This data article provides genome statistics, phylogenetic networks and trees for a phylogenetic study of Southern Hemisphere Buccinulidae 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 short-length DNA sequence data. We also investigate the proportion of variable sites per sequence length for a set of mitochondrial and nuclear ribosomal genes, in order to examine the phylogenetic information provided by different DNA markers. Sequence alignment files used for phylogenetic reconstructions in the main text and this article are provided here.

© 2017 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).
**Value of the data**

- Summary statistics for whole mitochondrial DNA sequences and 45S nuclear ribosomal genes are presented because such information for gastropods is currently rare, and base bias is known to influence phylogenetic inferences.
- Phylogenetic reconstructions (from short-length DNA sequence data) presented here include multiple buccinid and buccinulid taxa not included in the main-text trees, and may be useful to future evolutionary studies of Neogastropoda.
- DNA sequence variation and phylogenetic trees are provided because Southern Hemisphere taxa are currently under-sampled.
- The proportion of variable DNA sites for a selection of mitochondrial and nuclear genes from buccinulid whelks are compared. This information can improve genetic marker selection for future molluscan studies.

1. Data

The data presented here originates from a phylogenetic study of Southern Hemisphere whelks [1], which refers to a group of marine snails that can be classified within the taxonomic families Buccinulidae or Buccinidae [2–8]. The classification of these gastropod snails depends upon a biogeographic hypothesis and an assumption of reciprocal monophyly between the majority of lineages in the Northern and Southern Hemispheres [3,6–8]. Results from our study indicated that Buccinulidae and Southern Hemisphere whelks are not monophyletic [1].

32 putative buccinulid and buccinid marine snails, as well as three fasciolariid snails used as a phylogenetic outgroup, were high-throughput sequenced on the Illumina 2500 platform. Sequence data was assembled to provide mitochondrial (mtDNA) genomic and 45S nuclear ribosomal DNA (rDNA) sequence data for most taxa, although some individuals failed to successfully sequence for the entire mtDNA or rDNA. This data was complemented with short-length sequence data from the mitochondrial 16S RNA and *cox1* genes and nuclear ribosomal 28S RNA gene. This short-length
Fig. 1. Maximum-likelihood mtDNA phylogeny of buccinid and buccinulid whelks. A maximum-likelihood derived phylogeny generated using RAxML 8.2.8 [9], based on an alignment of 31 concatenated mitochondrial genome sequences (11,128 bp incorporating protein-encoding, tRNA and rRNA genes). No partitions were used. No outgroup or monophyly was enforced for this tree. Genera putatively belonging to Buccinulidae are shown in different colours.

Fig. 2. Maximum-likelihood 45S rDNA phylogeny of buccinid and buccinulid whelks. A maximum-likelihood derived phylogeny generated using RAxML 8.2.8 [9], based on a 4667 bp alignment of 31 concatenated nuclear rDNA gene sequences (18S, 5.8S, 28S rRNA). No partitions were used. No outgroup or monophyly was enforced for this tree. Genera putatively belonging to Buccinulidae are shown in different colours.
sequence data was acquired via PCR amplification and Sanger sequencing using universal primers. Sequence alignments used for analyses presented in the main text are attached to this paper. Using these sequence alignments, we present maximum-likelihood and Bayesian phylogenetic reconstructions for the sampled buccinulid whelks. These phylogenetic trees are alternative reconstructions that can be compared to trees presented in the main text. Splits networks are also estimated using the mtDNA genomic and nuclear ribosomal RNA (18S, 5.4S, 28S) sequence data. The proportion of variable sites per sequence length for a set of mitochondrial and nuclear ribosomal genes is investigated as well, which provides insight towards marker information for recent and distant evolutionary change in neogastropods (Figs. 1 and 9).

