



**VI International Heterobranch Workshop
2-5 September 2018 Fremantle, Australia**

PROGRAM



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2-5 September 2018

Esplanade Hotel, Fremantle, WA, Australia

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VI International Heterobranch Workshop Fremantle, Western Australia

Dear Participants,

Welcome to Fremantle and to the latest International Heterobranch Workshop! It's the first time we have thrown off our polyphyletic 'opisthobranch' moniker and have embraced our monophyletic heterobranch roots. We hope you enjoy all the talks and posters compiled for you here; such a diverse group of molluscs always results in a diverse range of topics.

Fremantle is the port town of Perth, Western Australia, and is located at the mouth of the Swan River. Historical collecting records of molluscs often list 'Swan River' as the locality, but this actually can refer to anywhere relating to the Swan River Colony, later known as the Colony of Western Australia. Fremantle is built on Whadjuk Noongar land, and was called Walyalup. It is a place known for trading, ceremonies and cultural practices, and a place where people feasted on fish and game in two different Noongar seasons, Djeran and Kambarang, loosely corresponding to spring and autumn.

Originally Fremantle and Perth were not convict settlements, and there was debate about their arrival from free settlers. Convicts were present for about 17 years (~1850-1867). Fremantle also played a significant role in the gold rush of the late 19th century and the Second World War. Fremantle has many well-preserved heritage buildings, including the Round House, the oldest intact building in Western Australia. We hope you enjoy your time outside of the workshop as well!

We have three wonderful keynote speakers, each of which examine broader patterns of ecology, biogeography and defense through the lens of evolution. We thank you for attending this workshop, and supporting our heterobranch community. We hope that the presentations here, and the fruitful discussions which follow, enrich your research and your collegial relationships

Best wishes for a productive meeting,

The organising committee

Organising Committee

Nerida Wilson - Chair - Western Australian Museum

Clay Bryce - Western Australian Museum

Gary Cobb - Nudibranch Central

Alex Hickling - Western Australian Museum

Lisa Kirkendale - Western Australian Museum

Kara Layton - University of Western Australia

Corey Whisson - Western Australian Museum

Useful Phone Numbers/Information

Emergency Police/Ambulance/Fire Services – 000

Non-Emergency Police – 131 444

Nerida Wilson – 0459 273 399

Clay Bryce – 0457 537 784

Esplanade Reception – 9432 4000

Maps of Perth, Fremantle and surrounds

<http://ontheworldmap.com/australia/city/perth/>

Program
Monday, 3rd September

8:30-9:00	Registration	
9:00-9:30	Opening session/welcome to country	
9:30-10:20	Patrick Krug	Keynote; Is diversity constrained by dispersal, feeding ecology or sexual selection? Comparative tests with herbivorous sea slugs
10:20-10:40	Katharina Jörger	On heterobranch worms: diversification and evolution of Rhodopemorpha
10:40-11:20	Morning Tea	
11:20-11:40	Monisha Bharate	The gastropod genus <i>Haminoea</i> (Heterobranchia: Cephalaspidea) from India
11:40-12:00	Nerida Wilson	An update on the <i>Moridilla brockii</i> Bergh, 1888 complex
12:00-12:20	Conxita Avila	Diving into the challenging taxonomy and systematics of Antarctic heterobranchs
12:20-12:40	Matt Nimbs	Is Port Stephens, eastern Australia, a global hotspot for biodiversity of Aplysiidae (Gastropoda: Heterobranchia)?
12:40-14:00	Lunch	
14:00-14:20	Heike Wägele	Marine Heterobranchia (Gastropoda, Mollusca) in Bunaken National Park, North Sulawesi, Indonesia – the more diversity studies, the less we know?
14:20-14:40	Anna Mikhlina	Animal machine: the buccal armature of nudibranchs and its relation to feeding preferences
14:40-15:00	Christina Egger	Inside the “chubby dude”: comparative microanatomy of <i>Cliopsis krohnii</i> Troschel, 1854 (Gymnosomata, Pteropoda, Euopisthobranchia) from Western Australia
15:00-15:10	Irina Ekimova	Lightning Talk; Well-known, but poorly studied nudibranch: a resolving of <i>Myja longicornis</i> (Bergh, 1896) phylogenetic placement
15:10-15:30	Poster Session, continues through	
15:30-16:00	Afternoon Tea	

Tuesday, 4th September

9:00-9:30	Registration	
9:30-10:20	Frank Köhler	Keynote; Surviving aridification – on the evolution of Australia’s most successful land snail group
10:20-10:40	John Stanisic	The land snail field guide project: volumes 1 & 2 unbound
10:40-11:20	Morning Tea	
11:20-11:40	Lorelle Holcroft	Protoconch sculpture as a taxonomic tool in Australian charopid systematics (Gastropoda: Eupulmonata: Charopidae)
11:40-12:00	Lisa Kirkendale	First molecular phylogeny of the Australian land snail genus <i>Bothriembryon</i> (Gastropoda, Orthalicoidea) reveals high levels of diversity in a global hotspot
12:00-12:20	Corey Whisson	A review of rare and endangered land snails from south-western Australia, <i>Bothriembryon</i> Pilsbry, 1894 (Stylommatophora: Bothriembryontidae)
12:20-12:40	Marc Widmer	Snails of biosecurity significance: A twenty year snapshot of snails as pests in WA
12:40-14:00	Lunch	
14:00-14:20	Guanglong Xie	The systematic significance of left-right reversal in <i>Pupoidea</i> land snails
14:20-14:40	Michael Curran	West-Australian land snails in environmental impact assessments
14:40-15:20	Land Snail Open Discussion, continues through	
15:20-16:00	Afternoon Tea	
17:30	Conference Dinner (by registration only)	

Wednesday, 5th September

9:30-10:20	Karen Cheney	Keynote; Chemical defences and colour patterns in nudibranchs
10:20-10:40	Cedric van den Berg	Studying the function and design of nudibranch colour pattern geometry
10:40-11:20	Morning Tea	
11:20-11:40	Kara Layton	Using exon capture phylogenomics to explore closely-related species in the sea slug genus <i>Chromodoris</i>
11:40-12:00	Bastian Brenzinger	Phylogenetic reconstruction of the lower Heterobranchia by Sanger sequencing with expanded taxon sampling
12:00-12:20	Vanessa Knutson	Applying transcriptomic data to long standing questions of phylogeny in Heterobranchia
12:20-12:40	Craig Hoover	Evaluating gene flow after regional extinction: The conservation status of <i>Felimare californiensis</i> (Mollusca: Nudibranchia)
12:40-14:00	Lunch	
14:00-14:20	Kathe Jensen	Sacoglossan penial armature revisited
14:20-14:40	Alexandre Lobo-da-Cunha	The male genital apparatus of the Haminoeidea: Comparative histological and ultrastructural study in <i>Haminoea solitaria</i> and <i>Haminoea navicula</i>
14:40-15:00	Stephen Smith	Slugging it out for science: Insights from the Sea Slug Census program in eastern Australia
15:00-16:00	Afternoon Tea	
16:00-16:15	Closing Session	

