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Varied environments drive rapid divergence in sponge (*Suberites diversicolor*) populations

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The nature of dispersal barriers for marine taxa often remains elusive. Here, we studied the relative role of stochastic and deterministic variables influencing population divergence, by comparing multiple replicate populations of sponges from marine lakes. Marine lakes are land-locked bodies of seawater with a variable connection with the surrounding sea via subterranean fissures. Furthermore, each lake has a distinct environmental regime (defined as water temperature, salinity and pH). Marine lakes with their discrete populations provide a unique model to study early stages of evolution in coastal marine taxa. We selected lakes that have comparable ages (~ 8000 years) and sizes (~15000 m^2), but which vary in degree of connection to the open sea and environmental regimes. Using population genomic methods (double-digest restriction site associated DNA, ddRAD) we studied populations of *Suberites diversicolor* from 8 marine lakes and three adjacent sea locations. In this study ddRAD proved to be a useful and cost-effective method for both phylogeographic and population genomic analyses of sponges. We found strong genetic structure and in most cases strong divergence between populations (pairwise F_{ST} ranged from 0.54 - 0.63). Admixture analyses furthermore showed little gene flow between marine lakes, even between lakes only 1-10 kilometres apart. We found that at large spatial scales (> 200 km), stochastic dispersal limitation plays a large role, while preliminary analysis showed that environment plays a significant role in the connectivity and divergence of marine lakes populations at smaller scales (< 30 km). Hence, varied environments can lead to rapid divergence of sponge populations. Understanding how gene flow corresponds with environmental gradients will improve predictions on adaptive capacities of marine species under different climate change scenarios.

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The freshwater sponge fauna of Madagascar: a first assessment

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Spongillida fauna of Madagascar was known only for a single record on *Spongilla alba* (family Spongillidae) since more than two centuries (1887) from the northern small island of Nosy-Bé. *Metania madagascariensis* (family Metaniidae) was recently described by us from the central highlands.

Two field campaigns were carried out in 2011 and 2016 for a total of *ca*. 80 sampling sites in a wide altitudinal range 0-1600 m asl, along (a) two transects in the Eastern slope and High Plateau, and (b) three transects in the North-Western slope, South-Western slope, and Central-Eastern High Plateau. Sampling season was selected on the basis of rainfalls trend, i.e. at the end of the dry season (September) characterised by the lowest water level in the major hydrographic basins, facing both East (Indian Ocean) and West (Mozambique Channel). A wide range of water bodies, of all climatic areas (*sensu* Köppen), were sampled i.e. springs, streamlets, streams, rivers, crater lakes, and reservoirs, from pristine rainforests to arid lands, and in areas where forests

are now relictual due to alteration by human activities (deforestation, agriculture, mining, and farming). Geographic coordinates, altitude, habitat, and micro-habitat data were collected.

Sponges (*ca*. 80 specimens) were discovered in 13 of the sampled sites, in both lentic and lotic water bodies, from 6 out of 9 Malagasy classified climatic areas. Here we report on new records for Madagascar of 5 genera of Spongillidae, i.e. *Corvospongilla*, *Ephydatia, Eunapius, Radiospongilla*, and *Trochospongilla*. The most widespread genera are *Radiospongilla* (5/13 sites), *Trochospongilla* (3/13 sites), and *Eunapius* (3/13 sites). The majority of the samples (over 50) is still problematic. In some cases it is not possible to ascribe them to a presently known genus of Spongillida. Further investigations at the species level are in progress.

From a biogeographic point of view the 7 genera recorded in Madagascar, including *Spongilla* and *Metania* from previous literature are well represented in several continents with many species. *Ephydatia, Eunapius, Spongilla*, *Radiospongilla*, and *Trochospongilla* are widespread worldwide, while *Corvospongilla* and *Metania* show a prevalent Gondwana range. All recorded genera are known from the Afrotropical Region. Once again field campaign, in unexplored lands, yielded the discovery of a diversified Spongillida fauna.

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Systematics of marine sponges from the Bay of Plenty, New Zealand

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Reliable taxonomic assignments are critical to marine conservation strategies, as is an understanding of how biodiversity is distributed. However, the morphological plasticity of marine sponges can make identifications difficult, hence records of distribution patterns can be unreliable and there are frequent gaps in biogeographic knowledge. The need to improve both morphological and molecular based taxonomic methods in order to make it easier to accurately record sponge diversity has been recognised. Here we present a case study of the first taxonomic examination of sponges from a north eastern New Zealand Harbour. Research focused on (1) recording sponge biodiversity from the Bay of Plenty region, (2) undertaking a systematic revision of the fauna correlating classical taxonomy with a modern phylogenetic assessment (3) determine whether identifications based on genetic barcoding are congruent with those produced via traditional morphological methods (alpha taxonomy). Fifty five species are described, of these; there is a possibility of a new genus with eighteen species remaining un-described. We conclude that for New Zealand Demospongiae, sequence variation present in the barcoding region of the COI gene is sufficient to allow for the identification of species.

Progress with Poecilosclerida (Demospongiae: Porifera) – more molecular insights into poecilosclerid phylogeny.

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Poecilosclerida with around 2210 species is the largest of the demosponge orders and also one of the most diverse in terms of spicule morphology. In a recent revision of Demospongiae (Morrow & Cardenas, 2015)[1], 5 of the 25 poecilosclerid families were assigned to other orders and the suborder classification, which was based mainly on the presence/absence, and morphology of the chela was abandoned. A new internal classification of Poecilosclerida was considered premature, as there was insufficient molecular data to support it.

The current study is an attempt to fill some the gaps in the molecular classification of Poecilosclerida by analysing newly obtained 18S & 28S rRNA sequences in combination with sequences obtained from previous studies. Species of Hymedesmiidae that possess pore sieves form a monophyletic clade with Crellidae. The