



MSA

THE
MALACOLOGICAL
SOCIETY OF
AUSTRALASIA



Molluscs 2018

Conference program and abstracts

2-5 December 2018

Museum of New Zealand Te Papa Tongarewa

Wellington, New Zealand

www.malsocaus.org



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Program and Abstracts for the 2018 meeting of the Malacological Society of Australasia (2nd to 5th December, Wellington, New Zealand)

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Malacological Society of Australasia, Triennial Conference

Table of contents

The Conference Venue	3
Venue floorplan	3
General Information.....	4
Molluscs 2018 Organising Committee.....	6
Our Sponsors.....	6
MSA Annual General Meeting and Election of Office Bearers	7
President's Welcome.....	7
Keynote Speakers.....	9
Conference Timetable	11
Posters	11
Scientific Program for Molluscs 2018	12
Abstract Index	17

The Conference Venue

Museum of New Zealand Te Papa Tongarewa
55 Cable Street, Wellington

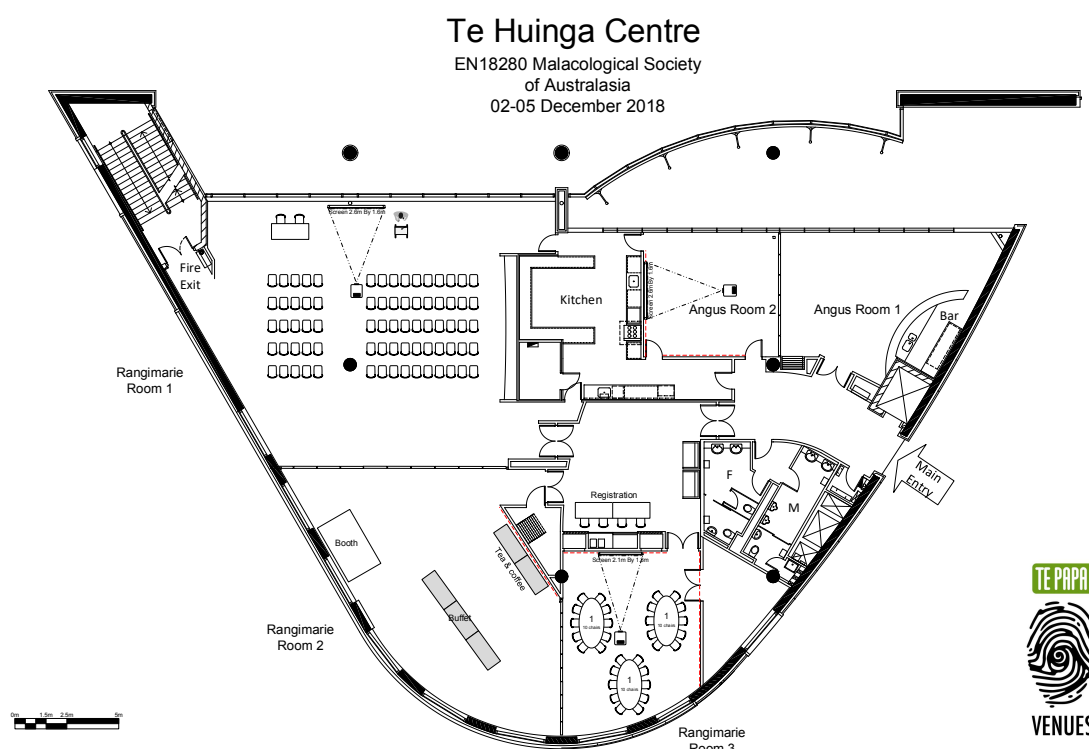
Coordinates 41.290589°S 174.782154°E

The Museum of New Zealand Te Papa Tongarewa is New Zealand's National Museum, located in the capital, Wellington. Known locally as Te Papa, or "Our Place", the museum opened in 1998 following the merging of the National Museum and the National Art Gallery. More than 1.5 million people visit every year.

Te Papa Tongarewa translates to "container of treasures". Te Papa's philosophy emphasises the living face behind its cultural treasures, many of which retain deep ancestral links to the indigenous Māori people. The Museum recognises the partnership that was created by the signing of the Treaty of Waitangi, te Tiriti o Waitangi, in 1840.

The five main collections areas are Natural History, Arts, History, Taonga Māori and Pacific Cultures.

Venue floorplan



General Information

The conference hosts and conference manager would like to welcome you to **Molluscs 2018 in Wellington**.

Below is essential information for helping make your stay at the conference more enjoyable. If you have any questions or require assistance, please do not hesitate to approach the conference registration/help desk in the conference area lobby.

Molluscs 2018 is a three-day program, commencing on the evening before presentations with a Welcome Function, Sunday 2nd December from 5pm. The program each day commences in the Rangimarie Rooms at Te Papa that are part of the Te Huinga Centre on Level 3.

For full details, please see the detailed timetable commencing on page 15.

Accommodation

Accommodation bookings have been handled direct by delegates with their own selected accommodation.

Check with your accommodation if luggage storage is required on Wednesday 5th or Thursday 6th December prior to your departure.

Conference Registration and Help Desk

The Conference Registration and Help Desk will be located in Te Papa outside the Rangimarie Rooms and will be open:

- Sunday 2nd December From 4:15pm adjacent to Icon at Te Papa
- Monday 3rd December 8am to 9am then all meal breaks
- Tuesday 4th December 8am to 9am then meal breaks
- Wednesday 5th December 8am to 9am then meal breaks

The conference desk is staffed by Conference Manager Julie Burton from Southern Cross Conference and Event Management Pty Ltd

Messages

Messages can be left for delegates during the conference by ringing the conference secretariat.

- Julie Burton Mobile + 61 (0)408 66 4053

Delegate Name Tags

The following key will be used for conference name badges:

White – Conference Delegate

Green – First Timer at Conference

Yellow – Student Helpers

Conference Organisers can be identified by their blue ribbons.

Conference Keynote Speakers will wear a red ribbon.

Conference Rooms

All conference sessions will be held in the Rangimarie Rooms at Te Papa on Level 3.

Rangimarie Room 1 is our plenary and catering space. Rangimarie Room 3 is our breakout conference session room.

Social Functions (included in full registrations)

- Welcome Reception Sunday 2nd December 5pm to 6pm at Icon, Te Papa
- MSA Conference Dinner Tuesday 4th December at Foxglove Bar and Kitchen, Queens Wharf from 6pm.

Entry will be with your delegate name tag - please ensure you wear it at all times during the conference. Additional Tickets for all functions can be purchased from the Registration Desk.

Dietary requirements can be catered for but please notify us in advance if you have not already done so via the conference registration process.

Welcome Function

The Welcome Function is a cocktail function with canapés and drinks to be held at Icon on level 2 at Te Papa from 5pm to 6pm.

Morning Teas, Lunches and Afternoon Teas

All morning teas, lunches and afternoon teas will be served in Rangimarie Room 2.

Conference Dinner

The Conference Dinner will commence with drinks on the deck of Foxglove Bar and Kitchen from 6pm. The function concludes at 10pm. Admission is included with all full registrations.



An optional, post-conference workshop will be hosted on Thursday 6th December.

Non-Model Genomics Workshop

A one day examination of current high-throughput DNA sequencing methods for use in an ecological/population biology context, and focused on molluscs.

Further information will be provided to those that have registered for the workshop.

This workshop will be at an additional cost of \$200 AUD.

See the registration desk for any last-minute registrations as numbers are limited.

Molluscs 2018 Organising Committee

Organising Committee

Simon Hills (Chair), Massey University

Carmel McDougall, Griffith University

Hamish Spencer, University of Otago

Bruce Marshall, Te Papa

Kerry Walton, University of Otago/Te Papa

Nicole Phillips, Victoria University of Wellington

Conference Secretariat

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Our Sponsors

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MSA Annual General Meeting and Election of Office Bearers

The MSA Annual General Meeting is on at 12:50 pm on Wednesday, December 5th.

The new Council will be nominated at this meeting, and voting will take place on changes to the MSA Constitution. All delegates are invited and encouraged to attend.

Malacological Society of Australasia, National Council 2018

PRESIDENT: Lisa Kirkendale
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COUNCIL MEMBERS:

Kirsten Benkendorff (NSW), Bob Creese (NSW), Simon Grove (TAS), Peter Hunt (SA), Wayne O'Connor (NSW), David Rudd (NSW), Steve Smith (NSW)

President's Welcome

Welcome to Molluscs 2018, the triennial conference of the Malacological Society of Australasia! We are very honoured to be holding our conference at the Museum of New Zealand Te Papa Tongarewa in Wellington, the nation's natural and cultural history 'container of treasures', at such a critical time for biodiversity research.

The Mollusca are a special group- they are well-known, diverse and widespread with a solid fossil record and heaps of novelty that make them an attractive study system for a range of ecological and evolutionary questions. From widespread tropical marine members to highly endemic faunas in our temperate (shout out to Wellington and New Zealand!) and polar regions, you can't help but bump into a mollusc doing something interesting somewhere.

Researchers have taken notice. Since our last triennial at the end of 2015, molluscs have been the subject of over 10,000 publications according to Google. The first few titles alone '*Miocene fossil sediments in Kachchh*', '*From molluscs to materials*' and '*Species identification of bivalve molluscs by pyrosequencing*' are telling in the diversity of questions made possible when you utilize molluscan study systems. The range of applied research on molluscs is vast and members of our favourite



phylum provision us with new materials, food and drugs, coastal erosion control and insight into climate change and invasions. Our range of symposia attempts to cover this span and I look forward to all of the talks.

I'm very pleased to welcome ~45 new attendees to the conference this year, a whopping 70% of our total attendance. These newbies not only highlight the continuing attraction of molluscs as a research topic, but also provide an opportunity to breathe fresh ideas into the MSA. I encourage our new members to interact widely over the course of the conference, but also to attend the AGM to learn more about the MSA. We welcome innovative approaches to invigorate the Society and keep molluscs in the spotlight, for example, through novel and targeted social media endeavors. We have wide representation at MSA 2018, with attendees from eight countries, but also a great local showing, with about half coming from our host country.

We are lucky to be a well-resourced society and this has certainly given us the courage to jump the pond for a New Zealand adventure. The ability to award seven MSA travel grants to students for attendance at MSA 2018 is a result of our healthy membership base. This has definitely helped to ensure students from far away have been able to make the conference, so we thank our many members for their continuing support. Longstanding society members are the pillars of the MSA and provide critical advice, guidance and perspective. At the other end of the spectrum are some of our newest members, many of whom are students, and we welcome you to the MSA also. An important emerging group is the molluscan enthusiasts and citizen scientists that represent a growing community that we embrace. We encourage all of you to mingle widely so that you come away from MSA 2018 with research ideas, career advice and hopefully, a new collaboration or two.

I'd like to thank Simon Hills and Carmel McDougall, as well as the rest of the local organizing committee, and Julie Burton, our event planner, for putting together a great conference and scientific program. It is a massive amount of work that occurs out of sight, out of mind, so please thank the organizers of Molluscs 2018 when you get a chance. I would also like to thank the MSA Council members over the past three years who have together ensured a range of voices guide our group. Thank you for the amazing level of commitment and loyalty to the organisation and its members.

Enjoy your time in Wellington and at Molluscs 2018 everyone!

Sincerely,



Lisa Kirkendale, MSA President

Dr. Lisa Kirkendale
Curator (Mollusca)
Department of Aquatic Zoology



Keynote Speakers

The keynote speakers at Molluscs 2018 are a wonderful mix of the finest researchers in malacological science. We value their input to our conference and thank each of them for their time and commitment to attend. The listing below is by presentation order at Molluscs 2018.

Dr. Phil Ross, University of Waikato



Phil Ross is a marine ecologist at the University of Waikato's Coastal Marine Field Station in Tauranga. His research is focused on past and present human impacts on the environment and the notion that knowledge of human-environment interactions will guide the sustainable use of natural resources. His recent research has had two key strands – the impacts and management of the Rena shipwreck, and the history, ecology and management of toheroa, a threatened surf clam. In his toheroa research he combines mātauranga Māori (Māori knowledge) with ecology, archaeology, history, anthropology and molecular ecology to gain a better understanding of factors impeding the recovery of toheroa, the early-human influences on toheroa distribution and the extent to which early-Maori manipulated their marine environment. Phil's research challenges the paradigm that species distributions are solely a consequence of natural processes and recent human activity, and provides important insights into the ecological impact of humans.

Dr. Serean Adams, Cawthron Institute

Serean Adams has been actively involved in mollusc research for almost 20 years specialising in hatchery technologies including cryopreservation and ploidy manipulation.

She currently leads the Aquaculture Group at the Cawthron Institute and is the Science Leader for Cawthron's Shellfish Aquaculture Research Platform.

Cawthron's aquaculture research spans across almost all areas of aquaculture from selective breeding and hatchery production through to seafood safety and value add.



Assoc. Prof. Amy Moran, University of Hawaii



Amy Moran has been working with molluscs for over 25 years, starting off with her PhD work at the University of Oregon on the development and life history ecology of littorinids and muricids in the eastern Pacific. She has also worked on the evolution, life history, and diversification of tropical arcid bivalves, and the physiology of larval development in oysters. Her recent molluscan research at the University of Hawai'i at Mānoa has focused on the physiology and functional morphology of gastropod embryos and egg masses in temperate and polar regions, with the particular goal of anticipating how early life history stages are likely to be affected by ocean warming.

Dr. Satoshi Chiba, Tohoku University



Since 1993, Satoshi Chiba has used molluscs as model systems for the study of speciation processes, evolution of behavior, genetic variation and phenotypic diversity, biogeography, and extinction processes. Particularly, land snails in Japan and surrounding islands are excellent materials to understand evolutionary processes because of their high phenotypic and genetic diversity. His current projects focus on conservation of ecosystems and endangered species of molluscs.

Prof. Robert Cowie, University of Hawaii

Robert Cowie has worked with snails for over 40 years, initially based in England where he obtained his PhD and undertook postdoctoral work on the ecology, genetics and behaviour of European Helicidae. He moved to Hawaii in 1990 to take charge of the Bishop Museum's spectacular Pacific malacological collections, subsequently moving to the University of Hawaii in Honolulu. His recent research has been on invasive snails in the Asia-Pacific region, with a focus on South American Ampullariidae, and on assessing rates of mollusc extinction globally in the context of the so-called "Sixth Extinction".



Prof. Pauline Ross, University of Sydney



Pauline Ross is a Professor of Biology, Teaching Principal for Life, Earth and Environmental Science (LEES), Associate Dean (Education) in the School of Life and Environmental Science, Faculty of Science at the University of Sydney and a National Teaching Fellow of the Office for Learning and Teaching, investigating the changing nature of the academic role. Pauline leads the internationally recognised research group at the University of Sydney investigating the impact of climate change on molluscs and molluscan habitat. Her team funded nationally by the Australian Research Council and internationally by the German Academic Exchange Service, is developing oysters with resilience to climate change to sustain an industry that generates more than one billion dollars per year in sales and employs thousands of Australians.

Conference Timetable

The full conference program from Monday 2nd to Wednesday 5th December is outlined in the following pages.

Abstracts are in alphabetical order by the last name of the first author, with the presenting author underlined.

Information Disclaimer

The speakers, topics and times are correct at the time of publishing. In the event of unforeseen circumstances, the organisers reserve the right to alter or delete items from the conference program.

PRESENTER INFORMATION

Speaker's preparation will be in the room in which the presentation is scheduled. You are encouraged to load your presentation well in advance of your talk to enable you to check your presentation well beforehand. Please do not leave this until the last moment.

Speaker Assistance will be available from 8am each day and during morning tea breaks. We encourage you to take advantage of this and have your presentation uploaded at least the session before your presentation.

Posters

Poster authors will be beside their posters during an extended morning tea break on Tuesday December 4th to discuss their work and answer questions.

