

XX Simpósio de Biologia Marinha

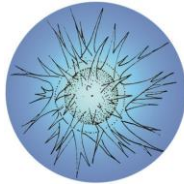
São Sebastião, SP, Brasil, 28 a 29 de novembro de 2019

CADERNO DE RESUMOS

CENTRO DE BIOLOGIA MARINHA
UNIVERSIDADE DE SÃO PAULO

CEBIMar **USP**

NP **BioMar**



XX Simpósio de Biologia Marinha

São Sebastião, SP, Brasil, 28 a 29 de novembro de 2019

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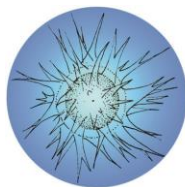
Imagem do logo:

Bjornberg, Tagea. Development stages of some tropical and subtropical planktonic marine copepods. Studies on the Fauna of Curaçao and Other Caribbean Islands, 60, 1972, p. 137, fig. 81 (*Centropages furcatus* egg).

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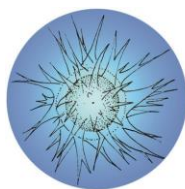


XX Simpósio de Biologia Marinha

São Sebastião, SP, Brasil, 28 a 29 de novembro de 2019

Lista de participantes

Nome completo	Categoria
Ágatha Nascimento Carpinelli	Estudante
Aline Aparecida Zanotti	Estudante
Alvaro Esteves Migotto	Profissional
Ana Carla Santin Massocatto	Estudante
Anabelle Klovrza	Estudante
André Luiz Veiga Conrado	Estudante
Andreia Cristina Câmara Barbosa	Estudante
Ariane Campos	Estudante
Augusto Alberto Valero Flores	Profissional
Aurea Maria Ciotti	Profissional
Camila de Rezende Barreto	Estudante
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Carla Brunner Pavone	Estudante
Carla Kuhl de Figueiredo	Estudante
Cassiano Riyu Kohori	Estudante
Claudia Francesca Vaga	Estudante
Claudio Gonçalves Tiago	Profissional
Cristiane Cassiolato Pires Hardoim	Profissional
David Santos Soares	Estudante
Diogo Destro Barcellos	Estudante
Gabriel Gonzalez Sonoda	Estudante
Gabriel Nascimento Silva	Estudante
Gisele Youkimi Kawauchi	Profissional
Gustavo Muniz Dias	Profissional
Isabela Galvão de Lossio e Seiblit	Estudante
Juliana de Souza	Estudante
Karine Bianca Nascimento	Estudante
Kátia Cristina Cruz Capel	Profissional
Laiza Cabral de Faria	Estudante

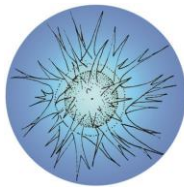


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São Sebastião, SP, Brasil, 28 a 29 de novembro de 2019

Lista de participantes

Nome completo	Categoria
Letícia Curvello Franco	Estudante
Licia Sales Oliveira	Profissional
Ligia Maria Salvo	Profissional
Liv Ascer	Estudante
Marcelo Visentini Kitahara	Profissional
Marcio Reis Custodio	Profissional
Marcos César de Oliveira Santos	Palestrante
Mariana Alves Roque Moraes	Estudante
Maximiliano Manuel Maronna	Profissional
Michelle Guzmán de Fernandes	Estudante
Otávio César Marchetti	Estudante
Priscilla Aparecida Dantas Araújo	Estudante
Rafael Campos Duarte	Profissional
Rafael Viana Amaral	Estudante
Raquel Renó de Oliveira	Profissional
Renata Stecca Lunes	Estudante
Renato Massaaki Honji	Profissional
Rodrigo Mosquera Tanasovici	Estudante
Silvia Neri Godoy	Profissional
Sônia Cristina da Silva Andrade	Profissional
Tadeu Salgado Ivahy Badaró Junior	Palestrante
Thainá Cortez	Estudante
Vanessa Silva Vicente	Estudante
Vinicius Queiroz Araújo	Estudante

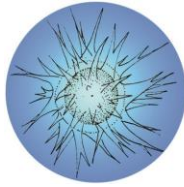


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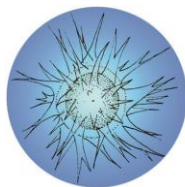
Apresentação

Dando sequência a um evento científico tradicional do Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), o XX Simpósio de Biologia Marinha (SBM) foi realizado de 28 e 29 de novembro de 2019. O SBM tem como objetivo central divulgar os trabalhos realizados por coordenadores, alunos e técnicos com o apoio do CEBIMar, incluindo resultados de projetos finalizados recentemente e em andamento.

Nesta edição foi mantido o formato do simpósio realizado em 2015, com sessões plenárias, apresentações orais curtas e exposição de pôsteres. Os coordenadores de projetos de longa duração, ou projetos temáticos, apresentaram painéis de divulgação, que puderam ser visitados durante todo o evento.

O Simpósio foi dividido em sessões nas principais áreas da Biologia Marinha: Biogeografia, Conservação, Ecologia, Ecofisiologia, Evolução, Biologia do Desenvolvimento e História Natural.

Contamos também com a presença do Prof. Marcos Tavares do Instituto Oceanográfico e do Dr. Tadeu Badaró Júnior, do Ministério Público do Estado de São Paulo, que apresentaram palestras de temas da atualidade.



Programação

28/11/2019 – Quinta-feira

8:30 – 12:00: Recepção dos participantes e distribuição de materiais

12:00 – 14:00: Almoço

14:00 – 14:15: Abertura da Exposição de fotos “CEBIMar 60 anos” – Local: Biblioteca do CEBIMar

14:15 – 14:30: Abertura - Pronunciamentos

Primeira Sessão: História Natural / Presidente: Kátia Capel

14:30 – 14:45: *Beania* Johnston, 1840 (Bryozoa): a problem of over 180 years old! / Nascimento, Karine B.; Vieira, Leandro M. ; Migotto, Alvaro E.

14:45 – 15:00: Coelomocytes of regular and irregular sea urchins: a comparative approach / Queiroz, Vinicius; Custódio, Márcio R.

15:00 – 15:15: Unraveling the function of the bursa copulatrix in sea slugs / Sales, Licia; Marian, José Eduardo A.R.

Segunda Sessão: Outra área temática - Presidente: Alvaro Migotto

15:15 – 15:35: Holobiome of three marine sponges from the north coast of São Paulo / Hardoim, Cristiane C.P.; Ramaglia, Andressa C.M.; Carrara, Virginia; Lobo-Hajdu, Gisele; Custódio, Márcio R.

15:30 – 15:45: Cellular localization of YB1 protein along gametogenesis in solitary and colonial styelid tunicates / Santos-Soares, David; Brown, Federico D.

Terceira Sessão: Fisiologia Marinha - Presidente: Renato Honji

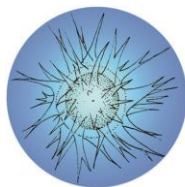
15:45 -16:00: The use of proteomics to assess the toxicity of DEHP in *Hymeniacidon heliophila* (Porifera, Desmosponge) / Ascer, Liv; Rozas, Enrique; Custódio, Márcio R.

16:00 – 16:15: Coffee break

16:15 – 17:15: Sessão de pôsteres - História Natural e Outras Áreas Temáticas

17:15 – 17:45: Palestra: Aplicação prática do conhecimento científico no Sistema de Justiça: importância, obstáculos e caminhos / **Badaró Júnior, Tadeu S.I.** (Ministério Público do Estado de São Paulo)

17:45 – 18:0: Entrega do Prêmio “Sérgio de Almeida Rodrigues”



Programação

29/11/2019 – Sexta-Feira

Quarta Sessão - Ecologia e conservação / Presidente: Aurea Ciotti

9:00 – 9:15: Temperature-driven secondary competence windows may increase the dispersal potential of invasive sun corals / **Barbosa, Andreia C.C.**; Vinagre, Catarina ; Mizrahi, Damian ; Flores, Augusto A.V.

9:15 – 9:30: Acoustic identification of odontocete cetaceans in coastal waters: Canal de São Sebastião and at the Anchieta Island, Ubatuba / **Barcellos, Diogo D.**; Oliveira, Amanda M. ; Santos, Marcos C.O.

9:30 – 9:45: Species-specific camouflage, colour and pattern diversity reflect contrasting life histories of two sympatric crab species / **Duarte, Rafael C.** ; Stevens, Martin ; Flores, Augusto A.V. ; Dias, Gustavo M.

09:45 – 10:00: Coffee break

Quarta Sessão (continuação) - Ecologia e conservação / Presidente: Augusto Flores

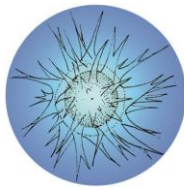
10:00 – 10:15: Does substrate complexity affect the structure of epifauna of the communities? / **Marchetti, Otávio C.** ; Oricchio, Felipe T.; Dias, Gustavo M.

10:15 – 10:30: Influence of oceanographic variables on methods of primary production rates in the São Sebastião channel / **Obata, Camila S.S.**; Regaudie-de-Gioux, Aurore ; Giannini, Maria F.C.; Ciotti, Áurea M.

10:30 – 10:45: Short-term and seasonal variability of sea surface salinity at the São Sebastião Channel (set/2014 - out/2018) / **Oliveira, Raquel R.**; Coelho, Stella C.C.; Ciotti, Áurea M.

10:45 – 11:45: Sessão de pôsteres - Ecologia e Conservação

11:45 – 14:00: Almoço



Programação

Quarta Sessão (continuação) - Ecologia e conservação / Presidente: Renato Honji

14:00 – 14:15: How does environmental complexity affect the fouling community? / **Rodrigues, Isadora D.**; Oricchio, Felipe T. ; Dias, Gustavo M.

14:15 – 14:30: Different abundances of sun coral (*Tubastraea* spp.) in a recreative marina on the São Sebastião Channel: investigating the importance of predation and hydrodynamism / **Tanasovici, Rodrigo M.**, Kitahara, Marcelo V., Dias, Gustavo M., Vieira, Edson A.

Quinta Sessão - Evolução e Biogeografia / Presidente: Marcelo Kitahara

14:30 – 14:45: A new species of *Paraturbanella* (Gastrotricha, Macrotrichida) from Brazilian coast / **Campos, Ariane**; Garraffoni, André R.S.

14:45 – 15:00: Genome-wide SNP analysis of a highly dispersal marine gastropod, *Littoraria flava* / **Cortez, Thainá**; Andrade, Sônia C.S.

15:15 - 15:30: What is going on? Taxonomy and population genetics of *Nemertopsis* aff. *bivittata* in the Brazilian Coast / **Mendes, Cecili B.**; **Andrade, Sônia C.S.**

15:30 – 15:45: The future of corals told by mito-phylogenomics / **Seibnitz, Isabela G.L.**; Capel, Kátia C.C.; Kitahara, Marcelo V.

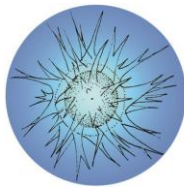
15:45–16:00: Coffee break

16:00 – 17:00: Sessão de pôsteres - Ecofisiologia Marinha, Fisiologia Marinha, Evolução e Biogeografia

17:00 – 17:30: Palestra: Innovative cetacean research towards conservation at the REVIS de Alcatrazes: IOUSP (CEBIMar/USP) and ICMBio onboard / **Santos, Marcos C.O.** (IO/USP)

17:30 – 17:45: Divulgação dos melhores trabalhos apresentados

17:45 – 18:00: Encerramento



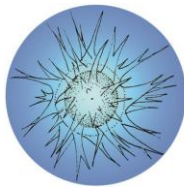
Palestra

Aplicação prática do conhecimento científico no Sistema de Justiça: importância, obstáculos e caminhos

Badaró Júnior, Tadeu S.I.

Ministério Público do Estado de São Paulo, São Sebastião, SP, Brasil.

Trata-se de palestra que, partindo de breves noções introdutórias sobre o papel atribuído ao Ministério Público pela Constituição Federal na defesa dos direitos coletivos, sobre o funcionamento do GAEMA-LN (Grupo de Atuação Especial em Defesa do Meio Ambiente do Litoral Norte do Estado de São Paulo) e sobre as ferramentas à disposição dos promotores de justiça para o exercício destas atribuições (inquéritos civis, ajustamento de condutas e ações civis públicas), buscou explorar as diversas formas em que o conhecimento científico pode agregar valor e fortalecer a defesa judicial e extrajudicial do meio ambiente, permitindo a aplicação prática do produto da atividade acadêmica. Assim, foi destacado que o trabalho de pesquisa científica pode servir como elemento deflagrador da atuação do GAEMA, notadamente quando revela que determinada atividade humana está provocando degradação ou ameaça de degradação ambiental; para o preenchimento de lacunas normativas relevantes, quando evidencia que uma dada atividade humana precisa ser melhor regulamentada para que atenda ao postulado do desenvolvimento sustentável; para subsidiar o judiciário diante de uma controvérsia de ordem técnico-científica, dado que o trabalho da academia tem presunção de imparcialidade; para suplementar a demanda do Ministério Público por laudos técnicos, dado que seu corpo técnico é insuficiente para esse fim e, em última análise, como subsídio geral da atuação do promotor de justiça, dado seu potencial de elevar o conhecimento do agente público acerca de questões sobre as quais não é especialista, mas suscitam conhecimento multidisciplinar. Em seguida, a palestra abordou os obstáculos para o aproveitamento da produção científica pelos órgãos públicos, com destaque para a dificuldade no custeio, sugerindo caminhos para sua superação, tais como o estabelecimento de convênios e a elaboração de um banco de demandas do Ministério Público local a ser disponibilizado aos pesquisadores que porventura tenham interesse em investigar aspectos a elas correlatos ou que já disponham de informações que possam, no todo ou em parte, atendê-las. Por fim, na parte final, dedicada às reflexões, debates e proposições, foi sugerido que o GAEMA e o CEBIMAR se reúnam periodicamente, a fim de estreitar essa relação e permitir um melhor aproveitamento da pesquisa científica pelo Ministério Público local.



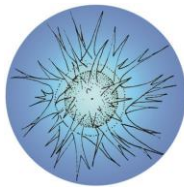
Palestra

Innovative cetacean research towards conservation at the REVIS de Alcatrazes: IOUSP (CEBIMar/USP) and ICMBio onboard

Santos, Marcos C.O.

Laboratório de Biologia da Conservação de Mamíferos Aquáticos (LABCMA), Departamento de Oceanografia Biológica, Instituto Oceanográfico da Universidade de São Paulo (IO/USP), São Paulo, SP, Brasil.

After a long-term investigation concluded by the “Universidade de São Paulo”, a total of 30 cetacean species were listed in records gathered since the 1800s along the coast of São Paulo state with *ca.* 600km in length. Considering the coastal waters, 7 of these species are seasonal visitors after migration movements (4 of which are considered as regular visitors), 16 are strays from their ordinary ranges of distribution and reported just in rare occasions, 2 are common visitors with poorly known patterns of movements, and 5 are residents year-round. In order to better understand the use of local waters by cetaceans, the “Instituto Oceanográfico – Universidade de São Paulo (IOUSP)”, the “Centro de Biologia Marinha da USP (CEBIMar USP)”, and the “Instituto Chico Mendes de Conservação da Biodiversidade (ICMBio)” joined together into an innovative new research program. Our aims are related to detect cetacean occurrences year-round through Passive Acoustic Monitoring (PAM), coped with a citizen scientist program. Monthly cruises to cover the whole extension of the “Refúgio e Vida Silvestre do Arquipélago de Alcatrazes (REVIS de Alcatrazes)”, São Paulo State northern coast, have been conducted since July 2019. The crew is composed of scientists and volunteers who passed through a capacity building program established by the ICMBio staff. Cruises are important to map cetacean occurrence, to record their sound emissions which will help to build a library on local cetacean sounds, and to share the knowledge on cetaceans with the ICMBio volunteers. From early 2019, two hydrophones were moored by the 3 teams of researchers at the REVIS de Alcatrazes to detect cetacean sound emissions through PAM. This tool provides innovative opportunities to detect cetaceans in moments that usually are not easily available for scientists in research vessels: in rough sea state, at night, and in a significant part of the year that cruising for cetaceans is economically prohibitive. Besides, PAM usually reduce noise pollution and the contamination of oceans when compared to regular and intense boat-based investigations. Since 2016 the IOUSP has been working towards the establishment of a library composed by cetacean sound emissions. In a mid-term, the aim is to optimize the strategy to seasonally and locally detect the occurrence of cetaceans, expanding this methodology to neighboring areas and to other Marine Protected Areas in Brazilian waters.



Comunicação oral - Primeira Sessão: História Natural

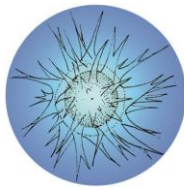
***Beania* Johnston, 1840 (Bryozoa): a problem of over 180 years old!**

Nascimento, Karine B. (1, 2); Vieira, Leandro M. (3); Migotto, Alvaro E. (1)

(1) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil; (2) Instituto de Biociências da Universidade de São Paulo (IB/USP), São Paulo, SP, Brasil; (3) Centro de Biociências da Universidade Federal de Pernambuco (CB/UFPE), Recife, PE, Brasil.

