

# Deep gastropod relationships resolved

Tauana Junqueira Cunha<sup>1</sup> and Gonzalo Giribet<sup>2</sup>

Museum of Comparative Zoology, Department of Organismic and Evolutionary Biology  
Harvard University, 26 Oxford Street, Cambridge, MA 02138, USA

<sup>1</sup>Corresponding author: [tauanacunha@g.harvard.edu](mailto:tauanacunha@g.harvard.edu) | [orcid.org/0000-0002-8493-2117](https://orcid.org/0000-0002-8493-2117)

<sup>2</sup>[ggiribet@g.harvard.edu](mailto:ggiribet@g.harvard.edu) | [orcid.org/0000-0002-5467-8429](https://orcid.org/0000-0002-5467-8429)

## Abstract

Gastropod mollusks are arguably the most diverse and abundant animals in the oceans, and are successful colonizers of terrestrial and freshwater environments. Here we resolve deep relationships between the five major gastropod lineages - Caenogastropoda, Heterobranchia, Neritimorpha, Patellogastropoda and Vetigastropoda - with highly congruent and supported phylogenomic analyses. We expand taxon sampling for underrepresented lineages with new transcriptomes, and conduct analyses accounting for the most pervasive sources of systematic errors in large datasets, namely compositional heterogeneity, site heterogeneity, heterotachy, variation in evolutionary rates among genes, matrix completeness and gene tree conflict. We find that vetigastropods and patellogastropods are sister taxa, and that neritimorphs are the sister group to caenogastropods and heterobranchs. With this topology, we reject the traditional Archaeogastropoda, which united neritimorphs, vetigastropods and patellogastropods, and is still used in the organization of collections of many natural history museums. Several traits related to development and life history support our molecular results. Importantly, the time of differentiation of the embryonic 4d cell (mesentoblast, responsible for mesoderm formation), differs between the two major clades, highlighting the degree of conservation and significance of development in the evolution of gastropods, as it is also known for spiralian animals more broadly.

## 20 1 Introduction

21 Gastropods are one of the most diverse clades of marine animals [1], and the only mollusk group to successfully  
22 colonize terrestrial environments. Besides the number of species, which is in the order of many tens of  
23 thousands considering just the described extant diversity, gastropods have a high degree of morphological  
24 disparity - snails, limpets and slugs with complex patterns in shell shape, coloration, sizes - and inhabit  
25 all kinds of environments and depths. Gastropods have spiral embryo cleavage, an array of developmental  
26 modes (direct and indirect, with more than one type of larva), and undergo torsion of the body during  
27 development. Five main lineages are currently recognized: Caenogastropoda (e.g., cowries, whelks, conchs,  
28 cones), Heterobranchia (e.g., bubble snails, nudibranchs, most terrestrial snails and slugs), Neritimorpha  
29 (nerites), Patellogastropoda (true limpets), and Vetigastropoda (e.g., abalones, keyhole limpets, turban snails,  
30 top shells).

31 Early classifications included members of the vetigastropods, patellogastropods and neritimorphs in the  
32 Archaeogastropoda [2, 3]. With the first numerical cladistic analysis of morphological data, patellogastropods  
33 were recovered as the sister group to all other gastropods, which were united in the clade Orthogastropoda [4,  
34 5]. The sister group relationship of the most diverse lineages, the heterobranchs and caenogastropods into the  
35 clade Apogastropoda, has been consistently recovered in most morphological and molecular analyses, but  
36 other than that, almost all possible topologies for gastropod relationships have been proposed [for a historical  
37 review, see 6], with early molecular studies having mixed success in recovering even the well-established  
38 monophyly of gastropods or some of the main lineages [7–11]. The first transcriptomic analyses of the group  
39 were able to reject several hypotheses, including the clade Orthogastropoda [12]. However, different methods  
40 still resulted in contrasting topologies, and three hypotheses remain [12]. The major uncertainty is the position  
41 of Neritimorpha, which is recovered either as the sister group to Apogastropoda, or as the sister group to a  
42 clade of Patellogastropoda and Vetigastropoda, in this case forming the traditional Archaeogastropoda. The  
43 third remaining hypothesis has vetigastropods as the sister lineage to all other gastropods [12].