	Presenter	Author(s)	Title of Poster
Poster 1	Carmel McDougall , (Griffith University)	Carmel McDougall, Bernard Degnan	Ependymins in molluscs – expansions of a multifunctional protein family
Poster 2	Amber McEwan (Victoria University of Wellington)	Amber McEwan, Aaria Dobson-Waitere, Jeff Shima	Comparing indigenous and western methods of kākahi translocation: implications for ecological restoration
Poster 3	Kao Akiyama (Tohoku University, Japan)	Kao Akiyama, Mary Morgan-Richards, Steve Trewick	The effect of environment to species composition and phylogenetic study of micro snails in New Zealand
Poster 4	Phuong-Thao Ho (Ewha Womans University)	Phuong-Thao Ho, Yong-Jin Won	Adaptive evolution of mud-tidal gastropod (genus Batillaria) to the salt stress

Poster 5	Rodrigo Salvador (Museum of New Zealand Te Papa Tongarewa)	Rodrigo Salvador	The role of video game molluscs in science communication and animal conservation
Poster 6	Kara Layton (University of Western Australia)	Kara Layton, Greg Rouse, Nerida Wilson	Exploring an undocumented diversification of endoparasitic gastropods in Antarctica
Poster 7	Natalí Delorme (Cawthron Institute)	Natalí Delorme, Norman Ragg, Zoë Hilton, Samantha Gale, Paul South, Leo Zamora, Thomas Wheeler, David Burritt	Development of stress and health biomarkers in the Green-lipped mussel <i>Perna canaliculus</i>
Poster 8	Simon Hills (Massey University)	Felix Vaux, Steven Trewick, James Crampton, Bruce Marshall, Alan Beu, Simon Hills, Mary Morgan-Richards	Identifying evolutionary lineages of marine snails
Poster 9	Mary Morgan-Richards (Massey University)	Michael Gemmell, Simon Hills, James Crampton, Alan Beu, Steve Trewick, Mary Morgan-Richards	Do New Zealand Olive Shells (<i>Amalda</i> spp.) support Punctuated Equilibria?

Scientific Program for Molluscs 2018

Program - Sunday 2nd December

16:15	Registration opens (Icon room)
17:00-18:00	Welcome Function – Te Papa (Icon room)

Program - Monday 3rd December

8:30-9:00	Welcome introduction by Lisa Kirkendale and Simon Hills (Rangimarie 1)	
9:00-9:45	Keynote presentation – Phil Ross (University of Waikato) Ancient aquaculture and the mystery of the disappearing surf clams	
9:45-10:30	Keynote presentation – Serean Adams (Cawthron Institute) Growing, enabling and securing New Zealand's mollusc aquaculture industry - a research perspective	
10:30-11:00	Morning Tea (Rangimarie 2)	
	Symposium: Systematics, taxonomy and biogeography (Rangimarie 1) Chair: Hamish Spencer	
11:00-11:20	Lisa Kirkendale (Western Australian Museum) The world in a shell: Aspects of cockle taxonomy, biogeography, phylogenetics and evolution reviewed	
11:20-11:40	Kerry Walton (University of Otago/Te Papa) Biodiversity, biogeography and vulnerability of hydrothermal vents: a case study using bathymodioline mussels	
11:40-12:00	Martyn Kennedy (University of Otago) The speed of semi-slug formation: Limacization of <i>Schizoglossa</i> (Mollusca: Pulmonata: Rhytididae)	
12:00-12:20	Isabel Hyman (Australian Museum) Widespread convergence in body form in Australian Helicarionidae (Pulmonata, Stylommatophora)	
12:20-13:30	Lunch (Rangimarie 2)	
	AFTERNOON PARALLEL SESSIONS	
	Symposium: Systematics, taxonomy and biogeography (Rangimarie 1) Chair: Kerry Walton	Symposium: Aquaculture, fisheries and human uses of molluscs (Rangimarie 3) Chair: Andrea Alfaro
13:30-13:50	Andy Davis (University of Wollongong) Biogeographic conundrum: why so many freshwater gastropod taxa in Fiji compared to Australia?	Sara Masoomi Dezfooli (Auckland University of Technology) Encapsulated feed for increased growth of farmed paua and reduced feed wastage
13:50-14:10	Olga Aksenova (Northern Arctic Federal University) Diversity, molecular taxonomy, biogeography and ecology of the radicine pond snails (Gastropoda: Lymnaeidae) in the Palearctic	Andrea Alfaro (Auckland University of Technology) Novel health assessment tools for shellfish aquaculture
14:10-14:30	Kirsten Donald (University of Otago) Using both barcoding and next generation sequencing to elucidate the complex New Zealand Maurea (Mollusca: Gastropoda: Calliostomatidae: <i>Calliostoma</i>) phylogeny	Paul South (Cawthron Institute) The retention of juvenile <i>Perna canaliculus</i> in aquaculture
14:30-14:50	Katherine Lockton (University of Otago) Phylogeography of <i>Lasaea hinemoa</i>	Leonardo Zamora (Cawthron Institute) Green-lipped mussel <i>Perna canaliculus</i> ' ability to cope with low seawater temperatures: Implications for survival, aerial exposure and heart rate
14:50-15:10	Ruthela Payawal (Polytechnic University of the Philippines)	Matt Miller (Cawthron Institute)

	Molecular identification of Conidae (Gastropoda) at Verde island, Batangas, Philippines using mitochondrial gene markers cytochrome oxidase 1 and 16s rRNA	Musseling-up program: Greenshell mussel and role in inflammation management and joint health
15:10-15:40	Afternoon Tea (Rangimarie 2)	
	Symposium: Systematics, taxonomy and biogeography (Rangimarie 1) Chair: Kara Layton	Symposium: Community engagement and citizen science (Rangimarie 3) Chair: Kirsten Benkendorff
15:40-16:00	Daniel Ramos Gonzalez (University of Nottingham) Evolutionary phenotype variation of <i>Cepaea nemoralis</i> in the Pyrenees	Caine Taiapa (Manaaki Te Awanui) Activating Kaitiakitanga (environmental custodianship) through pipi relocation “what are we enhancing”.
16:00-16:20	Priscila Salloum (The University of Auckland) Understanding local adaptation of <i>Onithochiton neglectus</i> (Polyplacophora:Chitonidae) across an environmental gradient based on genetic, genomic and morphological data.	Rodrigo Salvador (Museum of New Zealand Te Papa Tongarewa) The creepy, the slimy and the ugly: how scientists communicate science with invertebrates
16:20-16:40	Mathieu Quenu (Massey University) Snail shell shape and size suggests hybridisation of two species: a comparison of supervised and unsupervised learning algorithms with geometric morphometric data for species identification	Yuta Morii (Massey University) Activity of invasive slug <i>Limax maximus</i> in relation to climate conditions based on citizen's observations
16:40-17:00	Hamish Spencer (University of Otago) Contrasting phylogeography of two limpet genera in the Southern Ocean	

Program - Tuesday 4th December

8:55-9:00	Announcements (Rangimarie 1)
9:00-9:45	Keynote presentation - Amy Moran (University of Hawaii) Physiological effects of temperature and oxygen availability on molluscan development: lessons from the Antarctic
9:45-10:30	Keynote presentation – Satoshi Chiba (Tohoku University) Lessons from the ongoing mass extinction of land snails in Ogasawara: direct and indirect effects of multiple invasive species
10:30-11:40	Morning Tea and Poster Session (Rangimarie 2)
	Symposium: Paleontology/ Genomics and molecular biology (Rangimarie 1) Chair: Simon Hills
11:40-12:00	Tom Womack (Victoria University of Wellington) Resolving the Cenozoic mollusc fossil record of New Zealand: unravelling macroevolution

12:00-12.20	Frank Koehler (Australian Museum) Land snails (1) : dinosaurs (0) – phylogenomics resolves Late Mesozoic diversification of helicoid land snails		
12:20-13.30	Lunch (Rangimarie 2) Molluscan Research Editor’s meeting – (Rangimarie 3)		
	AFTERNOON PARALLEL SESSIONS		
	Symposium: Palaeontology (Rangimarie 1) Chair: Lisa Kirkendale	Symposium: Genomics and molecular biology (Rangimarie 3) Chair: Scott Cummins	
13:30-13:50	Alan Beu (GNS Science) New Zealand Cenozoic fossil Turbinidae: Indo-Pacific elements in southern New Zealand Oligocene–Miocene rocks	Carmel McDougall (Griffith University) A genomic approach to developing tropical oyster aquaculture	
13:50-14:10	Mary Morgan-Richards (Massey University) Morphological Stasis	Kara Layton (The University of Western Australia) Using exon capture to tease apart recently radiated mimetic sea slugs	
14:10-14:30	Rodrigo Salvador (Museum of New Zealand Te Papa Tongarewa) The importance of terrestrial and freshwater molluscs for palaeoecological studies: examples from the German Miocene	Felicity Masters (University Sunshine Coast) Stress in pearl oysters: Transcriptional investigation of responses to extreme temperature and salinity.	
14:30-14:50	Bryce Peebles (University of Otago) Resolving a quandary: The preservation of chiton valves	Scott Cummins (University Sunshine Coast) How investigation into secreted snail proteins can have massive health and economic implications	
14:50-15:10	Afternoon Tea (Rangimarie 2)		
15:10:17:30	Mini-Workshop: Major challenges in molluscan aquaculture (Rangimarie 1) Chair: Carmel McDougall	Mini-Workshop: Photography of molluscs and collection management (Rangimarie 3) Chair: Lisa Kirkendale, Platon Vafiadis and Kara Layton	Field Trip: Victoria University of Wellington marine lab and Taputeranga Marine Reserve
18:00	Conference dinner (Foxglove)		

Program - Wednesday 5th November

8:55-9:00	Announcements (Rangimarie 1)
9:00-9:45	Keynote presentation - Robert Cowie (University of Hawaii) Denying the Sixth Extinction: a counterpoint
9:45-10:30	Keynote presentation - Pauline Ross (University of Sydney) Resilience of Molluscs to a Changing Ocean

10:30-11:00	Morning Tea (Rangimarie 2)	
	PARALLEL SESSIONS	
	Symposium: Ecology, conservation and environmental restoration (Rangimarie 1) Chair: Don Colgan	Symposium: Climate Change (Rangimarie 3) Chair: Pauline Ross
11:00-11:20	Bob Creese (Southern Cross University) Brooding in Australasian chitons: are there any patterns?	Abby Smith (University of Otago) Skeletal carbonate mineralogy of abalone, especially <i>Haliotis iris</i> Gmelin, 1791.
11:20-11:40	Regan Fairlie (University of Waikato) The environmental history of Tauranga Moana	Sherry Sayco (University of the Philippines Diliman) Behavioural response of juvenile <i>Tridacna gigas</i> exposed to low salinity or elevated seawater temperature
11:40-12:00	Kath Walker (Department of Conservation) Diversity within and conservation of New Zealand's large land snail <i>Powelliphanta</i>	Le Ma (Murdoch University) Tolerance to acute and gradual increases in salinity in a freshwater mussel
12:00-12:20	Alison Duncan (Victoria University of Wellington) Gastropod Communities of Seagrass Meadows in a central New Zealand estuary	
12:20-13:50	Lunch (Rangimarie 2) MSA AGM (Rangimarie 1)	
	Symposium: Ecology, conservation and environmental restoration (Rangimarie 1) Chair: Nicole Phillips	Symposium: Biochemistry and Physiology (Rangimarie 3) Chair: Carmel McDougall
13:50-14:10	Fred Wells (Curtin University) Growth rates of potamidid snails in mangroves in northern Australia	Kirsten Benkendorff (Southern Cross University) Risks associated with neonicotinid pesticide exposure in Sydney Rock Oyster
14:10-14:30	Matthew Bennion (University of Waikato) Gas bubble disease and rickettsiosis in New Zealand surf clams	Kate Ballard (University of the Sunshine Coast) Molecular components of the trail mucus in the common garden snail, <i>Cornu aspersum</i>
14:30-14:50	Corey Whisson (Western Australian Museum/Murdoch University) Un-earting the true diversity of the Australian land snail genus <i>Bothriembryon</i> (Gastropoda, Orthalicoidae)	
14:50-15:20	Afternoon Tea (Rangimarie 2)	
15:20-15:40	Closing session: student prizes and concluding address by the MSA president (Rangimarie 1)	

Abstract Index

Oral presentations

Growing, enabling and securing New Zealand's mollusc aquaculture industry – a research perspective

Adams, Serean L.¹ 21

Diversity, molecular taxonomy, biogeography and ecology of the radicine pond snails (Gastropoda: Lymnaeidae) in the Palearctic

Aksenova, Olga^{1,2}, Ivan Bolotov^{1,2}, Maxim Vinarski³ and Alexander Kondakov^{1,2} 22

Novel health assessment tools for shellfish aquaculture

Alfaro, Andrea¹, Thao Van Nguyen¹ and Tim Young¹ 23

Molecular components of the trail mucus in the common garden snail, *Cornu aspersum*

Ballard, Kaylene¹ 24

Risks associated with neonicotinid pesticide exposure in Sydney rock oysters

Endurance, Ewere¹, Kirsten Benkendorff¹ and Amanda Reichelt-Brushett¹ 25

Gas bubble disease and rickettsiosis in New Zealand surf clams

Bennion, Matthew¹, Henry Lane², Anjali Pande², Ian McDonald³ and Phil Ross¹ 26

New Zealand Cenozoic fossil Turbinidae: Indo-Pacific elements in southern New Zealand

Oligocene–Miocene rocks

Beu, Alan¹ 27

Lessons from the ongoing mass extinction of land snails in Ogasawara: direct and indirect effects of multiple invasive species

Chiba, Satoshi^{1,2} 28

Denying the Sixth Extinction: a counterpoint

Cowie, Robert H.¹, Benoît Fontaine² and Philippe Bouchet² 29

Brooding in Australasian chitons: are there any patterns?

Creese, Bob¹ 30

How investigation into secreted snail proteins can have massive health and economic implications

Cummins, Scott F.¹, Conor E Fogarty¹, Donald P McManus² and Tianfang Wang¹ 31

Biogeographic conundrum: why so many freshwater gastropod taxa in Fiji compared to Australia?

Davis, Andy¹ and Winston Ponder² 32

Using both barcoding and next generation sequencing to elucidate the complex New Zealand

Maurea (Mollusca: Gastropoda: Calliostomatidae: *Calliostoma*) phylogeny

Donald, Kirsten¹, Ludovic Dutoit¹ and Hamish Spencer¹ 33

Gastropod communities of seagrass meadows in a central New Zealand estuary

Duncan, Alison¹ and Nicole Phillips¹ 34

The environmental history of Tauranga Moana

Fairlie, Regan^{1,2}, Phil Ross¹ and Caine Taiapa² 35

Widespread convergence in body form in Australian Helicarionidae (Pulmonata, Stylommatophora)	
Hyman, Isabel ¹ and Frank Köhler ¹	36
The speed of semi-slug formation: limacization of <i>Schizoglossa</i> (Mollusca: Pulmonata: Rhytididae)	
Kennedy, Martyn ¹ , James Cotton ² , Fred Brook ³ and Hamish Spencer ¹	37
The world in a shell: aspects of cockle taxonomy, biogeography, phylogenetics and evolution reviewed	
Kirkendale, Lisa ¹ , Jingchun Li ^{2,3,4} and Jan Johan ter Poorten ⁵	38
Land snails (1) : dinosaurs (0) – phylogenomics resolves Late Mesozoic diversification of helicoid land snails	
Köhler, Frank ¹ , Makiri Sei ² , Gary Rosenberg ³ and Adnan Moussalli ⁴	39
Using exon capture to tease apart recently radiated mimetic sea slugs	
Layton, Kara KS ^{1,2} , Jose I. Carvajal ² and Nerida G. Wilson ^{1,2}	40
Phylogeography of <i>Lasaea hinemoa</i>	
Lockton, Katherine ¹ and Hamish Spencer ¹	41
Tolerance to acute and gradual increases in salinity in a freshwater mussel	
Ma, Le ¹ , Alan Lymbery ¹ , Stephen Beatty ¹ and David Morgan ¹	42
Encapsulated feed for increased growth of farmed paua and reduced feed wastage	
Masoomi Dezfooli, Seyedehsara ¹ , Noemi Gutierrez-Maddox ² , Andrea Alfaro ² and Ali Seyfoddin ^{1,3}	43
Stress in pearl oysters: Transcriptional investigation of responses to extreme temperature and salinity	
Masters, Felicity ¹ , Scott Cummins ¹ , David Mills ¹ and Abigail Elizur ¹	44
A genomic approach to developing tropical oyster aquaculture	
McDougall, Carmel ^{1,2}	45
Musseling-up program: Greenshell mussel and role in inflammation management and joint health	
Miller, Matthew R. ¹ , Marlena C. Kruger ² , Fran M. Wolber ² , Parkpoom Siriarchavatana ² , Saima Rizwan ² and Hong Tian ³	46
Physiological effects of temperature and oxygen availability on molluscan development: lessons from the Antarctic	
Moran, Amy ¹ , Peter Marko ¹ , Jerry Harasewych ² and H. Arthur Woods ³	47
Morphological Stasis	
Morgan-Richards, Mary ¹ , James Crampton ^{2,3} , Alan Beu ² , Ian Henderson ¹ , Felix Vaux ¹ , Michael R Gemmell ¹ , Elizabeth Daly ^{1,4} and Steve Trewick ¹	48
Activity of invasive slug <i>Limax maximus</i> in relation to climate conditions based on citizen's observations	
Morii, Yuta ^{1,2} , Yusaku Ohkubo ³ and Sanae Watanabe ⁴	49
Molecular identification of Conidae (Gastropoda) at Verde Island, Batangas, Philippines using mitochondrial gene markers cytochrome oxidase 1 and 16s rRNA	
Payawal, Ruthela P. ¹ and Khristina J. Cruz	50
Resolving a quandary: the preservation of chiton valves	