2. Experimental design, materials and methods

The DNA extraction, purification, sequencing method and routine for sequence assembly is provided in the main text [1]. The main text also explains how the figures presented here were
Fig. 4. Bayesian cox1 phylogeny of buccinid and buccinulid whelks. A Bayesian phylogeny based on a 439 bp alignment of mitochondrial cox1 gene sequences obtained from 54 individual marine snails. The GTR + I + G substitution model was used [11]. The phylogeny was produced using a Bayesian method (100 million MCMC, 10% burn-in, 1000 sample frequency, node labels are posterior support values), via BEAST 1.8.3 [16]. For this tree no outgroup was specified explicitly but reciprocal monophyly was enforced for the Fasciolariidae and Buccinidae/Buccinulidae/Nassariidae. Genera putatively belonging to Buccinulidae are shown in different colours.

Fig. 5. Bayesian 28S RNA phylogeny of buccinid and buccinulid whelks. A Bayesian phylogeny based on an alignment of nuclear ribosomal 28S RNA gene sequences obtained from 44 individual marine snails (1486 bp). The GTR + I + G substitution model was used [11]. The phylogeny was produced using a Bayesian method (100 million MCMC, 10% burn-in, 1000 sample frequency, node labels are posterior support values), via BEAST 1.8.3 [16]. For this tree no outgroup was specified explicitly but reciprocal monophyly was enforced for the Fasciolariidae and Buccinidae/Buccinulidae/Nassariidae. Genera putatively belonging to Buccinulidae are shown in different colours.
Fig. 6. Bayesian 16S RNA phylogeny of buccinid and buccinulid whelks. A Bayesian phylogeny 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 phylogeny was produced using a Bayesian method (100 million MCMC, 10% burn-in, 1000 sample frequency, node labels are posterior support values), via BEAST 1.8.3 [16]. For this tree no outgroup was specified explicitly but reciprocal monophyly was enforced for the Fasciolariidae and Buccinidae/Buccinulidae/Nassariidae. Genera putatively belonging to Buccinulidae are shown in different colours.

Fig. 7. Proportion of variable sites at increasingly deep levels of divergence. The proportion of variable sites per sequence length (bp) for a selection of mtDNA and nuclear rDNA genes reflects different rates of DNA substitution. Values were calculated using Geneious 9.1.3 [17]. The trends plotted effectively represent change in the phylogenetic information provided by each gene for different levels of investigation. Average numbers of variable sites were used for groups in genus and family-level comparisons. For example, we used the average number of differences for all sampled whelk (Buccinidae/Buccinulidae) taxa from all sampled Fasciolariidae taxa. Sampling from Aeneator, Buccinulum and Penion was used to estimate generic-level differences as these groups contained more than two specimens. Likewise, only P. sulcatus, P. chathamensis, and P. c. cuvierianus were used for within-species estimates as these taxa were sampled twice. Since read coverage varies for some genes, not all individuals were included for estimates made for each gene.
Fig. 8. Splits network illustrating alternative phylogenetic signal in mtDNA sequence data for marine snails. The splits network is based on an alignment of 31 concatenated mitochondrial genome sequences (incorporating protein-encoding, tRNA and rRNA genes; 11,128 bp). Splits were generated using the Neighbor-Net algorithm in SplitsTree 4 [18]. The splits network presents a generalisation of all of possible topological solutions for the phylogenetic signal contained in the underlying sequence data, but it does not quantify the likelihood of alternative phylogenetic relationships. Edge length is proportional to split weight, and box structures within the network indicate signal for alternative topologies in the underlying sequence data.

Fig. 9. Splits network for illustrating alternative phylogenetic signal in 45S rDNA sequence data for marine snails. The splits network is based on a 4667 bp alignment of 31 concatenated nuclear rDNA gene sequences (18S, 5.8S, 28S rRNA genes). Splits were generated using the Neighbor-Net algorithm in SplitsTree 4 [18]. The splits network presents a generalisation of all of possible topological solutions for the phylogenetic signal contained in the underlying sequence data, but it does not quantify the likelihood of alternative phylogenetic relationships. Edge length is proportional to split weight, and box structures within the network indicate signal for alternative topologies in the underlying sequence data.
### 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 newly 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   |
| Austrofusus 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   |
| Volutopsis 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 adspersa       | 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. litorinoides| SFKH-TMP011 | 5340 | 24  | 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 | 24  | 24.7 | 30.1 | 22.0 | 54.8   |
| Aeneator benthicolus     | M.274111    | 5340 | 22  | 24.7 | 30.1 | 22.1 | 54.7   |
| Aeneator elegans         | SFKH-TMP015 | 5340 | 22  | 24.7 | 30.1 | 22.0 | 54.8   |
| Aeneator otogensis       | 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 kelleti         | 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          | Phoenix9    | 5339 | 23  | 24.4 | 30.0 | 22.3 | 54.4   |
| Penion sulcatus          | Phoenix1    | 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 | 22.3 | 54.3   |