Function Information

The Esplanade Hotel – Conference room



46-54 Marine Terrace & Essex Street, Fremantle WA 6160

Little Creatures Next Door – Welcome function



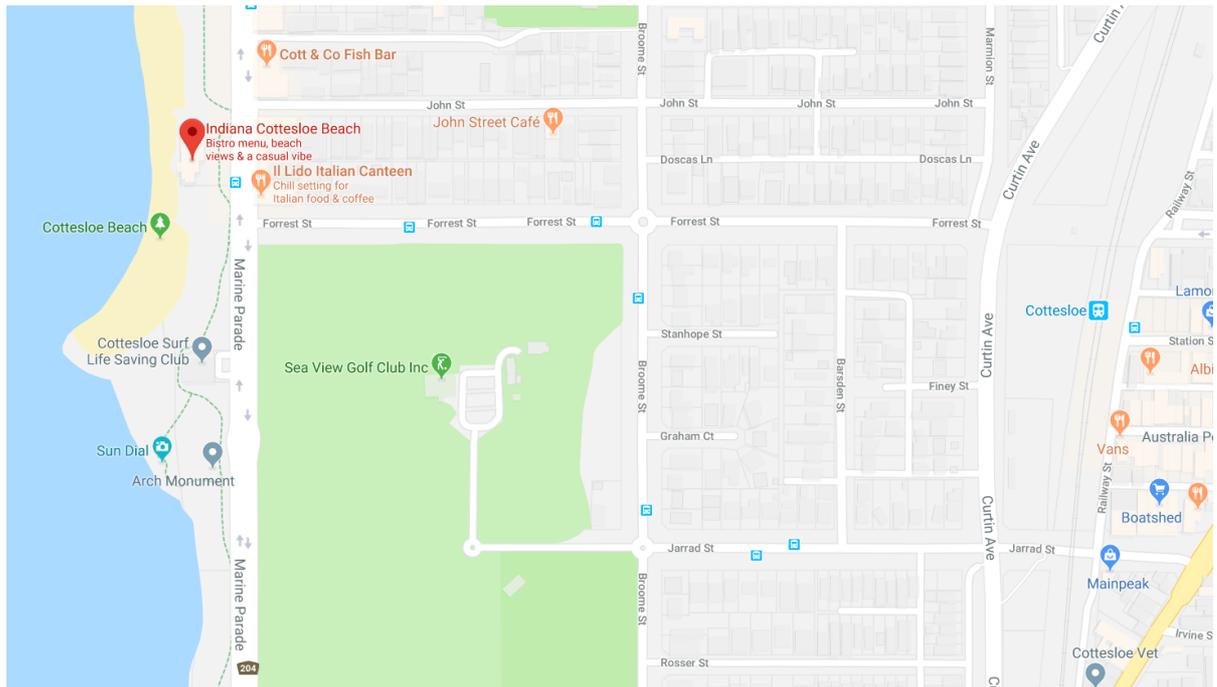
Sunday 2nd September, 3pm – 5:30pm

Drinks and canapés provided

42 Mews Road, Fremantle WA 6160 (not to be confused with the large brewery next door)

Please Note: Anyone aged 25 and under must provide proof of ID upon entry (passport for international visitors, drivers license/ID card for Australians).

Indiana Restaurant – Conference dinner



5:30pm for a sunset drink, followed by a three-course dinner

99 Marine Parade, Cottesloe WA, 6011

It's a 1km walk from Cottesloe train station with walking shoes

Please Note: Access to this function is only for people who have paid and registered for the conference dinner

Day 1 – Monday 3rd September

**Is diversity constrained by dispersal, feeding ecology or sexual selection?
Comparative tests with herbivorous sea slugs.**

Patrick J. Krug*

Department of Biological Sciences, California State University, Los Angeles, CA 90032-8201

Traits affecting dispersal, host use or sexual selection may influence rates of lineage diversification (speciation minus extinction). Although cases of species selection—where one character state increases diversification rate—are challenging to identify in most animal groups, marine heterobranchs present outstanding opportunities for tests of trait-dependent diversification. Shifts in larval type have occurred frequently, affecting the dispersal of descendent species. Most adult sea slugs are specialized consumers, permitting tests of whether diversity correlates with adult feeding niche or host characteristics. The complex reproductive systems and behaviors of heterobranchs also present distinctive opportunities for sexual selection to promote or constrain diversity. I will discuss how such traits may explain the uneven distribution of species richness across Sacoglossa, a group of herbivorous sea slugs. Using comparative methods, we modeled relationships between traits and diversity with a molecular phylogeny of 300 species, and original trait data supplemented by records for 420 taxa. Evolutionary quantitative-genetic models identified 27 shifts from planktotrophic to less dispersive lecithotrophic larvae. Contrary to 40 years of inference based on the paleontological record, our analyses showed species selection strongly favors planktotrophy; life-history evolution results in frequent shifts to short-lived larvae, which yields short-lived lineages. Kleptoplastic (photosynthetic) slugs have higher rates of shifting among host algae, and also higher background diversification rates. Ancestral reconstructions support recurring, sequential transitions from the tropical host family Halimedineae to hosts ranging into temperate zones, opening new niches and initially spurring cladogenesis; transitions to non-chlorophyte hosts were then frequent but decreased diversification, resulting in many evolutionary dead-ends. Diversification was higher for slug lineages feeding on uncalcified or chemically undefended algae, and positively correlated with the breadth of host diversity used by a slug genus. Lastly, I will discuss whether reproductive features including penial stylets vary more than expected among sympatric taxa, implicating sexual selection in speciation.

On heterobranch worms: diversification and evolution of Rhodopomorpha

Katharina M. Jörger^{1,2*}, Christina Laibl², Nerida G. Wilson³, Katrine Worsaae⁴, Jon L. Norenburg⁵,
Michael Schrödl^{1,2}, Bastian Brenzinger²

¹ *Systematic Zoology, Biozentrum, Ludwig-Maximilians-University, Munich, Germany*

² *SNSB-Bavarian State Collection of Zoology, Munich, Germany*

³ *Western Australian Museum, Welshpool, Australia*

⁴ *Marine Biology Section, University of Copenhagen, Copenhagen, Denmark*

⁵ *National Museum of Natural History, Smithsonian Institution, Washington D.C., USA*

Rhodopomorpha are the most aberrant free-living heterobranchs and have puzzled taxonomists for over 150 years. With their vermiform bodies, they externally resemble nemerteans or turbellarian flatworms and lack otherwise typical morphological characters of gastropods (such as foot, shell, head tentacles and radula). Molecular phylogenies contradict earlier hypotheses on ‘pulmonate’ or ‘opisthobranch’ relationships of rhodopomorphs, but place them outside Euthyneura, sister to shelled, ‘lower heterobranch’ Murchisonellidae. So far, little is known on the diversity and distribution of this small clade of heterobranch ‘worms’ with only eight described species. Here we present our phylogenetic analyses on the diversity and evolution of Rhodopomorpha, which include over 20 additional candidate species retrieved in a decade of dedicated sampling efforts in tropical and temperate zones. We comparatively discuss the morphological diversity of the two confirmed monophyletic genera (*Rhodope* and *Helminthope*) and present first 3D-microanatomical data based on histological semi-thin sections on a novel, worldwide distributed *Helminthope*-like form with conspicuous cruciform spicules. Our multi-marker molecular data reveals that the power of external characteristics and spicule morphology for species delineation of colorless species is limited and that many genetically distinct lineages of *Helminthope* are externally (and largely also microanatomically) cryptic. We show that hidden diversity of this largely meiofaunal yet biologically significant clade is underestimated by current taxonomy.

