



ECE 11

Lyon, France

ABSTRACT BOOK

11th European Conference on Echinoderms (ECE11)

October 16–20, 2023

Lyon, France

CONFERENCE SCHEDULE

	Monday 16 Oct.	Tuesday 17 Oct.	Thursday 19 Oct.	Friday 20 Oct.
08h00	Registration desk open	R. Mooi (S4)	Registration desk open	Registration desk open
08h15			Applied Biomedicine & Biomimetics (S7)	M. Nonclercq & C. Dupichaud (S11)
08h30				
08h45				
09h00	welcome address	Collections (S11)		
09h15	Palaeontology I (S4)			
09h30				P. Oliveri (S1)
09h45				
10h00		coffee break	coffee break	
10h15	coffee break	coffee break	Systematics II (S8)	Post-Metamorphosis Development (S12)
10h30	Embryonic & Larval Development (S1)	Ecophysiology, Ecotoxicology & Effects of Global Change Stressors (S5)		
10h45				
11h00				
11h15			Ecology, Functional Ecology & Morphology II (S13)	
11h30				
11h45				
12h00	lunch & Poster Session 1	lunch & Poster Session 1		lunch & Poster Session 2
12h15				
12h30				
12h45				
13h00	J. Croce (S1)	P. Dubois (S5)	T. O'Hara (S9)	J. Nebelsick (S14)
13h15				
13h30				
13h45				
14h00	Bioluminescence & Photoreception (S2)	Ecophysiology, Ecotoxicology & Effects of Global Change Stressors (S5)	Biogeography (S9)	Palaeontology II (S14)
14h15				
14h30				
14h45				
15h00	coffee break	coffee break	Revision of the <i>Treatise on Invertebrate Paleontology</i> (S10)	General Session (S15)
15h15				
15h30				
15h45				
16h00	Systematics I (S3)	coffee break	EMBRC	closing ceremony
16h15		Ecology, Functional Ecology & Morphology I (S6)		
16h30				
16h45				
17h00	ICE BREAKER		PUBLIC CONFERENCE	GALA DINNER
17h15				
17h30				
17h45				
18h00				
EVENING				

SUMMARY

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After previous successful editions in Brussels (Belgium, 1979 and 1989), Lecce (Italy, 1991), London (UK, 1995), Milano (Italy, 1998), Banyuls (France, 2001), Göttingen (Germany, 2010), Portsmouth (UK, 2014), Sopot (Poland, 2016) and Moscow (Russia, 2019), we are very pleased to invite you to the 11th European Conference on Echinoderms (ECE11), which will be held in Lyon (France) this autumn.

This meeting will be the first 'in person' echinoderm meeting after an almost four-year hiatus due to the covid pandemic, and we look forward to seeing you all again!

Chairs of the Organizing and Scientific committees

Bertrand Lefebvre (Lyon)

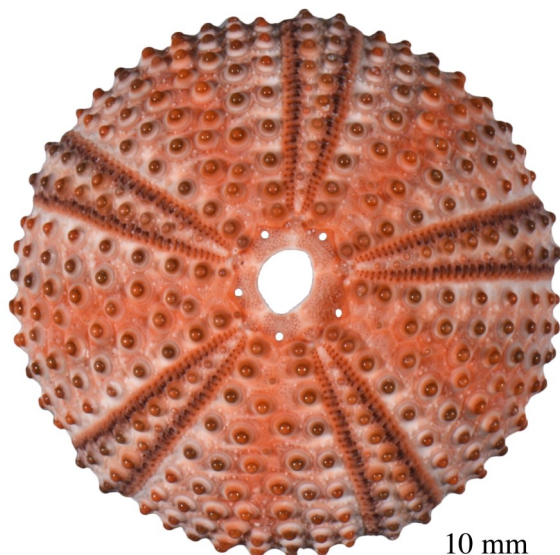
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 Jeffrey R. Thompson (Southampton, UK)
 Ben Thuy (Luxemburg City, Luxemburg)
 Loïc Villier (Paris, France)
 Samuel Zamora (Zaragoza, Spain)





DETAILED PROGRAM

Session 1

08:00 Registration desk open

09:00 Opening Ceremony

Session 1: Embryonic & Larval Development
chairs: Hugh Carter & Jenifer Croce

09:30 **P. Oliveri**, E. Parey, O. Ortega-Martinez, J. Delroisse, P. Martinez, K. Buckley & F. Marletaz
S1_01 **(keynote)**
Genomic control of regeneration

10:15 Coffee break

10:45 **G. Eviatar**, L. Roth & O. Bronstein
S1_02 Temporal effects on sperm motility and fertilization success across three echinoid species

11:00 **A. Rufino-Navarro**, T.J. Carrier & J.C. Hernández
S1_03 The developmental stages of the sea urchin *Arbacia lixula* associated with photosymbionts that influence host survival

11:15 **P. Cormier**, F. Pontheaux, S. Boulben, H. Chassé, A. Boutet, F. Roch & J. Morales
S1_04 Identification of neo-translated mRNAs regulating cleavage dynamics in early sea urchin embryos

11:30 **L. Piovani**, E. Parey, S. Mercurio, M. Sugni & F. Marlétaz
S1_05 Genomic and single cell insights into the metamorphosis of the crinoid *A. mediterranea*

11:45 **B. Delorme**, N. Cuny, G. Lhomond, G. Malandain, T.A. Basith, G. Salbreux, J. Croce
S1_06 & M. Rauzi
Mechanisms and mechanics of tubulogenesis in the embryo of *Paracentrotus lividus*

12:00 Lunch and **Poster Session 1**

13:30 **J. Croce**, G. Lhomond & M. Schubert **(keynote)**
S1_07 The canonical Wnt/ β -catenin signaling pathway and the control of sea urchin embryonic development

Session 2

Session 2: Bioluminescence & Photoreception
chairs: Constance Coubris & Jérôme Mallefet

14:15 **C. Coubris**, S. Dupont & J. Mallefet
S2_01 Ontogenic apparition of luminous capabilities in the brittle star *Amphiura filiformis*

14:30 **J. Mallefet**, P. Martinez-Soares, M.P. Eléaume, T.D. O'Hara & L. Duchatelet
S2_02 Amazing Bioluminescence of Crinoidea from Depths

14:45 **Y. Nonclercq**, P. Flammang, I. Eeckhaut & J. Delroisse
S2_03 Study of sea cucumber photoreception

15:00 **J. Delroisse**, W. Bayaert, J. Rousseaux, M. Majerova, E. Lau, J. Ullrich-Lüter, K. Buckley,
S2_04 O. Ortega-Martinez, P. Oliveri, F. Marletaz, P. Martinez, E. Parey, T. Oakley, M. Marek,
J. Mallefet & P. Flammang
Keep your eyes on the stars... and their genes! News insights into the bioluminescence of the brittle star *Amphiura filiformis*

15:15 **W.S. Bayaert**, L. Duchatelet, C. Coubris, P. Flammang, J. Mallefet & J. Delroisse
S2_05 Deep dive into the multi-level control of bioluminescence in the brittle star *Amphiura filiformis*

15:30 Coffee break

Session 3: Systematics I
chairs: Camille Moreau & Ruiyan Zhang

16:00 S3_01	R. Zhang & C. Wang Systematics of deep-sea starfish order Brisingida (Echinodermata: Asteroidea), with revised classification and remarks on character evolution
16:15 S3_02	X. Xie Integrative taxonomy of the order Euryalida (Echinodermata, Ophiuroidea) from the West Pacific
16:30 S3_03	P. Martinez-Soares , M. Roux, M.P. Eléaume & N. Améziane Atelecrinidae: using molecular data and X-ray tomography to look into the latest hypotheses
16:45 S3_04	A. Eichsteller , T. O'Hara, M. Christodoulou & P. Martinez Arbizu Ophiuroid phylogenomic: deep-sea species enrich the tree of life
17:00 S3_05	H.A. Lessios & L. Geyer Evolution of sperm and egg proteins in the sea urchin <i>Diadema</i>
17:15 S3_06	E. Courville , N. Mongiardino Koch, H. Lessios, A. Díaz, T. Saucède & E. Poulin New molecular phylogeny sheds new light on the evolutionary history of the genus <i>Arbacia</i> Gray, 1835 (Arbacioida, Echinoidea)
17:30 S3_07	A. Kroh & M. Kapun A novel UCE probe set for phylogenomics of echinoids
17:45 S3_08	M. Christodoulou , T. O'Hara, C. Mah, A. Gebruk, R. Mooi, M.P. Eléaume & P. Martinez Arbizu The echinoderm abyssal biodiversity of the Clarion Clipperton Zone
18:00 21:00	Icebreaker Reception

TUESDAY, OCTOBER 17, 2023

08:00 Registration desk open

Session 4: Palaeontology I
chairs: Pauline Guenser & Samuel Zamora

08:00 S4_01	R. Mooi (keynote) You can't get a head: Supporting a view in which the first echinoderms were pentaradial
08:45 S4_02	F. Saleh , B. Lefebvre, C. Dupichaud, E. Martin, M. Nohejlová & L. Spaccesi Skeletal elements controlled soft-tissue preservation in echinoderms from the Early Ordovician Fezouata Biota
09:00 S4_03	C. Dupichaud , B. Lefebvre, M. Nohejlová & S. Zamora The oldest African echinoderms (Morocco): Morphology and implications for the diversification of blastozoans in the early Cambrian
09:15 S4_04	S. Zamora The oldest record of stylophorans
09:30 S4_05	X. Zhuang , T.A.M. Ewin, I.A. Rahman, B. Clark, J.R. Thompson & M. Reich Virtual reconstruction and analysis of a new, exceptionally preserved Silurian cyclocystoid provides insights into soft tissue structures and the mode of life of an enigmatic extinct class

09:45 S4_06	E. Decaux , B. Lefebvre, N. Rivière, D. Lopez & S. Puijalon Scouring around a fossil organism (Cincta, Echinodermata): Physical modelling and morpho-functional analysis
10:00 S4_07	J. El Kabouri , E. Errami, B. Becker-Kerber, N. Ennih, U. Linnemann, C. Fellah, A. Triantafyllou & B. Lefebvre <i>Arkarua</i> -like fossils from the Anti-Atlas region (Morocco): A new opportunity to test the Ediacaran-Cambrian radiation
10:15	Coffee break
Session 5: Ecophysiology, Ecotoxicology & Effects of Global Change Stressors chairs: Guillaume Caulier & Lachan Roth	
10:45 S5_01	L. Roth , G. Eviatar, L.M. Schmidt & O. Bronstein Red Alert: Regional scale mass mortality of diadematoids in the Northern Red Sea
11:00 S5_02	E. Bossiroy , N. Wambreuse, F. David, C. Vanwinge, J. Delroisse, I. Eeckhaut & G. Caulier An innovative strategy for the isolation of circulating pigmented cells: The case of sea cucumber coelomocytes
11:15 S5_03	P. Gorzelak , D. Kołbuk, J. Stolarski & P. Dubois Effect of shifts in the Mg^{2+}/Ca^{2+} ratio of seawater on mechanical properties of the echinoderm skeleton
11:30 S5_04	R. Pérez-Portela , M. Peralta, S. González-Delgado & J.C. Hernández Local adaptation to temperature under high levels of gene flow in <i>Diadema africanum</i> , a key herbivore in the Canary Islands
11:45 S5_05	M. Pyl , H. Gharbia, K. Sdiri, F. Oberhänsli, J. Friedrich, B. Danis & M. Metian Comparative role of biofilm-covered microplastic and sediment particles as vectors of ^{14}C -PCB-153 to <i>Paracentrotus lividus</i>
12:00 S5_06	M. Aliende-Hernandez , S. González-Delgado, R. Pérez-Portela & J.C. Hernández Effect of ocean warming on clonal and sexual population of the starfish <i>Coscinasterias tenuispina</i> (Lamarck, 1816)
12:15	Lunch and Poster Session 1
13:45 S5_07	P. Dubois (keynote) Are macroalgal beds possible refuges for echinoderms facing ocean acidification?
14:30 S5_08	L.M. Schmidt , G.A. Benaim, A. Kroh & O. Bronstein Global trends of echinoid mass mortalities – insights from <i>Echinocardium</i> from the Eastern Mediterranean Sea
14:45 S5_09	M. Byrne , D.J. Deaker, P. Selvakumaraswamy & M. Clements Juvenile waiting stage crown-of-thorns sea stars are resilient in heatwave conditions that bleach and kill corals
15:00 S5_10	M. Martín-Huete , M. Peralta-Serrano, R. Fernández-Vilert & R. Pérez-Portela Metabolic plasticity of sea urchins to face ocean warming
15:15 S5_11	N. Wambreuse , E. Bossiroy, J. Delroisse, C. Vanwinge, I. Eeckhaut & G. Caulier Divergent function between perivisceral fluid and hydrovascular fluid under immunological stress in sea cucumbers (<i>Holothuria forskali</i>)
15:30 S5_12	G. Caulier , A. Lourtie, P. Gerbaux, E. Claereboudt, P. Flammang & I. Eeckhaut Saponins: Multitasking chemical signatures in asteroids and holothuroids
15:45 S5_13	M. Lamare , M. Byrne, B. Danis, D.J. Deaker, S. Dupont, S. Foo, T. Jowett, S. Karelitz, M.A. Sewell, L. Thomas & A. Agüera Antarctic sea star <i>Odontaster validus</i> larval performance is negatively impacted by long-term parental acclimation to warming ⁸

16:00	Coffee break
Session 6:	Ecology, Functional Ecology & Morphology I chairs: Maria Eugenia Majón-Cabeza & Loïc Michel
16:30 S6_01	M. Delleuze , G. Schwob, J. Orlando, B. Danis, E. Poulin & L. Cabrol Could two burrowing echinoid species coexist thanks to ecological niche differentiation driven by their gut microbiome?
16:45 S6_02	S. González-Delgado , O.S. Wangenstein, B. Alfonso & J.C. Hernández Echinoderms associated with different subtropical macroalgal communities revealed by metabarcoding
17:00 S6_03	L.F. Indriana , A. Kunzmann & M.J. Slater Dietary effect of fermented feed sources on growth performance of juveniles sea cucumber <i>Holothuria scabra</i>
17:15 S6_04	J. Pierrat , L. Urbistondoy, A. Modi, B. Viramoutou & P. Frouin What drives the patchy distribution of tropical sea cucumbers? A multispecific monitoring study
17:30 S6_05	M. Webb , M. Clements, P. Selvakumaraswamy, E. McLaren & M. Byrne Behavioural responses of juvenile Crown of Thorns Starfish (<i>Acanthaster</i> sp.) to flow and chemosensory cues from coralline algae, coral, and adult conspecifics
17:45 EMBRC	Nathalie Turque & Alex McDougall EMBRC - France: the French National Marine Biological Resource Centre
19:00	Open Public Conference by Thomas Saucède [in French]
20:00	La biodiversité marine des Terres australes françaises face aux changements climatiques

WEDNESDAY, OCTOBER 18, 2023

- Activity 1 Zoological Collections (Lyon 1 University)
- Activity 2 Palaeontological Collections (Lyon 1 University)
- Activity 3 Guided tour, Lyon Aquarium
- Activity 4 Field excursion to Ardèche (La Voulte Lagerstätte, Musée de l'Ardèche, ...)

THURSDAY, OCTOBER 19, 2023

Session 7:	Applied Biomedicine & Biomimetics chairs: Patrick Flammang & Michela Sugni
08:15 S7_01	V. Sardhalia & M. Albéric Bio-sourced hybrid pigments inspired by colored sea urchin spines
08:45 S7_02	R. Santos Screening for sea urchin adhesive proteins to develop new biomimetic adhesives for biotechnological and biomedical applications
09:00 S7_03	P. Flammang , N. Lemaire, N. Singh, A. Lin, J. Delroisse, C. Moraes & M.J. Harrington Mechanically tunable collagen scaffolds for tissue engineering applications inspired by sea cucumbers
09:15 S7_04	A. Whaite , B. Herlemont, J. Delroisse & P. Flammang Bonding with sea cucumbers: Identification of tube foot adhesive proteins from transcriptomic data

09:30 **G. Martinelli**, M. Roncoroni, A. Massironi, F. Bonasoro, S. Marzorati & M. Sugni
 s7_05 Sea urchin wastes valorization: Production of innovative composite biomaterials for tissue regeneration

09:45 Coffee break

Session 8: Systematics II
chairs: Magdalini Christodoulou & Jeffrey R. Thompson

10:15 **S. Stöhr**
 s8_01 Genital plates and associated structures in Ophiuroidea – morphology and phylogenetic implications

10:30 **J.R. Thompson**, I.A. Rahman, M. Reich, T.A.M. Ewin, N. Mongiardino Koch & S. Zamora
 s8_02 Origin and evolution of echinozoan body plans

10:45 **E. McLaren**, O. Bronstein, A. Kroh & M. Byrne
 s8_03 *Tripneustes australiae*, the senior synonym of *T. kermadecensis*: Taxonomy and museum distribution records of sea urchins in the genus *Tripneustes* in eastern Australia

11:00 **L. Vantomme**, K. Gérard, Q. Jossart, B. Danis & C. Moreau
 s8_04 Sea star (Asteroidea) diversity in the Magellanic region (south-Chile) and their affinities within the Southern Ocean

11:15 **T. Saucède**, Q. Jossart, J. Vandermeeren, M. Delleuze, B. Danis & C. Moreau
 s8_05 The taxonomic status of *Aporocidaris incerta* (Koehler, 1902): Such a long enigma for a common species

11:30 **D. Janies**, Y.Q. Hernandez-Días, F.A. Solís-Marín, K. Lopez, J. Fletcher & I. Bosch
 s8_06 Many cloning larvae and related juveniles are Oreasteridae

11:45 **K. Mezali**
 s8_07 The sea cucumber of the Algerian coastal waters: Taxonomy, ecology and their nascent fisheries and illegal trade

12:00 **D.L. Soualili**, A. Benarous & K. Mezali
 s8_08 First record of the echinid *Echinus melo* Lamarck, 1816 on the west coast of Algeria (Sidi- Madjdoub, Mostaganem)

12:15 Lunch and **Poster Session 2**

Session 9: Biogeography: Past, Present and Future in a Changing World
chairs: Angelina Eichsteller & Timothy D. O'Hara

13:45 **T. O'Hara (keynote)**
 s9_01 Biogeography and evolution of ophiuroids

14:30 **F. Ducarme**
 s9_02 Keeping up reliable biogeographic information in a changing taxonomy : Three asteroid tales

14:45 **K.C.K. Ma**, R. Trenholm, J.-F. Hamel & A. Mercier
 s9_03 Longitudinal gradient in the population size structure of the sea cucumber *Cucumaria frondosa* in the Northwest Atlantic

15:00 **H. Carter**, S. Williams & P. Oliveri
 s9_04 To brood or not to brood: Predicting larval strategies in the Asteroidea

15:15 **O. Bronstein**, R. Zirler, L.A. Leck, T. Feldstein Farkash, M. Holzknecht, A. Kroh,
 s9_05 V. Gerovasileiou, M.F. Huseyinoglu, C. Jimenez, V. Resaikos & M.B. Yokes
 From invasion to mass mortality- the ongoing saga of *Diadema setosum* in the Mediterranean Sea

15:30	Coffee break
Session 10:	Revision of the <i>Treatise on Invertebrate Paleontology</i> (S, T & U) chairs: Martina Nohejlová & Loïc Villier
16:00 S10_01	T. Saucède , A. Kroh, C. Mah, T.D. O'Hara, G. Paulay, M. Reich, S. Stöhr & B. Thuy Treatise on Invertebrate Paleontology, Part U, Echinodermata 3, Asterozoa - Echinozoa: Last updates and perspectives for the future
16:30 S10_02	B. Lefebvre Class Stylophora: What's new since the last IEC (Nagoya, 2018)?
16:45 S10_03	S. Zamora An overview of cinctans and ctenocystoids (stem-echinoderms)
17:00 S10_04	C.D. Sumrall A revised classification for Edrioasteroidea
17:15 S10_05	A. Kroh & M. Reich Holothuroid phylogeny inferred from mitogenome data
17:30 S10_06	Y. Makhlof , B. Lefebvre, E. Nardin & C.R.C. Paul Aristocystitidae (Echinodermata, Blastozoa): Systematic and taxonomic review
17:45 S10_07	M. Nohejlová , C. Dupichaud & B. Lefebvre <i>Quid novi Soluta?</i>
19:30 23:00	Gala Dinner

FRIDAY, OCTOBER 20, 2023

08:00	Registration desk open
Session 11:	Collections & History of Echinoderm Research chairs: Marie Nonclercq & Mike Reich
08:30 S11_01	M. Nonclercq, C. Dupichaud , B. Bärtschi & B. Kaufmann (keynote) The Caudan Expedition: History and legacy of the echinoderms collections of the Université de Lyon
09:15 S11_02	C. Conand , S. Purcell, J.-F. Hamel, A. Mercier, M. Di Simone, A. Horellou, K. Friedman & A. Lovatelli Conservation of commercially exploited sea cucumbers (Holothuroidea): Recent advances and knowledge gaps
09:30 S11_03	P. Guenser & B. Lefebvre Historical, sampling and gender bias in palaeontological collections: Stylophora (Echinodermata) as a case study

09:45	Coffee break
Session 12:	Post-Metamorphosis Development chairs: Philippe Dubois & Dorota Kolbuk
10:15 S12_01	J. Walker , I.A. Rahman, D. Doran & J.R. Thompson Chemical composition and distribution in sea urchin teeth using synchrotron X-ray fluorescence
10:30 S12_02	S.R. Stock , P.D. Shevchenko & A. Ziegler Novel 3D quantification of plate and needle/prism dimensions in teeth of the Odontophora (Echinoidea: Camarodonta)