### Table 2
A summary of the statistics for the length and nucleotide composition for the mitochondrial genomes newly sequenced as part of this study. Specimens marked with one asterisk (*) exhibit drops in read coverage for some small regions, for example K. kelletii 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   |
| Austrofusus 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   |
| Volutopsis 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 adspersa       | 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   |
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

This work was supported by the Royal Society of New Zealand Te Aparangi Marsden Fund grant (12-MAU-008), a Ministry of Business, Innovation and Employment Te Tipu Pataia Postdoctoral Fellowship (CONT-22922-TTP-MAU), and a funding contribution from the Department Of Conservation Taxonomic and Threat Status Information fund (RIF 4718).

This work includes samples collected as part of two Antarctic survey projects: TAN0402: A biodiversity survey financed by the former New Zealand Ministry of Fisheries.

TAN0802: Funded by the New Zealand Government under the New Zealand International Polar Year Census of Antarctic Marine Life Project (Phase 1: So001IPY; Phase 2; IPY2007-01).

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

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

| Species                  | Museum ID | mtDNA genome |
|--------------------------|-----------|--------------|
|                          | Length (bp) | % A | % C | % G | % T | GC bias |
| Buccinulum pallidum      | M.258277/6 | 15247 | 30.9 | 14.1 | 15.2 | 39.7 | 29.3 |
| Buccinulum p. finlayi    | M.302870/2 | 15247 | 30.1 | 14.8 | 15.9 | 39.1 | 30.7 |
| Buccinulum robustum      | M.314755/1 | 15244 | 29.6 | 15.2 | 16.1 | 39.0 | 31.3** |
| Buccinulum v. vittatum   | SFKH-TMP012 | 15244 | 29.6 | 15.1 | 16.4 | 38.9 | 31.5** |
| Aeneator benthicolus     | M.274111  | 15254 | 30.4 | 14.7 | 15.7 | 39.2 | 30.4 |
| Aeneator elegans         | SFKH-TMP015 | 15254 | 30.3 | 14.6 | 15.8 | 39.3 | 30.4 |
| Aeneator otagoensis      | M.279437  | 15249 | 30.3 | 14.7 | 15.5 | 39.5 | 30.2* |
| Aeneator recens          | M.190119  | 15264 | 30.0 | 14.9 | 16.0 | 39.1 | 30.9 |
| Aeneator valedictus      | SFKH-TMP013 | 15258 | 29.3 | 15.8 | 16.7 | 38.2 | 32.5 |
| Penion benthicolus       | M.183832  | 15229 | 29.5 | 16.2 | 17.0 | 37.3 | 32 |
| Kelletia kelletii        | KK12       | 15104 | 29.3 | 16.0 | 17.1 | 37.6 | 31* |
| Kelletia ischkei         | KL2        | 15225 | 29.6 | 16.1 | 16.8 | 37.5 | 32.9 |
| Penion mandarinus        | C.456980  | 15250 | 30.4 | 15.1 | 16.2 | 38.3 | 31.3 |
| Penion maximus           | C.487648  | 15249 | 30.6 | 15.1 | 16.0 | 38.2 | 31.1 |
| Penion sulcatus          | Phoenix9   | 15227 | 29.2 | 16.0 | 17.2 | 37.5 | 32 |
| Penion sulcatus          | Phoenix1   | 15227 | 29.2 | 16.1 | 17.2 | 37.4 | 33 |
| Penion chathamensis      | M.190085/3 | 15227 | 28.6 | 16.8 | 18.0 | 36.7 | 34.8 |
| Penion chathamensis      | M.190082/2 | 15228 | 28.5 | 16.8 | 18.0 | 36.7 | 34.8 |
| Penion c. cuvierianus    | M.183792   | 15235 | 28.6 | 16.9 | 17.8 | 36.7 | 34.7 |
| Penion c. cuvierianus    | M.183927   | 15241 | 28.3 | 17.1 | 18.0 | 36.6 | 35.1** |
References