Peebles, Bryce ¹ , Abigail Smith ¹ and Hamish Spencer ²	51
Snail shell shape and size suggests hybridisation of two species: a comparison of supervised and unsupervised learning algorithms with geometric morphometric data for species identification	
Quenu, Mathieu ¹ , Mary Morgan-Richards ¹ and Steve Trewick ¹	52
Evolutionary phenotype variation of <i>Cepaea nemoralis</i> in the Pyrenees	
Ramos Gonzalez, Daniel ¹ and Angus Davison ¹	53
Resilience of molluscs to a changing ocean	
Ross, Pauline M ¹	54
Ancient aquaculture and the mystery of the disappearing surf clams	
Ross, Phil ¹	55
Understanding local adaptation of <i>Onithochiton neglectus</i> (Polyplacophora:Chitonidae) across an environmental gradient based on genetic, genomic and morphological data	
Salloum, Priscila ¹ , Anna Santure ¹ and Shane Lavery ¹	56
The creepy, the slimy and the ugly: how scientists communicate science with invertebrates	
Salvador, Rodrigo B. ¹ , Julia Kasper ¹ , Daniel C. Cavallari ² , João V. Tomotani ³ and Barbara M. Tomotani ¹	57
The importance of terrestrial and freshwater molluscs for palaeoecological studies: examples from the German Miocene	
Salvador, Rodrigo B. ¹	58
Behavioural response of juvenile <i>Tridacna gigas</i> exposed to low salinity or elevated seawater temperature	
Sayco, Sherry Lyn ¹ , Odette Enricuso ¹ , Patrick C. Cabaitan ¹ and Cecilia Conaco ¹	59
Skeletal carbonate mineralogy of abalone, especially <i>Haliotis iris</i> Gmelin, 1791.	
Smith, Abigail M. ¹ , Cummings, Vonda J. ² and Peebles, Bryce A. ¹	60
The retention of juvenile <i>Perna canaliculus</i> in aquaculture	
South, Paul ^{1,2} , Oliver Floerl ¹ and Andrew Jeffs ²	61
Contrasting phylogeography of two limpet genera in the Southern Ocean	
Spencer, Hamish ¹ and Claudio González-Wevar ²	62
Activating Kaitiakitanga (environmental custodianship) through pipi relocation “what are we enhancing”	
Taiapa, Caine and Waiaria Rameka	63
Diversity within and conservation of New Zealand’s large land snail <i>Powelliphanta</i>	
Walker, Kath ¹ , Graeme Elliott ¹ , Steve Trewick ² and Rod Hitchmough ¹	64
Biodiversity, biogeography and vulnerability of hydrothermal vents: a case study using bathymodioline mussels	
Walton, Kerry ^{1,2} , Bruce Marshall ¹ and Ashley Rowden ^{3,4}	65
Growth rates of potamidid snails in mangroves in northern Australia	
Wells, Fred ^{1,2,3} and John Keesing ^{4,5}	66
Un-earthing the true diversity of the Australian land snail genus <i>Bothriembryon</i> (Gastropoda, Orthalicoidea)	

<u>Whisson, Corey</u> ^{1,2} , Lisa Kirkendale ¹ , Nerida Wilson ¹ , Diana Prada ^{1,3} and Abraham Breure ^{4,5}	67
Resolving the Cenozoic mollusc fossil record of New Zealand: unravelling macroevolution	
<u>Womack, Tom</u> ¹ , James Crampton ² and Michael Hannah ¹	68
Green-lipped mussel <i>Perna canaliculus</i>' ability to cope with low seawater temperatures: Implications for survival, aerial exposure and heart rate	
<u>Zamora, Leonardo</u> ¹ , Norman Ragg ¹ , Joanna Copedo ¹ , Natali Delorme ¹ and Serean Adams ¹	69

Poster presentations

The effect of environment to species composition and phylogenetic study of micro snails in New Zealand	
<u>Akiyama, Kao</u> ¹ , Mary Morgan-Richards ² and Steve Trewick ²	70
Development of stress and health biomarkers in the Green-lipped mussel <i>Perna canaliculus</i>	
<u>Delorme, Natalí J.</u> ¹ , Norman L. C. Ragg ¹ , Zoë Hilton ¹ , Samantha Gale ² , Paul South ¹ , Leo Zamora ¹ , Thomas Wheeler ¹ and David J. Burritt ³	71
Identifying evolutionary lineages of marine snails	
Vaux, Felix ¹ , Steven A. Trewick ¹ , James S. Crampton ^{2,3} , Bruce A. Marshall ⁴ , Alan G. Beu ² , <u>Simon F. K. Hills</u> ¹ and Mary Morgan-Richards ¹	72
Adaptive evolution of mud-tidal gastropod (genus <i>Batillaria</i>) to the salt stress	
<u>Ho, Phuong-Thao</u> ¹ and Yong-Jin Won ^{1,2}	73
Exploring an undocumented diversification of endoparasitic gastropods in Antarctica	
<u>Layton, Kara KS</u> ^{1,2} , Greg W. Rouse ³ and Nerida G Wilson ^{1,2}	74
Ependymins in molluscs – expansions of a multifunctional protein family	
<u>McDougall, Carmel</u> ^{1,2} , Degnan, Bernard M. ²	75
Comparing indigenous and western methods of kākahi translocation: implications for ecological restoration	
<u>McEwan, Amber Julie</u> ¹ , Aaria Dobson-Waitere ² and Jeff Shima ¹	76
Do New Zealand olive shells (<i>Amalda</i> spp.) support punctuated equilibria?	
Gemmell, Michael R ¹ , Simon F K Hills ¹ , James Crampton ^{2,3} , Alan Beu ² , Steve Trewick ¹ and <u>Mary Morgan-Richards</u> ¹	77
The role of video game molluscs in science communication and animal conservation	
<u>Salvador, Rodrigo B</u> ¹	78

Growing, enabling and securing New Zealand's mollusc aquaculture industry – a research perspective

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Globally, aquaculture currently represents around half of the world's fish production. As the world's population and middle class rapidly grows, so too does the demand for farmed seafood. For the New Zealand aquaculture industry, the opportunities to grow, diversify and add value are immense. Currently, New Zealand's shellfish aquaculture is predominantly based on two species, Greenshell mussels™ (*Perna canaliculus*) and Pacific oysters (*Crassostrea gigas*). These species make up around 68% of New Zealand's total aquaculture production by value and 86% by tonnage.

For both species, the industry has traditionally caught wild juveniles (spat) to on-grow. Today, with guidance and support from the Cawthron Institute, there is an increasing shift towards hatchery production, as it provides a reliable seed source where there is opportunity to incorporate selective breeding, and to perform manipulations such as triploidy to improve stock performance and product quality. Omics technologies such as genotyping by sequencing are increasingly being used to amplify the power and efficiency of mollusc breeding programmes. In an ever-changing environment, selective breeding programmes now need to consider characteristics such as resilience and robustness to emerging threats for example, from ocean warming, acidification and emerging pathogens. We have seen the importance of this for the Pacific oyster industry, where farming was significantly impacted by mass mortalities due to the Pacific oyster herpes virus in New Zealand waters since 2010. Now, after four generations of breeding for disease resilience, we are seeing recovery in the oyster industry and recognition of the benefits that come with selective breeding. Our work to understand underpinning mechanisms suggests that resilience to the virus may relate to the host's ability to respond to oxidative stress. Corresponding resilience studies in mussels include characterising the effects of ocean acidification on different life stages and genotypes. Early embryonic and shell forming stages (<48 h old) appear particularly sensitive to changes in pH, with the capacity to develop successfully being under significant genetic control. Through manipulation of the seawater environment in the hatchery and selecting specific families for production, there is opportunity to address some of the key impacts of near-future ocean acidification on mollusc hatchery production. Research and industry effort to establish farming for the high value New Zealand flat oyster (*Ostrea chilensis*) has been hampered by the discovery of the exotic parasite *Bonamia ostreae*, and the subsequent removal of farms in the areas where it was detected, to protect wild oyster populations; efforts now focus on other high value species such as geoduck (*Panopea zelandica*) and pāua (abalone, *Haliotis iris*).

Biofouling control imposes an enormous cost on the aquaculture industry, requiring a variety of management strategies and approaches. Tools such as blue mussel spat-fall forecasting and practical treatments such as acetic acid dipping enable farmers to better manage and reduce the cost of this threat. New approaches continue to be developed that will assist with pathway management and biofouling control.

Both Greenshell mussels™ and Pacific oysters are presently farmed in sheltered coastal waters throughout New Zealand but there is opportunity to grow the industry by farming in the open ocean; near Opotoki, in the Bay of Plenty, this has already begun. Farming in open ocean environments requires more robust infrastructure and new monitoring equipment compared to that traditionally used in nearshore aquaculture. Research is underway to address these challenges, using modelling and wave tank simulation trials to rapidly test whether different configurations can withstand the substantial hydrodynamic forces that are known to occur at open ocean sites. From these trials, prototypes are now being built for full-scale testing. Precision monitoring technology is also being developed that will better enable farmers to monitor stock health and condition, as well as the integrity of farm infrastructure from afar. This technology can also be used on coastal farms located in remote areas.

In addition to research focussed on improving the farming of these molluscs, there is also effort towards adding value by better understanding their human health benefits, targeting consumer preferences and extending post-harvest shelf-life and quality. Mollusc research underpins the New Zealand aquaculture industry in the 21st century and is well positioned to enable further growth of this important sector and increase industry resilience in the future.

Diversity, molecular taxonomy, biogeography and ecology of the radicine pond snails (Gastropoda: Lymnaeidae) in the Palearctic

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The Lymnaeidae snails represent a species-rich and widely distributed group, many species of which are key vectors of human and animal trematodoses. But the available data on diversity, taxonomy, biogeography and ecology of the Radicine Pond Snails is fragmentary. In recent years a considerable amount of work has been done in the study of the fauna and ecology of molluscs in the hot springs of different parts of the world. It is our purpose on this occasion to analyse some features of the gastropod snails inhabiting thermal springs. The authors studied the freshwater molluscs populations in different geothermal streams of North Eurasia. In the present study, we revised these taxa based on an integrative taxonomic approach, using newly collected topotypes from different geothermal springs and specimens sampled from other sites (cold waterbodies and rivers). Species identification was performed using shell morphology, soft body anatomy and molecular data. In addition, the type series of *Lymnaea* sp. from Zoological Institute of the Russian Academy of Sciences, (St. Petersburg, Russia) were studied. We used data inferred from the mitochondrial cytochrome oxidase subunit I (COI) and the nuclear internal transcribed spacer 2 (ITS2) genes, because the molecular analysis of the nuclear and mitochondrial markers provides the most representative taxonomic results. As a conclusion, we have confirmed that various widespread species of the family Lymnaeidae could successfully inhabit an extreme warm environment of different geothermal sources, e.g., *Radix auricularia* and *R. kamtschatica* in Siberia and the Russian Far East; *R. lagotis* in North-East Europe and *R. balthica* in Iceland, *Ladislavella tumrokensis* from Kamchatka Peninsula and other. Another main focus is clarify the taxonomy, distribution and evolutionary biogeography of the lymnaeids in the Palearctic Region based on the most comprehensive multi-locus molecular dataset sampled to date. We show that the subfamily Amphipepleinae is monophyletic and contains at least ten genus-level clades: *Radix* Montfort, 1810, *Ampullaceana* Servain, 1881, *Peregriana* Servain, 1881, *Tibetoradix* Bolotov, Vinarski & Aksenova gen. nov., *Kamtschaticana* Kruglov & Starobogatov, 1984, *Orientogalba* Kruglov & Starobogatov, 1985, *Cerasina* Kobelt, 1881, *Myxas* G. B. Sowerby I, 1822, *Bullastra* Bergh, 1901, and *Austropeplea* Cotton, 1942. With respect to our phylogeny, species-delimitation model and morphological data, the Old World fauna includes 35 biological species of radicles. Tibet and Eastern Europe harbor the richest faunas, while East Asia and Africa appear to be the most species-poor areas. The radicine clade could have originated near the Cretaceous – Paleocene boundary. The Miocene great lakes in Eurasia seems to be the most important evolutionary hotspots shaping spatial patterns of recent species richness. Finally, we present the first DNA barcode reference library for the reliable molecular identification of species within this group. The study was supported by the FASO (no. 0409-2016-0022), Ministry of Education and Science of Russian Federation (no. 6.2343.2017/4.6), by grants from the President of Russia (no. MD-2394.2017.4) and the RFBR (nos. 16-05-00854_a, 17-44-290016_r_a).

Novel health assessment tools for shellfish aquaculture

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Recent advancements in ‘omics’ approaches have opened the door for deep understanding of how an organism’s biology works inside cells, biofluids, tissues and organs. The most common ‘omics’ are genomics, transcriptomics, proteomics and metabolomics, and these have produced a wealth of genotype to phenotype research avenues. One of the newest ‘omics’, metabolomics (the study of metabolites in a biological sample), has shown considerable promise in health assessment, since it provides a new phenotyping tool to understand endogenous metabolic changes in response to diseases or environmental perturbations. In addition, specific metabolite biomarkers can be generated to diagnose each biological permutation.

Our recent work with GC-MS-based metabolomics applications on the New Zealand Greenshell™ mussel (*Perna canaliculus*) has allowed us to elucidate molecular mechanisms and markers associated with biological responses of haemocytes against pathogens (e.g., *Vibrio* sp.) and environmental contaminants (e.g., copper). We have also used this approach to characterize metabolic and immunological responses (e.g., oxidative stress, apoptosis) of mussels during a mass mortality event in a farm. Our results show that alterations of some specific metabolites could be used for future development of biomarkers for pathogen infections and pollutant-induced stress syndromes.

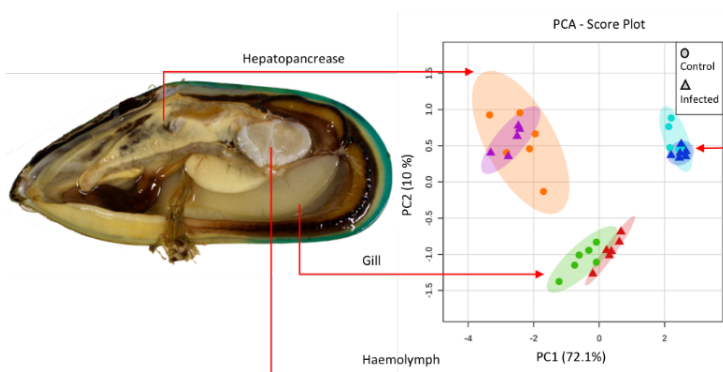


Figure. Principal Component Analysis (PCA) of metabolite profiles of hepatopancreas, gill and haemolymph of *Perna canaliculus* mussels infected with *Vibrio* sp.

Molecular components of the trail mucus in the common garden snail, *Cornu aspersum*

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Several species of land snail are a significant agricultural pest around the globe. *Cornu aspersum*, also known as the Common Garden Snail, has successfully colonized most continents, and is a pest of citrus orchards, vineyards and many other crops. As such, information regarding communication in land snails would be useful in developing a sustainable and effective pest control strategy. As several species of land snails have been shown to follow the mucus trail of conspecifics, this study investigated the components of snail trail mucus, with the goal of identifying a land snail pheromone. Using methods including LC-MS/MS, HPLC and GC-MS, we have identified the peptide components of the trail mucus of *C. aspersum*, along with volatiles that are emitted from the mucus trail. To date, several novel peptides have been identified, and numerous volatiles elucidated. Additionally, we will document the microbial diversity of trail mucus, including culture-dependent and culture-independent species. In particular, actinomycetes will be explored as a possible source of volatile components, which may also play a role in snail communication. Actinomycete species have been isolated and cultured from the mucus and are currently undergoing antifungal and antibacterial assays, while awaiting the results of microbial diversity profiling. These results will be combined with snail behavioural assays, in order to observe snail response to purified snail mucus-derived substances.

The outcomes of this project will utilize a multidisciplinary approach to provide knowledge into snail behaviour and pheromone communication, and therefore can be used to control pest snail species. Results may also facilitate the protection and conservation of native snail species. In addition, this study may have an impact on human health, by identifying the antimicrobial and antifungal components of snail mucus that may be beneficial in biomedical applications.

