The relationships of the enigmatic gastropod *Tritonoharpa* (Neogastropoda): New data on early neogastropod evolution?

Maria Vittoria Modica
Dipartimento di Biologia Animale e dell'Uomo
"La Sapienza" Rome University
Viale dell'Università 32
I-00185 Roma, ITALY
mariavittoria.modica@uniroma1.it

Alisa R. Kosyan
A.N. Severtsov Institute of Ecology and Evolution
Russian Academy of Sciences
33 Leninski Prospekt
Moscow 119071, RUSSIA
kosalisa@rambler.ru

Marco Oliverio
Dipartimento di Biologia Animale e dell'Uomo
"La Sapienza" Rome University
Viale dell'Università 32
I-00185 Roma, ITALY
marco.oliverio@uniroma1.it

ABSTRACT

In this paper, the relationships of *Tritonoharpa* Dall, 1908, within Neogastropoda are discussed. *Tritonoharpa* is indeed similar to *Colubraria* in the morphology of its head-foot, pallial complex, reproductive and excretory systems, in the presence of an extremely long and coiled proboscis, and a very large stomach. However, it differs from *Colubraria* in the rest of its foregut anatomy, revealing a cancellariid affinity, and a typical nematoglossan radula. The molecular data confirms Beu and Maxwell's placement of *Tritonoharpa* in the Cancellariidae, close to *Plesiotriton*. It is also suggested that cancellariids may be the sister-group to the rest of neogastropods. *Tritonoharpa* has a rather large and well developed midgut gland, resembling the gland of Leiblein. As previously studied cancellarioideans have been shown to lack a well differentiated gland of Leiblein, the present study raises some interesting questions about the evolution of the foregut in Neogastropoda. In fact, if this glandular structure were confirmed as a true homologue of the gland of Leiblein, and the cancellarioideans proved to be the sister group to the remaining neogastropods, the possession of the gland should be considered a synapomorphy of the Neogastropoda.

Additional keywords: Anatomy, phylogeny, molecular systematics, Neogastropoda, Cancellariidae

INTRODUCTION

Tritonoharpa antiquata (Hinds in Reeve, 1844) belongs to a small group of 19 Recent species, most occurring in the tropical Indo-West Pacific (Beu and Maxwell, 1987). These species had previously been referred to a *Colubraria*-like group, together with members of at least four families (Beu and Maxwell, 1987). Elongate and varicate shells, typical of *Colubraria*, have evolved through convergence several times in the families Ranellidae, Muricidae, Buccinidae, and Cancellariidae. A number of genera with columellar plaits and a nematoglossan radula, morphologically similar to *Plesiotriton*, Fisher, 1884, were placed in the Cancellarioidea. Among those, the genus *Tritonoharpa* Dall, 1908 (type species by original designation, *Tritonoharpa vexillata* Dall, 1908, Recent, from western America and the Galapagos Islands) was distinguished from *Plesiotriton* only by the absence of columellar plaits and the absence of radula (Beu and Maxwell, 1987).

Information on the anatomy of Cancellariidae is available (Harasewych and Petit, 1982; 1984; 1986), based on representatives of the subfamilies Cancellariinae and Admetinae. The anatomy and phylogenetic relationships of the Plesiotritoninae to the other cancellariids are still unknown.

Herein we describe the foregut anatomy of *Tritonoharpa antiquata* (Figure 18) and compare it with anatomical data already available for other cancellariids. A molecular dataset, based on two mitochondrial markers (12S and 16S rDNA) was used to construct a molecular phylogenetic framework for the systematics of the Plesiotritoninae.

MATERIALS AND METHODS

Taxon Sampling and Specimen Collection: The material for the present study was collected during field work and expeditions to the West Pacific (Panglao 2004, Philippines, and Santo 2006, Vanuatu, organized by the Muséum national d'Histoire naturelle, Paris), Panama (Neogastropod Workshop 2006 at the Smithsonian Tropical Research Institution, Panama), the Mediterranean Sea, and other localities, and supplemented by specimens provided by Museums and colleagues (see Table 1 for details). Vouchers are stored at BAU (Department of Animal and Human Biology, Rome), MNHN (Muséum national d'Histoire naturelle, Paris), NMSA (Natal Museum, Pietermaritzburg).

Representatives of 21 additional neogastropods, including representatives of 13 families were sequenced to provide a phylogenetic framework for the relationships of *Tritonoharpa* to other cancellariids and within the Neogastropoda. The cypraeid *Cypraea cervinetta* Kiener, 1843 has been chosen as an outgroup (see Table 2 for details).

Table 1. Species included in the molecular analysis, with collecting data, voucher numbers, length of the 12S and 16S sequences, and EMBL accession numbers. BAU, Department of Animal and Human Biology, Rome; MNHN, Muséum National d'Histoire Naturelle, Paris; NMSA, Natal Museum, Pietermaritzburg; and EMBL, The European Molecular Biology Laboratory, Heidelberg.

				12S		16S		
Family	Species	Locality	Voucher Number	EMBL	bp	EMBL	bp	References
Cypraeidae	*Cypraea cervinetta* Kiener, 1843	Venado (Panama), 8.89° N, 79.59° W, intertidal	BAU00799	FM999072	521	FM999103	492	Oliverio and Modica, in press
Cancellariidae	*Cancellaria cancellata* Linné, 1767	Off Malaga (Spain), 40–50 m	BAU00224	FM999074	541	FM999105	652	Oliverio and Modica, in press
Cancellariidae	*Cancellaria cooperi* Gabb, 1865	Off La Jolla (California, USA), 40 m	MNHN IM-2009-4611 BAU00797	FM999073	537	FM999104	616	Oliverio and Modica, in press
Cancellariidae	*Tritonoharpa antiquata* (Hinds in Reeve, 1844)	Mactan Is. (Philippines), 10.32° N, 124.03° E, 40–120 m, tangle nets, 15 May 2006	BAU00270	FN392228	521	FN392229	489	This work
Cancellariidae	*Plesiotriton vivus* Habe and Okutani, 1981	Bohol/Sulu sea sill (Philippines), PANGLAO 2005, st CP2359, 8.83° N 123.58° E, 437–476 m	MNHN32123	FM999075	523	FM999106	656	Oliverio and Modica, in press
Conidae	*Conus textile* Linnaeus, 1758	Philippines	–	DQ862058	535	DQ862058	609	Bandyopadhyay et al., 2007
Turridae	*Lophiotoma cerithiformis* Powell, 1964	Philippines	–	DQ284754	532	DQ284754	625	Bandyopadhyay et al., 2006
Muricidae	*Nucella lapillus* Linnaeus, 1758	Portobello (UK), 55.95° N, 3.10° W, intertidal	MNHN IM-2009-4617 BAU00187	FM999088	527	FM999119	679	Oliverio and Modica, in press
Muricidae	*Cronia* sp. 1	Tolo Channel, Hong Kong, 22.45° N, 114.26° E, 1 m depth	MNHN IM-2009-5118 BAU00619	FN391982	521	FM999120	669	Oliverio and Modica, in press
Muricidae	*Stramonita haemastoma* (Linné, 1767)	S. Marinella (Italy), 42.0° 3 N, 11.90° E, intertidal	BAU00696	FM999090	525	FM999121	661	Oliverio and Modica, in press
Muricidae	*Drupella cornus* Röding, 1798	Panglao Is., Catarman (Philippines), PANGLAO 2004, st. R18, 9.60° N, 123.86° E, 2–46 m	MNHN IM-2009-4601 BAU00192	FM999091	521	FM999122	657	Oliverio and Modica, in press
Buccinulidae	*Paraeuthria plumbea* (Philippi, 1841)	Ushuaia (Argentina), 54.78° S, 68.23° W, intertidal	MNHN IM-2009-4613 BAU00697	FM999095	530	FM999126	637	Oliverio and Modica, in press
Buccinidae	*Neobuccinum eatoni* (Smith, 1875)	Terra Nova Bay (Antarctic), 74.69° S, 164.1° 2 E	MNHN IM-2009-4614 BAU00785	FM999096	535	FM999127	657	Oliverio and Modica, in press
Nassariidae	*Ilyanassa obsoleta* (Say, 1822)	Not available		DQ238598	535	DQ238598	563	Simison et al., 2006
Nassariidae	*Nassarius pagodus* (Reeve, 1844)	Las Perlas Is. (Panama), 8.74° N, 79.20° W, 50 m	MNHN IM-2009-4620 BAU00237	FM999094	528	FM999125	659	Oliverio and Modica, in press
Melongenidae	*Melongena patula* (Broderip and Sowerby, 1829)	Venado (Panama), 8.89° N, 79.59° W, intertidal	MNHN IM-2009-4621 BAU00794	FM999093	533	FM999124	671	Oliverio and Modica, in press
Melongenidae	*Volema myristica* (Röding, 1798)	Panglao Is., Sungcolan (Philippines) PANGLAO 2004, st, M11, 9.64° N, 123.83° E, 0–3 m	MNHN IM-2009-4602 BAU00225	FM999091	534	FM999123	662	Oliverio and Modica, in press

