



Macroevolution of venom apparatus innovations in auger snails (Gastropoda; Conoidea; Terebridae)

M. Castelin^{a,b,c,d,1}, N. Puillandre^{d,e,1}, Yu.I. Kantor^f, M.V. Modica^{a,b,c}, Y. Terryn^g, C. Cruaud^h, P. Bouchetⁱ, M. Holford^{a,b,c,*}

^a Hunter College, The City University of New York, 695 Park Ave. NY, NY 10065, USA

^b The Graduate Center, The City University of New York, 365 5th Ave. NY, NY 10016, USA

^c The American Museum of Natural History, Central Park West at 79th St. NY, NY 10024, USA

^d UMR 7138, Muséum National d'Histoire Naturelle, Département Systematique et Evolution, 43, Rue Cuvier, 75231 Paris, France

^e Atheris Laboratories, Case postale 314, CH-1233 Bernex-Geneva, Switzerland

^f A.N. Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences, Leninski Pros. 33, Moscow 119071, Russia

^g NaturalArt, Kapiteinstraat 27, 9000 Gent, Belgium

^h GENOSCOPE, Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5706, 91057 Evry Cedex, France

ⁱ UMR 7138, Muséum National d'Histoire Naturelle, Département Systematique et Evolution, 55, Rue Buffon, 75231 Paris, France

ARTICLE INFO

Article history:

Received 21 October 2011

Revised 27 February 2012

Accepted 1 March 2012

Available online 14 March 2012

Keywords:

Character evolution

Key innovations

Predator–prey system

Radula

Teretoxins

Peptide toxins

ABSTRACT

The Terebridae are a diverse family of tropical and subtropical marine gastropods that use a complex and modular venom apparatus to produce toxins that capture polychaete and enteropneust preys. The complexity of the terebrid venom apparatus suggests that venom apparatus development in the Terebridae could be linked to the diversification of the group and can be analyzed within a molecular phylogenetic scaffold to better understand terebrid evolution. Presented here is a molecular phylogeny of 89 terebrid species belonging to 12 of the 15 currently accepted genera, based on Bayesian inference and Maximum Likelihood analyses of amplicons of 3 mitochondrial (COI, 16S and 12S) and one nuclear (28S) genes. The evolution of the anatomy of the terebrid venom apparatus was assessed by mapping traits of six related characters: proboscis, venom gland, odontophore, accessory proboscis structure, radula, and salivary glands. A novel result concerning terebrid phylogeny was the discovery of a previously unrecognized lineage, which includes species of *Euterebra* and *Duplicaria*. The non-monophyly of most terebrid genera analyzed indicates that the current genus-level classification of the group is plagued with homoplasy and requires further taxonomic investigations. Foregut anatomy in the family Terebridae reveals an inordinate diversity of features that covers the range of variability within the entire superfamily Conoidea, and that hypodermic radulae have likely evolved independently on at least three occasions. These findings illustrate that terebrid venom apparatus evolution is not perfunctory, and involves independent and numerous changes of central features in the foregut anatomy. The multiple emergence of hypodermic marginal radular teeth in terebrids are presumably associated with variable functionalities, suggesting that terebrids have adapted to dietary changes that may have resulted from predator–prey relationships. The anatomical and phylogenetic results presented serve as a starting point to advance investigations about the role of predator–prey interactions in the diversification of the Terebridae and the impact on their peptide toxins, which are promising bioactive compounds for biomedical research and therapeutic drug development.

© 2012 Elsevier Inc. All rights reserved.

* Corresponding author at: Hunter College, The City University of New York, NY, United States. Fax: +1 212 772 5332.

E-mail addresses: magcastelin@mnhn.fr (M. Castelin), puillandre@mnhn.fr (N. Puillandre), kantor@malaco-sevin.msk.ru (Yu.I. Kantor), mariavittoria.modica@uniroma1.it (M.V. Modica), yves@naturalart.be (Y. Terryn), cruaud@genoscope.cns.fr (C. Cruaud), pbouchet@mnhn.fr (P. Bouchet), mholford@hunter.cuny.edu (M. Holford).

¹ Present address: UMR 7138, Muséum National d'Histoire Naturelle, Département Systematique et Evolution, 43, Rue Cuvier, 75231 Paris, France.

1. Introduction

At the macroevolutionary level, it is hypothesized that the tempo of evolution can be viewed through the lens of key innovations (Sanderson and Donoghue, 1994). Key innovations are biological traits that promote lineage diversification (Heard and Hauser, 1995; Hodges and Arnold, 1995). The development of a venom apparatus in the marine gastropod superfamily Conoidea is a key innovation that can be used as an organizational framework to decipher the evolutionary history of this megadiverse group. Here

the evolution of the venom apparatus in auger snails (Neogastropoda; Conoidea; Terebridae) is investigated using a molecular phylogenetic scaffold.

The Terebridae are a diverse family of medium to large-sized (mostly 15–150 mm) marine gastropods distributed throughout most tropical and subtropical oceans. Terebrids use their venom apparatus to capture prey, and perhaps also to defeat competitors or predators (Olivera, 1997). Similar to the peptide toxins produced by cone snails (Neogastropoda; Conoidea; Conidae), the peptide toxins produced by terebrids, teretoxins, are promising bioactive compounds for biomedical research and therapeutic drug development (Puillandre and Holford, 2010). Peptide toxins from a venom source are of increasing interest in the pharmacological industry (Chin et al., 2006; Newman and Cragg, 2007; Butler, 2008; Casewell et al., 2009; Hong, 2011). As recently demonstrated (Fry et al., 2003; Modica and Holford, 2010; Puillandre et al., 2010; Saslis-Lagoudakis et al., 2011), understanding how the organisms that produce these toxins have emerged and evolved over time, may become central in the process of drug discovery. Specifically, in the case of the Terebridae, where not all species have a venom apparatus, identifying the lineages that have a venom apparatus is an effective route to peptide toxin characterization. Currently, the extent of species diversification of the Terebridae is largely underestimated and the evolutionary pathways explored by the terebrid groups, especially regarding the peptide toxins they produce, remains largely unknown.

Whether used for defense or attack, the diversity of toxins developed by venomous organisms is often attributed to the process of co-evolution in predator–prey relationships (Kordis and Gubensek, 2000; Lynch, 2007; Duda, 2008; Kozminsky-Atias et al., 2008; Barlow et al., 2009). Co-evolutionary predator–prey interactions may lead to the development of specialized adaptations in the predator that are followed by counter-adaptations in the prey, which in turn can lead to further adaptations in the predator, and so on, as dictated by biotic, “Red Queen” (Van Valen, 1973) or abiotic, “Court Jester” (Barnosky, 2001) pressures. For example, numerous plants produce toxic secondary compounds that influence the behavior, growth, or survival of insects and other herbivores. In addition, herbivores have developed ways to detoxify, sequester, or render ineffective specific plant poisons (Laycock, 1978; Fowler, 1983; Zangerl et al., 2008). In snakes, it has been demonstrated that venom diversity may result by adaptation toward specific diets (Daltry et al., 1996; Wüster et al., 1999; Barlow et al., 2009). In parallel, some snake prey have developed the ability to inhibit specific venom toxins (Heatwole and Poran, 1995; Biardi et al., 2005). By its indirect effect on fitness, the predator–prey arms race can represent a driving force of speciation and species diversification in both predator and prey populations. This is referred to as the “escalation/diversification hypothesis” (Ehrlich and Raven, 1964; but see also Berenbaum and Feeny, 1981; Berenbaum, 1983; Vermeij, 1993). Phylogenetic analyses can provide seminal evidence on rates and patterns of predation-traits evolution and species diversification (Farrell et al., 1991). However, the correlation between adaptative changes of predation-traits and species-diversification in predator–prey systems is difficult to study. Such a study requires a good understanding of the biology and the ecology of the species involved and necessitates a thorough taxonomic sampling of both predator and prey taxa. A good alternative, as attempted here with the Terebridae, is to obtain an exhaustive taxonomic sampling of one of the two taxa (predator or prey) and to study the traits or innovations that affect the ability to accomplish or avoid predation. Mapping these innovations on a phylogenetic tree then reveals patterns that may impact species diversification.

Understanding the evolutionary patterns of venom apparatus evolution in the Terebridae would significantly advance clarifying the phylogeny and systematics of the group, in addition to advancing

the characterization of terebrid peptide toxins for biomedical applications. Recent molecular phylogenies (Holford et al., 2009a, 2009b; Puillandre et al., 2011) of the family Terebridae based on samples from Western and Eastern Pacific demonstrated the monophyly of terebrids relative to the other families of conoideans. Also illustrated in these phylogenetic studies is the existence of five distinctive clades, *Pellifronia*, *Oxymeris* [= *Acus*], *Terebra*, *Hastula*, and *Myurella*, numbered clades A–E, respectively, with clade A, containing the recently revised *Pellifronia jungi* (Terry and Holford, 2008), as sister species of all the other terebrids. Previous molecular analyses combined with mapping of venom apparatus morphology also indicated that the Terebridae have lost the venom apparatus at least twice during their evolution (in clades B and E). However, these phylogenies were based on a limited number of species (~50 for the most complete, vs the ~400 currently described species), and sampling was limited to the Pacific Ocean. Additionally, only the presence and absence of the venom glands were studied, overlooking other morphological and anatomical innovations potentially linked to the evolution of terebrid predatory skills and toxin diversity. In contrast, the present expanded study of the molecular phylogeny of the family Terebridae almost doubles the number of species from 50 to 89, including 12 out of the 15 accepted genera, almost triples the number of specimens, and increases the geographical area sampled by including the western Indian Ocean. The molecular phylogeny in this study is based on the three mitochondrial genes, COI, 12S, 16S, previously used in conoidean phylogenies, with the addition of one nuclear gene, 28S, shown to be useful in resolving relationships at the genus level in Conoidea and other gastropods (Williams and Ozawa, 2006; Puillandre et al., 2008). The analysis of the venom apparatus, previously reduced to the presence or absence of the venom gland, and thus underestimating the diversity of the evolutionary pathways the terebrids may have explored, is here extended to other anatomical features linked to the venom apparatus. The morphology of the radula, in particular, has been linked to prey capture, and consequently different radula types may correlate to innovations in predatory behavior, including venom evolution.

2. Materials and methods

2.1. Taxon sampling

All the material studied herein was collected during several expeditions conducted by the Museum National d'Histoire Naturelle of Paris (MNHN), in partnership with Pro-Natura International (PNI), Instituto Español de Oceanografía (IOE), and Institut de Recherche pour le Développement (IRD), the Natural History Museum of London (NHM), and the Smithsonian Tropical Research Institute (STRI) (see Table 1 and acknowledgements). Samples include 406 specimens assigned to 89 species collected off New Caledonia (4 specimens), Philippine Islands (49), Vanuatu (115), Solomon Islands (12), Australia (4), the Coral Sea (4), Panama (50), Madagascar (87), Mozambique (75), Tahiti (4), New-Zealand (1) and Fiji (1) (Fig. 1). These samples originate from depths ranging from 0 m to ~800 m (Table 1). In the field, all specimens were specifically fixed for molecular analysis. Living specimens were anesthetized using magnesium chloride (MgCl₂), a piece of tissue was cut from the head-foot, and fixed in 95% ethanol. Shells were kept intact for identification. Vouchers are deposited in MNHN. Taxonomy follows Terry (2007), with updates in Terry (2011) (*Cinguloterebra* synonymized with *Triplostephanus*, *Impages* with *Hastula*, and *Acus* and *Perirhoe* with *Oxymeris*). Three specimens of the family Turridae (putative sister-group of the Terebridae – Puillandre et al., 2011), Cochlespiridae (Conoidea) and Conidae (Conoidea) were used as closely related outgroups. *Harpa*

Table 1
List of specimens analysed.

MNHN Ids	Genus	species	Country	Coordinates; depth (m)	Clade	BOLD ID	Genbank COI	GenBank 12S	GenBank 16S	GenBank 28S
MNHN IM200730401	<i>Clathroterebra</i>	<i>fortunei</i>	Philippines	9°39'N, 123°48'E; 255–268	E1	CONO284-08	EU685526	EU685371	EU685663	
MNHN IM200730391	<i>Clathroterebra</i>	<i>fortunei</i>	Solomon Islands	7°59' S, 157°33' E; 260	E1	CONO381-08	EU685535	EU685384	EU685675	
MNHN IM200730581	<i>Clathroterebra</i>	<i>fortunei</i>	Philippines	9°39'N, 123°48'E; 255–268	E1	CONO1130-12	EU685535	EU685384	EU685675	
MNHN IM20099971	<i>Clathroterebra</i>	<i>fortunei</i>	Mozambique	25°33'S, 33°13'E; 253–262	E1	CONO1134-12	EU685535	EU685384	EU685675	
MNHN IM200730455	<i>Clathroterebra</i>	<i>poppei</i>	Philippines	9°36'4"N, 123°53'8"E; 60–62	E3	CONO266-08	EU685523	EU685368	EU685660	JQ808947
MNHN IM200730546	<i>Clathroterebra</i>	<i>poppei</i>	Vanuatu	15°36'S, 167°03'E; 86–118	E3	CONO482-08	EU685596	EU685455	EU685748	
MNHN IM200910162	<i>Duplicaria</i>	<i>albofuscata</i>	South Madagascar	25°03'7'-8'S, 46°57'7'E; 3–4	F	CONO1154-12	EU685596	EU685455	EU685748	JQ808948
MNHN IM200910163	<i>Duplicaria</i>	<i>albofuscata</i>	South Madagascar	25°03'7'-8'S, 46°57'7'E; 3–4	F	CONO1254-12	EU685596	EU685455	EU685748	JQ808948
MNHN IM20099973	<i>Duplicaria</i>	<i>baileyi</i>	South New-Caledonia	22°06'S, 167°03'E; 190–200	E2	CONO1263-12	EU685596	EU685455	EU685748	JQ808949
MNHN IM20099977	<i>Duplicaria</i>	<i>baileyi</i>	South New-Caledonia	22°06'S, 167°03'E; 190–200	E2	CONO1262-12	EU685596	EU685455	EU685748	JQ808949
MNHN IM200910908	<i>Duplicaria</i>	<i>bernardi</i>	Australia	26°56'607"S, 153°23'813"E; 40	F	CONO1185-12	EU685596	EU685455	EU685748	JQ808950
MNHN IM20099951	<i>Duplicaria</i>	<i>raphanula</i>	North Madagascar	14°31'S, 47°25'E; 50–107	D	CONO1163-12	EU685596	EU685455	EU685748	JQ808950
MNHN IM20099952	<i>Duplicaria</i>	<i>raphanula</i>	North Madagascar	14°31'S, 47°25'E; 50–107	D	CONO1287-12	EU685596	EU685455	EU685748	JQ808951
MNHN IM200910111	<i>Duplicaria</i>	sp. 1	South Madagascar	25°04'4'-7'S, 46°55'3'-56'3"E; 19–26	F	CONO1218-12	EU685596	EU685455	EU685748	JQ808952
MNHN IM200910117	<i>Duplicaria</i>	sp. 1	South Madagascar	25°04'4'-7'S, 46°55'3'-56'3"E; 19–26	F	CONO1364-12	EU685596	EU685455	EU685748	JQ808952
MNHN IM200910113	<i>Duplicaria</i>	sp. 2	South Madagascar	25°03'7'-8'S, 46°57'6'-7"E; 2–7	F	CONO1253-12	EU685596	EU685455	EU685748	JQ808953
MNHN IM200910164	<i>Duplicaria</i>	sp. 2	South Madagascar	25°03'7'-8'S, 46°57'6'-7"E; 2–7	F	CONO1219-12	EU685596	EU685455	EU685748	JQ808953
MNHN IM200730432	<i>Duplicaria</i>	sp. 3	Vanuatu	15°35'4'S, 166°58'7"E; 3–8	E2	CONO1256-12	EU685596	EU685455	EU685748	JQ808953
MNHN IM200730466	<i>Duplicaria</i>	sp. 3	Vanuatu	15°35'4'S, 166°58'7"E; 3–8	E2	CONO1306-12	EU685596	EU685455	EU685748	JQ808953
MNHN IM200910122	<i>Duplicaria</i>	sp. 3	South Madagascar	25°26'1'-4'S, 44°55'2'-6"E; 17–20	E2	CONO1279-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910123	<i>Duplicaria</i>	sp. 3	South Madagascar	25°25'80'-8'S, 44°55'7'-8"E; 11–13	E2	CONO1214-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910124	<i>Duplicaria</i>	sp. 3	South Madagascar	25°24'1'-2'S, 44°51'1'-7"E; 24–26	E2	CONO1211-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910125	<i>Duplicaria</i>	sp. 3	South Madagascar	25°26'1'-4'S, 44°55'2'-6"E; 17–20	E2	CONO1342-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910126	<i>Duplicaria</i>	sp. 3	South Madagascar	25°24'1'-2'S, 44°51'1'-7"E; 24–26	E2	CONO1247-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910134	<i>Duplicaria</i>	sp. 3	South Madagascar	25°25'9'S, 44°55'1'-2"E; 18–20	E2	CONO1341-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910136	<i>Duplicaria</i>	sp. 3	South Madagascar	25°26'1'-4'S, 44°55'2'-6"E; 17–20	E2	CONO1220-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910137	<i>Duplicaria</i>	sp. 3	South Madagascar	25°25'80'-8'S, 44°55'7'-8"E; 11–13	E2	CONO1215-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910138	<i>Duplicaria</i>	sp. 3	South Madagascar	25°23'1'-2'S, 44°51'4'-6"E; 20–23	E2	CONO1361-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910139	<i>Duplicaria</i>	sp. 3	South Madagascar	25°24'1'-2'S, 44°51'1'-7"E; 24–26	E2	CONO1147-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910140	<i>Duplicaria</i>	sp. 3	South Madagascar	25°23'6'-7'S, 44°53'3'-5"E; 10–12	E2	CONO1176-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910141	<i>Duplicaria</i>	sp. 3	South Madagascar	25°24'1'-2'S, 44°51'1'-7"E; 24–26	E2	CONO1212-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910142	<i>Duplicaria</i>	sp. 3	South Madagascar	25°24'1'-2'S, 44°51'1'-7"E; 24–26	E2	CONO1248-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910145	<i>Duplicaria</i>	sp. 3	South Madagascar	25°24'1'-2'S, 44°51'1'-7"E; 24–26	E2	CONO1148-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910146	<i>Duplicaria</i>	sp. 3	South Madagascar	25°26'1'-4'S, 44°55'2'-6"E; 17–20	E2	CONO1343-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910148	<i>Duplicaria</i>	sp. 3	South Madagascar	25°26'7'S, 44°55'8"E; 15	E2	CONO1281-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910149	<i>Duplicaria</i>	sp. 3	South Madagascar	25°26'7'S, 44°55'8"E; 15	E2	CONO1282-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910150	<i>Duplicaria</i>	sp. 3	South Madagascar	25°26'7'S, 44°55'8"E; 15	E2	CONO1304-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910151	<i>Duplicaria</i>	sp. 3	South Madagascar	25°24'1'-2'S, 44°51'1'-7"E; 24–26	E2	CONO1149-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910152	<i>Duplicaria</i>	sp. 3	South Madagascar	25°24'1'-2'S, 44°51'1'-7"E; 24–26	E2	CONO1213-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910153	<i>Duplicaria</i>	sp. 3	South Madagascar	25°24'1'-2'S, 44°51'1'-7"E; 24–26	E2	CONO1150-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910154	<i>Duplicaria</i>	sp. 3	South Madagascar	25°24'1'-2'S, 44°51'1'-7"E; 24–26	E2	CONO1151-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910155	<i>Duplicaria</i>	sp. 3	South Madagascar	25°25'80'-8'S, 44°55'7'-8"E; 11–13	E2	CONO1299-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910156	<i>Duplicaria</i>	sp. 3	South Madagascar	25°25'80'-8'S, 44°55'7'-8"E; 11–13	E2	CONO1179-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910159	<i>Duplicaria</i>	sp. 3	South Madagascar	25°25'80'-8'S, 44°55'7'-8"E; 11–13	E2	CONO1178-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910160	<i>Duplicaria</i>	sp. 3	South Madagascar	25°26'1'-4'S, 44°55'2'-6"E; 17–20	E2	CONO1280-12	EU685596	EU685455	EU685748	JQ808954
MNHN IM200910112	<i>Euterebra</i>	<i>fusculeta</i>	South Madagascar	25°04'4'-7'S, 46°55'3'-56'3"E; 19–26	F	CONO1339-12	EU685596	EU685455	EU685748	JQ808955
MNHN IM200910114	<i>Euterebra</i>	<i>fusculeta</i>	South Madagascar	25°03'7'S, 46°57'8"E; 7	F	CONO1365-12	EU685596	EU685455	EU685748	JQ808955
MNHN IM200910127	<i>Euterebra</i>	<i>fusculeta</i>	South Madagascar	25°26'0'-1'S, 44°54'2'-9"E; 21–24	F	CONO1340-12	EU685596	EU685455	EU685748	JQ808955
MNHN IM200910133	<i>Euterebra</i>	<i>fusculeta</i>	South Madagascar	25°26'8'S, 44°54'9"E; 27	F	CONO1334-12	EU685596	EU685455	EU685748	JQ808955
MNHN IM200910147	<i>Euterebra</i>	<i>fusculeta</i>	South Madagascar	25°25'9'S, 44°55'1'-2"E; 18–20	F	CONO1155-12	EU685596	EU685455	EU685748	JQ808955
Museum of New Zealand	<i>Euterebra</i>	<i>tristis</i>	New-Zealand	35°13'20"S, 174°14'30"E, 2–8	F	CONO477-08	EU685592	HQ401611	HQ401677	
MNHN IM200730437	<i>Haustoria</i>	<i>albula</i>	Vanuatu	15°26'6'S, 167°15'2"E;	D	CONO478-08	EU685593	EU685451	EU685744	JQ808956
MNHN IM200730438	<i>Haustoria</i>	<i>albula</i>	Vanuatu	15°26'6'S, 167°15'2"E;	D	CONO501-08	EU685593	EU685471	EU685764	JQ808956
MNHN IM200730457	<i>Haustoria</i>	<i>albula</i>	Vanuatu	15°22'6'S, 167°11'6"E;	D	CONO511-08	EU685620	EU685480	EU685773	JQ808956
MNHN IM200730630	<i>Haustoria</i>	<i>albula</i>	Vanuatu	15°35'7'S, 166°59'3"E; 12	D	CONO511-08	EU685620	EU685480	EU685773	JQ808956

(continued on next page)

Table 1 (continued)