The genus *Beania*, established by Johnston in 1840 for *Beania mirabilis*, has been characterized by having colonies with connecting tubes linking the autozooids, an entirely membranous frontal surface, and rhizoids attaching the colony to the substrate. Several new species have been assigned to the genus, about 2/3 of which were poorly described and based on relatively few specimens. This and the fact that bryozoans commonly exhibit certain degree of morphological plasticity may lead to wrong assumptions regarding intraspecific variability of morphological characters and species delimitations, making the taxonomy of the genus rather complex and confuse. As a result, the evaluation of the diversity of the genus, as well as analyses of geographical distributions and the assessment of exotic and invasive species are impaired. We revised the genus, after examining, under light and scanning electron microscopy, and performing quantitative and qualitative analyses of morphological characters from about 700 specimens of *Beania* deposited at different biological collections (Victoria Museum, Australia; Natural History Museum of London, UK; National Institute of Water and Atmospheric Research, New Zealand; Zoological Museum of University of São Paulo, Brazil; National Museum of Rio de Janeiro, Brazil). Among this material, there were those gathered by 19th and early 20th century great expeditions, for instance, H.M.S. Herald (South Hemisphere, 1845), H.M.S. Rattlesnake (Australia and New Guinea, 1846-1850), H.M.S. Challenger (global, 1872-1876), H.M.S. Alert (Arctic, 1874-1876), H.M.S. Siboga (Indo-Pacific, 1899-1900), Discovery Expedition (Antarctic, 1901-1904), and Terra Nova Expedition (Antarctic, 1910-1913). Of the 73 species described for the genus, 54 were found deposited in at least one of the collections mentioned, including the type material (holotype or paratype) of 39. Our study revealed new characters for species discrimination within the genus, while the traditional characters currently used to distinguish the species of *Beania* proved to be more informative at higher taxonomic levels than genus and species levels. The new characters proposed include shape, size, position, and number of spines, avicularia, connecting tubes, rhizoids, and brood chambers for embryonic and larval incubation. We recognized 68 valid described species within the genus and propose the addition of 30 other new species to science (to be described). Additionally, 3 species are synonymized; 2 are considered invalid species; and 5 are possibly species complexes. The known species of *Beania* were categorized, employing the new characters, in five subgroups: 1) uniserial-long (n=4), 2) uniserial-short (n=6), 3) reticulated-basal (n=3), 4) reticulated-proximal (n=15) and, 5) reticulated-hexagonal (n=34). Whether these subgroups should be raised to genus-level depends on future morphological and molecular phylogenetic analyses.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq); Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq).



Comunicação oral - Primeira Sessão: História Natural

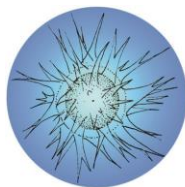
Coelomocytes of regular and irregular sea urchins: a comparative approach

Queiroz, Vinicius (1, 2); Custódio, Márcio R. (1, 2)

(1) Departamento de Fisiologia, Instituto de Biociências da Universidade de São Paulo (IB/USP), São Paulo, SP, Brasil; (2) Núcleo de Apoio à Pesquisa em Biodiversidade Marinha da Universidade de São Paulo (NPBioMar/USP), São Paulo, Brasil.

Echinoderms may have up to six main coelomic cell types, but only four (*viz.* phagocytes, vibratile cells, red and colorless spherulocytes) have been assumed to occur in sea urchins. Although echinoids are divided in two main groups, namely regular (sea urchins) and irregular (sand dollars and heart urchins), most studies rely on regular species, and data about irregular ones are scarce and punctual. Here, based on published literature and direct observations, we examined the diversity of coelomocytes in Echinoidea, and compared how these cells are distributed among regular and irregular echinoids. We collected data from 33 species of six orders and 15 families. Detailed morphological studies of six regular (*Eucidaris tribuloides*, *Arbacia lixula*, *Lytechinus variegatus*, *Echinometra lucunter*, *Paracentrotus lividus*, *P. gaimardi*) and two irregular (*Encope emarginata* and *Clypeaster subdepressus*) species were analyzed by live-cell observations, and cytochemical preparations. In addition to the four usual coelomocytes mentioned above, five additional spherulocyte subpopulations were identified: large, granular, green, yellow, and small-granular. Phagocytes, as well as red and colorless spherulocytes were recorded in almost all echinoids. Vibratile cells were found in all regular sea urchins, in all spatangoids echinoids, and in *C. subdepressus*. Granular spherulocytes were found only in the regular echinoids directly observed. Large spherulocytes were seen only in Mellitidae sand dollars, while green, yellow, and small-granule spherulocytes were seen only in *C. subdepressus*. Cells with basic physiological functions, such as phagocytosis, bactericidal activity, and cytotoxicity (*i.e.* phagocytes, red and colorless spherulocytes, respectively) were present in most species. Vibratile cells were restricted to echinoids with large coelomic cavities. Although the real function of this coelomocyte remains uncertain, it has been suggested to be involved with coelomic fluid agitation or clotting. Granular spherulocytes were found only in the regular echinoids directly observed, but the distributional pattern suggests its wide presence among regular species and maybe in Spatangoida. Clypeasteroida showed the highest number of different cell types, which indicates that other specialized functions of clypeasteroid coelomocytes remain to be found. Thus, in summary, three important aspects are raised in this work: I) cells which perform general functions (*e.g.* phagocytes) seems to be widespread among all groups; II) the diversity of coelomic cells in echinoids seems to be considerably underestimated, even for the well-studied regular species; III) possibly, the new physiological challenges due to the evolution of a infaunal lifestyle by the sand dollars were solved with the emergence of new cell types.

Apoio: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP) (Procs. 15/21460-5 and 18/14497-8), Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq)



Comunicação oral - Primeira Sessão: História Natural

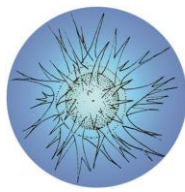
Unraveling the function of the bursa copulatrix in sea slugs

Sales, Licia (1); Marian, José Eduardo A.R. (1)

(1) Instituto de Biociências da Universidade de São Paulo (IB/USP), São Paulo, SP, Brasil.

Most sea slugs are simultaneous hermaphrodites with a complex reproductive system, including organs for sperm reception, digestion, and storage. Sperm storage is considered a function of the seminal receptacle, while sperm reception and digestion are generally attributed to the bursa copulatrix. However, considering that the bursa copulatrix is a blind-sac in sea slugs, if both functions are performed by this organ, it would require precise control over the digestion process – otherwise, all received allosperm would be under risk of being damaged before being transferred to the seminal receptacle. Also, although the occurrence of sperm digestion is known for several sea slugs, it remains obscure in which situations and how often sperm are digested. Here, we combined experimental manipulations and histological analyses of the sea slug *Okenia polycerelloides*, a dorid nudibranch, to investigate if the bursa copulatrix is the site of initial sperm reception, and how often sperm are digested when an individual mates with one or two partners. Sperm were initially received and stored by the seminal receptacle. Sperm digestion occurred continuously, and at least some amount of sperm received during each mating event was directed to the bursa copulatrix to be digested, corroborating the hypothesis of surplus sperm digestion. However, although rarely, all received sperm could also be directed to the bursa copulatrix, suggesting the possibility of cryptic female choice, which would support the hypothesis of its role in post-copulatory sexual selection. Gradual reduction of the contents of the bursa copulatrix with increasing post-copulation times suggests resorption of the digested materials, which could have physiological implications. In conclusion, this study provides (1) the first evidence against a function of sperm reception by the bursa copulatrix in dorid nudibranchs, (2) empirical evidence for the hypothesis of surplus sperm digestion, and (3) evidence for other possible functional meanings of sperm digestion in sea slugs.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq) - Finance Code 001; Núcleo de Pesquisa em Biodiversidade Marinha da Universidade de São Paulo (NPBioMar/USP)



Comunicação oral - Segunda Sessão: Outra área temática

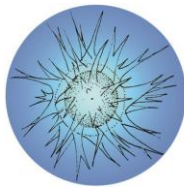
Holobiome of three marine sponges from the north coast of São Paulo

Hardoim, Cristiane C.P. (1); Ramaglia, Andressa C.M. (1); Carrara, Virginia (1,2); Lobo-Hajdu, Gisele (3); Custódio, Márcio R. (4)

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Marine sponges perform several processes that contribute to the functioning and health of the benthic ecosystems. They also harbor diverse archaeal, bacterial and fungal communities in which complex interactions are established and aid the host to grow and develop. Conversely, little is still known about the diversity and community structure of this microbiota. As such, there is a need to disclose their taxonomic and functional diversities within these animals. To tackle this, the sympatric species *Aplysina fulva*, *A. caissara* (endemic) and *Tedania ignis* were collected along with surrounding seawater and sediment at Praia Preta, in the north coast of São Paulo. The sponge species were identified using morphological characteristics and by barcoding using the genes cytochrome oxidase subunit 1 (*cox-1*), cytochrome *b* (*cob*), and the internal transcribed spacer regions (ITS, including ITS1, 5.8S, ITS2). The DNA from the sponges, seawater and sediment were extracted and subjected to Illumina MiSeq platform using the phylogenetic markers 16S (prokaryotic communities) and ITS (eukaryotic communities – Fungi). Even though three genes were used to identify the sponge species, only *cob* was capable to separate *A. fulva* and *A. caissara* into two distinct clusters. The Illumina sequences were analyzed with MOTHUR and showed that the highest Shannon diversity index and CHAO richness was observed for sediment, followed by seawater, *Aplysina* species and *T. ignis* for both 16S rRNA and ITS genes. The most abundant bacteria phyla were *Acidobacteria*, *Actinobacteria*, *Chloroflexi*, *Cyanobacteria* and *Proteobacteria* (*Gammaproteobacteria*, *Alphaproteobacteria*); whereas *Crenarcheota* was the dominant phyla in the Archaea domain. The abundance of these phyla was different between sponge species and environmental samples. For fungi the *Agaricomycetes* and *Basidiomycetes* were the major phyla associated with sponge species, where *Zygomycetes* dominated the environmental samples. When OTUs were assigned, it clearly showed that the holobiome associated with sponge species were distinct from the detected in seawater and sediment. This survey addressed for the first time the holobiome of the São Paulo sponge species and it demonstrated that the microbial communities associated with sponges were host-specific.

Apoio: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP), nr. 2016/17189-7.



Comunicação oral - Segunda Sessão: Outra área temática

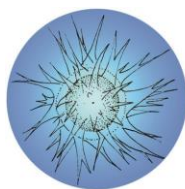
Cellular localization of YB1 protein along gametogenesis in solitary and colonial styelid tunicates

Santos-Soares, David (1, 2); Brown, Federico D. (1, 2)

(1) Departamento de Zoologia, Instituto de Biociências da Universidade de São Paulo (IB/USP), São Paulo, SP, Brasil. (2) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil.

Gametogenesis is a fundamental process in metazoans with sexual reproduction and is generally characterized by the differentiation of diploid cells into specialized haploid cells, including a number of intermediate cell types. Although the molecular mechanisms that control spermatogenesis and oogenesis, as well as the morphological changes involved in the process, are well studied in mammals and other non-colonial model organisms, there are few studies regarding the expression and cellular localization patterns of proteins that are specifically expressed in germ cells of tunicates. Tunicates are marine invertebrate chordates whose reproductive features have been studied due to various independent budding acquisitions, so that many species of the clade have concomitant sexual and asexual reproduction capabilities. Previous studies in *Ciona* (a solitary phlebobranch tunicate) performed by Tanaka et al. (2004) demonstrated the expression of YB1 protein in germ cells. It was shown that CiYB1 (homologous to vertebrate protein Y-box 1) repressed mRNA translation by forming a complex with CiPEM and Ci-macho1, which are proteins associated with the germlasm. By comparing expression patterns of YB1 in the solitary styelid tunicate *Styela canopus* and the colonial styelid *Symplegma rubra* using western blot, immunohistochemistry and confocal microscopy we find: (1) nuclear localization of YB1 during all stages of spermatogenesis (from spermatogonia to spermatids), as well as in the flagella of spermatids in the solitary ascidian *Styela canopus*; (2) CiYB1 antibody did not label any spermatogenic cells of the testis in the colonial ascidian *Symplegma rubra*; (3) YB1 labeled oocytes in the solitary ascidian *Styela canopus* and in the colonial *Symplegma rubra*, corroborating previous observations in *Ciona*. Therefore, our results show an unexpected expression of YB1 in spermatogenic cells in the testes of *S. canopus*, and confirms expression of YB1 protein during oogenesis of both *S. canopus* and *S. rubra*. The role of YB1 during *S. canopus* spermatogenesis remains elusive. Proteins of the Y-box 1 subfamily have nucleic acid binding domains and disordered domains that confer different functions to the protein, including controlling transcription in the nucleus or sequestration of mRNAs in ribonucleoprotein complexes in the cytoplasm, thus inhibiting their translation. The absence of YB1 expression during spermatogenesis in the colonial tunicate *S. rubra* or *Ciona* may suggest different and species-specific roles of YB1 proteins across tunicates.

Apoio: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP); Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior via PROEX (CAPES/CNPq-PROEX)



Comunicação oral - Terceira Sessão: Fisiologia Marinha

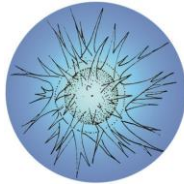
The use of proteomics to assess the toxicity of DEHP in *Hymeniacidon heliophila* (Porifera, Desmosponge)

Ascer, Liv (1); Rozas, Enrique (2); Custódio, Márcio R. (1)

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Living organisms respond to subtle changes in the environment by modulating the expression of multiple genes and proteins capable of helping survival. Based on toxicological results, several molecular biomarkers were developed focused on their differential chemical actions and targets. Although the use of those biomarkers is linked to the understanding of the pathway studied, all the molecular interactions downstream them are usually not well known, especially among those influenced by multiple cofounding factors (i.e. HSP). The “-omics” science advent is helping solve those problems, since the techniques can present all the molecules alterations specific to certain types of chemicals, revealing even concurrent biochemical reactions. The toxicity of chemicals found in ocean is a big part of ecotoxicological studies nowadays, since ocean pollution is of great importance for humans’ health and ecosystem and biodiversity balance. Among all the different types of ocean pollution, plastic is the one research focused its efforts the most for the last 10 years. Plastic particles may interact with pollution particles dissolved in ocean water and can leach other contaminants present in their structure. Phthalates are one class of compound present in plastic structure that are found in ocean the most. Their presence in medical and day-to-day use products are correlate to endocrine disruption in humans, specially infants, whereas once in the ocean, they were associated with toxicity in marine organisms, from algae to fishes. Surprisingly, among all studied organisms, marine sponges were not used as a model although their filter feeding habits could make them excellent ones. Using DEHP, a widely found phthalate, as the type of pollutant and *Hymeniacidon heliophila* as a sponge model, the aim of this study is to compare proteomic profiles from exposed and control organisms to find up and/or down-regulated pathways that could be involved in the response of this molecule toxicity. Although preliminary results show that important molecular functions such as catalytic activity and binding were maintained between exposed and control organisms, ionic channel regulators were detected only in DEHP exposed sponges. Further analysis identified that those regulators were linked to calcium channel activities. Histological and contractions experiments were realized, and observations indicate that DEHP changes calcium intake by cells leading to a blockage in the sponge contraction. The blockage of calcium ionic channels may inhibit calcium dependent contraction cells and/or alter cellular adhesion, affecting the contraction signal transfer between cells. The effect was reversible, and sponges recovered their contraction patterns 3 to 4 hours after exposure. To understand how sponges recovered from the exposure further experiments will focus on artificial calcium channels blockage and *in vivo* channel observations.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq); Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP)



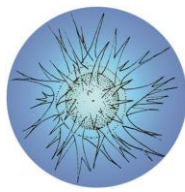
Comunicação oral - Quarta Sessão: Ecologia e conservação

Temperature-driven secondary competence windows may increase the dispersal potential of invasive sun corals

Barbosa, Andreia C.C. (1); Vinagre, Catarina (2); Mizrahi, Damian (3); Flores, Augusto A.V. (1)
(1) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil; (2) MARE - Centro de Ciências do Mar e do Ambiente, Universidade de Lisboa, Faculdade de Ciências, Lisboa, Portugal; (3) Instituto Oceanográfico, Universidade de São Paulo (IO/USP), Ubatuba, SP.

Invasive sun corals exhibit outstanding development plasticity during early ontogenesis, which may greatly affect the pelagic duration of propagules and hence their dispersal potential. Remarkably, a small proportion of larvae may not directly settle on the benthic habitat, but metamorphose to planktonic polyps. We show the latter may settle successfully, eventually opening a secondary competence window (SCW). Based on local conditions (Southeast Brazil), delayed SCWs were confirmed at average summer (26oC) and, especially, at heat-wave (30oC) temperature, allowing an escape response from habitats where larval mortality rates are high and mass-mortality events of colonies, later on, more likely. Despite a higher frequency of pelagic metamorphosis, no SCWs were observed at average winter (22oC) and cold-front (19oC) conditions. Climate change may thus favor large-scale dispersal of competent pelagic polyps and further promote range extensions to subtropical and warm-temperate regions where temperature conditions (ca. 22oC) for propagule survival and settlement success are best.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq); Núcleo de Pesquisa em Biodiversidade Marinha da Universidade de São Paulo (NPBioMar/USP)



Comunicação oral - Quarta Sessão: Ecologia e conservação

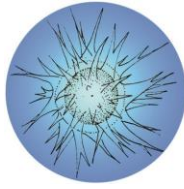
**Acoustic identification of odontocete cetaceans in coastal waters:
Canal de São Sebastião and at the Anchieta Island, Ubatuba**

Barcellos, Diogo D. (1); Oliveira, Amanda M. (1); Santos, Marcos C.O. (1)

(1) Laboratório de Biologia da Conservação de Mamíferos Aquáticos, Instituto Oceanográfico, Universidade de São Paulo (IO/USP), São Paulo, SP, Brasil.