44 Although the most diverse gastropod lineages were well sampled in the transcriptomic analyses of Zapata  
45 et al. [12], the dataset had only one species of Patellogastropoda and two of Neritimorpha, which are crucial  
46 for the proper rooting of the gastropod tree. Furthermore, several biases known to be present in large genomic  
47 datasets were not accounted for in the phylogenetic methods used so far to resolve gastropod relationships.  
48 Heterogeneity in the stationary frequency of amino acids among samples is one such issue that can artificially  
49 group taxa that are actually not closely related based on convergent amino acid composition [13]. Within-site  
50 rate variation through time (heterotachy) is another likely violation [14]. Some genes with slow rates of

51 evolution (e.g., ribosomal protein genes) have also been shown to bias phylogenetic inference [15, 16], while  
52 genes with fast rates and high levels of saturation can cause long-branch attraction [17]. An additional  
53 model violation comes from gene tree discordance, not accounted for by concatenation methods, that can  
54 be caused by incomplete lineage sorting and be particularly relevant in areas of the tree with short internal  
55 branches [18–20], such as the radiation of crown gastropods at the Ordovician [12, 21]. More commonly  
56 considered issues include rate heterogeneity between sites and missing data.

57 Our goal was to resolve between the three hypotheses for the early divergences of gastropods. We present an  
58 extended sampling of Neritimorpha and Patellogastropoda by producing new transcriptomes, and complement  
59 the dataset with the latest published gastropod transcriptomes and with increased representation for the  
60 closest outgroups - bivalves, scaphopods and cephalopods. We build a series of matrices and employ a variety  
61 of methods and models to account for the most common and relevant potential sources of systematic error in  
62 large datasets, namely compositional heterogeneity, site heterogeneity, heterotachy, variation in evolutionary  
63 rates among genes, matrix completeness and gene tree conflict.

## 64 2 Methods

### 65 2.1 Sampling and sequencing

66 We sequenced the transcriptomes of 17 species, mostly patellogastropods and neritimorphs, and combined  
67 them with published transcriptome sequences from 39 other gastropods and 18 mollusk outgroups, for a total  
68 of 74 terminals. All new data and selected published sequences are paired-end Illumina reads. New samples  
69 were fixed in *RNAlater* (Invitrogen) or flash frozen in liquid nitrogen. RNA extraction and mRNA isolation  
70 were done with the TRIzol Reagent and Dynabeads (Invitrogen). Libraries were prepared with the PrepX  
71 RNA-Seq Library kit using the Apollo 324 System (Wafergen). Quality control of mRNA and cDNA was  
72 done with a 2100 Bioanalyzer, a 4200 TapeStation (Agilent) and the Kapa Library Quantification kit (Kapa  
73 Biosystems). Samples were pooled in equimolar amounts and sequenced in the Illumina HiSeq 2500 platform  
74 (paired end, 150 bp) at the Bauer Core Facility at Harvard University. New sequences were deposited in the  
75 NCBI Sequence Read Archive (BioProject XXX); voucher information, library indexes and assembly statistics  
76 are available in the Supplementary Material.

## 77 2.2 Transcriptome assembly

78 Both new and previously published transcriptomes were assembled from scratch with a custom pipeline  
79 (full details and scripts in the Supplementary Material). Raw reads were cleaned with RCorrector [22] and  
80 Trim Galore! [23], removing unfixable reads (as identified by RCorrector), Wafergen library adapters and  
81 reads shorter than 50 bp. Filtered reads were compared against a dataset of mollusk ribosomal RNAs and  
82 mitochondrial DNA and removed with Bowtie2 v2.2.9 [24]. This dataset was created from the well-curated  
83 databases SILVA [25] (18S and 28S rRNAs), AMIGA [26] (mtDNA) and from GenBank [27] (5S and 5.8S  
84 rRNAs). Reads were assemble into transcripts with Trinity v2.3.2 [28, 29] (`-SS_lib_type FR` for our new  
85 strand-specific data generated with Wafergen kits; precise information was not available from published  
86 data, so the default non-strand-specific mode was used for reads downloaded from SRA). A second run of  
87 Bowtie2 was done on the assemblies, before removing transcripts with sequence identity higher than 95% with  
88 CD-HIT-EST v4.6.4 [30, 31]. Transcripts were then translated to amino acids with TransDecoder v3.0 [29],  
89 and the longest isoform of each gene was retained with a custom python script (*choose\_longest\_iso.py*). The  
90 completeness of the assemblies was evaluated with BUSCO by comparison with the Metazoa database [32].