MNHN Ids	Genus	species	Country	Coordinates; depth (m)	Clade	BOLD ID	Genbank COI	GenBank 125	GenBank 16S	GenBank 28S
MNHN IM20097100	<i>Hastula</i>	<i>albula</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	D	CONO1358-12	JQ809051	JQ808563	JQ808768	
MNHN IM20097101	<i>Hastula</i>	<i>albula</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	D	CONO1296-12	JQ809052	JQ808564	JQ808769	
MNHN IM20097102	<i>Hastula</i>	<i>albula</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	D	CONO1275-12	JQ809053	JQ808565		
MNHN IM20097103	<i>Hastula</i>	<i>albula</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	D	CONO1205-12	JQ809054		JQ808770	
MNHN IM200730407	<i>Hastula</i>	<i>hertica</i>	Philippines	07°38.5'N, 008°25.1'W; 883	D	CONO260-08	EU685518	EU685363	EU685655	JQ808957
MNHN IM200730426	<i>Hastula</i>	<i>hertica</i>	Vanuatu	15°35.4'S, 166°58.7'E; 3–8	D	CONO498-08	EU685610	EU685469	EU685762	
MNHN IM200910104	<i>Hastula</i>	<i>hertica</i>	South Madagascar	25°08.9'S, 46°45.4'E; 0–1	D	CONO1252-12	JQ809055	JQ808566	EU685771	
MNHN IM200911872	<i>Hastula</i>	<i>hertica</i>	Tahiti	17°30'28.28"S, 149°27'0.14"W; 0	D	CONO1222-12	JQ809056		JQ808772	
MNHN IM200911873	<i>Hastula</i>	<i>hertica</i>	Tahiti	17°30'28.28"S, 149°27'0.14"W; 0	D	CONO1223-12	JQ809057		JQ808773	
MNHN IM200911874	<i>Hastula</i>	<i>hertica</i>	Tahiti	17°30'28.28"S, 149°27'0.14"W; 0	D	CONO1367-12	JQ809058		JQ808774	
MNHN IM200911875	<i>Hastula</i>	<i>hertica</i>	Tahiti	17°30'28.28"S, 149°27'0.14"W; 0	D	CONO1368-12	JQ809059		JQ808775	
MNHN IM200730535	<i>Hastula</i>	<i>lanceata</i>	Philippines	9°33.0'N, 123°46.5'E; 8–14	D	CONO203-08	EU685495	EU685631	EU685776	JQ808958
MNHN IM20097089	<i>Hastula</i>	<i>lanceata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	D	CONO1274-12	JQ809060	JQ808567	JQ808776	
MNHN IM20097090	<i>Hastula</i>	<i>lanceata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	D	CONO1241-12	JQ809061	JQ808568	JQ808777	
MNHN IM20097091	<i>Hastula</i>	<i>lanceata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	D	CONO1140-12	JQ809062	JQ808569	JQ808778	
MNHN IM200730542	<i>Hastula</i>	<i>penicillata</i>	Vanuatu	15°22.6'S, 167°11.6'E;	D	CONO502-08	EU685613	EU685472	EU685765	JQ808959
MNHN IM200730540	<i>Hastula</i>	<i>penicillata</i>	Vanuatu	15°22.6'S, 167°11.6'E;	D	CONO503-08	EU685614	EU685473	EU685766	
MNHN IM200730550	<i>Hastula</i>	<i>solida</i>	Vanuatu	15°26.6'S, 167°15.2'E;	D	CONO476-08	EU685591	EU685448	EU685740	
MNHN IM200730417	<i>Hastula</i>	<i>solida</i>	Vanuatu	15°26.6'S, 167°15.2'E;	D	CONO1189-12	JQ809063	EU685450	EU685742	
MNHN IM200730549	<i>Hastula</i>	<i>solida</i>	Vanuatu	15°26.6'S, 167°15.2'E;	D	CONO1225-12	EU685449	EU685741	EU685741	
MNHN IM20097096	<i>Hastula</i>	<i>solida</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	D	CONO1207-12	JQ809064	JQ808570	JQ808779	
MNHN IM20097097	<i>Hastula</i>	<i>solida</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	D	CONO1329-12	JQ809065	JQ808571	JQ808780	JQ808960
MNHN IM20097098	<i>Hastula</i>	<i>solida</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	D	CONO1242-12	JQ809066	JQ808572	JQ808781	
MNHN IM20097099	<i>Hastula</i>	<i>solida</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	D	CONO1206-12	JQ809067	JQ808573	JQ808782	
MNHN IM200910110	<i>Hastula</i>	sp.	South Madagascar	25°03.7'S, 46°57.8'E; 7	D	CONO1303-12	EU685580	JQ808574	JQ808783	
MNHN IM200730608	<i>Hastula</i>	<i>strigilata</i>	Vanuatu	15°35.2'S, 167°59.4'E;	D	CONO465-08	EU685581	EU685434	EU685724	
MNHN IM200730420	<i>Hastula</i>	<i>strigilata</i>	Vanuatu	15°35.2'S, 167°59.4'E;	D	CONO466-08	EU685582	EU685435	EU685726	
MNHN IM200730416	<i>Hastula</i>	<i>strigilata</i>	Vanuatu	15°35.2'S, 167°59.4'E;	D	CONO1131-12	JQ809066	EU685435	EU685727	
MNHN IM200730435	<i>Hastula</i>	<i>strigilata</i>	Vanuatu	15°33.4'S, 167°12.4'E; 2–6	D	CONO1308-12	JQ809067	JQ808575	JQ808784	JQ808961
MNHN IM200730607	<i>Hastula</i>	<i>strigilata</i>	Vanuatu	15°35.2'S, 167°59.4'E;	D	CONO1132-12	JQ809068	EU685433	EU685725	
MNHN IM200910143	<i>Hastula</i>	<i>strigilata</i>	South Madagascar	25°23.6–7'S, 44°53.3–5'E; 10–12	D	CONO1177-12	JQ809068	JQ808576	JQ808785	JQ808962
MNHN IM200910161	<i>Hastula</i>	<i>stylata</i>	South Madagascar	25°08.9'S, 46°45.4'E; 0–1	D	CONO1302-12	JQ809069	JQ808577	JQ808786	
MNHN IM200730488	<i>Hastulopsis</i>	<i>amoena</i>	South Madagascar	24°47.1'S, 47°11.9'E; 0–1	D	CONO1363-12	JQ809070	JQ808578	JQ808787	JQ808963
MNHN IM200910909	<i>Hastulopsis</i>	<i>amoena</i>	Vanuatu	15°31.7'S, 167°09.4'E; 9–13	E1	CONO1259-12	JQ809071	JQ808579	JQ808788	JQ808964
MNHN IM200910910	<i>Hastulopsis</i>	<i>amoena</i>	Australia	26°56'607"S, 153°23'813"E; 40	E1	CONO1221-12	JQ809072	JQ808580	JQ808789	
MNHN IM200910911	<i>Hastulopsis</i>	<i>conspersa</i>	Vanuatu	15°33.1'S, 167°12.2'E; 3–40	E1	CONO1305-12	JQ809072	JQ808581	JQ808790	
MNHN IM200730619	<i>Hastulopsis</i>	<i>conspersa</i>	Vanuatu	15°33.1'S, 167°12.2'E; 3–40	E1	CONO437-08	EU685552	EU685403	EU685694	
MNHN IM200730623	<i>Hastulopsis</i>	<i>conspersa</i>	Vanuatu	15°33.1'S, 167°12.2'E; 3–40	E1	CONO443-08	EU685558	EU685409	EU685700	
MNHN IM200730463	<i>Hastulopsis</i>	<i>conspersa</i>	Vanuatu	15°33.1'S, 167°12.2'E; 3–40	E1	CONO445-08	EU685560	EU685411	EU685702	JQ808965
MNHN IM200730478	<i>Hastulopsis</i>	<i>conspersa</i>	Vanuatu	15°33.1'S, 167°12.2'E; 3–40	E1	CONO446-08	EU685561	EU685412	EU685703	
MNHN IM200730624	<i>Hastulopsis</i>	<i>conspersa</i>	Vanuatu	15°33.1'S, 167°12.2'E; 3–40	E1	CONO518-08	EU685623	EU685483	EU685776	
MNHN IM200910118	<i>Hastulopsis</i>	<i>mindanaensis</i>	Philippines	15°33.4'S, 167°12.4'E; 2–6	E1	CONO207-08	EU685499	EU685344	EU685635	JQ808966
MNHN IM200910119	<i>Hastulopsis</i>	<i>minipulchra</i>	South Madagascar	25°30.2'S, 45°46.3'E; 41–42	E5	CONO1183-12	JQ809073	JQ808581	JQ808791	
MNHN IM200910120	<i>Hastulopsis</i>	<i>minipulchra</i>	South Madagascar	25°28.6'S, 44°56.8'E; 12	E5	CONO1180-12	JQ809074	JQ808582	JQ808792	
MNHN IM200910128	<i>Hastulopsis</i>	<i>minipulchra</i>	South Madagascar	25°22.8–23.7'S, 44°51.1'E; 18–21	E5	CONO1216-12	JQ809075	JQ808583	JQ808793	
MNHN IM200910129	<i>Hastulopsis</i>	<i>minipulchra</i>	South Madagascar	25°22.8–23.7'S, 44°51.1'E; 18–21	E5	CONO1249-12	JQ809076	JQ808584	JQ808794	
MNHN IM200910129	<i>Hastulopsis</i>	<i>minipulchra</i>	South Madagascar	25°28.6'S, 44°56.8'E; 12	E5	CONO1335-12	JQ809077	JQ808585	JQ808795	
MNHN IM200910131	<i>Hastulopsis</i>	<i>minipulchra</i>	South Madagascar	25°22.8–23.7'S, 44°51.1'E; 18–21	E5	CONO1300-12	JQ809078	JQ808586	JQ808796	
MNHN IM200730480	<i>Hastulopsis</i>	<i>pertusa</i>	Vanuatu	13°25'S, 47°57'E; 71–158	E1	CONO444-08	EU685559	EU685410	EU685701	JQ808967
MNHN IM200730388	<i>Hastulopsis</i>	<i>pertusa</i>	Vanuatu	13°25'S, 47°57'E; 71–158	E1	CONO447-08	EU685562	EU685413	EU685704	
MNHN IM200730392	<i>Hastulopsis</i>	<i>pseudopertusa</i>	Vanuatu	13°25'S, 47°57'E; 71–158	E1	CONO448-08	EU685563	EU685414	EU685705	
MNHN IM200910080	<i>Hastulopsis</i>	<i>pseudopertusa</i>	North Madagascar	13°25'S, 47°57'E; 71–158	E5	CONO1145-12	JQ809079	JQ808587	JQ808797	JQ808968
MNHN IM20099954	<i>Hastulopsis</i>	<i>pseudopertusa</i>	North Madagascar	13°25'S, 47°57'E; 71–158	E5	CONO1146-12	JQ809080	JQ808588	JQ808798	
MNHN IM200910065	<i>Myurella</i>	<i>affinis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1116-10	JQ809081	EU685351	EU685799	
MNHN IM200730430	<i>Myurella</i>	<i>affinis</i>	Philippines	9°37.4'N, 123°54.5'E; 6–8	E1	CONO214-08	EU685506	EU685352	EU685642	
MNHN IM200730452	<i>Myurella</i>	<i>affinis</i>	Philippines	9°37.4'N, 123°54.5'E; 6–8	E1	CONO215-08	EU685507	EU685352	EU685643	

MNHN IM200730439	Myurella	<i>affinis</i>	Philippines	08°36.7'N, 079°00'W; 28	E1	CONO218-08	EU685508	EU685353	EU685644	JQ808969
MNHN IM200730460	Myurella	<i>affinis</i>	Philippines	9°35.7'N, 123°44.4'E; 0-2	E1	CONO239-08	EU685512	EU685356	EU685648	
MNHN IM200730481	Myurella	<i>affinis</i>	Philippines	9°35.7'N, 123°44.4'E; 0-2	E1	CONO283-08	EU685525	EU685370	EU685662	
MNHN IM200730414	Myurella	<i>affinis</i>	Vanuatu	15°26.6'S, 167°15.2'E;	E1	CONO467-08	EU685582	EU685436	EU685728	
MNHN IM200730412	Myurella	<i>affinis</i>	Vanuatu	15°26.6'S, 167°15.2'E;	E1	CONO468-08	EU685583	EU685437	EU685729	
MNHN IM200730594	Myurella	<i>affinis</i>	Vanuatu	9°32.8'N, 123°45.9'E; 2	E1	CONO475-08	EU685590	EU685447	EU685739	
MNHN IM200730541	Myurella	<i>affinis</i>	Vanuatu	15°36.8'S, 167°08.5'E; 1-42	E1	CONO485-08	EU685599	EU685458	EU685751	
MNHN IM200730415	Myurella	<i>affinis</i>	Vanuatu	9°32.8'N, 123°45.9'E; 2	E1	CONO1285-12	Q809082	Q808589	Q808800	
MNHN IM200730529	Myurella	<i>affinis</i>	Philippines	08°36.7'N, 079°00'W; 28	E1	CONO1133-12	Q809083	Q808590		
MNHN IM200730551	Myurella	<i>affinis</i>	Vanuatu	9°32.8'N, 123°45.9'E; 2	E1	CONO1226-12	Q809084	Q808591	Q808801	
MNHN IM200910021	Myurella	<i>affinis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1202-12	Q809085	Q808592	Q808802	
MNHN IM200910022	Myurella	<i>affinis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1325-12	Q809086	Q808593	Q808803	
MNHN IM200910056	Myurella	<i>affinis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1292-12	Q809087	Q808594	Q808804	
MNHN IM200910058	Myurella	<i>affinis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1201-12	Q809088	Q808595	Q808805	
MNHN IM200910059	Myurella	<i>affinis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1239-12	Q809089	Q808596	Q808806	
MNHN IM200910060	Myurella	<i>affinis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1171-12	Q809090	Q808597	Q808807	
MNHN IM200910061	Myurella	<i>affinis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1170-12	Q809091	Q808598	Q808808	
MNHN IM200910062	Myurella	<i>affinis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1326-12	Q809092	Q808599	Q808809	
MNHN IM200910063	Myurella	<i>affinis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1272-12	Q809093	Q808600	Q808810	
MNHN IM200910064	Myurella	<i>affinis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1353-12	Q809094	Q808601	Q808811	
MNHN IM200910066	Myurella	<i>affinis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1327-12	Q809095		Q808812	
MNHN IM200910067	Myurella	<i>affinis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1293-12	Q809096	Q808602	Q808813	
MNHN IM20097092	Myurella	<i>affinis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1169-12	Q809097	Q808603	Q808814	
MNHN IM20097093	Myurella	<i>affinis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1200-12	Q809098	Q808604	Q808815	
MNHN IM20097094	Myurella	<i>affinis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1139-12	Q809099	Q808605	Q808816	
MNHN IM20097095	Myurella	<i>affinis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1324-12	Q809100	Q808606	Q808817	
MNHN IM200730510	Myurella	<i>columellaris</i>	Philippines	9°35.7'N, 123°44.4'E; 0-2	E5	CONO237-08	EU685510	EU685646		
MNHN IM200730598	Myurella	<i>columellaris</i>	Vanuatu	15°26.6'S, 167°15.2'E;	E5	CONO469-08	EU685584	EU685438	EU685730	JQ808970
MNHN IM200910020	Myurella	<i>columellaris</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E5	CONO1357-12	Q809101	Q808607	Q808818	
MNHN IM200730465	Myurella	<i>flavofasciata</i>	Philippines	9°29.4'N, 123°56.0'E; 15-20	E1	CONO247-08	EU685515	EU685360	EU685652	JQ808971
MNHN IM20087436	Myurella	<i>flavofasciata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E1	CONO1141-12	Q809102		Q808819	JQ808972
MNHN IM200730459	Myurella	<i>kilburni</i>	Philippines	9°35.7'N, 123°44.4'E; 0-2	E5	CONO238-08	EU685511	EU685355	EU685647	
MNHN IM200730461	Myurella	<i>kilburni</i>	Vanuatu	15°42.7'S, 167°15.1'E; 2-3	E5	CONO491-08	EU685604	EU685463	EU685756	
MNHN IM200730612	Myurella	<i>lineaperlata</i>	Vanuatu	15°29'S, 167°14.9'E; 2-4	E2	CONO460-08	EU685575	EU685428	EU685719	
MNHN IM200730471	Myurella	<i>lineaperlata</i>	Vanuatu	15°29'S, 167°14.9'E; 2-4	E2	CONO461-08	EU685576	EU685429	EU685720	
MNHN IM200730635	Myurella	<i>lineaperlata</i>	Vanuatu	15°33.4'S, 167°12.4'E; 2-6	E2	CONO519-08	EU685624	EU685484	EU685777	JQ808973
MNHN IM200730408	Myurella	<i>nebulosa</i>	Philippines	9°29.4'N, 123°56.0'E; 15-20	E1	CONO248-08	EU685516	EU685361	EU685653	
MNHN IM200730378	Myurella	<i>nebulosa</i>	Vanuatu	15°33.1'S, 167°12.2'E; 3-40	E1	CONO407-08		EU685392	EU685683	
MNHN IM200730567	Myurella	<i>nebulosa</i>	Vanuatu	15°34.7'S, 167°13.8'E; 14-25	E1	CONO459-08	EU685574	EU685426	EU685717	
MNHN IM200730498	Myurella	<i>nebulosa</i>	Vanuatu	15°27.6'S, 167°14.3'E; 6-35	E1	CONO479-08	EU685594	EU685453	EU685746	JQ808974
MNHN IM200910098	Myurella	<i>nebulosa</i>	Mozambique	26°12'S, 35°03'E; 87-90	E1	CONO1312-12	Q809103	Q808608	Q808820	
MNHN IM200910099	Myurella	<i>nebulosa</i>	Mozambique	26°12'S, 35°03'E; 87-90	E1	CONO1161-12	Q809104	Q808609	Q808821	
MNHN IM20097437	Myurella	<i>nebulosa</i>	Mozambique	26°12'S, 35°03'E; 87-90	E1	CONO1348-12	Q809105	Q808610		
MNHN IM20097438	Myurella	<i>nebulosa</i>	Mozambique	26°12'S, 35°03'E; 87-90	E1	CONO1162-12	Q809106	Q808611	Q808822	
MNHN IM20097439	Myurella	<i>nebulosa</i>	Mozambique	26°12'S, 35°03'E; 87-90	E1	CONO1192-12	Q809107	Q808612	Q808823	
MNHN IM200730530	Myurella	<i>orientalis</i>	Chesterfield Islands	20°29'S, 158°42'E; 197-230	E3	CONO201-08	EU685493	EU685339	Q808823	
MNHN IM200730515	Myurella	<i>orientalis</i>	Chesterfield Islands	20°06'S, 160°23'E; 280-304	E3	CONO202-08	EU685494	EU685340	EU685629	
MNHN IM200730524	Myurella	<i>orientalis</i>	Solomon Islands	9°07' S, 158°21' E; 267-329	E3	CONO1250-12	Q809108	Q808613	Q808824	
MNHN IM20099974	Myurella	<i>orientalis</i>	New Caledonia	18°02'S, 163°04'E; 320-337	E3	CONO1260-12	Q809109	Q808614	Q808825	
MNHN IM200730453	Myurella	<i>paucistriata</i>	Vanuatu	15°29.6'S, 167°14.9'E; 2-5	E5	CONO480-08	EU685595	EU685454	EU685747	
MNHN IM200730513	Myurella	<i>sp.</i>	Philippines	9°36.4'N, 123°53.8'E; 60-62	E5	CONO265-08	EU685522	EU685367	EU685659	JQ808975
MNHN IM200910090	Myurella	<i>sp.</i>	North Madagascar	12° 35.92' S, 48° 35.22' E; 50-52	E5	CONO1174-12	Q809110	Q808615	Q808826	
MNHN IM200910091	Myurella	<i>sp.</i>	North Madagascar	12° 35.92' S, 48° 35.22' E; 50-52	E5	CONO1332-12	Q809111	Q808616	Q808827	
MNHN IM200910092	Myurella	<i>sp.</i>	North Madagascar	12° 35.92' S, 48° 35.22' E; 50-52	E5	CONO1244-12	Q809112	Q808617	Q808828	
MNHN IM200910094	Myurella	<i>sp.</i>	North Madagascar	15° 30.15' S, 46° 4.3' E; 29-36	E5	CONO1264-12	Q809113	Q808618	Q808829	
MNHN IM200910096	Myurella	<i>sp.</i>	North Madagascar	12° 35.92' S, 48° 35.22' E; 50-52	E5	CONO1298-12	Q809114	Q808619	Q808830	
MNHN IM200910097	Myurella	<i>sp.</i>	North Madagascar	12° 35.92' S, 48° 35.22' E; 50-52	E5	CONO1333-12	Q809115	Q808620	Q808831	
MNHN IM20097124	Myurella	<i>sp.</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E5	CONO1323-12	Q809116	Q808621	Q808832	
MNHN IM20097125	Myurella	<i>sp.</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E5	CONO1322-12	Q809117	Q808622	Q808833	

(continued on next page)

Table 1 (continued)