- 10:45 **G. Pria**, A. Barbaglio, L. Piovani, F. Marletaz, F. Bonasoro, P. Martinez,
S12_03 M.D. Candia Carnevali & M. Sugni
Cell commitment prevents larval regeneration in the crinoid *Antedon mediterranea*
- 11:00 **M. Albéric**, C. Dos Reis Ferreira, O. Spaeker, L. Bertinetti & Y. Politi
S12_04 The importance of red-spherule cells in the pigmented biomineralization processes of sea urchin spines

Session 13: Ecology, Functional Ecology & Morphology II
chairs: Maria Byrne & Frédéric Ducarme

- 11:15 **G. Corbisier**, G. Caulier, J.-F. Hamel & A. Mercier
S13_01 Comparative and morpho-functional investigation of the stone canal in Holothuroidea
- 11:30 **A. Deridoux**, P. Flammang & S. Gabriele
S13_02 Tube feet dynamics control sea star locomotion
- 11:45 **A. Lourtie**, G. Caulier, L. Mussoi, M. Isorez, I. Eeckhaut & J. Mallefet
S13_03 Impact of host separation on the echinoderms obligate symbionts
- 12:00 **L. Mussoi**, A. Lourtie, G. Lepoint, F. David & G. Caulier
S13_04 Chromatic harmony in symbiosis: Acquisition and characterization of pigments in *Zenopontonia soror*, associated with *Culcita novaeguineae*

12:15 Lunch and **Poster Session 2**

Session 14: Palaeontology II
chairs: Timothy A.M. Ewin & Elise Nardin

- 13:45 **J. Nebelsick (keynote)**
S14_01 Taphonomy and paleoecology of echinoids: Reconstructing the past
- 14:30 **M. Fau** & L. Villier
S14_02 Deep-sea Zoroasteridae (Asteroidea) are not living fossils: Evidences for a peramorphosis-driven evolution of this family
- 14:45 **T. Oji**, N. Landman, J.K. Cochran & A. Tajika
S14_03 CT-scans suggest that *Lakotacrinus brezinai* is a crinoid with a chemosynthetic mode of life
- 15:00 **B. Thuy**
S14_04 Was the Triassic ophiuroid radiation triggered by the Carnian Pluvial Event?
- 15:15 **L. Pauly**
S14_05 Test growth in Paleozoic echinoids: A short review and new morphological data from the Upper Devonian of Germany
- 15:30 **C. Voiculescu-Holvad**, B. Clark & T.A.M. Ewin
S14_06 The internal anatomy of Middle Jurassic comatulid cups (Comatulida, Articulata, Crinoidea), as revealed by X-ray microtomography, and its implications for the radiation of comatulid crinoids
- 15:45 **C.D. Sumrall**, N.S. Smith, B. Thuy & P.J. Holterhoff
S14_07 A new understanding of North American, Late Paleozoic brittle star faunas based on microfossils
- 16:00 **M. Reich**, A. Kroh & T.R. Stegemann
S14_08 Hidden diversity in Mesozoic fossil pluteus larvae (Ophiuroidea and Echinoidea)

16:15 Coffee break

Session 15: General Session
chairs: Marine Fau & Andreas Kroh

16:45	J.P. Féral
s15_01	Standards of initial training in occupational scientific diving (OSD), a necessity for the mobility of echinologists
17:00	M. Bonomo & O. Bronstein
s15_02	High-throughput non-invasive underwater DNA sampling methods – Red Sea echinoderms as a case study
17:15	Closing Ceremony & Next Echinoderm Conferences
17:30	

POSTER SESSION 1
MONDAY & TUESDAY, OCTOBER 16–17, 2023

Embryonic & Larval Development

P1_01. **A. Aleotti, M. Preti, A. Borsani, J. Devilliers, M. Elphick & M. Sugni**

Exploring the effects of neurotransmitters and neuropeptides on the swimming behaviour of crinoid larvae

Ecophysiology, Ecotoxicology & Effects of Global Change Stressors

P1_02. **M. Bayat, C. Moreau, L. Katz, M. Delleuze, M. Dogniez, I. George & B. Danis**

Exploring the impact of climate change on trophic plasticity and gut microbiome variability: Insights from a southern ocean sea urchin species

P1_03. **R. Fernández-Vilert, J.C. Hernández, S. González-Delgado, M. Martín-Huete & R. Pérez-Portela**

Effect of acidification on populations of the sea urchin *Paracentrotus lividus* (Lamarck, 1816) using natural gradients

P1_04. **A. Mercier & J.-F. Hamel**

Investigating the mystery of beaching events involving sea cucumbers

P1_05. **V. Dettling, Claire Laguionie-Marchais, J.B. Fini & S. Samadi**

Can holothurians from the deep-sea of New Caledonia be used to monitor microplastic pollution?

Ecology, Functional Ecology and Morphology

P1_06. **H. Chammem, C. Marcos, J. Ben Souissi & A. Pérez-Ruzafa**

Echinodermata assemblages from northern Tunisia (Central Mediterranean Sea)

P1_07. **H. Chammem, C. Zuleta, C. Aldea & C. Jofré**

Echinoderms (Echinodermata) from marine protected areas of Central Chile coast

P1_08. **J. Hurtado-García & M.E. Manjón-Cabeza**

Environmental control on the structure of asteroid assemblages in the Patagonia Argentina

P1_09. **J. Heijens, E. Courville, E. Poulin & T. Saucède**

Ecological niche evolution within the echinoid genus *Arbacia* Gray, 1835

P1_10. **E. McLaren, B. Sommer & M. Byrne**

Long term stability of *Centrostephanus* populations in coral associated habitat despite other sea urchin populations declining in the subtropical-to-temperate transition zone of east Australia

P1_11. **K.C.K. Ma, F. Gao, J.-F. Hamel & A. Mercier**

First observations and morphological descriptions of biogenic calcareous microcrystalline structures in an echinoderm

P1_12. **S. Williams, H. Carter, C. Laumer, C. Trimble, Y. Kano, S. Putschakarn, S. Banchongmanee & N.J. Kenny**

Genetic control of blue colour in tropical starfish *Linckia laevigata*

P1_13. **C. Trimble, S. Williams, M. Lamare, N.J. Kenny & M. Fellner**

Molecular investigations into the basis and role of colouration in the sea star *Linckia laevigata*

Systematics

P1_14. **J. Na, D. Zhang, H. Cheng, Y. Zhou & C. Wang**

Accelerated and variable evolution rates of Ophiuroidea based on comparative mitochondrial genome

P1_15. **S.F. Hiruta, D.H.E. Setiamarga & T. Fujita**

Molecular phylogeny of Neoasteroidea (Asteroidea) based on mitochondrial genome

P1_16. **A. Hugall, M. Byrne & T.D. O'Hara**

Amphipholis squamata is an allopolyploid swarm

P1_17. **J. Lee & T. Lee**

Comparative taxonomic analysis of *Holothuria* (*Thymiosycia*) *decorata* and *H. (Mertensiothuria) hilla*

P1_18. **C. Moreau, Q. Jossart, M. Cabessut, C. De Ridder, M. Delleuze, J. Vandermeeren, B. Danis & T. Saucède**

Systematics of the urchin *Ctenocidaris* (*Eurocidaris*) *nutrix* (Thomson, 1876)

P1_19. **Q. Jossart, A. Dettai, C. Moreau, B. Danis, I. Schön & M. Kochzius**

Sea star mitogenomes: characterization and utility for phylogenetics

P1_20. **T. Mogi, T. Fujita & Y. Kano**

Systematic revision of *Ctenodiscus* (Asteroidea, Paxillosida) in Japanese waters

P1_21. **C. Buron, C. Moreau, B. Danis & Q. Jossart**

Diversity in the deep sea: a case study of the Pterasteridae (Echinodermata: Asteroidea)

P1_22. **C. Yuan, C. Wang & D. Zhang**

Morphological and molecular phylogenetic analysis of sea cucumbers (Holothuroidea) collected in the Kyushu-Palau ridge

P1_23. **A. Lee & T. Lee**

Taxonomical revision of *Ophiopholis aculeata* and *O. japonica* based on the mitochondrial COI and morphological analysis

P1_24. **C. Moreau, A. Eichsteller, L. Vantomme, E. Kamyab, P. Martinez Arbizu & A. Brandt**

Echinoderm diversity in the northeast Aleutian Trench

P1_25. **E. Kamyab, S. Khodami, F. Bonk, S. Rossel, J. Taylor, S. Brix & P. Martínez Arbizu**

IceDivA Project: The study of diversity of deep-sea holothurians in the North Atlantic Ocean using molecular approaches

P1_26. **M. Fau**

Revision of the genus *Benthogenia* Fisher, 1911, with description of a new species, and detailed ossicle anatomy

P1_27. **A.A. Caballero-Ochoa, B.E. Buitrón-Sánchez, F.A. Solís-Marín, C.A. Conejeros-Vargas & D. Mireles-Velásquez**

Skeleton structure of *Nidorellia armata* (Gray, 1840) (Echinodermata: Asteroidea) as archaeological evidence of its presence in the offerings of Templo Mayor, Mexico

P1_28. **A. Eichsteller, A. Martynov, T.D. O'Hara, M. Christodoulou, T. Korshunova, G. Bribiesca-Contreras & P. Martinez Arbizu**

Ophiotholia saskia: a new brittle star from the Clarion Clipperton Zone

P1_29. **D.L. Soualili, Z. Lebouazda, I. Khodja & K. Mezali**

Focus on the morphological aspect of *Ophioderma* Müller & Troschel, 1840 from the Algerian west coast

POSTER SESSION 2

THURSDAY & FRIDAY, OCTOBER 19-20, 2023

Applied Biomedicine and Biomimetics

P2_31. **E. Kamyab, M.Y. Kellermann, M. Reverter, D. Praditya, A.W. Storjohann, M. Köck, J. Wink, E. Steinmann, D. Tasdemir & P.J. Schupp**

Molecular diversity and structure-activity relationship of saponin in Indo-Pacific sea cucumber *Bohadschia argus*

P2_32. **I. Ventura, V. Harman, R.J. Beynon & R. Santos**

Glycoproteins: Are they involved in sea urchin adhesion?

P2_33. **T.N. Olivares-Bañuelos, A.V. Colores-Mendoza & A. Ortega**

Expression of glia transporters GLAST and GLT-1 in the Mexican Pacific sea biscuit *Dendroaster excentricus*

P2_34. **N. Lemaire, N. Singh, A. Lin, R. Wattiez, J. Delroisse, M.J. Harrington & P. Flammang**

An investigation of the molecular and structural properties of the mutable collagenous tissue in the European sea cucumber *Holothuria forskali*

Post-Metamorphosis Development

P2_35. **J.R. Thompson, P. Paganos, Z.X. Schultz, L. McMonagle, G. Benvenuto, F. Caccavale, F. Marletaz, M.I. Arnone & P. Oliveri**

Accretionary skeletal growth in post-metamorphic *Paracentrotus lividus* (Echinodermata: Echinoidea)

P2_36. **S. Jobson, J.-F. Hamel & A. Mercier**

Autotomy in the apodid sea cucumber *Chiridota laevis*

P2_37. **J. Coakley & M. Lamare**

Quantifying *in situ* growth rates in the New Zealand sea star *Coscinasterias muricata* using tetracycline tag-recapture methods

Collections and History of Echinoderm Research

P2_38. **M. Christodoulou**

The echinoderm collection of the Biologiezentrum (OÖ Landes-Kultur GmbH), Linz, Austria

P2_39. **J. Thomas & Récolnat team**

Récolnat: a digital platform for the promotion of 350 years of natural history collections

P2_40. **H. Hagdorn, M. Reich, B. Gaitzsch & J.W. Schneider**

The type material of the iconic Muschelkalk 'stone lily' *Encrinurus liliiformis* Lamarck, 1801 (Triassic, Crinoidea)

Biogeography: Past, Present and Future in a Changing World

P2_41. **C. Moreau, L. Katz, A.N. Mironov, M. Christodoulou, P. Martinez Arbizu, A. Eichsteller, S. Brix, Q. Jossart, L. Vantomme & B. Danis**

Phylogeography of the deep-sea benthos: Results from the abyssal sea star family Porcellanasteridae (Asteroidea, Echinodermata)

P2_42. **A. Macías-Ramírez, L.M. García-Guillén & M.E. Manjón-Cabeza**

Ophiuroidea of the Avilés Canyons System (INDEMARES + LIFE Project)

P2_43. **A.A. Caballero-Ochoa, B.E. Buitrón-Sánchez & F.A. Solís-Marín**

Distributional congruence and species richness of echinoderms in the East Pacific

P2_44. **A. Bujalance Silva, J. Hurtado-García, F. Moya Ruiz, Th. Saucède & M.E. Manjón-Cabeza**

Preliminary results of the study of the echinoids of the Scotia Arc (Antartica)

P2_45. **M. Martín-Huete, C. Leiva, L. Pérez-Sorribes, M. Peralta-Serrano, S. González-Delgado & R. Pérez-Portela**

Adaptation and divergence patterns in the spiny sea star *Marthasterias glacialis*

Palaeontology

P2_46. **B. Lefebvre, Y. Candela, E. Nardin, T. Servais & B. Mottequin**

Late Ordovician echinoderms from the Brabant Massif (Belgium): Taxonomic revision, palaeoecology and palaeobiogeographic implications

P2_47. **B. Lefebvre, M.E. Cournoyer, P. Isotalo & T.E. Guensburg**

Taxonomic revision of the first described stylophoran echinoderm: *Ateleocystites huxleyi* Billings, 1858

P2_48. **A. Cincotta, B. Lefebvre, P. Guériau, S. Olive & B. Mottequin**

A possible peltocystid mitrate (Stylophora) in a new Praguian (Early Devonian) Konservat-Lagerstätte from Belgium

P2_49. **M. Nohejlová**

Cambrian gogiid eocrinoids from the Barrandian area: Re-evaluation of their diversity

P2_50. **T. Boisset, B. Lefebvre, R. Mooi, A. Kroh, V. Winkler, J. Adrien & M.J. Martin**

Insights into stylophoran anatomy and taphonomy based on an exceptionally preserved mitrate from the Lorraine Group (Upper Ordovician) of New York, USA

P2_51. **Y. Ishida, M. Tagiri, T. Kato, S. Tsunoda, Y. Nakajima, B. Thuy, L.D. Numberger-Thuy & T. Fujita**

Exceptionally well preserved *Stegophiura* (Echinodermata, Ophiuroidea) fossils from the Pliocene of central Japan

P2_52. **L.D. Numberger-Thuy, Y. Ishida, E. Doi & B. Thuy**

Unexpected brittle-star diversity in the Carnian (Upper Triassic) of SW-China and Japan

P2_53. **L. Pauly**

A new echinoid fauna from the Famennian of Velbert (W Germany) and its implications for Late Devonian evolution of sea urchins

P2_54. **F. Noirit, J.A. Waters, J.E. Bauer, J. Le Mort & B. Lefebvre**

First results of the revision of the eublastoids (Echinodermata) from the Devonian of the Armorican Massif (NW France)

P2_55. **E.E.O. Cutcliffe, E.G. Mitchell, J.R. Thompson, T.A.M. Ewin & I.A. Rahman**

Quantifying tiering of crinoid communities using a new echinoderm Lagerstätte from the Jurassic of Wiltshire, UK

P2_56. **F.A. Raquet, D.B. Blake & B. Lefebvre**

A new multiarmed asteroid from the Lower Devonian of Morocco

P2_57. **A. Salone, M. Fau, J. Bardin & L. Villier**

Deciphering evolutionary patterns in the fossil *Metopaster* (Valvatida, Asteroidea) using 3D geometric morphometrics on ultimate superomarginal ossicles

General Session

P2_58. **N.E.H. Belkacem, I. Khodja & K. Mezali**

Nutritional quality and culinary and nutraceutical valorization of sea cucumbers from the Mostaganem region (Algeria)

P2_59. **R. Hocde, G. Thouzeau, S. Bourquin, L. Borel, M. Coulange, J.P. Féral, E. Feunteun, S. Jacquet, P. Le Bras, L. Le Gall, S. Legrand, P. Lenfant, M. Lepage, C. Play, G. Saragoni & Q. Schull**

Scientific diving in France: an overview of the current practices in science

Proceedings of the conference

The proceedings of the conference will be published free of charge in a thematic volume of the journal ***Cahiers de Biologie Marine***, which is an international, indexed and peer-reviewed publication (IF = 0.527) edited by the Roscoff Marine Station (France). This journal has already edited the proceedings of the 14th International Conference on Echinoderms, held in Brussels in 2012 (*Cahiers de Biologie Marine*, volume 54, published in 2013).

The deadline for manuscript submission is **March 31st 2024**.



PRE-CONFERENCE EXCURSION TO VILLEFRANCHE-SUR-MER MARINE STATION (October 11th-15th, 2023)

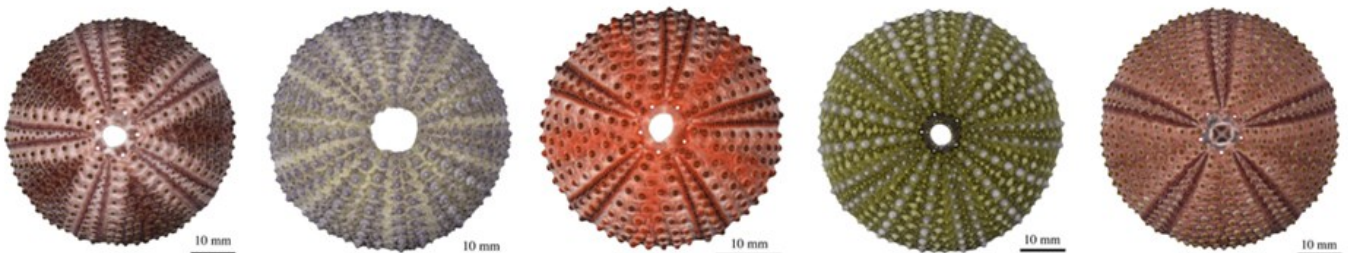


Overlooking one of the most beautiful harbours in the world, the city of Villefranches-sur-Mer (situated on the French Riviera, Côte d'Azur, southern France, between Nice and Monaco) offers an exceptional and unexpected setting with its 16th century Citadel, a historic monument housing the City Hall and cultural center (Museums, Auditorium, Théâtre de Verdure), Royal Port of "Darse", chapels (Saint-Pierre de Villefranche-sur-Mer chapel decorated by Jean Cocteau, Saint Elisabeth, Saint Elme and Saint Michael's church), and medieval and magical "rue Obscure" street. For those interested, the excursion may include a visit to the nearby Leyrens islands and Oceanographic Museum of Monaco.

Established in 1885 by Alexis de Korotneff (University of Kiev) and Carl Vogt (University of Geneva), the Villefranche-sur-Mer marine station (Institut de la Mer de Villefranche - IMEV) operates and maintains one of the three longest-running deep marine environmental monitoring stations in the world as well as an important long-term pelagic observation program. Research topics include developmental biology, pelagic and coastal oceanography, biological and biogeochemical cycles in marine environment, carbon cycle, phytoplankton production, and biological diversity of zooplankton communities.

Marine research facilities include access to the RV *Sagitta II* ship (trawler) for sea trip (plankton nets, oceanographic instruments for biological and physical monitoring), scuba diving for access to marine ecosystems and echinoderm sampling, laboratories, technological platforms, and climate control rooms with access to all basic research equipment (molecular biology, microscopic imaging).

More information: thomas.saucede@u-bourgogne.fr



MID-CONFERENCE ACTIVITIES (OCTOBER 18TH, 2023)

Four activities will be proposed to participants (and accompanying persons) on Wed. 18 Oct.

(1) Access to all facilities and visit of the Zoological Collections of Lyon 1 University. The University of Lyon Zoological collections are world-famous for hosting the collections of Pr. René Koehler (1860–1931), comprising over 800 vials containing echinoderm specimens (including 8 holotypes) collected during the sea campaign of the Caudan (1895) in the Gulf of Gascogne.

This activity is free, but registration is compulsory and limited to 15 participants on a first-come, first-served basis, according to the reservation order.



(2) Access to all facilities and visit of the Palaeontological Collections of Lyon 1 University. These collections are the second largest ones in France (after the Muséum national d'Histoire naturelle in Paris). They are hosting over 1,800 types and figured specimens of fossil echinoderms (e.g. Barrande, Caillet, Cotteau, Lissajous, Sayn, Thorall, de Verneuil, Vizcaino collections).

This activity is free, but registration is compulsory and limited to 15 participants on a first-come, first-served basis, according to the reservation order.



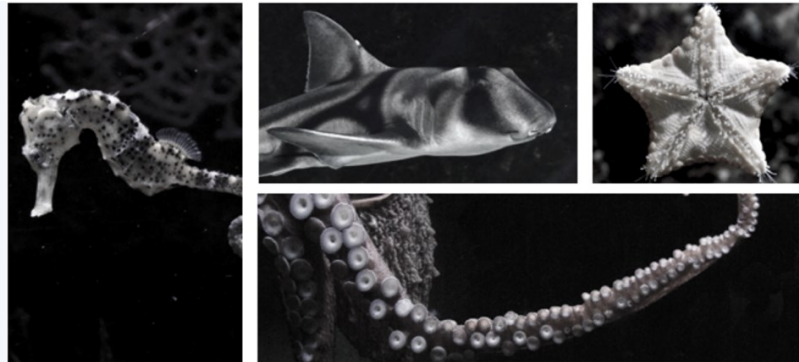
Please note that the Zoological and Palaeontological collections will be both closely associated to the conference, and will remain accessible to all participants before, during and after the meeting.