The gastropod genus *Haminoea* (Heterobranchia: Cephalaspidea) from India

Monisha P. Bharate¹, Trond R. Oskars², Deepak A. Apte¹ and Manuel A. E. Malaquias²

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² – Department of Natural History, Section of Taxonomy and Evolution, University Museum of Bergen, University of Bergen, PB7800 5020 Bergen, Norway. Trond.Oskars@uib.no and Manuel.Malaquias@uib.no

The heterobranch genus *Haminoea* Turton & Kingston [in Carrington], 1830 belongs to the family Haminoeidae and is characterised by thin fragile bubble shaped shells. To date approximately 70 species of *Haminoea* were recorded worldwide of which 11 are assigned to India. Several anomalies still exist in the identity of some of these 11 species as they were identified only on the basis of the shell (e.g. *H. crocata*), or refer to species from the Atlantic Ocean (e.g. *H. elegans*), species of temperate affinities (*H. alfredensis*), or have been meanwhile placed in other genera (e.g. *H. curta* now in genus *Liloa*). In order to establish the diversity of the *Haminoea* snails in India, field surveys were carried out between 2015-2018 in eight coastal states viz, Maharashtra, Gujarat, Goa, Kerala, Tamil Nadu, Andhra Pradesh, West Bengal and two archipelagoes; Lakshadweep Islands and Andaman and Nicobar Islands. Preliminary results based on DNA barcoding and morpho-anatomical studies using scanning electron microscopy (shell, radula, gizzard plates and reproductive system), have confirmed so far the presence of six species of *Haminoea* throughout India.

An update on the *Moridilla brockii* Bergh, 1888 complex

Nerida G. Wilson^{1*}, Peter U. Middelbart¹, Terrence M. Gosliner², Leila Carmona³

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2. Department of Invertebrate Zoology & Geology, California Academy of Sciences, San Francisco, CA 94118, USA

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Our understanding of cryptic (and not so cryptic) diversity continues to improve, especially as geographic coverage of taxon sampling increases, and additional data (eg DNA) becomes available. This study examines the monotypic taxon *Moridilla brockii*, thought to be widely distributed throughout the Indo-Pacific. The species name was based on a single individual from Indonesia, and was later redescribed from a large number of animals from the Gulf of Mannar, India; however, the redescription shows some deviations from the original species. We examine a range of specimens from the Indian Ocean and Coral Triangle to assess the level of diversity 'hiding' within *M. brockii*. We also present two new species, one from Western Australia and another from Papua New Guinea, and discuss a public engagement activity that was carried out using *Moridilla*. Accessing material from the type locality of *M. brockii* is now a priority to assist with establishing the valid taxon.

Diving into the challenging taxonomy and systematics of Antarctic heterobranchs

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The diversity of Antarctic heterobranchs has been considered low for more than a century. However, large areas and deep basins remain still underexplored and many groups are understudied. Up to 2015, there were about 80 species of heterobranchs described to live in Antarctica, with Nudibranchia (~35) and Cephalaspidea (~25) as the most speciose groups. Among them, several families and genera are endemic, often being essential for understanding the evolution of heterobranch lineages. Here, we review the results on the taxonomy and systematics of several Antarctic heterobranchs, in the light of the recent studies from our group. We provided integrative taxonomic evidence for the establishment of a new Cephalaspidea family (Newnesiidae), with eurybathic and circumpolar distribution, and the description of a new genus and two new species, namely *Newnesia abyssalis* and *Hocius joani*. This discovery traced the origin of the cephalaspideans, which are worldwide distributed, to Antarctica. Furthermore, our data support the hypothesis that herbivory is the plesiomorphic feeding condition in Cephalaspidea. We also described two new species of nudibranchs, *Doto carinova* and *Doridunculus punkus*, using non-destructive tomographic techniques. Detailed studies of several Tritonidae and Philinoidea species will also be discussed. In the philinoid species studied, our morpho-anatomical and molecular data suggest major changes in the systematics of the group, including the erection of a new family, two new genera, and three new species to embrace most of the species described in the Southern Ocean so far. Overall, our results highlight both the need and the importance of multidisciplinary approaches to estimate biodiversity in heterobranch molluscs from Antarctica, one of the still poorly studied areas of the planet.

Is Port Stephens, eastern Australia, a global hotspot for biodiversity of Aplysiidae (Gastropoda: Heterobranchia)?

Matt J. Nimbs^{a,b}, Richard C. Willan^c, Stephen D. A. Smith^{a,b}

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^bMarine Ecology Research Centre, Southern Cross University, Lismore, NSW 2456, Australia

^cMuseum and Art Gallery of the Northern Territory, G.P.O. Box 4646, Darwin, NT 0801, Australia.

Port Stephens, a large natural harbour on the central New South Wales coast, provides ideal oceanographic and benthic conditions for the growth of marine algae and seagrasses and this promotes a suite of herbivorous heterobranch sea slugs such as sea hares and sap-sucking sea slugs. In this paper we document both historic and recent observations of sea hares (family Aplysiidae) from Port Stephens with the intention of recording species diversity. The western South Pacific region has the richest aplysiid fauna in the world and with 16 species now recorded in Port Stephens. This location is the most taxonomically diverse for this family in Australia. Despite this hotspot of aplysiid diversity, the taxonomy and nomenclature of 12 species is uncertain, a fact highlighted by a series of nomenclatural notes included in this paper. We herein report the first observation of *Petalifera* sp. in Australian waters. *Dolabrifera jacksoniensis* Pilsbry, 1896 is newly synonymised with *D. brazieri* G. B. Sowerby II, 1870. Recent reports of southern range extensions for other heterobranch sea slugs, both in Port Stephens and elsewhere in NSW, highlight the importance of recording the existing aplysiid diversity in the Port. Thus, any future alteration to species composition and range shifts driven by climate change may be detected.

Marine Heterobranchia (Gastropoda, Mollusca) in Bunaken National Park, North Sulawesi, Indonesia – the more diversity studies, the less we know?

Heike Wägele^{1*}, Nani Undap¹, Adelfia Papu^{1,2}, Dorothee Schillo¹, Jobel Dialao³, Sven Reumschüssel³, Fontje Kaligis^{2*}, Robert Bara², Nathalie Yonow⁴, Jan-Hendrik Eisenbarth¹

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³ *Panorama Resort and Diving Centre, Manado, Bunaken Island, Indonesia*

⁴ *Swansea Ecology Research Team, Department of Biosciences, Swansea University, Singleton Park, Swansea SA2 8PP, Wales, United Kingdom*

Bunaken National Park has been surveyed four times in 14 years, in an attempt to establish the species composition of heterobranch sea slugs in a baseline study to enable protection of this special park. These molluscs are potentially good indicators of the health of an ecosystem, as many species are species-specific predators on a huge variety of marine benthic and sessile invertebrates from almost every taxonomic group. Additionally, they are known to contain bio-compounds of significance in the pharmaceutical industry. It is therefore of paramount importance not only to document the species composition from a zoogeographic point of view, but to assist in their protection for the future, both in terms of economics and aesthetics. These four surveys have documented a total of more than 200 species, with an approximate 50% of each collection found only on that survey and not re-collected. Many species new to science have also been documented, highlighting the lack of knowledge in this field.

Animal machine: the buccal armature of nudibranchs and its relation to feeding preferences

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³*Far Eastern Federal University, Sukhanova str., 8, 690950, Vladivostok, Russia*

The buccal armature usually plays important role in the feeding process of gastropods. By this term, the cuticular structures found in the buccal cavity, e.g., radula and jaws, are meant. In the case of nudibranchs, the features of buccal armature have a special importance in taxonomical studies due to specialization on different feeding objects and absence of other hard structures as shell and operculum. Nevertheless, data on the functional role of the buccal armature are insufficient. In the present study, we compared the general and fine morphology of the buccal armature in several species of nudibranchs with different feeding preferences. To understand the position of the buccal armature within the buccal complex, we constructed computer-based three-dimensional reconstructions for several species. To examine the morphology of the radula and the jaws we used methods of SEM and TEM. The arrangement of the radular teeth on the working plane (the odontophoral bend) was observed by SEM. The main characteristics depending on the feeding objects are the shape of the radular teeth, the shape of the denticles on the radular teeth and the masticatory processes of the jaws and the length of the cutting edge of the teeth (if present) as well. These characteristics may change during the ontogenesis, like in *Dendronotus frondosus* (Ascanius, 1774) or remain the same in size and shape, like in *Coryphella verrucosa* (M.Sars, 1829) and *Eubranchus rupium* (Møller, 1842). The changes in morphology of the buccal armature are the reflection of the changes in feeding preferences. This study was supported by the Russian Foundation of Basic Research, Grant No. 18-34-00251.