## 91 2.3 Matrix construction

92 We built four matrices to account for extreme evolutionary rates, amino acid composition heterogeneity and  
93 different levels of matrix completeness. Scripts and a detailed pipeline are available in the Supplementary  
94 Material. Orthology assignment of the peptide assemblies was done with OMA v2.0 [33]. We then used a  
95 custom python script (*selectslice.py*) to select all orthogroups for which at least half of the terminals were  
96 represented (50% taxon occupancy), resulting in a matrix with 1059 genes (Matrix 1) (Figure 1). Each  
97 orthogroup was aligned with MAFFT v7.309 [34], and the alignment ends were trimmed to remove positions  
98 with more than 80% missing data with a custom bash script (*trimEnds.sh*). To avoid possible biases, saturation  
99 and long-branch attraction, Matrix 2 was built by removing from Matrix 1 the 20% slowest and the 20% fastest  
100 evolving genes, as calculated with TrimAl [35], for a final size of 635 genes (Figure 1). Matrix 3 is the subset  
101 of 962 genes from Matrix 1 that are homogeneous regarding amino acid composition. Homogeneity for each  
102 gene was determined with a simulation-based test from the python package p4 [13, 36], with a script modified  
103 from Laumer et al. [37] (*p4\_compo\_test.py*) and a conservative p-value of 0.1. Finally, a subset of 149 genes  
104 with 70% taxon occupancy constitutes Matrix 4 (Figure 1). For inference methods that require concatenation,  
105 genes were concatenated using Phyutility [38]. We further reduced composition heterogeneity in Matrices 1  
106 and 2 by recoding amino acids into the six Dayhoff categories [39] with a custom script (*recdayhoff.sh*).

## 107 2.4 Phylogenetic analyses

108 Amino acid matrices were used for phylogenetic inference with a coalescent-based approach in Astral-II  
109 v4.10.12 [40], with maximum likelihood (ML) in IQ-TREE MPI v1.5.5 [41–43], and with Bayesian inference in  
110 PhyloBayes MPI v1.7a [44]. The two Dayhoff-recoded matrices were analyzed in PhyloBayes (Figure 1). Full  
111 details and scripts are explained in a custom pipeline in the Supplementary Material. For the coalescent-based  
112 method, gene trees were inferred with RAxML v8.2.10 [45] (-N 10 -m PROTGAMMALG4X) and then used  
113 as input for Astral-II for species tree estimation. For each concatenated matrix, we inferred the best ML  
114 tree with two strategies: a gene-partitioned analysis with model search including LG4 mixture models and  
115 accounting for heterotachy (-bb 1500 -sp partition\_file -m MFP+MERGE -recluster 10 -madd LG4M,LG4X  
116 -mrate G,R,E); and a non-partitioned analysis with model search also including the C10 to C60-profile mixture  
117 models [46] (ML variants of the Bayesian CAT model [47]) (-bb 1500 -m MFP+MERGE -recluster 10 -madd  
118 LG4M,LG4X,LG+C10,LG+C20,LG+C30,LG+C40,LG+C50,LG+C60 -mrate G,R,E). The search for the  
119 models LG+C60 (Matrices 1 and 3) and LG+C50 (Matrix 1) required more memory than available, and  
120 these models were disregarded for the respective matrices. PhyloBayes was run with the CAT-GTR model  
121 on a subset of the concatenated alignments (matrices 1, 2 and 4), discarding constant sites to speed up  
122 computation.

## 123 3 Results and discussion

### 124 3.1 Main gastropod relationships

125 Our main goal was to resolve the deep nodes of the gastropod tree and distinguish between three hypotheses of  
126 the relationships among its five main lineages. All but one of our inference methods and matrices congruently  
127 support a clade uniting Vetigastropoda and Patellogastropoda, and Neritimorpha as the sister group to  
128 Apogastropoda (Figure 2). The only exception is the coalescent-based analysis on the smallest dataset of 149  
129 genes (Astral, Matrix 4), in which these two key nodes were left unresolved (all tree files are available in the  
130 Supplementary Material). Accordingly, the few analyses with lower support on these nodes also refer to the  
131 smaller Matrix 4, which is unsurprising given that it comprises fewer informative sites in concatenated analyses,  
132 and less genes in the coalescent-based analysis [48]. In summary, the resulting topology is congruent based  
133 on an array of analyses testing for the major common sources of systematic error in phylogenomic datasets,  
134 including gene tree discordance, compositional heterogeneity, heterotachy, site heterogeneity, variation in  
135 evolutionary rates, and missing data.