(3) Guided tour of the **Lyon Aquarium**

(<https://www.aquariumlyon.fr/en/>)

Registration (15 €) is limited to 15 participants, on a first-come, first-served basis, according to the reservation order.



(4) One-day field excursion to Ardèche. This one-day excursion will bring all the participants to visit the palaeontological collections of the Musée de l'Ardèche (<https://museum-ardeche.fr/en/>), which is hosting iconic fossils from the famous Callovian (Middle Jurassic) La Voulte Lagerstätte. Several fossiliferous sites yielding Jurassic echinoderms (mostly crinoids and ophiuroids) will be also visited, including the La Voulte Lagerstätte itself. A convivial stop (wine tasting) in a local cellar is also scheduled.

Registration (80 €) is limited to 60 participants, on a first-come, first-served basis, according to the reservation order.



Photographie : Bernard Riou

Lyon is the third-largest city and the second-largest urban area of France. It is located at the confluence of the rivers Rhône and Saône, about 500 km southeast of Paris. Former capital of the Gauls at the time of the Roman Empire, birthplace of the cinema (Lumière brothers) in the late 19th century, Lyon is now recognized for its cuisine and gastronomy, as well as for its historical and architectural landmarks: e.g. the districts of Old Lyon, the Fourvière hill, the Presqu'île and the slopes of the Croix-Rousse that are registered on the UNESCO World Heritage List. For those interested in the Rugby World Cup, Lyon is hosting two matches the week before the pre-conference excursion: New Zealand - Uruguay (October 5th, 2023) and France - Italy (October 6th, 2023).

Its central position in France makes it very easy to reach by any means of transportation.

By train

Lyon has three main train stations (Part-Dieu, Perrache and Vaise stations) that are linked to many French and European cities (e.g. Paris-Lyon = 2h; Geneva-Lyon = 2h).

By plane

The Lyon Saint Exupéry airport is situated about 20 km east of the city centre and is connected to the main train station (Part Dieu) by the Rhône Express tramway (less than 30 min trip; departure every 15 minutes from 4.25am to midnight). The airport is connected to most major European cities.

By car

The central position of Lyon makes it also easy to reach it by car. But note that, in the city, it is difficult to find a parking spot and parking fees are expensive. Parking close to the conference venue is much cheaper/easier.

Public transport in Lyon

In your conference bag, you will be given five daily passes that will allow you to use freely the public transports of the city during all the conference.



CONFERENCE VENUE

The conference will be held next in the same building (Darwin) as the **Zoological and the Palaeontological Collections**.

The venue is situated just in front of the tramway T1 & T4 stop "Université Lyon 1", which is three stops away from the Metro lines A and B station "Charpennes".



The Charles Depéret lecture hall (250 seats) is equipped with computers, video projectors, and video cameras. Free wifi connection will be available in the lecture hall and in the congress building. Smaller rooms for meetings and workshops, equipped with computers and video projectors will be also available.

The University of Lyon Zoological collections are world-famous for hosting the collections of Pr. René Koehler (1860–1931), comprising over 800 vials containing echinoderm specimens (including 8 holotypes) collected during the sea campaign of the Caudan (1895) in the Gulf of Gascogne. The University of Lyon is also hosting the second largest palaeontological collections in France (after the Muséum national d'Histoire naturelle in Paris). They are hosting over 1,800 types and figured specimens of fossil echinoderms (e.g. Barrande, Caillet, Cotteau, Lissajous, Sayn, Thorall, de Verneuil, Vizcaino collections). The Zoological and Palaeontological collections will be closely associated to the conference, and will remain accessible to all participants before, during and after the meeting.

Université Claude Bernard Lyon 1

La DOUA

DARWIN D building

Tramway T1 & T4

"Université Lyon 1" Stop





TALKS

TALKS

The importance of red-spherule cells in the pigmented biomineralization processes of sea urchin spines

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Luca BERTINETTI² & Yael POLITI²

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Red-spherule cells (RSCs) are key players of the innate immune system of sea urchins through the release of poly-hydroxylated naphthoquinones (PHNQs) initially enclosed in their cytoplasmic vesicles as dense red granules (Coates *et al.*, 2018). RSC can be very abundant in the soft tissues of regenerated spines after fracture (Heatfield & Travis, 1975). Known for their demonstrated antimicrobial activity, PHNQs are also responsible for the multiple colors observed in sea urchin biominerals. However, the mechanism by which PHNQs are eventually released from the RSC and incorporated into the biomineral structure during its growth is yet unknown. Therefore, we here investigated biomineral pigmentation processes during the regeneration of mineralized spines of adult *Paracentrotus lividus* sea urchins. Spines were fractured at their extremities and let regenerate for few days either in pure or 20 μ M calcein enriched sea water. *In vivo* confocal imaging shows that RSCs move actively all around growing micro-spines, likely providing ideal conditions for biomineralization to occur. Many 500 nm to 10 μ m Ca-vesicles were observed. However, RSCs did not seem to contain any calcium ions. Tips of regenerated spines were then high-pressure-frozen and automatized frozen substituted for cryo-SEM and FIB-SEM observations. The characteristic epidermis and dermis zones as well as the well-described skeletogenic cells (sclerocytes), phagocytes and spherule cells, in particular RSC were identified (Dubois & Ameye, 2001). Serial FIB-SEM micrographs allow for 3D reconstruction of the different cellular features observed at the vicinity of growing micro-spines. Interestingly, not only sclerocytes were observed in contact with the trabeculae of the stereom but also RSCs. RSCs connect to micro-spines through a sheath that contain isolated pigment vesicles touching the growing mineral surface, showing the release and the later incorporation of PHNQs from the cells to the biomineral. Finally, TEM observations of ultrathin sections of fixed samples showed that pigment vesicles having different PHNQs granule density, were internally coated by a polysaccharide layer possibly acting as a protective barrier against acidic pH for the cell. We suggest that those polysaccharides play a role in vesicles opening possibly induced by pH variations required for CaCO₃ mineralization.

References

- Coates, C.J., McCulloch, C., Betts, J. & Whalley, T. 2018. Echinochrome A release by red spherule cells in an iron-withholding strategy of sea urchin innate immunity. *Journal of Innate Immunity*, **10**, 119–130.
- Heatfield, B.M. & Travis, B.M., 1975. Ultrastructural studies of regenerating spines of the sea urchin *Strongylocentrotus purpuratus*. *Journal of Morphology*, **145**, 51–72.
- Dubois, P. & Ameye, L. Regeneration of spines and pedicellariae in Echinoderms: a review. *Microscopy Research and Technique*, **55**, 427–437.

Effect of ocean warming on clonal and sexual population of the starfish *Coscinasterias tenuispina* (Lamarck, 1816)

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Rocío PÉREZ-PORTELA² & José Carlos HERNÁNDEZ¹

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Ocean warming is one of the greatest threats to the future of our oceans, it is modifying marine environments and subjecting many species to adverse conditions, consequently impacting their physiology. Studying the effect of climate change on keystone species is indispensable for safeguarding the future of the oceans. The aim of this study (Fig. 1) was to investigate the response of the fissiparous starfish *C. tenuispina* to increasing acute temperature changes (from 20°C to 28 °C) through metabolism experiments (O₂ consumption), from two populations: Mediterranean and Atlantic. This species was selected because of the different genetic structures between populations, while the Mediterranean is considered a clonal population, the Atlantic population is composed by several genotypes, which made the study even more interesting. The metabolism was measured using an intermittent close respirometer which registers accurate data. Our results revealed differences between the clonal and sexual population, caused by a greater energy demand from the individuals coming from the Mediterranean. Moreover, *C. tenuispina* tended to decrease its aerobic metabolism when exposed to high temperatures, which could imply disadvantages in coping with ocean warming. Nonetheless, this specie showed high survival rates to high temperatures. Could *C. tenuispina* be a potential candidate to face climate change?

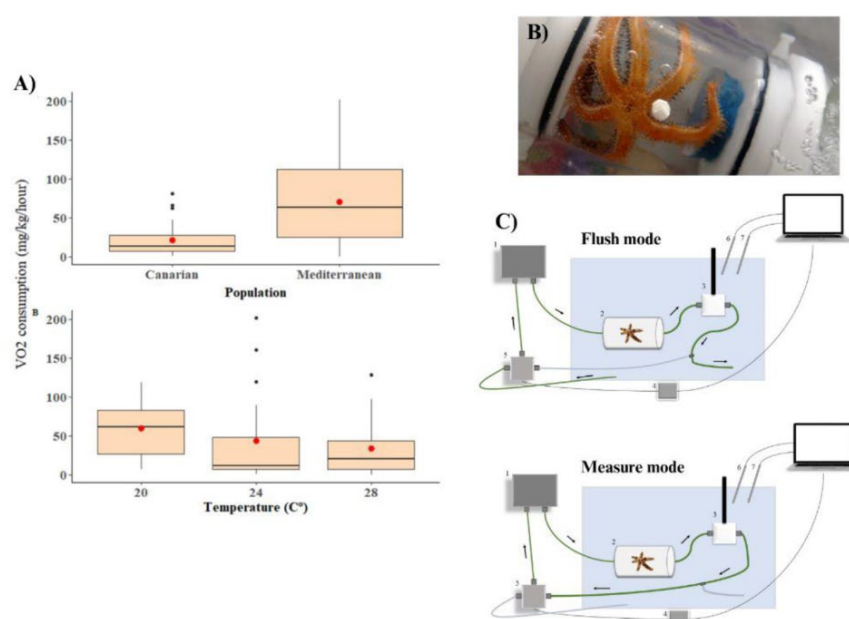


Fig. 1. Overview of the study: A) Preliminary results. B) *C. tenuispina* inside the respirometer. C) Respirometer.

Deep dive into the multi-level control of bioluminescence in the brittle star *Amphiura filiformis*

Wendy-Shirley BAYAERT¹, Laurent DUCHATELET², Constance COUBRIS²,
Patrick FLAMMANG¹, Jérôme MALLEFET² & Jérôme DELROISSE¹

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² Université catholique de Louvain - UCLouvain, Marine Biology Laboratory, ELIV, Louvain-La-Neuve, Belgium.

Bioluminescence is commonly associated with abyssal species. But luminous organisms can be found even in shallower waters. This is the case of certain brittle stars such as *Amphiura filiformis*. The light-emitting capability of the latter has become well-studied. However, the mechanisms behind its bioluminescence control are still largely unclear and puzzling! The multidisciplinary approach of this study, which combines molecular biology and functional morphology, has led to a better understanding on 3 levels:

(i) At the **molecular** level, the enzyme responsible for light production is called luciferase. *In silico* analysis of a new *A. filiformis* reference genome (Buckley *et al.*, unpublished data) revealed 11 genes coding for luciferase-like proteins.

(ii) At the **cellular** level, light-producing cells are presumably located at the basis of the spines. These same cells are thought to be associated with pigment cells that play a role in controlling the direction of the light emitted.

(iii) Potential mechanoreceptors are observed on the surface of the light-emitting **organ**, i.e. the spine. Analysis of their distribution suggests a functional link with photocytes.

While contributing to a broader understanding of *Amphiura filiformis* bioluminescence control, these findings may also provide clues to the evolution and process of bioluminescence in the marine world.

Reference

Buckley, K., Delroisse, J., Ortega-Martinez, O., Oliveri, P., Martelaz, F., Martinez, P., Parey, E., *et al.* Genome consortium working on the genome of *A. filiformis* (unpublished data).

High-throughput non-invasive underwater DNA sampling methods – Red Sea echinoderms as a case study

Mai BONOMO^{1,2} & Omri BRONSTEIN^{1,2}

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² Steinhardt Museum of Natural History, Tel Aviv, Israel.

Field DNA sampling is indispensable for analysis of species identification and diversity. Molecular tools are also crucial for distinguishing cryptic species, understanding phylogenetic relationships, and are an important supplement for field surveys. Underwater sampling methods are currently mostly limited to tissue collection and usually induce high stress or require whole animal sacrifice. This is particularly problematic when considering rare or endangered species. Furthermore, sampling in the underwater environment poses additional limitations such as time restraints while diving and maintaining DNA integrity and sterility. Here, we developed a procedure for an efficient, non-intrusive, and easily accessible underwater DNA sampling method which allows for larger sampling size per dive and facilitates high throughput molecular analysis. Given the difficulties regarding morphological species determination of some echinoderms and the confusion surrounding their phylogenetic relationships, we present the applicability of this method in the Gulf of Aqaba (Red Sea), where much of echinoderm phylogeny and taxonomy has yet to be characterized.

An innovative strategy for the isolation of circulating pigmented cells: The case of sea cucumber coelomocytes

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The immune system of sea cucumbers, which are marine invertebrates belonging to the phylum Echinodermata, relies on circulating cells known as coelomocytes. These cells are found in the fluids of the coelomic cavity and the ambulacral system of these organisms. In some sea cucumber species, hemocytes are the predominant type of coelomocytes in the ambulacral fluid and are stored in large numbers in an organ of this system, the Polian vesicle. Hemocytes have been recently studied for their role in encapsulating foreign particles (Caulier *et al.*, 2020). Interestingly, they are easily distinguishable from other coelomocytes due to their intense red color. It has long been assumed that this pigmentation was due to the presence of hemoglobin. However, our pigment analysis using HPLC revealed a high concentration of carotenoids in the ambulacral fluid and Polian vesicle, suggesting that these pigments are responsible for the hemocyte pigmentation. A comparative transcriptomics approach did not reveal a notable elevated expression of genes coding for globins relative to other coelomocytes, in contrast to the expression of genes involved in carotenoid metabolism. This finding corroborates the hypothesis that the observed pigmentation likely does not originate from hemoglobin. Additionally, hemocytes exhibit strong autofluorescence, and we took advantage of this property to isolate hemocytes using a combined approach of spectral flow cytometry and FACS. We successfully obtained a pure and viable cell population that can be processed for downstream analyses. This strategy could be extended to other pigmented cells and offer new perspectives for a more targeted study of hemocytes and their function(s) in the immune response of sea cucumbers.

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From invasion to mass mortality- the ongoing saga of *Diadema setosum* in the Mediterranean Sea

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The Eastern Mediterranean Sea is a marine biodiversity hot spot characterized by high levels of endemism. However, introduction of invasive species, particularly those of Indo-Pacific origin, poses a threat to this unique ecosystem. *Diadema setosum*, a key species on Red Sea and Indo-Pacific coral reefs, recently invaded the Mediterranean Sea. Owing to their intensive grazing, *Diadema* species are often recognized as environmental engineers, capable of altering the structure and composition of entire benthic communities. Since its first detection in the Levantine basin in 2006, *D. setosum* has experienced an exponential increase in abundance and range. Most recently, in July 2022, mass mortalities of *D. setosum* started occurring in the northern Levantine Basin, along the coasts of Turkey and Greece. Dead and dying individuals were seen detached from the substrate, showing extensive tissue and spines loss.

Here we summarize two decades of research on *D. setosum* in the Mediterranean Sea, from its initial appearance, through its accelerated population growth (population outbreak), to a most recent mass mortality event. We combined data from the literature, citizen-science reports, and a regional-scale sampling effort, to provide the most accurate and comprehensive account of the species' invasion dynamics and dispersal patterns in the Mediterranean. We further report and explore the progression of the recent die-offs in the Mediterranean Sea and described the pathologies of infected individuals.

We show an exponential population growth of *D. setosum* throughout the Eastern Mediterranean since 2018, following more than a decade of latent invasion. Molecular analysis illustrates the presence of a single genetic clade in the Mediterranean, matching Red Sea clade b, reinforcing the notion of Red Sea origin. The recent mass mortalities of *D. setosum* are rapidly spreading in the Eastern Mediterranean, and currently cover an area of over 1000 km in southern Turkey and Greece. The similar pathologies and modes of spread of observed mortalities highly resemble those of *D. antillarum* in the Caribbean, suggesting pathogenic infection as the cause of mortalities.

Juvenile waiting stage crown-of-thorns sea stars are resilient in heatwave conditions that bleach and kill corals

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The juveniles of predatory sea stars can remain in their recruitment-nursery habitat for some time before their ontogenetic shift to the adult habitat and diet. These small juveniles are vulnerable to a range of factors with their sensitivity amplified by climate change-driven ocean warming. We investigate the thermal tolerance of the waiting stage herbivorous juveniles of the keystone coral predator, the crown-of-thorns sea star (*Acanthaster* sp.), in context with the degree heating weeks (DHW) model that predicts coral bleaching and mass mortality. In temperature treatments ranging from +1–3 °C in prolonged heatwave acclimation conditions the juveniles exhibited ~100% survival in DHW scenarios that trigger coral bleaching (4 DHW), result in mass mortality of corals (8 DHW) and extreme conditions well beyond those that kill corals (12 DHW). This indicates that herbivorous juvenile COTS are far more resistant to heatwave conditions than the coral prey of the adults. The juveniles exhibited higher activity (righting) and metabolic rate after weeks in increased temperature. In separate acute temperature experiments the upper thermal limit of the juveniles was 34–36 °C. In a warming world, juvenile COTS residing in their coral rubble nursery habitat will benefit from an increase in the extent of this habitat due to coral mortality. The juveniles have potential for long term persistence as they wait for live coral to recover before becoming coral predators, thereby serving as a proximate source of COTS outbreaks on reefs already in a tenuous state due to climate change.

To brood or not to brood: Predicting larval strategies in the Asteroidea

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Larval strategies, the particular ways in which development progresses from fertilization, through metamorphosis and ultimately to settlement, and the degree of maternal input that characterizes such strategies, are fundamental to understanding biogeographic patterns in marine taxa. This is particularly true in the echinoderms, which, with a broadly sessile adult phase, are reliant on pelagic larvae as their primary means of dispersal and for the maintenance of genetic connectivity between disparate populations. Some of the greatest diversities of developmental strategies are found in the Asteroidea and these can, broadly, be categorized into three main types, free-swimming planktotrophs, lecithotrophic planktotrophs and benthic lecithotrophs (which are often brooded). Each strategy represents something of a trade-off between reproductive considerations: is it more advantageous to produce numerous planktonic larvae with individually low survival rates but greater potential for exploitation of suitable but disjunct habitats or is it more favourable to invest in greater maternal input and individual larval survival rates at the cost of massively reduced dispersal potential and vulnerability to stochastic events?

From a biogeographic perspective, each of these three major larval strategies have been shown to be geographically and bathymetrically distinct and work on this clade helped shape the seminal but now largely disregarded 'Thorson's Rule'. Although a free-swimming planktotrophic larvae is generally considered to be 'typical' for the class, developmental mode is only known for ~10% of asteroid species and is far less well characterised in the tropics than in temperate and polar waters. Here, we have utilised a large, near comprehensive dataset of asteroid distribution data to fully characterise the biogeographic patterns of each larval mode at a fully global scale. Building on this, we have further mapped reproduction across phylogeny and used the accumulated data to train models to predict, for the first time, across the unknown reproductive strategies of the class. We show substantial and surprising patterns of larval strategy distribution, discuss biological hypotheses to explain such patterns and suggest that the general paradigm of starfish development may be less settled than previously considered.

Saponins: Multitasking chemical signatures in asteroids and holothuroids

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Organisms live in a world of odors and flavors where each living or inert entity releases distinct molecules in the environment. Marine organisms, in particular, rely on environmental chemical cues during their entire life, from early developmental to adult stages (Hay, 2009). Particularly, the phylum Echinodermata presents specific chemicals for each class (Kornprobst, 2005). Saponins are triterpenic or steroidal glycosides that are produced by all investigated species of holothuroids and asteroids (Caulier *et al.*, 2011). Due to their amphiphilic properties, these molecules can interact with sterols in biological membranes, rendering saponins noxious and repellent to most organisms (e.g., ichthyotoxic effect). Despite this role of chemical defense, sea cucumbers and seastars harbor diverse symbiotic communities composed of crustaceans, polychaetes and even carapide fishes that developed biological adaptations to resist to saponins. Not only symbionts may benefit from the chemical defense of their hosts to reduce their predation rate, they can also use saponins as kairomones to specifically recognize their host by chemical communication (Caulier *et al.*, 2013). Recently, we even discovered that holothuroids use saponins as an aggregation pheromone, having a particularly important role in their reproduction (Claereboudt *et al.*, 2023).

This study highlights the diverse functions of saponins in seastars and sea cucumbers, ranging from repellent allomones to attractive pheromones and kairomones. These essential metabolites have been strongly selected throughout evolution, with each species possessing its unique chemical signature allowing it to interact with the environment.

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The echinoderm abyssal biodiversity of the Clarion Clipperton Zone

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The Clarion-Clipperton Zone (CCZ) covers about 6 million km² of the Pacific seabed and it's the largest polymetallic nodule province in the world. Other important occurrences are known from the Peru Basin and specifically from the DIS-turbance and re-COLonisation Experimental Area (DEA). CCZ is targeted for commercial-scale mining in the coming years, however there is a lack of adequate baseline information that may result in serious species declines before they are even discovered and described. The restricted knowledge on these dark taxa ensures that they remain in the shadows of research and conservation policies. Therefore, Echinodermata (Asteroidea, Crinoidea, Echinoidea, Holothuroidea, Ophiuroidea) collected during ten scientific cruises across the CCZ and the DEA were examined. More than 850 specimens were sorted and identified to the lowest possible level through imagery to propose primary species hypotheses, and the ensuring data were integrated with barcoding information (COI). Neighbour-joining trees were constructed, while tree- and distance-based methods of species delineation (ASAP, BINs, GMYC, mPTP) were employed to propose secondary species hypotheses (SSHs) among the echinoderms collected. Concordant results from the species delimitation analyses revealed 87 deep-sea echinoderm SSHs, uncovering an unexpectedly high diversity and showing that diversity of even the most conspicuous invertebrates in abyssal plains has so far been considerably underestimated. As a result, a curated DNA reference library for the CCZ-DEA echinoderms was created in BOLD, including DNA sequences, photographs, collection, and taxonomic data. This study provides the foundation for biogeographic and functional analyses that will aid policy-making as commercial ventures affect dark abyssal biodiversity.

