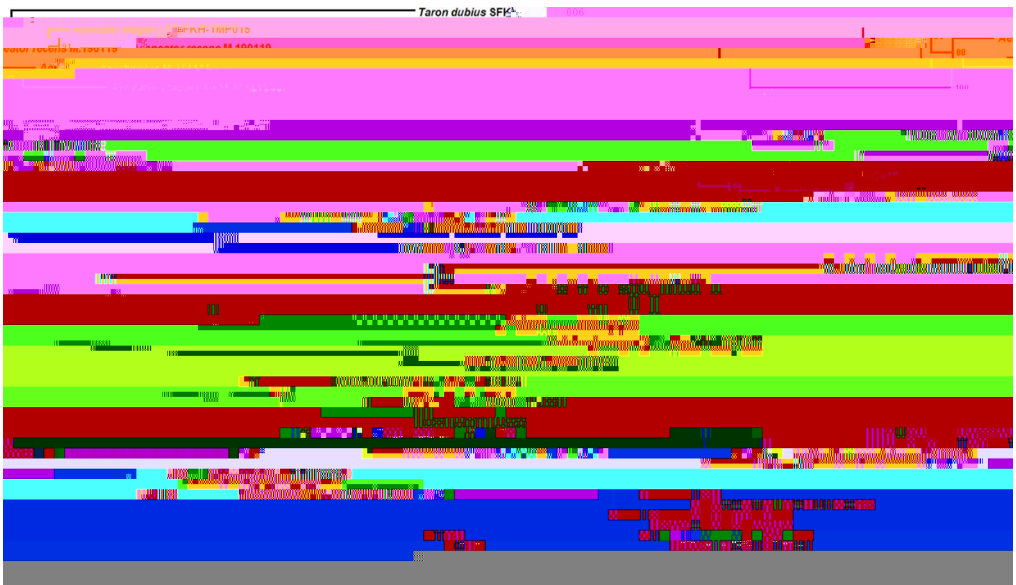


Fig. 2. Maximum-likelihood 45S rDNA phylogeny of buccinid and buccinulid whelks. A maximum-likelihood derived phylogenogram generated using RA ML 8.2.8 [9]



Fig. 6. Bayesian 16S RNA phylogeny of buccinid and buccinulid whelks. A Bayesian phylogenetic tree based on an alignment of mitochondrial 16S RNA gene sequences obtained from 35 individual marine snails (868 bp). The GTR + I + G substitution model was used [11]. The phylogenetic tree was produced using a Bayesian method (100 million MCMC, 10% burn-in, 1000 sample frequency, node labels are posterior probabilities), via BEAST 1.8.3 [16]. For this tree no outgroups were specified but reciprocal monophyly was enforced for the Fascioliariidae and Buccinidae/Buccinulidae/Nassariidae. Genera pertaining to Buccinulidae are shown in different colors.



Fig. 8.

Table 1

A summary of statistics for the length and nucleotide composition for the concatenated DNA sequences for the nuclear ribosomal RNA genes 18S, 5.8S and 28S (the internal transcribed spacer regions are not included). All listed specimens were sequenced for this study.

Species	Museum ID	Concatenated nuclear rDNA 18S, 5.8S, 28S					
		Length (bp)	% A	% C	% G	% T	GC bias
Pararetifusus carinatus	SFKH-TMP005	5337	23	24.5	30.0	22.2	54.5
Glaphyrina caudata	SFKH-TMP004	5339	23	24.5	30.0	22.2	54.5
Taron dubius	SFKH-TMP006	5339	23	24.7	30.1	22.0	54.8
Austrofuscus glans	SFKH-TMP014	5338	24	24.4	30.0	22.2	54.4
Colus islandicus	20140782	5334	24	24.5	30.0	22.2	54.5
Voluptosius norwegicus	20140781	5338	24	24.4	30.0	22.3	54.4
Buccinum undatum	20140783	5339	24	24.3	30.0	22.3	54.3
Cominella adpersa	SFKH-TMP009	5339	23	24.6	30.0	22.0	54.6
Cominella v. brookesi	SFKH-TMP010	5339	21	24.9	30.3	21.7	55.2
Buccinulum fuscozonatum	M.302907/2	5340	22	24.8	30.1	22.0	54.9
Buccinulum linea	SFKH-TMP016	5340	22	24.8	30.1	22.0	54.9
Buccinulum v. littorinoides	SFKH-TMP011	5340	22	24.7	30.1	22.0	54.8
Buccinulum pallidum	M.258277/6	5340	22	24.7	30.2	21.9	54.9
Buccinulum p. finlayi	M.302870/2	5340	22	24.7	30.1	22.0	54.8
Buccinulum robustum	M.314755/1	5340	22	24.8	30.1	21.9	54.9
Buccinulum v. vittatum	SFKH-TMP004	5340	22	24.7	30.1	22.0	54.8
Aeneator benthicolus	M.274111	5340	22	24.6	30.1	22.1	54.7
Aeneator elegans	SFKH-TMP015	5340	22	24.7	30.1	22.0	54.8
Aeneator otagoensis	M.279437	5340	22	24.7	30.2	21.9	54.9
Aeneator recens	M.190119	5340	22	24.6	30.1	22.1	54.7
Penion benthicolus	M.183832	5337	23	24.4	30.0	22.3	54.4
Kelletia kelleitii	KK12	5337	24	24.4	29.9	22.3	54.3
Kelletia lischkei	KL2	5337	24	24.3	29.9	22.4	54.2
Penion mandarinus	C.456980	5339	24	24.4	29.9	22.2	54.3
Penion maximus	C.487648	5339	25	24.4	29.9	22.2	54.3
Penion sulcatus	Phoeni 9	5339	23	24.4	30.0	22.3	54.4
Penion sulcatus	Phoeni 1	5339	23	24.4	30.0	22.3	54.4
Penion chathamensis	M.190085/3	5339	23	24.4	29.9	22.3	54.3
Penion chathamensis	M.190082/2	5339	23	24.4	29.9	22.3	54.3
Penion c. cuvierianus	M.183792	5339	23	24.3	30.0	22.3	54.3
Penion c. cuvierianus	M.183927	5339	23	24.3	30.0	22.4	54.3