Olividae	*Oliva spicata* (Röding, 1798)	Las Perlas (Panama), 8.53° N, 79.09° W, 20–22 m	MNHN IM-2009-4616 BAU00278	FM999083	524	FM999114	672	Oliverio and Modica, in press
	Olivella volutella (Lamarck, 1811)	Venado (Panama), 8.89° N, 79.59° W, intertidal	MNHN IM-2009-4615 BAU00241	FM999082	534	FM999113	665	Oliverio and Modica, in press
Pseudolividae	*Sylvanocochlis ancilla* (Hanley, 1859)	SW of Mossel Bay, Agulhas Bank, Western Cape (South Africa), 81 m	NMSA-E5279	FM999084	532	FM999115	489	Oliverio and Modica, in press
Costellariidae	*Vexillum plicarium* (Linnaeus, 1758)	Panglao Is.,Tangibilaran-Panglao Channel (Philippines), Panglao-2004, st. R67, 9.64° N , 123.86° E, 3.0–3.5 m	MNHN IM-2009-4603 BAU00207	FM999081	535	FM999112	489	Oliverio and Modica, in press
Volutomitridae	*Microvoluta* sp.	Bohol/Sulu Seas sill (Philippines), Panglao 2005 St. CP2358, 8.87° N, 123.62° E, 569–583 m	MNHN IM-2009-4609 BAU00699	FM999080	525	FM999111	651	Oliverio and Modica, in press
Ptychatractidae	*Latiromitra* sp.	Bellona West (New Caledonia), Coral Sea, Ebisco, st. CP2556, 21.1° S, 158.53° E, 741–791 m	MNHN IM-2009-4610 BAU00612	FM999085	525	FM999116	653	Oliverio and Modica, in press

Table 2. The specimens of *Tritonoharpa antiquata* with their shell measurements (in mm) and their use in this study. Abbreviations: **H,** shell length; **h,** length of the last whorl: **al,** aperture length.

Specimen/Voucher ID	locality	H	w	h	al	Sex	
BAU00268	Aliguay Is. (Philippines), 8.75° N, 123.23° E, 30–150 m, tangle nets, May 2006	15.7	5.4	9.4	6.8	male	dissected
BAU00269	Aliguay Is. (Philippines), 8.75° N, 123.23° E, 30–150 m, tangle nets, May 2006	18.5	6.1	9.9	7.2	female	dissected
BAU00270	Mactan Is. (Philippines), 10.32° N, 124.03° E, 40–120 m, tangle nets, 15 May 2006	14.1	4.6	8.4	6	female	DNA
BAU00301	Santo Is. (Vanuatu), Santo 2006, sta. DR74, SE Matewulu, 15.38° S, 167.19° E, 6 m (J. Pelorce leg.)	15.3	5.1	9.1	6.6	female	dissected
BAU00302	Santo Is. (Vanuatu), Santo 2006 sta. DR74, SE Matewulu, 15.38° S, 167.19° E, 6 m (M. Oliverio leg.)	20	6.5	10.3	8.1	female	sectioned
BAU00303	Santo, Vanuatu, Santo 2006 sta. DR55, Palikulo Bay, 15.48° S, 167.25° E, 3–7 m (J. Pelorce leg)	19.1	6.3	10.1	7.3	female	dissected

In the Results and the Discussion sections, we have used collective taxonomic names within quotation marks (e.g.: 'volutoid', 'buccinoid') as descriptive terms in the traditional context of the names (e.g., Ponder, 1974), but without attributing a specific taxonomic rank to them.

Anatomical Methods: Four specimens of *Tritonoharpa antiquata* were manually dissected (two from the Philippines BAU00268-9 and two from Vanuatu BAU00301, BAU00303). One female (from Vanuatu, BAU00302) was embedded in paraffin and serially sectioned at a thickness of 7 µm. The sections were stained either with hematoxylin and alcoholic eosin, or with hematoxylin, eosin and Alcian Blue. Radulae were cleaned in liquid bleach [NaOCl], air-dried, coated with gold, and examined using a JEOL scanning electron microscope.

DNA Extraction, PCR, Cloning, and Sequencing: Total DNA was extracted following a standard Phenol/Chloroform/Ethanol protocol (Hillis et al., 1990) with slight modification as previously described by Oliverio and Mariottini (2001). The QIAGEN QiAmp Extraction Kit was used for extraction of DNA from difficult samples, according to manufacturer's instructions.

Partial sequences of two mitochondrial genes encoding ribosomal DNA were PCR amplified. A region of the gene encoding 16S rDNA encompassing the domains IV and V (Gutell and Fox, 1988) was amplified using primers 16SA (5′-CGCCTGTTTATCAAAAACAT-3′) (Palumbi et al., 1991) and 16SH (5′-CCGGTCTGAACTCAGATCAC-3′) (Espiritu et al., 2001) or CGLeuR (5′-TATTTAGGGCT TAAACCTAATGCAC-3′) (Hayashi, 2005). A portion of the gene encoding 12S rDNA corresponding to the domains II and III was amplified with primers 12SI (5′-TG CCAGCAGCCGCGGTTA-3′) and 12SIII (5′-GAGC GACGGGCGRTTWGTAC-3′) (Oliverio and Mariottini, 2001). Amplification conditions were as follows (30–35 cycles): 94°C for 30 seconds, 45–50°C for 30 seconds, 72°C for 60 seconds. When a single band was obtained, the PCR product was purified using the Exo-Sap enzymatic method. In cases of persistent aspecific amplification, the PCR product was ligated into the pGEM-T-Easy vector according to manufacturer's (Promega) instructions and then used to chemically transform *E. coli* JM109 cells. Transformed colonies were selected by blue-white selection and clones containing the correct insert size were PCR-screened. Then, they were purified using the SIGMA miniprep kit. Purified products (amplicons and clones) were then double-strand sequenced with BigDye v. 2.0 (Applied Biosystems, Foster City, CA, USA) using the PCR primers and sequences visualized on automatic sequencer. Sequencing was performed by Macrogen Inc. (Seoul, South Korea). Chromatograms were analysed using the Staden Package (Version-1.6.0, Staden et al., 1998, 2005). All sequences have been deposited at EMBL (The European Molecular Biology Laboratory, Heidelberg; see Table 1 for accession numbers).