Risks associated with neonicotinid pesticide exposure in Sydney rock oysters

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Neonicotinoids are systemic insecticides that have broad applications in agriculture, with potential for spray drift and run-off into adjacent aquatic ecosystems. These water-soluble pesticides have been detected in surface waters and estuarine sediments around the world, along with increasing documentation of the risks to non-target species. However, few studies have investigated the impacts on commercially important seafood species, or whether the pesticides can accumulate in the flesh, thus posing risks to human consumers. Using preliminary exposure experiments, we investigated whether the water-soluble neonicotinoid imidacloprid (IMI) is absorbed into the flesh of Sydney rock oyster (*Saccostrea glomerata*). After exposure to various concentrations of IMI the flesh was extracted using acetonitrile and QuEChERS, then analysed using liquid chromatography-mass spectrometry. By comparison of the retention time, UV profile and mass spectra to standard solutions of IMI, we were able to positively identify IMI in the exposed oyster flesh, but not in unexposed controls. After just 24 hours of exposure to 0.25mg/L IMI, residues were detected in the oyster tissues at 0.4µg/g tissue, building up to a maximum of 1.8 µg/g after two days then levelling off. Significantly, higher levels were detected in the adductor muscle and gills, in comparison to the digestive gland. After 24 hours of depuration in IMI-free water there was a significant drop in IMI residues, with none remaining in any tissue by day 4 of depuration. Chronic exposure to IMI at 0.5 and 1 mg/L resulted in a reduction of oyster filtration rates after 4 days and a significant decrease in acetyl choline esterase activity was detected down to 0.25 mg/L exposure. Overall, this study indicates that Sydney Rock oysters can absorb IMI from the water column at concentrations that can well exceed maximum residue limits for meat (0.05 µg/g), and chronic exposure can lead to negative impacts on oyster physiology and feeding behaviour.

Gas bubble disease and rickettsiosis in New Zealand surf clams

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Globally, *Rickettsia*-like organisms (RLOs) are increasingly being recorded in association with shellfish mass-mortality events. Since their first detection in marine molluscs in the 1970s, RLOs have been recorded in a wide array of host species including clams, abalone, mussels, scallops and cockles. Since 2012, RLOs have been observed while investigating mass-mortality events in at least nine New Zealand shellfish species. Despite their increasing presence in the New Zealand shellfish-mortality landscape, there is currently only limited knowledge of the drivers of RLO infections or their ecological significance. In 2017, RLOs (and gas bubble disease) were observed in toheroa (*Paphies ventricosa*) in northern New Zealand for the first time. Toheroa is an iconic surf clam endemic to New Zealand. Formerly abundant on a handful of west coast beaches, toheroa have failed to recover from unsustainable harvesting of the early to mid-20th century. Several biotic and abiotic factors have been linked to this failure including, land use change, toxic algal blooms, and vehicle traffic. Now, we are investigating the role of RLOs in the continued decline of toheroa. In this study, we investigate the seasonality of RLO infections in New Zealand surf clams and the relationship between RLOs and gas bubble disease.

New Zealand Cenozoic fossil Turbinidae: Indo-Pacific elements in southern New Zealand Oligocene–Miocene rocks

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Astraea heliotropium appears on the conference logo, and Turbinidae is a good subject for revealing the shrinking of the Indo-Pacific warm province as temperatures fell during middle Miocene to Pleistocene time. Turbinidae are among many molluscs that show that the Indo-Pacific province extended at least as far south as the southern South Island during early Eocene to middle Miocene time (c.50–10 M yrs ago). Suzanne Williams's (2007) molecular phylogeny of the Turbinidae showed that *Astraea* (used here only for the lineage of *A. heliotropium*), *Modelia*, *Cookia*, *Bolma* and *Lunella* are genera distinct from *Turbo*.

At least 35 species of Turbinidae are represented in NZ Cenozoic rocks. *Astraea* (5–6 species) can be seen evolving from a *Bolma*-like ancestor in NZ late Eocene and early Oligocene rocks. The earliest species had a basal depression but a closed umbilicus; the umbilicus widens through Oligocene time. This is particularly interesting in view of at least three species in southern Australian late Eocene–Miocene rocks that resemble *Astraea heliotropium* quite closely, with a low spire and a widely open umbilicus, but they already had a wide umbilicus well before *Astraea* had evolved one in NZ, so this is presumably a distinct, convergent genus. This might also be interpreted as indicating that *Astraea* evolved in Australia and did not reach New Zealand until latest Oligocene time; the NZ Eocene–Oligocene species might then be referred to a genus resembling *Bolma*. *Cookia sulcata* and *Modelia granosa* are present in NZ late Oligocene rocks, so they evolved earlier than Oligocene and provide excellent examples of evolutionary stasis. A probable new *Cookia* species is present in middle Miocene deep-water rocks, but otherwise both genera are monotypic. *Lunella smaragda* has no record before late Pliocene time and is probably a recent arrival. The large species that Powell (1938) placed in his genus *Sarmaturbo* show no significant differences from *Turbo* (*Sarmaticus*), and this currently South African subgenus was quite diverse in NZ during Oligocene to late Miocene time (at least 5 species). One species from early Miocene rocks near Auckland has been referred to *T. (Marmarostoma)*, but the 5 mm-wide holotype should never have been described. *Bolma* and the probably distinct genus *Ormastralium* are also quite diverse, with one species of typical, large *Bolma* in Auckland early Miocene rocks and 6 or more species of *Ormastralium* throughout early Eocene to late Miocene rocks, and one still living off Northland.

The most surprising diversity, perhaps, is that of *Guildfordia* (at least 8 species). A typical, large species resembling *G. triumphans* is common in Waitakian (latest Oligocene–earliest Miocene) rocks around the Waitaki Valley in the South Island, and Andrew Grebneff collected a second, much less common species with a taller spire and weaker sculpture with the typical one in a few places. A similar species occurs in early Miocene rocks near Oamaru, and a species resembling the short-spined living species *G. aculeata* Kosuge, 1979 [for which the earliest name is *G. monilifera* (Hedley & Willey, 1896)] occurs in several Miocene localities. Finally, there is group of species with a markedly taller, straight-sided spire and many short, narrow spines around the base, for which Finlay proposed the genus *Opella*. These have the same arrangement of spines and sculpture around the peribasal angle as in *Guildfordia* species, so I think this group is at most a subgenus of *Guildfordia*. Three species are known, all in early Miocene rocks in the north, from Auckland to Parengarenga Harbour. The northernmost, at Parengarenga, has a very tall spire and is a surprising development for a *Guildfordia* relative. The tropical Indo-Pacific genus *Guildfordia* was unexpectedly diverse and extended to the southern South Island 25 M yrs ago.

Lessons from the ongoing mass extinction of land snails in Ogasawara: direct and indirect effects of multiple invasive species

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Designing preventive measures to reduce the risk of invasive alien species is crucial to conservation programs of native ecosystems. The potential severity of the impacts of non-native species can be assessed for effective conservation management. However, such risk assessments are often difficult—the possible harm of non-native species can be underestimated or even overlooked. In addition, invasive species can often have both negative and positive effects on native species. Here, I show examples of the catastrophic decline of land snail fauna in the oceanic Ogasawara Islands (Japan), a UNESCO World Heritage site, due to direct impacts of non-native predators and also indirect impacts of non-native land snails. The harm due to some of these non-native predators and most of the non-native land snails has previously gone unnoticed. For examples, the impacts of non-native ants *Pheidole megacephala* on native land snails have been underestimated in Ogasawara because no influence of *P. megacephala* on native snail fauna have been documented on other Japanese islands. Non-native land snails, with the exception of *Euglandina rosea*, promote an increase in the population of predatory nonnative flatworms. This situation results in the serious decline of native land snails. Conversely, a decline of malacophagous *Euglandina rosea* due to predation by nonnative flatworms has resulted in an increase in the population of small native land snails, which possess resistance against predation by non-native flatworms. Similarly, predatory impacts of black rats on native snails are mitigated by the presence of the non-native plant *Casuarina equisetifolia* introduced from Australia. An additional example of the difficulty of risk assessment of non-native species involves the non-native land nemertine, which has been believed to be malacophagous and potentially responsible for the decline of land snails. This animal is actually entomophagous, and our recent surveys documented that the land nemertine have caused serious declines in soil arthropods in Ogasawara. These findings highlight issues and limitations to recognizing the threats of non-native species. I introduce several programs concerning these issues to prevent the invasion and expansion of non-native species in Ogasawara.

Denying the Sixth Extinction: a counterpoint

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Most (almost all) students of biodiversity acknowledge that we are at least at the start if not in the middle of a major biodiversity extinction event, similar in significance to the previous “Big Five” mass extinctions the Earth has suffered over the last 500 million years since the burgeoning of life during the Cambrian. The so-called “Sixth Extinction” differs from the previous five in being caused entirely by human activities, beginning almost as soon as modern humans expanded out of Africa and continuing at an ever-increasing tempo today. There is overwhelming evidence for heightened rates of extinction globally. Yet, there are those who deny that such evidence really exists and argue that it has been wilfully and even disingenuously concocted or exaggerated by conservation and biodiversity scientists with self-serving agendas. Others accept the Sixth Extinction but argue that because humans are part of the natural world, this event is also a natural phenomenon, a part of the evolutionary trajectory of life on Earth and that we should embrace it and manipulate it for the almost sole benefit (however defined) of humanity. Both attitudes mean that extinctions will continue unchecked.

Prominent deniers have based their spurious interpretations on the IUCN Red List, listing extinctions - primarily of mammals and birds - since the year 1500. However, mammals and birds constitute a highly biased sample of biodiversity. Among animals, invertebrates constitute the vast majority, 95% of known species. But because of their vast diversity, the lack of knowledge of many species, and probable differences among major groups in their proneness to extinction, it is difficult to find a single well-understood group that could act as a surrogate for estimating overall rates of extinction.

We suggest that molluscs are one such group. They are relatively well known and, crucially, many species leave long-lasting remains (shells) when they die, making this group a good candidate for easily assessing species losses in a fairly rigorous way. Numerous studies, especially on oceanic islands and inland waters, have revealed a vanished fauna. Insects or other arthropods, which usually do not leave identifiable remains, cannot give such an insight into recent extinctions.

We have shown that more than twice as many mollusc species than are included in the Red List are known by the scientific community to be recently extinct. Furthermore, an expert assessment of a random global sample of land snail species estimated that 17% of them (extrapolated to 5,100 land snail species globally) have gone extinct. Under a series of assumptions, this extrapolates to 255,000 of all ~2 million known species (marine and non-marine) having gone extinct since around 1500. This is orders of magnitude greater than the 872 (0.04%) listed as extinct on the IUCN Red List (version 2018-1). But is it a biodiversity crisis, the Sixth Extinction?

Extinction deniers have attempted to show that such rates of extinction are exaggerated and that in reality the current extinction rate is no greater than the natural background rate of extinction. But even our most conservative estimates of extinction rate are an order of magnitude faster than the fastest estimate of the background rate. Our less conservative and perhaps more realistic estimates are two orders of magnitude faster. The Sixth Extinction is demonstrably in progress.

Brooding in Australasian chitons: are there any patterns?

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Chitons are an ancient group of molluscs that typically live on rocky substrata in intertidal or shallow subtidal environments. Australia and New Zealand both have a diverse chiton fauna, but the ecology and reproductive behaviour of most species have not been well documented. Most species are known, or assumed, to be broadcast spawners. Increased collections and more extensive field surveys in recent decades, however, have revealed that quite a few species brood their offspring to varying extents in their pallial grooves. Most chiton species that brood their young are small, reaching in the vicinity of 15-20 mm as fully grown adults, although there are some notable exceptions. Although a comprehensive review of brooding in Australasian chitons is not yet possible, several common features are emerging. The brooding characteristics of several species will be described with a view to developing a better understanding of the ecological significance of this behaviour.

How investigation into secreted snail proteins can have massive health and economic implications

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Aquatic animals utilize secreted proteins to relay or receive information from their environment such as conspecific or host attractiveness, predator avoidance or health. This includes freshwater snails that are found throughout the world in various habitats. Unfortunately, freshwater snails are widely recognized as intermediate hosts to a variety of animal parasites, including the trematode *Schistosoma*, which is particularly detrimental to humans (their primary host). Our recent research has pinpointed secreted proteins from the snail *Biomphalaria* that mediate strong attraction responses in invading *Schistosoma mansoni*. Here, I will present new research that confirms the importance of secreted snail proteins in parasite infection, through genomic, proteomic and behavioural studies. Water conditioned with *Oncomelania hupensis quadrasi*, a molluscan host for *Schistosoma japonicum*, was fractionated using RP-HPLC and the fractions were tested on *Oncomelania* free-living aquatic miracidia. One fraction was found to stimulate change in miracidia behaviour, including increasing tortuosity and duration of presence, even at 100× dilution. Candidate bioactive secreted proteins were identified using LC-MS/MS and a transcriptome-derived protein database from *O. hupensis quadrasi*. These proteins included some known proteins, as well as a novel protein.

This information and experimental workflow will help to support new approaches for control of snail-borne infections, including Schistosomiasis, fascioliasis and angiostrongyliasis.

Biogeographic conundrum: why so many freshwater gastropod taxa in Fiji compared to Australia?

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Small coastal streams on the high islands of Fiji and much of the South Pacific, support a rich freshwater gastropod fauna, predominantly drawn from two families - the Thiaridae and Neritidae. As an example, at least 19 gastropod taxa from these two families are found in the modest-sized Rukuruku creek on the Island of Ovala, Fiji. Here we focus attention on the Neritimorpha - a relatively small superorder of Gastropoda with a mix of marine and freshwater representatives totalling approximately 300 taxa. In Fiji, 23 freshwater neritimorphs have been recorded, with representatives in the genera, *Clithon*, *Neritina* and *Septaria*. All of these taxa lay the characteristic calcareous nerite egg cases and their larvae, very unusually for freshwater gastropods, undergo a marine dispersive phase before settling near the entrance of creeks and re-entering these freshwater systems as crawling juveniles. The striking diversity of this group in the small coastal streams of Fiji contrast with a paucity of taxa in tropical Australia, despite northern Australia occupying a similar latitude. Just three taxa have been reported from Australia, the same number as reported from Hawaii, while Fiji and Papua New Guinea each support 23 taxa. These patterns are in striking contrast to the wide distribution of many marine nerites in the Pacific and conflict with Island Biogeography Theory. In highlighting this biogeographic conundrum, we consider some of the processes that may explain the disparate patterns in distribution of these taxa.

Using both barcoding and next generation sequencing to elucidate the complex New Zealand *Maurea* (Mollusca: Gastropoda: Calliostomatidae: *Calliostoma*) phylogeny

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Calliostoma, which comprises approximately 250 carnivorous species inhabiting mostly rocky areas from the intertidal zone to deep waters, are currently treated as a broad genus. New Zealand is rich in calliostomatids, with 33 species currently recognised. The New Zealand species were originally placed, based on morphologically characteristics, into four subgenera: *Maurea* Oliver, 1926, *Mauriella* Oliver, 1926, *Calliotropis* Oliver, 1926 and *Mucrinops* Finlay, 1926 in the 1920s. However, due to overlap in shell characteristics and radular morphology between the four subgenera type species, they have more recently synonymised been into the single subgenus *Maurea* (Marshall, 1995). Recent New Zealand *Calliostoma* spp. have dissimilar shell morphology to the European *Calliostoma* type species, *C. conulus* and are exceptionally large. As molluscs often display high phenotypic plasticity, convergence and gigantism, morphology provides inadequate species delimitation, consequently we cannot ascertain, based on morphological data alone, whether the New Zealand *Maurea* subgenus is valid and if so, if it may be elevated to the status of genus.

Traditionally, molecular phylogenies have been constructed based on small fragments of small numbers of mitochondrial genes, particularly cytochrome oxidase I (COI), the “barcoding gene”. These molecular phylogenies are relatively easy to build and have provided useful information about the evolution and biogeography of numerous molluscan groups. However, phylogenies based on short fragments of one or two genes can be problematic. There are many instances of molecular phylogenies, constructed from reasonably short fragments of relatively few genes, showing unexpected relationships in which morphologically distinct molluscan species are genetically close, while morphologically cryptic species may be genetically more distant. This phenomenon is often explained by the decoupling of morphological convergence from genetic change. Perhaps however, unexpected relationships in molecular phylogenies are an artefact of the relatively small amount of data being analysed. Individual sequences are often not representative of the genome; COI, had only a 70% success rate in delimiting closely related but unambiguously distinct sister species (Dupuis et al., 2012). We initially attempted to resolve a New Zealand *Calliostoma* molecular phylogeny based on a small section of the barcoding mitochondrial gene, cytochrome oxidase I (COI), sequenced from a large number of New Zealand species (including *C. blacki*, *foveauxana*, *granti*, *osbornei*, *pellucida*, *punctulata*, *selecta*, *spectabile*, *tigris* and *waikanae*). The resulting Bayesian phylogenetic tree was problematic, with several poorly resolved clades.