Conservation of commercially exploited sea cucumbers (Holothuroidea): Recent advances and knowledge gaps

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Sea cucumbers have been harvested, particularly by the Chinese, for human consumption for thousand years. To service modern Asian seafood markets, fisheries have progressively expanded to countries around the tropical Pacific, then into the Indian Ocean and more recently across the world. The tropical fisheries are generally artisanal and multispecific, whereas temperate ones are often monospecific and industrialized. The number of exploited species has increased greatly in recent decades and the dried products (bêche de mer or trepang) can be classified according to their value. Harvesting often follows a 'boom-and-bust' cycle, with a rapid or steady increase in production, followed by over-exploitation and stocks collapsing. Illegal harvesting (IUU) is often observed, especially in low-income countries where fishing has been banned. Conservation issues have therefore been raised and research developed at both the specific level, relating to taxonomy, biology, and ecology and at the ecosystem level, regarding biodiversity, fisheries and markets. Advances in holothurian conservation is coming from the efforts of international bodies, including FAO, CITES, IUCN, as well as from regional ones such as SPC and WIOMSA, and national research and fisheries administrations. Present knowledge gaps are analyzed through the following questions: What are the main threats to the fishery, past and emerging? What biological and ecological data are most needed for conservation planning? For which species/groups are these data most lacking and why? Are there geographic areas that are especially data poor? What are the most effective processes for conserving sea cucumber populations?

Comparative and morpho-functional investigation of the stone canal in Holothuroidea

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Among the most enigmatic structures of echinoderms is the stone canal, which is part of the ambulacral system. It is typically connected to the exterior in echinoderms, however in the majority of Holothuroidea, this canal is opening in the main body cavity. While the morphology and function of the stone canal in Asteroidea and Echinoidea have been studied for the past two centuries, no consensus has been reached regarding its function. Most commonly, it is described as a pressure regulator, with ciliary inflow occurring at the surface of the apex of the stone canal. An excretory function has been hypothesized, however a bidirectional flow has also been suggested (Binyon, 1964).

Despite these hypotheses, the function of the stone canal remains poorly understood, and its function in the Holothuroidea class has not been investigated. The morphology of the stone canal in sea cucumber is also understudied, and only limited information is available on it (Erber, 1983).

To address these gaps in research, 6 species of sea cucumber have been studied and various morphological and in vivo analyses have been conducted. Morphological results have led to the discovery of an asymmetric canal inside the peduncle of the stone canal that can play a part in generating a bidirectional flow through ciliary movement. To strengthen this assumption, in vivo analyses were conducted using microbeads and carbon particles to track the movement within the organisms at different time points. Injections were made in the ambulacral system and inside the body cavity. Particles were tracked for 72 hours. These analyses have confirmed the existence of a bidirectional flow, where particles inside the body cavity entered the stone canal and particles inside the ambulacral system migrated to the body cavity via the stone canal.

These findings represent a step towards understanding the functions of the stone canal and further research may shed light on the various functions of this organ and on the broader concept of excretion in echinoderms.

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Identification of neo-translated mRNAs regulating cleavage dynamics in early sea urchin embryos

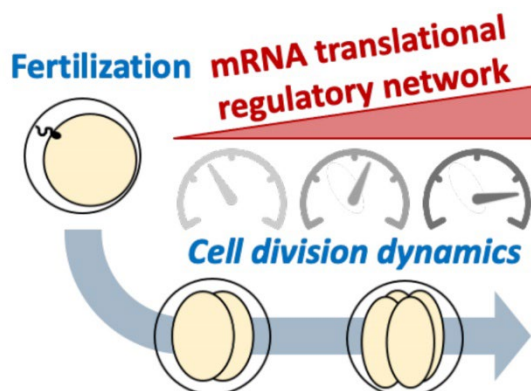
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In the sea urchin early embryo, protein synthesis is a highly regulated process that plays a key role during the mitotic divisions ensuing fertilization. In addition to the well-described mitotic cyclins, we hypothesized that active translation of other mRNAs could regulate cell division rates at the cleavage stage. Here, we show that the *de novo* synthesis of eIF4B (eukaryotic Initiation Factor 4B) controls embryonic cleavage dynamics in two sea urchin species, *Paracentrotus lividus* and *Sphaerechinus granularis*. The injection of a morpholino directed against eIF4B mRNA results in a downregulation of translational activity and delays cell division in these two echinoids. Conversely, the injection of an mRNA coding for eIF4B stimulates translation and significantly accelerates mitotic rates (Pontheaux *et al.*, 2022). Preliminary results suggest that translating the mRNA encoding a serine/threonine protein PIM kinase also controls the cell division dynamics following fertilization. Our findings provide new insights into the complex translational regulatory network that orchestrates the egg-toembryo transition in the sea urchin egg.



Fertilization triggers mRNA translation and protein synthesis, which contribute to finely tune cell division rates in sea urchin early embryo.

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Ontogenic apparition of luminous capabilities in the brittle star *Amphiura filiformis*

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Bioluminescence is the capability to emit light thanks to a biochemical reaction. This reaction implies the oxidation of a substrate called luciferin catalyzed by an enzyme named luciferase.

Today, the most widespread luciferin is the coelenterazine found in eight phyla. This broad phylogenetic distribution of this light-emitting molecule led to the hypothesis of its dietary acquisition so far demonstrated in one jellyfish (Haddock *et al.*, 2001), one lophogastrid shrimp (Frank *et al.*, 1984), and one brittle star species (Mallefet *et al.*, 2020). The latter, *Amphiura filiformis* is a suspensive feeder known to use coelenterazine in a luciferin-luciferase reaction (Mallefet *et al.*, 2013; Delroisse *et al.*, 2017). *A. filiformis* is a brittle star model species with an established aquaculture protocol allowing obtention of fertilized eggs, pluteus larvae, and juveniles.

As *A. filiformis* is a coelenterazine-dependent luminous organism needing exogenous supplies of this luciferin through its diet, this study aims to determine from which ontogenic larval stage the brittle star can produce luminescence. Our results showed (i) coelenterazine content and no luciferase activity from gametes to pluteus larvae (until day 13 post-fertilization) (ii) gametes and embryos are not able to produce light after potassium chloride depolarization. Work is still in progress to know when and how the juveniles of *A. filiformis* start to emit light. This work is supported by FRIA (FNRS) grant n°40004341.

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New molecular phylogeny sheds new light on the evolutionary history of the genus *Arbacia* Gray, 1835 (Arbacioida, Echinoidea)

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The echinoid genus *Arbacia* comprises five extant species distributed across the Pacific and Atlantic oceans. *A. punctulata* occurs along the Central and North Atlantic coasts of America, while *A. lixula* occurs in Brazil, off West Africa, and in the Mediterranean Sea. The remaining *A. stellata*, *A. spatuligera* and *A. dufresnii* are mainly present along the Pacific coasts of North, Central and South America, although *A. dufresnii* can be found across the Pacific and Atlantic Magellanic Province. Previous work suggests that *Arbacia* originated in temperate zones of the Southeastern Pacific and that Atlantic species originated after the closure of the Isthmus of Panama (approx. 3 Ma). A new phylogenetic analysis was performed based on multiple molecular markers (COI, 16s, Control Region, 18s, 28s, histone3), revealing a topology that differs drastically from previous ones. The phylogeny shows that a species of another genus, *Tetrapygyus niger*, is the sister species to *A. dufresnii*, hence questioning the taxonomic status of the monospecific genus *Tetrapygyus*. The topology strongly supports a reciprocally monophyletic grouping of the three Pacific species of *Arbacia* (plus *Tetrapygyus*), *vis a vis* those from the Atlantic when two outgroups are used to root the *Arbacia* phylogeny. Atlantic species show levels of intraspecific variation three to six times higher than those of Pacific ones, suggesting potential intraspecific phylogeographic structure. *A. punctulata* includes three distinct sub-entities restricted to the Caribbean Sea, the Gulf of Mexico, and the Atlantic coasts of North America, respectively. In *A. lixula*, distinct sub-entities are identified between populations from East Atlantic Islands and the Mediterranean Sea, and specimens from the coasts of Brazil. These genetic differences are associated with morphological variations.

This study suggests a different evolutionary history of the genus than previously thought, with a divergence between Atlantic and Pacific taxa occurring well before the closure of the Isthmus of Panama.

The canonical Wnt/ β -catenin signaling pathway and the control of sea urchin embryonic development

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Embryonic development, no matter the animal considered, commonly relies on the interplay of transcription factors and signaling pathways that control cell diversity, morphogenetic movements, and organogenesis. One of the most important signaling pathways for animal development is the canonical Wnt/ β -catenin pathway. This pathway is involved, for instance, in cell division and survival, embryonic axis establishment as well as germ layer specification and differentiation (Clevers, 2006). In some animals, canonical Wnt/ β -catenin has further been shown to exhibit duration-, stage-, context-, and/or dose-specific developmental functions (Pedone & Marucci, 2019). In sea urchins, perturbation experiments targeting the canonical Wnt/ β -catenin pathway have already revealed its critical requirement for the development of vegetal tissues (skeletogenic mesoderm, non-skeletogenic mesoderm, and endoderm) as well as for the spatial restriction, within the animal hemisphere, of the ectoderm and the anterior neuroectoderm lineages (Emily-Fenouil et al., 1998; Range *et al.*, 2013; Sun et al., 2021). The experiments documenting these effects have, however, all been initiated before or at fertilization, leaving open the questions of whether this pathway has duration-specific requirements as well as particular functions at specific later stages of sea urchin development. Using an inducible, conditional knockdown approach, we have determined that, during sea urchin embryogenesis, each vegetal tissue requires different exposure durations to the canonical Wnt/ β -catenin pathway to be properly specified and that canonical Wnt/ β -catenin is still required, up to 10 hours post-fertilization, to maintain some of these tissues through time. We also established that a gradual increase in nuclear β -catenin exposure duration has a gradual effect on the restriction of the ectoderm and of the anterior neuroectoderm along the animal-vegetal axis. Taken together, our work is the first to reveal the successive roles and duration requirements of the canonical Wnt/ β -catenin pathway during sea urchin embryogenesis, reinforcing the complex involvements of this signaling pathway during embryonic development.

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Scouring around a fossil organism (Cincta, Echinodermata): Physical modelling and morpho-functional analysis

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The study of atypical echinoderms like cinctans is problematic, because they cannot be anatomically compared to other taxa. Studying the hydrodynamics of feeding in this class is a promising source of information about their ecology (Rahman et al., 2015). We designed a protocol that aims to extend this study to the scouring processes around a representative cinctan species: *Protocinctus mansillaensis* (Cincta, Echinodermata). Three-dimensional models of the species were printed and placed in a racetrack flume and then exposed to various current velocities to study the scouring mechanisms around the body of *P. mansillaensis*. Quality of the current modelling was assessed using particle image velocimetry, reliefs and evolution of the produced scour marks were measured with a stream gauge, and current parameters were measured with an acoustic Doppler velocimeter. Our results show that this protocol can be used to model the cinctans' habitat and gives results that are consistent with literature. Analysing scouring around the cinctan models showed that this species has a maximized stability when it is oriented with its stele towards current. We also observed sedimentation inside the food grooves of the animal in this orientation, which supports the hypothesis that cinctans were passive suspension feeders with brachioles.

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Could two burrowing echinoid species coexist thanks to ecological niche differentiation driven by their gut microbiome?

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The niche concept proposed by Hutchinson (1957) refers to the position that a species or a population occupies in their environment and their relationship with it. Syntopic species (*i.e.*, species that occur in the same place at the same time) can gradually forge niche separation to reduce interspecific competition for resources. Niche separation relies on different patterns of resource use, such as diet, micro-habitat selection, space and time selection, and movement behaviors that allow them to coexist. The gut microbiota plays critical roles in host health and physiological functions by contributing to its nutrition, defence, immunity, development and behaviour. It has been shown that gut communities can confer host-specific capacities to occupy niches that would not otherwise be available (*e.g.*, the case of ruminants). Understanding the diversity and functionality of gut microbiota can provide new insights into the mechanisms of niche separation and coexistence between syntopic species. *Abatus agassizii* (Mortensen, 1910) and *Schizocosmus abatoides* (Clark, 1925) are two genera of irregular sea urchins that coexist in the Fildes Bay in King George Island, Antarctica. They live buried in the same sediment and are exposed to the same environmental conditions. Both species are deposit-feeders and ingest the surrounding sediments. In order to understand which mechanisms allow these two sea urchins to coexist in the same patches of sediment, we studied the taxonomic composition and potential functions of their associated microbial communities through 16S rRNA gene sequencing. We studied specifically the microbiota associated to (i) the surrounding sediment, (ii) the gut content (*i.e.*, ingested sediment transitory filling the gut) and (iii) the gut tissue (permanently attached to the intestinal membrane). Our results showed that gut microbiota (both gut content and gut tissue) of *A. agassizii* and *S. abatoides* were significantly different from the surrounding sediment microbiota. Although there was no discernible difference in the microbiota associated to the ingested sediment between the two sea urchin species, *A. agassizii* and *S. abatoides* presented a significantly different gut tissue microbiota both in terms of composition, relative abundance and predicted metabolic functions. Different bacterial phyla characterized the gut tissue microbiota of each sea urchin species; Bacteroidota and Spirochaetota were found in *A. agassizii* gut tissue microbiota (especially *Spirochaeta 2* genus known for its role in sulphur oxidation and nitrogen fixation, and *Bacteroidetes BD2-2* genus probably involved in carbon cycle) while Proteobacteria and Firmicutes were found in *S. abatoides* gut tissue microbiota (as *Methylobacterium-Methylorubrum* genus known to assimilate single carbon substrates via the serine cycle). These results suggest that specific bacterial lineages enable *A. agassizii* and *S. abatoides* to coexist by using environmental resources (organic matter and nutrients) in contrasted ways. Our study highlights the potential role of gut microbiota in shaping and separating the ecological niches of coexisting species sharing the same habitat.

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Mechanisms and mechanics of tubulogenesis in the embryo of *Paracentrotus lividus*

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Tubes: an apparently ordinary yet essential structure in the world of living organisms. They serve as the optimal conduit to transport metabolites inward and outward for multicellular organisms. As the fundamental framework of vital systems such as the respiratory, cardiovascular, or digestive systems, any improper formation or maintenance of tubes can result in severe developmental defects or diseases. The development of the larval gut, known as the archenteron, in sea urchin embryos is an outstanding example of tubulogenesis. The embryo's characteristics, including its simple geometry, single-layered epithelium, and optical transparency, make it an excellent model for investigating the mechanisms behind tube formation.

Regarding the signaling pathways, it has been demonstrated that Frizzled5/8 controls the formation of the archenteron via the Wnt/PCP pathway (Croce *et al.*, 2006). Downstream, on the level of physical forces, various mechanisms have been proposed to drive this event, but no conclusive evidence has settled the debate in favor of a particular mechanism (Kominami & Takata, 2004). To address this question, we have implemented state-of-the-art techniques to study the sea urchin embryo, including 3D+t light-sheet imaging followed by cell segmentation and tracking, epithelial micropipetting and sub-cellular laser dissection. Our investigations reveal that the invaginating epithelium consists of two distinct zones with different mechanical properties: an inner zone characterized by high apical tension and an active region of polarized tension controlled by Frizzled5/8. Through mathematical modeling, we demonstrate that the combined action of these two zones is necessary and sufficient for proper invagination of the archenteron. Our research sheds new light on sea urchin gastrulation and provides insights into the mechanisms involved in budding tubulogenesis.

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Keep your eyes on the stars... and their genes! New insights into the bioluminescence of the brittle star *Amphiura filiformis*

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The bioluminescence of brittle stars has long fascinated scientists and it's not over yet! Recent research found that the luciferase enzyme of the brittle star *Amphiura filiformis* shares homology with the luciferase of the sea pansy *Renilla* (Cnidaria). Surprisingly, these enzymes also share high sequence identity and structural similarity with haloalkane dehalogenases that are mostly microbial enzymes that cleave carbon-halogen bonds in diverse halogenated hydrocarbons. This suggests that ancestral non-luciferase enzymes were convergently co-opted into luciferases in cnidarians and echinoderms.

Using chromosome-scale genome and extensive transcriptome analyses, we identified multiple luciferase genes in the brittle star and studied their expression during development and arm regeneration. Luciferase mRNA and protein were detected in the light-emitting spines and the central nervous system of adults, and the peak of luciferase expression corresponded to the differentiation of spines during regeneration.

Recombinant protein expression and biochemical experiments confirmed the bioactivity of two luciferase candidates, one of which exhibited a dual function, supporting the idea that *Renilla*-type luciferases evolved from haloalkane dehalogenases. This research provides valuable insights into the morpho-functional characterization and evolution of brittle star bioluminescence.

Tube feet dynamics control sea star locomotion

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Even if for most of us sea stars seem motionless, they actually can move to catch their prey or climb the rocks. Indeed, their oral surface is covered by many small and active tubular projections, known as tube feet or podia, connected to their water vascular system. Extension and retraction of the tube feet make possible the highly organized stepping movement by which sea stars can move. While the morphology and internal architecture of sea star tube feet have been studied extensively, the locomotion mechanism and tube feet dynamics are still not fully understood.

To address this challenge, we developed an optical method based on frustrated total internal reflection (FTIR) to visualize and quantify in real time the number of tube feet adhering to the substrate. By using a wide range of sea star sizes, we showed that crawling speed is not related to sticking contact area, a metric which is linearly proportional to the mass. However, we found that the crawling speed is inversely proportional to tube foot adhesion time, which is itself dependent on the mass, suggesting a mechanical adaptation of the crawling speed to the mass. To confirm these observations, we equipped sea stars with a 3D-printed harness loaded with a weight corresponding to 25% or 50% of their initial mass. Our findings showed that the artificial increase in mass leads to a significant increase in the adhesion time of the tube feet, confirming the existence of an adaptation mechanism of the crawling speed to the mass through the modulation of the tube foot adhesion time. We then perturbed their locomotion by studying how the sea star tube feet dynamics can adapt to an inverted locomotion mode by placing them upside down, as observed in their natural environment.

Are macroalgal beds possible refuges for echinoderms facing ocean acidification?

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Calcifying metazoans with a low metabolism (therefore with a poor machinery to eliminate CO₂ and protons) and osmoconformers (organisms whose composition of extracellular fluids is close to that of seawater) were hypothesized to be particularly vulnerable to ongoing ocean acidification (OA) linked to global change. Echinoderms cumulate these characteristics, including an extensive high-magnesium calcite skeleton, and were therefore expected to be particularly affected by OA. Surprisingly, adult sea urchins resist OA rather well, even at long-term. This has been attributed to the ability of most sea urchins to compensate their extracellular pH (pH_e). However, this has an energetic cost and most echinoderms, including some basal echinoids, do not control their acid-base balance when facing OA. Macroalgal beds were suggested to be possible refuges in front of OA. This presentation will assess if they can act as such for echinoderms.

The acid-base physiology of echinoderms and associated effects of OA will be briefly reviewed. The carbonate chemistry of sea water in macroalgal beds will then be presented, including new data from *Macrocystis* beds in the Kerguelen islands. A risk assessment analysis comparing pH/pCO₂ levels in the macroalgal beds and threshold values for effects on echinoderms will then be implemented.

Keeping up reliable biogeographic information in a changing taxonomy: Three asteroid tales

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The number of described echinoderm species is constantly increasing, especially thanks to the progress of genetic studies. Many species once considered widely distributed are now separated into several variants, not always recognizable *in situ*. However, a large part of the biological information, especially concerning the ecology and distribution of the source species, is extremely difficult to reattribute, and large quantities of data are thus rendered obsolete, or even distorted because of misattribution (Ducarme, 2023). This fact has several worrying consequences, from both a scientific and conservation points of view, because the distribution ranges of these new species can become totally mysterious and easily overestimated. This contribution proposes to illustrate this problem with three Indo-Pacific examples: a sea star whose real range has been overestimated by faulty scientific consensus for a century (Ducarme, 2023), another whose problematic ecology must be completely re-evaluated since its separation into (at least) 4 new species (Haszprunar & Spies, 2014), and finally the history of the genus *Pentaceraster* Döderlein, 1916, originally described during Napoleon's Egyptian campaign (Audouin, 1826) without specimen and which has remained problematic for the last two centuries (Döderlein, 1916, 1936).