136 This exact topology for gastropod relationships has been previously recovered by a few molecular [12,  
137 49] and total evidence [6] analyses, with numerous alternatives proposed in the literature [e.g. 5, 6, 10,  
138 49–51], even within the same studies. With 17 analyses (combinations of four subsampled matrices, two  
139 data types - amino acids and Dayhoff recoding, and four inference methods/models), for the first time  
140 we find strong congruence and support for the tree presented in Figure 2. With that we reject the clade  
141 Archaeogastropoda, proposed almost a century ago by Thiele [2], which united Neritimorpha, Vetigastropoda  
142 and Patellogastropoda. Although this grouping had given way to other predominant hypotheses along the  
143 years (e.g., Eogastropoda *vs.* Orthogastropoda divergence), this classification is still used in the organization  
144 of malacology and paleontological collections of many natural history museums.

145 We find strong support for the position of neritimorphs as the sister group to apogastropods, a relationship  
146 that is further supported by important developmental characters [52, 53]. Vetigastropods and patellogastropods  
147 differ from neritimorphs and apogastropods in the time of differentiation of the 4d cell (mesentoblast), a key  
148 embryonic cell that gives rise to the mesoderm in spiralian [54–56]. In Vetigastropoda and Patellogastropoda,  
149 the mesentoblast is formed at the 63-cell stage; in the other gastropod lineages, formation of the mesentoblast  
150 is accelerated, happening sometime between the 24- and 48-cell stages depending on the species [52, 53]. Given  
151 the highly conserved nature of the early spiral cleavage program and of cell fates across spiralian phyla [54–56],  
152 the congruence between our molecular results and the variation in development highlights the significance of  
153 such traits also for the evolution of the main gastropod lineages. A few other reproduction and life history traits  
154 distinguish the two main clades of gastropods recovered here. While vetigastropods and patellogastropods are  
155 mostly broadcast spawners, neritimorphs and apogastropods have internal fertilization and often complex  
156 reproductive behaviors and anatomy [57]. For these latter groups, eggs are usually encapsulated, with either  
157 direct development or the release of a feeding veliger larva in the water, while embryos of vetigastropods  
158 and patellogastropods first develop into a non-feeding trochophore larva in the plankton [58]. In addition,  
159 neritimorphs and apogastropods have invaded freshwater and terrestrial environments several times. All of  
160 these traits are likely connected, but order of appearance and causal relations remain to be investigated.

161 Important questions that remain regarding major gastropod relationships include the position of  
162 Cocculiniformia, Neomphalina and the hot-vent taxa, smaller deep sea clades that have been considered  
163 somehow related to vetigastropods, neritimorphs, patellogastropods, or as independent branches in the  
164 gastropod tree. They are yet to be sampled in a phylogenomic analyses.

165 Regarding overall mollusk relationships, we recover a well supported clade of gastropods, bivalves and  
166 scaphopods in all analyses; however, as in previous phylogenomic efforts [59, 60], relationships between these

167 three groups are unstable (Figure 2). The Dayhoff datasets and most of the ML analyses with the profile  
168 mixture model result in a clade of gastropods and scaphopods; while most coalescent-based trees recover a  
169 clade of bivalves and scaphopods; and finally, the ML partitioned analyses produce a clade of gastropods and  
170 bivalves. Perhaps a way ahead to resolve such hard nodes will be to use other types of data, such as genomic  
171 rearrangements and presence/absence of genes from complete genomes.

### 172 3.2 A note about convergence in PhyloBayes

173 While PhyloBayes converged on Dayhoff-recoded datasets, analyses on the more complex amino acid matrices  
174 did not converge for all parameters. The problem was especially pronounced for the large matrices (a summary  
175 table for all analyses is given in the Supplementary Material). We observed that convergence issues were  
176 mostly due to small differences between chains regarding the position of one or few derived terminals within  
177 the outgroups or within apogastropods, whose relationships were not the goal of this study. We suspect this  
178 may be caused by a problem in topology proposals for these derived nodes, leading some of the chains to  
179 get stuck in local maxima. One example comes from the Dayhoff analysis of Matrix 1: the initial two chains  
180 seemed to be very far from topological convergence (maxdiff=1) even after more than 20,000 generations.  
181 Upon closer inspection, both trees were basically indistinguishable, with the only variation being the position  
182 of *Charonia* or *Crepidula* as the sister group to Neogastropoda. Removal of either one of the two terminals  
183 from the treelist file with a custom script (*remove\_terminal.py*) resulted in the same converged topology (tree  
184 files in the Supplementary Material). For that particular analysis, we ran two additional independent chains  
185 that converged without presenting this issue. This behavior was recently discussed [61], and perhaps has been  
186 underreported in the literature.