MNHN Ids	Genus	species	Country	Coordinates; depth (m)	Clade	BOLD ID	Genbank COI	GenBank 125	GenBank 16S	GenBank 28S
MNHN IM20097326	<i>Myurella</i>	sp.	Mozambique	25°59.0'S, 32°54.5'E; 0	E5	CONO1271-12		JQ808623	JQ808834	
MNHN IM200730629	<i>Myurella</i>	<i>undulata</i>	Vanuatu	15°33.1'S, 167°12.2'E; 3–40	E5	CONO408-08	EU685542	EU685393	EU685684	
MNHN IM200730628	<i>Myurella</i>	<i>undulata</i>	Vanuatu	15°33.1'S, 167°12.2'E; 3–40	E5	CONO409-08	EU685543	EU685394	EU685685	
MNHN IM200730620	<i>Myurella</i>	<i>undulata</i>	Vanuatu	15°31.3'S, 167°10.4'E; 3–18	E5	CONO440-08	EU685557	EU685406	EU685697	JQ808976
MNHN IM200730384	<i>Myurella</i>	<i>undulata</i>	Vanuatu	15°26.6'S, 167°15.2'E; 3–18	E5	CONO472-08	EU685587	EU685441	EU685733	
MNHN IM200730570	<i>Myurella</i>	<i>undulata</i>	Vanuatu	15°38.1'S, 167°05.9'E; 3–18	E5	CONO494-08	EU685606	EU685465	EU685758	
MNHN IM20097115	<i>Myurella</i>	<i>undulata</i>	Vanuatu	25°59.0'S, 32°54.5'E; 0	E5	CONO1208-12	EU685118	JQ808624	JQ808835	
MNHN IM200730587	<i>Oxymeris</i>	<i>areolata</i>	Philippines	9°37.4'N, 123°46.9'E; 3–20	B	CONO241-08	EU685513	EU685357	EU685649	
MNHN IM200730371	<i>Oxymeris</i>	<i>areolata</i>	Vanuatu	15°28.7'S, 167°15.2'E; 19	B	CONO406-08	JN589001	HQ401637	HQ401700	JQ808977
MNHN IM200910013	<i>Oxymeris</i>	<i>cerithina</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	B	CONO1138-12	JQ809119	JQ808625	JQ808836	
MNHN IM200910014	<i>Oxymeris</i>	<i>cerithina</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	B	CONO1291-12	JQ809120	JQ808626	JQ808837	
MNHN IM200910015	<i>Oxymeris</i>	<i>cerithina</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	B	CONO1199-12	JQ809121	JQ808627	JQ808838	
MNHN IM20097083	<i>Oxymeris</i>	<i>cerithina</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	B	CONO1270-12	JQ809122	JQ808628	JQ808839	
MNHN IM20097084	<i>Oxymeris</i>	<i>cerithina</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	B	CONO1268-12	JQ809123	JQ808629	JQ808840	
MNHN IM20097085	<i>Oxymeris</i>	<i>cerithina</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	B	CONO1168-12	JQ809124	JQ808630		
MNHN IM20097086	<i>Oxymeris</i>	<i>cerithina</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	B	CONO1269-12	JQ809125	JQ808631	JQ808841	
MNHN IM20099979	<i>Oxymeris</i>	<i>cerithina</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	B	CONO1238-12	JQ809126	JQ808632	JQ808842	JQ808978
MNHN IM200730490	<i>Oxymeris</i>	<i>chlorata</i>	Vanuatu	15°22.6'S, 167°11.6'E; 9	B	CONO504-08	EU685615	EU685474	EU685767	JQ808979
MNHN IM200730494	<i>Oxymeris</i>	<i>clenulata</i>	Vanuatu	15°34.4'S, 167°13.1'E; 9	B	CONO441-08	EU685556	EU685407	EU685698	JQ808980
MNHN IM200730377	<i>Oxymeris</i>	<i>clenulata</i>	Vanuatu	15°34.4'S, 167°13.1'E; 9	B	CONO442-08	EU685557	EU685408	EU685699	
MNHN IM200730373	<i>Oxymeris</i>	<i>dimidiata</i>	Vanuatu	15°32.5'S, 167°10.5'E; 5–10	B	CONO449-08	EU685564	EU685415	EU685706	JQ808981
MNHN IM200730379	<i>Oxymeris</i>	<i>dimidiata</i>	Vanuatu	15°32.5'S, 167°10.5'E; 5–10	B	CONO486-08	EU685600	EU685459	EU685752	
MNHN IM200730372	<i>Oxymeris</i>	<i>dimidiata</i>	Vanuatu	15°32.5'S, 167°10.5'E; 5–10	B	CONO487-08	EU685601	EU685460	EU685753	
MNHN IM200730428	<i>Oxymeris</i>	<i>dimidiata</i>	Vanuatu	15°38.1'S, 167°05.9'E; 3–37	B	CONO495-08	EU685607	EU685466	EU685759	
MNHN IM200730381	<i>Oxymeris</i>	<i>dimidiata</i>	Vanuatu	15°35.4'S, 166°59.7'E; 3–37	B	CONO510-08	EU685619	EU685479	EU685772	
MNHN IM20097087	<i>Oxymeris</i>	<i>dimidiata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	B	CONO1209-12	JQ809127	JQ808633	JQ808843	
MNHN IM20097088	<i>Oxymeris</i>	<i>dimidiata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	B	CONO1331-12	JQ809128	JQ808634	JQ808844	
MNHN IM200730443	<i>Oxymeris</i>	<i>felina</i>	Philippines	9°37.4'N, 123°54.5'E; 6–8	B	CONO208-08	EU685500	EU685345	EU685636	JQ808982
MNHN IM200730445	<i>Oxymeris</i>	<i>felina</i>	Philippines	9°37.4'N, 123°54.5'E; 6–8	B	CONO210-08	EU685502	EU685347	EU685638	
MNHN IM200730370	<i>Oxymeris</i>	<i>maculata</i>	Philippines	9°37.4'N, 123°54.5'E; 6–8	B	CONO204-08	EU685496	EU685341	EU685632	
MNHN IM200730389	<i>Oxymeris</i>	<i>maculata</i>	Vanuatu	15°28.7'S, 167°15.2'E; 19	B	CONO405-08	EU685541	EU685391	EU685682	JQ808983
MNHN IM200742093	<i>Oxymeris</i>	<i>strigata</i>	Panama	08°11.8'N, 078°57.1'W; 22	B	CONO974-09	FJ707455.1	FJ707388.1	FJ707422.1	
MNHN IM200742105	<i>Oxymeris</i>	<i>strigata</i>	Panama	08°11.8'N, 078°57.1'W; 22	B	CONO979-09	FJ707460.1	FJ707393.1	FJ707428.1	
MNHN IM200742137	<i>Oxymeris</i>	<i>strigata</i>	Panama	08°14.7'N, 079°05.6'W; 18	B	CONO990-09	FJ707471.1	FJ707404.1	FJ707439.1	
MNHN IM200730395	<i>Pellifrontia</i>	<i>jungi</i>	Philippines	9°38'N, 123°40'E; 606–631	A	CONO292-08	EU685530	EU685375	EU685666	JQ808984
MNHN IM200730584	<i>Pellifrontia</i>	<i>jungi</i>	Philippines	9°38'N, 123°38'E; 729–733	A	CONO347-08	EU685532	EU685380	EU685671	
MNHN IM200730501	<i>Pellifrontia</i>	<i>jungi</i>	Solomon Islands	8°26' S, 159°26' E; 543–593	A	CONO1286-12		EU685385	EU685676	
MNHN IM200730539	<i>Pellifrontia</i>	<i>jungi</i>	Vanuatu	15°44'S, 167°03'E; 618–722	A	CONO1261-12	JQ809129	JQ808634	JQ808845	
MNHN IM200730450	<i>Striotebrum</i>	<i>brunneobandatum</i>	Philippines	9°43'N, 123°49'E; 123–135	E1	CONO256-08	EU685517	EU685362	EU685654	
MNHN IM200730522	<i>Striotebrum</i>	<i>brunneobandatum</i>	Solomon Islands	8°38' S, 157°22' E; 195–197	E1	CONO1345-12	JQ809130	JQ808635		
MNHN IM200730454	<i>Striotebrum</i>	<i>dedonderi</i>	Philippines	9°36.4'N, 123°53.8'E; 60–62	E1	CONO263-08	EU685521	EU685366	EU685658	
MNHN IM200730425	<i>Striotebrum</i>	<i>nitidum</i>	Vanuatu	15°35.4'S, 166°58.7'E; 3–8	E2	CONO506-08	EU685616	EU685475	EU685768	
MNHN IM200730473	<i>Striotebrum</i>	<i>nitidum</i>	Vanuatu	15°35.4'S, 166°58.7'E; 3–8	E2	CONO507-08	EU685617	EU685476	EU685769	
MNHN IM200730614	<i>Striotebrum</i>	<i>nitidum</i>	Vanuatu	15°31.7'S, 167°09.4'E; 9–13	E2	CONO1188-12		EU685424	EU685715	
MNHN IM200910157	<i>Striotebrum</i>	<i>nitidum</i>	South Madagascar	25°26.1'–4'S, 44°55.2'–6'E; 17–20	E2	CONO1184-12	JQ809131	JQ808636	JQ808846	JQ808985
MNHN IM200910158	<i>Striotebrum</i>	<i>nitidum</i>	South Madagascar	25°24.1'–2'S, 44°51.1'–7'E; 24–26	E2	CONO1277-12	JQ809132	JQ808637	JQ808847	
MNHN IM20097114	<i>Striotebrum</i>	<i>nitidum</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	E2	CONO1273-12	JQ809133	JQ808637	JQ808848	
MNHN IM200730558	<i>Striotebrum</i>	<i>plumbeum</i>	Vanuatu	15°31.7'S, 167°09.4'E; 9–13	E2	CONO455-08	EU685570	EU685421	EU685712	
MNHN IM200730469	<i>Striotebrum</i>	<i>plumbeum</i>	Vanuatu	15°31.7'S, 167°09.4'E; 9–13	E2	CONO456-08	EU685571	EU685422	EU685713	
MNHN IM200730610	<i>Striotebrum</i>	<i>plumbeum</i>	Vanuatu	15°35.2'S, 167°59.4'E; 3–8	E2	CONO463-08	EU685578	EU685431	EU685722	
MNHN IM200730609	<i>Striotebrum</i>	sp. 1	Vanuatu	15°35.2'S, 167°59.4'E; 3–8	E2	CONO464-08	EU685579	EU685432	EU685723	JQ808986
MNHN IM200730611	<i>Striotebrum</i>	sp. 2	Vanuatu	15°35.2'S, 167°59.4'E; 3–8	E2	CONO462-08	EU685577	EU685430	EU685721	
MNHN IM200730543	<i>Striotebrum</i>	sp. 3	Vanuatu	15°35.4'S, 166°58.7'E; 3–8	E2	CONO499-08	EU685611	EU685470	EU685763	
MNHN IM200742068	<i>Terebra</i>	<i>argosyia</i>	Panama	08°37.2'N, 079°01.1'W; 25	C	CONO962-09	FJ707443.1	FJ707376.1	FJ707408.1	
MNHN IM200742069	<i>Terebra</i>	<i>argosyia</i>	Panama	08°37.2'N, 079°01.1'W; 25	C	CONO963-09	FJ707444.1	FJ707377.1	FJ707409.1	
MNHN IM200742072	<i>Terebra</i>	<i>argosyia</i>	Panama	08°15.6'N, 078°51.6'W; 24	C	CONO964-09	FJ707445.1	FJ707378.1	FJ707411.1	

MNHN IM200742073	<i>Terebra</i>	<i>argosyia</i>	Panama	08°15.6'N, 078°51.6'W; 24	C	CONO965-09	FJ707446.1	FJ707379.1	FJ707412.1	
MNHN IM200742087	<i>Terebra</i>	<i>argosyia</i>	Panama	08°11.8'N, 078°57.1'W; 21	C	CONO969-09	FJ707450.1	FJ707383.1	FJ707417.1	
MNHN IM200742089	<i>Terebra</i>	<i>argosyia</i>	Panama	08°11.8'N, 078°57.1'W; 21	C	CONO970-09	FJ707451.1	FJ707384.1	FJ707418.1	
MNHN IM200742090	<i>Terebra</i>	<i>argosyia</i>	Panama	08°11.8'N, 078°57.1'W; 21	C	CONO971-09	FJ707452.1	FJ707385.1	FJ707419.1	
MNHN IM200742091	<i>Terebra</i>	<i>argosyia</i>	Panama	08°11.8'N, 078°57.1'W; 21	C	CONO972-09	FJ707453.1	FJ707386.1	FJ707420.1	
MNHN IM200742092	<i>Terebra</i>	<i>argosyia</i>	Panama	08°11.8'N, 078°57.1'W; 21	C	CONO973-09	FJ707454.1	FJ707387.1	FJ707421.1	
MNHN IM200742099	<i>Terebra</i>	<i>argosyia</i>	Panama	08°11.8'N, 078°57.5'W; 24	C	CONO975-09	FJ707456.1	FJ707389.1	FJ707423.1	
MNHN IM200742100	<i>Terebra</i>	<i>argosyia</i>	Panama	08°11.8'N, 078°57.5'W; 24	C	CONO976-09	FJ707457.1	FJ707390.1	FJ707424.1	
MNHN IM200742103	<i>Terebra</i>	<i>argosyia</i>	Panama	08°11.8'N, 078°57.5'W; 22	C	CONO977-09	FJ707458.1	FJ707391.1	FJ707426.1	
MNHN IM200742104	<i>Terebra</i>	<i>argosyia</i>	Panama	08°11.8'N, 078°57.5'W; 22	C	CONO978-09	FJ707459.1	FJ707392.1	FJ707427.1	
MNHN IM200742119	<i>Terebra</i>	<i>argosyia</i>	Panama	08°11.8'N, 078°57.5'W; 22	C	CONO981-09	FJ707462.1	FJ707395.1	FJ707430.1	
MNHN IM200742122	<i>Terebra</i>	<i>argosyia</i>	Panama	08°11.8'N, 078°57.5'W; 22	C	CONO984-09	FJ707465.1	FJ707398.1	FJ707433.1	
MNHN IM200742123	<i>Terebra</i>	<i>argosyia</i>	Panama	08°11.8'N, 078°57.5'W; 22	C	CONO985-09	FJ707466.1	FJ707399.1	FJ707434.1	
MNHN IM200742124	<i>Terebra</i>	<i>argosyia</i>	Panama	08°11.8'N, 078°57.5'W; 22	C	CONO986-09	FJ707467.1	FJ707400.1	FJ707435.1	
MNHN IM200742125	<i>Terebra</i>	<i>argosyia</i>	Panama	08°11.8'N, 078°57.5'W; 22	C	CONO987-09	FJ707468.1	FJ707401.1	FJ707436.1	
MNHN IM200730383	<i>Terebra</i>	<i>argus</i>	Vanuatu	15°26.6'S, 167°15.2'E;	C	CONO1190-12	QJ809134	EU685442	EU685734	JQ808987
MNHN IM200730380	<i>Terebra</i>	<i>babylonia</i>	Vanuatu	9°32.8'N, 123°45.9'E; 2	C	CONO474-08	EU685589	EU685446	EU685738	
MNHN IM200730375	<i>Terebra</i>	<i>babylonia</i>	Vanuatu	9°32.8'N, 123°45.9'E; 2	C	CONO1227-12	QJ809135	EU685445	EU685737	JQ808988
MNHN IM200742144	<i>Terebra</i>	<i>berryi</i>	Panama	08°14.7'N, 079°05.6'W; 18	E4	CONO1351-12	QJ809136	QJ808638	QJ808849	
MNHN IM200742167	<i>Terebra</i>	<i>berryi</i>	Panama	08°33'N, 079°04'W; 19	E4	CONO1290-12	QJ809137	QJ808639	QJ808850	
MNHN IM200742097	<i>Terebra</i>	<i>cf. variegata</i>	Panama	08°11.8'N, 078°57.1'W; 26	E4	CONO1195-12	QJ809138	QJ808640	QJ808851	
MNHN IM200742128	<i>Terebra</i>	<i>cf. variegata</i>	Panama	08°14.9'N, 079°05.7'W; 14	E4	CONO1366-12	QJ809139	QJ808641	QJ808852	
MNHN IM200742133	<i>Terebra</i>	<i>cf. variegata</i>	Panama	08°14.8'N, 079°05.9'W; 13	E4	CONO1318-12	QJ809140	QJ808642	QJ808853	
MNHN IM200742135	<i>Terebra</i>	<i>cf. variegata</i>	Panama	08°14.8'N, 079°05.9'W; 13	E4	CONO1319-12	QJ809141	QJ808643	QJ808854	
MNHN IM200742146	<i>Terebra</i>	<i>cf. variegata</i>	Panama	08°14.7'N, 079°05.6'W; 18	E4	CONO1135-12	QJ809142	QJ808644	QJ808855	
MNHN IM200742158	<i>Terebra</i>	<i>cf. variegata</i>	Panama	08°24.5'N, 079°04.7'W; 18	E4	CONO1136-12	QJ809143	QJ808645	QJ808856	
MNHN IM200716735	<i>Terebra</i>	<i>cingulifera</i>	Philippines	9°36'N, 123°44'E; 382-434	C	CONO340-08	EU015735	EU685379	EU685670	EU015620
MNHN IM200730487	<i>Terebra</i>	<i>cingulifera</i>	Solomon Islands	8°40' S, 157°23' E; 214-243	C	CONO382-08	EU685536	EU685386	EU685677	
MNHN IM200730485	<i>Terebra</i>	<i>cingulifera</i>	Vanuatu	15°32.5'S, 167°10.5'E; 5-10	C	CONO490-08	EU685603	EU685462	EU685755	
MNHN IM200730382	<i>Terebra</i>	<i>cingulifera</i>	Vanuatu	15°26.6'S, 167°15.2'E;	C	CONO1347-12	QJ809144	EU685443	EU685735	JQ808989
MNHN IM200730562	<i>Terebra</i>	<i>cingulifera</i>	Solomon Islands	8°38' S, 157°22' E; 195-197	C	CONO1186-12	QJ809145	QJ808857	QJ808857	
MNHN IM200730563	<i>Terebra</i>	<i>cingulifera</i>	Philippines	16°04'N, 121°57'E; 98-107	C	CONO1158-12	QJ809146	QJ808858	QJ808858	
MNHN IM200730484	<i>Terebra</i>	<i>cingulifera</i>	Philippines	16°05.85'N, 121°58.85'E; 83	C	CONO1283-12	QJ809147	QJ808859	QJ808859	
MNHN IM200730564	<i>Terebra</i>	<i>cingulifera</i>	Philippines	15°54'N, 121°42'E; 125-198	C	CONO1129-12	QJ809148	QJ808860	QJ808861	
MNHN IM200730576	<i>Terebra</i>	<i>cingulifera</i>	Vanuatu	15°36.8'S, 167°08.7'E; 3-36	C	CONO1191-12	QJ809149	QJ808862	QJ808862	
MNHN IM200910171	<i>Terebra</i>	<i>cingulifera</i>	South Madagascar	25°04.7'S, 47°03.4'E; 64-65	C	CONO1337-12	QJ809150	QJ808646	QJ808862	
MNHN IM200742095	<i>Terebra</i>	<i>elata</i>	Panama	08°11.8'N, 078°57.1'W; 26	E4	CONO1316-12	QJ809151	QJ808647	QJ808863	
MNHN IM200742096	<i>Terebra</i>	<i>elata</i>	Panama	08°11.8'N, 078°57.1'W; 26	E4	CONO1317-12	QJ809152	QJ808648	QJ808864	
MNHN IM200742111	<i>Terebra</i>	<i>elata</i>	Panama	08°11.8'N, 078°57.5'W; 22	E4	CONO1165-12	QJ809153	QJ808649	QJ808865	
MNHN IM200742127	<i>Terebra</i>	<i>elata</i>	Panama	08°11.8'N, 078°57.5'W; 22	E4	CONO1267-12	QJ809154	QJ808650	QJ808866	
MNHN IM200742147	<i>Terebra</i>	<i>elata</i>	Panama	08°14.7'N, 079°05.4'W; 18	E4	CONO1320-12	QJ809155	QJ808651	QJ808867	
MNHN IM200742155	<i>Terebra</i>	<i>elata</i>	Panama	08°24.5'N, 079°04.7'W; 18	E4	CONO1137-12	QJ809156	QJ808652	QJ808868	
MNHN IM200742162	<i>Terebra</i>	<i>elata</i>	Panama	08°31.2'N, 079°06.8'W; 32	E4	CONO1352-12	QJ809157	QJ808653	QJ808869	
MNHN IM200742163	<i>Terebra</i>	<i>elata</i>	Panama	08°31.2'N, 079°06.8'W; 32	E4	CONO1166-12	QJ809158	QJ808654	QJ808870	
MNHN IM200730423	<i>Terebra</i>	<i>fijiensis</i>	Vanuatu	15°33'S, 167°16.7'E; 92	E2	CONO520-08	EU685625	EU685485	EU685778	
MNHN IM200742152	<i>Terebra</i>	<i>formosa</i>	Panama	08°16.9'N, 079°02.7'W; 39	C	CONO091-09	FJ707472.1	FJ707405.1	FJ707440.1	JQ808990
MNHN IM200730394	<i>Terebra</i>	<i>funiculata</i>	Vanuatu	25°59.0'S, 32°54.5'E; 0	C	CONO450-08	EU685565	EU685416	EU685707	
MNHN IM20097108	<i>Terebra</i>	<i>funiculata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1198-12	QJ809157	QJ808655	QJ808871	
MNHN IM20097109	<i>Terebra</i>	<i>funiculata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1237-12	QJ809158	QJ808656	QJ808872	
MNHN IM20097110	<i>Terebra</i>	<i>funiculata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1236-12	QJ809159	QJ808657	QJ808873	
MNHN IM200730387	<i>Terebra</i>	<i>funiculata</i>	Mozambique	15°33.1'S, 167°12.2'E; 3-40	C	CONO438-08	EU685553	EU685404	EU685695	
MNHN IM200730376	<i>Terebra</i>	<i>guttata</i>	Vanuatu	15°33.1'S, 167°12.2'E; 3-40	C	CONO439-08	EU685554	EU685405	EU685696	
MNHN IM200730431	<i>Terebra</i>	<i>guttata</i>	Philippines	9°36.8'N, 123°52.2'E;	C	CONO262-08	EU685520	EU685365	EU685657	
MNHN IM200730632	<i>Terebra</i>	<i>laevigata</i>	Vanuatu	15°31.7'S, 167°09.4'E; 9-13	C	CONO457-08	EU685572	EU685423	EU685714	
MNHN IM200730613	<i>Terebra</i>	<i>laevigata</i>	Vanuatu	15°31.7'S, 167°09.4'E; 9-13	C	CONO458-08	EU685573	EU685425	EU685716	
MNHN IM200730597	<i>Terebra</i>	<i>laevigata</i>	Vanuatu	15°26.6'S, 167°15.2'E; 6	C	CONO471-08	EU685586	EU685440	EU685732	
MNHN IM200730603	<i>Terebra</i>	<i>laevigata</i>	Vanuatu	15°43.4'S, 167°15.0'E; 6	C	CONO484-08	EU685598	EU685457	EU685750	
MNHN IM200730573	<i>Terebra</i>	<i>laevigata</i>	Vanuatu	15°29.6'S, 167°14.9'E; 2-5	C	CONO1157-12	QJ809160	QJ808658	QJ808874	
MNHN IM200910016	<i>Terebra</i>	<i>laevigata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1172-12	QJ809160	QJ808659	QJ808875	

(continued on next page)

Table 1 (continued)