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The oldest African echinoderms (Morocco): Morphology and implications for the diversification of blastozoans in the early Cambrian

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Since their first appearance in the fossil record (Cambrian Stage 3, ~520 Ma ago), echinoderms were already relatively diverse (classes Edrioasteroidea, Eocrinoidea, Helicoplacoidea, and Lepidocystoidea) and cosmopolitan. This suggests a possible earlier origin of the phylum, although no evidence for this has been found due to the absence of Lagerstätten able to preserve non-mineralized ancestral forms. The major diversification of echinoderms during the Cambrian and Ordovician (about twenty classes, so four times the number of extant classes) renders particularly difficult the identification of homologous structures and the construction of a phylogeny encompassing the whole phylum. The goal of this study is to clarify whether feeding appendages of blastozoans (brachioles) and crinoids (arms) are homologous (or not) and thus if those two groups belong (or not) to a same clade Pelmatozoa. In this context, the gogiid genus *Alanisicystis* -the oldest echinoderm known so far from the African continent, situated in Western Gondwana- is of particular interest. Its morphology was analyzed based on abundant and remarkably preserved specimens from the Issafen Formation (Cambrian Series 2, Stage 3; Morocco). This eocrinoid has a short stem composed of small, irregularly arranged circular plates. The theca is made of a mosaic of irregularly polygonal plates, ornamented with a fine granulation and numerous respiratory structures (epispines). Its aboral end consists of a single basal plate. The brachioles consist of two series of alternating flooring plates and two series of alternating cover plates. Those long appendages branch from the adoral end of the theca, at the edges of the oral frame.

Ophiuroid phylogenomics: deep-sea species enrich the tree of life

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The Clarion Clipperton Zone (CCZ) in the Northeast Pacific Ocean contains the largest deposits of polymetallic nodules in the world, at abyssal depths of 4000-6000 m. These nodules are rock formations containing valuable metals and minerals targeted for mining. Polymetallic nodules support a rich sessile and mobile fauna. Little is known so far on the taxonomy, natural history and biogeography of these deep-sea animals, which is vital for accurate assessment of the risk of species extinctions from large-scale mining. One of the most abundant megafaunal groups in the CCZ is the Ophiuroidea (brittle stars). To classify the 43 species collected in the CCZ, we used the exon capture system presented by Hugall *et al.* (2015), and extend the existing phylogenomic tree to include the deep-sea individuals. This method not only placed them into the global context but also revealed some old lineages appearing in CCZ species. It also pointed out that some widely distributed species show a partitioned genetic pattern. A closer focus is given to the species *Amphiophiura bullata* (Thomson, 1877) and *Amphiophiura convexa* (Lyman, 1878), only recently morphologically separated and raised to species level by Stöhr & O'Hara (2021), and we support their results in a worldwide genetical context including specimens from the Atlantic, Indian and Pacific Ocean. The samples were identified using COI Barcoding and their global population connectivity was studied using 2b RAD.

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***Arkarua*-like fossils from the Anti-Atlas region (Morocco): A new opportunity to test the Ediacaran–Cambrian radiation**

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The Ediacaran period represents a remarkable stage in the diversification of life on Earth. During this time, the first complex ecosystems were established in shallow and deep marine environments, and were inhabited by a wide range of macro-organisms known as the Ediacaran biota. The study of the biological aspects of the Ediacaran biota focuses mainly on classic localities (Nama, Newfoundland, Flinders Ranges...), and therefore the search for and study of new fossiliferous localities is of key importance.

This contribution describes a new fossiliferous locality in the Ougnate inlier, in the Anti-Atlas region (Morocco). The fossiliferous unit is the Izelf Formation (567-550 Ma), which belongs to the Ouarzazate Group. Sedimentological surveys indicate that the Izelf Formation consists of 200 meters of siliciclastic (sandstone, siltstone) and carbonate (stratified carbonate, carbonate stromatolites, and carbonate phosphate levels) sediments deposited in a shallow marine environment.

The fossil-bearing sediments of the Izelf Formation yielded four types of fossils: *Aspidella*, ivesheadiomorphs, *Charniodiscus*, and *Arkarua*-like forms. *Arkarua* is represented by four specimens with pentaradial symmetry. These *Arkarua*-like specimens are very similar to those found in Australia (Gehling, 1987), offering a new opportunity to test the link between the Ediacaran fauna and the Cambrian radiation of echinoderms.

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Temporal effects on sperm motility and fertilization success across three echinoid species

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Sexual reproduction, the primary process for generating new genetic lineages, is fundamental to our understanding of biodiversity, biogeography, and evolution at large. Heterogeneities in the distributions of adult broadcast spawners in the field, water flow, and the timing of spawning, can lead to high variations in egg and sperm concentrations along the water column. The result is either sperm limitation or sperm competition. Various aspects of sperm performance, such as sperm morphology, longevity, and motility, are directly linked to fertilization success.

This study aims to evaluate the influence of gametes age on sperm motility and fertilization success, and ultimately assess the optimal timeframe for fertilization (hereafter referred to as Effective Fertilization Time; EFT) across key Red Sea echinoids. We examined one commercially cultivated species (*Paracentrotus lividus*), and two wild, native Red Sea species (*Echinometra* EZ and *Tripneustes gratilla elatensis*). Sperm was collected dry (i.e. extracted outside of the water) during the peak reproductive season of each species. Within the testis sperm is immotile, motility is activated by dilution in seawater. Hyperactivation, defined as a change in sperm movement pattern associated with intensifying flagellum beating, initiates once egg pheromones are sensed by sperm. The sperm was activated and hyperactivated by dilution in filtered seawater and egg-water, respectively. Motility parameters such as velocity and progressivity, were evaluated over three hours following spawning in 15 min intervals. Sperm performance and kinematics were evaluated using a Computer Assisted Sperm Analysis (Microoptics) system, generating high-throughput motility profiling of individual sperm cells. Fertilization capacity was also evaluated during three hours in 15 min intervals for *P. lividus* and five hours in 30 min intervals for *Echinometra* EZ and *T. gratilla elatensis*. Comparisons were conducted between ‘old-activated’ (i.e. sperm activated in $t=0$) and ‘freshly-activated’ (i.e. sperm activated just prior to the fertilization assay in each time interval). Fertilization using freshly-activated sperm was conducted to isolate the effect of the aging egg on fertilization success.

In all species, sperm velocity and motility decreased as the sperm aged in both activated and hyperactivated states, yet the rate of decline is not uniform between species. Mean sperm velocity of cultivated *P. lividus*, was almost half of that of the wild species studied, with significantly lower sperm motility overall. Fertilization success decreased after 90 min when eggs were fertilized with old-activated sperm. In contrast, freshly-activated sperm exhibited ca 90% fertilization success at each time point across all species. Our study demonstrates the narrow EFT window for high percentage fertilization in echinoids and stresses the limitation of aging sperm in the processes. Furthermore, our data suggest an interesting link between sperm longevity and the different life histories of the studied species.

Deep-sea Zoroasteridae (Asteroidea) are not living fossils: Evidences for a peramorphosis-driven evolution of this family

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The family Zoroasteridae is an extant clade of sea stars found exclusively in deep marine environments (200-6000 meters). In the fossil record, seven extinct species, from the Middle Jurassic to the Miocene, have been compared and/or assigned to the Zoroasteridae. Here, we describe a new taxon from the Cenomanian of Le Mans (Sarthe, France) and reappraise the morphology of two important extinct species, the Jurassic *Terminaster cancriformis* and the Early Cretaceous *Protothyrastrer priscus*. The phylogenetic relationships of 6 well-preserved putative extinct zoroasterids were assessed using the character/taxon matrix published by Fau & Villier (2020). The character/taxon matrix was revised, and in total contains 118 characters and 37 taxa, including two valvatid outgroups. The character/taxon matrix was analysed using both parsimony-based phylogenetic analysis and Bayesian inference methods. In the parsimony-based analysis, all six extinct taxa are more closely related to the extant Zoroasteridae than to any other extant taxa. In the Bayesian-based phylogenetic tree, the position of *T. cancriformis* and *P. priscus* is unresolved and they are nested within a polytomy at the base of the Forcipulatacea. Our results confirm extant Zoroasteridae as a clade, and show a progressive acquisition of characters historically used to define the family, with many characters not appearing in the fossil record before the Cenozoic. The family name is maintained for the crown group only. The family Terminasteridae, that accounted for the genera *Terminaster* and *Alkaidia*, is found paraphyletic in both analyses. The order Zorocallida, initially erected for the family Zoroasteridae only, is redefined as the sister clade to the Forcipulatida that includes the crown group Zoroasteridae and its stem relatives.

Many synapomorphies of the Zoroasteridae are characters appearing late during ontogeny. We compared the sizes of Mesozoic and Cenozoic Zorocallida to assess possible heterochrony of development. Our results show that Mesozoic Zorocallida are significantly smaller than Cenozoic Zorocallida and express morphological characters that are typical of juvenile Zoroasteridae (Fau & Villier, 2018). The emergence of the modern forms is likely associated with peramorphic evolution. The apparent similarities between Extant Zoroasteridae and Late Palaeozoic and Triassic forms reflect convergent characters, but no homology. Although rooted deep into the Asterooid phylogenetic tree, the living deep-sea Zoroasteridae are highly derived taxa probably evolving from shallow marine ancestors.

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Standards of initial training in occupational scientific diving (OSD), a necessity for the mobility of echinologists

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Echinoderms live in all oceans, from the coast to the abyssal depths. Diving is the best tool for observing, collecting, or experimenting with them in situ, down to depths of a few dozen meters, or even a hundred meters (using rebreathers). The ability to use these diving techniques is not just a question of training. Legal and administrative aspects can also stand in the way, especially when collaborations involve several countries.

Getting SCUBA diving recognised as a scientific technique has long been a challenge in most European countries because of the "recreational" image associated with its practice. Another important difficulty for its administrative acceptance has been its supposed danger and the chain of responsibilities that an accident could initiate.

As early as the 1980s, it was understood that an essential aspect of making underwater interventions possible in the various scientific disciplines that needed them was the definition and implementation of an initial training that would guarantee maximum safety. A long process led to the proposal to establish European standards for scientific diving and to make visible a "European Scientific Diving Panel" through the European Marine Board between 2008 and 2017. This panel is currently receiving organisational support from the European Network of Marine Institutes and Stations (MARS). Currently, 16 countries recognise and apply these standards (or equivalent).

These standards have been defined in the context of the *occupational* practice of professional scientists. However, the use of the term "scientific diving" in the world of recreational diving, which does not follow the same rules of professional training and is aimed at volunteers, is currently blurring the original concept of scientific diving.

Mechanically tunable collagen scaffolds for tissue engineering applications inspired by sea cucumbers

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As the average human lifetime increases, so does the incidence of failing tissues and organs in the elderly. Thus, it becomes essential to develop strategies for regenerating replacement tissues in the lab. However, there are still major challenges to effectively engineer artificial tissues and organs with complex 3D structures – most notably the temporal and spatial regulation of tissue scaffold mechanics. To address this challenge, we take inspiration from a unique biological model – the mutable collagenous tissue (MCT) of sea cucumbers (Bonneel *et al.*, 2023). MCT is a collagen-based tissue that can be stiffened and softened through the addition of effector proteins. We hypothesize that sea cucumber-sourced collagen will enable dynamic modulation of mechanical properties for tissue engineering applications, providing several functional advantages over current mammalian-sourced collagen. In particular, MCT scaffolds will provide the ability to tune local mechanical properties in a controlled manner that is not possible with current natural or synthetic tissue scaffold materials.

Yet, harnessing MCT as a dynamically mechanoresponsive scaffold first requires an in-depth understanding of the molecular and structural mechanisms underlying mechanical mutability. Here, we undertook a comparative compositional and structural investigation of two distantly related sea cucumber species–*Holothuria forskali* and *Cucumaria frondosa*. For both species, it is known that the effector protein tensilin can rapidly induce a transformation between the soft and standard (stiffer) mechanical states of the dermis (Bonneel *et al.*, 2023). However, the other effector proteins, including softener, have only been partially purified based on their activity, and their identity and sequence remain unknown. Proteomic analyses coupled to transcriptomics first allowed us to investigate the specific molecular components of the MCT from the dermis of *H. forskali*. Then, we investigated the mechanical, compositional, and structural differences between *H. forskali* and *C. frondosa* dermis using a range of cross-disciplinary techniques including histology, tensile testing, FT-IR spectroscopy, X-ray diffraction and confocal Raman spectroscopy. This multi-length scale approach provides new insights into the similarities and differences between MCT from these two species, furthering our understanding of the mechanisms of tunability in this distinctive mechanically adaptive collagenous tissue.

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Echinoderms associated with different subtropical macroalgal communities revealed by metabarcoding

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In the past, identifying the actual diversity of an ecosystem was challenging due to the difficulty in detecting small, endemic, and cryptic species. Consequently, scientists often underestimated biodiversity. Fortunately, molecular techniques, such as DNA metabarcoding, have provided a breakthrough in ecological and diversity-based studies (Blaxter, 2016; Peters et al., 2015; Wangensteen & Turon, 2017). In this study, we used metabarcoding to determine the diversity of Echinodermata associated with common marine communities in the Macaronesia archipelagos. We collected at least 3 scrapings of 20x20 cm quadrants from each community to retrieve DNA and analysed the mitochondrial cytochrome c oxidase, subunit I marker for each sample (Wangensteen & Turon, 2017). We obtained a total of 2,739,293 reads, which were identified as Metazoan, with 1558 reads belonging to 17 echinoderms. The Shannon diversity index did not show significant differences, but ANOVA revealed a significant difference between the communities of the Azores and Canary Islands, as well as among some communities within each archipelago. The envfit analysis on the MDS graph indicated that the differences were due to the presence of *Diadema africanum* in the community of *Gongolaria abies-marina* and Gelidiales from the Canary Islands and *Sphaerechinus granularis* in all communities from the Azores. Additionally, we found *Coscinasterias tenuispina* only in the Canary Islands and *Holothuria sanctori* only in the *Halopteris* sp. community from the Azores. Finally, we were able to differentiate six lineages of the genus *Amphipholis*, one of which is unique to the Canary Islands and another to the Azores, with four lineages shared between them but in different abundances (Figure). This study highlights the importance of metabarcoding for the conservation of marine biodiversity, providing important data for echinoderm communities and laying the foundation for further research on these species, especially the small ones.

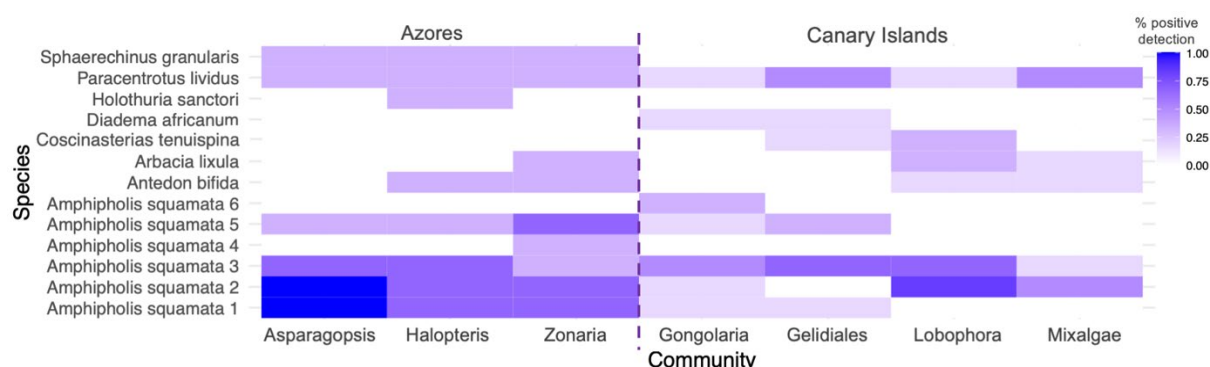


Fig. 1. Heatmap showing the ratio of replicates with positive detections for each echinoderm taxon by archipelago and macroalgal community.

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Effect of shifts in the $\text{Mg}^{2+}/\text{Ca}^{2+}$ ratio of seawater on mechanical properties of the echinoderm skeleton

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Theoretically, the occlusion of magnesium within calcite should improve its hardness, because impurities of Mg induce lattice distortion, which in turn increases both the sliding resistance of dislocations and deformation resistance in crystal. However, our understanding of the relations between Mg content and mechanical properties of the echinoderm skeleton is limited (e.g., Ma *et al.*, 2008; Moureaux *et al.*, 2010; Lemloh *et al.*, 2013). In our project we conducted experiments aimed to investigate the effect of ambient $\text{Mg}^{2+}/\text{Ca}^{2+}_{\text{sw}}$ ratio on skeletal Mg/Ca ratio and mechanical properties of spines in two echinoid species (*Paracentrotus lividus* and *Arbacia lixula*). We found that echinoids cultured in low $\text{Mg}^{2+}/\text{Ca}^{2+}_{\text{sw}}$ ratio produced a skeleton with lower Mg content and nanohardness than the controls. These results, if confirmed by studies of field-collected specimens, may have a number of implications, the most obvious of which are in the realm of paleontology. Although the modern variability in $\text{Mg}^{2+}/\text{Ca}^{2+}_{\text{sw}}$ ratio is relatively minor, throughout the geological history this ratio has varied substantially, which is believed to have affected the skeletal Mg/Ca ratio in fossil echinoderms (e.g., Dickson, 2002, Kołbuk *et al.*, 2020). Thus, if mechanical properties of echinoderm biomineral are to some extent related to its Mg content, it seems that at certain times in the past (during the so-called calcite seas) echinoderms with decreased skeletal Mg content were probably more susceptible to predation and post-mortem taphonomic processes (e.g., abrasion). Additionally, this effect might had some consequences in terms of energy allocation and higher energetic costs of calcification. [The project was funded by NCN grant 2020/37/B/ST10/01460].

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Historical, sampling and gender bias in palaeontological collections: Stylophora (Echinodermata) as a case study

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The class Stylophora corresponds to a relatively small clade of extinct echinoderms (around 130 species and 70 genera) known from the middle Cambrian (Wuliuan) to the Late Carboniferous (Bashkirian). From their first descriptions in the 1850s (Billings, 1858; Hall, 1859) to the 1950s, stylophorans were almost exclusively described from Europe and North America.

We analysed an extensive data set that includes all stylophoran species, the publication year and the location of the holotypes, the nationality and the gender of the taxonomists who described them. Based on multivariate statistics analyses, we assessed two main biases. First, although stylophoran occurrences have been documented from all continents except Antarctica for the last 75 years, our knowledge of this class remains strongly biased historically. Indeed, about 75% of all described taxa are from only four countries (France, Czech Republic, USA, and UK). Moreover, prolific countries (e.g., Morocco) do not have holotypes registered in their public collections, although the material was discovered in their territory. Second, although female geologists sometimes contributed extensively to fieldwork and the discovery of new taxa (the most famous example being Mrs Elizabeth Gray, after whom *Cothurnocystis elizae* Bather, 1913 was named), only a single species was described by a female palaeontologist, "*Phyllocystis*" *salairica* by Yulia Dubatulova (*in Rozova et al.*, 1985).

We might explain this pattern with parachute palaeontology (or scientific colonialism). The impact of colonialism on biodiversity study in deep time has been recently approached in the literature (Monarrez *et al.*, 2022, Raja *et al.*, 2022, Chacon-Baca *et al.*, 2023). Women in paleontology is an older topic (e.g., Aldrich, 1982, Berta and Turner, 2020), even if gender parity has not been reached yet (Warnock *et al.*, 2020). We rely on these studies to propose perspectives in order to foster diversity and inclusion in the stylophorans research community such as: supporting women and local collaborators in fieldwork and the description of the material; keeping the material in its country of origin after primary study; maintaining strong scientific collaborations with foreign universities that hold the material to diversify author nationalities in publications and generate fundings.

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Dietary effect of fermented feed sources on growth performance of juveniles sea cucumber *Holothuria scabra*

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Sea cucumber *Holothuria scabra* is one of the marine species with a high economic value that has the potential as a source of luxury seafood. A suitable diet is still a limiting factor in the growth of farmed sea cucumbers, particularly in large-scale cultivation. The objective of this study is to evaluate the effect of fermented diet on the growth and survival of early juveniles of *H. scabra*. Seven treatments were conducted with 4 replicates each, with the following main components: seagrass *Enhalus acoroides* (control), seaweed *Halimeda* sp., *Ulva* sp., *Padina* sp., *Sargassum* sp., microphytobenthos, and moss. Juveniles with an initial average wet weight of 0.16-0.18 g were maintained in experimental tanks in East Lombok, Indonesia. There were significant differences in the growth rate of juvenile *H. scabra* fed different fermented diets ($p < 0.05$). The highest and the lowest values of growth rate (0.09 ± 0.023 and 0.01 ± 0.001 g d⁻¹) were observed in treatments fed with klekap and *Ulva* sp., respectively. Specific growth rates of the diet *Halimeda* sp., (3.17 ± 0.183 % d⁻¹) and control *Enhalus* sp., (4.17 ± 0.058 % d⁻¹) are statistically significantly different ($p < 0.05$). The survival rates of the diets microphytobenthos, *Halimeda* sp. and moss were significantly lower than the control feed (*Enhalus* sp.) which had the highest value of $80.63 \pm 4.38\%$.

Many cloning larvae and related juveniles are Oreasteridae

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Two specimens of starfish were collected at Parque Nacional Arrecife Alacranes and Triángulos Oeste in the Southern Gulf of Mexico. We used DNA of mitochondrial loci to identify these specimens as members of the same clade as cloning larvae found abundantly in the tropical and subtropical western North Atlantic ocean. These results demonstrate that cloning larvae persist as clones but also metamorphose and settle to the benthos with typical asteroid morphology. We also demonstrate that this clade of starfish with cloning larvae is related to but distinct from *Oreaster clavatus* and *Oreaster reticulatus*, the two known species of Oreasteridae in the North Atlantic. Subsequent to our paper, another research group has shown that the clade of interest includes adults of *Valvaster striatus* and has sequenced a number of larvae from the coastal seas off Panama (Atlantic and Pacific). Notably the *Valvaster striatus* specimens that were sequenced by this research group were from the Cook Islands in the South Pacific, ~9000 KM from the specimens from the southern Gulf of Mexico.