Inside the “chubby dude”: comparative microanatomy of *Cliopsis krohnii* Troschel, 1854 (Gymnosomata, Pteropoda, Euopisthobranchia) from Western Australia

Christina Egger^{1,2*}, Peter C. Kohnert^{1,2}, Nerida G. Wilson³ and Michael Schrödl^{1,2}

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³*Western Australian Museum, Kew Street, Welshpool, Perth, Australia*

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Pteropoda is a monophyletic group of holoplanktonic gastropods which are characterized by having paired parapodial “wings” which they use for swimming. They are traditionally subdivided into shelled Thecosomata and shell-less Gymnosomata. While thecosomes feed by means of a mucus net, gymnosomes are carnivorous predators which prey exclusively on specimens of their shelled sister clade. For that purpose, gymnosomes possess hyper diverse feeding organs to grasp their prey and extract the soft body from the protective shell. Most gymnosome species have a streamlined body shape and are very agile swimmers, which enables them to hunt and pursue thecosomes. In contrast, *Cliopsis krohnii* has a rather clumsy appearance with small wings and a bulbous visceral sac and is reported to slowly sneak upon feeding thecosomes. Since most morphological and anatomical information on *Cliopsis krohnii* dates to the beginning of the 20th century we re-evaluated a specimen from Western Australian waters by means of histological serial sectioning and virtual 3D-reconstruction. The proboscis is extremely long (3 times the body size) and can be completely withdrawn into the head. Paired hook sacs, jaws and a radula for extraction of their prey are present. Cerebrobuccal connectives are very long and allow the buccal apparatus to be extended far into the proboscis. A typical digestive gland as present in most gastropods has been replaced by a voluminous sac lined with glandular digestive epithelium. The hermaphrodite reproductive system consists of a huge gonad, a fused complex of female glands and a cephalic copulatory organ. Noticeable is an enigmatic and yet undescribed organ of unknown function and systemic affiliation which fills a large part of the visceral sac. Our results are compared with newly generated microanatomical data of representatives of other gymnosome families (Clionidae and Pneumodermatidae) with an emphasis on the neuroanatomy and innervation of feeding organs.

Well-known, but poorly studied nudibranch: a resolving of *Myja longicornis* (Bergh, 1896) phylogenetic placement

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Myja longicornis (Bergh, 1896) is a well-known and remarkable nudibranch species. Its specific habitat and crypticity as well as astonishing external morphology made this species desirable for divers and underwater photographers. Nevertheless, there have not been any modern studies of its internal and external morphology since the original description. In the case of taxonomy, *Myja longicornis* was initially assigned to the family Tergipedidae, what then considered questionable. Recently the taxonomic division of this family and other fionid families underwent major changes, thus the validity and phylogenetic position of the genus *Myja* requires an additional testing.

We studied ten specimens of *Myja longicornis* collected in southern Vietnam, Nha Trang Bay, using anatomical dissections, SEM and CLSM techniques. Molecular phylogenetic analysis based on three independent markers (COI, 16S and H3) and expanded dataset was also implemented.

Our results show that *Myja longicornis* belongs to the family Facelinidae *sensu stricto*. Unexpectedly it is not recovered as a separate clade, but nests within the genus *Cratena* as a sister species of *C. minor* Padula et al., 2014. Synapomorphies of this clade are hard to determine. In addition, the recovered phylogenetic relationships show family Facelinidae and some of its genera to be polyphyletic, suggesting the future group revision.

Morphological study was supported by Russian Foundation of Basic Research, Grant No. 18-34-00251, molecular study – by Russian Science Foundation, Grant No. 18-74-00062.

Day 2 – Tuesday 4th September

Surviving aridification – on the evolution of Australia’s most successful land snail group

Frank Köhler*

Australian Museum, 1 William St, Sydney NSW 2010, Australia.

Representing Australia’s taxonomically and ecologically most diverse family of land snails, the Camaenidae inhabit a wide range of habitats, from rainforest to desert, and occur throughout most of the continent except Tasmania and the far southwest. This family contains about one third of all Australian land snail species, and their morphological and behavioural diversity surpasses that of any other Australian group. At the same time, many species exhibit remarkable patterns of narrow-range endemism, which are indicative of rather limited dispersal abilities. Molecular phylogenetic studies appear to be consistent with the hypothesis that Australian camaenids have originated from Southeast Asia in the mid-Cenozoic. Progressive aridification has since caused the retreat and the fragmentation of once widespread mesic and the emergence of arid biomes. In this talk I am exploring how these major environmental shifts have shaped the patterns of phenotypic and phylogenetic differentiation in the Australian Camaenidae.

The land snail field guide project: volumes 1 & 2 unbound

Dr J. Stanisic*

Honorary Research Fellow, Queensland Museum. PO Box 3300, South Brisbane, 4101, Qld. Email: john.stanisic@qm.qld.gov.au

The publication of 'Land snails of Australia, Volume 2: a field guide to the southern central and western species' completes a 14 year odyssey aimed at bringing Australia's native land snails into popular literature. The first volume in the series targeted the extensive eastern Australian fauna and featured 794 species of which 308 were newly described and illustrated in colour for the first time. At this stage of the project the aim was merely to showcase the fabulous diversity of the eastern rainforest snails. However, even before the print was dry, a second volume covering the land snails of the rest of Australia was in the planning phase. The second volume is now a reality and features 756 species from the southern rainforests of Victoria and Tasmania, the semi-arid and arid areas of southern and central Australia as well as the enormously diverse fauna of the Kimberley. Common names, distribution maps, key localities as well as live snail and habitat images have been designed to make snails more appealing to a general as well as a professional audience. Media interest and emanating research suggest that this strategy is working. A third volume is planned as the odyssey continues!!

Protoconch sculpture as a taxonomic tool in Australian charopid systematics (Gastropoda: Eupulmonata: Charopidae)

Lorelle Holcroft *

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Charopidae represent one of the most speciose land snail faunas in Australia with an estimated 750 species, mostly being less than 5 mm in shell diameter. The majority of the family's species are undescribed. With limited available material suitable for molecular analysis, morphological methods remain the primary technique for the identification of charopid species, and recent studies have shown that the sculptural patterns on the protoconch are diagnostic in establishing a generic signature. This talk elucidates the results of a recent study which formalised the formal framework for the description of the protoconch patterns for those species currently considered to be members of the eastern Australian group of charopids. Target species included the *Gyrocochlea*-grade group of charopids and those with finely cancellate protoconchs. Eleven major configurations were identified, coded, defined and described. It is intended that this terminology be the benchmark for future descriptions of the protoconch characteristics of these Australian charopid species and their generic placement. Evidence from this study also indicates that there is local geographic consistency in the distribution of the protoconch patterns and a broad latitudinal sequence of pattern turnover.