Sequence and Phylogenetic Analysis: Sequences were aligned using Clustal X (Thompson et al., 1994; 1997) using the default settings, then edited manually. The aligned dataset is available from the authors upon request. Analyses of nucleotide sequences were performed using Mega3.1 (Kumar et al., 2004). The uncorrected 'p' and the ML distances between the sequences were calculated. To test for the presence of mutational saturation, uncorrected 'p' pairwise distances, transition (Ts) and transversion (Tv) were plotted against the estimated ML distance (Nichols, 2005; Philippe et al., 1994) in DAMBE (Xia and Xie, 2001; Xia, 2000). The χ^2 test implemented in PAUP* v. 4b10 (Swofford, 2002) was used to test for base composition homogeneity of the aligned sequence data. The aligned sequences were analysed under the assumptions of Maximum Parsimony, Maximum Likelihood (ML, Felsenstein, 1981) and with a Bayesian approach (Rannala and Yang, 1996), using the packages PAUP* v. 4b10 (Swofford, 2002), Modeltest v. 3.7 (Posada and Crandall, 1998), MrModeltest v. 2.2 (Nylander, 2004), MrBayes v. 3.1.2 (Ronquist and Huelsenbeck, 2003), and Treefinder, June 2007 version (Jobb et al., 2004; Jobb, 2007). Each locus (12S and 16S) was first analysed separately. A partition homogeneity test (Mickevich and Farris, 1981; Farris et al., 1995a, 1995b; Cunningham, 1997), implemented as ILD test in PAUP*, was performed before combining the two loci (but see Darlu and Lecointre, 2002, and Yoder et al., 2001 for criticisms on ILD's efficiency in determining data compatibility). The combined dataset was analyzed by MP, and partitioned ML and Bayesian analyses. ML analyses were performed by Treefinder, using for each partition the substitution models chosen after evaluation by Modeltest using the Akaike information criterion. Base frequencies, relative rates of the six substitution types and model parameters were estimated separately for each partition by the software during phylogenetic reconstruction. Confidence for the nodes was estimated in Treefinder using 1000 bootstrap replicates and compared with the LR-ELW Edge Support (Expected Likelihood Weights on the Local Rearrangements: Strimmer and Rambaut, 2002; Jobb, 2007). A Bayesian analysis (BI) was performed to obtain posterior probabilities of branches using the software MrBayes, which adopts the Markov Chain Monte Carlo method to sample from posterior densities (Larget and Simon, 1999; Yang and Rannala, 1997). The substitution model used was estimated for each partition using the software MrModeltest. Base frequencies, the relative rates of the six substitution types and model parameters were estimated during the analysis, separately for each partition (using the command 'unlink' in MrBayes). A four chain metropolis-coupled Monte Carlo analysis was run twice in parallel for 10^6 generations, and trees were sampled every 1.000 generations, starting after a burn-in of 250,000 generations. Stationarity was considered to be reached when the average standard deviation of split frequencies shown in MrBayes was less than 0.01 (Ronquist and Huelsenbeck, 2003). Bayesian posterior probabilities (BPP) of a branch were estimated as the percentage of trees (after burn-in) which showed that specific node.

RESULTS

Anatomy of *Tritonoharpa antiquata:* External Morphology: Animal uniform cream in base color, with bright orange spots most frequently situated on surface of kidney and digestive gland (Figures 1–3). Foot (Figures 1–3, **ft**) partly contracted, with a deep propodial groove separating narrow propodium. Operculum absent in all specimens. Head small (Figure 4), on well-defined neck, with short, narrow, apparently non-retractable snout (**sn**) and pair of long, thick tentacles (**t**), each with a large black eye (**e**) on outer side of a basal swelling. Penis (Figure 7, **p**) of male (spm. No. 2) rather large, flattened, slightly widening distally, with small rounded orifice (**so**) at right upper angle.

Mantle: Mantle margin smooth (Figure 8). Siphon (**s**) short, muscular. Osphradium (**os**) occupying 1/3 of mantle length, approximately 1/10 of mantle width. Osphradium with broad axis, 2 equal rows of short lamellae. Ctenidium (**ct**) long, crescent-curved, slightly wider than osphradium, occupying almost entire mantle length. Females with broad capsular gland (**cg**) covering rectum. Female genital orifice (**fo**) small, slit-like, terminal. Area between ctenidium and capsular gland occupied by numerous high folds of hypobranchial gland (**hg**).

Digestive System: Proboscis extremely long, narrow (Figure 6, **pr**), folded within body haemocoel into > 10 coils (Figure 13, **pr**). In histological sections, proboscis wall consisting of columnar epithelium with basal nuclei (Figure 12, **ep**), a layer of circular muscles (**cml**) and a thick inner layer of longitudinal fibers (**lm**). Mouth opening large, terminal (Figure 6, **m**). Oral tube short, lined with thick cuticle (Figure 16, **ctc**). Buccal mass short, thick (Figure 5, **bm**), occupying ~1/10 proboscis length, consisting of buccal musculature and folded cartilages (Figures 9, 11, 15, **crt**). Buccal mass surrounded by well-developed, cuticularized, funnel-like jaw plate (Figures 9, 15, 16 **jw, ctc**), tubular anteriorly, expanded posteriorly into two small wings surrounding odontophore. Radula slightly shorter than odontophore (Figure 5, **r**), nematoglossan, consisting of a thin membrane and one central longitudinal row of rachidian teeth (Figure 19). Each tooth long, narrow (length >10×width), with three short cusps on distal end. Median cusp bearing vertical row of short secondary cusps (Figures 20, 21). Teeth closely set, distance between them approximately equal to their width.

Accessory salivary glands paired, strongly-coiled, thick-walled, tubular (Figure 5, **asg**), running parallel to buccal mass, tapering toward buccal tube, opening by two ducts (**asd**) into medial region of buccal cavity. Glands consisting of very thin layer of circular fibers and layer of tall columnar glandular epithelium with basal nuclei (Figure 16, **asg**). Lumen of gland filled with mucous secretion (staining blue with Alcian: Figure 16, **asg**). Proximal ends of accessory salivary glands fused together and connected to ventral part of proboscis wall by a strip of connective tissue (Figure 5, **cnt**). Buccal mass attached to bottom of buccal tube by multiple retractor muscles. Anterior esophagus thin-walled (Figure 5, **aoe**). Proboscis cavity containing thick proboscis nerves (Figure 5, **n**) and ducts of primary salivary glands.

Single proboscis retractor muscle running from base of proboscis to floor of body haemocoel (Figure 6, **prr**). Esophagus penetrating massive nerve ring (**nr**) then continuing ventrally. Spirally coiled valve of Leiblein (**vl**) situated within proboscis. Long midgut gland posterior to nerve ring, provisionally referred to as gland of Leiblein (Figure 6, **gl**), running along posterior part of esophagus. Gland well developed, easily recognized by its dark-brown color. Tissue of gland compact in histological sections, represented by globular cells with large nuclei and multiple granules, indicating strong apocrine secretion (Figure 16, 17, **gl**). Globular cells with large nuclei situated along septa internally dividing gland into distinct lobes. Gland filled with vesicles containing multiple secretion granules. Duct of this gland not found. Anterior aorta thick, running parallel to gland of Leiblein after passing through nerve ring. Primary salivary glands paired, whitish, tightly fused (Figure 6, **sg**), situated posterior to gland of Leiblein. In histological sections (Figure 17, **sg**), primary salivary glands appear clearly tubular, consisting of thin outer layer of connective tissue, and thick layer of high columnar epithelium, with cells having long necks and basal nuclei. Ducts of primary salivary glands (Figure 6, **sd**) thin, not passing through nerve ring, forming a loop, entering proboscis base parallel to esophagus. Ducts entering buccal mass posterior to ducts of accessory salivary gland.

Stomach long, narrow, situated beneath kidney and digestive gland, spanning one whorl. Stomach imperfectly preserved, transversal folds on its walls could not be clearly recognized.