Reliable estimation of wild animal populations is very important for effective wildlife management, conservation and ecology. Some species produce readily identifiable sounds, providing an opportunity to use passive acoustic data to estimate species richness. This is a preliminary study that establish a library of odontocete whistles for passive acoustic monitoring program in southeastern Brazil. Delphinid species of the southwestern Atlantic Ocean *Tursiops truncatus* (Tt), *Orcinus orca* (Oo), *Stenella longirostris* (Sl), *Sotalia guianensis* (Sg), *Stenella frontalis* (Sf) were visually confirmed during recordings with a 96 kHz sample rate. Seven acoustical parameters were extracted from 967 whistles. With autonomous acoustic recorders, data were collected during from 2015 to 2017 in the northern coast of São Paulo state, specifically at the Canal de São Sebastião (CSS, 23°49' S; 45°24' W) and at the Parque Estadual da Ilha Anchieta (PEIA, 23°33' S; 45°04' W). A total of 30 (CSS) and 137 (PEIA) odontocete detection events were recorded and acoustical variables were extracted from 5,644 whistles identified. Most detection events occurred in the absence of sunlight. PCA was used for analyses using the averages of the acoustic parameters of whistles of the five delphinids in relation to the whistles of each detection event. Simultaneously the prediction from the Random Forest (RF) classification model was considered to identify the species. The values of each acoustic parameter of whistles of the five delphinids were utilized to train the RF model. RF multivariate analysis presented 64% accuracy in species identification predictions. Based on mean decrease in accuracy, the most important variables for classification were duration, and the final, minimum, central and bandwidth frequencies. The best species classification was Sg, with 91% accuracy predictions. Sg was identified in 17% of detection events from CSS and in 71 events (52% of detections) in PEIA, where Sg was present in almost every month. Sf was identified in one detection event at PEIA. The acoustic detector database was enriched in training data with 3,274 whistles of Sg identified in the detection events. The new RF model presented 89% accuracy in predictions, increased the accuracy identification to 98% for Sg. It is necessary to continue the acquisition of acoustic records of odontocete whistles with visual identification to be incorporated into the RF model of identification of whistles. The description of the acoustic repertoire of odontocetes present in South Atlantic Ocean is a crucial step for the development of a classification system capable of determining the presence, distribution, use of area and abundance of species which can be passively detected on the coast of the São Paulo state.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq) Finance Code 001; Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP) n° 2011/51543-9, Programa Temático Baía do Araçá (FAPESP) n° 2011/50317-5); Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) - 163148/2015-5.



Comunicação oral - Quarta Sessão: Ecologia e conservação

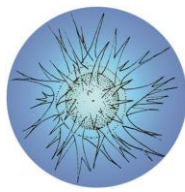
Species-specific camouflage, colour and pattern diversity reflect contrasting life histories of two sympatric crab species

Duarte, Rafael C. (1,2); Stevens, Martin (3); Flores, Augusto A.V. (2); Dias, Gustavo M. (1)

(1) Centro de Ciências Naturais e Humanas, Universidade Federal do ABC (UFABC), São Bernardo do Campo, SP, Brasil (2) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, Brasil (3) Centre for Ecology and Conservation, University of Exeter, Cornwall, United Kingdom.

Animal species frequently exhibit considerable variation of coloration and pattern, especially those living in colour heterogeneous habitats. Colour polymorphic populations may benefit from differential concealment of individuals, which would resemble both the general colour and pattern of the substrates (i.e. camouflage by background matching). However, while background matching is assumed to be one of the most common anti-predatory strategies in nature, little is known about how microhabitat use and other life history traits may affect how organisms resemble the backgrounds. Here, we used the mud crab *Panopeus americanus* and the mottled shore crab *Pachygrapsus transversus* to answer these questions since both species exhibit considerable intraspecific colour and pattern variation and occupy the same habitat but differ in some aspects of life history. Crabs were sampled in the Araçá region (São Sebastião) from different backgrounds (e.g. mudflats with large gravels, pebbles and rocky boulders covered with macroalgae) and photographed in the field in conjunction with the substrates. Using different tools of image analysis, we first linearised and equalized all the images to correct for changes in illumination and obtained estimates of light reflectance in the RGB channels. We used the reflectance data to calculate different colour parameters (e.g. brightness and hue) and performed a granularity analysis to obtain a set of pattern metrics, which were compared between species and crab's size to test for interspecific differences in crab's appearance and for possible ontogenetic changes in crab's coloration. We also compared the colour between crabs and the different backgrounds to test for differences in the level of camouflage of each species. Mud crabs exhibit brighter and more patterned carapace in comparison with shore crabs, which were darker and smoother. In addition, small mud crabs were more diverse in brightness than large individuals, indicating an ontogenetic change of crab's appearance. On the other hand, shore crabs, especially large individuals, exhibit larger hue values than mud crabs, indicating that as shore crabs grow they tend to become greener. Finally, mud crabs are better camouflaged against all substrate types, especially to mudflats and pebbles, compared to shore crabs, which are more conspicuous over all backgrounds. Mud crabs are habitat specialists and resident to the backgrounds, which would explain their great level of camouflage and the large variation in colour and pattern, especially in juveniles that are more vulnerable to predation than adults. On contrary, shore crabs are more generalist and mobile, moving to macroalgal patches when adults, which would explain why large crabs are greener. Here we show that differential habitat use in crabs can be associated to different colour patterns and camouflage strategies as a mean to avoid predation.

Apoio: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP); Núcleo de Pesquisa em Biodiversidade Marinha da Universidade de São Paulo (NPBioMar/USP)



Comunicação oral - Quarta Sessão: Ecologia e conservação

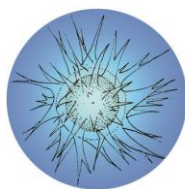
Does substrate complexity affect the structure of epifauna of the communities?

Marchetti, Otávio C. (1); Oricchio, Felipe T. (1); Dias, Gustavo M. (1)

(1) Centro de Ciências Naturais e Humanas, Universidade Federal do ABC (CCNH/UFABC), São Bernardo do Campo, SP, Brasil.

Epifauna is composed of mobile organisms, mainly crustaceans, polychaetes and mollusks, which live associated to sessile organisms such as algae and invertebrates. Marine ecosystems have been heavily modified due to the intensification of anthropogenic activity increasing pollution and construction of artificial structures such as marinas. Coastal constructions tend to be homogeneous structures, reducing the natural complexity of the environment, which favors the monopolization of resources by few species. Thus, to understand how the variation of environment complexity changes the structure of the epifaunal community, we carried out an experiment in five marinas from Southeastern Brazil that varied in environmental degradation. In each marina, 10 PVC plates were divided into two groups representing artificial habitats, simulating simple, bi-dimensional and complex tri-dimensional environments. Plates were submerged for 4 months and then mobile communities were collected, organisms were identified in large taxonomic groups and quantified. We assessed the effect of complexity and location on community richness, abundance and structure using univariate and multivariate analyzes of variance. Environmental complexity did not affect species richness or abundance, traits that were determined by the studied location. Locations exposed to intense anthropogenic (pollution) or natural (freshwater) disturbs, supported lower richness but greater abundance of organisms than less disturbed environments. Complexity effect was generally observed only for polychaetes, and its abundance was higher in low complexity, a possible result of the way how polychaetes interact with substrate. Complexity reduced the abundance of copepods in Ilhabela, but increased the abundance of crabs in Niterói, the most disturbed habitat. Although habitat complexity only presents localized effects when the taxonomic groups were analyzed separately, it altered the community structure, possibly by reducing hydrodynamism and promoting escape of predation. Our results show that complexity of the environment mediates the relative abundance of species, but its effect differs between taxonomic groups and may depend on other specific characteristics of the site. Thus, conservation strategies aiming to produce artificial habitats more similar to natural ones should not only concern themselves with increasing small-scale environmental complexity, but also reduce the regional selective pressures caused by anthropogenic disturbances normally associated with these constructions.

Apoio: Universidade Federal do ABC (UFABC); Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP).



Comunicação oral - Quarta Sessão: Ecologia e conservação

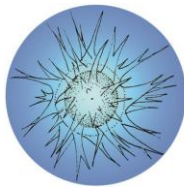
Influence of oceanographic variables on methods of primary production rates in the São Sebastião channel

Obata, Camila S.S. (1,2); Regaudie-de-Gioux, Aurore (2); Giannini, Maria F.C. (2); Ciotti, Áurea M. (1)

(1) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil; (2) Instituto Oceanográfico da Universidade de São Paulo (IO/USP), São Paulo, SP, Brasil.

It is a consensus that primary production (PP) studies in the ocean are important due to its role in the global carbon cycle. In the last few decades, efforts were applied to develop fast and non-invasive techniques to measure rates of PP to improve temporal and spatial data acquisition, and thus overcome the disadvantages and gaps associated with classical methods using incubation of samples. The aims of this work are: (1) to compare two techniques, Bio-optical (PPabs) and Active Variable Fluorescence (PPFire), to the classical method involving oxygen evolution by the planktonic community metabolism (represented here by the Gross Primary Production - GPP), and, (2) to determine the influence of oceanographic variables, such as temperature, salinity, chlorophyll-a concentration and Secchi Disk depth in PP prediction in the São Sebastião channel. Our results showed that GPP varied between 47.55 and 341.94 mg C m⁻³ d⁻¹, PPabs between 73.7 ± 6.9 and 454.9 ± 25.8 mg C m⁻³ d⁻¹ and PPFire between 9.0 and 57.8 mg C m⁻³ d⁻¹ in the summer of 2018. The relationships between methods were significant (GPP vs. PPabs, $p = 0.007$, GPP vs. PPFire, $p = 0.01$ and PPabs vs. PPFire, $p = 0.01$). A multiple linear regression test show that GPP ($p = 0.003$) and PPFire ($p < 0.001$) were predicted by surface temperature and chlorophyll-a concentration, and additionally, PPabs ($p = 0.007$) was also predicted by salinity. As expected, the compared methods yielded different PP magnitudes. Nonetheless, it is important to highlight that each method provides distinct ancillary information: GPP gives the gross primary production of the overall planktonic community, while PPabs supplies insights on pigments composition and species size, and PPFire adds phytoplankton cell photophysiology parameters. The correlations found between the PPs estimated from the different methods and both temperature and salinity indicate that all are sensitive to changes in local water masses, resulting from intrusions of upwelled South Atlantic Central Water as well as the input of diffuse freshwater discharges at the surface, which modulate light and nutrients availability. In conclusion, the significant proportionality found among each of the methods encourage further uses of non-invasive methods (PPabs and PPFire) to improve the temporal and spatial resolution of PP regionally. In addition, the supplemental information provided by each method incites the development of hybrid models in the future.

Apoio: Programa de Excelência Acadêmica da Coordenação de Aperfeiçoamento de Pessoal de Nível Superior, Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq/PROEX); Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq); Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP); Núcleo de Pesquisa em Biodiversidade Marinha da Universidade de São Paulo (NPBioMar/USP); Sistema de Monitoramento da Costa Brasileira (SIMCosta); Instituto Nacional de Ciência e Tecnologia Oceanografia Integrada e Usos Múltiplos da Plataforma Continental e Oceano Adjacente - Centro de Oceanografia Integrada (INCT-Mar COI)



Comunicação oral - Quarta Sessão: Ecologia e conservação

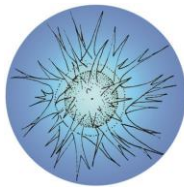
Short-term and seasonal variability of sea surface salinity at the São Sebastião Channel (set/2014 – out/2018)

Oliveira, Raquel R. (1,2); Coelho, Stella C.C. (3); Ciotti, Áurea M. (2)

(1) Sistema de Monitoramento da Costa Brasileira (SiMCosta), São Sebastião, SP, Brasil; (2) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil; (3) Instituto Nacional de Pesquisas Espaciais (INPE), São José dos Campos, SP, Brasil.

Global changes influence the global water cycle, which implies in salinity changes, especially at the coastal oceans. Variation in nearshore salinity can favor the growth of certain species and even promote red tides. Therefore, it is important to observe and predict salinity variability. In the São Sebastião Channel (SSC), located at the north of São Paulo state, hydrodynamics are not substantially influenced by river runoffs. Seasonally, salinity is expected to be influenced by the warm and salty Tropical Water in autumn and winter, and the cold and less salty South Atlantic Central Water in spring and summer. In addition, the SSC receives a mix of local diffuse and variable remote continental runoff, characterized as the Coastal Water. The climate of this region is characterized by storms during summer and by the passage of strong cold-front systems during winter. Episodic but extreme low-salinity conditions are anticipated during summer as a result of intense precipitation. The objective of this study is to characterize the variation of salinity at the surface waters of the SSC using four years of hourly observations (Sep. 2014 to Oct. 2018) acquired from a moored buoy (SP-01) linked to the *Sistema de Monitoramento da Costa Brasileira* (www.simcosta.furg.br/), and investigate its relationship to the variation of sea surface temperature (SST), air temperature and precipitation volume and rate. We report the longest and continuously validated salinity time series at the SSC, showing median salinity values around 34.50 and a remarkable interannual variability. During 2015 and 2017, salinity tended to be stable year-round. Differently, low salinity values were registered throughout winter and spring of 2016 and also during February 2018, when precipitation rates appear to explain the low values of salinity (28.91). High precipitation volume was observed during winter of 2016 (44.57 mm), but rainfall events were rather episodic compared to the more protracted salinity drops, suggesting an important remote contribution of freshwater to the SSC. It is interesting to note that red tides were reported in the region during both low-salinity events, suggesting that continental outflows could be an important source of nutrients. These preliminary results highlight the challenges for understanding and predicting changes in salinity at the SSC. Nonetheless, extreme low salinity values may be strong proxies of changes in this environment.

Apoio: Núcleo de Pesquisa em Biodiversidade Marinha da Universidade de São Paulo (NPBioMar/USP); Sistema de Monitoramento da Costa Brasileira (SiMCosta)



Comunicação oral - Quarta Sessão: Ecologia e conservação

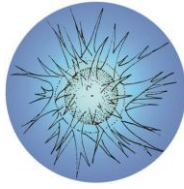
How does environmental complexity affect the fouling community?

Rodrigues, Isadora D. (1); Oricchio, Felipe T. (1); Dias, Gustavo M. (1)

(1) Centro de Ciências Naturais e Humanas da Universidade Federal do ABC (UFABC), Santo André, SP, Brasil.

The natural environment is altered by biotic and abiotic factors that combined affect the survival of species. Environmental complexity can dramatically change community organization as it increases microhabitat diversity, creating refuges against predation and reducing monopolization of resources by a single species. However, we have modified coastal habitats, building piers, platforms and ports, which tend to degrade the environment and provide new hard homogenous substrates, which are very distinct from natural rocky shores. Consequently, marine infrastructure tends to increase bioinvasion in coastal regions. To understand the effects of complexity on diversity of sessile marine organisms, we simulated substrates of high and low complexity using PVC panels that were suspended in five marinas along the southeast coast of Brazil. After four months, we collected the substrates and analyzed the effect of complexity on the following attributes of the fouling communities: biomass, richness and community structure. All factors were site-specific. We registered 66 species, with the largest average richness found in Ilhabela with 25 species (38 species in total) and the lowest in Angra dos Reis and Paraty with only 10 species each (Total $An = 21$, $Pa = 17$). The highest values for biomass were found in Paraty and Niterói, places with low richness. Niterói supported the largest number of exotic species while native species were more abundant in Ilhabela and Angra dos Reis, corroborating that human-disturbed environments as Guanabara Bay restrict the occurrence of native species, promoting a high dominance by exotics. Complexity increased biomass only in Angra dos Reis and reduced biomass in Paraty. Community structure was consistently affected by habitat complexity across all sites. In general, low complexity habitats were dominated by calcified organisms, mainly barnacles and bryozoans, while in complex habitats ascidians were the dominant organisms. Our results suggest that environmental tri-dimensionality provides refuges for soft-bodied organisms that are usually prone to predation. We concluded that habitat complexity affects fouling community mediating interactions between organisms, therefore altering their relative abundances, but the effect of habitat complexity can be affected by local conditions.