As next-generation sequencing (NGS) has become more affordable and user friendly, large amounts of data may now be analysed fairly routinely. We have used NGS to produce more accurate phylogenies and improve delimitation success among the New Zealand *Calliostoma* species. The entire mitochondrial genome (approximately 16 kb) was assembled for *C. waikanae*, *C. selecta*, *C. granti*, *C. punctulata*, *C. pellucida* and *C. spectabile*. The Bayesian tree produced of these six entire mitochondrial DNA sequence correlates with the COI analysis, placing *C. granti* and *C. punctulata* as sister species, with *C. spectabile* sister to this pair. Also, *C. waikanae* and *C. pellucida* were sister species, with *C. selecta* grouping next. These entire mitochondrial sequences allowed us to design primers to additional mitochondrial genes (16S and ND5), thus allowing construction of a phylogenetic tree based on more data (2838 bp), providing a more robust, well-supported phylogenetic tree. Although the COI phylogenetic tree provided much useful data, the addition of more genes allowed clearer resolution of previously confused relationships, e.g. *C. granti* and *C. punctulata* formed two separate clades and the position of *C. osbornei* became clear. Although COI barcoding is a useful, relatively cheap method of identifying species and building quick phylogenies, NGS of entire mitochondrial sequences allowed an easy method of increasing the data set to iron out issues that could not be resolved by COI sequencing alone. Based on both the COI dataset and the larger mitochondrial dataset we agree with Marshall’s 1995 finding that the four New Zealand *Calliostoma* subgenera should be synonymised into the subgenus *Maurea*.

Dupuis JR, Roe AD, Sperling FAH. 2012. Multi-locus species delimitation in closely related animals and fungi: one marker is not enough. *Molecular Ecology* 21, 4422-4436. Marshall BA. 1995. A revision of the recent *Calliostoma* species of New Zealand (Mollusca: Gastropoda: Trochoidea). *The Nautilus* 108: 83-127.

Gastropod communities of seagrass meadows in a central New Zealand estuary

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Seagrass meadows provide a spatial refuge for a variety of organisms, including gastropod molluscs. The structure provided by the seagrass likely reduces desiccation stress for gastropods during low tide, by trapping water near the blades and/or providing shade from direct sun light. In summer and winter of 2016, gastropods were collected, along with seagrass, from the upper and lower shore of three sites in a large lower North Island estuary. These sites vary in their exposure to natural and anthropogenic influences. At each site eight 25 x 25 cm quadrats were sampled at each tidal height. A total of 1380 gastropods from 15 species were identified, with species presence in each quadrat varying from zero to seven. Gastropod densities were spatially and temporally variable, with two of the three sites showing significantly higher densities in the upper shores than lower shores in summer. Densities were similar across all tidal heights in winter. Of the species sampled, two micro-gastropods (*Notoacmea scapha* and *Potamopyrgus estuarinus*) were numerically dominant across all sites. Principal component analysis indicates complex positive and negative associations between species collected. The trends exhibited by species appear to be strongly influenced by season and the different biotic and abiotic conditions at each site.

The environmental history of Tauranga Moana

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Management of the environment is a key area of discussion within the emerging space of Treaty co-governance between Māori and Government agencies. Successive waves of human occupation and the associated anthropogenic activities throughout Aotearoa have resulted in the degradation of estuarine environments and changes in estuarine ecology. In Tauranga Moana, mātauranga Māori indicates that kaimoana have declined in size and abundance over time, however the scientific repository of historical information related to these changes is limited to the recent past.

To improve our knowledge of the pre-human ecology of Tauranga Moana and the ecological consequences of human-induced environmental change, we are combining Māori knowledge of customary kaimoana sites with geological and ecological methods. Working with kaitiaki and hapū of Tauranga Moana, we have identified customary kaimoana sites and are examining the changing status of these biological resources over time. Sediments and bivalve shells from the present, recent and distant pasts, are currently being gathered through a sediment-coring approach, providing a window into the environmental history of Tauranga Moana.

Through understanding historical and pre-historic ecosystem responses to changing land use, we are gaining insight into future environmental and ecological trajectories and providing data to inform environmental management within the co-governance domain.

Widespread convergence in body form in Australian Helicarionidae (Pulmonata, Stylommatophora)

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The Helicarionidae is a family of snails and semislugs with its greatest diversity on the eastern coast of Australia, where there are around 100 described species. This group of rainforest specialists is one of Australia's most diverse land snail families. Around half of all species are semislugs, with a reduced shell into which they cannot fully retract. Helicarionids also occur in some islands of the Pacific, southeast Asia, Madagascar and the Mascarene Islands.

As in many land snails, the taxonomy of this group has historically been based primarily on shell morphology, made difficult by the thin, glossy shells with little sculpture, and the high incidence of shell reduction. We have revised the Australian species based on comparative morphology (including genital anatomy) and molecular phylogenetics (using mitochondrial genes COI and 16S). We have found that shell reduction has evolved independently multiple times in the Australian helicarionids.

Major radiations within the Australian Helicarionidae can be identified by molecular phylogenetics as well as by a combination of several significant morphological characters, including the presence or absence of a vagina, epiphallic caecum and/or epiphallic flagellum, the shape of the flagellum and the spermatophore that it produces, and the position of attachment of the penial retractor muscle. Some such radiations comprise a single body form, while others contain a mixture of snails and semislugs.

The extent of shell reduction in this group varies from slight to extreme, although there are no true slugs. Shell reduction results in not only convergence in gross morphology, but also convergence in some anatomical features, particularly in extreme semislugs with shells of fewer than 3 whorls. These modifications include the formation of an oesophageal crop, the shortening of the vagina, and the development of a unilobed ovotestis. However, individual semislug radiations can often be identified by a unique pattern of reproductive tract folding.

The speed of semi-slug formation: limacization of *Schizoglossa* (Mollusca: Pulmonata: Rhytididae)

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Phenotypic innovation is at the heart of many biological questions, but the rate at which major phenotypic change occurs is not well understood. Many differences among closely related taxa seem to be more ‘variations on a theme’ than significant evolutionary novelties. Nevertheless, major phenotypic changes are evident in a number of groups. Possibly one of the better examples (because it has happened repeatedly in the course of gastropod evolution) is the evolution of the slug body form from shelled gastropod ancestors, so-called ‘limacisation’. Apart from the obvious morphological change involved in the loss or reduction of the shell, major changes in basic anatomy, physiology and behaviour also occur. Moreover, a number of taxa, ‘semi-slugs’, have not completely lost their shell and offer insights into the processes required during limacisation, which are sometimes obscured in fully shell-less slugs by the wholesale nature of the changes. Members of the rhytidid genus *Schizoglossa*, known as paua slugs, are carnivorous semi-slugs from the northern North Island. Apart from the paua slugs all members of the subfamily Paryphantinae are snails, suggesting that limacisation occurred after the schizoglossan ancestors split from the rest of the paryphantines, but before speciation within the genus. We use nuclear and mitochondrial DNA sequences for multiple samples of all the extant species of *Schizoglossa*, together with relaxed molecular clock methods for dating evolutionary events in a phylogenetic context, in an effort to more precisely estimate the time involved in these first steps towards slugdom.

The world in a shell: aspects of cockle taxonomy, biogeography, phylogenetics and evolution reviewed

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Cardiid bivalves or cockles are a well-known, moderately diverse and widespread marine molluscan family with a solid fossil record. They include photosymbiotic members such as the giant clams (all Tridacninae) but also the lesser known heart cockles (some Fraginae). Together these attributes make them a viable molluscan system to tackle challenging questions about species diversity and distribution as well as adaptation through time. We will discuss highlights of several recent large scale initiatives that draw together work by a number of research teams worldwide. These efforts have resulted in updated assessments of biodiversity in Western Australia, including discovery of four new species and a doubling of the known fauna. Considered in context of other work in the region, we find additional evidence for a distinct diversity bulge in northern Australia. We then shift focus to discuss phylogenetic relationships and life history evolution in the family. While much progress has been made, poor signal has prevented attempts to resolve some critical relationships necessary to understand the evolution of cardiid photosymbiosis. However, new work utilizing a transcriptomic approach, although challenging, has provided clarity. Overall, our results support a sister relationship between Tridacninae and Fraginae with divergence around 78 million years ago. Although a sister relationship is recovered, ancestral state reconstruction still reveals two independent origins of photosymbiosis, one within Tridacninae, the other within the symbiotic Fraginae clade. Lastly, we discuss photosymbiont identity in the understudied photosymbiotic Fraginae and examine nutritional importance of these symbionts by scrutinizing evidence for nutrient transfer between host and symbiont.

Land snails (1) : dinosaurs (0) – phylogenomics resolves Late Mesozoic diversification of helicoid land snails

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During the Cretaceous–Paleogene mass extinction event, approximately 66 million years ago, up to three quarters of all plant and animal species suddenly vanished from Earth (including the dinosaurs). It is widely accepted that the cause of these extinctions was the collision with a massive meteorite, whose impact created the 180-kilometre-wide Chicxulub crater in the Gulf of Mexico and on Yucatan. For the few survivors, however, the devastation also provided new opportunities: in the wake of global disaster, many groups of animals and plants diversified into the live forms that surround us today. Latest molecular techniques enable us to reconstruct the events that have shaped the diversity of present life forms by analysing genome-scale genetic data. We have used such novel genomic methods to investigate the evolutionary history of one of the most diverse extant land snail superfamilies, the Helicoidea. Comprising approximately 4,700 extant species in 16 families, helicoids have a nearly global distribution and considerable evolutionary antiquity. Consequently, these snails offer a suitable model to investigate how major tectonic and paleoclimatic events since the late Mesozoic have shaped contemporary global biotic patterns. By using a molecular dataset of unprecedented size that included almost 175,000 base pairs from 477 nuclear protein-coding genes of 87 species representing all families but one as well as several stylommatophoran outgroups, our analyses result in a strongly supported phylogeny that shines new light on the spatiotemporal patterns of helicoid diversification on a global scale. To recapitulate their extraordinary evolutionary journey takes us further back than 66 million years ago... Together with their sister group Sagdoidea, Helicoidea are well represented in Central America by several distinct lineages that have diverged from one another between the mid-Cretaceous and early Paleogene (about 100 to 50 million years ago). Our analyses demonstrate that these lineages have persisted in Central and/or western North America through the Cretaceous–Palaeogene mass extinction. By incorporating plate tectonic models, we have reconstructed potential biogeographic pathways of their global diversification since the K/Pg boundary.

Using exon capture to tease apart recently radiated mimetic sea slugs

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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 eleven 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. Most species-level entities and sister species relationships were highly supported in both the concatenated ML and ASTRAL analysis, although these trees showed some discordance. An ASTRAL tree was reconstructed using 149 genes previously identified from eupulmonate gastropods, and this was largely congruent with the full gene ASTRAL tree. In some analyses, *C. aspersa* and *C. orientalis* were sister to the rest of the *Chromodoris*, suggesting that spots may be a plesiomorphic trait that were not reacquired in derived taxa. This work also corroborated a previous finding of regional mimicry for one species but revealed mitonuclear discordance in three others, likely resulting from mitochondrial introgression or capture. In all, this work has demonstrated that exon capture is informative for resolving species boundaries in a group of recently radiated nudibranchs and has advanced our understanding of evolutionary relationships in this group.

Phylogeography of *Lasaea hinemoa*

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Lasaea is a genus of molluscs that primarily consists of minute, hermaphroditic bivalves that occupy rocky shores worldwide. The majority of *Lasaea* species are asexual, polyploid, direct developers. However, two Australian species are exceptions (Ò Foighil & Thiriot-Quiévreux, 1999); *L. australis* is sexual, diploid and has planktotrophic development, whereas *L. colmani* is sexual, diploid and direct developing. The nominal species *Lasaea australis* has recently been found to consist of three cryptic genetic species occurring in different biogeographic provinces (Li, Ò Foighil, & Park, 2013).

The widespread New Zealand *Lasaea* species (*L. hinemoa*) has at present only had a sample from a Wellington population genetically evaluated; it remains relatively unexplored on a genetic level. Through sequencing the mitochondrial gene Cytochrome Oxidase III (COIII) and the nuclear gene Internal Transcribed Spacer 2 (ITS2), we investigated the phylogeny and biogeography of *Lasaea hinemoa*.

Both genes revealed that two distinct clades within what is currently recognized as *L. hinemoa* are present throughout much of the two main islands of New Zealand. Although there are no obvious morphological differences between members of these two clades, there is evidence of some biogeographic structure, with North Island and northern South Island populations dominated by one clade, which is less common further south. This latter southern clade also includes previously reported individuals from Kerguelen Island (Taylor & Ò Foighil, 2000).

The phylogenetic placement of these clades suggests that *L. hinemoa* is likely to be an asexual, polyploid, direct developer. Indeed, as did Booth (1979), we often observed larval shells within adult individuals, confirming the inference of direct development. Two of our sampled individuals, however, did not fall into either of the two *L. hinemoa* clades, instead grouping with samples reported by Li, Ò Foighil and Park (2013) from Australia, Hong Kong, Japan and Florida, which in turn group with *L. australis*. The species status and mode of reproduction of these two individuals are not clear.

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Tolerance to acute and gradual increases in salinity in a freshwater mussel

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Freshwater mussels play major roles in aquatic ecosystems by improving water quality through filter feeding, providing shelter to other animals, and enhancing the connection between benthic and pelagic systems through burrowing, depositing nutrients and releasing biological waste. Carter's freshwater mussel, *Westralunio carteri*, is the only freshwater mussel species in south-western Australia and is endemic to the region. The range of *W. carteri* has declined by 49% over the past 50 years, resulting in its classification as Vulnerable by both international and Australian conservation regulatory bodies. Secondary salinisation has been primarily responsible for the dramatic recent decline in the range of *W. carteri* and remains a major threat to the survival of the species. Laboratory assessment of tolerance to acute increases in salinity in adult mussels from two populations found LC50 values of 5.87-5.96 gL⁻¹, substantially greater than values found in a previous study. Mussels were able to acclimatise to gradual increases in salinity, with gradual LC50 values ranging from 6.43-6.45 gL⁻¹ and survival times increased by a slower rate of increasing salinity. Future research should determine both the salinity tolerance of glochidia and juvenile mussels and the non-lethal impacts of increased salinity on mussel fitness, so that the impacts of rising salinity levels in the rivers of south-western Australia can be more accurately predicted. The salinity tolerance of teleost hosts for the glochidia also warrants attention, as the decline in host abundance or presence may also impact mussel viability.

Encapsulated feed for increased growth of farmed paua and reduced feed wastage

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The slow growth rate of New Zealand abalone (*Haliotis iris*) and high feed cost are major industrial bottlenecks in New Zealand paua farming. Moreover, current commercial feed have a quick disintegration rate in seawater and poor consumption rate by farmed paua. In this study, an encapsulation technique was used to produce new encapsulated feed with significantly low disintegration rate in seawater and higher consumption rate. Natural polymers were used to produce encapsulated feed. The developed feed pellets were stable in seawater for up to 10 days. The matrix erosion test confirmed 3.2 ± 0.3 , 20 ± 1.8 and 26.5 ± 1.8 percent weight loss after 3, 4 and 10 days of incubating encapsulated feed pellets in seawater respectively. Ninety juvenile paua were fed with encapsulated and non-encapsulated feed over one-month feeding trial. The percentage of feed wastage were 11.7 ± 1.5 and 30.1 ± 2.3 for encapsulated and non-encapsulated feed respectively. A significant improvement in growth was achieved with the encapsulated feed that included 27.95% wet weight gain (0.1647 gr) and 87.61% increase in shell length (0.7 mm) compared to animals treated with non-encapsulated feed over one-month feeding trial. The results of this study can reduce feed cost associated with paua aquaculture and boost production significantly.

Stress in pearl oysters: Transcriptional investigation of responses to extreme temperature and salinity

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In northern Australia, the pearl oyster *P. maxima* has been identified as vulnerable to a range of factors known to cause significant physiological stress including increased sea surface temperatures and decreased salinity. Responding to stress conditions is energy costly and decreases the overall fitness of the oyster. In order to detect whether oysters are experiencing or responding to stress conditions detailed 'omics data can be used to identify key biomarkers that can be used diagnostically on a routine basis to improve farm management practices.