MNHN Ids	Genus	species	Country	Coordinates; depth (m)	Clade	BOLD ID	Genbank COI	GenBank 125	GenBank 16S	GenBank 28S
MNHN IM200910017	<i>Terebra</i>	<i>laevigata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1142-12	JQ809161	JQ808660	JQ808876	
MNHN IM200910018	<i>Terebra</i>	<i>laevigata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1144-12	JQ809162	JQ808661	JQ808877	
MNHN IM200910019	<i>Terebra</i>	<i>laevigata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1173-12	JQ809163	JQ808662	JQ808878	
MNHN IM20097104	<i>Terebra</i>	<i>laevigata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1143-12	JQ809164	JQ808663	JQ808879	
MNHN IM20097105	<i>Terebra</i>	<i>laevigata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1330-12	JQ809165	JQ808664	JQ808880	
MNHN IM20097106	<i>Terebra</i>	<i>laevigata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1297-12	JQ809166	JQ808665	JQ808881	JQ808991
MNHN IM20097107	<i>Terebra</i>	<i>laevigata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1359-12	JQ809167	JQ808666	JQ808882	
MNHN IM20099947	<i>Terebra</i>	<i>laevigata</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1276-12	JQ809167	JQ808667	JQ808883	
MNHN IM200742083	<i>Terebra</i>	<i>larvaeformis</i>	Panama	08°11.8'N, 078°57.1'W; 21	E4	CONO1265-12	JQ809168	JQ808668	JQ808884	
MNHN IM200742106	<i>Terebra</i>	<i>larvaeformis</i>	Panama	08°11.8'N, 078°57.5'W; 22	E4	CONO1350-12	JQ809169	JQ808669	JQ808885	
MNHN IM200742113	<i>Terebra</i>	<i>larvaeformis</i>	Panama	08°11.8'N, 078°57.5'W; 22	E4	CONO1196-12	JQ809170	JQ808670	JQ808886	
MNHN IM200742149	<i>Terebra</i>	<i>larvaeformis</i>	Panama	08°14.7'N, 079°05.4'W; 18	E4	CONO1197-12	JQ809171	JQ808671	JQ808887	
MNHN IM200742131	<i>Terebra</i>	<i>omata</i>	Panama	08°16.9'N, 079°02.7'W; 39	C	CONO988-09	FJ707469.1	FJ707402.1	FJ707437.1	
MNHN IM200730374	<i>Terebra</i>	<i>punctatostriata</i>	Vanuatu	15°31.4'S, 167°09.7'E; 4-18	C	CONO1344-12	JQ809172	JQ808672	JQ808888	
MNHN IM200742070	<i>Terebra</i>	<i>puncturosa</i>	Panama	08°15.6'N, 078°51.6'W; 24	E4	CONO1229-12	JQ809173	JQ808673	JQ808889	
MNHN IM200742081	<i>Terebra</i>	<i>puncturosa</i>	Panama	08°11.8'N, 078°57.1'W; 21	E4	CONO1315-12	JQ809174	JQ808674	JQ808890	
MNHN IM200742116	<i>Terebra</i>	<i>puncturosa</i>	Panama	08°11.8'N, 078°57.5'W; 22	E4	CONO1266-12	JQ809175	JQ808675	JQ808891	
MNHN IM200742171	<i>Terebra</i>	<i>puncturosa</i>	Panama	08°33'N, 079°04'W; 19	E4	CONO1167-12	JQ809176	JQ808676	JQ808892	
MNHN IM200971116	<i>Terebra</i>	<i>quoygaimardi</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1233-12	JQ809177	JQ808677	JQ808893	
MNHN IM20097118	<i>Terebra</i>	<i>quoygaimardi</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1234-12	JQ809177	JQ808678	JQ808894	
MNHN IM20099946	<i>Terebra</i>	<i>quoygaimardi</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1235-12	JQ809177	JQ808678	JQ808894	
MNHN IM200730464	<i>Terebra</i>	sp. 1	Philippines	9°35.3'N, 123°52.2'E; 84-87	E2	CONO206-08	EU685498	EU685343	EU685634	
MNHN IM200730516	<i>Terebra</i>	sp. 2	Chesterfield Islands	24°46'S, 159°43'E; 400-418	E3	CONO1159-12	JQ809178	JQ808679	JQ808895	
MNHN IM200730617	<i>Terebra</i>	sp. 3	Vanuatu	15°31.7'S, 167°09.7'E; 18-21	E2	CONO430-08	EU685549	EU685400	EU685691	
MNHN IM200730618	<i>Terebra</i>	sp. 3	Vanuatu	15°31.7'S, 167°09.7'E; 18-21	E2	CONO431-08	EU685550	EU685401	EU685692	
MNHN IM200730633	<i>Terebra</i>	sp. 4	Solomon Islands	9°07' S, 158°21' E; 267-329	E3	CONO1251-12	JQ809179	JQ808680	JQ808896	JQ808993
MNHN IM200730946	<i>Terebra</i>	sp. 5	Chesterfield Islands	20°21'S, 158°46'E; 345-351	E5	CONO1228-12	JQ809180	JQ808681	JQ808897	
MNHN IM200742151	<i>Terebra</i>	<i>speciata</i>	Panama	08°16.9'N, 079°02.7'W; 39	E4	CONO1321-12	JQ809181	JQ808682	JQ808898	
MNHN IM200742168	<i>Terebra</i>	<i>speciata</i>	Panama	08°24.5'N, 079°04.7'W; 18	E4	CONO1232-12	JQ809182	JQ808683	JQ808899	
MNHN IM200742168	<i>Terebra</i>	<i>speciata</i>	Panama	08°33'N, 079°04'W; 19	E4	CONO1289-12	JQ809182	JQ808684	JQ808900	
MNHN IM200730444	<i>Terebra</i>	<i>subulata</i>	Philippines	9°37.4'N, 123°54.5'E; 6-8	C	CONO209-08	EU685501	EU685346	EU685637	
MNHN IM200730483	<i>Terebra</i>	<i>subulata</i>	Philippines	15°36.6'S, 167°10.1'E; 8-20	C	CONO277-08	EU685524	EU685369	EU685661	JQ808994
MNHN IM200730386	<i>Terebra</i>	<i>subulata</i>	Vanuatu	15°36.6'S, 167°10.1'E; 8-20	C	CONO436-08	EU685551	EU685402	EU685663	
MNHN IM200730582	<i>Terebra</i>	<i>succincta</i>	Philippines	9°39'N, 123°48'E; 255-268	E3	CONO285-08	EU685527	EU685372	EU685669	EU015617
MNHN IM200730582	<i>Terebra</i>	<i>succincta</i>	Philippines	9°30'N, 123°42'E; 356-396	E3	CONO331-08	EU685544	EU685378	EU685672	
MNHN IM200716731	<i>Terebra</i>	<i>succincta</i>	Solomon Islands	7°14' S, 158°29' E; 286-423	E3	CONO379-08	EU685534	EU685381	EU685686	
MNHN IM200730479	<i>Terebra</i>	<i>succincta</i>	Vanuatu	15°31.7'S, 167°09.7'E; 18-21	E2	CONO425-08	EU685545	EU685396	EU685687	JQ808995
MNHN IM200730626	<i>Terebra</i>	<i>succincta</i>	Vanuatu	15°31.7'S, 167°09.7'E; 18-21	E2	CONO426-08	EU685546	EU685397	EU685688	
MNHN IM200730440	<i>Terebra</i>	<i>succincta</i>	Vanuatu	15°31.7'S, 167°09.7'E; 18-21	E2	CONO427-08	EU685547	EU685398	EU685689	
MNHN IM200730456	<i>Terebra</i>	<i>succincta</i>	Vanuatu	15°31.7'S, 167°09.7'E; 18-21	E2	CONO428-08	EU685548	EU685399	EU685690	
MNHN IM200730458	<i>Terebra</i>	<i>succincta</i>	Vanuatu	15°31.7'S, 167°09.7'E; 18-21	E2	CONO429-08	EU685548	EU685399	EU685690	
MNHN IM200730634	<i>Terebra</i>	<i>succincta</i>	Vanuatu	15°31.7'S, 167°09.7'E; 18-21	E2	CONO451-08	EU685566	EU685417	EU685708	
MNHN IM200730475	<i>Terebra</i>	<i>succincta</i>	Vanuatu	15°31.7'S, 167°09.7'E; 18-21	E2	CONO452-08	EU685567	EU685418	EU685709	
MNHN IM200730476	<i>Terebra</i>	<i>succincta</i>	Vanuatu	15°26.6'S, 167°15.2'E;	E2	CONO470-08	EU685585	EU685439	EU685731	
MNHN IM200730385	<i>Terebra</i>	<i>succincta</i>	Vanuatu	15°41'S, 167°00'E; 517-614	E2	CONO492-08	EU685605	EU685464	EU685757	
MNHN IM200730601	<i>Terebra</i>	<i>succincta</i>	Vanuatu	15°33.4'S, 167°12.4'E; 2-6	E2	CONO516-08	EU685621	EU685481	EU685774	
MNHN IM200730433	<i>Terebra</i>	<i>succincta</i>	Vanuatu	15°33.4'S, 167°12.4'E; 2-6	E2	CONO517-08	EU685622	EU685482	EU685775	
MNHN IM200730434	<i>Terebra</i>	<i>succincta</i>	Vanuatu	15°35.4'S, 166°58.7'E; 3-8	E2	CONO1307-12	JQ809183	JQ808685	JQ808901	
MNHN IM200730419	<i>Terebra</i>	<i>succincta</i>	Vanuatu	15°35.4'S, 166°58.7'E; 3-8	E2	CONO1224-12	JQ809184	JQ808686	JQ808902	
MNHN IM200730468	<i>Terebra</i>	<i>succincta</i>	Vanuatu	15°35.4'S, 166°58.7'E; 3-8	E2	CONO1257-12	JQ809185	JQ808687	JQ808903	
MNHN IM200730470	<i>Terebra</i>	<i>succincta</i>	Vanuatu	15°35.4'S, 166°58.7'E; 3-8	E2	CONO1160-12	JQ809186	JQ808688	JQ808904	
MNHN IM200730622	<i>Terebra</i>	<i>succincta</i>	Vanuatu	20°17'S, 163°50'E; 590-809	E3	CONO1187-12	JQ809187	JQ808689	JQ808905	
MNHN IM200910085	<i>Terebra</i>	<i>succincta</i>	North New-Caledonia	9°36.8'N, 123°52.2'E;	E2	CONO261-08	EU685519	EU685364	EU685656	
MNHN IM200730451	<i>Terebra</i>	<i>textilis</i>	Philippines	15°31.3'S, 167°09.9'E; 1-6	E2	CONO453-08	EU685568	EU685419	EU685710	
MNHN IM200730621	<i>Terebra</i>	<i>textilis</i>	Vanuatu		E2	CONO454-08	EU685569	EU685420	EU685711	
MNHN IM200730616	<i>Terebra</i>	<i>textilis</i>	Vanuatu		E2	CONO496-08	EU685608	EU685467	EU685760	

MNHN IM200730545	<i>Terebra</i>	<i>textilis</i>	Vanuatu	15°31.3'S, 167°09.9'E; 1-6	E2	CONO497-08	EU685609	EU685468	EU685761	
MNHN IM200730474	<i>Terebra</i>	<i>textilis</i>	Vanuatu	15°35.4'S, 166°58.7'E; 3-8	E2	CONO508-08	EU685618	EU685477	JQ808996	
MNHN IM200717938	<i>Terebra</i>	<i>textilis</i>	Vanuatu	15°35.4'S, 166°58.7'E; 3-8	E2	CONO509-08	EU015750	EU685771	EU015635	
MNHN IM200730441	<i>Terebra</i>	<i>textilis</i>	Vanuatu	15°33.4'S, 167°12.4'E; 2-6	E2	CONO1258-12	JQ809188	JQ808906	JQ808997	
MNHN IM200910088	<i>Terebra</i>	<i>textilis</i>	North Madagascar	14° 31.9' S, 47° 26.54' E; 46-54	E2	CONO1311-12	JQ809189	JQ808907	JQ808908	
MNHN IM200910093	<i>Terebra</i>	<i>textilis</i>	North Madagascar	15° 30.15' S, 46° 4.3' E; 29-36	E2	CONO1194-12	JQ809190	JQ808908	JQ808909	
MNHN IM200910095	<i>Terebra</i>	<i>textilis</i>	North Madagascar	15° 30.15' S, 46° 4.3' E; 29-36	E2	CONO1349-12	JQ809191	JQ808909	JQ808998	
MNHN IM20099957	<i>Terebra</i>	<i>textilis</i>	North Madagascar	12° 35.92' S, 48° 35.22' E; 50-52	E2	CONO1243-12	JQ809192	JQ808910		
MNHN IM200730409	<i>Terebra</i>	<i>tricolor</i>	Vanuatu	15°33.1'S, 167°17.8'E; 15-25	C	CONO404-08	EU685540	EU685681		
MNHN IM200730493	<i>Terebra</i>	<i>tricolor</i>	Vanuatu	15°38.5'S, 167°15.1'E; 13	C	CONO488-08	EU685602	EU685754		
MNHN IM200730424	<i>Terebra</i>	<i>trismacaria</i>	Solomon Islands	8°37' S, 157°21' E; 150-160	E2	CONO380-08		EU685383	JQ808999	
MNHN IM200730579	<i>Terebra</i>	<i>trismacaria</i>	Solomon Islands	8°40' S, 157°23' E; 214-243	E2	CONO383-08	EU685537	EU685678		
MNHN IM200730492	<i>Terebra</i>	<i>trismacaria</i>	Solomon Islands	8°40' S, 157°23' E; 214-243	E2	CONO384-08	EU685538	EU685679		
MNHN IM200730499	<i>Terebra</i>	<i>trismacaria</i>	Solomon Islands	8°40' S, 157°23' E; 214-243	E2	CONO385-08	EU685539	EU685680		
MNHN IM200730446	<i>Terenolia</i>	<i>pygmaea</i>	Philippines	9°37.4'N, 123°54.5'E; 4-5	E1	CONO211-08	EU685503	EU685639		
MNHN IM200730448	<i>Terenolia</i>	<i>pygmaea</i>	Philippines	9°37.4'N, 123°54.5'E; 4-5	E1	CONO212-08	EU685504	EU685640		
MNHN IM200730449	<i>Terenolia</i>	<i>pygmaea</i>	Philippines	9°37.4'N, 123°54.5'E; 4-5	E1	CONO213-08	EU685505	EU685641		
MNHN IM200730511	<i>Terenolia</i>	<i>pygmaea</i>	Philippines	9°35.7'N, 123°44.4'E; 0-2	E1	CONO236-08	EU685509	EU685645		
MNHN IM200910121	<i>Terenolia</i>	<i>pygmaea</i>	South Madagascar		E1	CONO1231-12	JQ809193	JQ808690	JQ809000	
MNHN IM200730552	<i>Triplostephanus</i>	<i>anilis</i>	Vanuatu	15°35.2'S, 167°59.4'E;	C	CONO473-08	EU685588	EU685736	JQ809001	
MNHN IM200730421	<i>Triplostephanus</i>	<i>anilis</i>	Vanuatu	15°35.4'S, 166°58.7'E; 3-8	C	CONO493-08	JQ809194	JQ808912		
MNHN IM200910068	<i>Triplostephanus</i>	<i>anilis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1354-12	JQ809195	JQ808913		
MNHN IM200910069	<i>Triplostephanus</i>	<i>anilis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1294-12	JQ809196	JQ808914		
MNHN IM200910070	<i>Triplostephanus</i>	<i>anilis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1295-12	JQ809197	JQ808915		
MNHN IM200910071	<i>Triplostephanus</i>	<i>anilis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1328-12	JQ809198	JQ808916		
MNHN IM200910072	<i>Triplostephanus</i>	<i>anilis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1355-12	JQ809199	JQ808917		
MNHN IM20097120	<i>Triplostephanus</i>	<i>anilis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1204-12	JQ809200	JQ808918		
MNHN IM20097121	<i>Triplostephanus</i>	<i>anilis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1203-12	JQ809201	JQ808919		
MNHN IM20097122	<i>Triplostephanus</i>	<i>anilis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1240-12	JQ809202	JQ808920		
MNHN IM20097123	<i>Triplostephanus</i>	<i>anilis</i>	Mozambique	25°59.0'S, 32°54.5'E; 0	C	CONO1356-12	JQ809203	JQ808921		
MNHN IM200730402	<i>Triplostephanus</i>	<i>cumingii</i>	Fiji	18°26.4'S, 178°02.4'E; 50-51	C	CONO1156-12	EU685487	EU685779		
MNHN IM200730418	<i>Triplostephanus</i>	<i>fenestratus</i>	Philippines	9°39'N, 123°48'E; 255-268	C	CONO286-08	EU685528	EU685664		
MNHN IM200730410	<i>Triplostephanus</i>	<i>fenestratus</i>	Philippines	9°39'N, 123°48'E; 255-268	C	CONO287-08	EU685529	EU685665		
MNHN IM200730390	<i>Triplostephanus</i>	<i>fenestratus</i>	Philippines	9°29'N, 123°44'E; 271-318	C	CONO305-08	EU685531	EU685374		
MNHN IM200730538	<i>Triplostephanus</i>	<i>fenestratus</i>	Philippines	9°39'N, 123°48'E; 255-268	C	CONO1284-12	JQ809204	EU685376		
MNHN IM200730553	<i>Triplostephanus</i>	<i>fenestratus</i>	Vanuatu	15°42'S, 167°02'E; 268-445	C	CONO1346-12	JQ809205	JQ808701		
MNHN IM200730559	<i>Triplostephanus</i>	<i>fenestratus</i>	Philippines	9°39'N, 123°48'E; 255-268	C	CONO1309-12	JQ809206	JQ808922		
MNHN IM200910073	<i>Triplostephanus</i>	<i>fenestratus</i>	North Madagascar	14°30'S, 47°27'E; 274-325	C	CONO1313-12	JQ809207	JQ808923		
MNHN IM200910074	<i>Triplostephanus</i>	<i>fenestratus</i>	North Madagascar	14°30'S, 47°27'E; 274-325	C	CONO1230-12	JQ809208	JQ808924		
MNHN IM200910075	<i>Triplostephanus</i>	<i>fenestratus</i>	North Madagascar	14°30'S, 47°27'E; 274-325	C	CONO1193-12	JQ809209	JQ808925		
MNHN IM200910076	<i>Triplostephanus</i>	<i>fenestratus</i>	North Madagascar	14°30'S, 47°27'E; 274-325	C	CONO1288-12	JQ809210	JQ808926		
MNHN IM200910077	<i>Triplostephanus</i>	<i>fenestratus</i>	North Madagascar	14°30'S, 47°27'E; 274-325	C	CONO1164-12	JQ809211	JQ808927	JQ809002	
MNHN IM200910078	<i>Triplostephanus</i>	<i>fenestratus</i>	North Madagascar	14°30'S, 47°27'E; 274-325	C	CONO1314-12	JQ809212	JQ808928		
MNHN IM200730482	<i>Triplostephanus</i>	<i>fujitai</i>	Vanuatu	15°42'S, 167°02'E; 268-445	C	CONO181-08	EU685492	JQ808929		
MNHN IM200715724	<i>Triplostephanus</i>	<i>fujitai</i>	Philippines	9°27'N, 123°49'E; 273-356	C	CONO306-08	EU685377	EU685628	EU015610	
MNHN IM200730544	<i>Triplostephanus</i>	<i>jenningsi</i>	Vanuatu	15°28.6'S, 167°15.1'E; 3-31	C	CONO483-08	EU685597	EU685749	JQ809003	
MNHN IM200730534	<i>Triplostephanus</i>	sp.	Philippines	9°42.1'N, 123°51.4'E; 3-4	E2	CONO243-08	EU685514	EU685651		
MNHN IM200730533	<i>Triplostephanus</i>	sp.	Philippines	9°42.1'N, 123°51.4'E; 3-4	E2	CONO1310-12	JQ809212	JQ808930	JQ809004	
MNHN IM200730404	<i>Triplostephanus</i>	<i>triseriatus</i>	Philippines	9°35.3'N, 123°52.2'E; 84-87	C	CONO205-08	EU685497	EU685633		
MNHN IM200910082	<i>Triplostephanus</i>	<i>triseriatus</i>	North Madagascar	12° 35.92' S, 48° 35.22' E; 50-52	C	CONO1245-12	JQ809213	JQ808931		
MNHN IM200910084	<i>Triplostephanus</i>	<i>triseriatus</i>	North Madagascar	12° 35.92' S, 48° 35.22' E; 50-52	C	CONO1246-12	JQ809214	JQ808932		
MNHN IM200910100	<i>Triplostephanus</i>	<i>triseriatus</i>	South Madagascar	25°22.4'S, 47°02.8'E; 89-95	C	CONO1181-12	JQ809215	JQ808933		
MNHN IM200910102	<i>Triplostephanus</i>	<i>triseriatus</i>	South Madagascar	25°02.4'-5'S, 47°03.2'-6'E; 54-56	C	CONO1338-12	JQ809216	JQ808934		
MNHN IM200910108	<i>Triplostephanus</i>	<i>triseriatus</i>	South Madagascar	25°22.4'S, 47°02.8'E; 89-95	C	CONO1152-12	JQ809217	JQ808935		
MNHN IM200910166	<i>Triplostephanus</i>	<i>triseriatus</i>	South Madagascar	25°04.7'S, 47°03.4'E; 64-65	C	CONO1278-12	JQ809218	JQ808936		
MNHN IM200910167	<i>Triplostephanus</i>	<i>triseriatus</i>	South Madagascar	25°04.7'S, 47°03.4'E; 64-65	C	CONO1301-12	JQ809219	JQ808937		
MNHN IM200910168	<i>Triplostephanus</i>	<i>triseriatus</i>	South Madagascar	25°04.7'S, 47°03.4'E; 64-65	C	CONO1362-12	JQ809220	JQ808938		
MNHN IM200910169	<i>Triplostephanus</i>	<i>triseriatus</i>	South Madagascar	25°04.7'S, 47°03.4'E; 64-65	C	CONO1182-12	JQ809221	JQ808939		
MNHN IM200910170	<i>Triplostephanus</i>	<i>triseriatus</i>	South Madagascar	25°04.7'S, 47°03.4'E; 64-65	C	CONO1217-12	JQ809222	JQ808940		

(continued on next page)

Table 1 (continued)

MNHN Ids	Genus	species	Country	Coordinates; depth (m)	Clade	BOLD ID	Genbank COI	GenBank 12S	GenBank 16S	GenBank 28S
MNHN IM200910172	<i>Triplostephanus</i>	<i>triseriatus</i>	South Madagascar	25°04.7'S, 47°03.4'E; 64–65	C	CONO1153-12	JQ809223	JQ808720	JQ808941	
MNHN IM200910173	<i>Triplostephanus</i>	<i>triseriatus</i>	South Madagascar	25°04.7'S, 47°03.4'E; 64–65	C	CONO1336-12	JQ809224	JQ808721	JQ808942	
MNHN IM200910911	<i>Triplostephanus</i>	<i>triseriatus</i>	Australia	27°02'069"S, 153°19'00"E; 3.5–7.8	C	CONO1255-12	JQ809225		JQ808943	
MNHN IM20099948	<i>Triplostephanus</i>	<i>triseriatus</i>	North Madagascar	12° 35.92' S, 48° 35.22' E; 50–52	C	CONO1175-12	JQ809226	JQ808722	JQ808944	
MNHN IM20099949	<i>Triplostephanus</i>	<i>triseriatus</i>	North Madagascar	12° 35.92' S, 48° 35.22' E; 50–52	C	CONO1360-12	JQ809227	JQ808723	JQ808945	
MNHN IM20099950	<i>Triplostephanus</i>	<i>triseriatus</i>	North Madagascar	12° 35.92' S, 48° 35.22' E; 50–52	C	CONO1210-12	JQ809228	JQ808724	JQ808946	
MNHN IM200740568	<i>Cochlespira</i>	<i>pulchella</i>			Outgroup	FRANZ207-08	EU685627	EU685488	EU685781	
MNHN IM200717922	<i>Conus</i>	<i>neris</i>			Outgroup	CONO339-08	EU015734	EU685489	EU685782	EU015619
MNHN IM200740569	<i>Harpa</i>	<i>kajiyamai</i>			Outgroup		EU685626	EU685491	EU685783	
MNHN IM200717685	<i>Iolyris</i>	<i>cingulifera</i>			Outgroup	CONO515-08	EU127881	EU685490	EU685780	EU127890

kajiyamai, belonging to another neogastropod family (Harpidae), was used as a distant outgroup to root the tree.