First molecular phylogeny of the Australian land snail genus *Bothriembryon* (Gastropoda, Orthalicoidea) reveals high levels of diversity in a global hotspot

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Bothriembryon Pilsbry, 1894 is an endemic genus of Australian land snail most diverse in the cool temperate region of southwest Western Australia. It is a member of the larger superfamily Orthalicoidea but also forms part of a discretely Gondwanan group, the Bothriembryontidae, with relictual distributions in South America, Africa, Polynesia and Australia. While the taxonomy of the family has been recently revised, no targeted phylogenetic analysis has been constructed to test species boundaries in the genus. We present the first molecular phylogenetic analyses of *Bothriembryon* with sampling of over 300 individuals, comprising 32 described species. Three gene regions were sequenced to build the phylogenetic trees; 745 mtDNA sequences (431 16S rRNA, 16S and 314 cytochrome c oxidase subunit I, COI) as well as 245 sequences from the nuclear gene, ANT. A number of clearly distinct lineages have been identified (min. 17) and several of these correspond to previously synonymized names (e.g. *kingii* group, *barretti* group). Many of these lineages have restricted ranges and/or are found in highly specific habitats. Similar to work on other terrestrial invertebrates in the southwest of WA, these findings provide early evidence for a number of short range endemics and call attention to the ongoing need for conservation in a global biodiversity hot spot.

A review of rare and endangered land snails from south-western Australia, *Bothriembryon* Pilsbry, 1894 (Stylommatophora: Bothriembryontidae)

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Eight species of *Bothriembryon* Pilsbry, 1894 (22% of all extant species) are listed as threatened at state and international levels. All but one of these nominally threatened taxa is found in south-western Western Australia (SWWA). The taxonomy of the group has not been recently studied and little data exist on the biogeography and ecology of most species. Detailed curatorial and field work from 2011 to 2016 has provided new ecological and behavioural data and, importantly, almost doubled the number of records of the seven nominally threatened SWWA species in Australian Museum and University collections. *Bothriembryon bradshawi* Iredale, 1939 was collected live for the first time, and the other threatened species *B. brazieri* (Angas, 1871), *B. glauerti* Iredale, 1939, *B. irvineanus* Iredale, 1939 and *B. perobesus* Iredale, 1939 were collected live in the field. The presumed extinct species *B. praeceus* Iredale, 1939 may have been collected live for the first time, awaiting more detailed analysis. The other presumed extinct species, *B. whitleyi* Iredale, 1939, was not collected live during this project, but recently dead shells were found during detailed study of WAM collections. Notes on live animal colour are recorded for the first time. Threatening processes are discussed which may place these species at risk. These findings have revealed the need for future, quantitative ecological surveys so an updated conservation assessment can be made.

Snails of biosecurity significance: A twenty year snapshot of snails as pests in WA

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Of all the species of snails that exist, most are innocuous and only a small handful of them are classified as pests. Snails can be charming or fascinating and some are truly magnificent and even beneficial. The Department of Primary Industries and Regional Development has long been involved with snails as pests in agriculture, home gardens, the environment and those of quarantine significance. In the past 20 years the Department has handled thousands of snail inquiries, but less than 1% of these were species of quarantine significance, including the exotic green snail, *Cantareus apertus*. This talk will offer the audience a snapshot view of the snail concerns to WA biosecurity, farmers and gardeners alike, and demonstrate an interesting trend in what species have been of greatest concern over the years. We will delve into the pitfalls and difficulties experienced during a failed exotic pest snail eradication attempt, and hear of a spectacular agricultural snail control success. Finally, we will touch on the challenges brought to us by shifts in climate, agricultural practices and the removal of effective treatment options over the years and even have a light-hearted look at some interesting alternatives in snail control.

The systematic significance of left–right reversal in *Pupoides* land snails

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Australian land snails are well-known for their high levels of endemism. About 97% of all land snail species native to Australia are endemic to the continent, and most of them are indeed narrowly endemic to much smaller areas. However, this paradigm of marked endemism in Australian land snails does not apply to the same extent to the Pupillidae, a family of minute snails. One member of this family is *Pupoides* Pfeiffer, 1854, a genus containing about nominal 30 species from all over the world, fifteen of which known from Australia. Interestingly, Some Australian species have sinistrally and others dextrally coiled shells. Generally, sinistral shells are rare among gastropods as more than 90% of all living species have dextral shells. However, sinistral shell coiling has evolved multiple times in several different groups. In several land snail groups the reversal of shell coiling is an evolutionarily conserved trait. Changes in chirality have also been identified as a driver of speciation in groups where dextral and sinistral forms become reproductively isolated from each other for their inability to mate. In other groups, however, different chiral morphs are known to occur within the same species indicating that changes in chirality may be evolutionarily less conserved. As the taxonomy of *Pupoides* rests entirely on morphological analyses, the evolutionary origin and systematic significance of changes in shell coiling in this group are not well understood. We have used mitochondrial phylogenetics to reconstruct the evolutionary history of the Australian species in order to better understand how often shifts in chirality have occurred in this group and whether these changes have promoted lineage differentiation in Australia.

West-Australian Land Snails in Environmental Impact Assessments

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Despite being identified and listed as short-range endemics (SREs) in WA legislature, there are several issues hindering the protection of land snails. For example, most consultant work is conducted in the Pilbara and Goldfields where identifications are largely reliant on decades old taxonomy. Additionally, consultants tasked with assessing impacts to such species often find themselves with timelines of between three and six months, inclusive of field work, identifications and reporting. Field work often coincides with dry conditions when most snails are aestivating (mostly shells are collected) and molecular work for live animals is not routine, let alone mandatory. I will be discussing land snails in several environmental impact assessments to illustrate the importance of, and challenges facing consultant work. I believe three changes are needed to provide better conservation outcomes for land snails in WA: 1) a robust and comprehensive taxonomy of land snails in WA; 2) a requirement for adequate surveys (i.e. collect live animals); and 3) molecular work is routinely applied.

Day 3 – Wednesday 4th September

Chemical defences and colour patterns in nudibranchs

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Nudibranchs exhibit an amazing diversity of colour patterns that are used to prevent detection from potential predators (camouflage) or to warn predators they contain toxic and/or unpalatable secondary metabolites as chemical defences (aposematism). Indeed, nudibranchs house an intriguing array of compounds that are produced de novo, obtained from dietary sources and stored directly without selection or modification, or selectively sequestered or biotransformed. We predict that storage strategies should be optimized to produce effective defence mechanisms but also prevent autotoxicity of the host.

We have identified secondary metabolites in over 40 species of nudibranch from Australia, which include macrolides, diterpenes and sesquiterpenes. Using toxicity and anti-feedent assays with shrimp and fish, we have also estimated the strength of these chemical defences. We relate these findings to nudibranch colour signals, which are investigated from the perspective of potential predators using a range of colour vision modelling and pattern analyses.

In this talk, I will present an overview of our findings on nudibranch colour patterns and chemical defences over the past 5 years. I will discuss whether camouflaged species often contain defensive compounds and whether brightly patterned nudibranchs are the most toxic and distasteful. I will also present work on a potential red-spot group mimicry complex found on the east coast of Australia and how colour pattern variation in nudibranch signals can persist between populations.

Studying the Function and Design of Nudibranch Colour Pattern Geometry

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Nudibranchs have evolved in thousands of shapes and colours spanning from near-perfect camouflage to eye-catching warning colouration. This diversity in form and colour is accompanied by sophisticated defensive weaponry or the complete lack thereof. The fact that they only possess rudimentary vision themselves makes nudibranchs the perfect model organism for the study of the function and evolution of defensive animal colouration. However, to understand how and why defensive animal colouration works and evolves we need to be able to understand how it appears to potential predators. Thus, a fundamental hurdle for our progress is our ability to approximate the way animals perceive their visual environment. As the saying goes, “Beauty is in the eye of the beholder”.

I have been busy for the last three years combining a variety of hardware, software and statistical components into a comprehensive framework for quantitative colour pattern analysis (QCPA). QCPA allows to interpret the colour pattern of an animal in its natural context, through the eyes of animal observers. In my talk I will highlight how calibrated digital photography in combination with sophisticated image analysis software and statistical tools can help us understand the design, function and evolution of animal colouration. I will do this by presenting some of the work I and collaborators have been or are involved in using nudibranch molluscs as a model organism for the study of defensive animal colouration and its evolution.