We obtained and sequenced DNA of specimens of *Valvaster striatus* that were collected in Indonesia and the Cook Islands. We reanalyzed the *Valvaster* sequences, sequences of larvae collected off Panama, with all existing data. We found that many of the larvae from Panama are sister to the clade of cloning larvae, *Valvaster*, and the starfish collected in the southern Gulf of Mexico. This clade of interest includes *Valvaster striatus* (nominally Asteropseidae) nested deep within a clade including many Oreasteridae taxa. Nominal Oreasteridae is monophyletic for two genes studied. In two other genes, nominal Oreasteridae is rendered non-monophyletic by inclusion of taxa that are nominally Goniasteridae, Archarsteridae, and Asteropseidae. In analyses of each gene, Oreasteridae is not broken up across the tree, but rather remains intact with members of the other families broken up across the tree including nesting within Oreasteridae. Thus a taxonomic revision of these families, especially Oreasteridae which subsumes members of other families (e.g., Valvasteridae, Goniasteridae, Archarsteridae, and Asteropseidae). In summary, our phylogenetic analyses underscores how small and monotypic families impair understanding of echinoderm evolution and life histories. Our phylogenetic analyses provide bases for evaluation of the taxonomic breadth, global distribution, life cycle, and ecology of cloning larvae related to Oreasteridae.

A novel UCE probe set for phylogenomics of echinoids

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In order to facilitate usage of museum materials in the quest for resolving the echinoid tree of life we have developed a custom genomic bait dataset to more efficiently target and capture ultraconserved elements (UCEs) within the class Echinoidea and its sister-group the Holothuroidea. UCEs are highly conserved genomic regions and provide a powerful tool for phylogenomic analyses that can be used as anchors for molecular markers. Sequence variation in their flanking regions has proven to be a valuable source of phylogenetically informative data in studies on vertebrates, arthropods, scleractinians and molluscs, to name just a few.

We employed a modified version of the phyluce pipeline (Faircloth, 2016) to identify conserved regions in the genomes of interest. In order to generate the UCE bait set, we used a set of eight previously published draft- and completed echinoid and holothuroid genomes for downstream phylogenetic inference within the class Echinoidea. We tested the bait set in silico by an extended dataset of publicly available raw whole-genomic Illumina sequencing data of 13 additional echinoid species from the NCBI short read archive (SRA).

Our custom bait set contains 4,754 UCE loci, 2,300-3,200 are also present in the holothuroid outgroups. Facilitating available chromosome-scale assemblies of *Lytechinus variegatus* and *L. pictus* we were able to explore the distribution of the UCE loci in the echinoid genome. Distribution of UCE's is non-random, with some chromosomes (four, six, and nine) harbouring very few loci, while others (three, seven, ten, and twelve) contain many loci. UCEs further tend to occur in clusters rather than being homogeneously distributed across chromosomes. In terms of position in relation to genic/intergenic regions, our analysis showed that UCEs often span exon-intron boundaries, followed by positions within exons. Only few UCE loci were located in intergenic regions, introns or the boundaries between exons and intergenic regions. From a functional point of view UCE loci appear to be enriched for genes of the GO-term „microtubule-based movement“. However, other GO-terms (e.g. DNA_integration or UDP-glycosyltransferase_activity) show a significant deficiency of genes, which may indicate that genes of these categories are under rapid evolution.

Usage of the novel bait set to capture UCE loci in WGS sequence data of a variety of different echinoid groups highlights the ability of these loci to increase the phylogenetic resolution of the group and to inform taxonomy. A mean of 3,535 (SD=975) loci were captured per taxon, and a 75% complete concatenated alignment of 21 taxa (18 Echinoid and 3 Holothurian) samples included 4,613 loci and ~1,788,915 base pairs. Maximum likelihood analyses recovered a highly supported tree and revealed that relationships within the Echinoidea are largely congruent with traditional morphological groupings.

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Holothuroid phylogeny inferred from mitogenome data

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Over the last decade an increasing number of mitochondrial genomes for echinoderms have been published and currently more than 230 echinoderm mitogenomes representing ca. 200 different species are available. Thanks to high-throughput sequencing it is now easier than ever to assemble mitochondrial genomes. Because of the high number of mitochondrial copies per cell, mitochondrial reads typically represent a few percent of the sequence data from most sequencing experiments, even if mitochondrial DNA was not the focus of the experiment in question. These data can often be used to assemble complete mitochondrial genomes of high quality and high genomic coverage (sequencing depth). Using published and newly assembled mitochondrial genomes from around the half of the known families of the major groups of sea cucumbers (Apodida, Elasipodida, Holothuriida, Molpadida, Synallactida, Dendrochirotida), we examined the phylogeny of the Holothuroidea and compared the results with phylogenomic analyses based on nuclear markers from transcriptomic data and morphological data.

This is a contribution to the efforts for the revised *Treatise on Invertebrate Paleontology, Part U, Echinodermata 3, Asterozoa – Echinozoa*.

Antarctic sea star *Odontaster validus* larval performance is negatively impacted by long-term parental acclimation to warming

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Cross generational responses, when the environment of the parents influences offspring performance, may contribute to species responses to climate change in rapidly warming regions such as coastal Antarctica. We conditioned adult Antarctic sea stars *Odontaster validus* in the laboratory to two temperature treatments (ambient (0°C) and warming (+3°C)) for two years, and used their gametes to generate larval offspring. The response of their larvae to five temperatures (0°C, 1°C, 2°C, 3°C, and 4°C) was examined over 145 days. Adults conditioned to 3°C produced significantly smaller eggs compared with those from 0°C conditioned adults. Following fertilisation, larval size and survival were initially higher in offspring from the 3°C conditioned parents compared with those from the 0°C adults. After 34 days of development, while survival was greater in offspring of the 3°C adults, reduced offspring size emerged at a time coinciding with the transition from the gastrula to the bipinnaria larval stage. After around 50 days, survival in larvae from 3°C conditioned adults decreased. By the end of the experiment (145 days), offspring of the 0°C conditioned adults had greater survival (17.6 - 34.3%) and growth (final size = 697 to 773 µm), compared to those from the 3°C conditioned adults (survival 7.0 - 19.3%; growth final size = 380 to 624 µm). Our results suggest that acclimation of adults to warmer temperatures resulted in negative carryover effects in terms of offspring performance, a pattern that emerged over time. While *O. validus* adults may survive exposure to moderate warming and produce viable gametes, their larval offspring may be less able to complete development. The downstream effects of poor recruitment of a key species such as *O. validus* would have important outcomes for coastal Antarctica ecosystems.

Class Stylophora: What's new since the last IEC (Nagoya, 2018)?

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Stylophorans are a clade of Palaeozoic (Wuliuan–Bashkirian) vagile echinoderms consisting of a single articulated appendage (aulacophore) and a more or less asymmetrical flattened theca. Along with glyptocystitid rhombiferans, eocrinoids and solutans, they were one of the major components of the cosmopolitan, low diversity echinoderm assemblages typical of soft substrate communities across the Cambrian–Ordovician boundary. In the first edition of the *Treatise on Invertebrate Paleontology*, stylophorans were elevated to class level (Ubaghs, 1968), and they were subdivided into the two orders Cornuta and Mitrata originally defined by Jaekel (1918). Over the past 50 years, the debates about their anatomy, mode of life and phylogenetic position within the deuterostomes have fueled an abundant literature, so that stylophorans have become one of the most studied and best known groups of Palaeozoic echinoderms.

Since the last International Conference on Echinoderms in Nagoya (2018) and the launch of the revision of volume S of the *Treatise on Invertebrate Paleontology*, major advances have been achieved for the chapter on Stylophora. The description of exceptionally preserved soft parts in the aulacophore and the theca (ambulacral and digestive systems) of cornutes from the Fezouata Lagerstätte (Lower Ordovician, Morocco) has provided new critical data on their anatomy (Lefebvre *et al.*, 2019), which confirmed the interpretation originally proposed by Ubaghs (1968). Extensive monographic studies devoted to mitrates (Lefebvre & Ausich, 2021; Lefebvre *et al.*, 2022a) and cornutes (Lefebvre *et al.*, 2022b) summarized and updated current knowledge on stylophoran anatomy, morphology, taphonomy, plate homologies and systematics, thus providing a firm framework for the chapter on Stylophora in the revised edition of the *Treatise*. Ongoing and future research includes additional reports of exceptionally preserved soft parts, as well as the description of several Cambro–Ordovician taxa from China and Morocco, which are essential for elucidating plate homologies and stylophoran phylogeny.

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Evolution of sperm and egg proteins in the sea urchin *Diadema*

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How gamete recognition proteins evolve is directly relevant to how species become reproductively isolated. We studied, in the sea urchin *Diadema*, the evolution of bindin, the molecule on the acrosome process of the sperm that mediates attachment and fusion to the egg; we also studied the evolution of EBR1 and Obi1, egg molecules that are receptors for bindin. Bindin of *Diadema* is longer than in any other sea urchin genus studied to date (418 amino acids), but its architecture is similar to that of bindin in other orders of Echinoida. There is a conserved core of 55 residues that does not vary between species and two flanking regions. Most of the variation is in the first exon. Like bindins of *Arbacia*, *Tripneustes*, *Lytechinus* and *Pseudoboletia*, (and unlike bindins in *Echinometra*, *Heliocidaris*, *Strongylocentrotus* and *Paracentrotus*) it evolves mostly under stabilizing selection. The gene genealogy of this molecule resembles that of mitochondrial genes, suggesting that time alone can account for variation between species. Sympatric species (with the exception of *D. clarki*) do not show evidence of diversifying selection, as would have been expected from the hypothesis of reinforcement of species recognition traits to avoid hybridization. The evolution of egg reproductive molecules has not yet been studied in any sea urchin other than *Diadema*. EBR1 in *Diadema* is composed of 3786 amino acids. It resembles EBR1 of *Mesocentrotus franciscanus*, rather than that of *Strongylocentrotus purpuratus* (the only two species in which the entire EBR1 had been sequenced) in lacking hyalin-like repeats. It consists of a signal peptide, single domains of M12B propeptide, repolysin, and ADAM moieties followed by multiple TSP1 and CUB repeats. The gene genealogy of EBR1 differs from that of mitochondrial genes, suggesting that factors other than time alone are important in its evolution. However, different modes of analysis fail to agree as to which sites in this long, repetitive molecule evolve under diversifying selection. Like bindin, EBR1 evolves mostly under stabilizing selection in *Diadema*. Divergence between species in one section of EBR1, where most of the putatively positively selected sites are located, is positively correlated with divergence in the first exon of bindin, suggesting coevolution between sperm and egg molecules. Obi1, the other egg molecule involved in fertilization, is 877 amino acids long. Its gene genealogy coincides with that of mitochondrial genes and of bindin. This molecule also evolves mostly under stabilizing selection. However, in Obi divergence between species is not significantly correlated with divergence in bindin. More work on the egg receptor molecules is needed to assess intraspecific variation, which may be relevant to the role of sexual selection, and their expected coevolution with bindin.

Impact of host separation on the echinoderms obligate symbionts

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Symbioses refer to long-lasting associations between different species, typically a host and a symbiont. Some symbionts have evolved to become highly dependent on their hosts, developing various adaptations to maintain this relationship. Recent research has revealed a new type of dependency in which symbionts rely on the chemical environment produced by their host (Brasseur *et al.*, 2018). This dependency can lead to a condition called "host separation syndrome," in which symbionts experience changes in health and coloration, and potentially death, when isolated from their host. This syndrome was studied on *Echinometra mathaei* and two of its symbionts (*Arete indicus* and *Tuleariocaris holthuisi*). In addition, we investigate this phenomenon in two other decapods-echinoderm associations: (i) the sea star *Culcita noveaguineae* and the sea star shrimp *Zenopontonia soror*, and (ii) the crinoid *Phanogenia distincta* and the pistol shrimp *Synalpheus stimpsonii*. We tested three different conditions, namely (i) the symbionts remaining on their host (control), (ii) the symbionts being isolated from their host, and (iii) the symbionts being isolated in water containing semiochemicals produced by their host. Our results indicate that all the symbionts experienced the separation syndrome, but only *Synalpheus stimpsonii* and *Tuleariocaris holthuisi* showed chemical dependency on their respective host. Additionally, our findings suggest that the phenomenon of symbiont discolouration is more complex than previously described. Overall, our study sheds light on the importance of chemical dependency in symbiotic relationships and provides further insights into the host separation syndrome.

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Longitudinal gradient in the population size structure of the sea cucumber *Cucumaria frondosa* in the Northwest Atlantic

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In response to declines in finfish fisheries, commercial harvests of underutilised species such as whelks and sea cucumbers were developed in many jurisdictions to generate or maintain economic growth. The sea cucumber *Cucumaria frondosa* is an abundant benthic echinoderm found on the continental shelves of eastern Canada and several other countries in the North Atlantic, making it a good candidate for a commercial fishery. On the St. Pierre Bank off the southern coast of insular Newfoundland (NAFO Division 3Ps) in Canada and France (Saint-Pierre-et-Miquelon), the biomass of sea cucumbers was estimated around 255,000 metric tonnes in 2016. In this study, this stock was assessed by examining the population size structure from three areas across a longitudinal gradient. We found an increasingly greater proportions of smaller individuals in the eastern area of the fishing ground. This pattern remained robust even after accounting for individual variability in size, which can range between 10 and 20% depending on the metric tested (e.g., body length, whole wet weight). Differences in size structure among populations were linked with local fluctuations in primary production (a proxy for food availability), temperature, and current velocity at the seafloor. These findings advocate for the importance of using site-specific size structure in the future management across the whole distributional range of *C. frondosa* in the Northwest Atlantic.

Aristocystitidae (Echinodermata, Blastozoa): Systematic and taxonomic review

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The Early Palaeozoic represents a critical time interval of life's history, during which echinoderms, as most other metazoans, underwent a major radiation. In this context, the subphylum Blastozoa Sprinkle, 1973 is of particular interest, as its morphological diversity was significantly concentrated early in its history (Foote, 1992). Aristocystitid specimens are generally poorly preserved (incomplete theca) and, very frequently, they do not show the oral surface, which is of prime taxonomic importance. Frequently, the taxonomic identification of many aristocystitid taxa simply relies on fragmentary portions of theca, mostly aboral regions, and is based on characters such as the shape and size of the theca; the shape, size and arrangement of thecal plates; the structure and arrangement of respiratory pores; and the occurrence of anatomical elements added as tubercles (Escribano Ródenas *et al.*, 1999; Gutiérrez-Marco & Aceñolaza, 1999; Gil Cid & García Rincón, 2012). In addition, aristocystitids are one of the blastozoan clades displaying the widest morphological diversity, which makes precise definition and taxonomy very difficult (Kesling, 1968; Paul & Kesling, 1968).

Since the last works of Chauvel (1980) and Chauvel & Meléndez (1986), systematic revisions were carried out on several aristocystitid taxa: *Aristocystites* (Parsley, 1990; Paul & Parsley, 2019), *Enodicalix* (Gutiérrez-Marco & Aceñolaza, 1999; Paul & Gutiérrez-Marco, 2020), *Binocalix* (McDermott & Paul, 2019), *Lepidocalix* (Makhlouf *et al.*, 2017), *Oretanocalix* (Gutiérrez-Marco, 2000; Paul & Gutiérrez-Marco, 2022), and *Prokopius* (Paul, 2018). However, the identification of the Ordovician aristocystitid *Calix* remains problematic, and will require to review the morphology of all taxa assigned to it, to critically reevaluate their assignment to that genus, and ultimately, to identify key characters for the diagnosis of *Calix* (Makhlouf *et al.*, in progress). However, although the characters of the type species of *Calix* are well established, all other species currently assigned to *Calix* require thorough morphological review, to reevaluate their assignment to that genus (Makhlouf *et al.*, in progress). The same work has to be done for all other problematic aristocystitid genera, such as *Glaphocystis*, *Phlyctocystis*, and *Maghreboecystis*. The systematics of the family Aristocystitidae remain unclear, and would benefit from a thorough revision, including a phylogenetic analysis and the systematic review of several taxa (Makhlouf *et al.*, in progress).

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Amazing Bioluminescence of Crinoidea from Depths

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Bioluminescence in echinoderms has been known since the early 19th century. Of the four luminous classes known, Crinoidea is the least studied, with only five bioluminescent species reported. The research conducted during the RV Southern Surveyor 2005 "Mapping benthic ecosystems" and the RV Investigator 2017 "Sampling the Abyss" cruises aimed to systematically sample deep benthic habitats along Australia's eastern and southwestern margins. These cruises allowed us to acquire the first *in vivo* pictures of light-emitting crinoids and luminometric measurements on fresh tissue samples. Four new records of bioluminescence in deep-sea Comatulida from three distinct clades, double the number of known Crinoidea species with bioluminescent capacity. *In vivo* photography and histology suggest that, in some species, light emission might originate from the sacculi. Pharmacological assays reveal that Thalassometridae light emission is under adrenergic control. Biochemical data indicates the presence of a coelenterazine-based luciferin-luciferase system in *Thalassometra* cf. *gracilis* similar to the one described in the ophiuroid *Amphiura filiformis*. Phylogenetic distribution of bioluminescence among Crinoidea and differences in this trait phenotype could be indicative of multiple acquisitions of luminescent capability in crinoids, possibly promoted by the ecological role that bioluminescence might fulfill in the vastness of the deep benthic habitat.

"Mapping benthic ecosystems on the deep continental shelf and slope in Australia's South west Region" was led by CSIRO under chief scientist Dr. A. Williams; "Sampling the Abyss" was led by Museums Victoria under Chief Scientist Dr. T O'Hara and supported by CSIRO Marine National Facility and NESP Marine Biodiversity Hub.

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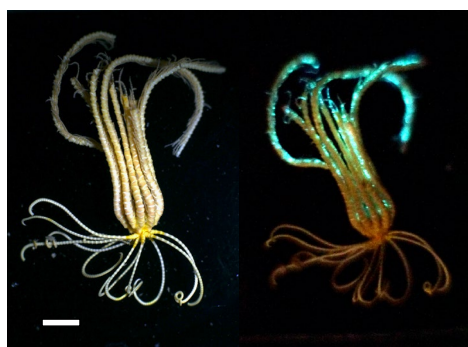


Fig. 1. Daylight and bioluminescence pictures of *Thalassometra* cf. *gracilis*.
© Dr.J. Mallefet. Scale bar = 1cm

Metabolic plasticity of sea urchins to face ocean warming

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One of the first responses of organisms under changing conditions is to adjust their behaviour to reduce stress, but when this is insufficient to maintain biological efficacy, environmental changes have an impact on physiological traits such as metabolism (Guillou *et al.*, 2013). With the future warming of the oceans and the increase of extreme heat events, the phenotypic plasticity of the organisms is going to be a key factor to their resistance to the upcoming temperatures. We here evaluate how two echinoderm species with different evolutionary origins, but whose distribution ranges overlap in the Mediterranean, *Arbacia lixula* (sub-tropical) and *Paracentrotus lividus* (temperate-cold) respond to a temperature increase and ocean warming according to their phenotypic plasticity. We analysed changes in basal metabolism to artificial temperature increase under controlled conditions in aquarium using Digital Respirometry System (Qubit Systems). We subjected individuals of both species collected from the same NW Mediterranean locality to a gradual increase of the temperature, over four days, from 16°C to 20°C, 23°C, and 26°C sequentially, for 22 hours (each temperature). Oxygen consumption was measured independently for each individual to calculate basal metabolism at each temperature. The results showed similar responses for both species for 16°C, 20°C and 23°C, with a progressive increase in the oxygen consumption for each increased temperature, meaning the significant rise of its metabolisms as a respond to the temperature stress. However, an opposite pattern between the species was observed at the highest temperature. Whereas *A. lixula* continued increasing its metabolism at 26°C, in *P. lividus* the metabolism rate dramatically fell down approaching the lowest oxygen consumption values and suggesting that this species reached its physiological maximum before 26°C. The results may be potentially related to the origin and distribution of these species, despite both overlap at large areas of the SE Atlantic and Mediterranean, being the subtropical species potentially more resistant to the warming of the Mediterranean Sea.

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Sea urchin wastes valorization: Production of innovative composite biomaterials for tissue regeneration

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Edible sea urchins are well known worldwide as food delicacies however their gonads are the only eatable part, while all the rest (about the 70-90% of total mass) is discarded as waste. Nonetheless we recently showed that the latter can still be valorized and recycled towards high added-value products, in line with a circular economy approach. Particularly, we previously demonstrated that these waste can be a source of valuable molecules, such as 1) fibrillar and GAG-rich collagen, used to produce innovative and biomimetic biomaterials for skin regeneration (Benedetto *et al.*, 2014; Ferrario *et al.*, 2020) and 2) antioxidant pigments (spinochromes) with a high free-radical scavenging activity (Marzorati *et al.*, 2021). As a step forward, in this work we attempted to combine both sea urchin collagen and spinochromes to develop a novel composite and second-level biomaterial, with both biomimetic and bioactive features.

Native collagen was obtained from a well known mutable collagenous tissue, the peristomial membrane, while spinochromes were extracted from the remaining waste (test, spines, soft tissues residues). The obtained composite biomaterials were characterized in terms of morphology, degradation kinetics, release kinetics of the spinochromes and antioxidant activity. SEM analyses indicate that biomaterials are morphologically similar to the simple collagen-based counterpart (as well to native connective tissues), with homogeneous fibrils organization pattern in the absence of undesired aggregates. Porosity was confirmed to be ideal for cells infiltration, settlement and growth. Furthermore, UPLC and ABTS assay indicate that antioxidants remain adsorbed onto the collagenous matrix, without any significant release. Additionally, degradation kinetics in both physiological and enzymatic (collagenase) conditions showed an improvement of the stability of the antioxidants/collagen composites, in comparison to simple collagen-based biomaterial. In addition, the degradation kinetics resulted similar to a commercial bovine membrane used as control (Integra®) in physiological conditions. Subsequently, the antioxidant activity of composite biomaterials was evaluated using ABTS assay directly on the solid composite materials. The results confirmed that the antioxidant activity was maintained on the biomaterial, even after freeze-drying even without antioxidants release in solution.