Apoio: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP)



Comunicação oral - Quarta Sessão: Ecologia e conservação

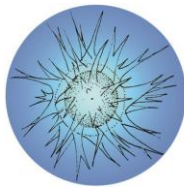
Different abundances of sun coral (*Tubastraea* spp.) in a recreative marina on the São Sebastião Channel: investigating the importance of predation and hydrodynamism

Tanasovici, Rodrigo M. (1), Kitahara, Marcelo V. (2,3), Dias, Gustavo M. (1), Vieira, Edson A. (1,4)

(1) Centro de Ciências Naturais e Humanas da Universidade Federal do ABC (CCNH/UFABC), São Bernardo do Campo, SP, Brasil; (2) Instituto do Mar da Universidade Federal de São Paulo, IMAR/UNIFESP, Santos, SP, Brasil; (3) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil; (4) Departamento de Oceanografia e Limnologia da Universidade Federal do Rio Grande do Norte (DOL/UFRN), Natal, RN, Brasil

Biological Invasions are one of the biggest threats to biodiversity nowadays, mainly due the increase in human mobility in the last few decades. Invasion success is conditioned both by invader traits (high competitive potential and escaping predation) and by the biotic and abiotic characteristics of the novel habitat. Recently, Brazil is facing the increase of the invasive sun coral (*Tubastraea* spp.), which has been causing a decrease in the diversity of both sessile and mobile associated organisms. In the Yacht Club of Ilhabela, in São Sebastião Channel, SP, the sun coral presents distinct abundances in the two different locations across the marina, being more abundant in the interior of the marina than in the breakwater. Previous studies show that sessile communities in the breakwater are more exposed to predation by fish and water circulation than those inside the marina. Therefore, the objective of this project was to quantify, through an experimental approach, the effect of predation and hydrodynamics in the growth of sun coral recruits. We observed that the predation pressure reduces sun coral clonal growth. Besides, variation in hydrodynamics induced plastic responses in the sun coral, which invested in the production of new polyps under highly hydrodynamic conditions, but increased the area occupied by the colony, producing larger polyps, in calm waters. Our results show that growth plasticity can be a crucial factor for the establishment and expansion of sun coral in Brazil, and that predators could also play an important part in retarding sun coral expansion.

Apoio: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP)



Comunicação oral - Quinta Sessão: Evolução e biogeografia

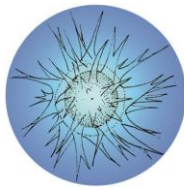
A new species of *Paraturbanella* (Gastrotricha, Macrodasysida) from Brazilian coast

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(1) Laboratório de Evolução de Organismos Meiofaunais, Departamento de Biologia Animal, Instituto de Biologia da Universidade Estadual de Campinas (IB/UNICAMP), Campinas, SP, Brasil.

Gastrotricha is a monophyletic phylum of microscopic metazoans ranging in size from 50 μm to 3500 μm and inhabit distinct marine and freshwater ecosystems throughout the world. Until now, more than 830 species have been described and divided into two orders, Chaetonotida and Macrodasysida. The latter order comprises 10 families and one of them, Turbanellidae, includes six genera: *Desmodasys*, *Dinodasys*, *Paraturbanella*, *Prostobuccantia*, *Pseudoturbanella* and *Turbanella*. Despite that the monophyly of these genera was not satisfactorily tested, 23 species belonging to the genus *Paraturbanella* are distinguished from turbanellids by sharing a peculiar group of tubes in ventro-lateral side of the anterior region known as "dohrni" tubes. In this study, one new species, *Paraturbanella* sp. is described from the intertidal zone of a sandy beach in Paraty (Rio de Janeiro State, Brazil). Living individuals were detected sorting the sediment poured into Petri dishes under a stereomicroscope; they were mounted singly on glass slides, observed *in vivo* and anaesthetized under a light microscope equipped with differential interference contrast optics. Eight of the 12 live specimens were recovered and were subsequently fixed for scanning electron microscopy analysis and 4 of 12 were used for extraction of genomic DNA. The new species can be distinguished from all other paraturbanellids: 6 anterior adhesive tubes (TbA) are arranged in "fleshy-hands" on each side, and 7 posterior adhesive tubes (TbP) on each side, presenting a pattern 1-5-1. The body tapers in the caudal region, where there is a central median cone. There are two rows of ventral ciliation in the anterior region of the body and in the posterior region there are four rows. This study is the first record of *Paraturbanella* species from Brazil and the second record from South America, so the marine gastrotrichs are poorly known and sampled not only in Brazil but in the whole of South America.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq); Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP)



Comunicação oral - Quinta Sessão: Evolução e biogeografia

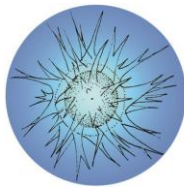
Genome-wide SNP analysis of a highly dispersal marine gastropod, *Littoraria flava*

Cortez, Thainá; Andrade, Sônia C.S.

Departamento de Genética e Evolução, Instituto de Biociências da Universidade de São Paulo (IB/USP), São Paulo, SP, Brasil.

The dispersal potential might directly reflect on populations connectivity and differentiation rates. For marine gastropods, this capability is influenced by the larvae development: species with planktotrophic larvae are able to remain for long periods in the water column, which may increase the dispersal amplitude and geographic distribution. Here we performed a fine-scale genetic structure of a marine gastropod with planktotrophic larvae, *Littoraria flava* (King, 1832), across the Southeast Brazilian coast. We performed the samplings on three states - São Paulo (SP), Rio de Janeiro (RJ) and Espírito Santo (ES) - with two sites each. To test a microgeographic structuring hypothesis, the samples were collected using horizontal transects, from the zero to 64 meters along the rock shore. Given that, we could obtain samples located at distances in micro and macro spatial scales - from a few meters until about 1,000 kilometers. A total of 58 samples were processed by GBS technique. We used the softwares Seqclean, iPyrad, PLINK, STRUCTURE and the package adegenet from R to implement the bioinformatics analysis over 3895 SNPs. The results show high genetic similarity among all individuals, with few exceptions. There is little genetic differentiation among the six sites ($F_{ST} = 0.04$, p -value = 0). The AMOVA showed that the 95% of the genetic variation is within each site, while only 0,23% is contained among the states. Furthermore, it is not possible to establish groups according to genetic similarity through the PCA (Principal Components Analysis). The results from DAPC (Discriminant analysis of Principal Components) and STRUCTURE suggest that all individuals belong to one large and panmictic population distributed along the Brazilian coast, with no evidences of subpopulations within each site. The planktotrophic development seems to be an important factor that shapes the migratory capacity and connectivity of the species. Additional analysis might reveal if there is any significant correlation between the landscape configuration and the currently genetic distribution of these *L. flava* populations.

Apoio: Instituto de Biociências da Universidade de São Paulo (IB/USP).



Comunicação oral - Quinta Sessão: Evolução e biogeografia

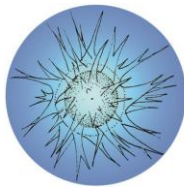
What is going on? Taxonomy and population genetics of *Nemertopsis* aff. *bivittata* in the Brazilian Coast

Mendes, Cecili B.; Andrade, Sônia C.S.

Laboratório de Diversidade Genômica, Instituto de Biociências da Universidade de São Paulo (IB/USP), São Paulo, SP, Brasil.

Many marine invertebrate are commonly found to be complex of cryptic species, especially the ones with less morphological diversity. Among nemerteans this is very common, once they lack any kind of external appendages and have a very simple morphology. *Nemertopsis bivittata* is a Hoplonemertean species with two longitudinal blackish stripes on the entire dorsal surface, and two pair of eyes. This species is known for its color pattern variation (presence or absence of a crossbar between the first pair of eyes) and a cosmopolitan distribution. Because of that, the species had many described synonyms, being now considered only one species. In Brazil both morphotypes can be found along the coast. To assess the taxonomic validity of this species in Brazil, and also its population structure, we collected 49 animals in nine different states in the Brazilian coast. Genomic DNA was extract and libraries were prepared using a modified GBS (genotyping-by-sequencing) protocol. 224.440.236 reads of 100bp were obtained and the demultiplex, filter, clustering and SNPs prospection were performed in the softwares Seqclean, Ipyrad and Plink. The graphic visualization of SNPs matrix was done using Matrix condenser and the genomic population and ancestry analyses, using Adegnet and Structure. During the SNP prospection analysis it was detect three different groups in *N. bivittata*: two of them are morphologically distinct (one with the crossbar and another without), being two morphotypes present along the entire coast and one restrict to Alagoas state, in the Northeast region of Brazil. Most of the 9500 prospect SNPs were exclusive of each group, probably due a long-term isolation of these populations. Surprisingly, however, the populations inside each group show no signs of structure independent of the geographic distance. This can indicate either the presence of long living planktonic larvae, or the transport of adults probably by biofouling, since this species complex live in fouling communities as oyster and barnacle banks.

Apoio: Instituto de Biociências da Universidade de São Paulo (IB/USP)



Comunicação oral - Quinta Sessão: Evolução e biogeografia

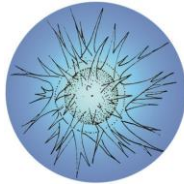
The future of corals told by mito-phylogenomics

Seiblitiz, Isabela G.L. (1, 2); Capel, Kátia C.C. (2); Kitahara, Marcelo V. (1, 2)

(1) Departamento de Ciências do Mar da Universidade Federal de São Paulo (DCMAR/Unifesp), Santos, SP, Brasil; (2) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil.

Scleractinian corals are basal metazoans pertaining to phylum Cnidaria, which is characterized by having urticating cells denominated nematocytes. Approximately half of these corals have a symbiotic relationship with dinoflagellates of family Symbiodiniaceae (zooxanthellae). Ocean acidification and global warming are a threat to this order, being associated to either loss or death of zooxanthellae (i.e. coral bleaching) as well as to the dissolution of coral carbonatic skeleton. The order Scleractinia is currently divided in three main clades based on molecular data: Basal, Complex and Robust. However, the evolutionary history of Scleractinia has not been completely resolved yet, as its monophyly has been previously questioned and the phylogeny of its suborders is still under debate. This uncertainty is likely due to the small number of taxa used, especially from azooxanthellate species, as well as the use of few molecular markers in phylogenetic analyses. Such discrepancies seem to have led to variations among topologies of different evolutionary reconstructions. Therefore, the aim of the present project is to recover the evolutionary history of Scleractinia based on complete mitochondrial genome (mitogenome) sequences of approximately 100 species of scleractinian corals. Specimens have been sequenced using Next Generation Sequencing (NGS) on Illumina platform, followed by assembly and annotation of complete mitogenomes. Data from 80 species have already been obtained, from which thirteen complete mitogenomes were successfully circularized to date and another four had the majority of genes annotated. Gene sequences from the obtained mitogenomes were aligned and used in phylogenetic analyses. Divergence times of each lineage will be estimated by molecular clock followed by mapping of palaeo-environmental data to the obtained tree. By using this technique, it should be possible to determine when some morphological and ecological features emerged or disappeared in representatives of this order, as well as to hypothesize about the fate of corals towards future anthropogenic impact. Preliminary results indicate that the Basal clade, which is composed of families Micrabaciidae and Gardineriidae, may not be monophyletic. All three species of Micrabaciidae (*Rhombopsammia niphada*, *Letepsammia superstes* and *Letepsammia formosissima*) were recovered as monophyletic and sister to Gardineriidae+Complex+Robust. Even though molecular phylogenies support Basal clade monophyly, there are anatomical similarities between Micrabaciidae and Corallimorpharia, as well as morphological dissimilarities to Gardineriidae that reinforce the pattern recovered in the present study.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq); Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP).



Pôster – História Natural

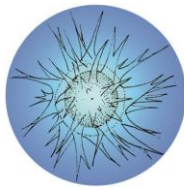
Development and culture of *Okenia polycerelloides* (Gastropoda: Nudibranchia) in laboratory: a potential model organism for experimental studies

Sales, Licia (1); Marian, José Eduardo A.R. (1); Migotto, Alvaro E. (2)

(1) Instituto de Biociências da Universidade de São Paulo (IB/USP), São Paulo, SP, Brasil (2) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil.

To fit into the role of a good model organism, the species should meet a set of important criteria, such as being abundant, widely distributed, ecologically relevant, and experimentally manageable in the laboratory. The sea slug *Okenia polycerelloides* fits most of these conditions. Here, we present a culture protocol and describe the whole development of the species, from spawning to adult. Based on its characteristics, we propose that *O. polycerelloides* is a potential model organism for experimental studies. Adult sea slugs were collected with its host, the bryozoan *Amathia verticillata*, at Araçá Bay (São Paulo state, Brazil), brought to the Center for Marine Biology of the University of São Paulo, and kept in the laboratory. The egg masses were individualized in glass bowls with filtered (0.22 µm) seawater (FSW) (daily changed) and maintained at 24°C in a germination chamber in a 12h light/12h dark photoperiod. Egg masses were cylindrical gelatinous cords varying in length and with hundreds of eggs, in which each egg was involved by one oval capsule. Cleavage was holoblastic and spiral, the first one occurring approximately 2h after egg posture (AEP), and second and third cleavages within a 1h interval each. Blastula and gastrula were formed 12h and 24h AEP, respectively. Trochophore larva stage was reached 36h AEP. Veliger larva, which is characterized by the presence of the velum, foot, and shell, was formed about 60h AEP, still encapsulated. Larval movements increased near hatching; the oval capsules ruptured and the veligers swam freely inside the matrix of the egg mass until hatching, which occurred about 77h AEP. After hatching, the larvae were moved to glass beakers (1L) with 800 ml of FSW with 25mg/L of penicillin, and under mild aeration. Larvae were daily transferred into a clean beaker with new FSW, antibiotic, and food (live microalgae *Isochrysis galbana*, at 25,000 cells/mL). When the larvae started to swim near the bottom, pieces of *A. verticillata* were added to the cultures. After 9–12 days on the water column, the larvae settled on the branches of *A. verticillata*, which were maintained as substrate and food for juveniles and adult sea slugs. The metamorphosis took around 24 h, during which the velar lobes were shed and after which the larval shell was discarded. From then on, the juvenile started to feed on the bryozoan, later developing rhinophores, gill, and papillae. It took about 15 days for the juvenile to attain the adult stage. Therefore, the complete development of *O. polycerelloides* were reached in around 30 days. Fast development associated with abundance year-round (which is rare in sea slugs), plus the fact that it is easy to collect, maintain and rear in the laboratory, all make *O. polycerelloides* a potential model organism for experimental studies.

Apoio: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP) - grant 2013/08425-0; Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq) - Finance Code 001; Núcleo de Pesquisa em Biodiversidade Marinha da Universidade de São Paulo (NPBioMar/USP)



Pôster – História Natural

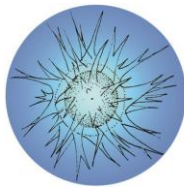
Distribution patterns of an interstitial annelid in the subtidal ripple marks at Marine National Park of Currais Islands, southern Brazil

Massocatto, Ana C.S. (1); Di Domenico, Maikon (1)

(1) Centro de Estudos do Mar da Universidade Federal do Paraná (CEM/UFPR), Pontal do Paraná, PR, Brasil.

Interstitial annelids are a frequent and diverse group of meiofauna. Their morphological plasticity allows them to inhabit several marine sediments. They are closely associated with sedimentary features responding to the granulometric composition and hydrodynamics. Among the interstitial annelids, the oligochaetes of the family Enchytraeidae are neglected in ecological studies of marine meiofauna. Among its representatives, the monophyletic genus *Grania* is the only one of the Enchytraeidae family that is found exclusively in marine sediments, comprising more than 70 species. We investigated the distribution pattern of the interstitial annelid species *Grania* sp. in two spatial scales in the ripple marks found subtidal at the Marine National Park of the Currais Islands, state of Paraná. We tested whether its distribution can be predicted by the sediment texture and by the crests or troughs of the ripples. The samples were carried out at two sites distant 200 meters apart; the sites were divided into two areas, and in each area we sampled six randomly replicates on the crests and the troughs of the ripples. We used hierarchical ANOVA considering sites (two levels, A and B) nested to the ripples (two levels, crests, and trough). The response of *Grania* sp. abundances to the sediment texture was determined with a model selection approach, applying on GLMs. Our results show that for site A crests and troughs do not explain the distribution of *Grania* sp.; in site B, the higher abundance of *Grania* sp. was found in the troughs. The relationship between the distribution of *Grania* sp. and sediment texture showed a positive correlation between sorting and a negative correlation with the mean grain size and kurtosis. All in all, *Grania* sp. distribution was related to fine sand, extremely poorly selected, with platy- to mesokurtic distribution.

Apoio: Programa de Pós-Graduação em Sistemas Costeiros Oceânicos (PGSISCO)



Pôster – História Natural

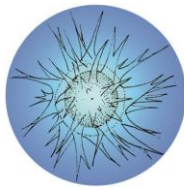
The amazing world of bryozoans: morphological complexity of polymorphs

Nascimento, Karine B. (1, 2); Vieira, Leandro M. (3); Santos, Ariely D. (1); Migotto, Alvaro E. (1)

(1) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil; (2) Instituto de Biociências da Universidade de São Paulo (IB/USP), São Paulo, SP, Brasil; (3) Centro de Biociências da Universidade Federal de Pernambuco (CB/UFPE), Recife, PE, Brasil.