**Using exon capture phylogenomics to explore closely-related species in the sea slug genus
*Chromodoris***

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Chromodoris is a genus of toxic nudibranch with 39 closely related species in the Indo-Pacific, some of which mimic congeners on a regional scale. Existing mitochondrial phylogenies for this group are unresolved with short branch lengths and polytomies, suggesting additional data is needed to clarify species boundaries. This study employs a transcriptome-based exon capture approach for resolving the phylogeny of *Chromodoris*. Two *Chromodoris* and four outgroups were first selected for transcriptome sequencing to assist with bait design, and 69 samples were chosen for exon capture. This work produced a novel bait set targeting 2,925 informative exons from 1,630 genes across the genus, and is the first study to test this approach on a group of recently diverged taxa. The resulting ML and ASTRAL trees had slightly different topologies and short branch lengths at interior nodes, but both show high support for species-level entities. Both trees were also reconstructed using 149 genes previously identified from eupulmonate gastropods, which were predicted to have broad utility for phylogenetic reconstruction. A Treespace analysis revealed that trees generated with the full gene and 149-gene exon datasets had slightly different topologies but were more similar to each other than to mitochondrial trees, which showed the greatest topological variability. In some analyses, *C. aspersa* and *C. orientalis* are sister to the rest of the *Chromodoris*, suggesting that spots are a plesiomorphic trait and were not reacquired in derived taxa. This work also corroborates a previous finding of regional mimicry for some individuals, but recovers others as introgressive hybrids, providing the first evidence of introgression in *Chromodoris*. In all, this work has demonstrated that exon capture is informative for resolving species boundaries in a group of recently diverged nudibranchs and has advanced our understanding of evolutionary relationships in this group.

Phylogenetic reconstruction of the lower Heterobranchia by Sanger sequencing with expanded taxon sampling

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Heterobranchia is one of the major gastropod clades with such well-known euthyneuran taxa as nudibranch sea slugs, pteropod sea butterflies and panpulmonate land snails. It remains poorly understood, however, how so-called “lower” heterobranchs – mostly minute, marine and still shell-bearing snails originating as early as the Devonian – have evolved to these highly specialized forms. To illuminate the early evolutionary history of the Heterobranchia, we collected specimens of lower heterobranchs for phylogenetic and 3D-anatomical reconstructions.

Our present dataset contains novel COI sequences (~658 bp) for all 14 extant families and more than half of the genera in the lower Heterobranchia, mainly from waters of Japan, Europe, and also various Indo-Pacific countries targeted by the biodiversity expeditions of the Muséum National d'Histoire Naturelle, Paris. To our surprise, this single marker could resolve many relationships that were unclear or not suggested in previous studies and gives the first insights into the internal phylogenies of most families and superfamilies.

Four major clades have been identified, namely: 1) re-defined Valvatoidea snails (Valvatidae, Hyalogyrinidae, Cornirostridae) including at least two further marine lineages; 2) Architectonicoidea *sensu lato* with Architectonicidae, Mathildidae and re-defined Omalogyridae; 3) a new clade containing snails with highspired or flatspired shells (Orbitestellidae, Cimidae, and others); and 4) a clade of somewhat euthyneuran-like animals, including Rhodopidae and possibly paraphyletic Murchisonellidae, that is sister to Euthyneura. We expect full resolution within the four clades by adding other traditional markers and by conducting detailed morphological comparisons, approaching a fully resolved backbone tree of the heterobranchs.

Applying Transcriptomic Data to Long Standing Questions of Phylogeny in Heterobranchia

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Phylogenetic relationships within Heterobranchia have been researched extensively, but have been difficult to resolve because of the independent or parallel evolution of many morphological features, including, but not limited to, shell reduction and/or loss, gill placement, and miniaturisation. While our knowledge of the heterobranch phylogeny has improved drastically through the use of cladistic methods combined with the Sanger sequencing of traditional genetic markers, relationships remain largely unresolved at the generic and familial levels, likely due to a lack of sufficient phylogenetic signal in these loci. Recently, a handful of studies have applied next-generation sequencing (NGS) technologies to data collection for phylogenomic analysis of heterobranch relationships, with promising results. However, this approach has yet to be applied to Heterobranchia on a large scale, and due to limited taxon sampling, many relationships remain untested or unresolved. To address this, we gathered, sequenced, and assembled *de novo* dozens of Heterobranchia transcriptomes, sampling more or less at the family level, focussing on marine heterobranchs. We then analysed these data using a variety of phylogenomic methods in order to resolve evolutionary relationships within this charismatic group. Here we present our methods and preliminary results for a subset of our samples. Answering long-standing questions of phylogeny in Heterobranchia will better enable the study of the evolution of fascinating characters and behaviours including shell loss, gill placement, chemical ecology, and diet in this diverse and speciose clade of gastropods.

Evaluating gene flow after regional extinction: The conservation status of *Felimare californiensis* (Mollusca: Nudibranchia)

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The conservation status of the nudibranch *Felimare californiensis* was evaluated during a recovery period that followed twenty years of regional extinction in Southern California. Evaluation addressed questions about relative genetic diversity, connectivity and isolation among eight populations representing the two regions, Southern California and Mexico, to determine if regional extinction was likely to threaten the species through a loss of genetic diversity and thus adaptability. Mitochondrial genes CO1, 16S and three nuclear microsatellites were tested using a variety of population genetics approaches. The Southern California region showed relatively high genetic diversity and low connectivity with Mexico. Clipperton Island was a remote isolated population. Considering the recent recovery these results indicated high gene flow throughout most of the population. We found no evidence that regional extinction was likely to have caused a loss of genetic diversity, and therefore conclude that *F. californiensis* does not qualify for threatened status based on that criteria. Considering present trends in climate change and that the conservation status of only ten percent of molluscs have been evaluated by the IUCN we recommend more comprehensive study to fill this gap in scientific knowledge.

Sacoglossan penial armature revisited

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In 1974 Tom Gascoigne (1903-2000) published a short paper reviewing penial armature of 13 species of Sacoglossa (Gastropoda: Panpulmonata). At that time few observations existed on copulatory behaviour, and most of these were on the common European shallow-water species of *Limapontia* and *Alderia modesta*, which are easily kept in small petri-dishes. At the 11th International Malacological Congress in Siena, Italy in 1992, Tom Gascoigne made an unforgettable presentation (paper published in 1993) in which he elaborated on his former work, this time focusing on function. Since then many new species have been described, and SEM is now the preferred method to illustrate shape of penial stylets. Also, copulatory behaviour has been studied in several species. In the present study a review of penial armature and copulatory behaviour will be presented, as well as new information on penial stylets from almost all known genera of Sacoglossa. Examination has shown discrepancies with old descriptions in both size and shape of penial stylets. The significance of this will be discussed.

The male genital apparatus of the Haminoeidea: Comparative histological and ultrastructural study in *Haminoea solitaria* and *Haminoea navicula*

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The genus *Haminoea* occurs in shallow marine and estuarine habitats all over the world and currently contains about 40 species recognized as valid, many of them described based only on shell characters. However, features of the male copulatory apparatus have been considered more reliable to discriminate between species. Nevertheless, despite the general morphology of this apparatus in *Haminoea* being depicted in several studies, detailed data on its internal anatomy and histology is lacking. Ongoing molecular phylogenetic studies of the family Haminoeidae (Cephalaspidea) suggest that the traditional genus *Haminoea* is not monophyletic, and therefore, the histological study of the male genital apparatus of species with distinct anatomies can contribute to clarify these taxonomic issues. For this purpose, the male genital apparatus of *H. navicula* (a native European species) and *H. solitaria* (an American species introduced in the Baltic Sea with a unique morphology of the male reproductive apparatus) were processed for light and transmission electron microscopy.