Overall, these data indicate that sea urchin wastes can be profitably exploited to obtain valuable molecules and develop innovative biomimetic and bioactive biomaterial, potentially effective in the promotion of tissue regeneration. As a future perspective, 3D bioprinting technology and sea urchin-derived bioink is currently under development to produce collagen-based bioactive biomaterials with enhanced mechanical properties and tuneable morphologies.

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Atelecrinidae: using molecular data and X-ray tomography to look into the latest hypotheses

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Atelecrinidae is a remarkable family of deep-sea/abyssal feather-stars characterized by the presence of a complete basal ring, a high conical centrodorsal with horseshoe-like structures flanking the cirrus-sockets and absence of pinnules on the proximal arm. They are even more outstanding when one considers that molecular studies place them within Bourgueticrinina, a clade composed of crinoids with a xenomorphic stalk (Hemery *et al.*, 2013). A recent revision by Messing (2013) based solely on morphological characters established two new genera inside this clade, *Adelatelecrinus* and *Paratelecrinus*, and suggested inter-relationships among the now four genera (*Sibogacrinus* as sister to all others). Here we present the first molecular phylogeny (COI, 16S, 28S) of the family including 9 of the 13 currently described species. Our molecular results show that some genetic distances between “species” are more congruent with inter-generic rather than inter-specific distances. Tree topology is not entirely resolved and some inter-relationships must be taken with caution. Of the morphological characters used, a lot of importance was put into the presence of (coelomic?) pits on the adoral rim of the centrodorsal and the articular facet on the aboral surface of the basals. In this study, we use X-ray tomography to reobserve these characters on the Atelecrinidae from the MNHN collections which contain all four of Messing’s genera and some type material that was not dissected in his study. We further add the analysis of two other morphological characters: the “knobby-process” (a unique character of primibrachials shared by extant Bourgueticrinina families except Phrynocrinidae) and the mode of articulation between radials. We suggest new hypotheses on species interrelationships based on the combination of both molecular and morphological methods. Their consequences on classification at the genus rank are discussed.

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***Tripneustes australiae*, the senior synonym of *T. kermadecensis*: Taxonomy and museum distribution records of sea urchins in the genus *Tripneustes* in eastern Australia**

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Accurate taxonomy and descriptions of species are key to understanding biodiversity. The echinoid genus *Tripneustes* is an ecologically and commercially important taxon that includes the pan tropical *Tripneustes gratilla gratilla* (Linnaeus, 1758) and the recently described *T. kermadecensis* by Bronstein *et al.* (2017) from Australia and New Zealand. Occurrences of *T. kermadecensis* along the coast of New South Wales, Australia was previously considered to indicate a range extension of the tropical *T. g. gratilla*. We used the Australian Museum collections to clarify the distributions of these two species in eastern Australia and show a clear tropical distribution of *T. g. gratilla* and a subtropical/temperate distribution of *T. kermadecensis*. Material described as *Evechinus australiae* by Tenison-Woods (1878) from Sydney Harbour was examined using molecular and morphological techniques. These techniques included micro-computed tomography, quantification of test traits, and molecular genetic analysis using the mitochondrial marker cytochrome oxidase subunit I (COI), which was used for phylogenetic analysis. We found that the material described by Tenison-Woods was identical to *T. kermadecensis* as described by Bronstein *et al.* (2017) and so *T. kermadecensis* is a junior synonym of *Evechinus australiae* which was transferred to the genus *Tripneustes* by the Australian Museum in May 1909. So, the correct designation is *Tripneustes australiae* (Tenison-Woods, 1878).

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The sea cucumbers of the Algerian coastal waters: Taxonomy, ecology and their nascent fisheries and illegal trade

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The present work aims to provide an overview of the various studies carried out on sea cucumber species from the Algerian coastal areas. The main contributions relate to the discovery of the new genus *Paraleptopentacta* and the separation of the new species *Holothuria algeriensis* formerly called *Holothuria tubulosa* "B" (Mezali *et al.*, 2020, 2021). Various studies have focused on the reproduction of *Holothuria sanctori* and *Holothuria poli*, the population dynamics of *Holothuria tubulosa* and *Holothuria poli*, the feeding behavior and the analysis of the digestive contents of some species of the genus *Holothuria*, as well as the species *Parastichopus regalis* (Mezali *et al.*, 2022). The biochemical aspect was approached by elucidating the proximate composition of the species of the genus *Holothuria* as well as the characterization of the saponins present in the tegument and Cuvierian tubules of *Holothuria sanctori*, *Holothuria algeriensis* and *Holothuria arguinensis*. In Algeria, the harvesting of sea cucumbers is growing rapidly and is capable of extracting significant amounts of these benthic animals (Mezali & Slimane-Tamacha, 2020). Hence, there is an urgent need for effective management in order to avoid destruction of the stock.

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You can't get a head: Supporting a view in which the first echinoderms were pentaradial

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Echinoderms are so highly derived compared with other deuterostomes, including their sister group, hemichordates, that comparisons of body plans are sometimes accompanied by points of view enjoying varying levels of morphological, paleontological, and especially, embryological support. Conceptual models, usually imbued with Haeckelian principles, consider the absence of a single character (pentaradial symmetry) as a recapitulation of the pre-metamorphic larval stage of echinoderms, forcing unusual taxa that also lack pentaradiality, such as carpoids, down the phylum's phylogenetic tree. Such scenarios assume that first echinoderms had a bilaterian-type anterior-posterior axis. Empirical models rely on comparison of non-pentaradial early forms with a wide array of data obtained from extant and fossil echinoderms, suggesting that pentaradial symmetry was secondarily lost in such taxa. Is it worth considering non-pentaradial echinoderms as members of a well-known group of echinoderms, the blastozoans, which already includes many secondarily-derived, non-pentaradial members? Followers of the empirical model think so, presenting an alternative that integrates paleontology, embryology, body wall homology, and image analysis, deriving echinoderms from a bilaterian, archimeric *larva*, not bilaterian *adults*. Unprecedented modification of a single mesocoel (hydrocoel) initiated the pentaradial adult echinoderm, most parsimoniously with five primary lobes at the outset in stem forms of each major clade within the phylum. The unique water vascular system led to rearrangement of adult axes that literally have no parallel with those of any other invertebrate, representing an iconic synapomorphy for the Echinodermata. There are few, if any, developmental or stratigraphic data parsimoniously defending carpoids or stylophorans as 'bilateral' in the same sense as hemichordates. Furthermore, the supposed 'tail' of these puzzling taxa is now shown to be an ambulacrum, undermining any supposition of a 'head', 'tail', or 'gill slits' in any echinoderm. Pentaradial hydrocoel patterning that induces adult pentaradiality is also key to understanding features allowing exploitation of epibenthic habitats. The water vascular system (axial region) in the oldest known echinoderms originally served in suspension and detritus feeding, facilitated by small tube feet in narrow ambulacra radiating from an upward-facing mouth. A subset of blastozoans exploited motility as a feeding mode, leading to extraordinary adaptations that belie their interpretation as ancestral echinoderms.

Chromatic harmony in symbiosis: Acquisition and characterization of pigments in *Zenopontonia soror*, associated with *Culcita novaeguineae*

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Coloration change is a common phenomenon in the marine environment, particularly for organisms that are cryptic or use passive/active camouflage (e.g. cephalopods). When two organisms are symbiotically associated, they may harbor similar colors that improve their survival by decreasing their predation rate. However, when the symbiont is separated from its host, it may suffer from host separation syndrome, which may have an impact on the discoloration of the symbiont resulting from stress. This study examines the symbiotic relationship between the shrimp *Zenopontonia soror* and the sea star *Culcita novaeguineae* living in Moorea (French Polynesia) to understand the pigment acquisition of the symbiont. To address this question, stomach content, stable isotopes and pigment extraction analyses were performed on the two associates to demonstrate the potential link between pigment acquisition and coloration of these organisms. The results of the pigment extraction showed similar carotenoid pigments in the tissues of the host and the symbiont. The gut contents analysis has revealed that both associates share a common food sources and the presence of sea star spicules. These results were confirmed by the stable isotopes analysis. This study describes, for the first time, the chemical composition of the pigments contained in symbionts tissues and provide further insights on how the coloration of the symbiont is impacted by its association with its host.

Taphonomy and paleoecology of echinoids: Reconstructing the past

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The study of echinoid evolution, diversity, and paleoecology is highly dependent on the fact that they are represented by taxa, which not only inhabited a large range of marine environments, but also possessed widely differing architectural designs of their multi-plated skeletons. This results in highly varying taphonomic biases dictating the presence of skeletal remains. The role of fossil echinoids in their environment can be interpreted with respect to functional morphology, direct comparison to modern counterparts as well as by studying taphonomic pathways. Although special preservation features can be found in mass accumulations and exceptional conditions, most sedimentary environments in which fossils are found show incompletely preserved remains.

A long-standing tenant of studies on preservation potentials is that taphonomic loss inherent during destructive processes is counteracted by information gain with respect to those abiotic and biotic interactions, which are duly recorded in skeletal remains. Echinoderm taphonomy not only follows the predicament of skeletons and their remains in their natural environment, but also draws upon interactions with other components of their ecosystems. Since echinoderms very much thrive in most marine environments, paleontologist not only incorporate recent observation from biological and ecological literatures, but can also to conduct actualistic experimental studies to specifically study destructive processes.

Two ecological interactions of special interest to paleontologist will be highlighted: Predator-prey relationship and organism-substrate interactions. The first analyzes how predators eat their prey, what kind of wounds are incurred, and if they can be recognized. Encrustation and bioerosion can occur during the life of the animals or as post-mortem occurrences on dead skeletons, which often represent stable substrates in otherwise particulate, mobile sedimentary environments. Finally, the role and history of echinoids in dictating the structure and composition of the environments in which they thrived will be discussed. This entails various processes where echinoids serve as “ecosystem engineers” structuring the environment and the composition of the sediment in which they are represented. Furthermore, echinoderms eventually contribute skeletal elements and fragments to the composition of the sediment on which and in which they live.

Quid novi Soluta?

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Solutans are a small clade of extinct non-radiate echinoderms. Their stratigraphic range extends from the middle Cambrian (Miaolingian, Drumian) to the Lower Devonian (Emsian). Solutans are characterized by two distinct and unequal appendages inserted at opposite ends of their theca: a single free ambulacral structure (brachiole), and a longer stem-like appendage (homoioostele). Due to their unusual morphology, the taxonomic position of the class is still controversial. Solutans are considered either as a distinct class of blastozoans or as basal, pre-radial hemichordate-like echinoderms. This contribution aims at reviewing the major advances achieved since Caster's (1968) chapter on Soluta in the *Treatise on Invertebrate Paleontology*, with a special emphasis on the main results obtained since the last IEC in Nagoya (2018) and ongoing studies.

The description of *Pahvanticystis utahensis* (Guzhangian, Utah) confirmed the probable Laurentian origin of the class (Lefebvre & Lerosey-Aubril, 2018). Work in progress lead by S. Zamora and X. Zhu will describe the earliest non-Laurentian solutan from the Guole Biota (Jiangshanian, South China). The Fezouata Biota (late Tremadocian–late Floian) yielded exceptionally preserved soft parts (gut) in a *Castericystis*-like solutan, as well as abundant remains of *Plasiacystis mobilis* (originally described in the Darriwilian of the Czech Republic) and a new taxon, morphologically intermediate between *Minervaecystis* and *Plasiacystis* (Dupichaud & Lefebvre, 2022). The revision of late Tremadocian solutans from the Montagne Noire provided the first detailed reconstruction of *M. vidali* and the first report of *P. mobilis* in that region (Dupichaud *et al.*, in press). The very unusually-shaped Hope Shale solutan (Darriwilian, Shropshire) is still awaiting description (work in progress by K. Derstler & B. Lefebvre). The Late Ordovician genus *Dendrocystites* was reported for the first time in North Africa (Nohejlová & Lefebvre, 2022) and from a new echinoderm Lagerstätte in the Prague Basin (Nohejlová *et al.*, 2019). The Neuville Formation (lower Katian, Quebec) yielded abundant remains of a new solutan, with a surprisingly plesiomorphic ('*Castericystis*-like') morphology (work in progress by K. Derstler). Finally, the first ever described Silurian solutan, *Dehmicystis ariasi*, was recently documented in the Ludlow of Spain (Zamora & Gutiérrez-Marco, in press), thus filling a long stratigraphic gap between the Late Ordovician and the Early Devonian. Another Silurian solutan from Wales is also awaiting description (Dupichaud, in progress).

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The Caudan Expedition: History and legacy of the echinoderms collections of the Université de Lyon

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The Caudan departed from Lorient (France) on the 19th of August 1895, for 14 days of scientific exploration in the Gulf of Gascony (Atlantic Ocean). The scientific team on board was comprised of René Koehler, professor from the Faculté de Lyon, Louis Roule, professor from the Faculté de Toulouse, Julien Thoulet, professor from the Faculté de Nancy, and Félix Le Dantec, preparer from the Faculté de Paris. During the expedition, 32 iterations of deep sea probing and 28 iterations of dredging were conducted, from 180 to 2200 meters deep, leading to a total of 550 animal species collected, among which 94 were unknown at the time. The goal of this expedition was to bring back to the Université de Lyon deep sea specimens that only the Muséum National d'Histoire Naturelle of Paris had at the time. The Caudan was one of the last expeditions in the Gulf of Gascony before a 60 years long period of disinterest for studying the fauna of this region, and it was the first to have been launched from private initiative and without funding from the French state. To this day, 256 marine animal taxa are still preserved in the Caudan collections of the Université de Lyon, including around 270 specimens of echinoderms. Representing a total of 52 species - 23 asteroids, 11 echinoids, nine holothuroids, seven ophiuroids, and two crinoids -, the Caudan collections also holds 14 type specimens of eight new – at the time – taxa: *Cribella bascayensis*, *Cribella caudani*, *Ophiactis corallicola*, *Antedon flava*, *Pentagonaster kergroheni*, *Asteronyx locardi*, *Benthogone rosea*, and *Holothuria roulei*.

Study of sea cucumber photoreception

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It has been known that echinoderms, despite lacking complex eye structures, exhibit photosensitivity mediated by opsins, photoreceptor proteins also found in other bilaterians. Recent studies on sea urchins, sea stars, and brittle stars, have revealed opsins in various body parts such as tube feet, spines, and the nervous system (Ullrich-Lüter *et al.*, 2011; Delroisse *et al.*, 2014). The eyespot located at the sea star arm tips has also been studied extensively. Some species have even demonstrated low-resolution extraocular spatial vision (e.g., Sumner-Rooney *et al.*, 2020). However, photoreception in sea cucumbers has remained largely unexplored, with only sporadic data available, such as observations of species moving away from a light source or retracting their oral tentacles under strong light exposure. To fill this knowledge gap, we conducted a comprehensive investigation of sea cucumber photoreception using a multidisciplinary approach. Firstly, we analyzed genomes and transcriptomes of multiple holothuroid species, revealing the presence of six ancestral opsin types in this group. Secondly, we highlighted the expression of rhabdomeric opsins, commonly found in protostome eyes, in oral tentacles and tube feet of *Holothuria (Panningothuria) forskali*, a European species belonging to the Holothuriida order. Our investigation also focused on the Apodida order, a group of sea cucumbers with snake-shaped bodies lacking tube feet. Previous authors have proposed the presence of visual-like structures at the base of the tentacles and/or in association with the oral nerve ring in different species (e.g., Ludwig, 1889; Yamamoto & Yoshida, 1978). Our study revealed the expression of ciliary opsins, typically found in vertebrate eyes, in the neuroepithelial structures forming eyespots at the base of tentacles in the tropical species *Euapta godeffroyi*. We also detected the expression of ciliary opsins in the sensory cupules of *Oostergrenia digitata*, a burrowing European species. Until now, the functions of these cupules located on the inner surface of tentacles had remained unexplored. Finally, ethological tests conducted on both Holothuriida and Apodida species revealed that *H.(P.) forskali* and *E. godeffroyi* moved away from a light source, while *Synapta maculata* exhibited a movement toward it, specifically in response to blue and green lights. These findings provide new insights into the mechanisms and evolution of photoreception in sea cucumbers.

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Biogeography and evolution of ophiuroids

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The compilation of a global phylogenomic and distributional dataset of ophiuroids has the potential to vastly improve our knowledge of the distribution and evolution of deep-sea life and our ability to identify priority areas for conservation. We now have genetic data (275 kbp, 1500 exons and COI) for 2300 samples across 1300 nominal species. We are currently focusing on the biogeography of the group, as geographic, bathymetric and habitat traits can be compiled from museum records, and readily mapped onto phylogenetic trees. At a global scale, the biogeography of the group follows two trajectories. Firstly, there is a shallow water (0-200 m) tropical-temperate fauna, whose distribution is limited by strong environmental gradients, disjunct habitats, and (except for rafting asexual species) an inability to disperse widely. The biogeography of this fauna has been strongly influenced by the Cenozoic cooling of the earth and by tectonic re-arrangements, including closure of the Tethys and Panamanian seaways and opening of the Drake Passage. Secondly, there is the bathyal and abyssal fauna which also emerges to occupy shallow water in polar regions. The biogeography of this group is strongly structured by the availability of dispersal pathways over the Cenozoic. The massive ranges occupied by many deep-sea ophiuroid lineages demonstrate an impressive ability to disperse widely. North Atlantic species range all the way around South Africa to Tasmania and some southern-ocean species-complexes extend along the eastern and northern rim of the Pacific, sometimes to Japan. Speciation appears to often occur along bathymetric gradients. Antarctica currently is experiencing particularly high diversification rates, with some species complexes having up to ~50 recognisable clades. Finally, there are numerous rare, often phylogenically-divergent, species spread across the world's oceans, particularly at tropical upper bathyal depths.

CT-scans suggest that *Lakotacrinus brezinai* is a crinoid with a chemosynthetic mode of life

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Lakotacrinus brezinai is an unusual crinoid that occurs in the Pierre Shale (Upper Campanian) of South Dakota. This crinoid has many longitudinal tubuli throughout the column, as well as an axial canal and ligamentary passages, both of which are present in most crinoids. Because this crinoid occurs only in association with methane seep carbonates, it is suspected to have had a chemosynthetic mode of life. We conducted a preliminary morphological analysis by thin sections and CT-scans to clarify the internal morphology of the columnals. Longitudinal tubuli extend from near the distal end of columnals to the most proximal end of the columnals, without any bifurcation or clear change in diameter. These tubuli proximally extend to and open into the thecal cavity where the main soft tissue is housed. Therefore, these tubuli were directly in contact with the main soft body in the theca. Considering the large volume provided by the tubuli in the columnals, the most probable scenario is that the tubuli were used to harbor chemosynthetic microbes and served as the passage connecting the columnals to the main soft body. An alternative scenario is that the tubuli housed extensions of the coelom, but most crinoids have a central axial canal for this purpose. Because this crinoid occurs in a seep environment, and has only five arms, it may have given up the "normal" suspension feeding mode and relied instead on nutrients supplied from chemosynthetic microbes. Carbon isotope analysis of two samples of columnals reveals values of $\delta^{13}\text{C}$ of -8.3 – -9.8 ‰ VPDB, suggesting incorporation of methane-derived carbon associated with hydrocarbon seeps, although further study is required to validate this assertion. Thus, to date, *Lakotacrinus brezinai* may be the only known crinoid to have followed a chemosynthetic lifestyle.

Genomic control of regeneration

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Echinoderms are well known to regenerate tissues, organs and even the entire body, however this capacity varies between species and/or stages of the lifecycle. *Amphiura filiformis*, a prevalent species of brittle star found in the northern East Atlantic, possesses a remarkable ability to regenerate its arms after injury. In the wild, over 90% of adult individuals display evident signs of regeneration. This provides an excellent system for investigating the regeneration of complex structures. Through a combination of genome sequencing and analysis of transcriptome data, we aim to elucidate the genomic control governing arm regeneration in *A. filiformis*. The high-quality chromosome-scale genome assembly enabled the comparison with other echinoderms, which revealed several genomic rearrangements and a complex pattern of gene loss and gain within the *A. filiformis* genome. The analysis of the dynamics of gene expression during different stages of regeneration identified three distinct phases of gene activity. These phases encompassed genes associated with immune responses, cell proliferation, and tissue differentiation, collectively orchestrating the regenerative process. Drawing parallels between our datasets and analogous ones from other species undergoing appendage regeneration, we pinpointed sets of genes that are commonly expressed during the regeneration processes. Moreover, our analysis of differential gene expression during explant regeneration identified potential regulators responsible for maintaining positional identity, shedding light on the intricate regulatory control underlying *A. filiformis* arm regeneration.