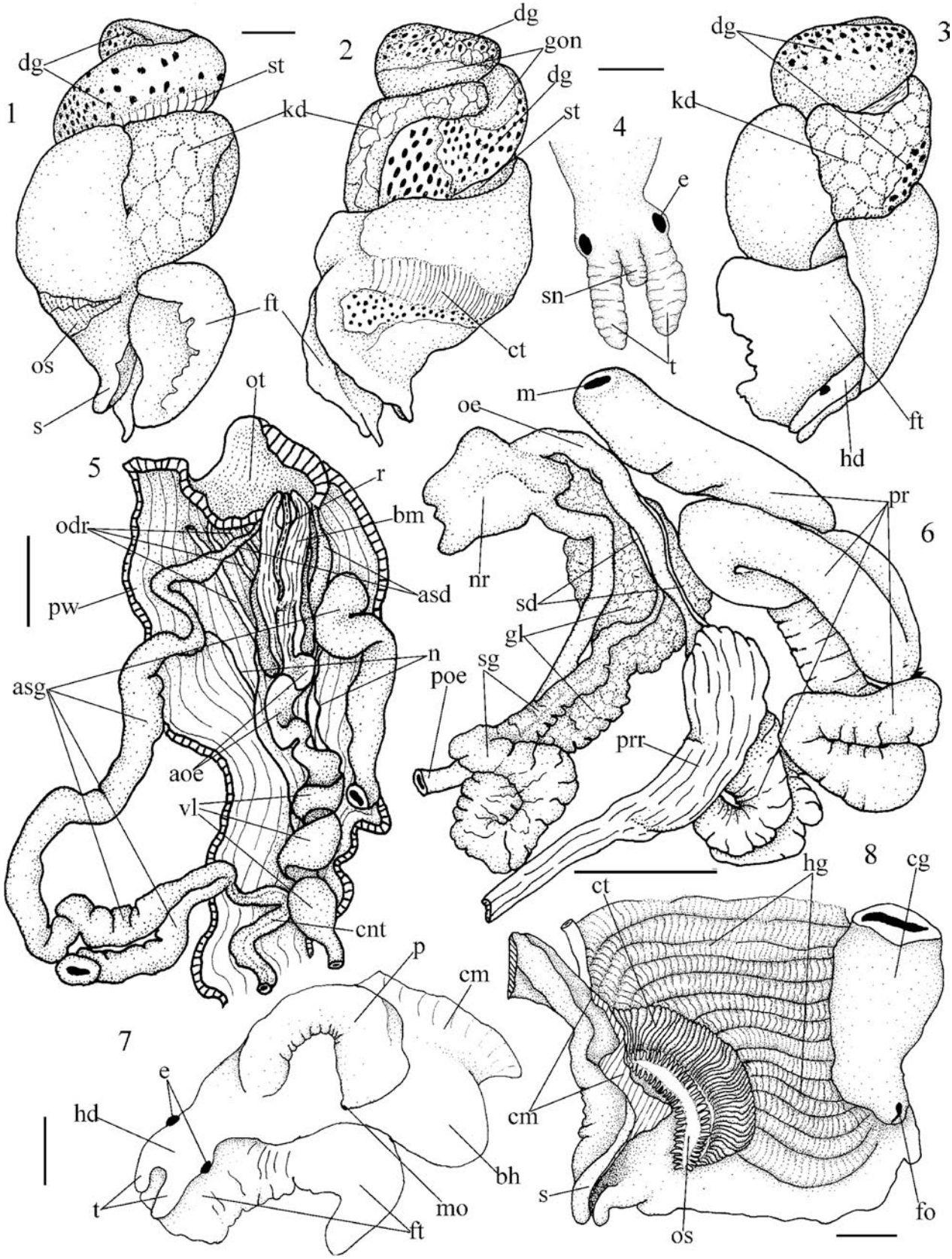
DNA Analysis: A total of 23 sequences were obtained for each of the two genes (including the outgroup *Cypraea cervinetta*). The sequences in the trimmed alignment were 521–541 bp for 12S and 489–679 bp for 16S. A χ^2 test of base homogeneity, uncorrected for phylogeny, indicated that base composition at each partition was not significantly different across all sites (16S: P=1.000; 12S: P=0.999).

Mutational saturation plots (results not shown) displayed evidence of saturation for both 12S and 16S sequences at the level of the ingroup-outgroup comparisons.

A partition homogeneity test performed in PAUP* (Swofford, 2000) did not reveal significant incongruence between the 16S and 12S datasets (P value=0.65).

The combined aligned dataset comprised 1300 nucleotide positions (12S: 581; 16S: 719), with the alignment of 301 positions considered uncertain, and thus excluded from subsequent analysis. Of the 999 included positions 536 were constant, 136 variable positions were parsimony-uninformative and 327 variable positions were parsimony-informative.

The MP analyses of each partition and of the combined dataset, produced topologies with very few nodes


1
dg
st
kd
ft
os
s
2
dg
gon
dg
st
ct
3
dg
kd
ft
hd
4
e
sn
t
5
ot
r
bm
odr
asd
pw
n
asg
aoe
vl
cnt
6
m
oe
pr
nr
sd
gl
sg
poe
prr
7
p
cm
e
hd
t
bh
mo
ft
8
hg
cg
ct
cm
s
os
fo

supported by bs>50% (Figure 22). In all MP trees, the Rachiglossa, the Toxoglossa, the Muricidae, and the Buccinidae emerged as polyphyletic. In the analysis of the combined dataset, *Tritonoharpa+Plesiotriton* and the *Cancellaria* spp. comprised a nematoglossan clade, sister to the Olividae. Only seven nodes received a bootstrap support >90%.

Model test 3.7 selected by AIC the following models of nucleotide evolution: the TrN+I+G for 12S rDNA only and the TVM+I+G (transversional model) for 16S rDNA only. These models were adopted for ML analysis. MrModelTest2.2 selected by AIC the GTR+I+G substitution model both for 16S rDNA and for 12S rDNA; this model was used in the Bayesian analysis.

In the ML topology obtained for the concatened dataset (Figure 23), a sister-group relationship between *Tritonoharpa* and *Plesiotriton* was strongly supported (bs=99 and BPP=1). The Plesiotritoninae emerged as the sister group of the other Cancellariidae included in our analysis (*C. cooperi* and *C. cancellata*), albeit without strong support (bs=50 and BPP=0.89); the clade comprising all the nematoglossans (Cancellarioidea) was the sister-group of the remaining neogastropods (rachiglossans and toxoglossans). Toxoglossans (Conoidea) emerged as polyphyletic and basal to the stenoglossans. Within the rachiglossate group, a clade Olividae was basal (bs=95; not recovered in bayesian analysis), followed by a 'volutoid' clade (bs=95 and BPP=0.99), comprising Volutomitridae (*Microvoluta* sp.) and Costellariidae (*Vexillum* sp.) plus Ptychatractidae (*Latiromitra* sp). A clade formed exclusively of Muricidae (bs=92 and BPP=0.97) was the sister taxon to a clade of consisting of the 'buccinoid' families Nassariidae, Buccinidae, and Melongenidae) (bs=95 and BPP=0.95).