[1] F. Vaux, S.F.K. Hills, B.A. Marshall, S.A. Trewick, M. Morgan-Richards, A phylogeny of Southern Hemisphere whelks (Gastropoda: Buccinulidae) and concordance with the fossil record, Mol. Phylogenet. Evol. 114 (2017) 367–381.
[2] J. Thiele, Die antarktischen Schecken und Muscheln, Dtsch. Südopolar-Exped. 1901–1903 13 (1912) 183–285.
[3] H.J. Finlay, The recent Mollusca of the Chatham Islands, Trans. NZ Inst. 59 (1928) 232–286.
[4] A.W.B. Powell, The recent and Tertiary species of the genus Buccinulum in New Zealand, with a review of related genera, Trans. NZ Inst. 60 (1929) 57–101.
[5] W. Wenz, Gastropoda. Teil 1: allgemeiner Teil und Prosobranchia, in: G.H. Schinderwolf (Ed.), Handbuch der Paläozoologie, Borntraeger, Berlin, 1941.
[6] A.W.B. Powell, Antarctic and subantarctic Mollusca: Pelecypoda and Gastropoda, Discov. Rep. 26 (1951) 47–196.
[7] M.G. Harasewy, Y.I. Kantor, A revision of the Antarctica genus Chlanidota (Gastropoda: Neogastropoda: Buccinulidae, Proc. Biol. Soc. Wash. 112 (1999) 253–302.
[8] S. Hayashi, The molecular phylogeny of the Buccinidae (Caenogastropoda: Neogastropoda) as inferred from the complete mitochondrial 16S rRNA gene sequences of selected representatives, Molluscan Res. 25 (2005) 85–98.
[9] A. Stamatakis, RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies, Bioinformatics 30 (2014) (1312–131).
[10] M. Hasegawa, K. Kishino, T. Yano, Dating the human-ape splitting by a molecular clock of mitochondrial DNA, J. Mol. Evol. 22 (1985) 160–174.
[11] S. Tavaré, Some probabilistic and statistical problems in the analysis of DNA sequences, Lect. Math. Life Sci. 17 (1986) 57–86.
[12] A. Kaim, A.L. Beisel, Mesozoic gastropods from Siberia and Timan (Russia). Part 2: Neogastropoda and Heterobranchia, Pol. Polar Res. 26 (2005) 41–64.
[13] E.C. Allison, Middle Cretaceous Gastropoda from Punta China, Baja California, Mexico, J. Paleo 29 (1955) 400–432.
[14] S. Tracey, J.A. Todd, D.H. Erwin, Mollusca: Gastropoda, in: M.J. Benton (Ed.), The Fossil Record, Chapman & Hall, London, 1993, pp. 131–167.
[15] A.G. Beu, P.A. Maxwell, Cenozoic Mollusca of New Zealand, New Zealand Geol. Surv. Bull. (1990) 58.
[16] A.J. Drummond, M.A. Suchard, D. Xie, A. Rambaut, Bayesian phylogenetics with BEAUti and the BEAST 1.7, Mol. Biol. Evol. 29 (2012) 1969–1973.
[17] M. Kearse, R. Moir, A. Wilson, S. Stones-Havas, M. Cheung, S. Sturrock, S. Buxton, A. Cooper, S. Markowitz, C. Duran, T. Thierer, B. Ashton, P. Mentjies, A. Drummond, Geneious basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data, Bioinformatics 28 (2012) 1647–1649.
[18] D.H. Huson, D. Bryant, Application of phylogenetic networks in evolutionary studies, Mol. Biol. Evol. 23 (2006) 254–267.