2.2. PCR amplification and DNA sequencing

Total genomic DNA was extracted from muscle tissue using NucleoSpin[®] 96 Tissues (Macherey–Nagel) and following the manufacturer's instructions. Fragments of the mitochondrial genes Cytochrome Oxidase I (COI), 16S rRNA and 12S rRNA as well as the nuclear 28S rRNA were amplified (Table 2). PCR reactions were performed in 25 µL final volume, containing approximately 3 ng template DNA, 1.5 mM MgCl₂, 0.26 mM of each nucleotide, 0.3 µM of each primer, 5% DMSO and 0.75 U of Taq Polymerase (Qbiogene). Amplification products were generated by an initial denaturation step of 4 min at 94 °C followed by 35 cycles at 94 °C for 40 s, annealing at 50 °C for COI, 52 °C for 28S, 51 °C for 12S rRNA and 16S rRNA for 40 s and by an extension at 72 °C for 1 min. PCR products were purified using ExonucleaseI and Phosphatase and sequenced using BigDye Terminator V3.1 kit (Applied biosystem) and the AB3730XL sequencer. All genes were sequenced for both directions to confirm accuracy of each sequence. Chromatograms were edited using CodonCode Aligner version 3.7.1.1. All the sequences were deposited in GenBank and BOLD (Table 1).

2.3. Datasets

Six datasets were analyzed. The first three datasets were analyzed for all taxa listed in Table 1 and consisted of three independent gene analyses performed from COI, 16S and 12S genes. The fourth dataset consisted of a combined data set of COI, 16S, and 12S and is referred to as CD1. To evaluate the robustness of the mitochondrial phylogeny, a fifth dataset corresponding to the nuclear 28S gene set was built, with one representative for most of the species. This reduced dataset was then combined with the three mitochondrial genes and is referred to as CD2.

2.4. Phylogenetic analyses

Sequences were aligned for each gene independently using MUSCLE (Edgar, 2004). The accuracy of automatic alignments was confirmed by eye using BioEdit version 7.0.0.0 (Hall, 1999). Hyper-variable regions of 12S and 16S rRNA genes were excluded from further analyses to avoid ambiguities in the homology hypotheses. Best-fit substitution models were identified for each gene separately and for each combined dataset using Modelgenerator V.85 (Keane et al., 2006). Best-scoring Maximum Likelihood (ML) trees were estimated using RaxML (Stamatakis, 2006) from 100 independent searches each starting from distinct random trees. Robustness of the nodes were assessed using the thorough bootstrapping algorithm (Felsenstein, 1985a) with 1000 replicates. Bayesian Analyses (BAs) were performed running two parallel analyses in MrBayes (Huelsenbeck and Ronquist, 2001), consisting each of eight Markov chains of 100,000,000 generations with a sampling frequency of one tree each ten thousand generations. The number of swaps chains was set to 5, and the chain temperature at 0.02. Convergence of each analysis was evaluated using Tracer 1.4.1 (Rambaut and Drummond, 2007) to check that ESS values were all greater than 200. A consensus tree was then calculated after omitting the first 25% trees as burn-in. For the treatment of combined data using ML and BA, the data were separated into six unlinked partitions: 16S, 12S, 28S and the three codon positions of the COI gene. Analyses were performed on the Cipres Science Gateway (<http://www.phylo.org/portal2>), using the RAXML-HPC2 on TG tool for ML and the MrBayes on TG tool for BA.



Fig. 1. Map showing localities sampled for Terebridae study. AU, Queensland, Australia; CH, Coral Sea; FI, Fiji; SMA, South Madagascar; MO, Mozambique; NMA, North Madagascar; NNC, North New Caledonia; PA, Pacific Panama; PH, Philippines; SO, Solomon Islands; TA, Tahiti; VA, Vanuatu.

2.5. Overview of Terebridae anatomy and foregut characters

Foregut anatomy was examined by dissecting sequenced specimens. The radulae were cleaned with diluted bleach (1 part of commercially available bleach to 3–4 parts of water), rinsed several times in distilled water, mounted on clear glass cover-slips and air-dried. The cover-slips were glued to stubs, coated with gold and examined by scanning electron microscopy. The terminology previously used for description of the foregut structures in Terebridae is inconsistent and can be confusing (Miller, 1970, 1975, 1979). Here the terminology of Taylor et al. (1993), which reflects the supposed homologies within the entire Conoidea was followed. Six characters of the foregut were examined and used for tracing evolutionary pathways on the molecular tree (Table 3):

2.5.1. Character 1

Proboscis (PR): 0 – absent, 1 – present. PR is very variable in length, from extremely short to very long. In long proboscises, walls often form telescopic folds, while the proboscis can be coiled within the rhynchodaeum. The proboscis contains the buccal tube, i.e., the portion of the alimentary canal extending between the buccal cavity and the true mouth, which is situated at the distal end of the proboscis (Taylor et al., 1993). The buccal tube is absent only in those species where the proboscis is lost. All examined terebrid species possess a more or less long rhynchodeal introvert (also known as labial tube – Miller, 1970). The length of the introvert correlates with the presence of the proboscis: in species without proboscis, the rhynchodeal introvert is much longer than in species with proboscis.

2.5.2. Character 2

Venom gland (VG): 0 – absent, 1 – present. VG, sometimes called venom duct, is an autapomorphy of Conoidea (Taylor

et al., 1993); when present it always has a muscular bulb, also referred to as the venom bulb. The venom gland in Terebridae opens just posterior to the radular sac.

2.5.3. Character 3

Odontophore (OD): 0 – absent, 1 – present. OD, consisting of subradular cartilages and muscles, usually present in species having a radula with a strong subradular membrane. In Terebridae it can vary from being massive (e.g., *Duplicaria bernardii*) to being vestigial and hardly recognizable (e.g., *Terebra succincta*, clade E3).

2.5.4. Character 4

Accessory proboscis structure (APS): 0 – absent, 1 – present. APS is an extensible muscular structure that arises from the wall of the rhynchodaeum. It can be branching or club-shaped, distally papillated, or simple, stalk-shaped. A somewhat similar structure, named rhynchodeal outgrowth, is found in other Conoidea–Horaiclavidae and *Zemacies* (Borsoniidae) (Fedosov and Kantor, 2008).

2.5.5. Character 5

Radula (RadT): 0 – absent, 1 – consists of duplex marginal teeth, 2 – consists of solid recurved marginal teeth, 3 – consists of flat marginal teeth, 4 – consists of semi-enrolled marginal teeth, 5 – consists of hypodermic marginal teeth. Radula in Terebridae consists only of a pair of marginal teeth per transverse row. The radula was completely lost in several lineages, but when present the marginal teeth exhibit a range of morphological types, and five major types are here recognized: (1) *Duplex teeth* (Fig. 2A–C), consisting of a major element (limb), attached to the subradular membrane along most of its length, and an accessory limb, which is the thickened edge of the major element, usually somewhat elevated above the membrane. Here, the radula has about 20–25 rows of teeth; (2) *solid recurved teeth* (Fig. 2F–G) with a broad flattened base, which is

Table 2

Primers used for gene amplification and sequencing. PCG = Protein Coding Gene.

Gene	Primer name	Primer Sequences (5'–3')	Sens	Tm	References	Length of amplification	Gene type
COI	LCOI1490	GGT CAA CAA ATC ATA AAG ATA TTG G	F	48/50	Folmer et al. (1994)	660	mtDNA PCG
COI	HCOI2198	TAA ACT TCA GGG TGA CCA AAA AAT CA	R	48/50	Folmer et al. (1994)		
16S	16Sa-L	CGC CTG TTT ATC AAA AAC AT	F	51	Palumbi (1996)	460	mtDNA rRNA
16S	16Sb-H2	CTC CGG TTT GAA CTC AGA TCA	R	51	Palumbi (1996)		
12S	12SA	AAA CTG GGA TTA GAT ACC CCA CTA T	F	51	Palumbi (1996)	370	mtDNA rRNA
12S	12SB	GAG GGT GAC GGG CGG TGT GT	R	51	Palumbi (1996)		
28S	C1'	ACC CGC TGA ATT TAA GCA T	F	56	Jovelín and Justine (2001)	830	nDNA rRNA
28S	D2	TCC GTG TTT CAA GAC GGG	R	56	Jovelín and Justine (2001)		

attached to the relatively strong subradular membrane. In species with this type of teeth, the radula is short, with only 15–20 rows; (3) *flat and simple teeth* (Fig. 2D–E), attached by a narrow base to the subradular membrane. Two, not clearly delimited, variants – *broad triangular* (Fig. 2E) and *long irregular* (Fig. 2D) – are coded as the same radular type in the analysis. The subradular membrane is usually very thin and fragile, and easily tears apart. Radulae with this type of teeth consist of 20 or more rows; (4) *semi-enrolled teeth* (Fig. 3Q) with tooth edges overlapping at the base, forming a loosely enrolled tube, while closer to the tip the tooth is trough shape in section. Radulae with this type of teeth are very short, with only about 10 rows; (5) *hypodermic hollow teeth* (Fig. 3A–P), rather similar to the hypodermic teeth present in other Conoidea. Such teeth have a very broad basal opening of the tooth canal, with usually a reflected outward edge of the tooth, forming a collar-like structure; the apical opening can be unarmed or it can have small barb(s) or blade(s). The subradular membrane is usually very thin

and vestigial. The number of rows of teeth varies from about 10 (*Terebra jenningsi*) to about 30 (*Hastula hectica* and *H. penicillata*).

2.5.6. Character 6

Salivary glands (SGs): 0 – absent, 1 – present. SGs can be paired, but are more often fused, bipartite with paired ducts. In some species, a single gland is present.

Accessory salivary gland(s) are present in different species of Terebridae, as well as in some other conoideans. They usually are very small and difficult to find by dissection, therefore not used in the analysis.

2.6. Evolution of the anatomy

A reduced dataset was built for the 46 species (including the four outgroups) for which anatomical data were available. To minimize the risk of undetected cryptic species, the dissected

Table 3

Matrix of the anatomical characters used for the character mapping. Numbers in parentheses in the column “MNHN vouchers” correspond to specimens used to reconstruct the phylogenetic tree when the dissected specimen was not available or when its sequencing failed. JDT and YK: species dissected by John D. Taylor and Yuri Kantor.

Species	MNHN vouchers	Clade	PR	VG	OD	APS	RadT	SG
<i>Clathrotrebra poppei</i>	IM_2007_30546	E3	1	1	0	?	1	1
<i>Duplicaria bernardi</i>	IM_2009_10908	F	0	0	1	0	2	1
<i>Duplicaria</i> sp. 1	IM_2009_10111	F	0	0	1	0	2	1
<i>Duplicaria</i> sp. 2	IM_2009_10164	F	0	0	1	0	2	1
<i>Duplicaria</i> sp. 3	IM_2009_10134	E2	0	0	0	0	0	0
<i>Euterebra fuscolutea</i>	IM_2009_10127	F	0	0	1	0	2	1
<i>Hastula hectica</i>	YK (IM_2009_10104)	D	1	1	0	0	5	1
<i>Hastula lanceata</i>	IM_2007_30535	D	1	1	0	0	5	?
<i>Hastula penicillata</i>	IM_2007_30540	D	1	1	0	0	5	1
<i>Hastula strigillata</i>	IM_2007_30607	D	?	1	1	0	5	?
<i>Hastula stylata</i>	IM_2009_10106	D	1	1	0	0	4	1
<i>Hastulopsis amoena</i>	IM_2009_10909	E1	0	0	0	?	0	?
<i>Hastulopsis conspersa</i>	IM_2007_30619	E1	0	0	0	0	0	0
<i>Hastulopsis minipulchra</i>	IM_2009_10129	E5	0	0	0	0	0	0
<i>Hastulopsis pseudopertusa</i>	IM_2009_9953 (9954)	E5	0	0	0	0	0	1
<i>Myurella affinis</i>	IM_2007_30439	E1	0	0	0	1	0	0
<i>Myurella flavofasciata</i>	IM_2007_30465	E1	0	0	0	?	0	?
<i>Myurella kilburni</i>	IM_2007_30461	E5	1	1	0	0	5	1
<i>Myurella lineaperlata</i>	IM_2007_30635	E2	1	1	1	0	3	1
<i>Myurella nebulosa</i>	IM_2007_30408	E1	0	0	0	1	0	1
<i>Oxymeris dimidiata</i>	JDT (IM_2007_30373)	B	0	0	0	0	0	1
<i>Oxymeris felina</i>	IM_2007_30443	B	0	0	0	0	0	0
<i>Oxymeris maculata</i>	JDT (IM_2007_30389)	B	0	0	0	0	0	1
<i>Pellifronia jungi</i>	IM_2007_30591 (30395)	A	1	1	1	?	1	?
<i>Strioterebrum nitidum</i>	IM_2009_7114	E2	1	1	1	0	3	1
<i>Terebra argosyia</i>	IM_2007_42087	C	?	?	?	?	?	1
<i>Terebra berryi</i>	IM_2007_42167	E4	0	0	0	0	0	0
<i>Terebra cf. variegata</i>	IM_2007_42128	E4	0	0	0	0	0	1
<i>Terebra cingulifera</i>	IM_2007_30382	C	1	1	0	?	5	1
<i>Terebra elata</i>	IM_2007_42095	E4	1	1	?	0	?	1
<i>Terebra funiculata</i>	IM_2007_30394	C	?	1	0	?	5	?
<i>Terebra guttata</i>	IM_2007_30376	C	1	1	0	0	5	1
<i>Terebra puncturosa</i>	IM_2007_42171	E4	1	0	0	1	0	?
<i>Terebra specillata</i>	IM_2007_42168	E4	0	0	0	0	0	1
<i>Terebra subulata</i>	JDT (IM_2007_30444)	C	1	1	0	0	5	1
<i>Terebra succincta</i>	IM_2007_30385	E2	1	0	0	1	0	1
<i>Terebra succincta</i>	IM_2007_30582	E3	1	1	1	?	1	1
<i>Terebra textilis</i>	IM_2007_30547	E2	1	1	1	0	3	1
<i>Terebra trismacaria</i>	IM_2007_30579	E2	1	1	0	0	3	1
<i>Terenolla pygmaea</i>	IM_2007_30449	E1	0	0	0	0	0	0
<i>Triplostephanus fenestratus</i>	IM_2007_30418	C	1	1	0	0	5	1
<i>Triplostephanus triseriatus</i>	IM_2007_30404	C	1	1	0	?	5	?
<i>Cochlespira pulchella</i>	IM_2007_40568	Out	1	1	1	0	1	1
<i>Conus nereis</i>	IM_2007_17922	Out	1	1	0	0	5	1
<i>Harpa kajiyamai</i>	IM_2007_40569	Out	1	0	1	0	0	1
<i>Iotyrrius cingulifera</i>	IM_2007_17685	Out	1	1	1	0	1	1

1. Proboscis (PR): 0 – absent, 1 – present.

2. Venom gland (VG): 0 – absent, 1 – present.

3. Odontophore (OD): 0 – absent, 1 – present.

4. Accessory proboscis structure (APS): 0 – absent, 1 – present.

5. Marginal radular teeth (RadT): 0 – radula absent, 1 – duplex, 2 – solid recurved, 3 – flat, 4 – semi-enrolled, 5 – hypodermic.

6. Salivary glands (SGs): 0 – absent, 1 – present.

7. Unresolved observation: ? – data missing.

and sequenced specimens were the same in most cases. However, for *Pellifronia jungi* and *Hastulopsis pseudopertusa* (Table 3), sequences were not obtained from the dissected specimens, and a conspecific specimen was used. Four species, *Oxymeris dimidiata*, *O. maculata*, *Terebra subulata* and *Hastula hectica*, were dissected by YK and John D. Taylor using non-sequenced material, and conspecific specimens were used for sequencing. ML analyses were performed using the method described above. The evolution of the six characters listed in Table 3, and described in the anatomy overview above, was assessed with Mesquite V2.74 (Maddison and Maddison, 2009), using the option “tracing character history” and the parsimony ancestral reconstruction method. The characters PR (proboscis), VG (venom gland), OD (odontophore), and RadT (marginal radular teeth anatomy) were treated as ordered characters (using a stepmatrix), prohibiting some of the transformation sequences, in our case from absent to present, as reappearance of these features is highly unlikely. Other characters were treated as unordered. Additionally, Bayestrans (Pagel and Meade, 2006) was used to test if the evolution of foregut characters were correlated. As Bayestrans cannot compare characters with more than two states, the character 5 (RadT) were recoded in two different characters, RadT1 and RadT2, with the states 0 “radula absent” and 1 “radula present” for RadT1, and states 0 “radula solid” and 1 “radula hypodermic” for RadT2. In the latter case, an absence of radula was coded as missing data. Independent and dependent models of Bayesdiscrete were compared. MCMC were run with default parameters, except for the number of generations, which were set to 2,050,000.

3. Results

3.1. Genetic diversity

Of the total of 406 samples of Terebridae used to reconstruct the molecular phylogeny of the family, 389 were sequenced for the COI gene, 400 for the 16S gene, 369 for the 12S gene and 63 for the 28S gene. For COI, 658 bp were sequenced and no indels were found. After the alignments and the removal of ambiguously aligned sites, fragments of 591, 654 and 761 bp in length were obtained for the 16S, 12S and 28S genes, respectively. For the COI gene, 218 different haplotypes were found, displaying 121 polymorphic sites and 278 parsimony informative sites. For the 16S gene, 162 different haplotypes were found, displaying 277 polymorphic sites and 235 parsimony informative sites. For the 12S gene, 164 different haplotypes were found, displaying 412 polymorphic sites and 369 parsimony informative sites. Representatives of the mitochondrial diversity were also sequenced for the 28S gene (62 specimens, including 2 outgroups). Overall, the variability for the 28S gene was less important than for the mitochondrial genes, with 127 polymorphic sites and 94 parsimony informative sites.

3.2. Phylogenetic analyses: single-gene data sets

Modelgenerator results indicated that GTR + I + G model was the best-fit model of evolution for the four genes analyzed (COI: $I = 0.47$, $\alpha = 0.55$; 16S: $I = 0.56$, $\alpha = 0.6$; 12S: $I = 0.3$, $\alpha = 0.6$ and 28S: $I = 0.63$, $\alpha = 0.4$). Parameters of the models were estimated during the maximum likelihood and bayesian analyses for both single-gene and concatenated datasets (see below). For each gene analyzed, no supported conflict was found between the different analyses. In each of the four single gene analyses, the consensus tree showed the Terebridae to be monophyletic however, the relationships within terebrids were generally poorly resolved, with few well-supported clades (Supplementary data 1–4). Therefore only the results obtained for the combined datasets CD1 and CD2 are presented.

3.3. Phylogenetic analyses: combined data set 1 (CD1)

The best-fit model of evolution was GTR + I + G ($I = 0.45$, $\alpha = 0.59$). Topologies derived from ML analyses of the combined data set 1 (CD1) were congruent with the topology derived from BA analyses. From these combined analyses, the Terebridae were found monophyletic, CD1, Posterior Probabilities PP = 0.99, Bootstraps B = 96% (Fig. 4). Within the Terebridae, the five major clades, *Pellifronia*, *Oxymeris* [= *Acus*], *Terebra*, *Hastula* and *Myurella* (clades A–E, respectively) previously identified in Holford et al. (2009a) were recovered. Each were still strongly supported (PP > 0.90, B > 70%), and the topological relationships among the clades were similar, e.g., clades B–E were grouped together (PP = 0.99, B = 90%) (Fig. 4, and see Fig. 2 in Holford et al. (2009a)). A sixth clade, hereafter designated as clade F, is novel in the molecular analysis and presented here for the first time. Intra-clade relationships for clades A–F are detailed in Figs. 5 and 6, and some shells are illustrated for each clade in Fig. 7. Clade F appeared to be the sister group to clades B–E, although the corresponding node is not supported (PP = 0.93, B = 46%). It is comprised of six newly-sampled species, four from South Madagascar, one from Australia and one from New-Zealand. The species composition of clade A remained unchanged compared to Holford et al., 2009a, 2009b, still including a single species, and appearing to be the sister group to all the other clades (although without statistical support). A newly-sampled species from South Mozambique was added to clade B, now totalling eight species (PP = 0.99, B = 100%). Three newly-sequenced species, one from South Madagascar, one from South Mozambique, and one from Philippines and the Solomon Islands, were added to clade C, now comprising nineteen species (PP = 0.99, B = 73%). Clade D included eleven species, of which one species, sampled in Madagascar, was new to the taxon set (PP = 1, B = 100%). Clade E contained five well-supported subclades (E1–E5), but the relationships among these were in general poorly resolved. Clade E1 (PP = 1, B = 96%) included eleven species of which one, from Vanuatu and Australia, was new to the taxon set. Two newly-sequenced species, one from New Caledonia and one from Vanuatu and South Madagascar, were added to the thirteen species previously included in clade E2 (PP = 1, B = 97%). Clade E3 (PP = 0.97, B = 66%) included five species of which two, from the Coral Sea and Solomon Islands respectively, were new to the taxon set. Clade E4 (PP = 1, B = 75%) was new to the taxon set, with six species from Pacific Panama. Two newly-sampled species from Madagascar were added to clade E5, now comprising eight species (PP = 1, B = 94%).