Bryozoans are colonial animals formed by unities called zooids. Although the main individual – the autozooids – are characterized by a retractable lophophore (for food capture) and digestive system with mouth, intestine, and anus, the colony may also have heterozoids, modified multifunctional polymorphic zooids responsible for different functions, including defense, protection, support and larval incubation. In addition, other structures formed from the wall of the autozooid may have these same functions. Morphologies of these zooidal structures are suitable to be used to identify and differentiate species, as well as to infer phylogenetic relationships between different taxa. Thus, here we provide illustrations and characterization of polymorphic structures found in Beaniidae family (Cheilostomata, Bryozoa). Between 2015 and 2019, about 700 specimens of Beaniidae from zoological collections were analyzed and more than 3000 images were generated using scanning electron microscopy. At least five heterozoids were characterized: (i) spines (oral, lateral, abfrontal and opercular), (ii) avicularia (bird's head avicularia, formed by cystid, rostrum, mandible and peduncle), (iii) rhizoids, (iv) stolon and (v) oecia. Besides this, two kinds of structures formed from the autozooid wall were also characterized: i) oral projections and ii) connecting tubes. Spines are sessile structures that provide protection for the soft parts of the autozooids, mainly the frontal membrane, oral opening and ovicell, but may also keep the abfrontal part of the autozooid away from the substrate, freeing the colony from accumulation of sediment. Avicularia are mobile, often located near the oral region and may have different functions, such as removing debris, capturing motile organisms and deterring possible predators. Rhizoids are elongate structures in abfrontal or basal region that attach the autozooid to the substrate. Stolons and connecting tubes connect the autozooids to each other and allow the exchange of nutrients for the entire colony through communication pores. Oecia are the skeletal structure of the embryonic and larval incubation chambers, which may be well-developed or vestigial at the distal part of the autozooid. In addition to these, a lanceolate structure situated at the distal part of the autozooid, possibly a modified spine, unique to a *Beania* species is also characterized. The genus *Beania* has not yet been subjected to a comprehensive revision, and so far neither morphological nor molecular phylogenetic analyses were done for any taxa of the family Beaniidae. The morphological study performed is an important step toward the recognition of homologies so that hypotheses of phylogenetic relationships can be proposed and the taxonomical results obtained for these taxa validated.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq); Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq).



Pôster – Outra área temática

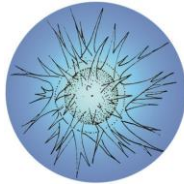
Correlations between weight and total length of blue shark embryos *Prionace glauca* (Chondrichthyes: Carcharhiniformes)

Conrado, André L.V. (1); Lunes, Renata S. (1); Amorim, Alberto F. (2); Bruno, Carlos Eduardo M. (3); Silva, José Roberto M.C.(1)

(1) Instituto de Ciências Biomédicas da Universidade de São Paulo (ICB/USP), São Paulo, SP, Brasil; (2) Centro de Pesquisa do Pescado Marinho do Instituto de Pesca (APTA/SSA), Santos, SP, Brasil; (3) Departamento de Cirurgia, Faculdade de Medicina Veterinária e Zootecnia da Universidade de São Paulo (FMVZ/USP), São Paulo, SP, Brasil.

The blue shark, *Prionace glauca* is commercially exploited and is on the International Union for Conservation of Nature (IUCN) red list with almost threatened status. Populational studies have observed that females of *P. glauca* with gravid uteri present embryos with up to 45 cm of furcal length. However, knowledge about the reproduction of this species in the Southern Atlantic Ocean requires more information. Thus, the objective was to evaluate the morphometric development of *P. glauca* embryos at different stages of development and correlate the weight and total length. Nine gravid uteri of five blue sharks were collected in the South Atlantic Ocean between May 2013 and April 2015 by the commercial trawling fleet of Itajaí, State of Santa Catarina, Brazil. The embryos were euthanized *in situ* by desensitization and fixed in 10% formalin. Subsequently, the embryos were weighed (W, in grams) and taken as total lengths (TL, in centimeters). Data were evaluated by Pearson's correlation between the weight and the length of the embryos and underwent exponential regression using the Microsoft Excel Office statistical package. This work was approved by the Ethics Committee on Animal Use (CEUA/FMVZ/USP) nº 9396271113 and authorized by the Brazilian Institute of Environment and Renewable Natural Resources (SISBIO/ICMBio/MMA) nº 47691-1. In total, 221 embryos were collected with a mean of 25.4 ± 8.5 embryos per uterus, weight of 10.39 ± 9.84 g and total length of 11.33 ± 4.21 cm. The regression equation was $W = 0.0207TL^{2.4627}$ ($R^2 = 0.95$, F-test = 1938, $P < 0.0001$). Regression equations between weight and total length are useful in assessing populations of different species *in situ* where it is not possible to use scales, a reality in scientific cruises on commercial fishing vessels. Mathematically, exponential regression showed a high correlation between weight and total length of the embryos, with favorable use for future evaluations of *P. glauca* shark embryos.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq)



Pôster – Outra área temática

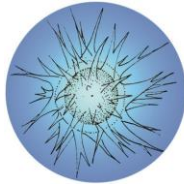
Morphological and molecular identification of octocorals (Cnidaria; Anthozoa) potentially invasive of Brazilian southeastern

Carpinelli, Ágatha N. (1); Cordeiro, Ralf T.S. (1); Moura, Rodrigo L. de (2); Kitahara, Marcelo V. (1) (3)

(1) Universidade Federal de São Paulo (UNIFESP), Santos, SP, Brasil; (2) Universidade Federal do Rio de Janeiro (UFRJ), Rio de Janeiro, RJ, Brasil; (3) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil.

Biological invasions are characterized when organisms are introduced to a region outside their native range, being able to establish and reproduce mainly because of their fast reproductive rate and lack of natural predators. Non-indigenous species are today the second greater cause of biodiversity loss, which can also affect the ecosystem, society and economy. In this sense, the present work aimed to identify octocoral (Cnidaria; Anthozoa) invaders, collected in Angra dos Reis - RJ, whose probable vector was aquarium trade. The identification of the organisms was based on morphological aspects, with emphasis on sclerites analyzes by scanning electron microscopy. In addition, genetic analyzes were performed using partial sequencing of the molecular markers CO1, msh1 and 28S. Evolutionary reconstruction corroborated morphological data, in a reciprocal illuminating process. The results corroborate previous studies on the occurrence of *Clavularia sp.* and *Sansibia sp.* in Angra dos Reis, as well as to report the occurrence of another invasive species in Brazil, *Erythropodium caribaeorum*.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq)



Pôster – Outra área temática

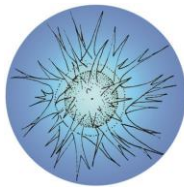
Photophores description of toadfish *Porichthys porosissimus* (Cuvier 1829), Batrachoidiformes, Batrachoididae, from Guarujá inshore, Brazil

lunes, Renata S. (1); Conrado, André L.V. (1), Silva, José Roberto M.C. (1)

(1) Instituto de Ciências Biomédicas da Universidade de São Paulo (ICB/USP), São Paulo, Brasil

Toadfish *Porichthys porosissimus* is a subtropical marine benthic fish species, reaching up to 32 cm body length. It is found from Espírito Santo, Brazil to eastern Argentina in depths ranging between 20 and 50 meters. Toadfish is one of the most abundant by-catch species in sea-bob shrimp fishery and are totally discarded as it has no economic value. The presence of photophores on the skin accompanying the lateral line is possibly related to camouflage for predation, mimicry, defense and recognition among the same or different species. Among species, photophores shape, dimension, number and arrangement can vary. Thus, the goal was to describe the photophores of the toadfish *P. porosissimus* skin from Guarujá inshore, Brazil. The specimen was captured dead as by-catch of a shrimp trawl fishery, held in February 2019. Skin samples with photophores were collected from different regions and fixed in 10% formalin for 24-48h, stored in alcohol 70% and embedded in histological resin (Historesin, Leica, Germany). Sections of 3 µm thick were stained with methylene blue, toluidine blue, hematoxylin-floxin and periodic-acid Schiff (PAS). In light microscopy, it was observed that the skin of the toadfish is covered by pavement epithelium, presenting six to eight epithelial layers, with photophores and mucous glands between them. The photophores appear as round elliptical shaped structures ranging in size from 59.0 x 66.4 µm to 117.8 x 40.4 µm (length x height). Larger photophores are covered by one to two layers of epithelial cells upheld by smooth connective fiber sheaths. Photophores are filled with an amorphous eosinophilic material with neutral to slightly acidic pH, with globular structures close to upper pole. The mucous skin glands have oval, goblet and fusiform forms, filled by neutral (PAS positive) and acid (metachromasia to toluidine blue) mucus, with a single pore on the surface. The dermis showed wavy, acidic collagen fibers, blood vessels, and thin layers of melanin deposition near the basement membrane. Unlike other species of the genus *Porichthys*, the photophores of toadfish do not have lens.

Apoio: Instituto de Ciência Biomédicas- USP (ICB/USP)



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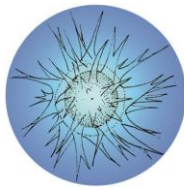
Radiographic and tomographic description of marlin sucker *Remora osteochir*, Pisces: Echeneidae. Preliminary data of one specimen

Conrado, André L.V. (1); Lunes, Renata S. (1); Bruno, Carlos Eduardo M. (2); Rocha, Aline T.S. (3); Silva, José Roberto M.C. (1)

(1) Instituto de Ciências Biomédicas da Universidade de São Paulo (ICB/USP), São Paulo, SP, Brasil; (2) Faculdade de Medicina Veterinária e Zootecnia da Universidade de São Paulo (FMVZ/USP), São Paulo, SP, Brasil; (3) Centro Avançado de Diagnóstico por Imagem, CADi, São Sebastião, SP, Brasil.

Remoras are commensal fish of various marine animal species such as sharks, turtles, dolphins, manta rays and whales. The aim of this study was to evaluate the anatomy of a marlin sucker *Remora osteochir* using computed tomography and digital radiology. One marlin sucker was collected as part of the companion fauna of the swordfish and shark fishery in South Atlantic Ocean, 35° S. It presented 19 cm of furcal length and 22 cm of total length, weight around 54 g and undetermined sex. This specimen was euthanized by the excess of benzocaine (1 gL⁻¹), fixed in 10% formalin solution and stored in 70% alcohol until laboratory evaluation. The tomographic and radiographic exams were performed in São Sebastião/SP and in São Paulo/SP, respectively. For the tomographic evaluation, it was utilized a HiSpeed CT/e Dual helical tomograph (GE Medical Systems, GE Healthcare Life Sciences, USA). The radiographic images were acquired by the AGFA DX-D 400 digital radiography equipment (AGFA Healthcare, AGFA-Gevaert, Belgium). This work was approved by the Ethics Commission of the School of Veterinary Medicine and Animal Sciences of the University of São Paulo, Brazil # 9396271113 and the collection was authorized by the Brazilian Institute of Environment and Renewable Natural Resources # 47691-1. From the tomographic images and reconstructions, it was possible to identify the intercalar bones of the cephalic disc; spine with vertebral bodies composed of neural arches and ventral ribs; and pectoral girdle formed by posttemporal, cleithrum and scapulocoracoid bones. In radiographic images it was possible to observe otoliths in the center of the neurocranium, to count 27 vertebrae, nine pairs of ribs and to detect the presence of two epural and three hipural bones near of the caudal fin. The neurocranium is a compact structure formed by small bones, which hampers a reliable image. Taking into account the relationship between age/otolith rings (Y) and total length (TL) described by the von Bertalanffy equation for marlin suckers *R. osteochir* from Mediterranean Sea $TL=27.37 (1-e^{-0.248(Y-(-1.36))})$, where e is the mathematical constant with numerical value about 2.71 (based on data from the specialized literature), the specimen should be around 3-4 years when it was collected. It was concluded that computed tomography and digital radiology were able to describe anatomical structures of marlin sucker *R. osteochir* without dissection.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq)



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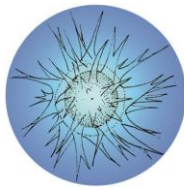
Recognizing the diversity of jellyfishes (Medusozoa, Rhopaliophora)

Morandini, André C. (1, 2); Cavalcante, Arthur S. (1); Gamero-Mora, Edgar (1); Jordano, Mayara A. (1); Klovrza, Anabelle (1); Lawley, Jonathan W. (3); Maronna, Maximiliano M. (1); Molinari, Clarissa G. (1); Tiseo, Gisele R. (1); Schiariti, Agustin (4); Stampar, Sergio N. (5)

(1) Departamento de Zoologia, Instituto de Biocências da Universidade de São Paulo (IB/USP), São Paulo, SP, Brasil (2) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil (3) Sea Jellies Research Laboratory, School of Environment and Sciences, Griffith University, Gols Coast, QLD, Australia (4) Instituto Nacional de Investigación y Desarrollo Pesquero, Mar del Plata, Argentina (5) Departamento de Ciências Biológicas, Faculdade de Ciências e Letras, Universidade Estadual de São Paulo (UNESP), Assis, SP, Brasil

The main objective of the project is to generate knowledge about the systematics of jellyfish, focusing on morphological aspects and using molecular tools. The differential of the project lay in using an integrative approach [life cycle, biology, detailed morphology, molecular data] to diagnose and define species. It is composed of several smaller projects including different students and collaborators. Concerning the systematics part: a book with all species of scyphozoans and cubozoans of the world was finished containing descriptions of 271 valid species; we advanced in resolving the identification of species of the genera *Aurelia* (6 redescribed, 4 resurrected, 17 new species being 2 from the Brazilian coast), *Cassiopea* (at least 12 redescribed, and 1 new species), *Linuche* (4 redescribed) and *Nausithoe* (22 redescribed, 1 new species for Brazil) using both morphology and molecular data; the species *Lychnorhiza lucerna* has little genetic variability (COI, ITS) throughout its distributional range (0.7% between Argentina and N Brazil); data from the ultrastructure of the sperm of jellyfishes cannot be used for separating species, but can help in distinguishing the classes Scyphozoa and Cubozoa. Concerning the biology of species: the investment in gonad formation corresponds to 20-30% of total wet weight of medusa of *L. lucerna* and *Chrysaora lactea*; the species *Catostylus tagi* from the Portuguese coast has a metagenetic life cycle (polyp obtained from *in vitro* fertilization); in the species studied (*N. aurea*, *C. plocamia*, *L. lucerna*) the cnidae types do not vary throughout the life cycle, only size; higher temperatures (+ 5° C) under laboratory conditions affect the development and swimming abilities of *L. lucerna* and *C. andromeda*. The genome size of 29 species of Scyphozoa and Cubozoa were generated and data showed that species with reduced or abbreviated metagenesis have larger genomes.

Apoio: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP) 2015/21007-9); Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq 304961/2016-7); Núcleo de Pesquisa em Biodiversidade Marinha da Universidade de São Paulo (NPBioMar/USP)



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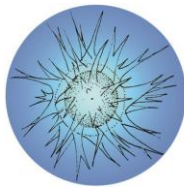
Sipuncula diversity: an integrative approach using larvae and adults form

Kawauchi, Gisele Y. (1); Franco, Letícia C. (1); Tiago, Claudio G. (2); Migotto, Alvaro E. (2)

(1) Departamento de Zoologia, Instituto de Ciências Biomédicas da Universidade Federal de Minas Gerais (ICB/UFMG), Belo Horizonte, MG, Brasil; (2) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil.

In the later Metazoa phylogenies, Sipuncula has been considering as a member of the Annelida clade. They are exclusive marine worms important to the bioerosion process in the ocean and the ecological dynamic in the benthic community. Recent studies using molecular and morphological data pointed out that some cosmopolitan sipunculans are non-monophyletic and can be hiding a species diversity among this group of invertebrates that has 150 described species. In a study focusing in molecular data of the most known species of Sipuncula, *Sipunculus nudus*, from different parts of the world, recovered multiple clades and indicated that some morphological characters could possibly distinguish them from each other. The wide distribution of some adult species has been presumably based on the larvae (called pelagosphaera) long distance capability of dispersion, maintaining the genetic connectivity between isolated populations. Studies on larvae from the Florida Current have described ten different types by external characters as body size, color, ciliation pattern, texture of the surface and head morphology. From these ten larvae, six were already linked to their adults using the DNA barcoding approach. Our study aims to identify sipunculans larvae found in the São Sebastião Channel and link them to the adults also found in the same locality, using the DNA barcoding method and describing the external morphological characters observed from each larval type. In this study, we collected seven different types of pelagosphaera and adults from nine species in eight genera. After collection each type of larva was photographed and described using the characters suggested by the study from Florida Current larvae. We sequenced individuals from both stages of life for cytochrome c oxidase subunit 1 gene (CO1) (649 bp) and the nuclear gene Histone H3 (327 bp). Phylogenetic analyses were performed using Likelihood approach for both genes in two separated analysis. For now, we could find correspondence for three larvae and their adults. For the others, we were able to determine the genus in which they belong. The study of pelagosphaera larvae will contribute to the knowledge of zooplankton diversity, provide insight into population connectivity of widespread species, and larval morphology can give us an additional suite of characters useful for differentiating species in future taxonomic studies.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq); Núcleo de Pesquisa em Biodiversidade Marinha da Universidade de São Paulo (NPBioMar/USP)



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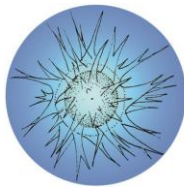
The high and low microbial abundance dichotomy in marine sponges from the north coast of São Paulo (Brazil)

Hardoim, Cristiane C.P. (1); Ramaglia, Andressa C.M. (1); Carrara, Virginia (1, 2); Lobo-Hajdu, Gisele (3); Custódio, Márcio R. (4)

(1) Laboratório de Interações Hospedeiro-Microbiota, Instituto de Biociências da Universidade Estadual Paulista (IB/UNESP), São Vicente, SP, Brasil; (2) Laboratório de Bioprospecção de Produtos Naturais, IB-UNESP, São Vicente, SP, Brasil; (3) Departamento de Genética, Instituto de Biologia Roberto Alcântara Gomes, Universidade do Estado do Rio de Janeiro, Rio de Janeiro, Brasil; (4) Laboratório de Biologia Celular de Invertebrados Marinhos, Departamento de Fisiologia Geral, Instituto de Biociências da Universidade de São Paulo (IB/USP), São Paulo, SP, Brasil e Núcleo de Pesquisa em Biodiversidade Marinha da Universidade de São Paulo (NPBioMar/USP), São Sebastião, SP, Brasil.