We have developed proteomes and transcriptomes for oysters exposed to high temperature and low salinity conditions, our results show expression of many of the key proteins and genes required for cellular stress response, however with a high degree of variation being found between individuals. Up to 50% of the transcripts found to be differentially expressed in response to stress conditions compared to control oysters appear to be long noncoding RNAs that may play a role in transcriptional regulation.

A genomic approach to developing tropical oyster aquaculture

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Australian rock oyster aquaculture predominantly occurs in southern temperate areas and focuses on two species that are heavily impacted by disease. As a result, production values have been in decline since 2010. One potential solution for the industry is the development of aquaculture for additional native species. Of particular interest is the expansion of the industry to include farming of tropical species, which would significantly increase production and open up new areas of Australia's coastline to this form of sustainable aquaculture. Despite a very confused taxonomic picture of the oyster species that exist in tropical Australia, a number of candidates for aquaculture have been identified. One such candidate is the 'black-lip oyster', a large *Saccostrea* species variably referred to as '*Striostrea mytiloides*' or '*Saccostrea echinata*'. Favourable characteristics of this oyster include tolerance of environmental fluctuations, fast growth, acceptance by consumers, and perceived resistance to existing oyster diseases. There are some reports in the literature regarding hatchery culture of black-lip oyster larvae, and poor larval survival and poor settlement represent significant barriers to production. This presentation outlines current efforts to understand the phylogenetic relationships of this (and other) tropical oyster species, to improve black-lip hatchery performance, and to use comparative transcriptomics to fast-track efficient production of this species. It is envisioned that the approaches used within this research could easily be extended to other oyster species with aquaculture potential.

Musseling-up program: Greenshell mussel and role in inflammation management and joint health

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Lipid extracts from New Zealand's iconic Greenshell mussel (GSM) are the world's most expensive nutritional oil (~\$2000 USD/kg). Traditional use of GSM by coastal Maori has been associated with improved joint health and a number of studies have examined the anti-inflammatory effects of GSM extracts.

This paper looks at outputs of Musseling up program a 3-year program under the New Zealand National Science Challenge "High Value Nutrition" by a) identifying, discriminating and verifying GSM active ingredients; b) producing novel GSM food/extract products; c) determining the mechanism and efficacy in pre-clinical and clinical trials.

We have determined GSM lipid content over seasons, developed rapid near infrared analytical methods and developed novel food applications. Efficacy of GSM was tested 1) in-vitro analysis in macrophage, cartilage osteoclast and pre-osteoblast cell lines, 2) in-vivo in female Sprague-Dawley rats with obesity-induced osteoarthritis and 3) in a clinical trial on bioavailability of the lipids fraction.

We have determined the variation in GSM with female spring mussels having the highest lipid content. Novel stable GSM rich food ingredients have been made through emulsification and spray drying techniques. The inclusion of GSM in the rat diet significantly reduced blood levels of a cartilage degradation biomarker in rats In vitro, a non-polar lipid extract of GSM significantly reduced osteoclast differentiation in a dose-dependent manner.

GSM food products, food ingredients and extracts provide exciting opportunities for improving joint health and inflammation management.

Physiological effects of temperature and oxygen availability on molluscan development: lessons from the Antarctic

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One of the fundamental tasks of metazoans is acquiring and transporting oxygen to support aerobic metabolism. Many molluscs deposit embryos in egg masses, which lack mechanisms for active oxygen uptake or transport. In aquatic environments, diffusion-driven metabolic systems such as egg masses are oxygen-limited because of the comparatively low solubility and diffusion rates of O₂ in water, and this limitation increases with the size of the metabolizing structure or organism. Metabolic rate of ectotherms also increases with temperature, leading to predictions that the size of metabolizing structures such as egg masses or individual organisms is increasingly constrained by oxygen limitation as environmental temperatures rise. We tested these ideas using models, laboratory measurements, and field experiments with egg masses and embryos of gastropod species from temperate and Antarctic regions. In both groups, metabolic rate of embryos increased at warmer temperatures, driving a concurrent increase in oxygen limitation for internal embryos in both natural and experimentally-manipulated masses. Field measurements of internal oxygen levels in Antarctic masses showed that masses were mostly normoxic under ambient conditions of flow and temperature (-1.8°C). However, as for many ectothermic taxa, the thermal sensitivity of metabolism of the Antarctic embryos was much higher than that of temperate species; thus, small changes in temperature are likely to lead to hypoxia for embryos in Antarctic egg masses. Compared to temperate masses, egg masses in the Antarctic were larger had much longer diffusion distances (i.e. were much thicker), supporting the hypothesis that the stable, extremely cold temperatures in the Southern Ocean allow structures or organism that require oxygen to reach larger sizes. Field tests with Antarctic gastropods also showed that in keeping with Thorson's Rule, Antarctic taxa have large offspring and nonplanktotrophic larvae. Field outplants also showed that some species spend an extraordinarily long time – up to 8 years or more – in the egg capsule prior to hatching. If the thermal sensitivity of developmental rate is as high as the thermal sensitivity of metabolism, then even small increases in the temperature of the Southern Ocean are likely to profoundly change both the physiology and development of embryos, and the life history dynamics of Antarctic ectotherms in general.

Morphological Stasis

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Although examples of morphological stasis are widely recognised from the fossil record, the mechanisms that maintain a constant phenotype over many generations are still debated. Many biologists regard constraining (stabilising) selection as an adequate explanation. However, constraining selection for an optimal phenotype requires a constant environment, something that palaeontologists are less confident about. The time scale of morphological stasis can be measured in any unit but a lineage that survived for half a million years (or more) is unlikely to have lived without environmental variation. Taxa possibly shift their range to track their optimal habitat while maintaining an ‘optimal’ phenotype. It has also been suggested that gene flow among populations can limit morphological change, which might contribute to morphological stasis in the fossil record. We have tackled the problem of morphological stasis using real fossil snail data and simulated datasets to consider model selection. Our ability to differentiate stasis from a random walk is greatly influenced by the number of population samples in a time series, suggesting that our current datasets might be skewing our view of what is “normal”. Using fossil datasets of the marine snail *Penion* we show that defining a single “lineage” will influence our inferences. Using fossil land snails *Placostylus* we observe shell shape stasis even when environments were not constant, suggesting a role for gene flow in limiting or slowing morphological change.

Activity of invasive slug *Limax maximus* in relation to climate conditions based on citizen's observations

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Citizen science is a powerful tool that can be used to resolve the problems of introduced species. An amateur naturalist and presenter of this talk, S. Watanabe, recorded the total number of *Limax maximus* (Limacidae, Pulmonata) individuals along a fixed census route almost every day for two years on Hokkaido Island, Japan. *L. maximus* is considered one of the most widely spread terrestrial molluscs in the world and is a pest of agricultural and horticultural crops. We investigated how weather conditions were correlated to the intensity of slug activity using for the first time in ecology the recently developed statistical analyses, Bayesian regularization regression with comparisons among Laplace, Horseshoe and Horseshoe+ priors for the first time in ecology. The slug counts were compared with meteorological data from 5:00 in the morning on the day of observation (OT- and OD-models) and the day before observation (DBOD-models). The OT- and OD-models were more supported than the DBOD-models based on the WAIC scores, and the meteorological predictors selected in the OT-, OD- and DBOD-models were different. The probability of slug appearance was increased on mornings with higher than 20-year-average humidity (%) and lower than average wind velocity (m/s) and precipitation (mm) values in the OT-models. OD-models showed a pattern similar to OT-models in the probability of slug appearance, but also suggested other meteorological predictors for slug activities; positive effect of solar radiation (MJ) for example. Five meteorological predictors, mean and highest temperature (°C), wind velocity (m/s), precipitation amount (mm) and atmospheric pressure (hPa), were selected as the effective factors for the counts in the DBOD-models. Therefore, the DBOD-models will be valuable for the prediction of slug activity in the future, much like a weather forecast.

Molecular identification of Conidae (Gastropoda) at Verde Island, Batangas, Philippines using mitochondrial gene markers cytochrome oxidase 1 and 16s rRNA

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The Verde Island Passage is home to a great diversity of marine organisms. Given its diversity, this presents an opportunity for discovering economically and pharmacologically important Conidae species. Hence, a record on the available and remaining *Conus* species in the area is needed in building data on the regional collection of this group. To gather accurate data, identification using mitochondrial gene markers 16S rRNA and COI were employed.

Forty-five (45) samples were collected and initially separated by phenotype. DNA was extracted and the mitochondrial COI and 16S gene markers were amplified through Polymerase Chain Reaction using specific primers. Sequences were assembled and subjected to NCBI BLAST for identification. Molecular phylogeny was generated using Neighbor Joining, Maximum Parsimony and Maximum Likelihood Methods.

Twenty-one (21) distinct species were identified for both the gene markers. Phylogenetic analysis in both gene markers of majority of the samples revealed consistency with the molecular phylogeny of *Conus* species. Twenty six (26) samples had matching identities using the two gene markers, thereby confirming their species identification. Eleven samples (11) had differences in identification. Tree topologies in both COI and 16S rRNA were essentially similar. Most species formed well defined lineages and consistent clades with robust statistical supports. This study contributes to a growing Conidae data, particularly contributing pertinent identification of the species inhabiting an ecologically significant marine habitat, the Verde Island.

Resolving a quandary: the preservation of chiton valves

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Chitons are marine molluscs common worldwide and are rare in the fossil and sediment records. Although their rarity in the fossil records does not seem to be surprising due to their aragonitic shell, previous work suggests that they may be able to resist dissolution. If their mineralogy does not explain why chitons are removed from the record, then the effect of taphonomic forces on chiton valves should be examined. Chitons have been understudied in literature discussing taphonomy and only 37 species have had their microstructure and mineralogy described; therefore describing valve ultrastructure and determining the effects of taphonomic forces on chiton skeletal material is worthwhile. X-ray Diffractometry (XRD) and Scanning Electron Microscopy (SEM) were used to determine the valve ultrastructure of eight New Zealand chiton species (*Acanthochitona zelandica*, *Notoplax violacea*, *Chiton glaucus*, *Onithochiton neglectus*, *Sypharochiton pelliserpentis*, *Sypharochiton sinclairi*, *Ischnochiton maorianus*, and *Leptochiton inquinatus*). Chiton valves from these species have three to seven mineral sublayers and aesthete channels (nerve tissue) running through their dorsal most layer, the tegmentum. Isolated valves from these eight species were either tumbled in a rock tumbler to test their ability to resist abrasion or subjected to one of two pH treatments to determine their ability to resist dissolution. Valve ultrastructure and the aesthete channels were found to play a key role in the preservation of chiton valves. These channels initially protect the tegmentum against dissolution but allow it to be easily abraded away whereas the ventral layer, the articulamentum, is more vulnerable to dissolution than abrasion. Since these forces act in tandem in the marine environment they can wear away at both surfaces of the valve. It is likely that once the organic tissue within the tegmentum decays, the valve structure is either destroyed or rendered unrecognizable.

Snail shell shape and size suggests hybridisation of two species: a comparison of supervised and unsupervised learning algorithms with geometric morphometric data for species identification

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The combination of machine learning and geometric morphometric offers new opportunities to investigate morphological variation in groups of related individuals. We applied both supervised and unsupervised learning algorithms to a geometric morphometric dataset to investigate morphological variation in an endemic land snail from the New Caledonia, Isle of Pines, where two species of *Placostylus* snails coexist. Using a training dataset based on genetic identification of specimens supervised learning algorithms failed to classify all of our individuals into the two described species. Unsupervised learning supported this result and found the optimal separation of our data was into three clusters. Two of these clusters correspond to the established species *Placostylus fibratus* and *Placostylus porphyrostomus* while the third group identified was intermediate in both shape and size. Here we discuss biological and methodological implications of these result, and compare morphological variation with mitochondrial genetic diversity.

Evolutionary phenotype variation of *Cepaea nemoralis* in the Pyrenees

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Species with short generation times, such as many invertebrates, may offer a quick evolutionary vision to changing selection pressures. Perhaps the pre-eminent model, the snail *Cepaea nemoralis* will help to understand polymorphism variation. *C. nemoralis* is a predominantly west European species with a polymorphic shell for three main inherited features, and shell ground colour, banding and band pigmentation. There are many examples of polymorphisms such as classic examples as Müllerian mimic butterfly (*Heliconius numata*), the two-spotted ladybird (*Adalia bipunctata*) or the scarlet tiger moth (*Callimorpha dominula*). Maintenance of phenotype variation of species during rapid climate changes will depend on the efficacy of evolutionary adaptation. Furthermore, to avoid population declines due to significant environmental changes, selective factors may lead to shift in genetically adaptive traits. Therefore, how does changing climate affect the distribution of the different phenotypes due to selection? There is debate on how the phenotype is affected by environmental selective factors. Therefore, one of the emerging strengths of working with *Cepaea* is that historic collections can be compared against modern day samples, for instance to understand the impact of changing climate and habitat upon shell morph frequencies, and so infer the potential impact of natural selection. In nearly all studies reported to date, absolute change in frequencies of the various shell morphs have been reported, but the direction is not always consistent. The climate and human activity in the Pyrenees has significantly changed since 1960 which the average of temperature has increased by 2.8–4.0 degrees, more than in Europe. Furthermore, Central Pyrenees shows a particular local associations of phenotype variation. A comparison of shell features in *C. nemoralis* from historical data against actual sampling in the same location in the Pyrenees has been done. Considerable changes in almost all the main valleys in various phenotypes have occurred.

Resilience of molluscs to a changing ocean

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Predicting the impact of warmer and more acidic oceans on molluscs is a critical endeavor. Early experiments, at the start of this century, were based on acute, single life-history stage studies and unsurprisingly found overall negative impacts on larval, juvenile and adult stages. With improved experimental designs, chronic transgenerational studies where parents were exposed to ocean acidification during reproductive conditioning created resulted in resilient offspring. Such resilience persisted to adulthood and into the next generation. Most recent experiments, based in the real multistressor world, paint a more negative picture of resilience of molluscs to changing oceans. When offspring from exposed parents were reared under elevated CO₂ in combination with other environmental stressors they had lower survival compared to offspring from non-exposed parents. Experiments where molluscs were exposed to elevated CO₂ either in natural or experimental conditions show altered sex ratios (more females than males), increased predation rates and shifts in the composition of biogenic habitat which molluscs create which alters assemblage biodiversity. Understanding the impacts of climate change on molluscs along our coastlines and the capacity for resilience is sure to be the focus of the next decade of research.

Ancient aquaculture and the mystery of the disappearing surf clams

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The toheroa (*Paphies ventricosa*), is a New Zealand endemic surf clam of huge cultural importance to both Māori and Pakeha. With a disjunct geographic distribution, unlike that of any other New Zealand marine invertebrate, toheroa were formally abundant on a handful of New Zealand's west coast beaches until unsustainable harvesting during the early to mid-20th century led to their collapse and the closure of the fishery. Despite having been protected for over 40 years, toheroa have, for unknown reasons, failed to recover, with some populations continuing to decline. Current research has led us to hypothesise that the present-day distribution of this taonga (treasured) species is influenced by historical aquaculture, in the form of human-mediated translocations. This hypothesis is now being tested through a multidisciplinary research programme combining mātauranga Māori (Māori knowledge) and oral history with archaeology, anthropology and molecular ecology. Through this transdisciplinary research programme we are gaining a better understanding of the ecology of toheroa, the extent to which early Māori manipulated their marine environment and developing new strategies for the restoration of this iconic species.

Understanding local adaptation of *Onithochiton neglectus* (Polyplacophora:Chitonidae) across an environmental gradient based on genetic, genomic and morphological data

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The New Zealand marine environment has complex oceanographic features and extends over 23° of latitude, spanning a gradient of sea surface temperature. These factors influence population connectivity and local adaptation of many species, as reported by previous population and seascape genetic studies. This project aims to evaluate the degree of population connectivity and local adaptation of the morphologically variable etched chiton (*Onithochiton neglectus*), distributed along the New Zealand coast. This is a species endemic to New Zealand, with brooding behaviour and very low mobility, possibly leading to low gene flow. Using mitochondrial DNA markers (mt-DNA), we will assess *O. neglectus* phylogeography and genetic diversity. The mt-DNA results will be compared with results from genome-wide Single Nucleotide Polymorphisms (SNP) generated by Genotyping by Sequencing. The SNP will also be used in genomic scans to detect genomic regions that are putatively under natural selection, and in a seascape genomics approach to test for genomic-environment association. In addition, we will assess spatial variation in shell shape, and compare it with the variation of mt-DNA and SNP. The preliminary results for mt-DNA show three separate groups: Northern North Island, Central New Zealand and Southern New Zealand (including the New Zealand South Island and the Sub-Antarctic Islands). The first SNP results match the mt-DNA pattern, but more populations are still to be included. The shell shape results only separate Northern samples from all the others, but these analysis are not yet complete. The downstream analyses using SNPs will be important to understand which evolutionary forces are possibly driving such a pattern. This study contributes to our understanding of how different marine species respond to the factors shaping their habitat, and ultimately advances our fundamental knowledge for biodiversity protection and sustainability in the oceans of a changing world.