In *H. navicula* the penial sheath surrounds a muscular penis containing a penial duct, which is continuous with the seminal duct that connects the penis to the prostate. In *H. solitaria* a real penis is absent. Instead, a muscular papilla without a duct was found inside an atrium that is connected to prostate by the seminal duct.

The histological study of the prostate also revealed considerable differences between the two species. In *H. naivcula* the prostate is divided in two lobes. The proximal lobe being formed by tubules containing four types of secretory cells, and the distal lobe being formed by tubules containing a single type of secretory cells. In *H. solitaria* the prostate consists of a central lumen surrounded by pouches lined by an epithelium formed by a single type of secretory cells. These profound differences in anatomy and histology support the division of the traditional genus *Haminoea*, also suggested by molecular studies.

Slugging it out for science: insights from the *Sea Slug Census* program in eastern Australia

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The *Sea Slug Census* is a citizen-science-based program which was developed to improve the body of information on the diversity and distribution of heterobranch sea slugs in eastern Australia. Commencing at Nelson Bay, New South Wales, in December 2013, the program has now expanded to a total of 8 locations between south-east Queensland and Melbourne, Victoria (~1500 km) and engaged with >1000 volunteers. The data accumulated have been used to: evaluate the ability of volunteers to document species richness by comparison to data acquired by scientists; determine if short-term (1-2 days), intense sampling closely reflects data generated over a longer time period (1 month); generate location-specific species lists; and evaluate biotic patterns and temporal variation over a scale of up to 4 years. These analyses validate the utility of the program to generate accurate, cost-effective data on sea slug assemblages, including evidence of recent range-extensions putatively resulting from a changing climate. However, the potential benefits of the *Sea Slug Census* go far beyond the generation of data to address specific research questions, helping to deliver and reinforce information about sustainability to a broad audience in a time of changing environmental conditions

Posters

New heterobranch records associated with marine surveys undertaken during the Woodside Collection Project (Kimberley) 2009–2014

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The marine environments off the Kimberley coast are being subjected to ever increasing human-induced pressures, with little known of the region's marine biodiversity, and therefore, appropriate conservation approaches. Consequently, the Western Australian Museum with partner agencies undertook to survey the region over a six year period (2009–2014). Molluscs were one of the nine marine taxa targeted during the surveys with the results currently in preparation for publication. Of the seventy five heterobranch species recorded, a number of new records with regional significance are presented here.

How many groups of meiofaunal Cephalaspidea?

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Microscopic and worm-shaped slugs living between the interstices of marine sands have evolved at least 6 times in Heterobranchia and occur in all oceans, especially in tropical and subtropical waters. We here present first molecular data on the internal phylogeny of meiofaunal Cephalaspidea that belong to the families Philinoglossidae and Philinidae *sensu lato*. We found that fragmentary COI, 16S and H3 sequences proved informative in teasing apart diversity, yet so far fail at accurately placing the groups within Cephalaspidea.

Philinoglossidae are split into two geographically distinct groups that are reasonably delimited by current taxonomy, one Indo-Pacific and Eastern Atlantic group (“Philinoglossinae” with at least 4 species) and another group on both sides of the Atlantic and tropical western America (“Plusculinae”, also 4 species). These fully lack a shell or a gizzard and have modified morphology to the constraints of interstitial life.

We also found several morphospecies of meiofaunal “philinids” at various localities in the Indo-Pacific. These are 1-3 millimeter-sized, “typical”, meiofaunal worms yet bear a peculiar posterior shell and asymmetric gizzard plates similar to African benthic *Spiniphiline* Gosliner, 1988. However, a closer relationship to that genus or to equally meiofaunal *Philine exigua* Challis, 1969 from the Solomon Islands still remains questionable according to genetic data. Placement within Philinoidea also remains unclear due to restricted taxon sampling.

Meiofaunal “philinids” may have evolved several times independently, potentially making Cephalaspidea another hotspot of interstitial heterobranchs besides panpulmonate Acochlidia (Acochlidimorpha) and nudipleuran Pseudovermidae. They present an additional field for ongoing study for morphology of Cephalaspidea, including potentially paedomorphic ones.

Another weird secondarily coiled acochlidian slug - 3D-reconstruction of *Helicohedyle* sp. from Lord Howe Island

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Recently, *Helicohedyle dikiki* from Guam was described as new marine mesopsammic lineage of the Acochliidomorpha characterized by a long, coiled visceral sac unique within the highly diverse body plans of sea slugs. Here we present new findings of helicoid-coiled sea slugs discovered in 2011 on Lord Howe Island, Tasman Sea, Australia. The two encountered specimens are externally similar to each other with a highly coiled visceral sac, but differ in the appearance of the body surface and in the length of the cephalic tentacles.

We reconstructed and comparatively analyzed the microanatomy of both specimens using 3D-reconstructions based on histological semi-thin sections. The prepharyngeal central nervous system of both specimens is in concordance with other acochlidians, but lacks eyes and gastro-oesophageal ganglia. Peculiar are the long, coiled visceral nerves surrounded by a muscular sheath. Both specimens differ by the shape of the radula. The circulatory and excretory systems consist of a sac-like kidney and a short nephroduct; a heart or a pericardium could not be detected. Both specimens are simultaneous hermaphrodites with a follicular ovotestis, a tripartite ampulla and three nidamental glands. The male copulatory organs comprise a penis lacking any cuticular stylets. While one specimen is characterized by an internal vas deferens, the other specimen possesses an external sperm groove.

Molecular analyses are needed to evaluate if slight morphological differences within both specimens are due to interspecific or ontogenetic variation. Based on morphological characters, the present specimens are probably congeners of *Helicohedyle dikiki* characterized by a synapomorphic coiled visceral sac, but differing from *H. dikiki* in the peculiar visceral nerves, the shape of the radula, the ampulla and the external sperm groove. The presented findings show that this unique clade of helicoid sea slugs has diversified not only in the Western Pacific but also in the Tasman Sea/Southern Pacific.

Marine slugs off the Caribbean coasts of Panama.

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Species of "opisthobranchs" (Mollusca: Gastropoda: Heterobranchia) recorded up to the present in coastal or deep waters of the Panamanian Caribbean coasts are presented. The list is based on citations published in the literature or on the internet and in photographs of internet species whose identification has been confirmed. Bibliographical references certifying their presence on the Caribbean coasts of Panama are indicated for each species. In these Caribbean waters, a total of 129 opisthobranch species have been recorded: three Acteonoidea, five Pleurobranchida, 59 Nudibranchia (34 Doridina and 25 Cladobranchia), two Umbraculida, 29 Cephalaspidea, nine Aplysiida and 23 Sacoglossa. Of all these species, 27 of them have amphiphillan distribution, 10 are also found in the Panamanian Pacific (*Berthella agassizii* (MacFarland, 1909), *Doriprismatica sedna* (Ev. Marcus & Er. Marcus, 1967), *Tyrinna evelinae* (Er Marcus, 1958)), *Coryphellina marcusorum* (Gosliner & Kuzirian, 1990), *Limenandra nodosa* Haefelfinger & Stamm, 1958, *Tylodina fungina* Gabb, 1865, *Umbraculum umbraculum* (Lightfoot, 1786), *Aplysia juliana* Quoy & Gaimard, 1832, *Dolabrifera dolabrifera* (Rang, 1828) and *Elysia velutinus* Pruvot-Fol, 1947) and four others have not been clarified their specific status (*Trapania* sp., *Polycera* sp.2, *Paradoris* sp. and *Doto* sp.2). Taking into account the coastal extensions of the Panamanian Caribbean coasts (1287.7 Km) compared to the species found in other countries of the same continent such as Costa Rica, Colombia and Venezuela, it can be concluded that they are very rich in biodiversity of "opisthobranchs".