Marine sponges harbor diverse microbial communities in which complex interactions are established. Based on the microbial abundance, the species have been classified in high microbial abundance (HMA) and low microbial abundance (LMA) sponges. Even though dozens of sponge species have been classified worldwide as HMA or LMA, there is none sponge from Brazilian coast. To address this, the sponge species *Aplysina fulva*, *A. caissara* (endemic), *Tedania ignis*, *Ptilocaulis walpersi*, *Dragmacidon reticulatum*, *Halichondria cebimarensis* (endemic) and *Mycale angulosa* were collected at Praia do Segredo, Praia Preta, Prainha and Ponta do Recife, in the north coast of São Paulo State (Brazil). The sponge species were identified using morphological characteristics and by barcoding using the genes cytochrome oxidase subunit 1 (*cox-1*) and cytochrome *b* (*cob*). The DNA was subjected to Illumina MiSeq platform using the phylogenetic marker 16S rRNA. The *cob* was capable to separate *A. fulva*, *A. caissara*, *T. ignis*, *P. walpersi* and *D. reticulatum* into distinct clusters, whereas *cox-1* was able to distinguish *H. cebimarensis* (endemic) and *M. angulosa*. Preliminary results from the Illumina sequences showed that the highest alpha diversity metrics were detected in *A. fulva*, *A. caissara* and *D. reticulatum* than in *P. walpersi*, *M. angulosa*, *H. cebimarensis* and *T. ignis*. Several phyla, classes, and OTUs were found differentially abundant in either group. Additionally, HMA and LMA indicators were also detected. These results demonstrated for the first time that *A. fulva*, *A. caissara* and *D. reticulatum* are HMA, whereas *P. walpersi*, *M. angulosa* and *H. cebimarensis* are LMA.

Apoio: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP), nr. 2016/17189-7.



Pôster – Ecologia e Conservação

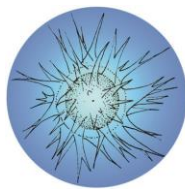
Assessment of the functional and histological parameters associated with the exposure of the fish cobia *Rachycentron canadum* (Linnaeus, 1766) a sublethal concentrations of polycyclic aromatic hydrocarbons (PAHs)

Neto, Gabriel M.S. (1); Salvo, Lígia M. (1); Moreira, Renata G. (2); Rezende, Karina F.O. (1); Silva, José Roberto M.C. (1); Borella, Maria I. (1)

(1) Departamento de Biologia Celular, Instituto de Ciências Biomédicas da Universidade de São Paulo (ICB/USP), São Paulo, SP, Brasil. (2) Departamento de Fisiologia, Instituto de Biociências da Universidade de São Paulo (IB/USP), São Paulo, SP, Brasil.

Petroleum is one of the most used xenobiotics by humanity and its water soluble fraction (WSF) is mainly composed of hydrocarbons (97% of the general composition). Among hydrocarbons, highlights the Polycyclic Aromatic Hydrocarbons (PAHs) which are organic pollutants of great environmental persistence, and its derivative compounds are potential carcinogens that can affect any biota in which they are involved. Thus, the objective was to evaluate the effects of the sublethal exposure to PAHs at the concentration of 0.3 ppm in marine fish *Rachycentron canadum* by means of morphometric, metabolic and histological parameters. The methodology is based on the ethical principles in the animal experimentation of the ICB / USP and consists, initially, in the extraction and evaluation of the WSF by means of fluorescence spectrometry. Then, *R. canadum* with mean weight of 52.26g (± 3.77), were divided into 3 groups of ten individuals each, being, CG- Control group; GE7- Group exposed to 0.3 ppm WSF for a period of 7 days, and; GE14- Group exposed to 0.3 ppm of WSF for a period of 14 days. After the exposure period, hepatic tissue was assessed according to the Hepatosomatic Index (HSI) and the Histological Alteration Index (HAI). In addition, the metabolic parameters (cortisol, glucose and total proteins) were determined by the ELISA test and lactate was performed using the Vet Test 8008 equipment. The results show that the mean \pm standard deviation of the HSI referring to the CG (3.47 ± 0.40) were statistically different from GE7 (7.08 ± 0.81) (ANOVA; $p=0.033$) and GE14 (5.69 ± 2.28) (ANOVA; $p=0.045$). With the application of HAI, was obtained $I = 0$ to CG, characterized as normal functioning organ, $I = 22$ to GE7 and $I = 23$ to GE14, both characterized as organ with moderate to severe alterations. However, no statistical differences were observed in relation to the metabolic parameters analyzed. It is concluded that exposure to the sublethal concentration of PAHs (0.3 ppm) overloads the liver of *R. canadum* revealed by the increase in HSI, probably due to the histological alteration of moderate to severe, after a period of 7 and 14 days. On the other hand, the absence of alterations in metabolic parameters may indicate an adaptation of the animals to stressors factors, such as PAHs. The *R. canadum* species was an excellent bioindicator, due to its behavioral characteristics and responses to the parameters analyzed, showing an effective response in all bioassays. The present study adds another tool to intensify biomonitoring of areas that may be impacted by PAHs.

Apoio: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP) : 10/50548-7;



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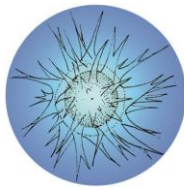
Biodiversity of macroalgae-associated Ophiuroidea in the Alcatrazes Archipelago, São Sebastião, SP

Vicente, Vanessa S. (1); Serrano, Helena (1); Mansur, Karine F. R. (1); Longo, Pedro A. S. (1); Leite, Fosca P.P. (1)

(1) Instituto de Biologia da Universidade Estadual de Campinas (IB/UNICAMP), Campinas, SP, Brasil.

The Alcatrazes Archipelago, located on the north coast of the state of São Paulo, in São Sebastião, is the largest marine protected area in the South and Southeast regions of Brazil, which comprises two main Conservation Units: the “Tupinambás” Ecological Station and the “Wildlife Refuge.” In 2019, the Refuge has been partially opened for SCUBA diving tourism, which reinforces the importance of raising knowledge of coastal biodiversity in order to minimize the impact of ecotourism on these areas. Invertebrates are of great ecological importance in marine coastal habitats, acting as key elements for structuring marine trophic webs. However, knowledge on the biodiversity of marine invertebrates in the Alcatrazes Archipelago is still lacking. In coastal habitats, macroalgae act as important biological substrates for a wide range of associated invertebrates species, providing food resources, breeding sites, shelter and protection against predators, natural impacts and wave action. Among the associated fauna, the Ophiuroidea (Echinodermata) are often very abundant in these habitats. Thus, this study aims to present the biodiversity of ophiuroids associated to macroalgae habitats in two areas within the Alcatrazes Archipelago: one recently opened for visit and one of total restricted access. Through SCUBA diving, ten samples, in each area, of the predominant macroalgae species were taken at depths between 7 to 10 m. Sampling was carried out during the summer of 2018 and 2019, and during the winter of 2018. Specimens were fixed in 70% alcohol and identified at species level under a stereomicroscope. Seventy-nine individuals from three families, three genera and four species were recorded. The species found were *Ophiactis lymani* (45%), *Ophioplocus januarii* (44%), *Amphipholis squamata* (7.5%) and *Ophiactis savigny* (2.5%). The predominant macroalgae differed between seasons: *Sargassum* sp. in summer and *Dictyota* sp. in winter. The abundance of each ophiuroid species, as well as their total abundance, were compared in two different ANOVA designs: a two-way ANOVA for only the 2018 samples (two factors: local and algae type) and a two-way ANOVA for only the summer samples (two factors: local and year). All comparisons were statistically non-significant ($p > 0.05$). Therefore, the abundance for all ophiuroid species was relatively similar between areas and among the different macroalgal hosts. Microhabitats provided by both brown algae might be functioning as shelter for these highly adaptable animals, resulting in similar abundances in all seasons. It is noteworthy that the few *Ophioplocus januarii* individuals found in samples were mostly juveniles, suggesting these macroalgae are “nursery” habitats for this species. Finally, we highlight the importance of monitoring the biodiversity of invertebrate species such as Ophiuroidea in the following years after the partial opening of Alcatrazes for ecotourism in order to assure conservation.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq); Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP)



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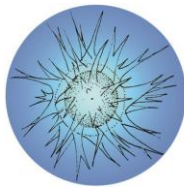
Colour change and behavioural choice facilitate chameleon prawn camouflage against different seaweed backgrounds

Green, Samuel D. (1); Duarte, Rafael C. (2,3); Kellett, Emily (1); Alagaratnam, Natasha (1); Stevens, Martin (1)

(1) Centre for Ecology and Conservation, University of Exeter, United Kingdom; (2) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil; (3) Centro de Ciências Naturais e Humanas, Universidade Federal do ABC (UFABC), São Bernardo do Campo, SP, Brasil.

Camouflage is driven by matching the visual environment, yet natural habitats are rarely uniform and comprise many backgrounds. Therefore, species often exhibit adaptive traits to maintain crypsis, including colour change and behavioural choice of substrates. However, previous work largely considered these solutions in isolation, whereas many species may use a combination of behaviour and appearance to facilitate concealment. Here we show that green and red chameleon prawns (*Hippolyte varians*) closely resemble their associated seaweed substrates to the vision of predatory fish, and that they can change colour to effectively match new backgrounds. Prawns also select colour-matching substrates when offered a choice. However, colour change occurs over weeks, consistent with seasonal changes in algal cover, whereas behavioural choice of matching substrates occurs in the short-term, facilitating matches within heterogeneous environments. We demonstrate how colour change and behaviour combine to facilitate camouflage against different substrates in environments varying spatially and temporally.

Apoio: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP)



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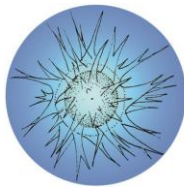
Effects of population connectivity on individual fitness: a case-study on pea crabs associated to sand dollars

Souza, Juliana (1); Flores, Augusto A.V.(1)

(1) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil.

Landscape ecology utilizes connectivity metrics as a fundamental measurement for modelling and analyzing the spatial dynamics of populations. Many natural populations are organized as metapopulations although this concept is mostly related to landscape fragmentation and habitat loss by anthropogenic effects. Those populations are maintained by migration patterns of the individuals, therefore, population structure and reproductive patterns persist because of the balance between immigration and emigration rates. However, little is known about how physical and biological properties of the connectivity matrix, usually a secondary and impoverished environment, affect the stability of populations and the performance of the individuals. This study approaches this issue in a particularly tractable system: pea crabs distributed on sand dollars, the latter working as discrete habitat patches separated by distances that can be easily covered by SCUBA diving. In the first phase of the study, we constructed distribution maps of the sand dollars and their pea crab guests along the São Sebastião channel, in different sampling areas of São Sebastião and Ilhabela. From these maps we ran analysis of the connectivity between habitat patches and on crab populations to identify the degree of aggregation, and the effects of habitat connectivity on the formation of reproductive units of the crabs. Also, in each sampling area we collected sediment samples that compose the matrix for granulometry and organic matter content analysis, and we measured the predation potential of each area by field experimentation, to investigate the composition, quality and predation risk of the matrix that could influence the migration rates of the crabs. In a second phase, the larval release rate of each combination of adult crabs found on sand dollars will be estimated in the laboratory to assess individual fitness. The analyses of these data will allow to (i) identify the environmental variables that most likely contribute to crab connectivity, (ii) assess how connectivity may influence crab clustering in sand-dollars (number of individuals and sex ratio), and (iii) understand how connectivity may ultimately affect crab per capita reproductive value. We also planned to conduct a secondary laboratory experiment in which the environmental variables identified above are manipulated to (iv) verify whether correlational evidence truly reflect cause-effect relationships. The preliminary results have shown that the sand dollars are randomly distributed in each area sampled, but the crab populations show a more clustered distribution and form reproductive units on patches closer to each other. We also verified high predation potential on the matrix that could lead to reduced migration rates and the consequent colonization of nearest patches.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq)



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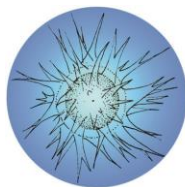
Evidence for trophic facilitation of habitat-limited grazers and edge effects at novel seagrass habitats in SE Brazil

Pavone, Carla B. (1,2), Gorman, Daniel (3), Flores, Augusto A.V. (1)

(1) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil; (2) Instituto de Biologia da Universidade Estadual de Campinas (UNICAMP), Programa de Pós-Graduação em Ecologia, Campinas, SP, Brasil; (3) Instituto Oceanográfico da Universidade de São Paulo (IO/USP), São Paulo, Brasil

Seagrasses may potentially enhance the abundance and diversity of benthic invertebrates, providing important trophic resources to demersal consumers. Two seagrass species occur in the São Sebastião Channel (SSC), Brazil: *Halodule emarginata*, a well-established species, and *Halophila decipiens*, a more tropical species that has recently extended southwards and become increasingly abundant. We compared several metrics of invertebrate assemblages at replicate sites populated by either *Halodule* or *Halophila* by sampling vegetated patches, bordering and isolated bare habitats to better understand how these seagrasses subsidize higher-order consumers. Despite the relatively low seagrass biomass at sampled meadows and the very high spatial variation between and within-sites of nearly all measured variables, we found evidence for bottom-up forcing within *Halophila* (not *Halodule*) patch boundaries through trophic facilitation of small grazing gastropods. Since this effect was only observed where baseline invertebrate abundance was high, we conclude that grazing gastropods may be habitat-limited in the area. Rather than spillover effects, changes in community structure from patch to bordering bare grounds indicate marked edge effects, with increased dominance of free-living polychaetes at the transitional habitat. Away from vegetated patches, sipunculid worms further discriminated isolated bare habitats from seagrass edges. Through soft-bottom re-engineering and trophic provisioning, the current spread of *H. decipiens* may critically change seascapes and the spatial distribution of ecological functions along the SCC.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq); Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP)



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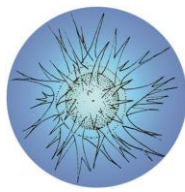
Floating alien coral: a journey through the oceans

Faria, Laiza C. (1,2); Kitahara, Marcelo V. (1,2,3)

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Ocean plastic pollution is a global concern. Plastic ingestion by animals and their capability to absorb chemicals are increasing scientific and non-scientific community attention. Recently, plastic debris was reported in the deep sea, indicating that anthropogenic effects are probably reaching even the most unexplored places on Earth. One plastic derivate highly consumed, and commonly found in the ocean is polystyrene foam (Styrofoam). Besides the pollution problem itself, Styrofoam can become a substrate for some sessile organisms and due to its buoyancy properties, becomes a dispersion vector for them. Once the organism is attached to the floating substrate, it can drift through the wind-driven currents. Here, we report the first record of *Tubastraea coccinea* floating attached to Styrofoam in São Sebastião, Brazil. Commonly known as sun corals, *T. coccinea* is an invasive azooxanthellate scleractinian. The first record of the species in Brazil occurred in the 1980s, on oil and gas platforms in the Campos Basin, Rio de Janeiro state. Nowadays, *T. coccinea* can be found on approximately 3500km through the Brazilian coastline, on natural and artificial substrates. Due to the lack of natural predators, rapid reproduction and extensive defense mechanisms, the sun coral has been spreading rapidly on the Brazilian coast, affecting marine biodiversity and modifying ecosystem functions. Many efforts are being made to control, and even try to reverse the situation of sun coral in Brazil. Now, we have a new sun coral propagation manner to worry about.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq); Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP)



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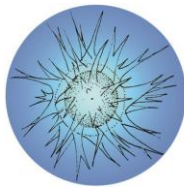
Genotoxicity effects in marine fish from the Araçá Bay (Brazil) after an oil spill

Lígia, Salvo M. (1); Andrews, Emerenciano K. (1); Divinomar, Severino (2); Junqueira, Helena (2), Felipe, Souza C. (1), Rossi-Wongtschowski, Carmen (3); Silva, José Roberto M.C. (1)

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Polycyclic aromatic hydrocarbons (PAHs) are toxic lipophilic compounds that accumulates in organisms and undergo bioaccumulation and biomagnification processes along the trophic chain. Here we evaluated the effects of PAHs on fish collected in the Araçá Bay, northern coast of São Paulo State, southeast Brazil, soon after and one year after a severe oil spill from an oil depot located on the São Sebastião Channel near the bay. Specimens of the fish *Mugil curema* (White mullet), *Epinephelus marginatus* (dusky grouper) and *Haemulon steindachneri* (roughneck grunt) were collected in the Araçá Bay during the 2013 winter and 2014 summer. The fish were evaluated for the presence of PAHs in bile and genotoxicity induction by erythrocyte nuclear abnormalities (ENAs) and micronucleus (MN) formation. Synchronous fluorescence UV spectrophotometry (SPEX Fluorolog 1681) was used in the analysis of PAHs, both for the waters collected from the bay and the fish bile. Morphometric parameters were calculated using the hepatosomatic index (HSI) and Fulton's condition factor (K). The results showed significant alterations in the frequencies of ENAs and MN when comparing the two evaluated periods. For *M. curema*, very significant differences ($p < 0.01$) in the frequency of ENAs and MN were found between the samples from the 2013 winter and 2014 summer. When comparing the three species evaluated, we also found very significant differences in the ENAs frequency of *E. marginatus* (S) ($p < 0.01$) and *H. steindachneri* (S) ($p < 0,05$) concerning *M. curema* (W). Somatic indexes indicate the general state of the fish, allowing to estimate their health state, the results showed a statistically significant difference for K between samples of *M. curema* collected in the winter and summer. No statistically significant differences were found regarding other parameters. The use of biomarkers of environmental contamination at different levels of biological organization, have constituted an important instrument in the assessment of the possible effects and in the biomonitoring of aquatic pollutants in the environment.