The creepy, the slimy and the ugly: how scientists communicate science with invertebrates

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Invertebrates comprise over 97% of the species known to science and their ecological importance is unmistakable, a fact which remains largely unknown to the public. These animals are typically perceived as ugly, bizarre, or even repulsive creatures, not being charismatic enough for people to bond with. As such, discussing invertebrate-related topics is uncomfortable for most of the public. Contrary to vertebrates and plants, science communication regarding invertebrates often come from scientists themselves, through museums, outreach activities, and social media.

Given the weight that public opinion has in conservation, it is vital to make people aware of invertebrates. The public, however, needs to “connect” with the topic, so the manner in which communication is approached is critical. Unfortunately, science communication has long been based on assumptions of how to better do it and of what the public wants; thus, more research on methodology and effectiveness is needed. We conducted an online survey with over 200 scientists worldwide to uncover their approaches and practices. We presented them a questionnaire with 18 questions: 9 related to personal information, 9 pertaining to science communication; different types of questions (e.g., open-ended or close-ended) were used depending on circumstances.

Most respondents were male (54%), and most live in the USA (40%). Their positions within their institutions varied greatly, but, as expected, most science communicators are researchers or professors (~25% each), with many graduate students also involved (~17%). The majority was involved with one or two science outreach events per month and North Americans engaged in more activities than everyone else. Most of the respondents identified themselves as malacologists (~33%), followed by entomologists (~19%). In their experience, the invertebrate groups that tend to fascinate the public the most are lepidopterans and cephalopods (~12.5% each). Some species were singled out as being particularly good in capturing the public’s attention: *Danaus plexippus*, *Octopus vulgaris*, *Apis mellifera*, *Architeuthis dux*, and *Nautilus* spp.

The most common overarching topic usually addressed by respondents was biodiversity, with conservation and evolution also being commonly used. The main approaches to engage the public were the pleasing aesthetics of some invertebrate groups and the perceived amazing feats some animals are capable of. “Disturbing” facets of the animals’ biology were also commonly employed. Regarding hands-on activities, respondents typically used preserved museum specimens during outreach activities. A final (optional) open-ended question asked personal experiences and stories and most respondents pointed out the importance of science communication being done by scientists and including outdoor and hands-on activities. The power of social media for science communication was also a recurring topic.

Science communication is not simply a one-way, top-down process, but rather it should be an ongoing dialogue between communicators and the public. As such, the next step of our research will focus on how the public responds to invertebrate-related topics and what they hope to receive from communicators.

The importance of terrestrial and freshwater molluscs for palaeoecological studies: examples from the German Miocene

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Terrestrial and freshwater molluscs are present in most continental settings, including fossiliferous deposits. However, their potential is often overlooked in paleontological studies, which until relatively recently rarely went beyond alpha taxonomy. These animals can be used for a broad range of studies, including palaeobiogeography, biostratigraphy and, more importantly for the present discussion, palaeoecology and palaeoenvironmental reconstructions. In fact, new methodologies and tools have led to an increase in studies investigating the latter areas. There are some main venues of research in which molluscs can be used in palaeoecological studies and typically they are complementary to one another: (1) actualistic ecological approach, (2) taphonomy, and (3) isotope analysis. Naturally, other information can also be critical, such as faunal composition and ichnofossils.

(1) The actualistic approach is widely used, albeit in an almost informal way. This approach joins two known palaeoecological methodologies: the Extant Phylogenetic Bracket (used to infer the probability of the existence of an unpreserved trait) and the Nearest Living Relative method (used in palaeobotanical studies for climate reconstruction). In short, it uses natural history data of close extant relatives (typically congeners) of the fossil molluscs to define a range of possible traits and habitats for them. (2) Taphonomy studies the events that take place between the death of an organism and its fossilisation. It can define to which extent the fossil assemblage reflects a living community and thus inform ecological interpretations. (3) Molluscan shells, if properly preserved, retain the isotopic signature of the living animal, which in turn reflects the environment. The analysis of stable (carbon and oxygen) and radiogenic (e.g., strontium) isotopes of the shell can help determine a wide range of ecological and environmental features, such as: diet, water chemistry, rainfall, seasonality and hydrology.

Nevertheless, while palaeoecological studies are on the rise, taxonomy became seen as an outdated branch of science, despite being inextricably intertwined with it. This is especially clear for the case of actualistic analyses, where a solid taxonomic framework and proper species identification are key to a successful study. Furthermore, the link between palaeontology and zoology, that is between fossil and living organisms, is also integral to success; for instance, taphonomy and isotope studies would greatly benefit from more systematic research on extant species.

The German Miocene counts with several fossil Lagerstätten, where terrestrial and freshwater molluscs abound. These deposits (e.g., Sandelzhausen and Randeck Maar) can be used to illustrate each of the above mentioned research strategies. They also allow us to explore the strengths and shortcomings of each methodology, as well as to understand how a joint approach can extract the most palaeoecological information.

Behavioural response of juvenile *Tridacna gigas* exposed to low salinity or elevated seawater temperature

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Giant clams have evolved large shells that protect them from harsh environments. However, little is known on the response of juvenile *Tridacna gigas* when exposed to different stressful conditions. We examined the behavioural responses of juvenile *T. gigas* when exposed to either low salinity or elevated temperature. At low salinity (20 ppt) and ambient temperature (29°C), most of the giant clams (90%) remained closed for up to 4-6 hours of exposure, a response that may help maintain the salinity inside the clam shells. The clams were also unable to attach firmly to substrate and did not exhibit a shadow response. After 24 hours of exposure to low salinity, 82% of the clams showed retracted mantles, an indication of stress, and 9% died. On the other hand, at elevated temperature (34°C) and ambient salinity (32 ppt), most clams exhibited open valves and strong substrate attachment. About 55% of the clams demonstrated a shadow response, while 44% had retracted mantles and 4% died. When surviving clams were allowed to recover for 48 hours at ambient temperature and salinity, more clams exhibited the shadow response (68% to 75%) and 48% from the low salinity treatment were able to attach to the substrate. Results suggest that juvenile *T. gigas* respond differently when exposed to different types of stressful conditions, which will have implications on their survival under changing environmental conditions.

Skeletal carbonate mineralogy of abalone, especially *Haliotis iris* Gmelin, 1791.

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Shell structure in the gastropod genus *Haliotis* (abalone) is well known. Protoconch skeletons are mostly amorphous calcium carbonate, which in the veliger stage gradually crystallise into aragonite. Juvenile shells in most species are monomineralic (usually aragonitic), but adult shells differentiate into discrete layers: an inner nacreous aragonitic layer overlain by a prismatic layer, which in turn lies under an organic periostracum protecting the shell from sea water. The outer prismatic layer is the most variable; it may be calcitic (e.g., *H. rufescens*), aragonitic (e.g., *H. asinina*) or both (e.g., *H. rubra*). A thorough literature review provided mineralogical information on at least 18 species in this genus – which is 30% of the ~60 extant species.

We acquired and measured skeletal carbonate mineralogy of several New Zealand and Australian species. It became clear that adult shells of *Haliotis iris* (black-footed paua endemic to New Zealand) had an unusual mineralogical signature, with both low and high-Mg calcite as well as aragonite present.

To investigate this further, we developed a new method for determining proportions of three carbonate minerals in a single powdered shell sample using X-Ray Diffractometry. We then applied it to *Haliotis iris* shells of various ages and sizes from aquaculture farms, from other experiments, and from local subtidal kelp forests in the South Island, New Zealand. Using our data alongside published data, we have acquired mineralogical measurements for over 300 specimens of *Haliotis iris*, many of which have robust replication. Such a rich data set allows us to examine the effects of ontogeny, locality, encrustation and environment on skeletal mineralogy in this important shell fishery.

The retention of juvenile *Perna canaliculus* in aquaculture

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New Zealand's mussel industry is worth around NZ\$250 million and accounts for over 70% of the total export earnings from aquaculture. This important industry is heavily reliant on wild-caught juveniles of the green-lipped mussel, *Perna canaliculus*, and can be heavily impacted by fluctuations in their supply. Furthermore, the first months of the aquaculture cycle are plagued by high losses of juveniles, an issue commonly referred to as poor 'retention' that is a significant constraint to the production and growth of the mussel aquaculture industry. However, the timing and magnitude of losses of juvenile mussels, let alone their causes, are unknown and therefore cannot be managed. To address this research gap, we carried out a series of field experiments and followed deployments of juveniles for the first 3 – 5 months of the aquaculture cycle. Greater than 65% of the initial starting densities of juvenile *P. canaliculus* were lost during these experiments. The greatest numbers of juveniles (> 40 %) were lost soon after deployment (< 2 weeks) with the losses continuing at reduced rates throughout the remainder of the study periods. We use experimental data to consider the roles of biofouling development, behaviour of the mussels, and their mortality as potential causes underlying the massive losses of mussels observed in this study. Finally, we discuss routes for future research to address the issue of juvenile-losses in mussel aquaculture in New Zealand.

Contrasting phylogeography of two limpet genera in the Southern Ocean

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Molecular techniques are increasingly used to elucidate the phylogenetic relationships among molluscan species and to delineate their various geographical ranges. Such approaches have been particularly useful in groups of cryptic species and those with few or confusing conchological characters. Here we examine the relationships among two groups of limpets that are abundant on rocky coasts of the Southern Ocean. Both groups are associated to a greater or lesser degree with the bull kelp, *Durvillaea antarctica*, which is now recognized as an efficient long-distance rafter that is capable of carrying a host of invertebrate species vast distances across the Southern Ocean. Nevertheless, the two limpet groups show very different phylogeographic patterns. Members of the patellogastropod genus *Nacella* occur on numerous subantarctic islands, with most island groups having endemic species that are closely related to species on islands upstream or downstream in the Antarctic Circumpolar Current. Apparently, colonization by *Nacella* of new island groups shortly after their emergence often leads to speciation. By contrast, two cryptic species in the pulmonate genus *Siphonaria*, *S. lateralis* and *S. fuegiensis*, are broadly co-distributed across the sub-Antarctic and exhibit low levels of genetic diversity across this range. Understanding the evolutionary history of these groups clearly requires further information, which we suggest comes from an understanding of their ecology and reproductive biology.

Activating Kaitiakitanga (environmental custodianship) through pipi relocation “what are we enhancing”

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Pipi (*Paphies australis*) is a shellfish of cultural significance to the indigenous Maori of Tauranga Moana, Bay of Plenty. With the impending threat of losing a large portion of a prominent pipi bed to dredging, the Kaitiaki (indigenous custodians) of Tauranga Moana activated and developed a Pipi Relocation Programme, which involved moving pipi from the proposed dredged area to selected sites within the Tauranga Harbour. This presentation will provide an overview of the Pipi Relocation Programme. We will discuss how both Mātauranga Māori (indigenous knowledge) and western science were synergistic in their utilisation, to guide and enhance community experiences and involvement in the project.

Mātauranga Māori is a living and breathing knowledge system, it is the basis of Maori environmental custodianship and it is a vital and central component to understanding New Zealand’s natural ecological systems. The Māori world view sees people as part of the natural ecosystem, as a result the Māori language and culture are inextricably linked to the environment. Ecological restoration, species specific or integrated, can be regarded as a restorative action toward Māori traditions and cultural resilience. We will discuss how Mātauranga Māori provided the foundations of the pipi project and as a result saw the development of a unique Māori approach to species-based enhancement and community restorative action. We will share some of the major outcomes of the pipi relocation project and discuss how pipi were key to activating and empowering kaitiakitanga.

Finally, we will talk about the role western science has played in a Māori approach to species restoration and education as well as how western science contributed to outcomes and objectives based on Māori principles of environmental custodianship.

Diversity within and conservation of New Zealand's large land snail *Powelliphanta*

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The carnivorous land snail *Powelliphanta* is endemic to New Zealand and notable for its large, brightly patterned and coloured shells. As spot endemics in a land invaded by many new predators since the late arrival of humans, their numbers have dwindled. The challenge has been to determine whether the spectacular radiation of shell morphology was confounding taxonomy, and if not, how to protect all that diversity. Results from recent genetic and morphological examination of the genus are briefly outlined. Efforts over the last 30 years to protect *Powelliphanta* from invasive species are described, and the cautionary tale of a snail species whose dangerous habitat niche was valuable coal measures is told.

Biodiversity, biogeography and vulnerability of hydrothermal vents: a case study using bathymodioline mussels

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Hydrothermal vent habitats represent a very small proportion of the seafloor, yet they host diverse, unique and poorly-known faunas. Due to their formations of high-value poly-metallic deposits, many vent fields are being evaluated for mineral extraction, necessitating an improved understanding of vent communities and connectivity. Correct taxonomic determination of specimens is important to assay the sensitivity of habitats to exploitation and to accurately quantify patterns of regional connectivity. Restriction of analyses to named species or broad genus-level identifications fails to account for the most sensitive taxa: regional endemics. We present a genetic dataset of bathymodioline mussels with a focus on the southwest Pacific and discuss what such datasets can tell us about the vulnerability of venting systems and, more importantly, what they can't.

Growth rates of potamidid snails in mangroves in northern Australia

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Mudwhelks of the genera *Terebralia* and *Telescopium* dominate the sessile invertebrate epifauna of many Indo-West Pacific mangroves and play an essential role in converting mangrove detritus into animal tissue available to higher trophic levels in the system. Growth rates were obtained for three species using data from tagging experiments fitted to the von Bertalanffy growth equation. *Terebralia palustris*, *Ter. semistriata* and *Telescopium telescopium* were tagged in Darwin, Northern Territory. *Terebralia palustris* and *Ter. semistriata* were tagged at two sites near Dampier, Western Australia. These are the largest snails in mangroves. Both species of *Terebralia* grew faster and larger in Darwin, near the centre of their ranges; growth and adult sizes were less in Dampier, near their southern range limit. The small (up to 6cm) *Terebralia semistriata* matures in about four to six years, *Ter. palustris* (up to 19cm) in 10 to 12 years and *Tel. telescopium* (up to 13cm) in about 10 to 12 years. However, the high proportion of adults in some populations of all three species suggest the lifespans may be much longer.

Un-earthing the true diversity of the Australian land snail genus *Bothriembryon* (Gastropoda, Orthalicoidea)

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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 relict distributions in South America, Africa, Polynesia and Australia. In collaboration with the Naturalis Biodiversity Centre, the Western Australian Museum commenced a large study on the group resulting in firstly a catalogue of Australian type material in 2012. During this work it was revealed the nomenclatural history of the generic name *Bothriembryon* was invalid and a submission was made to the ICZN in 2018 to conserve the name. No targeted phylogenetic analysis has been constructed to test species boundaries in the genus *Bothriembryon* and little data exist on the biogeography and ecology of most species. 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. The work to document new lineages has already begun, with CT scanning used to document the anatomical morphology of *B.sophiarum*. During this study the WA Museum modern mollusc collection was curated, and combined with fieldwork, emphasis was given to better understanding the eight threatened species of *Bothriembryon* Pilsbry, 1894 (22% of all extant species) listed at state and international levels. All but one of these nominally threatened taxa is found in south-western Western Australia (SWWA). New ecological and behavioural data was generated and, importantly, the number of records of the seven nominally threatened SWWA species in Australian Museum and University collections was almost doubled. *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. praecelsus* 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. In addition, the WA Museum fossil mollusc collection was curated to provide a spatial and temporal aspect to species distributions. 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.

Resolving the Cenozoic mollusc fossil record of New Zealand: unravelling macroevolution

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Despite centuries of research and debate, biologists and paleontologists still don't know what fundamentally controls biodiversity. Patterns of biodiversity over geological timescales intrinsically represent macroevolution. Fossilised marine molluscs provide an important resource for understanding patterns of biodiversity change due to their high preservation potential and long geological history. Prior research has focused on global patterns of marine mollusc biodiversity through the Phanerozoic, with limited focus on smaller spatial scales and their relationship to the stratigraphic record. Is there an overarching global force that controls patterns in biodiversity, or is variation manifested as regional or local changes, or both, that cumulatively contribute to the global signal? In order to address these questions, all spatial scales must be considered.