Amphiboreal species: are they real? Lessons from cladobranch genera *Dendronotus* and *Coryphella* s.l. (Nudibranchia)

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Until recently many species of nudibranch molluscs were believed to have a wide distribution range. It was also the case of amphiboreal species, which distribution pattern includes both north Pacific and north Atlantic areas with a breaking-up in the Arctic. However, molecular phylogenetic data often suggest the presence of cryptic species complex with a strong geographic correlation. It caused a tendency to describe Atlantic and Pacific populations as two distinct species even when molecular data were limited or not available. In this study we focused on testing the species identity of eight species from genera *Dendronotus* and *Coryphella sensu lato*. The main goal was to explore the genetic structure using mtDNA data of either amphiboreal species (*Dendronotus frondosus* and *D. kalikal*) or phylogenetically sister species with exclusively Pacific and Atlantic distribution (*Coryphella pseudoverrucosa* and *C. verrucosa*, *C. amabilis* and *C. gracilis*, *Dendronotus dalli* and *D. niveus*). In all cases a comprehensive morphological analysis was also provided to test inter- and intraspecific variations of taxonomically important characters.

Our results indicate a strict correlation between genetic structure and distribution pattern of each species. All studied species are not panmictic, but the level of divergence between Atlantic and Pacific populations/species is different. *Coryphella verrucosa* and *C. pseudoverrucosa* were found to be a single species due to the low level of genetic divergence (only 3 substitution rates). This is also the case of trans-Arctic populations of *Dendronotus frondosus* and *D. kalikal*. The species identity of sister *Microchlamylla gracilis* and *M. amabilis*, *Dendronotus dalli* and *D. niveus* was confirmed.

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Heterobranch sea slugs from the Southern Ocean. A Biodiversity and Biogeographical approach

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The Southern Ocean, which is located between the Antarctic continent and the southern tip of the American, African and Australian continents, is a large ocean with no strictly defined boundaries. Here, to study marine heterobranch sea slugs, we consider the Southern Ocean as referring to all the area south of latitude 41°S. We subdivide it into eight sub-Antarctic areas (South American Region, Falkland Islands, South Georgia Islands, South Orkney Island, Bouvet Island, Crozet and Prince Edward Islands, Kerguelen Islands and Macquarie Islands), four different Antarctic areas (Weddell Sea, West Antarctica, Ross Sea and East Antarctica), the coasts of the island of Tasmania and those of New Zealand. The marine heterobranchs of Tasmania (109 species cited) and New Zealand (222 registered species) are well known as they have been studied by renowned specialists. The heterobranch faunas of the Antarctic and sub-Antarctic regions have been the subject of several studies, however there are still many gaps in knowledge across different areas of both regions. 68 different species of marine heterobranchs have been recorded so far in strictly Antarctic waters (West Antarctica 37 species; Weddell Sea 36 species; Ross Sea 40 species; East Antarctica 30 species) while in the different subantarctic regions considered here 93 species have been cited (36 species in South Georgia, 16 species in South Orkneys, 10 species in Bouvet, 8 species in Prince Edwards and Crozet Islands, 11 species in Kerguelen, 2 species in Macquarie, 20 species in Falkland and 51 species in South America coasts). Using all available literature and unpublished records of the authors, a presence and absence data table was created for each of the Antarctic and Sub-Antarctic zones, New Zealand and Tasmania islands. Subsequently, a Sørensen-Motyka matrix was constructed and used to create Multi Dimensional Scale – Principal Component Analysis plots to find cluster groups of different areas.

Chemical defence strategies of nudibranchs in relation to visual signals

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Nudibranch chemical defences are often associated with their visual signals: many species are aposematic and possess bright colours to warn predators of their toxic defences. In contrast, the few studies on less conspicuous species suggest that camouflaged nudibranchs are not chemically defended. Nudibranchs commonly sequester defensive metabolites from their dietary sponges and store these compounds in different ways. Hence, this study investigates the differences in chemical defence strategies of sponge-feeding nudibranchs in relation to their visual signals, namely the highly conspicuous *Chromodoris*, the moderately conspicuous *Glossodoris* and the camouflaged *Sebadoris* genera. Through spectroscopic analyses, compounds in the rim, mantle and viscera of each species and their dietary sponges were identified and quantified. The rim and mantle of *Chromodoris kuiteri* contained only the toxic latrunculin A while the viscera contained a variety of dietary metabolites, suggesting that this species fed on multiple different sponges while selectively sequestering latrunculin A. *Glossodoris vespa* and *G. rufomarginata* were shown to biotransform their dietary metabolites. An anti-feedant assay using a dietary sponge extract of *G. vespa* suggested that these biotransformations enhanced a compound's potency for defensive purposes. This study provides further evidence that *Glossodoris* nudibranchs are capable of enzymatically oxidizing their metabolites, and also suggests other possible biotransformations. In contrast, the inconspicuous *Sebadoris fragilis* and its dietary sponges did not possess terpene chemical defences. This study expands on previous research on the chemical defences and feeding biology of *Chromodoris* and *Glossodoris* nudibranchs and represents the first chemical investigation of the cryptic *S. fragilis*, by offering a detailed characterization of the chemical profiles of these nudibranchs and their dietary sponges. Overall, this study highlights the range of mechanisms that nudibranchs use for chemical defences and provides intriguing insights into the chemistry and ecology of visual signals.

An illustrated inventory of the sea slugs of New South Wales, Australia (Gastropoda: Heterobranchia)

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Although the Indo-Pacific is the global centre of diversity for the heterobranch sea slugs, their distribution remains, in many places, largely unknown. On the Australian east coast, their diversity decreases from approximately 1,000 species in the northern Great Barrier Reef to less than 400 in Bass Strait. Whilst occurrence records for some of the more populated sections of the coast are well known, data are patchy for more remote areas. Many species have very short life-cycles, so they can respond rapidly to changes in environmental conditions. The New South Wales coast is a recognised climate change hot-spot and southward shifts in distribution have already been documented for several species. However, thorough documentation of present distributions is an essential pre-requisite for identifying further range extensions. Whilst distribution data are available in the public realm, much is also held privately as photographic collections, diaries and logs. This paper consolidates the current occurrence data from both private and public sources as part of a broader study of sea slug distribution in south-eastern Australia and provides a complete inventory by region. A total of 382 species, 155 genera, and 54 families is reported from the mainland coast of New South Wales.

Resolving the phylogeny of Chromodorididae using exon capture

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The sea slug family Chromodorididae Bergh, 1891 is one of the largest and most colourful, and contains many hundreds of species. The diversity of animals within this group has been under concerted attention from systematists for nearly the last 50 years. With the addition of technologies such as Scanning Electron Microscopy to examine radular characters, and more recently DNA data, new genera have been raised, and others synonymized. Although still in flux, the World Register of Marine Species recognises 17 genera. Mitochondrial phylogenies have greatly advanced our understanding of generic boundaries, and biogeographic patterns. But to robustly resolve the relationships among genera requires the addition of large amounts of data. We are employing a transcriptome-based exon capture approach to address the phylogeny of Chromodorididae. We have sequenced 13 additional transcriptomes of chromodorid genera and outgroups, and are designing capture baits for the approximately 3000 loci identified in previous work on *Chromodoris*. These data will be subjected to a variety of bioinformatic and phylogenetic analyses, including a summary coalescent analysis. A robust understanding of the phylogenetic relationships among Chromodorididae genera will enable many comparative tests of trait-based evolutionary patterns, and leverage its full potential as a model system.