Apoio: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP) : 10/50547-8; BIOTA/FAPESP (Araçá);



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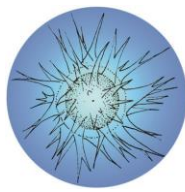
Spatial and temporal patterns of mobile invertebrate assemblages associated to canopy and turf-forming macroalgae

Figueiredo, Carla K. (1); Flores, Augusto A.V. (2)

(1) Faculdade de Filosofia, Ciências e Letras de Ribeirão Preto (FFCLRP/USP), Ribeirão Preto, SP, Brasil; (2) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil.

Canopy-forming macroalgae can play important ecosystem functions, adding complexity to coastal and terrestrial trophic webs, promoting a highly complex environment that is often colonized by a rich fauna of mobile invertebrates. This associated fauna benefits from shelter against predation and from trophic resources that are available, directly or indirectly, in this environment. These benthic canopy-forming macroalgae generally predominate in advanced stages of succession, overlapping with algae turfs of less structural complexity. Nonetheless, environmental disturbances can prevent the establishment of canopy-forming, leading to a permanent phase-shift to turf domination. State transitions between turfs and canopies are well documented for temperate reef habitats however is unknown how much of an impact is generated owing to the loss of vagile invertebrates and it is important to understand the potential ecological effects that this loss of habitat can generate. On the coast of southeastern Brazil, the *Sargassum* spp. macroalgae predominate, which oscillate in a seasonal and predictable way, allowing the conduction of studies on the impact of these processes on the secondary production. Thus, this project aims to (1) investigate the differences of the mobile communities associated with canopy and turf-forming macroalgae, and to estimate the importance of vegetation habitats in the São Sebastião Channel, SP, Brazil and (2) examine the temporal dynamics of the mobile invertebrate communities associated with *Sargassum* beds. For this purpose, fieldwork took place throughout the *Sargassum* blooming season¹ (December/2017 - March/2018) for objective 1 and December – February/2019 for objective 2. Canopies formed by *Sargassum* spp. and *Galaxaura marginata* (brown and red algae) also turfs composed of filamentous and articulated calcareous algae were collected in different locations in the São Sebastião Channel - SP. The associated mobile fauna was separated into different size classes, counted and identified in large groups. Previous results show we obtained a significant amount of different taxonomic groups, a greater abundance and diversity of individuals in the macroalgae samples in relation to the turfs, we found in larger quantities gastropods and amphipods in the macroalgae, while in the turfs were found in greater amounts polychaetes and tanaidaceans. Most of the individuals were concentrated between the sizes of 1.7 - 2.8 mm and only the canopy-forming presented specimens larger than 12 mm. Red and brown macroalgae presented similar numbers of individuals and groups while filamentous turfs were more inhabited in relation to calcareous, being the habitat chosen for comparison during the second stage of this project which is under development.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq); Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP)



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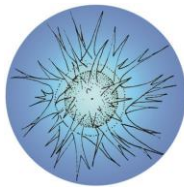
Sun coral (*Tubastraea* spp.) population growth in a marina from Southeastern Brazil and its consequences to the diversity of benthic organisms

Tanasovici, Rodrigo M. (1), Kitahara, Marcelo V. (2,3), Dias, Gustavo M. (1)

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Marine facilities create physical and biotic conditions distinct from those in natural habitats, modifying sediment deposit, organic and inorganic pollutants, hydrodynamics and biological communities. Those modifications can facilitate the establishment of non-indigenous species (NIS) in coastal ecosystems. The sun corals *Tubastraea coccinea* and *T. tagusensis* are harmful NIS in the Southeastern of Brazil, where they impact benthic communities and local economy. Herein, using a series of images spanning 9 years, we detected for the first time and followed the expansion of sun corals populations in a region where the sun corals are not frequent in the natural substrate. We described population growth in two locations from a recreational marina (Yacht Club of Ilhabela, São Sebastião Channel, SP): inside the marina and at the breakwater. As sun corals are known to reduce diversity in natural environments, we also evaluated how the variation in the density of sun corals inside the marina affected the community of both sessile and mobile benthic organisms. Sun corals have grown exponentially from 2010 to 2019 inside the marina, but not in the breakwater, where population stopped growing in 2016. While the increase in coverage of the sun corals did not affect species richness for both sessile and mobile groups, they are associated to a reduction in the area covered by the native bryozoan *Amathia Braziliensis*, and an increase of the area covered by the exotic bryozoan *Schizoporella errata*. Besides, areas with higher sun coral coverage also tended to show reduced abundance of gammarids and crabs. Small-scale variation in the population growth across the marina is probably associated to the high productivity and larval retention inside the marina. The maximum sun coral coverage found in this study was 59%. In a neighboring island further of the coast, only coverages nearing 100% resulted in loss of diversity, but considering that sun coral population is still growing inside the marina and promoting a replacement of a native species, management initiatives must be employed to prevent more intense damages to the benthic biota, especially considering that the sun corals are still scarce in the natural substrate of the São Sebastião channel, where the marina is located.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq); Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP)



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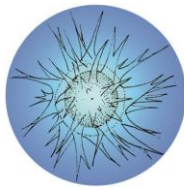
***Terrazoanthus* sp.: an undescribed zoantharian species from the Alcatrazes Archipelago**

Vaga, Claudia F. (1); Migotto, Alvaro E. (1); Santos, Maria E.A. (3); Reimer, James (3,4); Kitahara, Marcelo V. (1,2)

(1) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil; (2) Departamento de Ciências Marinhas, Universidade Federal de São Paulo, Santos, SP, Brasil; (3) Molecular Invertebrate Systematics and Ecology Laboratory, Graduate School of Engineering and Science, University of the Ryukyus, Japan; (4) Tropical Biosphere Research Center, University of the Ryukyus, Japan.

Although ubiquitous in many marine regions of the world from shallow waters to the deep sea, zoantharians (Cnidaria, Anthozoa) compose an order for which studies in the Southwestern Atlantic are scarce. The classification of many zoantharians is challenging due to extensive phenotypic plasticity, morphological convergence, and difficulties related to the examination of their anatomy, the latter caused by their capability to incorporate sand into their mesoglea. Consequently, the actual number of zoantharian species is unknown. In this study, using specimens collected by SCUBA diving at different sites from the main island of the Alcatrazes Archipelago, a new Southwestern Atlantic genus record representing an undescribed species (*Terrazoanthus* sp.) is reported. Some specimens of this undescribed species were kept in aquarium and some were preserved in 100% ethanol. Photographs were taken both *in situ* and from specimens kept in aquarium. For molecular analyses, mitochondrial 16S ribosomal DNA (mt 16S rDNA) and cytochrome oxidase subunit I (COI), as well as the nuclear internal transcribed spacer region of ribosomal DNA (ITS-rDNA) were amplified. With the obtained sequences both Bayesian and Maximum-Likelihood analyses were performed. Although *Terrazoanthus* sp. appears phylogenetically very closely related with other *Terrazoanthus* species in analyses, this species has unique sequences for all molecular markers examined. For morphological analyses, polyp dimension (oral disk diameter, polyp height), tentacle numbers and polyp colour were examined. Undischarged nematocysts were classified and measured from tentacles and polyps' column. Moreover, histological sections of the column were prepared and analysed for internal morphological examinations. *Terrazoanthus* sp. belongs within the family Hydrozoanthidae and can be distinguished from the other members of the genus by both molecular and morphological characters. Undescribed *Terrazoanthus* sp. inhabits hard substrates in highly hydrodynamic areas and is distinguished from congeners by its striped brown pigmentation, 28-30 tentacles, the presence of spirocysts and basitrichs in the column and small holotrichs in the tentacles. The report of *Terrazoanthus* to Brazil is also the first record of the family Hydrozoanthidae to this province.

Apoio: Conselho Nacional de Desenvolvimento Científico (/CNPq); Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP)



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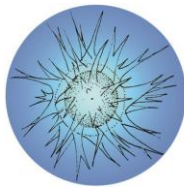
Can phenanthrene change the behavior and physiology of the marine protogynous dusky grouper *Epinephelus marginatus* (Serranidae: Perciformes)?

Honji, Renato M. (1); Campos, Mariana F. (2); Araújo, Bruno C. (2); Mello, Paulo H. (2); Lo Nostro, Fabiana L. (3); Cuña, Rodrigo H. (3); Moreira, Renata G. (2)

(1) Centro de Biologia Marinha da Universidade de São Paulo (CEBIMar/USP), São Sebastião, SP, Brasil; (2) Instituto de Biociências da Universidade de São Paulo (IB/USP), São Paulo, SP, Brasil; (3) Departamento de Biodiversidad y Biología Experimental da Universidad de Buenos Aires, UBA, Buenos Aires, Argentina.

This study is part of a program that aims to develop and improve the production potential and conservation status of the dusky grouper through a better knowledge of its biology. This species is a protogynous hermaphrodite, typical of rocky bottoms and listed as endangered in the Red List of Threatened Species of the International Union for the Conservation of Nature. The reproductive complexity makes this species vulnerable to environmental degradation, as well as overfishing, due to its great commercial value. These fish mature first as females; later in adult life, the ovaries are replaced by testes, changing the fish into reproductive males (protogynous species). This process is modulated mainly by steroid pattern modification, started when 17β -estradiol (E2) levels decrease whereas testosterone (T) and 11-ketotestosterone (11-KT) levels increase, promoting masculinization. Phenanthrene (Phe) is the main hydrocarbon in crude oil (with high toxicity) and in the São Sebastião Channel, harboring Brazil's greatest oil port, environmental monitoring (2004) of the area registered up to 79mg/L of oil waste in the water and 16.2ng/g of Phe in sea sediments. Animal biology can be altered in some way when individuals are exposed to Phe and, therefore, we investigated the effect of Phe exposure on the general behavior and reproductive physiology of the dusky grouper. Specimens were captured along the São Sebastião coast and held in fiberglass tanks with running sea water for at least 15 days before bioassays. To evaluate Phe effects on behavior/physiology, a 96h sub-lethal bioassay was performed. Fish were exposed to Phe at nominal concentrations of 0.1mg/L (PHE1) and 1mg/L (PHE2) and control groups were also carried out, with ethanol (ETOH, 0.004%) and without vehicle. During the exposure to Phe, animals were evaluated by video recordings (3 to 5min) for their general behavior at 4, 24 and 96h. At 4h, control, ETOH and PHE1 showed a normal behavior, i.e., natural opercular beats and swimming, normal mucus production and fed normally. However, the PHE2 treatment caused changes in behavior. Fish became inactive ("lying" in the bottom of the tank), with high mucus production (water became "cloudy") and did not feed (they regurgitated the food of the previous day). After 24 and 96h, fish behavior in the PHE2 treatment worsened. Fish lost their orientation, with their abdomen facing upwards. Also, some fish remained on the bottom while others floated on the surface, suggesting a change in the swim bladder and, along with the tremor of pectoral fins, an impairment of the nervous system. Continuous production of mucus and lack of feeding activity also differed the PHE2 group from the other treatments. No such effects were observed in the T and E2 plasma concentration during the experimental period, but 11-KT decreased in all groups compared to the control. These results may support future studies on anthropogenic contamination by this hydrocarbon in marine fish.

Apoio: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP)



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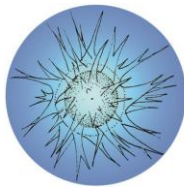
Effects of internal and external medium on the thermoregulation of *Pachygrapsus transversus*

Araújo, Priscilla A.D. (1); Guerrero, Agustín C. (1); Custódio, Márcio R. (1, 2)

(1) Instituto de Biociências da Universidade de São Paulo (IB/USP), São Paulo, SP, Brasil; (2) Núcleo de Pesquisa em Biodiversidade Marinha da Universidade de São Paulo (NPBioMar/USP/USP), São Sebastião, SP, Brasil.

Understanding how animals cope with oscillations in environmental conditions is fundamental to subsidize the modelling of their survival and distribution in the face of climatic changes. Based on this, we tested whether different osmolarities affect the weight and maximum voluntary temperature (vtmax) of crabs. The experiments were carried out at CEBIMar (USP) and at the Laboratory of Cellular Biology of Marine Invertebrates (IB-USP). The animals were kept in three aquariums, representing the range of tolerated salinities (24,33-35,40 unit) according to literature. Before the water treatment and after measuring the maximum voluntary temperature, we measured the fresh weight of the crab's body by simply wiping with a napkin and weighing it on a semianalytic scale. The crabs were heated within 200 ml of sea water with the heating rate identical to an initial temperature of 23-26°C. After the measurement of vtmax, the animals were again divided into three groups and subjected to the same three water conditions for 24 hours. The animals heated in higher osmolarities did not lose more weight during the maintenance of each heavy animal after at least 72 h in osmolarity 33-35 (control) and after 72 h in 25,33-35 and 44. There was no effect of water osmolarity on the weight lost by the crabs during heating. There were no effects of 72 h treatments on the osmolarity of the animals. There were no treatment effects for 72 hours of weight or shift at the maximum voluntary temperature (media, range). Despite being considered extreme for these crabs, the osmolarity levels of the different solutions did not change the hemolymph weight, osmolality, or maximum voluntary temperature, either along long treatments or short heating periods to their maximum tolerated water temperature.

Apoio: Núcleo de Pesquisa em Biodiversidade Marinha da Universidade de São Paulo (NPBioMar/USP); Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq)



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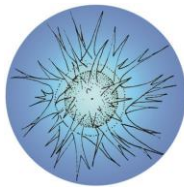
Bacteria degrading Trichlorophenol isolated from sponge *Hymeniacidon heliophila* (São Sebastião, SP)

Moraes, Mariana A.R. (1); Rozas, Enrique (2); Custódio, Márcio R. (3)

(1) Instituto de Biociências da Universidade de São Paulo (IB/USP), São Paulo, SP, Brasil; (2) Escola Politécnica da Universidade de São Paulo (EP/USP), São Paulo, SP, Brasil; (3) Instituto de Biociências da Universidade de São Paulo (IB/USP), São Paulo, SP, Brasil.

Sponges are ancient multicellular animals currently living in a wide variety of environments, including some highly polluted. Their resistance may be associated with bacteria that can eliminate toxic compounds, avoiding accumulation and potentially harmful effects. *Hymeniacidon heliophila* is a sponge commonly found in polluted areas on the Brazilian coast. To understand the role of the bacterial association to *H. heliophila* on the improvement of resistance to pollution, we performed selection tests to isolate strains capable of degrading Trichlorophenol (TCP). This compound is used as a fungicide, herbicide, insecticide, and antiseptic, and is connected to increases in leukemia and liver cancer in animals. Therefore were formed aggregates of *Hymeniacidon heliophila*, collected near CEBIMAR (São Sebastião-SP). The aggregates were initially treated with antibiotics to eliminate transient bacteria and then exposed to TCP for 24 hours. After, were made cultures of bacteria and two bacterial strains were successfully isolated. Bacteria isolated were exposed to TCP for one week and the samples were collected three times a week to observe for growth. On the last day, the supernatant was analyzed for metabolites and the analyses shows TCP degradation.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq); Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPQ); Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP); Instituto de Biociências da Universidade de São Paulo (IB-USP); Escola Politécnica da Universidade de São Paulo (Poli-USP)



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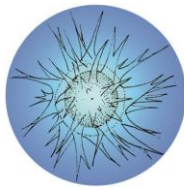
Coelomic elements of *Phascolosoma stephensoni* (Sipuncula): cell types and physiological aspects

Queiroz, Vinicius (1); Nascimento, Gabriel (1); Custódio, Márcio R. (1, 2)

(1) Departamento de Fisiologia, Instituto de Biociências da Universidade de São Paulo (IB/USP), São Paulo, SP, Brasil; (2) Núcleo de Apoio à Pesquisa em Biodiversidade Marinha da Universidade de São Paulo (NP/BioMar), São Paulo, Brasil.