### 187 3.3 Relationships within gastropod lineages

188 This is the first genomic-scale dataset for Patellogastropoda and Neritimorpha. Internal relationships of  
189 patellogastropods have presented incongruent results even among studies using the same type of data (reviewed  
190 in Lindberg [62] and Nakano & Sasaki [63]). We consistently recover Nacellidae (*Cellana*, *Nacella*) as the  
191 sister group of Patellidae (Figure 2), a clade originally supported by some of the earliest morphological [64]  
192 and mitochondrial phylogenies [65]. Nacellids have also been placed either as a grade at the base of the  
193 tree [66] or closer to Lottiidae [67], and the current taxonomic classification has Nacellidae in the superfamily  
194 Lottioidea [68]; our results indicate the family should be transferred to Patelloidea. Another interesting  
195 finding regards *Eoacmaea*, which had gained family and superfamily status due to being recovered as the

196 sister taxon to all other patellogastropods with mitochondrial markers [67]. None of our results recover this  
197 position, but rather indicate that the genus is either part of Lottiidae (most ML and Bayesian results), which  
198 was its original assignment, or is sister group to the Lottioidea families Neolepetopsidae (*Paralepetopsis*) and  
199 Lottiidae (*Patelloida*, *Nipponacmea*, *Lottia*, *Testudinalia*) (coalescent-based trees and one ML tree) (Figure 2).

200 Neritimorphs had mostly congruent phylogenies recovered from 28S rRNA data [69] and mitogenomes [70].  
201 Our reconstruction supports the same topology, with Neritopsoidea (*Titiscania*) as the sister group to all other  
202 neritimorphs, followed by the divergence between Helicinoidea (*Pleuropoma*) and Neritoidea. Within the latter,  
203 we also recover a monophyletic Neritidae as the sister group of Phenacolepadidae (*Thalassonerita*). The nested  
204 position of *Smaragdia* inside Neritinae disagrees with its current classification in its own subfamily [68].

205 Vetigastropoda and Heterobranchia had similar taxon representation as in Zapata et al. [12] (restricted  
206 to only transcriptomes with high sequencing quality, and with newly sequenced replacements for some  
207 vetigastropod families). As expected, the relationships are the same, and highlight the need for future studies  
208 focused on each group, given the uncertain position of *Haliotis* in Vetigastropoda, and low resolution of  
209 internal relationships of panpulmonates in Heterobranchia.

210 We substantially increased sampling of Caenogastropoda by adding the latest published transcriptomes of  
211 eight families. Despite that, caenogastropods are the most diverse gastropod lineage, with over a hundred  
212 families, and the following results are still limited in sampling. We recover a monophyletic Neogastropoda;  
213 its internal relationships differ from a molecular study with denser taxon sampling [71], in that we find  
214 Buccinoidea (*Cumia*, *Volegalea*) closer to Conoidea (*Conus*, *Crassispira*) than to Muricoidea (*Urosalpinx*).  
215 We also recover a monophyletic Truncatelloidea (*Bithynia*, *Oncomelania*) as the sister group to all other  
216 Hypsgastropoda. The relative position of Tonnoidea (*Charonia*) and Calyptraeidea (*Crepidula*) regarding  
217 Neogastropoda is unclear, nonetheless, this close relationship between them, and also of Stromboidea (*Lobatus*),  
218 agrees with previous molecular studies [71, 72]. The branching pattern of the closest relatives of neogastropods  
219 reveal a paraphyletic Littorinimorpha [68].

## 220 Supplementary material and data access

221 New transcriptomes were deposited in the NCBI Sequence Read Archive (BioProject XXX). Supplementary  
222 materials include detailed pipelines, tree files, images and tables, deposited in Harvard Dataverse doi:XXX.  
223 Scripts are available on [github.com/tauanajc/phylo\\_scripts](https://github.com/tauanajc/phylo_scripts).



## 224 **Competing interests**

225 The authors have no competing interests.

## 226 **Authors' contributions**

227 TJC and GG conceived the study, collected and identified specimens. TJC carried out lab work, analyzed  
228 the data and drafted the manuscript. Both authors improved the manuscript and gave final approval for  
229 publication.