A major problem for paleontologists is bias, related to both the quality and quantity of preserved sedimentary rock and sampling of the fossil record, warping our perception of true biodiversity patterns. Sampling biases have largely been accounted for, however, quantifying patterns in the sedimentary rock record and understanding their relationship to biodiversity patterns is key to resolving the fossil record and unravelling macroevolution. New Zealand provides a model system to test some of these questions due to its isolation and relatively complete molluscan fossil and sedimentary rock records.

Here I focus on patterns of change in sedimentary environment and biodiversity of marine molluscs in New Zealand through the Cenozoic, 66 million years ago (Ma) to present. Data sources include the Fossil Record Electronic Database, and new Pleistocene (2.58 Ma to 0.13 Ma) samples collected from shallow marine paleoenvironments in Hawke's Bay. Molluscan biodiversity patterns are compared to proxies for environmental heterogeneity at relevant scales. Preliminary results suggest regional marine biodiversity fluctuates greatly throughout the Cenozoic with a notable decrease in spatial turnover of faunas during the Late Oligocene (27.82 Ma to 23.03 Ma), coinciding with maximum flooding, and between 3 Ma and present. Local scale patterns show high variability of biodiversity between 2.58 Ma and 0.13 Ma in Hawke's Bay, with a notable change in fauna spatially and temporally.

Green-lipped mussel *Perna canaliculus*' ability to cope with low seawater temperatures: Implications for survival, aerial exposure and heart rate

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Seawater temperature fluctuations particularly affect marine ectotherms such as mussels. In New Zealand the thermal biology of the green-lipped mussel, *Perna canaliculus*, has been widely studied due to its ecological, cultural, and economic importance. The majority of these studies have focused on the upper limits of the thermal window of this species; however, within its natural bathymetrical and latitudinal distribution this mussel can also be exposed to cold temperatures, especially during winter. The aquaculture industry in New Zealand has also shown an interest in understanding the response of *P. canaliculus* to lower temperatures as that information can be applied to the management and handling of mussels after harvest. Therefore, considering the above, we have conducted a series of studies aiming to understand the effect of exposure to colder seawater temperatures on mussel survival at 0 °C, mussel heart rate, and aerial exposure survival after sub-lethal cold shock.

Mussels survived an acute transfer to 0 °C seawater for up to ten days, however, the mussels died 48h after transfer back to warmer seawater (13 °C). When mussels were exposed to a slower decrease in seawater temperature (~0.5 °C h⁻¹), their heart rate decreased with temperature until it was undetectable at temperatures close to 0 °C at which they remained for ~14h. Surprisingly, when the seawater temperature was increased back up, the mussels recovered, and their heart rate reached normal levels. Moreover, from a practical point of view, exposure to cold seawater (i.e., sublethal cold shock) induced behavioural (gaping) and physiological changes that allowed the mussels to cope better with the emersion stress during aerial exposure, enhancing their survival.

In summary, this mussel species can survive exposure to very low seawater temperatures. However, survival depends upon the temperature, time of exposure and the rate of temperature change. Depending on the conditions of the exposure, the ability of this species to handle lower temperatures can be used to harness their behaviour and physiological capabilities to improve survival during transportation of live mussels.

The effect of environment to species composition and phylogenetic study of micro snails in New Zealand

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New Zealand has the highest species diversity of land snails in the world (Solem 1984). Furthermore, 96% of species of snails in New Zealand are endemic (Spencer et al. 2009). Some large endangered species within the genera *Powelliphanta*, *Placostylus* and *Paryphanta* have been studied, but the more numerous micro snails have received little attention. Due to their extremely high species diversity the New Zealand micro snails provide excellent material to understand basic processes in evolution & ecology, study New Zealand phylogeography, and identify biodiversity hotspots. Therefore, we focus on micro snails and have started to assemble basic information about the distribution of genetic and species-level diversity. In this study, we examined the relationship between species composition and environmental factors on lime stone outcrops and moist forest in central North island, New Zealand. We obtained snail samples from the leaf litter from three locations, and classified micro snails on the basis of shell traits. Species diversity and faunal similarity were compared among the three sampling locations. We examined mtDNA sequence variation for about 200 individuals from 20 putative species, and inferred phylogenetic relationships. Our data suggests species composition is very similar among our three sampling locations. However, even at this small geographic scale we did detect regional genetic variation within some morpho-species. More study is required to explain this interspecific variation and expansion to sample more distant sites is planned.

Development of stress and health biomarkers in the Green-lipped mussel *Perna canaliculus*

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The green-lipped mussel, *Perna canaliculus*, is an important keystone species as well as one of New Zealand's most significant aquaculture crops. Therefore, this mollusc was selected as a model organism for the development of stress and health biomarkers. Stressful conditions, caused by abiotic (e.g., environmental, pollutants) or biotic (e.g., pathogens) factors, can result in cellular damage in an organism (i.e., oxidative stress) due to an accumulation of reactive oxygen species (ROS). The accumulation of these damaging agents can affect overall performance in an organism. However, under stressful conditions, organisms have the capacity to mitigate some of the effects of these damaging agents through an increase in the production of antioxidant enzymes and chaperone proteins such as heat shock proteins (HSP). Thus, our focus is to quantify and understand the production dynamics of these biomarkers. To achieve this, we are developing an enzyme-linked immunosorbent assay (ELISA) to quantify production of HSP70, as well as assessing the suitability of assays for a suite of oxidative stress markers, including protein carbonyls, lipid hydroperoxides, enzymatic antioxidants and oxidative DNA damage. In addition, we are developing fluorescence microscopy assays to determine the nutritional status of animals and the digestibility of food.

Larval settlement, metamorphosis and juvenile byssal attachment collectively represent a critical developmental bottleneck for *P. canaliculus*, determining net recruitment in both wild and commercial cultured populations. While the biomarkers detailed above are currently being applied to larvae and juveniles of the green-lipped mussel, they will also be tested for use in other molluscs (e.g., oysters, geoducks, abalone). Overall, the development of these biomarker assays will improve the understanding of the effects of key stressors associated with disease, husbandry and climate change upon key New Zealand molluscs of economic and ecological importance.

Identifying evolutionary lineages of marine snails

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Overlapping intra and interspecific variation in shell shape and size is a recurrent challenge for buccinoid marine snail taxonomy, especially for three Pacific genera: *Kelletia*, *Antarctoneptunea* and *Penion*. We estimated molecular phylogenetic trees and digitised shell morphology for all living species of these genera. We investigated if variation in shell shape and size aligned with deep phylogenetic splits reflecting generic-level classification. Results revealed a surprising level of concordance, given that alternative information (e.g. geography, ecology) was absent from morphometric analyses. *Penion* and *Kelletia* were readily distinguished based on shell shape and size, and although *Antarctoneptunea* was somewhat similar in shape to *Penion*, it was easily separated where shell size was included. The molecular and geometric morphometric results agreed even where they disputed previous taxonomic hypotheses. Results supported the recognition of a new species and the reclassification of another.

Adaptive evolution of mud-tidal gastropod (genus *Batillaria*) to the salt stress

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Salinity is one of the most crucial environmental factors that structures biogeographic boundaries of aquatic organisms, affecting distribution and contributing to successful biological invasion, abundance, and behaviour. However, relatively little research has focused on effects of salt stress on coastal invertebrates. In this study, we investigated the effects of biotic (genotype) and abiotic factors (origin of organisms, and past exposure to different salinity fluctuation profile) on response to salt stress of the intertidal gastropod *Batillaria attramentaria* through observation on behaviour (locomotion) and patterns of gene expression (using RNA-seq). We conducted behavioural and transcriptomic experiments to the *B. attramentaria*, that were collected from native (Korea and Japan) to introduced (the USA) ranges, through long-term (30 day) acclimation to a range of salinities (43, 33 (control), 23, 13, and 3 Practical Salinity Unit (PSU)). We found that the intertidal *B. attramentaria* is able to tolerate a broad range of salinity from 13 to 43 PSU, but not the low salinity of 3 PSU. Behavioural experiments showed that salt stress significantly influenced snails' movement, with lower salinity resulting in shorter movement distance. Transcriptomic analyses revealed critical metabolic pathways and genes potentially involved in acclimation to salt stress of this species. Results from a comparative behavioural and transcriptional analyses suggested that long-term introduction of the *B. attramentaria* to the coastline of USA have resulted in different tolerant capacity to salt stress of the introduced snails to the native congeners, and that is possibly caused by the past exposure to different salinity fluctuation profiles. Additionally, the comparative transcriptomic analyses also acknowledged potential genes that may contribute to successful biological invasion the species. In general, our study presents a robust, integrative laboratory-based approach to investigate the effects of salt stress on a non-model gastropod, which is facing detrimental consequences of environmental change. The current genetic data provide a wealth of reference data for further research on mechanisms of ionic and osmotic regulation underneath the successful invasion of this non-model marine organisms and adaptive evolution of this coastal gastropod.

Exploring an undocumented diversification of endoparasitic gastropods in Antarctica

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Benthic marine invertebrates are diverse in Antarctica, but little is known about their parasitic counterparts. *Asterophila*, a genus of eulimid gastropod, is endoparasitic in asteroid sea stars. There are four known members in this genus, one of which has been described from the Antarctica Peninsula and forms part of a putative radiation of species in this region. In order to further explore this radiation, 61 *Asterophila* specimens were collected from 36 hosts in Antarctica. Four genes were used for phylogenetic reconstruction and species delimitation and a test of host-parasite co-evolution was conducted by employing global congruence and event-based reconciliation analyses. The resulting *Asterophila* phylogeny shows high support for nine species-level entities in Antarctica, suggesting undocumented diversity in this group. These nine putative species show varying degrees of host specificity and species with more extensive sampling show higher host diversity. Significant global congruence between host and parasite phylogenies was detected, suggesting these groups are co-evolving, but the majority of links were explained by host switching rather than strict co-speciation. Investigating co-phylogenetic patterns provides insight into whether host and parasite lineages are evolving in synchrony, which may have important implications for biodiversity conservation. In all, these results advance our understanding of diversity and the processes driving this diversity in Antarctica.

Ependymins in molluscs – expansions of a multifunctional protein family

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Ependymins were originally identified in fish where they perform essential roles in memory consolidation and the development of the nervous system. Since this discovery, related proteins (ependymin-related proteins, EPDRs) have been identified in a range of animal taxa, where they are expressed in a range of different tissues and have been found to perform roles as diverse as conspecific signalling, connective tissue development, and regeneration. Large expansions of the EPDR gene family can be observed within some animal groups, and especially within the molluscs. Phylogenetic analysis reveals that some EPDR clades contain representatives from most of the surveyed gastropod and bivalve taxa, indicating that diversification occurred early within molluscan evolution whereas others are restricted to particular classes or to individual species. Previous research has implicated ependymin genes within molluscan shell formation, however *in-situ* hybridisation reveals that EPDRs may play a wide range of roles within molluscan development.

Comparing indigenous and western methods of kākahi translocation: implications for ecological restoration

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Population translocation is an important tool in conservation ecology. Improper handling of organisms during translocation can negatively affect their performance, and this could ultimately undermine the translocation effort. Freshwater mussels (Family Unionidae) burrow into the substrate to reduce the risk of physical displacement and predation, and newly translocated mussels are at heightened risk of displacement and predation until they have secured a position in the substrate. Indigenous peoples have been carrying out population translocations for some time prior to the development of ‘western science’, thus indigenous methods likely have much to offer to the modern conservation space. In Aotearoa/New Zealand, tangata whenua traditionally used kete (woven baskets made of natural materials) to translocate aquatic animals (including mussels—locally known as kākahi) to new environments as part of ahumoana tawhito (ancient aquaculture). In this study we investigated the influence of transport method: traditional (kete stuffed with wet moss), modern (lidded plastic bucket with an aerator), and combination (bucket containing submerged kete and an aerator) on the behaviour (probing propensity) and short-term performance (burrowing rate) of kākahi, as well as the influence of probing propensity on burrowing rate directly. We also tested whether assistance (planting kākahi in the substrate) resulted in enhanced burrowing rates. We found no difference between the modern and hybrid method of transport, however kākahi that were transported using the traditional methods were slower to probe and burrow. Kākahi that were quicker to probe were also quicker to bury, and assistance resulted in faster burrowing rates. We conclude that both handling procedures and individual behavioural traits influence the short-term performance of translocated kākahi and recommend procedures for future translocation projects.

Do New Zealand olive shells (*Amalda* spp.) support punctuated equilibria?

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The olive shells of the genus *Amalda* are a speciose group of neogastropod mollusc with an extensive distribution. In New Zealand there is an excellent fossil record and three endemic species have been cited as providing support for morphological stasis in the fossil record, a prerequisite for punctuated equilibrium. To be confident that the New Zealand *Amalda* species form a continuous evolutionary lineage in the fossil record the assumption that the New Zealand taxa have evolved in geographic isolation was tested. Monophyly of New Zealand species would help exclude the possibility of past dispersal of related species misleading inferences from the fossil record. The hypothesis that New Zealand *Amalda* species evolved in isolation was examined using whole mitogenome and nuclear (45S rDNA) markers from 11 *Amalda* species collected from New Zealand and around the world. The reconstructed phylogenies from both the mitochondrial and nuclear DNA sequences support the hypothesis that within the context of our current sampling the New Zealand *Amalda* are monophyletic. We estimated the timing of cladogenesis within the New Zealand taxa and resolved dates compatible with the fossil record for extant species. We used geometric morphometrics to study the evolution of shell size and shape through time for three lineages. We examined how well morphological change fitted three models: directional change, random walk and stasis. Although we did not detect examples of directional change only half of the traits examined (7/13) provided evidence for morphological stasis.

The role of video game molluscs in science communication and animal conservation

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There is scarcely any doubt that works of fiction can contribute to science communication and environmental education, especially when considering that the most effective way to convey new information is through narratives. Beyond movies and books, video games have grown considerably in the last decade; presently, this new industry far out-performs Hollywood. Therefore, it is only natural to start using games in science communication and education. This can be done via scientific exploration of some aspects of a given game by scientists or communicators, as done by the *Journal of Geek Studies*, *Geek Anthropologist*, and *Journal of Interdisciplinary Science Topics*.

Furthermore, games themselves can educate. The use of games in education, however, has a difficult past: firstly involving concerned parents and secondly because “educational games” are typically so off-putting that they may actually do more harm than good. Even so, there are “actual games” that also bring informative content. *Never Alone* (Upper One Games, 2014), made in partnership with Inuit storytellers, is a perfect example: certain in-game actions unlock short documentaries about the Arctic, its fauna and its people, focusing mainly on Inuit culture and myths, but with an ecological undertone. Another brilliant example is *Assassin's Creed: Origins* (Ubisoft, 2017), which offers a phenomenal tour of Ancient Egypt created in partnership with archaeologists and historians.

The companies behind the games can also have a more direct approach, although they almost never do that. One of the few examples is Rovio Entertainment, responsible for the *Angry Birds* franchise, who joined forces with several environmental organisations (e.g., BirdLife, WWF) in actual bird conservation efforts. In fact, environmental education and more specifically animal conservation, are areas that could greatly benefit from the tremendous untapped potential of video games. Games are chockful of cute creatures and linking them to conservation is an easy task (as *Angry Birds* above). However, games can also easily give the spotlight to more uncommon animals. The last three years saw the release of two games (*Splatoon* and *Abzû*) that prominently feature animals that hardly ever get the public's attention: molluscs. Even though invertebrates are not usually flagship species for environmental issues, I argue that molluscs are well suited for it, especially cephalopods, which have been receiving increased attention from the public mostly thanks to videos of charismatic critters circulating on social media.

In *Splatoon* (Nintendo, 2015), the player controls an inkling, a cartoonish squid-person that can alter between a squid form and a humanoid form, and battle against other players by shooting colourful ink on them. The second game (Nintendo, 2017) made the octolings (octopus versions of the inklings) playable characters. The developers took great care to integrate actual facets of the animals' biology into the game. *Abzû* (Giant Squid, 2016) is a game about underwater exploration, where the player encounters artistic (but still reasonably accurate) renditions of animals, with faithful depictions of behaviour. A remarkable section of the game takes place in the depths where *Architeuthis* lives, but other molluscs can be found, including other squid species, octopuses, nautilus and even living ammonoids. It is unfortunate that the companies behind these games failed to seize the momentum and invest in environmental education, because the potential is certainly there – especially with the runaway success of *Splatoon*, which greatly raised awareness of cephalopods among its public.

As science and the entertainment industry hardly cross paths, it falls to environmental bodies, universities and research institutions to forge this link. In this manner, it would be possible to explain to video game companies that they hold an immense untapped force for conservation and to guide them to take more direct measures towards this end.