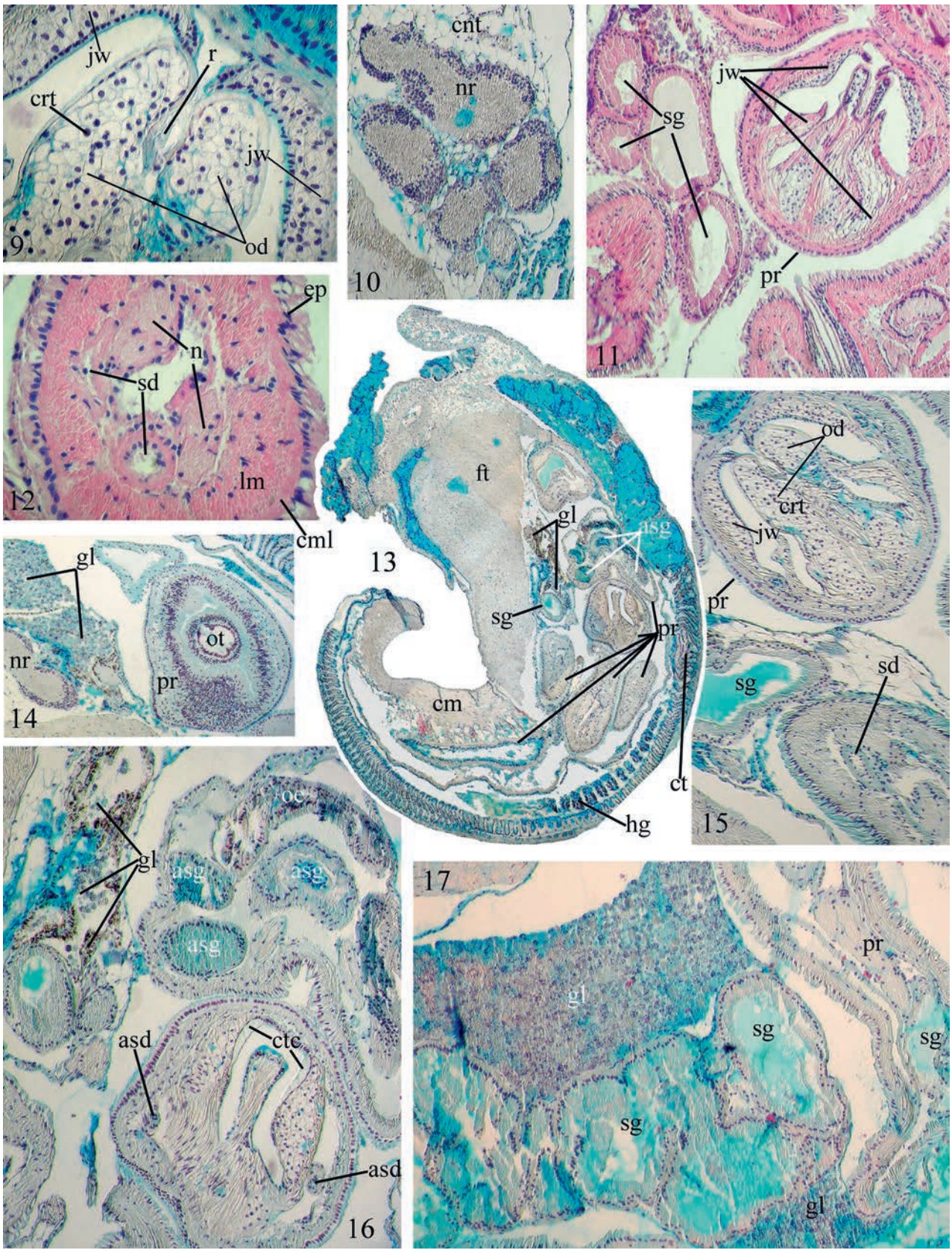
DISCUSSION

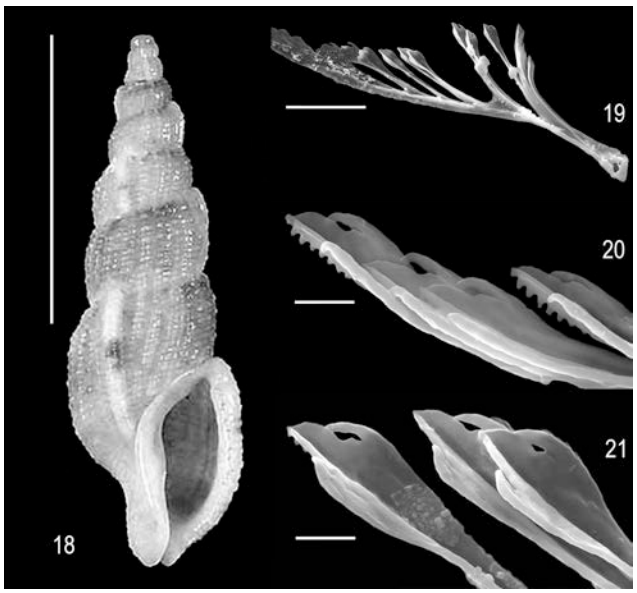
Morphology and Anatomy: Although *Tritonoharpa* is similar to the Colubrariidae and other neogastropods in the morphology of its head-foot, pallial complex, reproductive and excretory systems, and extremely long, coiled proboscis, it differs in its foregut anatomy. Beu and Maxwell (1987: 7) reported the lack of a radula in *T. antiquata* based on the examination of two specimens (one result admittedly "inconclusive", due to the extreme fragmentation of the specimen). We have observed the presence of a radula in at least three specimens. It is possible that Beu and Maxwell did not recognize a radula due to its extremely reduced size (<200 μm long). In some cancellariid species the radula may be present or absent (at different stages), as Oliver (1982) reported a radula only in the largest of two specimens of *Nothoadmete tumida* Oliver, 1982. The radula of *Tritonoharpa* has the typical nematoglossan structure, and is very similar to those of *Plesiotriton vivus* Habe and Okutani, 1981, and *Africotriton crebriliratus* (G. B. Sowerby III, 1903) (Beu and Maxwell, 1987, pls. 1 a–f and 13 a–d, respectively), comprising a single row of long, narrow, ribbon-like teeth. The peculiar tubular jaw surrounding the odontophore is typical of all Cancellariidae examined so far (Oliver, 1982; Harasewych and Petit, 1984, 1986; Simone and Birman, 2006) and may represent a synapomorphy of the Nematoglossa. Conceivably, the modification and reduction of the nematoglossan radula prompted the formation of protective jaws (**jw** in Figures 9, 15) around the median part of the odontophore (Figure 9, 15, **od**). This innovation was possibly induced by the necessity to either (1) raise the thin and long radular teeth, improving operational efficiency, and/or (2) strengthen the tip of the proboscis, which may be useful for suctorial feedng.

Tritonoharpa antiquata has two pairs of salivary glands. The accessory salivary glands have the typical tubular structure and location as described for other cancellariids (Graham, 1966; Harasewych and Petit, 1982, 1984, 1986). The primary salivary glands are tubular and located in the body haemocoel rather than in the proboscis. Such a position is unusual in cancellariids: it may be explained by the large size of these glands in *Tritonoharpa*, or alternatively it may be a plesiomorphic feature of the neogastropods.

Tritonoharpa antiquata has a large and well developed midgut gland located posterior to the nerve ring, which strongly resembles the gland of Leiblein of other neogastropods in its form and coloration. Although we have not detected any real duct connectig the gland to the esophagus, the only possible connection can be where the tissue of the gland and the esophagus are in contact, i.e. in the anterior portion of the gland, still posterior to the nerve ring. The tissue of this gland appears less structured than in the gland of Leiblein of other neogastropods (e.g., *Nucella lapillus*, Andrews and Thorogood, 2005; A. Richter, personal communication), although it is known that the general appereance of the gland can be related to feeding habits and the physiolog-

Figures 1–8. Anatomy of *Tritonoharpa antiquata*, Santo Is. (Vanuatu) and Aliguay Is. (Philippines). **1–3.** External view of the soft body of a female (BAU00303, Vanuatu). **4.** Head of a female (BAU00269, Philippines). **5.** Anterior section of the proboscis of a female (BAU00301, Vanuatu), dissected dorsally. **6.** Foregut anatomy of a female (BAU00268, Philippines). **7.** Head-foot of a male (BAU00269, Philippines). **8.** Mantle of a female (BAU00268, Philippines). Scale bar – 1 mm. Abbreviations: **aoe,** anterior esophagus; **asd,** accessory salivary duct; **asg,** accessory salivary gland; **bh,** body haemocoel; **bm,** buccal mass; **cg,** capsule gland; **cm,** columellar muscle; **cnt,** connective tissue; **ct,** ctenidium; **dg,** digestive gland; **e,** eye; **fo,** female orifice; **ft,** foot; **gl,** gland of Leiblein; **gon,** gonad; **hd,** head; **hg,** hypobranchial gland; **kd,** kidney; **m,** mouth; **mo,** male orifice; **n,** nerves; **nr,** nerve ring; **odr,** odontophoral retractors; **oe,** esophagus; **os,** osphradium; **ot,** oral tube; **p,** penis; **poe,** posterior esophagus; **pr,** proboscis; **prr,** proboscis retractors; **pw,** proboscis wall; **r,** radula; **s,** siphon; **sd,** salivary duct; **sg,** salivary gland; **sn,** snout; **st,** stomach; **t,** tentacles; **vl,** valve of Leiblein.


jw
r
crt
jw
od
9
cnt
nr
10
jw
sg
pr
11
ep
n
sd
lm
cml
12
ft
gl
asg
sg
pr
cm
ct
hg
13
od
crt
jw
pr
sg
sd
15
gl
ot
nr
pr
14
oe
gl
asg
asg
asg
asd
ctc
asd
16
17
pr
gl
sg
sg
sg
gl