Molecular analyses highlighted several incongruencies at the genus and species levels. With the exception of three genera (*Oxymeris* – clade B, *Pellifronia* – clade A and *Terenolla* – clade E1, the last two represented each by a single species), all the analyzed genera were found to be non-monophyletic. Clade B comprises eight species of the genus *Oxymeris*. As previously found (Holford et al., 2009a), clade C consists of six species of *Triplostephanus* and 13 of *Terebra* (s.s.), including *Terebra subulata*, the type species of *Terebra*. Clade D comprises eight species of *Hastula* and one *Duplicaria*. Clade E, the largest clade in terms of number of species, comprises primarily species of the genera *Myurella*, *Clathroterebra*, *Terenolla*, *Hastulopsis*, *Strioterebrum*, and the “*Terebra*” *textilis*-group (Terry, 2007). However, as shown in Holford et al. (2009a), all these genera (except *Terenolla*) are polyphyletic, with species of each genus placed in several of the five clades E1–E5. Specifically, *Myurella* species were found in E1, E2, E3 and E5, *Clathroterebra* in E1 and E3, *Hastulopsis* in E1 and E5, *Strioterebrum* in E1 and E2, and species of *Terebra* (s.s.) are distributed in clades C, E2, E3, E4 and E5. Also, the addition of newly sampled species impacted the generic composition of clade E. For example, clade E2 now includes two species that were attributed to *Duplicaria*, *D. baileyi* and a new species *D. sp3*, and one

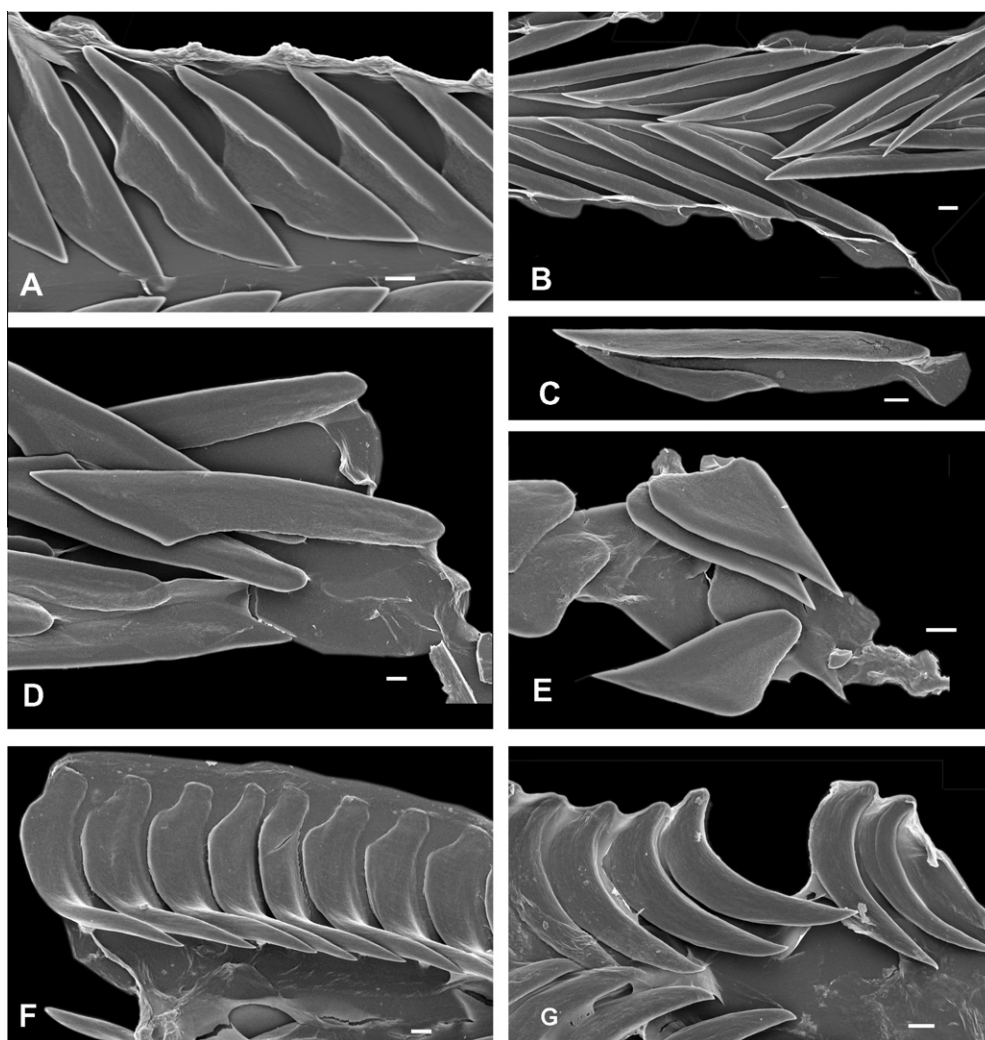


Fig. 2. Radula teeth of Terebridae. Duplex (A–C). Flat (D–E). Solid recurved (F–G). (A) *Pellifronia jungi* (IM_2007_30591), ventral view of radular membrane, only half shown; (B) *Clathroterebra poppei* (IM_2007_30546), ventral view of radular membrane; (C) *Terebra succincta* (IM_2007_30582), separate marginal tooth; (D) *Terebra trismacaria* (IM_2007_30579), ventral view of radular membrane; (E) *Myurella lineaperlata* (IM_2007_30635), group of teeth attached to the subradular membrane; (F) *Euterebra fuscolutea* (IM_2009_10133), ventral view of radular membrane, only half shown; (G) *Duplicaria* sp. 2 (IM_2009_10164), ventral view of radular membrane, only half shown. Scale bars – 10 μ m.

species currently attributed to *Triplostephanus*. A newly sampled species, currently attributed to *Hastulopsis* (*H. pseudopertusa*), was included in clade E5. The new lineage, clade F, includes both *Duplicaria* and *Euterebra* species.

At species level, *plumbeum*, *pertusa*, *strigilata*, *succincta* and *textilis* each end up in two distinct clades, revealing cryptic species. The COI pairwise genetic distances (K2P) between the two clades were 9.6% for *plumbeum*, 9.9% for *pertusa*, 6.4% for *strigilata*, 12.47% for *succincta* and 7.73% for *textilis*. Fourteen different lineages (five in the genus *Terebra*, three in *Strioterebrum*, three in *Duplicaria*, and one each in *Myurella*, *Triplostephanus* and *Hastula*) were not identified to species level and may represent new species. Conversely, two specimens identified as *Triplostephanus cumingii* and *Terebra punctatostriata* (clade C, Fig. 5) share almost identical sequences (no difference in the 16S gene and only four mutations in the 12S gene); revealing initial misidentification and/or synonymy of a species in the *T. anilis* complex.

3.4. Phylogenetic analyses: combined-gene data set 2 (CD2)

The best-fit model of evolution was GTR+I+G ($I = 0.58$, $\alpha = 0.55$). The combined data set 2 (CD2) included 62 specimens

for which at least two mitochondrial genes and the nuclear 28S gene were available. Topologies derived from both ML and BA analyses using CD2 were similar and consistent with the topology derived from analyses of the CD1 data set (Fig. 8). The family Terebridae was confirmed monophyletic (PP = 1, B = 89%). The nine clades (A–D, E1, E2, E3, E5 and F) represented in this dataset were also strongly supported, some with PP and/or B superior to the supports obtained in CD1 analysis. Relationships between and within the main clades are generally similar, except for some non-supported nodes. For example, clade A is sister-group to all the other terebrids in CD1, but in CD2 its position is inverted with clade F.

3.5. Evolution of foregut characters

Reconstruction of the evolution of the proboscis (character 1) clearly demonstrates that it was lost six times in Terebridae: in clades F, B, E1 (all species), and partially in clades E2, E4, and E5 (Fig. 9A). The venom gland (character 2) was lost eight times – in clades F, B, and E1 (all species), and partially in clades E2 (twice), E4 (twice), and E5 (Fig. 9B). In many lineages the odontophore (character 3) is completely absent (including all species having

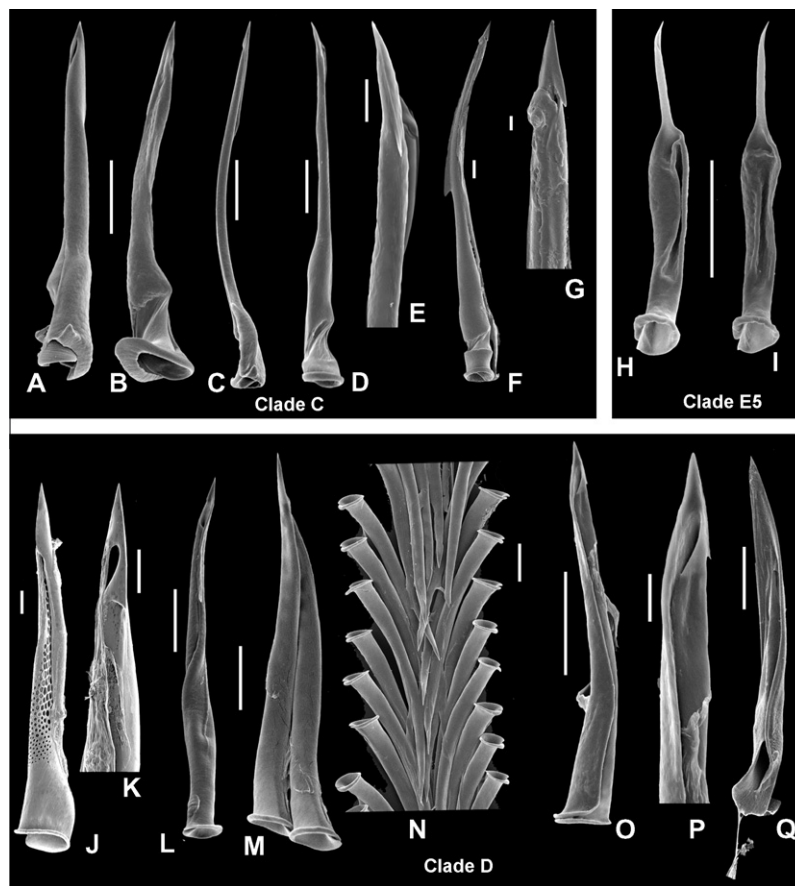


Fig. 3. Hypodermic (A–O) and semi-enrolled (Q) teeth in Terebridae. Clade C (A–G): A and B – *Terebra cingulifera* (IM_2007_30382); C – *Triplostephanus fenestratus* (IM_2007_30418); D–E – *Triplostephanus triseriatus* (IM_2007_30404); F–G – *Terebra guttata* (IM_2007_30376); clade E5 (H–I) – *Myurella kilburni* (IM_2007_30461); clade D (J–P): J–K – *Hastula hectica*, Philippines, Panglao Island; L – *Hastula lanceata* (IM_2007_30535); M–N – *Hastula penicillata* (IM_2007_30540), N – central part of the radular membrane; O–P – *Hastula strigilata* (IM_2007_30607); Q – *Hastula stylata* (IM_2009_10106). Scale bars: 50 μ m (except E, G, P – 10 μ m).

hypodermic marginal radular teeth) (Fig. 9C). Reconstruction of the presence of the odontophore showed that it was lost in most of the clades independently. It is present in clades A and F, and in some species of clades D, E3 and E2. It is vestigial, and hardly discernable in *Hastula strigilata*, to the extent that its presence was revealed only on serial histological sections (J.D. Taylor, personal communication). It is possible that a rudiment of the odontophore may be present in some other species of *Hastula* as well. Reconstruction of the presence of accessory proboscis structure (character 4) showed that it appeared independently in clades E1, E2, and E4 (Fig. 9D).

Reconstruction of the presence of the radula and of the morphology of marginal radular teeth (character 5) revealed a complicated evolutionary history of radular transformations (Fig. 9E). The radula was lost several times: in the entire clades B and E1, and in some species of clades E2 and E5. The most parsimonious ancestral state for the Terebridae radular teeth is the duplex type. Duplex teeth are variable in shape: in some species (*Terebra succincta*, clade E3, and *Clathroterebra poppei* – Figs. 2B and C) the limb also has a thickened edge, while in *Pellifronia jungi* (Fig. 2A) the limb edge is not thickened. Analysis suggests that duplex teeth are the most parsimonious ancestral state for the entire clade E and that flat teeth originated from duplex ones in clade E2. Analysis was not able to resolve a single most parsimonious state for clade D, with duplex and semi-enrolled teeth being equally parsimonious. Solid recurved teeth appeared in the single clade F. Semi-enrolled teeth were found so far in a single of the species examined here, *Hastula stylata* (Fig. 3Q). Teeth of rather similar shape were re-

corded in *Hastula bacillus* (Taylor and Miller, 1990). Finally, hypodermic teeth appeared independently three times – in clade C, in clade D and in the single species, *Myurella kilburni*, from clade E5. However, the structure of the hypodermic teeth is slightly different in these three lineages. In the species belonging to clade C (Fig. 3A–G), the teeth are slender, have a constriction at the base, and usually a basal spur, i.e. an anterior projection on the base of the tooth. Another important character for the hypodermic radula of clade C is that the teeth are attached to the subradular membrane at their bases. In species of clade D (*Hastula* spp.), the hypodermic teeth are conical, without constriction at the base and without spur. Contrary to the species of clade C, the teeth are attached along most of their length to the subradular membrane. Species in clade D can have a barb or blade at the tip of the tooth. In *Hastula hectica* the walls of the tooth are penetrated by numerous holes as previously described (Imperial et al., 2007) (Fig. 3J). The only species in clade E5 with hypodermic teeth (*Myurella kilburni*) has teeth with a peculiar syringe-like shape, with very narrow, attenuated distal end (slightly less than half of tooth length) and broad and probably rather flacid basal part of the tooth. As the specimen examined was badly damaged, it was not possible to examine the radula of the single species of clade E4, *Terebra elata*, that possesses a venom gland, although the presence of a venom duct was noticed (Holford, personal observation) and the presence of a radula is highly probable.

Although found in several species, such as *Triplostephanus fenestratus* and *Hastula hectica*, the presence or absence of the accessory salivary glands cannot be confirmed without histological

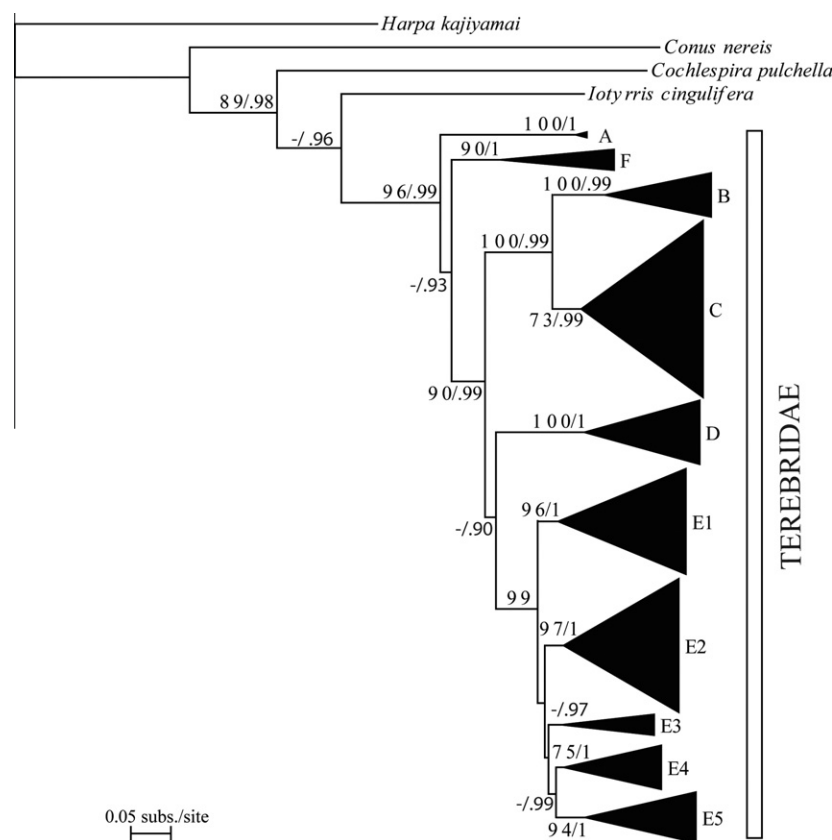


Fig. 4. Likelihood phylogenetic tree obtained with 410 specimen sequences for the COI, 12S and 16S genes. Bootstraps and Posterior Probabilities are indicated for each node (when >B = 70% and >PP = 0.90 respectively). The 10 collapsed clades of Terebridae (A, B, C, D, E1, E2, E3, E4, E5 and F) are detailed on Figs. 2–5.

sections and therefore the character was excluded from the analysis. Reconstruction of the presence and absence of salivary glands (character 6) suggested independent loss in one species of clade B (*Oxymeris felina*), in most species of clade E1, in one species of clade E5 (*Hastulopsis minipulchra*) and one species of clade E2 (*Duplicaria* sp. 3) (Fig. 9F).

Bayestraits analyses revealed that the evolution of several characters is strongly correlated. As shown in Table 4, the results from Bayestraits analyses indicate that the evolution of the proboscis and the venom gland, of the proboscis and the radula (presence/absence), of the venom gland and the radula (presence/absence) and of the odontophore and the radula (solid/hypodermic) are all strongly correlated with bayes factors >10. Additionally, the evolution of the proboscis and salivary glands, of the venom gland and the salivary glands, and of the radula (presence/absence) and the salivary gland are weakly correlated with bayes factors between 5 and 10 (Table 4).

4. Discussion

A robust phylogenetic context was used to both clarify the phylogenetic relationships of the Terebridae and to provide a framework to trace the evolution of several anatomical features linked to the venom apparatus, a key innovation of the Conoidea. The molecular phylogeny of the Terebridae presented here was based on an extended dataset compared to the previous large-scale phylogeny of the group (Holford et al., 2009a, 2009b; Puillandre et al., 2011), tripling the number of specimens, doubling the number of species to include 12 out of the fifteen accepted genera, extending the sampled diversity to the West-Indian Ocean, and including an

additional nuclear gene that strengthened the initial phylogeny exclusively based on mitochondrial genes. Analysis of terebrid foregut anatomy for the characters related to the presence of a venom apparatus, namely proboscis, venom gland and radula, and other characters, such as odontophore, accessory proboscis structure and salivary glands, identified unexpected evolutionary traits within the Terebridae, with implications for the whole superfamily Conoidea. Summarized below are our findings on the taxonomy, venom apparatus evolution, and predator–prey and toxin relationships in the Terebridae.

4.1. Taxonomy

The phylogenetic trees in this analysis confirmed the monophyly of the family Terebridae (Holford et al., 2009a, 2009b) and the existence of five major clades previously identified as *Pellifronia*, *Acus* [now *Oxymeris*], *Terebra*, *Hastula*, and *Myurella*, clades A–E, respectively (Holford et al., 2009a). A novel result for terebrid molecular analysis is the discovery of a new lineage, clade F, which includes *Euterebra* and *Duplicaria* species, and appears to be the sister group to clades B–E.

Our results suggest that taxonomic diversity of the family Terebridae is still inadequately understood. In several cases molecular data suggest the existence of at least two distinct species within what has been identified as a single morphospecies. In three cases (*S. plumbeum*, *H. pertusa* and *T. succincta*), the two cryptic species identified morphologically as one, were collected sympatrically, i.e. co-occurring in the same region, and sometimes syntopically, i.e. co-occurring at the same sampling station. This is the case for *H. pertusa* with includes two molecular species sampled at the same station in Santo, Vanuatu. The detection of several new cryptic

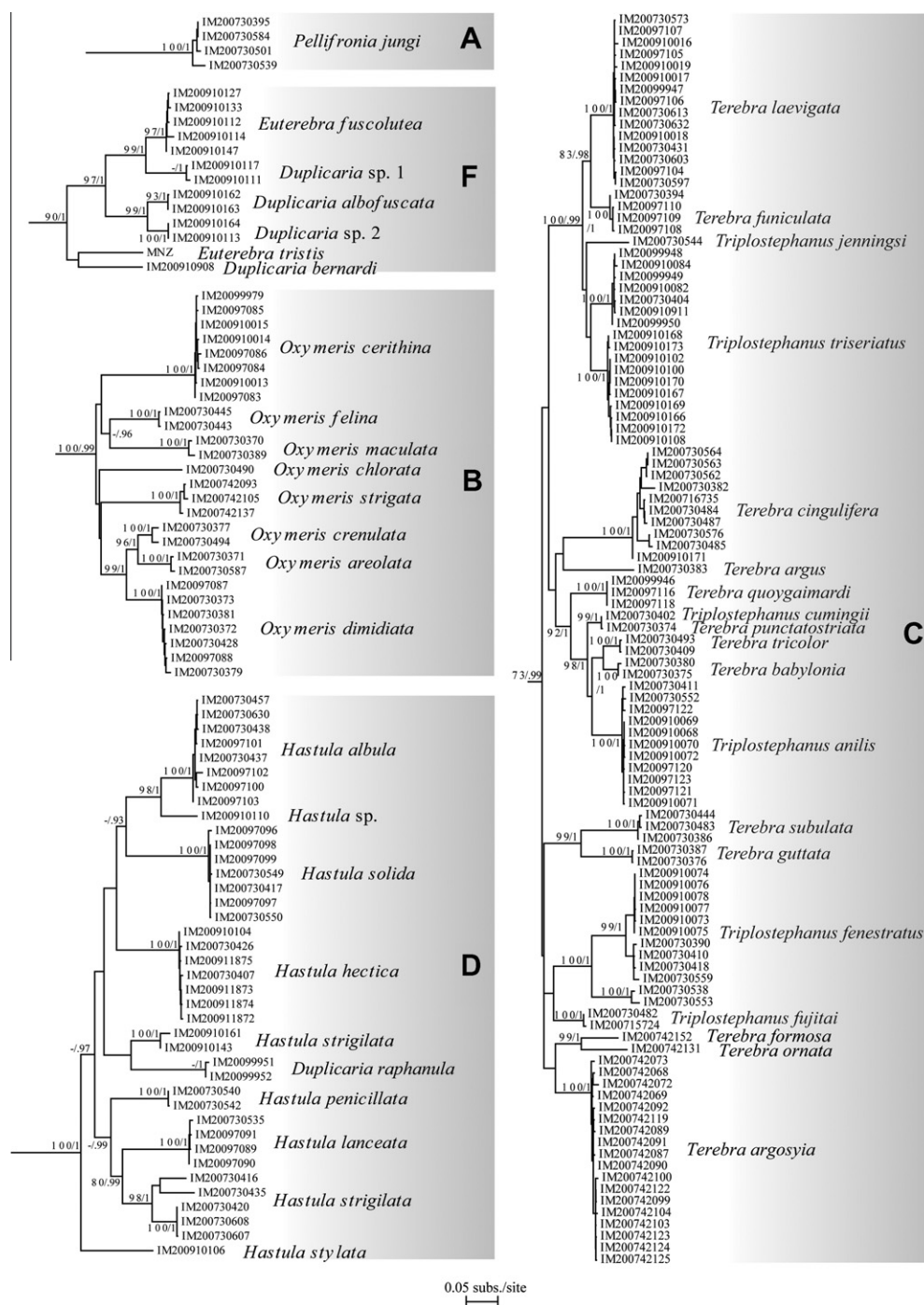


Fig. 5. Likelihood phylogenetic tree for clades A, B, C, D, F. Bootstraps and Posterior Probabilities are indicated for each node (when >70 and >0.90 respectively). For clarity purposes, intraspecific support values are not shown.

tic lineages emphasizes that species diversity in the family Terebridae may be underestimated. Additionally, among the ca. hundred species analyzed in this study, about twenty could not be attributed to a species name according to the taxonomic literature, suggesting that they could represent new species or nominal species currently treated as synonyms.