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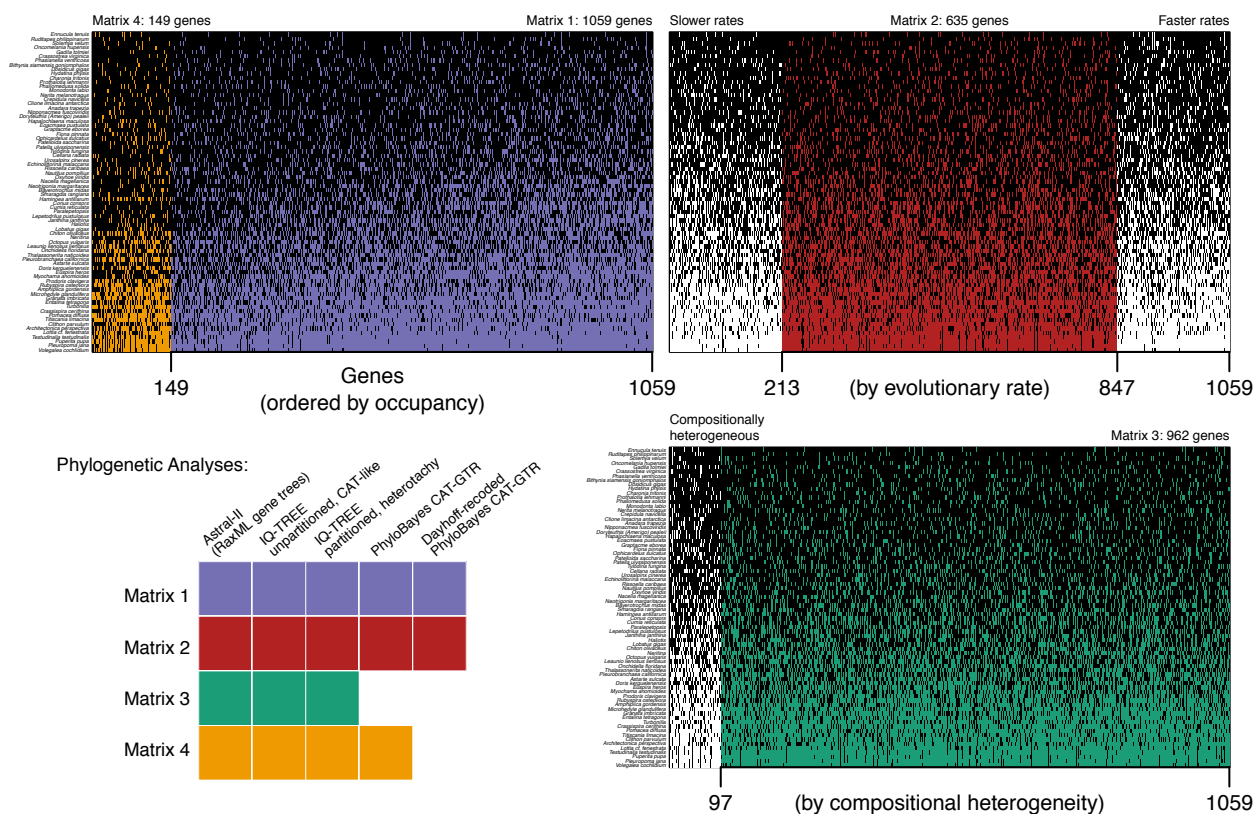
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**Figure1:** Matrices and phylogenetic methods used to infer gastropod relationships. With 50% taxon occupancy, Matrix 1 is the largest, with 1059 genes. Matrix 4 is the subset of the best sampled 149 genes, with 70% taxon occupancy. Genes and species are sorted with the best sampling on the upper left. Matrix 2 is the subset of 635 genes after ordering all genes by evolutionary rate and removing the 20% slowest and 20% fastest evolving genes. Matrix 3 includes the 962 genes that are homogeneous in amino acid composition; genes are ordered by p-value of the homogeneity test. Black cells indicate genes present for each species. Check Methods for details.



**Figure2:** Gastropod phylogeny inferred from the largest matrix (M1) with Maximum Likelihood and a profile mixture model (IQTREEcat). A single square marks branches where all analyses had full support; branches where at least one analysis had less than full support are marked with a plot, colored in a continuous scale according to support value, from 0 to 1. Grey squares in the plots represent splits that were absent in a given analysis. M1-M4: Matrices 1-4; IQTREEpart: ML partitioned analysis; Dayhoff-PB: Bayesian analysis on a matrix recoded according to the 6 Dayhoff categories. Check Methods for details.