Figures 18–21: Shell and radula of *Tritonoharpa antiquata*. **18.** Shell, off Tayud Is., Lilo-an (Cebu, Philippines) (photo courtesy, G. and P. Poppe). **19–21.** Radula, Mactan (Philippines; BAU00269). Scale bars: 10 mm (18), 50 µm (19), 5 µm (20–21).

ical state of the specimens (Andrews and Thorogood, 2005; A. Richter, personal communication). Large globular cells of this gland, with large nuclei and multiple nucleoli and granules in the cytoplasm indicate high secretion activity; the presence of vesicles filled with granules suggests an apocrine secretion mechanism. While the diet of *Tritonoharpa antiquata* is unknown, it is likely that individuals in this species are suctorial, feeding on body fluids as do other cancellarioideans. This conjecture is supported by the extreme modification of the radula, which suggests use for piercing rather than rasping (Oliver, 1982; Petit and Harasewych, 1986), by the tubular nature of the jaw, and by the large stomach resembling that of the haematophagous Colubrariidae (Ponder, 1968; Oliverio and Modica, in press). Furthermore, haematophagy has been already reported for the cancellariine *Cancellaria cooperi* Gabb, 1865 (O'Sullivan et al., 1987), while other cancellariid species have been observed feeding on bivalves (*Trigonostoma scalariformis* (Lamarck, 1822)), sand-dwelling gastropods (*Trigonostoma scalata* (Sowerby, 1832)) and, in aquarium, on fish pieces and squid eggs (Loch, 1987).

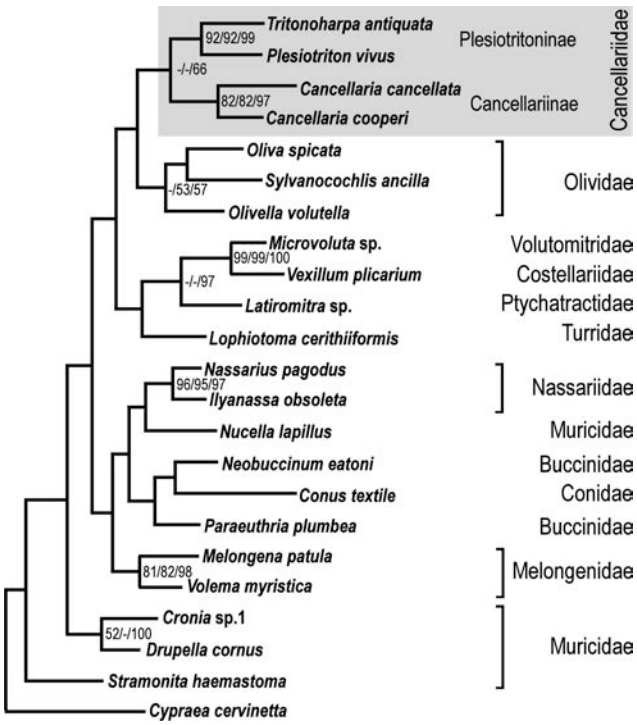


Figure 22: Maximum Parsimony topology obtained for the combined molecular dataset. Numbers at nodes represent Bootstrap values (1000 replicates) in the anlysis of the 12S, 16S, and combined datasets, respectively.

During several days of aquarium observations (SANTO 2006 expedition: MO, unpublished), two specimens of *T. antiquata* did not show any feeding activity in the presence of living specimens of various species of fishes.

The peculiar long and spirally convoluted valve of Leiblein, which differs from the pyriform valve of other Neogastropoda, has been also reported in *Plesiotriton vivus* (Kantor and Fedosov, 2009). Its functional significance deserves further investigation.

PHYLOGENY: The MP analyses of each partition and of the combined dataset, produced highly implausible results, particularly as the Rachiglossa, the Muricidae and the Buccinidae all emerged as polyphyletic (Figure 22), yet with a very few nodes with strong bootstrap support. This was probably due to the inclusion in our dataset of some highly divergent sequences (e.g., *Stramonita haemastoma* (Linnaeus, 1767), and *Conus textile* Linnaeus, 1758), a

Figures 9–17. Histology of *Tritonoharpa antiquata*, Santo Is. (Vanuatu; BAU00302, female. **9.** Cross-section of odontophore and radula. **10.** Nerve ring. **11.** Anterior part of the proboscis with buccal mass and salivary glands, stained with hematoxylin and eosin. **12.** Cross-section through the posterior part of the proboscis with primary salivary ducts and nerves. **13.** General view of the cross-section through the medial region of the last whorl of the animal. **14.** Cross-section of the proboscis at the level of the oral tube and medial part of the midgut gland. **15.** Anterior part of the proboscis with buccal mass and salivary glands, stained with alcian blue. **16.** Cross-section of the proboscis with accessory salivary glands and their ducts. **17.** Longitudinal section through the posterior parts of the midgut gland and salivary glands. Abbreviations: **asd,** accessory salivary duct; **asg,** accessory salivary gland; **cm,** columellar muscle; **cml,** circular muscles; **cnt,** connective tissue; **crt,** odontophoral cartilages; **ct,** ctenidium; **ctc,** cuticle; **ep,** epithelium; **ft,** foot; **gl,** gland of Leiblein; **hg,** hypobranchial gland; **lm,** longitudinal muscles; **lw,** lateral wings of the odontophoral cartilage; **modr,** middle part of the odontophoral cartilage; **n,** nerves; **nr,** nerve ring; **oe,** esophagus; **ot,** oral tube; **pr,** proboscis; **r,** radula; **sd,** salivary duct; **sg,** salivary gland.

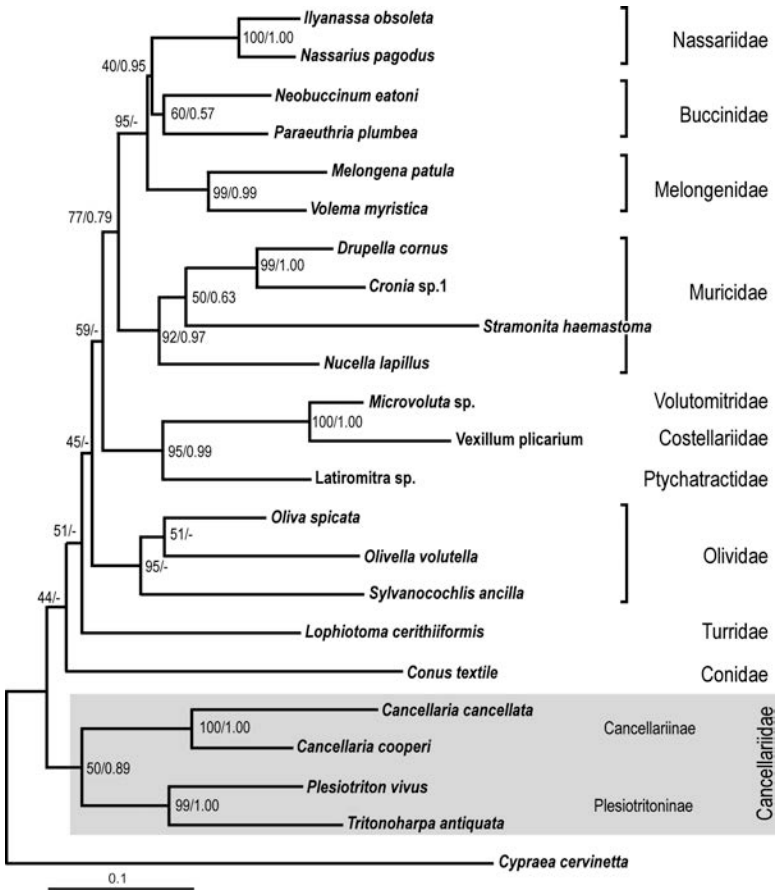


Figure 23: Partitioned Maximum Likelihood topology obtained for the molecular dataset. Numbers at nodes represent Bootstrap values/Bayesian Posterior Probability.

situation in which MP is expected to perform poorly (Felsenstein, 1978; Kim, 1996; Holder and Lewis, 2003). Therefore, MP results will not be described and discussed in details.