Increasing the geographic and species diversity of Terebridae analysed in the molecular tree demonstrates that the current genus-level classification of the group is not tenable. Most of the genera recognized in the last working identification guide of the family are non-monophyletic (10 out of the 12 genera analyzed). For example, the genus *Duplicaria*, represented by six

species, and sampled for the first time in this study, was found in three distinct clades (D, E2 and F). This was an unanticipated finding since *Duplicaria*, which is characterized by a shell axially ribbed, and a well-marked suture doubled on the whorls by an axial sculpture on the subsutural band (Terry, 2007), is widely accepted in the taxonomy community and was one of the unambiguous genera recognized by Bratcher and Cernohorsky (1987). Similar problems were observed for *Terebra* and *Myurella*, where species were found in five (C, E2–5) and three (E3–5) distinct clades, respectively (see also *Clathrotrebra*, *Hastulopsis*, *Striotrebra*, *Triplostephanus* – Figs. 5 and 6). These examples imply that shell morphology, used to describe the diversity of terebrids,

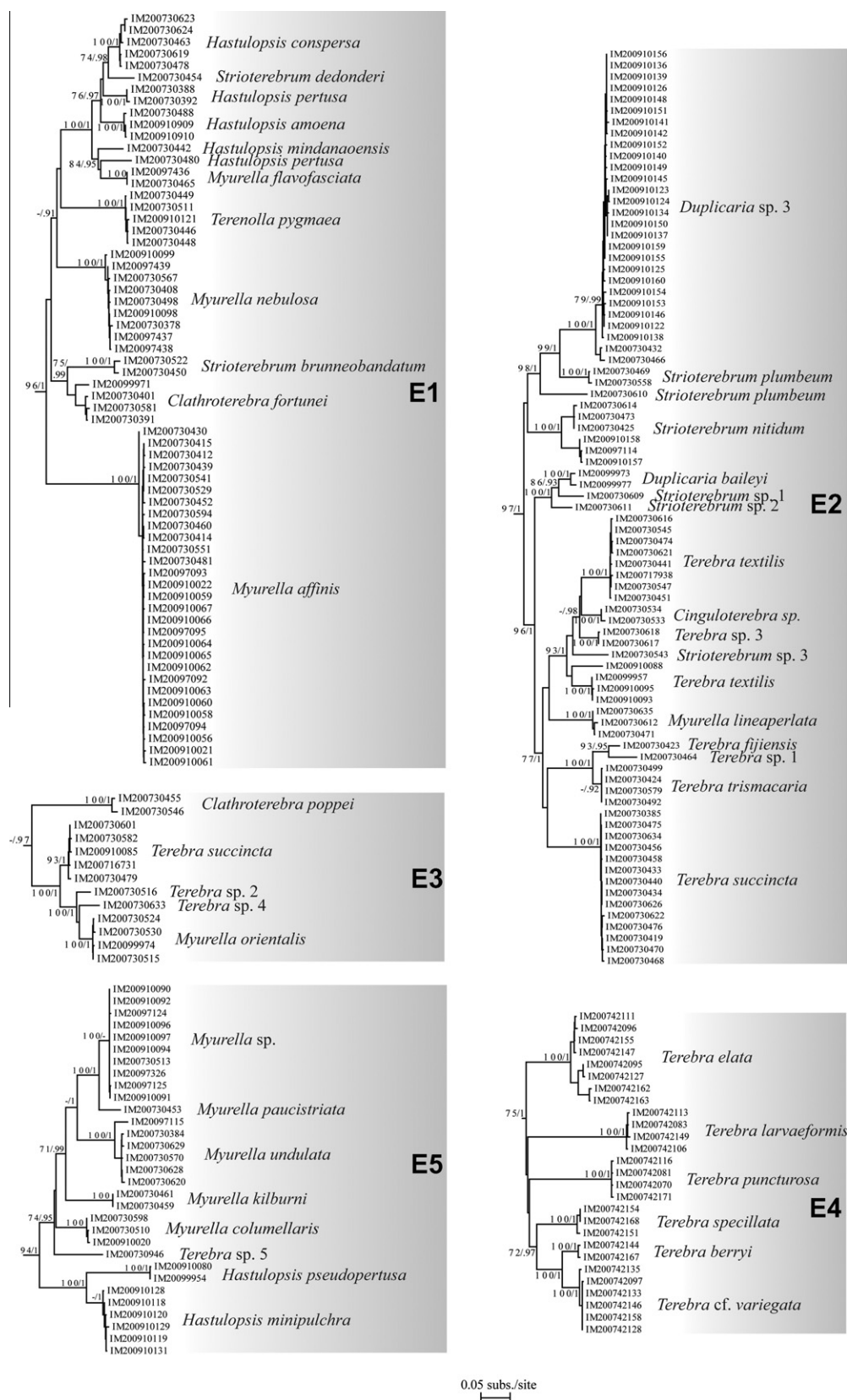


Fig. 6. Likelihood phylogenetic tree for the clades E1–E5. Bootstraps and Posterior Probabilities are indicated for each node (when B > 70% and PP > 0.90 respectively). For clarity purposes, intraspecific support values are not shown.

can be misleading at both genus and species levels, and can lead to an incorrect classification of the family if relied upon independent of other evidence.

Despite the extensive sampling efforts deployed to complete the taxonomic coverage, our dataset is still not exhaustive. It covers less than one quarter of the species diversity of the family, with

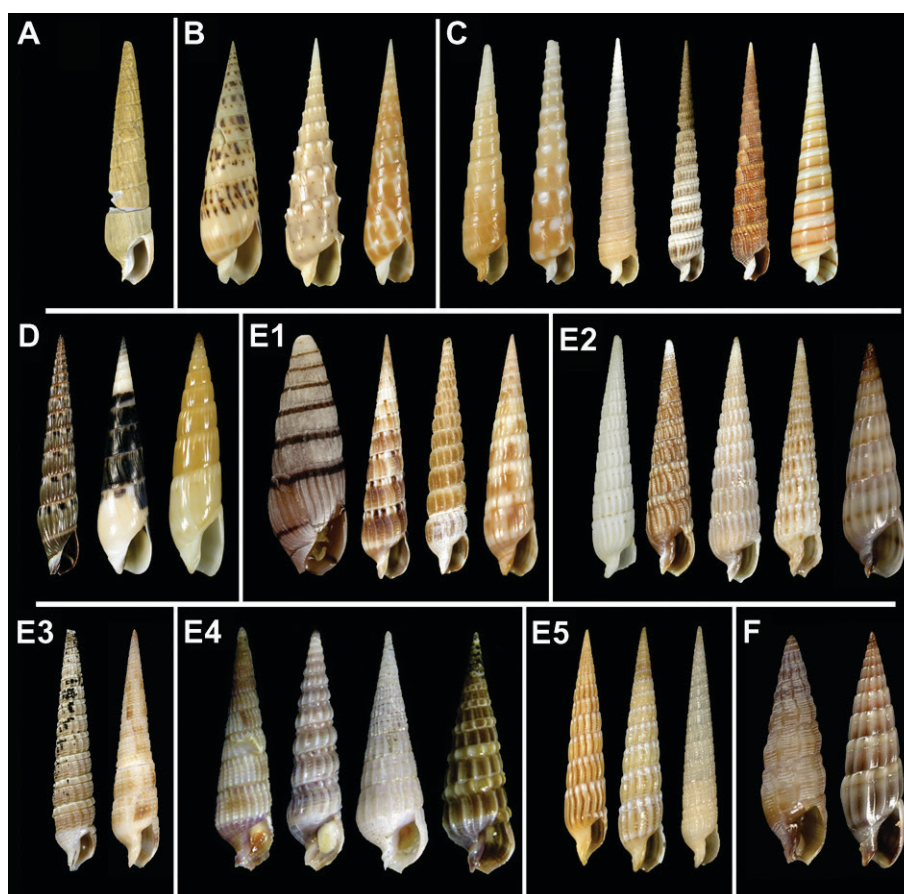


Fig. 7. Illustration of some specimens in each clade. From left to right: clade A: *Pellifronia jungi* IM_2007_30539; clade B: *Oxymeris maculata* IM_2007_30370, *Oxymeris crenulata* IM_2007_30377, *Oxymeris dimidiata* IM_2007_30379; clade C: *Terebra argus* IM_2007_30383, *Terebra guttata* IM_2007_30387, *Terebra funiculata* IM_2007_30394, *Triplostephanus fujitai* IM_2007_30482, *Terebra cingulifera* IM_2007_30485, *Terebra tricolor* IM_2007_30493; clade D: *Hastula strigilata* IM_2007_30416, *Hastula hectica* IM_2007_30426, *Hastula albula* IM_2007_30437; clade E1: *Terenolla pygmaea* IM_2009_10121, *Hastulopsis pertusa* IM_2007_30388, *Clathroterebra fortunei* IM_2007_30391, *Myurella affinis* IM_2007_30415; clade E2: *Terebra fijiensis* IM_2007_30423, *Terebra succincta* IM_2007_30433, *Terebra textilis* IM_2007_30451, *Myurella lineaperlata* IM_2007_30471, *Duplicaria* sp. 3 IM_2009_10151; clade E3: *Terebra succincta* IM_2007_16731, *Myurella orientalis* IM_2007_30515; clade E4: *Terebra elata* IM_2007_42111, *Terebra larvaeformis* IM_2007_42113, *Terebra puncturosa* IM_2007_42116, *Terebra berryi* IM_2007_42144; clade E5: *Myurella undulata* IM_2007_30384, *Myurella paucistriata* IM_2007_30453, *Terebra* sp. 5 IM_2007_30946; clade F: *Euterebra fuscolutea* IM_2009_10112, *Duplicaria albofasciata* IM_2009_10162.

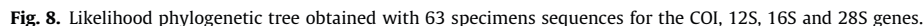
100 analyzed species out of the ~400 currently accepted species (WoRMS – www.marinespecies.org), representing 12 out of the 15 currently accepted genera. Further sampling is needed to obtain the missing genera *Granuliterebra*, *Microtrypetes* and *Pristiterebra*. In addition, among the genera analyzed, numerous type-species are not represented. Considering that recent studies have shown that most terebrid genera are non-monophyletic, it will also be essential to include the numerous synonymised genera. Although further taxonomic investigations are needed to stabilize the classification of the family, the phylogeny presented here provides a robust framework to analyze the evolution of several characters linked to the venom apparatus in the Terebridae.

4.2. Venom apparatus evolution

The formation of the venom gland and the appearance of the feeding mechanism of Conoidea was the initial key apomorphy of the group (Kantor and Puillandre, in press). The unique mechanism of prey envenomation is the most outstanding character of Conoidea and includes use of individual marginal radular teeth (detached from the subradular membrane) at the proboscis tip for stabbing and injecting neurotoxins into prey (Taylor et al., 1993). Teeth of very different morphologies, i.e. not only hypodermic, are used in a similar manner. This was observed directly (e.g.,

Kohn, 1956) and inferred from serial sectioning of different conoideans (Kantor and Taylor, 1991). Until recently, the Terebridae remained relatively poorly studied anatomically and existing data confirmed a great disparity of anatomy of the foregut, with loss of major organs, including proboscis, venom gland and radula in many species. Nevertheless, due to the absence of a robust phylogeny, the evolution of the foregut remained largely uncertain, and loss and apparition of novel features were considered anecdotal. The results from this study indicate that the evolution of the venom apparatus is not straightforward, as key features, together with the loss of various structures of the foregut anatomy, have arisen independently on at least three occasions within terebrids. These anatomical modifications appear to be the rule rather than the exception.

Terebridae were always treated as a major independent lineage of Conoidea until the recent molecular phylogeny of the Conoidea superfamily was published (Puillandre et al., 2011). The Conoidea molecular phylogeny suggests that Terebridae is a sister group of the family Turridae (s.s.), the component species of which can possess a venom gland, a radula with strong subradular membrane, and have duplex marginal teeth. The discovery of true duplex teeth, and flat teeth, their derivatives in Terebridae was thus quite unexpected. Prior to this study only two types of radula were known in Terebridae, solid recurved teeth and hypodermic teeth.



As suggested by the Bayestraits analyses, the reduction and losses of foregut characters in many lineages of the Terebridae are not casual and have a functional explanation. All species possessing a venom gland have a corresponding radula and proboscis, as the bayes factors > 10 for these characters indicate (Table 4). This is explained by the peculiarities of conoidean feeding mechanism, where envenomation of the prey requires the aid of the tooth gripped at the proboscis tip and used for stabbing the prey, or channelling the toxins through the internal lumen of hypodermic teeth. Currently, feeding of radulate terebrids was observed only in different *Hastula* and *Terebra* species with hypodermic radular teeth (Marcus and Marcus, 1960; Miller, 1970, 1979; Taylor, 1990; Taylor and Miller, 1990). The observations established that

Analysis of the anatomical characters revealed that hypodermic teeth originated three times independently in Terebridae, in clades C, D, and in a single species from clade E5, *Myurella kilburni*. As detailed in the results section, the hypodermic teeth of these three groups appear to be rather different (Fig. 3). Independent apparitions of hypodermic teeth suggest increasing the effectiveness of prey envenomation. A very interesting peculiarity was found in *Hastula cinerea* and *H. hectica*, both in clade D, where in most of the specimens examined, a tooth was held at the proboscis tip even when the species was not feeding, concealed within the proboscis with its base resting on the large sphincter (Marcus and Marcus, 1960; Imperial et al., 2007). This can be explained by the presence

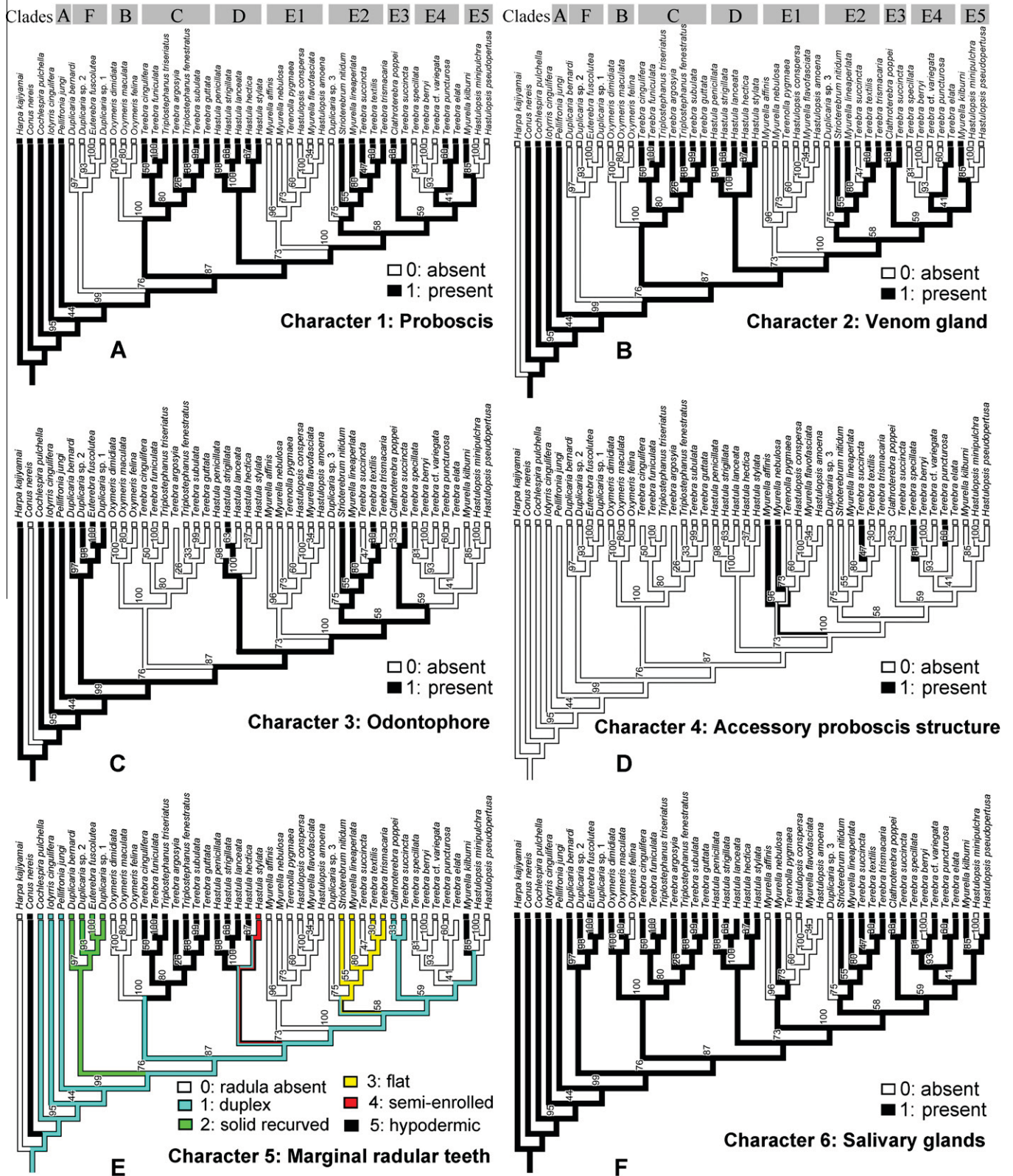


Fig. 9. Character mapping of the six characters presented in Table 2. Bootstraps are shown for each node.

of a relatively strong subradular membrane and tough attachment of the teeth to the membrane. In *Hastula*, because the teeth in the radular cecum are still attached to the membrane, they cannot be

immediately used for stabbing prey when required. In the process of radular growth, the oldest part of the membrane, situated in the radular cecum, is permanently destroyed and the teeth are dis-

Table 4

Bayesfactor obtained with bayestraits from comparing the posterior probabilities of the independent and dependent models for seven discrete characters (PR = proboscis, VG = venom gland, OD = odontophore, APS = accessory proboscis structure, RadT1 and 2 = marginal radular teeth – see text for details, SG = salivary glands).

	PR	VG	OD	APS	RadT1	RadT2	SG
PR							
VG	35.16						
OD	–4	–0.82					
APS	–2.48	1.16	–7.6				
RadT1	14.9	27.48	4.14	4.3			
RadT2	1.58	0.04	11.56	–2.72	–0.38		
SG	8.38	6.68	–0.12	–1.38	7.54	–2.64	

lodged. When the tooth is separated from the membrane, it is transferred to the proboscis tip, where it is presumably held until it is used. This is also assumed for members of the other families of “turrids” that have a strong subradular membrane. In most turrid specimens examined, there was a tooth at the proboscis tip held by the sphincter(s) (Kantor and Taylor, 1991).

Although nothing is known on the feeding of species with duplex/flat teeth, it is reasonable to suppose that they are used on the proboscis tip in a manner similar to other conoideans with non-hypodermic teeth. In this respect it was interesting to find in *Terebra textilis* at the proboscis tip flat teeth very similar to those of *Terebra trismacaria* (Fig. 2D). A group of four teeth attached to the subradular membrane was found in the buccal tube somewhat posterior to the proboscis tip. It is obvious that in this case the teeth cannot be used separately for stabbing the prey, but the mechanism of transport of the teeth from radular sac to the proboscis tip persists in this species. A probable explanation in this case represents an intermediate stage of reduction of radulae and transition to feeding without use of marginal teeth at the proboscis tip.

An odontophore is present in species that have a more or less strong subradular membrane and non-hypodermic radular teeth (bayes factor > 10, Table 4). It is large and powerful in species of clade F, *Duplicaria* and *Euterebra*, which lack proboscis and venom gland and therefore do not utilize teeth for stabbing and envenomation of the prey. A well-developed odontophore suggests that the radula is functioning as a whole organ only, probably for transferring the prey from rhynchodaeum to oesophagus. There is no observation on feeding of species of this clade and diet is known for only one species with similar anatomy, *Terebra nassoides*, feeding on capitellid polychaetes (Taylor, 1990). Similarly to species with hypodermic radulae, an active role of the introvert in prey capture was also shown in *Terebra gouldi*, a species lacking venom apparatus, radula, proboscis, and preys on the enteropneust *Ptychodera flava*, which is swallowed alive.

While reduction of the venom gland provides economy of energy that is otherwise used for producing toxins and constant formation of the radula, the rhynchostomal introvert, which is present and well-developed in all terebrids, may explain the numerous independent losses of the venom gland and associated organs. With the rhynchostomal introvert present, feeding becomes possible without stabbing and envenomation of the prey. In addition, the proboscis also becomes unnecessary, as its primary function, gripping the tooth, does not exist any more. The muscular buccal lip, which is well developed in radular-less species, serves for transferring the swallowed prey further into oesophagus. Although very little is known about diet of terebrids with such foregut anatomy, Miller (1975) suggested that they feed on different hemichordates. The family Raphitomidae is the only other taxon of Conoidea that possesses a developed rhynchostomal introvert. In that family numerous independent reductions and

losses of the venom gland and radula were hypothesized (Kantor and Taylor, 2002). It was also suggested that these reductions were connected with the role of introvert in prey capture.