Table 2

A summary of the statistics for the length and nucleotide composition for the mitochondrial genomes were sequenced as part of this study. Specimens marked with one asterisk (*) exhibit drops in read coverage for some small regions, for example *K. kelleitii* has 54 bp missing from *cox1*. Specimens marked with two asterisks (**) have genomes with large gaps in genome coverage for some regions, such as *B. v. vittatum* that has 266, 151 and 64 bp missing from the *ATP6*, *cox1* and *ND2* genes respectively.

Species	Museum ID	mtDNA genome					
		Length (bp)	% A	% C	% G	% T	GC bias
Pararetifusus carinatus	SFKH-TMP005	15204	31.5	14	15.0	40.1	28.4
Glaphyrina caudata	SFKH-TMP004	15235	31.5	13	14.6	40.7	27.9
Taron dubius	SFKH-TMP006	15189	29.3	15.7	17.0	38.0	32.7
Austrofuscus glans	SFKH-TMP014	15195	31.1	14.5	15.3	39.1	29.8
Colus islandicus	20140782	15158	30.5	14.9	15.8	38.7	30.7
Voluptosius norwegicus	20140781	15232	29.3	15.7	16.5	38.4	32.2
Buccinum undatum	20140783	15231	29.5	15.6	16.3	38.7	31.9
Cominella adpersa	SFKH-TMP009	15251	30.4	15.7	16.0	38.0	31.7
Cominella v. brookesi	SFKH-TMP010	15263	29.6	15.9	16.7	37.8	32.6
Buccinulum fuscozonatum	M.302907/2	15246	30.2	14.8	15.8	39.1	30.6

Table 2 (continued)

Species	Museum ID	mtDNA genome					GC bias
		Length (bp)	% A	% C	% G	% T	
<i>Buccinulum pallidum</i>	M.258277/6	15247	30.9	14.1	15.2	39.7	29.3
<i>Buccinulum p. finlayi</i>	M.302870/2	15247	30.1	14.8	15.9	39.1	30.7
<i>Buccinulum robustum</i>	M.314755/1	15244	29.6	15.2	16.1	39.0	31.3**
<i>Buccinulum v. vittatum</i>	SFKH-TMP012	15244	29.6	15.1	16.4	38.9	31.5**
<i>Aeneator benthicolus</i>	M.274111	15254	30.4	14.7	15.7	39.2	30.4
<i>Aeneator elegans</i>	SFKH-TMP015	15254	30.3	14.6	15.8	39.3	30.4
<i>Aeneator otagoensis</i>	M.279437	15249	30.3	14.7	15.5	39.5	30.2*
<i>Aeneator recens</i>	M.190119	15264	30.0	14.9	16.0	39.1	30.9
<i>Aeneator valedictus</i>	SFKH-TMP013	15258	29.3	15.8	16.7	38.2	32.5
<i>Penion benthicolus</i>	M.183832	15229	29.5	16.2	17.0	37.3	32
<i>Kelletia kelleitii</i>	KK12	15104	29.3	16.0	17.1	37.6	31*
<i>Kelletia lischkei</i>	KL2	15225	29.6	16.1	16.8	37.5	32.9
<i>Penion mandarinus</i>	C.456980	15250	30.4	15.1	16.2	38.3	31.3
<i>Penion maximus</i>	C.487648	15249	30.6	15.1	16.0	38.2	31.1
<i>Penion sulcatus</i>	Phoeni 9	15227	29.2	16.0	17.2	37.5	32
<i>Penion sulcatus</i>	Phoeni 1	15227	29.2	16.1	17.2	37.4	33
<i>Penion chathamensis</i>	M.190085/3	15227	28.6	16.8	18.0	36.7	34.8
<i>Penion chathamensis</i>	M.190082/2	15228	28.5	16.8	18.0	36.7	34.8
<i>Penion c. cuvierianus</i>	M.183792	15235	28.6	16.9	17.8	36.7	34.7
<i>Penion c. cuvierianus</i>	M.183927	15241	28.3	17.1	18.0	36.6	35.1**

generated, including the software and settings used. Legends for tables and figures presented below specify which sequence alignments were used (again referenced in the main text) (Tables 1 and 2).

Acknowledgements

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Transparency document. Supporting information

Transparency data associated with this article can be found in the online version at <https://doi.org/10.1016/j.dib.2017.11.021>.

Appendix A. Supporting information

Supplemental data associated with this article can be found in the online version at <https://doi.org/10.1016/j.dib.2017.11.021>.

References