The ML and BI phylogenetic analyses of the molecular datasets confirms Beu and Maxwell's placement of *Tritonoharpa* in the Cancellariidae within a plesiotritonine group. It also suggests that cancellariids could be the sister-group to other neogastropods, in agreement with neogastropod phylogenetic hypotheses based on anatomical characters (Kantor, 1996, 2002; Strong, 2003) and larger molecular datasets (Oliverio and Modica, in press).

The presence of a midgut gland resembling (and possibly homologous to) the neogastropod gland of Leiblein in *Tritonoharpa* raises some interesting questions on the evolution of the foregut. In fact, current hypotheses interpret the lack of separation between the midgut gland and esophagus in the cancellariids as indicating that the elongation site is the mid-esophagus. In the rachiglossans the elongation site is the anterior esophagus, causing the detachment of the glandular tissue from the oesophageal walls and the formation of the gland of Leiblein (Ponder, 1974). If further studies on the midgut gland of the Plesiotritoninae (e.g., biochemical characterization of the secretion, exact localization of the connection to the esophagus) will confirm its homology with the neogastropod gland of Leiblein, the possession of a separate gland should be considered as an apomorphy of the Neogastropoda (instead of only of rachiglossans + toxoglossans). It may thus not be the site of elongation of the esophagus that determined the formation of the gland of Leiblein. The presence of glandular band of tissue, and not a separate gland, in other cancellariids (Harasewych and Petit, 1982; 1984; 1986) could be considered as a secondary reduction. Alternatively, either the plesiotritonine midgut gland or the separate glandular tissue of other cancellariids may not be homologous to the true gland of Leiblein. The development of a compensatory glandular region, has already been reported for other neogastropods, where it is associated with a reduced or absent gland of Leblein (e.g., the glandular mid-posterior esophagus of Colubraridae: Ponder, 1968, 1973; Oliverio and Modica, in press).

The buccal mass is displaced posteriorly from the proboscis tip of cancellarioideans by the length of the oral tube. This condition does not correspond to a basal position (as in the toxoglossans), which has been hypothesized as the plesiomorphic state for the ancestral neogastropod

(Kantor, 1996; 2002). An intermediate and variable condition in the buccal mass position is observed in olivids (Kantor, 1996; 2002), which our ML tree shows to be a basal clade within the rachiglossan radiation (Figure 23).

In our phylogeny, several clades are well supported (Figure 23). In a 'volutoid' clade, comprising *Latiromitra*, *Vexillum,* and *Microvoluta* (members of Ptychatractidae, Costellariidae, and Volutomitridae respectively), at least the first two species exhibit a primitive arrangement of the foregut (Bouchet and Kantor, 2000; Ponder, 1972). Ptychatractids have been recently treated as a separate family (Bouchet and Rocroi, 2005), but they had been included as a subfamily of the Turbinellidae (e.g., Bouchet and Warén, 1985), which are a group displaying remarkable variation among the recognized subfamilies (Ponder, 1974; Kantor and Bouchet, 1997). The placement of *Latiromitra* in our analysis suggests that a 'volutoid' affinity of the ptychatractids may exist, as suggested by, e.g., Thiele (1929) or Cernohorsky (1970). A 'buccinoid' clade is recognizable in a more derived position (including members of the families Nassariidae, Buccinidae, and Melongenidae), sister to a clade constituted exclusively by Muricidae. This result is in agreement with a recent morphology-based phylogenetic hypothesis (Strong, 2003).

It is evident that cancellariids are a key group for understanding neogastropod evolution, although their anatomical disparity is still largely unexplored. As more anatomical data on *Plesiotriton* and other cancellariids become available, a new light could be shed on the evolution of the foregut in Neogastropoda and on the early radiation of the group.

ACKNOWLEDGMENTS

We are grateful to Jerry Harasewych, Yuri I. Kantor, Alexandra Richter, and Ivan Marin for helpful discussion and comments on various aspect of neogastropod evolution. We wish to thank the organizers of the WCM 2007, and particularly Jerry Harasewych and Ellen Strong, for having organized the symposium "Neogastropod Origins, Phylogeny, Evolutionary Pathways and Mechanisms." The second author was supported by a 2007 Unitas Malacologica Young Scientists Award. Thanks are due to Philippe Bouchet who allowed the participation of MO in the Panglao 2004 and Santo 2006 expeditions, to the participants in the expeditions who helped in various ways and, in particular to Jacques Pelorce, who collected two of the specimens of *T. antiquata* in Vanuatu. We also wish to thank John Jackson (San Diego, USA), who provided the specimens of *Cancellaria cooperi*; Serge Gofas (Malaga, Spain), for the specimens of *C. cancellata*; Richard Kilburn and Dai Herber (Pietermaritzbutrg, South Africa), and Luiz Simone (São Paulo, Brazil), for the material of *Sylvanocochlis ancilla*. Jerry Harasewych and a reviewer provided very helpful comments and suggestions to the manuscript.

LITERATURE CITED

Andrews, E.B. and K.E. Thorogood. 2005. An ultrastructural study of the gland of Leiblein of muricid and nassariid neogastropods in relation to its function, with a discussion on its homologies in other caenogastropods. Journal of Molluscan Studies 71: 269–300.

Bandyopadhyay, P.K., B.J. Stevenson, M.T. Cady, B.M. Olivera, and D.R. Wolstenholme. 2006. Complete mitochondrial DNA sequence of a Conoidean gastropod, *Lophiotoma (Xenuroturris) cerithiformis*: Gene order and gastropod phylogeny. Toxicon 48: 29–43.

Bandyopadhyay, P.K., B.J. Stevenson, J.-P. Ownby, M.T. Cady, M. Watkins, and B.M. Olivera. 2007. The mitochondrial genome of Conus textile, coxI–coxII intergenic sequences and Conoidean evolution. Molecular Phylogenetics and Evolution 46: 215–223.

Beu, A.G. and P.A. Maxwell. 1987. A revision of the fossil and living gastropods related to *Plesiotriton* Fischer, 1884 (Family Cancellariidae, Subfamily Plesiotritoninae n. subfam.) with an appendix: Genera of Buccinidae Pisaniinae related to *Colubraria* Schumacher, 1817. New Zealand Geological Survey Paleontological Bulletin 54: 1–14.

Bouchet, P. and Yu.I. Kantor. 2000.The anatomy and systematics of *Latiromitra*, a genus of deep-water Ptychatractinae (Gastropoda: Turbinellidae). The Veliger 43: 1–23.

Bouchet, P. and J.-P. Rocroi. 2005. Classification and nomenclator of gastropod families. Malacologia 47: 1–397.

Bouchet, P. and A. Warén. 1985. Revision of the north-East Atlantic bathyal and abyssal Neogastropoda excluding Turridae (Mollusca: Gastropoda). Journal of Molluscan Studies, Supplement 1: 120–296.

Cunningham, C.W. 1997. Can tree incongruence test predict when data should be combined? Molecular Biology and Evolution 14: 733–740.

Darlu, P. and G. Lecointre. 2002. When does the incongruence length difference test fail? Molecular Biology and Evolution 19: 432–437.

Espiritu, J.D., M. Watkins, V. Dia-Monje, G.E. Cartier, L.J. Cruz, and B.M. Olivera. 2001. Venomous cone snail: molecular phylogeny and the generation of toxin diversity. Toxicon 39: 1899–1916.

Farris, J.S., M. Källersjö, A.G. Kluge, and C.J. Bult. 1995a. Testing significance of incongruence. Cladistics 10: 313–319.

Farris, J.S., M. Källersjö, A.G. Kluge, and C.J. Bult. 1995b. Constructing a significance test for incongruence. Systematic Biology 44: 570–572.

Felsenstein, J. 1978. Cases in which parsimony or compatibility methods will be positively misleading. Systematic Zoology 27: 401–410.