The coelomic fluid of sipunculid worms performs many physiological and immune functions, and the coelomocytes are the main effectors. However, coelomocytes are not the only elements in the coelomic fluid since gametes can also be found in this cavity. Most knowledge on the coelomic elements in this phylum has been based on *Sipunculus nudus*, and data about other species are scarce. Here, based on live cells and cytochemical preparations, we make a detailed characterization of the coelomic elements of *Phascolosoma stephensoni*. Additionally, some physiological/immune aspects (*viz.* clotting and phagocytosis respectively) are analyzed. Coelomocytes were collected using a syringe needle preloaded with anticoagulant solution and live cells were observed just after collection. For cytological preparations, cells were attached on histological slides using a cytocentrifuge, fixed for 45 min in formaldehyde sublimate and stained with toluidine blue (TB) or Mallory trichrome (MT). Coelomocytes collected in Ca²⁺ enriched artificial sea water were used to observe clotting, while in phagocytosis assays we observed which cell type was able to phagocyte autoclaved yeast. Hemerythrocytes, hyaline cells, morula, signet-ring cells and two subpopulations of granulocytes (GI and GII) were found in the coelomic fluid of *P. stephensoni*, as well as sperm plates (male gametes). In cytochemical preparations using MT, hemerythrocytes and GI stained pinkish, while GII and morula cell stained blue. Still, GI nucleus was smaller ($3.01 \pm 0.3 \mu\text{m}$) than GII ($6.3 \pm 0.5 \mu\text{m}$). Signet ring cells and hyaline cells do not showed specific reactions, and sperm plates stained purple with TB. Clotting reaction consisted on a fast cell aggregation, with no sign of gelation or extracellular strands, and can be easily separated after soft agitation. Phagocytosis was performed by granulocytes. Hemerythrocytes, granulocytes, morula and signet-ring cells were common cell types in *P. stephensoni*, fact also observed to *S. nudus*. Granulocytes have traditionally been identified based on live cells, and this makes difficult to perform comparisons with *P. stephensoni* cells. However, morphological and cytochemical features were remarkably different, suggesting the presence of two different subpopulations. The absence of eggs in the coelomic fluid of *P. stephensoni* suggests that only males were analyzed. The pinkish color on MT preparations indicates protein content, and hemerythrocytes are well-known by carry the respiratory pigment hemerythrin. The bluish color on MT preparations indicates glycosaminoglycan. As in other invertebrates, clotting and phagocytosis are important physiological strategies that ensure the maintenance of the *milieu intérieur*. In summary, this works provides interesting information about the coelomic elements of *P. stephensoni*, bringing data on a new granulocyte subpopulation and showing that this species is a suitable model to physiological studies.

Apoio: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP) Procs. 15/21460-5; 18/14497-8 and 19/04707-8), Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq)



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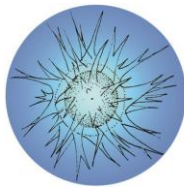
Isolation of Labyrinthulomycota present in primary cell culture of marine sponge *Hymeniacidon heliophila*

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Sponges (phylum Porifera) are multicellular organisms that play a vital role in many aquatic ecosystems. They are considered the first animals to derive within Metazoa, with fossil records dating from the Pre-Cambrian. Sponges have a remarkable capacity for association with microorganisms, hosting a complex microbiota that influences the animal at various levels of biological organization. Despite its importance, several aspects of this microbiota-host interface are still poorly studied. Besides bacteria, one of the groups frequently found, and one of the most unknown, are protists of phylum Labyrinthulomycota (Straminipila). These fungus-like microorganisms are saprophytic, osmotrophic, and omnipresent in marine ecosystems. It is known that these organisms have a little-explored biotechnological potential, such as enzymatic activities and the production of metabolites of economic interest. Currently there are many records of marine invertebrates reported to harbor Labyrinthulomycota, however, the nature of their association with sponges is unknown. Using the method for the cultivation of primary cell culture of sponges, aggregates of Porifera cells (from *Hymeniacidon heliophila*) denominated primmorphs were maintained for 2 months straight in a specific medium. During this time a variety of fungi and fungi-like organisms were documented by light microscopy including protists with morphological characteristics of Labyrinthulomycota being two morphotypes frequently observed in primary sponge cell culture. Seeking isolation for precise identification of these organisms, samples of cell cultures were inoculated in a variety of medium for microorganisms with antibiotics (penicillin/streptomycin [1g/L] and nystatin [10.000 UI/mL]). Were used the medium (agar and liquid) BHI (Brain-Heart-Infusion), YNBG (Yeast Nitrogen Base and Glucose), YTG (Yeast Extract, Tryptone, and Glucose) modifying the concentration of components, salinity of medium (~20ppt - 34ppt) and temperature (18°C - 25 °C). In none of these experiments, perceptible growth was observed. Considering its association with Porifera and the characteristics of its physiology, preliminary results indicate that Labyrinthulomycota associated to sponges may have specific needs that are supplied by these animals. Nevertheless, more experimentation is needed for elucidating a functional protocol for isolation of these protists from primary cell culture of marine sponges and enlighten the nature of the association of those organisms.

Apoio: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP), Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq); Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq); Núcleo de Pesquisa em Biodiversidade Marinha da Universidade de São Paulo (NPBioMar/USP)



Pôster – Fisiologia marinha

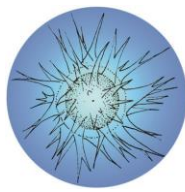
Marine and freshwater sponge-associated bacteria: evolution of the host-bacteria relationship along the freshwater colonization process and biotechnological potential

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Sponges (phylum Porifera) are basal metazoans originated more than 800 million years ago. One of its remarkable characteristics is the presence of several associated microorganisms such as bacteria, that represent up to 40% of an individual's volume. These sponge-associated bacteria are known for producing secondary metabolites of biotechnological interest such as antibiotics, antifungal and antitumor compounds. The presence of endosymbiont bacteria suggests that those bacteria avoid rejection from the host sponge producing some kind of immunosuppressor compound. In this type of association, host and symbiont are connected anatomically, as well as, in physiological, immunological, genetic and evolutionary aspects, in a way that every organism is a functional part of a virtual organism known as holobiont. This relationship between bacteria and sponges dates back to more than 600 million years ago, even before the irradiation of most of Porifera groups. This event induced the marine sponges and their associated microbiota to unknown adaptations that permitted the freshwater environments colonization. This project aims to study the bacteria profile of marine and freshwater sponges to determine the relationship between both bacteria stock, suggesting a possible marine ancestral stock. Preliminary results of the isolation of the associated bacteria of two sponges, a marine and a freshwater one, already showed evidence on the difference of their microbiota. The freshwater sponge (*Radiospongilla inesi*) had only 2 strains isolated, the marine one (*Haliclona melana*) on the other hand, had 10 strains isolated. It is known that most marine sponges are often classified as having a high microbial abundance (HMA), while freshwater ones are commonly part of the low microbial abundance group (LMA). Thus, those preliminary results could be an indicative that these sponges follow those patterns of microbial abundance. Also identification attempts using mass spectrometry (MALDI-TOF) led to scores lower than 1.500, therefore the result was considered insufficient for a reliable identification of both genus and species level. Further metagenomic analysis, that are already taking place, will help clear up the identity of the associated microbiota of those sponges. Also proteomic analysis of the isolated bacteria strains, will help us understand how the host-bacteriome complex was constructed during the freshwater colonization process. Another step on this project is the screening of bacterial extracts on Porifera and Mammal cells, that will indicate the presence of inhibitors or immunomodulators with potential biotechnological applications. Thus, the present work intends, by using the bacteria data distribution in sponge and immunosuppressive activity, to establish which bacteria were carried in the freshwater colonization process.

Apoio: Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES/CNPq); Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq); Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP)



Pôster – Evolução e biogeografia

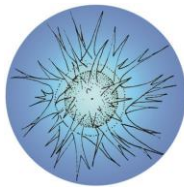
A genetic framework for Rhopaliophora evolution

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Any culture-related laboratory would be considered the optimal starting point for a genetic project, mainly if they are considered as desired main objectives genomics and evolution. Cnidaria is a well known animal group (~11,000 extant species) but besides a few species, they lack genetic information in classical and new fronts like genome sizes, cytogenetics and genome sequencing. From these premises/context we developed an evolutionary genomics approach to take advantage of Rhopaliophora species in culture, starting with genome sizes. We defined the genome size of 97 cnidarian species using Flow Cytometry technique, including the new smallest and biggest genome size for the group; from these, 40 are related to Scyphozoa and 8 to Cubozoa. From this first outcome and taking account their phylogenetic context, we targeted a selected group of species as priorities to genome sequencing. They included Coronatae (*Nausithoe aurea*, *Thecoscyphus zibrowiii* and *Linuche anguila*), Semaestomeae (*Sanderia malayensis*) and Rhizostomeae species (*Rhopilema esculentum*, *Lichnorhiza lucerna* and *Stomolophus meleagris*); as outgroups, we sequenced a cerianthid and a zoanthid species (*Palythoa mizigama* and *Ceriantheomorpha Braziliensis*, respectively). All these datasets are being explored in several hypotheses, mainly in terms of macroevolution and evolutionary dynamics (ex, genome sizes, life cycles and non coding regions). As an additional outcome, new collaborations were established with international groups and we are proposing a new international network of cnidarian culture experts to enhance cnidarian research from culture and living specimens.

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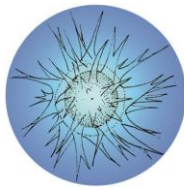
A phylogeographic approach of a gastropod with high dispersal capacity in the Brazilian coastline

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In marine gastropods, the range of the geographic distribution may be related to the type of larval development. Species developed from a planktotrophic larvae are prone to present higher dispersal potential. This factor directly reflects in the differentiation rates and populational genetics structuring. In this study, we analyzed the mitochondrial regions COI (Cytochrome c oxidase I) and 16SrRNA from *Littoraria flava* (King, 1832), a gastropod with planktotrophic larvae commonly found in Brazilian rocky coasts. The sampling was done along the Brazilian coastline, in 10 locations at São Paulo, Rio de Janeiro, Espírito Santo, Santa Catarina, Ceará and Alagoas. The intra and interpopulational genetic differentiation were evaluated at micro and macro geographical extent along the Brazilian coastline using 80 samples. The preliminary COI and 16SrRNA analysis did not recover evidences of genetic distribution associated to geographic locations. The AMOVA values revealed that the most of the variability is within the populations in both regions (100% in COI, 88% in 16SrRNA). There is only significant evidence of genetics structuring in the 16SrRNA region (F_{ST} 16SrRNA = 0.114). These preliminary results point to a unique panmictic populational unity with constant maintenance of gene flow along the studied area. However, previous studies with a codominant marker suggested that *L. flava* distribution in a micro geographic scale consists in genetically structured subpopulations highly responsive to constant recolonizations. More samples are being analyzed along with the amplification of the nuclear ITS region that together might clarify the genetic distribution of *Littoraria flava*.

Apoio: Instituto de Biociências da Universidade de São Paulo (IB/USP);



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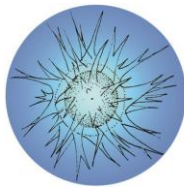
Detecting positive selection on toxin genes in ribbon worm transcriptomes

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Worms from the phylum Nemertea are known to produce toxins, which may be used for both predation or defense. Although some studies concerning these toxins have been done, their variety and evolution are poorly known. Besides the toxins which were effectively extracted from ribbon worms mucus, a study based in in silico analyses revealed that transcriptomes of different species of nemertea contained several putative transcripts of toxins previously unknown to be produced by nemerteans. The objective of this study is to describe and analyze the evolution of toxin genes of Brazilian ribbon worms. In order to describe feeding preference of nemerteans, which could be a factor involved in the selective pressure of toxins, feeding tests were performed. Barnacles were offered to *Nemertopsis bivittata* specimens, which are known to prey mainly on sessile invertebrates. Polychaetes, isopods, gastropods and the mantle of an oyster were offered to a single *Lineus bonaerensis*. None of the experiments resulted in any feeding event. In the *in silico* analyses, several putative toxin sequences were found in the previously assembled transcriptomes of different species of Nemertea. From these sequences the plancitoxin-1, first described in the echinoderm *Acanthaster planci*, was chosen for analysis. Of the four species selected for this study (*Lineus bonaerensis*, *Nemertopsis bivittata*, *Ototyphlonemertes erneba* and *O. lactea*), only *L. bonaerensis* had available transcriptome reads of a closely related species (*L. sanguineus*). These reads were used to assemble new transcriptomes, in which toxin sequences were searched for. These new transcriptomes were not only used for designing primers which would anneal to conserved regions of these transcripts, but were also used to make selection tests of these transcripts. The plancitoxin-1 transcripts were found to be under positive selection (average omega for models M1 and M2 are, respectively, 0.516 and 1.203, $p < 0.0001$). As for the *Ototyphlonemertes* and the *Nemertopsis* species, the lack of a transcriptome from a closely related species demands the assembly of de novo transcriptomes from total RNA extractions. Toxin transcripts found in these transcriptomes will be used for designing primers to amplify these regions through PCR, which will be assayed for further selection analyses.

Apoio: Instituto de Biociências, Universidade de São Paulo (IB/USP)



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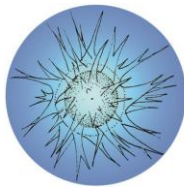
Disentangling *Astrangia* (Scleractinia, Rhizangiidae)

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Belonging within the family Rhizangiidae (Cnidaria, Anthozoa), the genus *Astrangia* is composed by 15 recent species of which two are recorded in Brazil. In general, the taxonomy of its representatives has been presenting several challenges towards morphological characterization and, consequently, the nomenclature of these species. Although *Astrangia rathbuni* is the only officially reported species through the coast of São Paulo state, sightings of these corals in situ suggest that at least three species of the genus occur sympatrically in the northern shores of São Paulo state as they present distinct changes in their colonial shape and color. Therefore, in order to deepen our knowledge on the most abundant scleractinian corals of São Paulo coast, 32 specimens of potential astrangiids corals were collected mostly around the Arquipélago de Alcatrazes area and analyzed through integrative systematics, including morphology and genetic analysis. The morphological analysis suggested the occurrence of two more species that have never been officially reported previously in the area, *A. solitaria* and one more species that is being called *A. sp.* as the study continues. However, despite the morphological characters suggesting the occurrence of three species, evolutionary reconstructions using the 28S rDNA molecular marker has not shown the support for the morphological analysis as the marker didn't present the precision required to distinguish three different clades within the genus. More studies on the 16S rDNA molecular marker are being carried out.

Apoio: Instituto Chico Mendes de Conservação a Biodiversidade (ICMBio)



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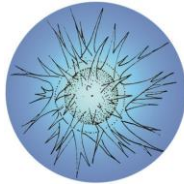
Identification of colonial species of coronatae scyphozoans (Cnidaria: Scyphozoa: Coronatae): the genus *Linuche* Eschscholtz, 1829

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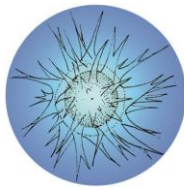
The order Coronatae is considered the basal group of the class Scyphozoa. The members of this order have at the polyp stage a peridermal tube that totally surrounds the soft parts, distinguishing them from other Scyphozoa. The characters used for species differentiation consists in external measurements and observations of structures inside the peridermal tube. As far as coloniality is concerned, there are 4 species recorded with this habitus: *Nausithoe punctata*; *Nausithoe racemosa*; *Linuche unguiculata*; and *Stephanoscyphistoma allmani*. The aim of this project was to verify if there were differences in the colonial polypoid stages from different regions identified as '*Linuche unguiculata*'. For the observations and comparisons, two types of colonies were used: in vivo (cultures) and preserved (SEM) animals from Atlantic and Pacific Oceans. The following characters from the colonies were observed: type of ramification, tube diameter, number of external rings, and presence/absence and patterns of their internal cusps. Regarding the external features, no differences were found between the number of rings among the specimens analysed, and the diameters of the tubes for all the colonies were similar and isodiametric. We recognized 3 shapes for the colonies: stolonal, cauliflower, and verticil type. For internal features, we noticed 3 patterns of cusps: absent; cup-shaped cusps with regular projections at the margin (serrated); and cup-shaped cusps with irregular projections at the margin and surface. Regarding the medusoid stage, all of the colonies produced medusae that had a large number of symbionts (zooxanthellae), 4 pairs of gonads, 8 rhopalia, 16 marginal lobes, 1 shallow coronal groove, and developing subumbrellar sacs. From the data obtained, it can be concluded that the species present in the Caribbean region (Cuba) and in the Brazilian coast comprise a single taxonomic entity, which should be named *Linuche unguiculata*. Regarding the samples from the Pacific Ocean, we concluded that there are at least 3 different species: the first, with a colony structure very similar to the Atlantic Ocean (stolonal), classified in the genus *Linuche*. We were unable to differentiate between the two *Linuche* species described in the Pacific, as live material would be necessary for analysis of the ephyrae and adult medusae. For now, we choose to name this species as *Linuche* sp. The second species was *Nausithoe racemosa*, which has a characteristic colonial structure (cauliflower shaped) and absence of internal cusps. Finally, the third recognized species was *Stephanoscyphistoma allmani*, which has a different colonial growth (verticil type). However, we can not associate this species with any known jellyfish as we did not obtained living material for further comparative studies.

Apoio: Programa Unificado de Bolsas da Universidade de São Paulo (PUB /USP); Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP); Núcleo de Pesquisa em Biodiversidade Marinha da Universidade de São Paulo (NPBioMar/USP)



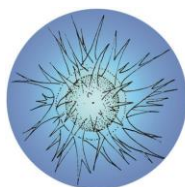
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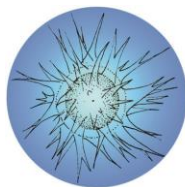
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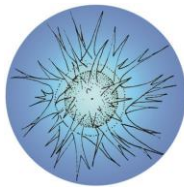
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