Bayestraits analysis revealed only weak correlations between presence of the salivary glands and proboscis, and of venom gland and presence/absence of radula, with bayes factors between 6.68 and 8.38 (Table 4). The low bayes factors suggest that salivary glands are not directly involved in process of envenomation of the prey. It should be noted however, that the salivary glands of cone snail species *Conus pulicarius* contained peptide toxins when analysed by transcriptome data (Biggs et al., 2008). The functions of the accessory proboscis structure remain unclear as its presence is not correlated with other foregut structures. It was suggested that it has chemosensory functions (Taylor, 1990; Taylor and Miller, 1990). The present data supports the idea that the accessory proboscis structure is not used directly in feeding processes, but may be related to detection of the prey.

4.3. Predator–prey and toxins

Numerous terebrid lineages have lost the venom apparatus, and by contrast the lineages that kept it each developed novel anatomical features, such as hypodermic marginal radular teeth. The components of the venom apparatus, radular, venom duct, venom bulb, and proboscis, were thought to be so complicated that they certainly evolved once or twice. However, the Terebridae acquired or lost similar structure several times, resulting in an anatomy sometimes convergent with that of other conoideans. A remarkable finding is that in the Terebridae alone the hypodermic teeth, in association with reduction of the odontophore, have likely evolved on multiple and independent occasions. Additionally, the detailed anatomy demonstrates not only different origins of the teeth but also suggests differences in functional use. Analysis of radular evolution in the entire Conoidea indicate that besides terebrids, hypodermic teeth appeared only once in a major clade that unites the families Conidae, Conorbidae, Borsoniidae, Clathurellidae, Mitromorphidae, Mangeliidae and Raphitomidae (Kantor and Puillandre, in press).

The diversity of foregut anatomy in the single family Terebridae is as large as in the whole superfamily Conoidea, which includes 14 other families. For example, all major types of conoidean radular marginal teeth were recorded in the Terebridae. From prototypic duplex teeth they evolved: solid recurved teeth, which appeared independently in some Pseudomelatomidae; flat teeth, which appeared from duplex in some Drilliidae; and hypodermic teeth, which appeared independently in common ancestor of a major clade of Conoidea (Bouchet et al., 2011; Kantor and Puillandre, in press). Moreover, the flat triangular teeth of some Terebridae are unique among Conoidea. The overview of the foregut anatomy presented in this study revealed an inordinate diversity of features in the family Terebridae. These results suggest that predator–prey relationships have played an important role in the evolutionary history of Terebridae. Indeed, repeated innovations in the foregut anatomy of terebrids suggest that they adapted to different diets (e.g., deposit-feeding or carnivorous polychaetes). To date, this hypothesis remains untested as the prey of most of the analyzed terebrid species are unknown. This could be analysed by direct observation, or by indirect approaches, such as DNA-barcoding of the gut contents (Garros et al., 2008; Oliverio et al., 2009) or analysis of stable isotopes composition (Fujikura et al., 2009).

Based on the hypothesis that the diversity of foregut structures in the Terebridae is linked to the diversity of feeding types and preys, it could also be argued that the species diversity of the Terebridae could be linked to the prey diversity, and thus to foregut

anatomy. However, the results also illustrate that several species may share an apparently identical foregut structure, suggesting that the diversity of the foregut and the prey are not the only factor at the origin of the species diversity in the Terebridae and other features of the prey-capture system should be investigated e.g., reduced dispersion abilities and geographical isolation (Bouchet, 1981; Duda and Palumbi, 1999; Cunha et al., 2005, 2008; Meyer et al., 2005; Castelin et al., 2010), or differential selection by abiotic factors such as depth (Chase et al., 1998; Quattro et al., 2001; Zardus et al., 2006). Given the rate of evolution of conopeptides in cone snails, it can be argued that various Terebridae species evolved different toxins as an answer, or a consequence, to prey adaptation. Integrative approaches will be employed to complete the phylogeny of the Terebridae, identify their respective preys, and compare their foregut anatomy and the peptide toxins they produce. An integrated approach is not only a promising way to identify the factors that led to the diversification of the Terebridae and potentially the (co-)evolution of their prey, but is also a step forward in the characterization of novel terebrid toxins with novel function and potentially new therapeutic applications. Terebrids have clearly evolved different responses to the costs and benefits of having a venom apparatus under varying conditions. Using, for example, phylogenetic independent contrasts (Felsenstein, 1985b), the large-scale phylogeny presented here could assist in analysing the potential correlation between the anatomical innovations developed by the Terebridae and various biotic and abiotic parameters.

Acknowledgments

In addition to the sources enumerated in Holford et al. (2009b), a large part of the material used in the present paper was collected in Mozambique and Madagascar in 2009–2010 during expeditions Mainbaza, Miriky and Atimo Vatae, a cluster of expeditions funded by the Total Foundation, Prince Albert II of Monaco Foundation, and Stavros Niarchos Foundation, and conducted by MNHN and Pro-Natura International (PNI) as part of their “Our Planet Reviewed” programme. The authors also thank Felix Rodriguez, Edwin Diaz, Trinidad Pardo, Moises Bernal, and the crew of the RV-Urraca with collection efforts in Panama. This work was supported by a grant from The Alfred P. Sloan Foundation (B2010-37), NSF (0940108), and NIH-NIGMS (GM088096) to MH; by the “Consortium National de Recherche en Génomique” and the “Service de Systématique Moléculaire” (UMS 2700 CNRS-MNHN) as part of agreement 2005/67 between Genoscope and MNHN for the project “Macrophylogeny of life” directed by Guillaume Lecointre; and by grant RFBR 11-04-01284 “Evolution of digestive system of carnivorous gastropods: testing of morphologically-based hypotheses by molecular data” (PI Yu. Kantor). NP was partly funded by CONCO, the cone snail genome project for health, funded by the European Commission: LIFESCIHEALTH-6 Integrated Project LSHB-CT-2007-037592. The phylogenetic analyses were performed on the Cipres Science Gateway. The authors want to thank Dr. John Taylor for sharing unpublished information on terebrid anatomy and providing material from Australia, and Barbara Buge and José Utge for processing and curation of the molecular collection. The authors thank Dr. Thomas F. Duda, Jr. and Dr. Suzanne Williams for constructive comments on the manuscript.

Appendix A. Supplementary material

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.ympev.2012.03.001>.

References

- Barlow, A., Pook, C.E., Harrison, R.A., Wüster, W., 2009. Coevolution of diet and prey-specific venom activity supports the role of selection in snake venom evolution. *Proc. Roy. Soc. Biol. Sci. Ser. B* 276, 2443–2449.
- Barnosky, A.D., 2001. Distinguishing the effects of the Red Queen and Court Jester on Miocene mammal evolution in the northern Rocky Mountains. *J. Vertebr. Paleontol.* 21, 172–185.
- Berenbaum, M., 1983. Coumarins and caterpillars: a case for coevolution. *Evolution* 37, 163–179.
- Berenbaum, M., Feeny, P., 1981. Toxicity of angular furanocoumarins to swallowtail butterflies: escalation in a coevolutionary arms race? *Science* 212, 927–929.
- Biardi, J.E., Chien, D.C., Coss, R.G., 2005. California ground squirrel (*Spermophilus beecheyi*) defenses against rattlesnake venom digestive and hemostatic toxins. *J. Chem. Ecol.* 31, 2501–2518.
- Biggs, J.S., Olivera, B.M., Kantor, Y.I., 2008. [alpha]-Conopeptides specifically expressed in the salivary gland of *Conus pulicarius*. *Toxicon* 52, 101–105.
- Bouchet, P., 1981. Evolution of larval development in eastern Atlantic Terebridae (Gastropoda), Neogene to Recent. *Malacologia* 21, 363–369.
- Bouchet, P., Kantor, Y.I., Syssoev, A., Puillandre, N., 2011. A new operational classification of the Conoidea (Gastropoda). *J. Mollus. Stud.* 77, 273–308.
- Bratcher, T., Cernohorsky, W.O., 1987. Living Terebras of the World: A Monograph of the Recent Terebridae of the world. American Malacologists, Melbourne.
- Butler, M.S., 2008. Natural products to drugs: natural product-derived compounds in clinical trials. *Nat. Prod. Rep.* 25, 475–516.
- Casewell, N., Harrison, R., Wüster, W., Wagstaff, S., 2009. Comparative venom gland transcriptome surveys of the saw-scaled vipers (Viperidae: *Echis*) reveal substantial intra-family gene diversity and novel venom transcripts. *BMC Genomics* 10, 564–576.
- Castelin, M., Lambourdiere, J., Boisselier, C., Lozouet, P., Couloux, A., Cruaud, C., Samadi, S., 2010. Hidden diversity and endemism on seamounts: focus on poorly dispersive neogastropods. *Biol. J. Linn. Soc.* 100, 420–438.
- Chase, M.R., Etter, R.J., Rex, M.A., Quattro, J.M., 1998. Bathymetric patterns of genetic variation in a deep-sea protobranch bivalve, *Demimacula atacellana*. *Mar. Biol.* 131, 301–308.
- Chin, Y.W., Balunas, M.J., Chai, H.B., Kinghorn, A.D., 2006. Drug discovery from natural sources. *AAPS J.* 8, 239–253.
- Cunha, R.L., Castilho, R., Rber, L., Zardoya, R., 2005. Patterns of cladogenesis in the venomous marine gastropod genus *Conus* from the Cape Verde Islands. *Syst. Biol.* 54, 634–650.
- Cunha, R.L., Tenorio, M.J., Afonso, C., Castilho, R., Zardoya, R., 2008. Replaying the tape: recurring biogeographical patterns in Cape Verde *Conus* after 12 million years. *Mol. Ecol.* 17, 885–901.
- Daltry, J.C., Wüster, W., Thorpe, R.S., 1996. Diet and snake venom evolution. *Nature* 379, 537–540.
- Duda, T.F., 2008. Differentiation of venoms of predatory marine gastropods: divergence of orthologous toxin genes of closely related *Conus* species with different dietary specializations. *J. Mol. Evol.* 67, 315–321.
- Duda Jr., T.F., Palumbi, S.R., 1999. Molecular genetics of ecological diversification: duplication and rapid evolution of toxin genes of the venomous gastropod *Conus*. *Proc. Natl. Acad. Sci. USA* 96, 6820–6823.
- Edgar, R.C., 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucl. Acids Res.* 32, 1792–1797.
- Ehrlich, P.R., Raven, P.H., 1964. Butterflies and plants: a study in coevolution. *Evolution* 18, 586–608.
- Farrell, B.D., Dussourd, D.E., Mitter, C., 1991. Escalation of plant defense: do latex and resin canals spur plant diversification? *Am. Nat.* 138, 881–900.
- Fedosov, A., Kantor, Y., 2008. Toxoglossan gastropods of the subfamily Crassispirinae (Turridae) lacking a radula, and a discussion of the status of the subfamily Zemaciinae. *J. Mollus. Stud.* 74, 27.
- Felsenstein, J., 1985a. Confidence limits on phylogenies: an approach using the bootstrap. *Evolution* 39, 783–791.
- Felsenstein, J., 1985b. Phylogenies and the comparative method. *Am. Nat.* 125, 1–15.
- Folmer, O., Black, M., Hoeh, W., Lutz, R., Vrijenhoek, R., 1994. DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates. *Mol. Mar. Biol. Biotechnol.* 3, 294–299.
- Fowler, M., 1983. Plant poisoning in free-living wild animals: a review. *J. Wildl. Dis.* 19, 34–43.
- Fry, B.G., Wüster, W., Kini, R.M., Brusic, V., Khan, A., Venkataraman, D., Rooney, A.P., 2003. Molecular evolution and phylogeny of elapid snake venom three-finger toxins. *J. Mol. Evol.* 57, 110–129.
- Fujikura, K., Sasaki, T., Yamanaka, T., Yoshida, T., 2009. Turrids whelk, *Phymorhynchus buccinoides* feeds on *Bathymodiolus* mussels at a seep site in Sagami Bay, Japan. *Plank. Benth. Res.* 4, 23–30.
- Garros, C., Ngugi, N., Githeko, A.E., Tuno, N., Yan, G., 2008. Gut content identification of larvae of the *Anopheles gambiae* complex in western Kenya using a barcoding approach. *Mol. Ecol. Res.* 8, 512–518.
- Hall, T.A., 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucl. Acid. Symp. Ser.* 41, 95–98.
- Heard, S.B., Hauser, D.L., 1995. Key evolutionary innovations and their ecological mechanisms. *Hist. Biol.* 10, 151–173.
- Heatwole, H., Poran, N.S., 1995. Resistances of sympatric and allopatric eels to sea snake venoms. *Copeia* 1, 136–147.

- Hodges, S.A., Arnold, M.L., 1995. Spurring plant diversification: are floral nectar spurs a key innovation? *Proc. Biol. Sci.* 343–348.
- Holford, M., Puillandre, N., Modica, M., Watkins, M., Collin, R., Bermingham, E., Olivera, B., 2009a. Correlating molecular phylogeny with venom apparatus occurrence in Panamic auger snails (Terebridae). *PLoS One* 4, e7667.
- Holford, M., Puillandre, N., Terryn, Y., Cruaud, C., Olivera, B., Bouchet, P., 2009b. Evolution of the Toxoglossa venom apparatus as inferred by molecular phylogeny of the Terebridae. *Mol. Biol. Evol.* 26, 15–25.
- Hong, J., 2011. Role of natural product diversity in chemical biology. *Curr. Opin. Chem. Biol.* 15, 350–354.
- Huelsenbeck, J.P., Ronquist, F., 2001. MrBayes: a program for the Bayesian inference of phylogeny. *Bioinformatics* 17, 754–755.
- Imperial, J.S., Kantor, Y., Watkins, M., Herald III, F.M., Stevenson, B., Chen, P., Hansson, K., Stenflo, J., Ownby, J.P., Bouchet, P., 2007. Venomous auger snail *Hastula (Impages) hectica* (Linnaeus, 1758): molecular phylogeny, foregut anatomy and comparative toxinology. *J. Exp. Zool. B: Mol. Dev. Evol.* 308, 744–756.
- Jovelin, R., Justine, J.-L., 2001. Phylogenetic relationships within the *Polyopisthocotylean* monogeneans (Platyhelminthes) inferred from partial 28S rDNA sequences. *Int. J. Parasitol.* 31, 393–401.
- Kantor, Y., Puillandre, N., in press. Evolution of the radular apparatus in Conoidea (Gastropoda: Neogastropoda) as inferred from a molecular phylogeny. *Malacologia*.
- Kantor, Y.I., Taylor, J.D., 1991. Evolution of the toxoglossan feeding mechanism: new information on the use of the radula. *J. Mollus. Stud.* 57, 129.
- Kantor, Y.I., Taylor, J.D., 2002. Foregut anatomy and relationships of raphitomine gastropods (Gastropoda: Conoidea: Raphitominae). In: Oliverio, M., Chemello, R. (Eds.), *Systematics, Phylogeny and Biology of the Neogastropoda*. Bollettino Malacologico, Roma, pp. 161–174.
- Keane, T., Creevey, C., Pentony, M., Naughton, T., McInerney, J., 2006. Assessment of methods for amino acid matrix selection and their use on empirical data shows that ad hoc assumptions for choice of matrix are not justified. *BMC Evol. Biol.* 6, 29.
- Kohn, A.J., 1956. Piscivorous gastropods of the genus *Conus*. *Proc. Natl. Acad. Sci. USA* 42, 168–171.
- Kordis, D., Gubensek, F., 2000. Adaptive evolution of animal toxin multigene families. *Gene* 261, 43–52.
- Kozminsky-Atias, A., Bar-Shalom, A., Mishmar, D., Zilberberg, N., 2008. Assembling an arsenal, the scorpion way. *BMC Evol. Biol.* 8.
- Laycock, W., 1978. Coevolution of poisonous plants and large herbivores on rangelands. *J. Range Manag.* 31, 335–342.
- Lynch, V., 2007. Inventing an arsenal: adaptive evolution and neofunctionalization of snake venom phospholipase A2 genes. *BMC Evol. Biol.* 7, 2.
- Maddison, W.P., Maddison, D., 2009. Mesquite: a modular system for evolutionary analysis Version 2.01. Available from: <<http://mesquiteproject.org>>.
- Marcus, E., Marcus, E., 1960. On *Hastula cinerea*. *Boletim da Faculdade de Filosofia Ciências e Letras. Universidade de São Paulo (Zoologia)*, pp. 25–66.
- Meyer, C.P., Geller, J.B., Paulay, G., 2005. Fine scale endemism on coral reefs: archipelagic differentiation in Turbinid gastropods. *Evolution* 59, 113–125.
- Miller, B., 1970. Studies on the Biology of Indo-Pacific Terebra (Ph.D. Dissertation). University of New Hampshire, Durham.
- Miller, B.A., 1975. The biology of *Terebra gouldi* Deshayes, 1859, and a discussion of life history similarities among other terebrids of similar proboscis type. *Pac. Sci.* 29, 227–241.
- Miller, B.A., 1979. The biology of *Hastula inconstans* (Hinds, 1844) and a discussion of life history similarities among other *Hastulas* of similar proboscis type. *Pac. Sci.* 33, 289–306.
- Modica, M.V., Holford, M., 2010. The Neogastropoda: evolutionary innovations of predatory marine snails with remarkable pharmacological potential. In: Pontarotti, P. (Ed.), *Evolutionary Biology – Concepts, Molecular and Morphological Evolution*. Springer, Heidelberg, pp. 249–270.
- Newman, D.J., Cragg, G.M., 2007. Natural products as sources of new drugs over the last 25 years. *J. Nat. Prod.* 70, 461–477.
- Olivera, B.M., 1997. *Conus* venom peptides, receptor and ion channel targets and drug design: 50 million years of neuropharmacology (EE Just Lecture, 1996). *Mol. Biol. Cell* 8, 2101–2109.
- Oliverio, M., Barco, A., Modica, M., Richter, A., Mariottini, P., 2009. Ecological barcoding of corallivory by second internal transcribed spacer sequences: hosts of coralliophiline gastropods detected by the cnidarian DNA in their stomach. *Mol. Ecol. Res.* 9, 94–103.
- Pagel, M., Meade, A., 2006. Bayesian analysis of correlated evolution of discrete characters by reversible-jump Markov chain Monte Carlo. *Am. Nat.* 167, 808–825.
- Palumbi, S.R., 1996. Nucleic acids II: the polymerase chain reaction. In: Hillis, D.M., Mable, B.K., Moritz, C. (Eds.), *Molecular Systematics*. Sinauer Associates., Sunderland, pp. 205–247.
- Puillandre, N., Holford, M., 2010. The Terebridae and teretoxins: combining phylogeny and anatomy for concerted discovery of bioactive compounds. *BMC Chem. Biol.* 10, 7.
- Puillandre, N., Samadi, S., Boisselier, M.C., Sysoev, A.V., Kantor, Y.I., Cruaud, C., Couloux, A., Bouchet, P., 2008. Starting to unravel the toxoglossan knot: molecular phylogeny of the “turrids” (Neogastropoda: Conoidea). *Mol. Phylogenet. Evol.* 47, 1122–1134.
- Puillandre, N., Sysoev, A., Olivera, B., Couloux, A., Bouchet, P., 2010. Loss of planktotrophy, fragmentation and speciation: the deep-water gastropod genus *Bathytoma* (Gastropoda, Conoidea) in the western Pacific. *Syst. Biodivers.* 8, 371–394.
- Puillandre, N., Kantor, Y.I., Sysoev, A., Couloux, A., Meyer, C., Rawlings, T., Todd, J., Bouchet, P., 2011. The dragon tamed? A molecular phylogeny of the Conoidea (Gastropoda). *J. Mollus. Stud.* 77, 259–272.
- Quattro, Chase, Rex, Greig, Etter, 2001. Extreme mitochondrial DNA divergence within populations of the deep-sea gastropod *Frigidoalvania brychia*. *Mar. Biol.* 139, 1107–1113.
- Rambaut, A., Drummond, A.J., 2007. Tracer.
- Sanderson, M.J., Donoghue, M.J., 1994. Shifts in diversification rate with the origin of angiosperms. *Science* 264, 1590–1593.
- Saslis-Lagoudakis, C.H., Klitgaard, B.B., Forest, F., Francis, L., Savolainen, V., Williamson, E.M., Hawkins, J.A., 2011. The use of phylogeny to interpret cross-cultural patterns in plant use and guide medicinal plant discovery: an example from *Pterocarpus* (Leguminosae). *PLoS One* 6, e22275.
- Stamatakis, A., 2006. RAXML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics* 22, 2688–2690.
- Taylor, J., 1990. The anatomy of the foregut and relationships in the Terebridae. *Malacologia* 32, 19–34.
- Taylor, J., Miller, J., 1990. A new type of gastropod proboscis: the foregut of *Hastula bacillus* (Gastropoda: Terebridae). *J. Zool.* 220, 603–617.
- Taylor, J.D., Kantor, Y.I., Sysoev, A.V., 1993. Foregut anatomy, feeding mechanisms, relationships and classification of the Conoidea (=Toxoglossa) (Gastropoda). *Bull. Natl. Hist. Mus. Zool. Ser.* 59, 125–170.
- Terryn, Y., 2007. A Collectors Guide to Recent Terebridae (Mollusca: Neogastropoda). *ConchBooks/Natural Art, Hackenheim*.
- Terryn, Y., 2011. Family Terebridae Mörch, 1852. In: Severns, M. (Ed.), *Shells of the Hawaiian Islands. The Sea shells. Conchbooks, Hackenheim*, pp. 370–381.
- Terryn, Y., Holford, M., 2008. The Terebridae of the Vanuatu archipelago with a revision of the genus *Granuliterebra* Oyama 1961. *Visaya Suppl.* 3, 6–118.
- Van Valen, L., 1973. A new evolutionary law. *Evol. Theor.* 1, 1–30.
- Vermeij, G.J., 1993. *Evolution and Escalation: An Ecological History of Life*. Princeton University Press, Princeton.
- Williams, S.T., Ozawa, T., 2006. Molecular phylogeny suggests polyphyly of both the turban shells (family Turbinidae) and the superfamily Trochoidea (Mollusca: Vetigastropoda). *Mol. Phylogenet. Evol.* 39, 33–51.
- Wüster, W., Daltry, J.C., Thorpe, R.S., 1999. Can diet explain intraspecific venom variation? Reply to Sasa. *Toxicon* 37, 253–258.
- Zangerl, A., Stanley, M., Berenbaum, M., 2008. Selection for chemical trait remixing in an invasive weed after reassociation with a coevolved specialist. *Proc. Natl. Acad. Sci. USA* 105, 4547–4552.
- Zardus, J.D., Etter, R.J., Chase, M.R., Rex, M.A., Boyle, E.E., 2006. Bathymetric and geographic population structure in the pan Atlantic deep sea bivalve *Deminucula atacellana* (Schenck, 1939). *Mol. Ecol.* 15, 639–651.