Felsenstein, J. 1981. Evolutionary trees from DNA sequences: a maximum likelihood approach. Journal of Molecular Evolution 17: 368–376.

Graham, A. 1966. The fore-gut of some marginellid and cancellariid prosobranchs. Studies in Tropical Oceanography, University of Miami 4, pp. 134–151.

Gutell, R.R. and G.E. Fox. 1988. A compilation of large subunit RNA sequences presented in a structural format. Nucleic Acids Research 16: r175–r269.

Harasewych, M.G., S.L. Adamkewicz, J.A. Blake, D. Saudek, T. Spriggs, and C.J. Bult. 1997. Neogastropod phylogeny: a molecular perspective. Journal of Molluscan Studies 63: 327–351.

Harasewych, M.G. and R.E. Petit. 1982. Notes on the morphology of *Cancellaria reticulata* (Gastropoda: Cancellariidae). The Nautilus 96: 104–113.

Harasewych, M.G. and R.E. Petit. 1984. Notes on the morphology of *Olssonella smithii* (Gastropoda: Cancellariidae). The Nautilus 98: 37–44.

Harasewych, M.G. and R.E. Petit. 1986. Notes on the morphology of *Admete viridula* (Gastropoda: Cancellariidae). The Nautilus 100: 85–91.

Hayashi, S. 2005. The molecular phylogeny of the Buccinidae (Caenogastropoda: Neogastropoda) as inferred from the complete mitochondrial 16S rRNA gene sequences of selected representatives. Molluscan Research 25: 85–98.

Hillis, D.M., C. Moritz, B.K. Mable. 1996. Molecular Systematics, 2nd Edition. Sinauer Associates, Sunderland, 655 pp.

Holder, M. and P.O. Lewis. 2003. Phylogeny estimation: traditional and bayesian approaches. Nature Reviews, Genetics 4: 275–284.

Huelsenbeck, J.P. and F. Ronquist. 2001. MRBAYES: Bayesian inference of phylogeny. Bioinformatics 17: 754–755.

Jobb, G. 2007. Treefinder. June 2007 Version. Distributed by the author at http://www.treefinder.de.

Jobb, G., A. von Haeseler, and K. Strimmer. 2004. Treefinder: a powerful graphical analysis environment for molecular phylogenetics. BMC Evolutionary Biology 4: 18.

Kantor, Yu.I. 1996. Phylogeny and relationships of Neogastropoda. In: Taylor, J. (ed.) Origin and Evolutionary Radiation of the Mollusca. Oxford University Press, Oxford, pp. 221–230.

Kantor, Yu.I. 2002. Morphological prerequisite for understanding neogastropod phylogeny. Bollettino Malacologico, Supplemento 4: 161–174.

Kantor, Yu.I. and P. Bouchet. 1997. The anatomy and systematics of Ceratoxancus, a genus of deep-water Ptychatractinae (Gastropoda: Turbinellidae) with labral spine. The Veliger 40: 101–120.

Kantor, Yu.I. and A. Fedosov. 2009. Morphology and development of the valve of Leiblein in eogastropoda: possible evidence for paraphyly of the group. The Nautilus 123: 73–82.

Kim, J.H. 1996. General inconsistency conditions for maximum parsimony: effects of branch lengths and increasing numbers of taxa. Systematic Biology 45: 363– 374.

Kumar, S., K. Tamura, and M. Nei. 2004. MEGA3: Integrated software for Molecular Evolutionary Genetics Analysis and sequence alignment. Briefings in Bioinformatics 5: 150–163.

Larget, B. and D. Simon. 1999. Markov chain Monte Carlo algorithms for the Bayesian analysis of phylogenetic trees. Molecular Biology and Evolution 16: 750–759.

Loch I. 1987. Man bites dog. Australian Shell News 59–60: 9.

Nylander, J.A.A. 2004. MrModeltest 2.1. Program distributed by the author. Evolutionary Biology Centre, Uppsala University.

O'Sullivan, J.B., R.R. McConnaughey, and M.E. Huber. 1987. A blood-sucking snail: the Cooper's nutmeg *Cancellaria cooperi* Gabb, parasitizes the California electric ray, *Torpedo californica* Ayres. Biological Bulletin 172: 362–366.

Oliver, P.G. 1982. A new species of cancellariid gastropod from Antarctica with a description of the radula. British Antarctic Survey Bulletin 57: 15–20.

Oliverio, M. and P. Mariottini. 2001. A molecular framework for the phylogeny of *Coralliophila* and related muricoids. Journal of Molluscan Studies 67: 320–324.

Oliverio, M. and M.V. Modica. In press. Relationships of the haematophagous marine snail *Colubraria* (Rachiglossa: Colubrariidae), within the neogastropod phylogenetic framework. Zoological Journal of the Linnean Society.

Palumbi, S.R., A. Martin, S. Romano, W.O. McMillan, L. Stice, and G. Grabowski. 1991. The simple fool's guide to PCR. University of Hawaii Press, Honolulu.

Petit, R.E. and M.G. Harasewych. 1986. New Philippine Cancellariidae (Gastropoda: Cancellariacea), with notes on the fine structure and function of the nematoglossan radula. The Veliger 28: 436–443.

Ponder, W.F. 1968. Anatomical notes on two species of the Colubrariidae (Mollusca, Prosobranchia). Transactions of the Royal Society of New Zealand, Zoology 10 (24): 217–223.

Ponder, W.F. 1972. The morphology of some mitriform gastropods with special reference to their alimentary and reproductive system (Neogastropoda). Malacologia 11: 295–342.

Ponder, W.F. 1974. The origin and evolution of the Neogastropoda. Malacologia 12: 295–338.

Posada, D. and K.A. Crandall. 1998. Modeltest: testing the model of DNA substitution. Bioinformatics 14: 817–818.

Ronquist, F. and J.P. Huelsenbeck. 2003. MRBAYES 3: Bayesian phylogenetic inference under mixed models. Bioinformatics 19:1572–1574.

Simone, L.R.L. and A. Birman. 2006. A new species of *Iphinopsis* (Caenogastropoda: Cancellariidae) from Brazil. Journal of Conchology 39: 141–144.

Simison, W.B., D.R. Lindberg, and J.L. Boore. 2006 Rolling circle amplification of metazoans mitochondrial genomes. Molecular Phylogenetics and Evolution 39: 562–567

Staden, R., D.P. Judge, J.K., and J.K. Bonfield. 2005. Sequence assembly and finishing methods bioinformatics. In: Baxevanis, A.D. and B.F. Francis Ouellette (eds.) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. Second Edition. John Wiley and Sons, New York, pp. 303–322.

Strimmer, K. and A. Rambaut. 2002. Inferring confidence sets of possibly misspecified gene trees. Proceedings of the Royal Society of London, Series B, 269: 137– 142.

Strong, E.E. 2003. Refining molluscan characters: morphology, character coding and a phylogeny of the Caenogastropoda. Zoological Journal of the Linnean Society 137: 447–554.

Swofford, D.L. 2002. PAUP*. Phylogenetic Analysis Using Parsimony (*and Other Methods). Version 4 [1998], beta 4.0b10 [2002]. Sinauer Associates, Sunderland.

Thompson, J.D., D.J. Higgins, T.J. and Gibson. 1994. ClustalW: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position specific gap penalties and weight matrix choice. Nucleic Acid Research 22: 4673–3680.

Thompson, J.D., T.J. Gibson, F. Plewniak, F. Jenmougin, and D. J. Higgins. 1997. The clustalX windows interface: flexible strategies for multiple sequences alignment aided by quality analyls tools. Nucleic Acid Research 25: 4876–4882.

Yang, Z. and B. Rannala. 1997. Bayesian phylogenetic inference using DNA sequences: a Markov chain Monte Carlo method. Molecular Biology and Evolution 14: 717–724.

Yoder, A.D., J.A. Irwin, B.A. Payseur. 2001. Failure of the ILD to determine data combinability for slow loris phylogeny. Systematic Biology 50: 408–24.