Test growth in Paleozoic echinoids: A review and new morphological data from the Upper Devonian of Germany

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While the test of crown-group echinoids is always composed of biserial ambulacra and interambulacra, many stem-lineage echinoids had more complex, often multiseriate plate arrangements. Earlier research has identified two major modes of test growth in echinoids: (1) addition of new plates at the margin of the apical disk, and (2) growth of existing plates by accretion of stereom. In crown-group echinoids, plate accretion is the dominant mechanism of skeletal growth. In more plesiomorphic Paleozoic forms, the test was highly flexible and composed of thin, imbricating plates. In these groups, there was little or no accretionary growth of plates and size increase of the corona was accomplished primarily by insertion of new, undifferentiated plates that were subsequently shifted to various positions in a complex pattern resulting in multiseriate plate arrangements. These forms always lack a differentiated peristomial membrane and the mouth opening was instead surrounded by the first-formed (coronal) ambulacral plates which were flexible enough to compensate for vertical movement of the lantern. Two lineages, the palaechinids and the archaeocidarids (which would later give rise to the echinoid crown group), convergently developed stronger and more regular, isotropic plate growth along with decreased plate imbrication. Development of more rigid tests also resulted in resorption of the first-formed plates around the mouth and acquisition of a “true”, more flexible peristomial membrane in both lineages. The acquirement of strong accretionary growth in the archaeocidarid lineage is of particular evolutionary importance because it enabled the various modifications to overall test morphology that would eventually lead to the establishment of the crown-group body plan.

Newly described echinoid fossils from the Famennian (Upper Devonian) of Velbert near Düsseldorf, Germany, provide new insights into the test growth of archaeocidarids and hyattechinids. A new archaeocidarid shows the earliest known evidence of strong accretionary growth and stereom remodelling of interambulacral plates including outward migration of scrobicular tubercles. While these plates are very similar to those of later archaeocidarids such as *Archaeocidaris*, the construction of the interambulacra is unique: there are two continuous and two discontinuous columns of large interambulacral plates with large primary tubercles and an interradial zone of much smaller plates that show no evidence of accretionary growth. This mixture of plesiomorphic and derived expressions of plate growth could be seen either as an intermediary evolutionary step or as a specialized body plan, although the functional use of confinement of plate growth to only some columns remains unclear.

The new fossils also include many well-preserved oral surfaces of a new species of *Hyattechinus* representing a growth series. There is clear evidence that the specialization and enlargement of adoral ambulacral plates typical for the hyattechinid-proterocidarid lineage was accomplished by modification and growth of adoral plates during ontogeny rather than by early specification of test plating as in irregular echinoids. This growth was confined to a small growth zone just below the ambitus and apparently terminated later in ontogeny when the maximum number of enlarged ambulacral plates was reached. The fossils further show that growth patterns of the ambulacra and interambulacra were very tightly linked. This new data shows that the hyattechinid-proterocidarid lineage represents a third case of specialized test growth derived from the plesiomorphic condition.

Local adaptation to temperature under high levels of gene flow in *Diadema africanum*, a key herbivore in the Canary Islands

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In this study, we analyse the sea urchin, *Diadema africanum*, a key herbivore in the rocky reef systems of the subtropical northeastern Atlantic area. This species is currently expanding north, associated with recent climate-driven changes in ocean conditions. Despite the increase in the abundance of this species in the Canary Islands, which led to the formation of barren grounds since the late 80s through its grazing activity, during the last two decades, mass mortality events across populations of several islands of the Canary Archipelago likely associated the propagation of pathogens, have been recorded. In order to understand the potential effect of these mass mortality events and the seawater temperature on the genomic architecture of this species were performed a study with the objectives of: a) analysing the populations' genomic structure of *D. africanum* in the Canary Islands to identify patterns of connectivity and local adaptation, and b) determining the effect of population decreasing on the genomic diversity by comparing affected and not-affected populations by mass mortality events. To do so, we generated double digestion Restricted-Associated DNA sequencing data for 179 individuals from thirteen localities from El Hierro, Tenerife, and Lanzarote. We obtained 9,109 Single Nucleotide Polymorphisms (SNPs), from which 405 SNPs were identified as candidate loci (genes) under selection to temperature. Our study demonstrated that the species passed through recent demographic expansions and holds low levels of diversity and absence of population structure when all genomics markers are considered, although a sub-structure was evidenced due to local adaptation to temperature. Recent divergence of the species from an ancestor, followed by a strong founder effect, and the current process of demographic expansion could explain the genomic features observed. Recent mass mortality events seem to have had a minimum impact on the populations' diversity. The high connectivity among islands has led to a homogenisation of populations and the rapid recovery of the decimated populations.

What drives the patchy distribution of tropical sea cucumbers? A multispecific monitoring study

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Three species of sea cucumbers, *Holothuria atra*, *Holothuria leucospilota* and *Stichopus chloronotus*, are patchily distributed within coral reefs of Reunion Island. They exhibit high density ($> 1 \text{ ind.m}^2$). Factors involved in the distribution and spatio-temporal dynamics of these populations are not well understood yet. The aim of this study is to identify the key factors which drive the dynamics of sea cucumbers populations of Reunion Island. Sea cucumber populations and sedimentary factors (substrates composition, total organic matter, fine particles, chlorophyll *a*, $\Delta^{13}\text{C}$ and $\Delta^{15}\text{N}$) were monitored along a back-reef and shore-to-ocean gradient during four consecutive seasons. Feeding behaviour was assessed by measure of motility and excretion rate. Multiseasonal monitoring revealed that the three species have their own dynamics, with an increase of density for *H. leucospilota*, a stability observed for *H. atra*, but a decrease for *S. chloronotus*, since 1990s. Meanwhile, the use of asexual reproduction has ceased for *H. atra* and *H. leucospilota*, and some signs of decline for *S. chloronotus* were observed. *Stichopus chloronotus* seems specialist while the two other generalists. Sedimentary factors with signs of anthropogenic disturbances (high organic matter, chlorophyll *a* and $\Delta^{13}\text{C}$) was related to *H. atra* distribution, while seagrasses variable was correlated with *H. leucospilota*. Conspecific attraction may drive the high-density patchy distribution of these two species. Finally, no sedimentary factor was correlated with *S. chloronotus*. The drastic diminution of the populations of *S. chloronotus* could be linked to unstudied factors such as illegal harvesting, diseases, predation or climate change. Further studies should focus on other environmental factors in other reef compartments to fully explain to patchy distribution of sea cucumbers at Reunion Island.

Genomic and single cell insights into the metamorphosis of the crinoid *Antedon mediterranea*

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Many marine animals have the striking ability to generate different body plans out of the same genome during their life cycle: the larva and the adult. Planktonic larval stages allow animals to disperse before metamorphosing into usually benthic adult forms. Larval stages are widely distributed across animal phyla (from sponges to molluscs) but one of the most distinctive larvae is that of echinoderms. In this phylum of marine organisms, larval metamorphosis proceeds through a complete reorganisation of the bilateral larval body to give rise to a five-fold symmetrical adult body. This dramatic change makes echinoderms an essential model to study how gene expression can create two different bodies and body axes from the information encoded in the same genome.

While larval life can last several weeks in some echinoderms such as sea stars, crinoid larvae only take a few days and will settle easily on glass or plastic substrate making them a great model to study metamorphosis. To help unravel the molecular events involved in this process, we generated a chromosome-scale genome for the crinoid *A. mediterranea* and applied single-cell transcriptomics to successive stages from larva to juvenile. These datasets allow us to monitor gene expression, changes in cell populations and cell molecular signature through settlement and body plan shift. Moreover, we performed a comparison of cell types of the short-lived larva of crinoid with that of other echinoderms and larvae across metazoan to shed light on the evolutionary origins of larval stages.

Cell commitment prevents larval regeneration in the crinoid *Antedon mediterranea*

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Regeneration is a widespread phenomenon along the phylogenetic tree, however few animal groups display remarkable regenerative abilities as Echinoderms do. Indeed regeneration is consistently present in all the extant classes, both in adults and larval stages. While adult regeneration has been deeply studied, comparatively less studies focused on larval regeneration. Nonetheless the latter is well documented for all echinoderm classes, except for Crinoidea. Hence, the aim of this work was to assess if the larval (doliolaria) and post-metamorphic stages of the crinoid *Antedon mediterranea* are able to regenerate, as the adult form perfectly does at the level of almost any tissue/organ. In normal conditions, free-swimming *A. mediterranea* doliolaria settle and metamorphose in a temporary sessile and stalked stage (pentacrinoid) which is provided with an apical calyx; the latter will eventually develop the ten arms (advanced pentacrinoid) and then detach originating the free-swimming adult individual. Adult specimens of *A. mediterranea* were collected at Le Grazie (Ligurian Sea, Italy). After hatching, doliolaria larvae were transversally bisected and the obtained anterior and posterior halves were monitored for 2-3 weeks. For each fragment type we defined different post-amputation “developmental” stages which were characterized by light (confocal) and electron microscopy (SEM, TEM). Results showed that none of the surviving halves was able to completely regenerate. Rather, after a wound-healing phase each half continued its “developmental program” so that the obtained post-metamorphic stage lacked structures deriving from the missing half: anterior fragments originated a stalk without a calyx whereas the posterior halves produced a calyx without a stalk. Noteworthy, this inability to regenerate is progressively rescued upon the transition from pentacrinoid to free-swimming juvenile, as advanced pentacrinoids (close to the stalk detachment event) show albeit minimal regenerative ability while freshly “detached” juveniles are perfectly able to regenerate their tissues/structures (even more than adults).

Overall, these data suggest that: doliolaria cells are strictly committed to their original fate; cellular plasticity/dedifferentiation is temporary blocked and/or “stem cells” are missing or in a “stand-by” state. To answer this question the presence and expression of stemness markers (e.g. c-myc, pou, piwi) is currently under investigation.

Considering the basal phylogenetic position of Crinoidea these results are particularly significant to better understand the evolutionary trajectories which led to gain or loss of (larval) regenerative abilities among echinoderms and metazoans.

Comparative role of biofilm-covered microplastic and sediment particles as vectors of ^{14}C -PCB-153 to *Paracentrotus lividus*

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Microplastics (MPs) are contaminants of concern *per se*, but also based on their ability to concentrate environmental contaminants (such as polychlorinated biphenyls; PCBs), acting as vectors for the transfer of toxic chemicals into marine organisms. However, the relevance of the role of MPs as vectors of contaminants adsorbed onto their surfaces (i.e., co-contaminant) is currently a matter of debate with the argument that MPs would play a minor role as vectors compared to naturally occurring particles (e.g. sediments) because of their relative abundance in the environment. The present study compares the role of biofilm-covered microplastics (500-600 μm ; negatively buoyant polyethylene beads) and sediment particles as vectors of ^{14}C -PCB-153 into adult specimens of the sea urchin *Paracentrotus lividus*. Results showed that after 14 days of exposure, the transfer of ^{14}C -PCB-153 from biofilm-covered particles to sea urchin tissues occurred to a similar extent for both types of particles, suggesting that MPs located on the seafloor may act as vectors of PCB-153 in a similar way than other natural particles such as sediments.

Hidden diversity in Mesozoic fossil pluteus larvae (Ophiuroidea and Echinoidea)

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Echinoderm larvae are common and ecologically important members of the marine plankton in all oceans today. It has been recognized that all modern echinoderm representatives, with the exception of Crinoidea, have feeding (planktotrophic) larvae, whereas benthic, free-living feeding larvae are missing. Lecithotrophic (non-feeding) larvae with benthic or planktonic habits have been reported in all modern echinoderms. All of these types of echinoderm larvae have unique morphologies, and, with the exception of the bipinnaria larvae of Asteroidea, a calcitic skeleton. In contrast to modern representatives, the fossil record of echinoderm larvae is essentially non-existent and biased due to missing studies and lack of awareness of such small and fragile fossils. However, modified laboratory techniques and detailed study of sieve residues below 0.1 millimetre have the promise to provide microscopic larval skeletons as shown recently by the first author (Reich, 2021).

Our study reports a few hundreds of ophiopluteus and echinopluteus skeletons from Early Jurassic strata of Germany (Lower Saxony, Saxony-Anhalt), Austria (Salzburg), and France (Ardennes), as well as Late Triassic sediments of Italy (Dolomites).

Most of the specimens found (>95%) belong to ophiuroids, only a few correspond well to echinoid larval skeletons. All plutei skeletons found are of compound type including unique characteristics, revealing evolutionary changes between Mesozoic and Cenozoic forms. Our new findings provide a window into the poorly known fossil record of echinoderm larvae, showing a hidden diversity of such fragile microfossils and the possibility of direct geological recording.

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Red Alert: Regional scale mass mortality of diadematoids in the Northern Red Sea

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Echinoderms are characterized by boom-and-bust fluctuations, where extreme and rapid population declines may be regarded as mass mortality events (MME). Major die-offs of echinoid populations may lead to large-scale algal outbreaks as the key herbivores are removed. On coral reefs, algae proliferation may lead to coral degradation, as the fast growth rate of algae outcompetes that of corals.

Here, we report for the first time, an extensive, regional-scale MME of two Diadematidae species in the Gulf of Aqaba (GoA) and the Red Sea, *Diadema setosum* (Leske, 1778) and *Echinothrix calamaris* (Pallas, 1774). Starting January 2023, we observed a significant decline in *D. setosum* and *E. calamaris* populations in Eilat (Israel) and Aqaba (Jordan), reaching up to 99% decline in some sites. Surveys along the Egyptian coasts of the GoA showed a significant decline of 100% in *D. setosum* populations in some locations between February and May, 2023. Additional mortalities were observed near the coasts of Hurghada (Egypt), indicating the MME is expanding beyond the GoA reaching more Southern parts of the Red Sea. Mass mortalities of *D. setosum* and *E. calamaris* were also observed in land-based open seawater system facilities, suggesting a water-born agent as the mortality source. Moreover, symptoms characterizing dying individuals were highly similar to those documented in the Caribbean *D. antillarum* 2022 MME, caused by a water-born ciliate-like pathogen (Hewson et al., 2023). These together imply the current Red Sea MME is potentially caused by a water-born pathogen.

We raise a red flag and warn against a potential quick and uncontrolled spread of this MME. The absence of *D. setosum* and *E. calamaris* as a major grazing force in the GoA may potentially lead to a severe, regional-scale phase-shift, from a coral-dominated reef to an algae-dominated system, threatening the unique and diverse coral communities of the Red Sea.

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The developmental stages of the sea urchin *Arbacia lixula* associated with photosymbionts that influence host survival

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The larvae of marine invertebrates (*e.g.*, sea urchins) spend weeks to month—and sometimes years—in the water column. During this extensive dispersal period they are challenged from the energetic point of view because the presence of food in the open seas is irregular and scarce. As is common for sea urchins, *Arbacia lixula* provides its offspring with a very little amount of nutrients. Nevertheless, this species has a trans-Atlantic distribution that ranges from the Mediterranean Sea to the coast of Brazil. The mechanism(s) that allow larvae to endure the nutrient-limited conditions required to travel such distances remains unknown. Symbiosis between marine invertebrates and their associated microbiome has been documented in many cases and it is widely thought that these animals obtain a nutritional benefit. Here, we characterized the developmental microbiome of *A. lixula*. We show that photosynthetic microbes are present in each developmental stage (Fig. 1.A). We then tested whether these photosynthetic microbes influence survival during development. We found that survival was significantly lower for larvae in dark (*i.e.*, without functional photosymbionts) than their siblings in light (Fig. 1.B). This result was consistent with (5µm filtered seawater) and without (0.22µm filtered seawater) microbes in the environment. This further supports that these photosymbionts are present in the eggs (*i.e.*, are vertically/maternally transmitted). Taken together, our data supports the idea that the early stages of *A. lixula* establish a symbiotic association with photosynthetic microbes that are provided by their parents and influences their survival.

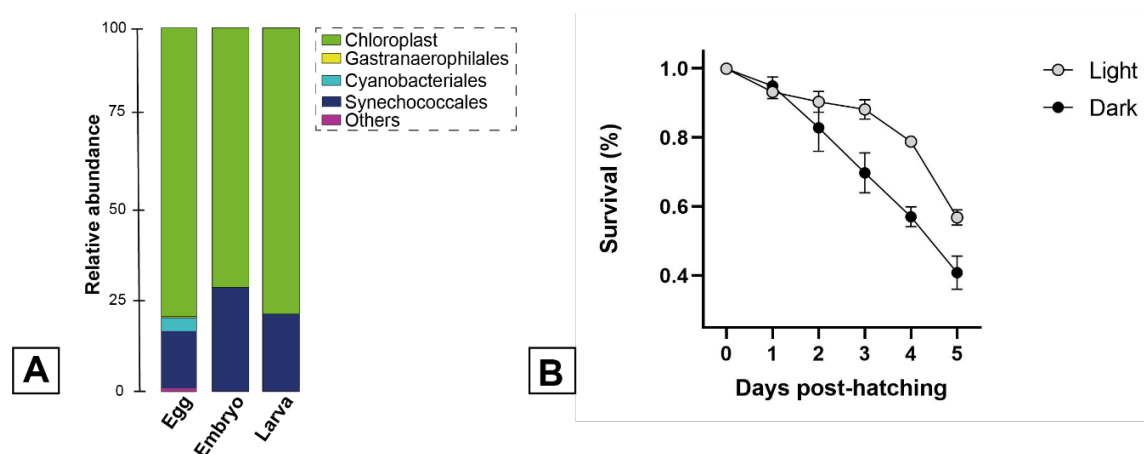


Fig. 1. **A.** Relative abundance of the photosynthetic microbes of the early stages of *A. lixula*. **B.** Differences in survival between treatments (light cultures vs dark cultures).

Skeletal elements controlled soft-tissue preservation in echinoderms from the Early Ordovician Fezouata Biota

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Exceptional fossils preserve non-biomineralized tissues in the geological record and provide crucial information on the evolution of life on Earth. Exceptionally preserved fossils are rarely discovered complete, challenging their morphological description and their palaeontological interpretation. Although decay experiments reconstructing degradation sequences in modern animals are necessary to better understand taphonomic processes involved in exceptional preservation, their applicability to some enigmatic and/or extinct fossil taxa is limited. Here, based on a representative sample of 423 specimens collected from a single stratigraphic level from the Early Ordovician Fezouata Biota, we reconstruct the degradation sequence of both skeletal remains and soft tissues of stylophorans, an extinct clade of echinoderms. The rare preservation of the water vascular system can be explained by the rapid post-mortem opening of cover plates resulting from the fast decay of associated muscles and the action of ligaments. In contrast, the proximal aulacophore and associated stylocone formed a particularly decay-resistant closed module, thus favouring the preferential preservation of included soft parts (foregut). The non-random location and frequency of pyritized intra-skeletal structures strongly suggest that skeletal elements dictated the preservation of underlying soft parts. As such, taphonomic investigations should not only focus on the environment surrounding a decaying animal, but also on the different micro-environments created within a particular carcass.

Screening for sea urchin adhesive proteins to develop new biomimetic adhesives for biotechnological and biomedical applications

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Bioadhesion is vital for sea urchins, since it is through the production of adhesive secretions that these marine invertebrates attach, move, feed, and defend themselves. Understanding these processes and what defines the uniqueness of bioadhesives, is important from a biological point of view, but has also a major biotechnological impact, considering the high demand for biomimetic adhesives. Indeed, wet-effective, biocompatible and ecological adhesives are vastly needed in medical and biotechnological applications, as surgical adhesives or promoters of cellular adhesion for *in-vitro* cultures and 3D organ printing.

Most marketed adhesives perform badly in wet conditions, precluding certain applications. Synthetic adhesives (e.g. cyanoacrylate) have outstanding adhesion, but are cytotoxic, carcinogenic and pollutant. On the other hand, biological adhesives (e.g. fibrin glue), are biocompatible and biodegradable, but have low adhesion (Balkenende *et al.*, 2019).

Sea-urchins bioadhesives have the potential to overcome these limitations since they have the strongest adhesives among known non-permanent adhesives (up to 0.5 MPa) (Santos & Flammang, 2008) and have evolved in the presence of seawater that has high dielectric and ionic strength like physiological fluids (Balkenende *et al.*, 2019).

Sea urchin bioadhesives are made up of proteins and sugars, and through a combination of different techniques progress has been made towards the identification of the key molecular components that are worth mimicking. An integrative analysis of the transcriptome and proteome of *Paracentrotus lividus* tube feet and its adhesive secretion, conjugated with gene expression analysis by *in situ* hybridization, pinpointed six adhesion related proteins (Pjeta *et al.*, 2020) which share a significant homology with sea star orthologue adhesion-related genes, indicating conservation of some functional domains among non-permanent adhesives (Davey *et al.*, 2021). A complementary analysis using lectin-histochemistry, -pull downs and -blots applied to the tube feet and adhesive secretions from four sea urchin species belonging to different taxa and habitats (*P. lividus*, *Sphaerechinus granularis*, *Diadema africanum* and *Arbacia lixula*) demonstrated that there is interspecific variability of the glycans involved in sea urchin adhesion. However, there seems to be more conservation among taxonomically closer species, such as *P. lividus* and *S. granularis*, which have high molecular weight glycoproteins bearing chitobiose (glucosamine units linked by β -1,4 bonds) in their tube foot adhesive epidermis and in their adhesive footprints (Gaspar *et al.*, 2021). In *P. lividus*, it was demonstrated that at least five of the previously identified adhesion related proteins are chitobiose-bearing glycoproteins (Ventura *et al.*, 2023).

As a proof of concept, one adhesion related protein, *P. lividus* Nectin, which contains six repeated discoidin-domains, is being produced recombinantly in bacteria. To simplify the production of biomimetic adhesives, the adhesive performance of the full length-protein will be compared with designed truncated versions bearing one to a few domains, to better understand the relevance of these domains to the sought adhesive function.

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Bio-sourced hybrid pigments inspired by colored sea urchin spines

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Because organic dyes generally fade under sunlight, organic-inorganic hybrid pigments have been developed to improve their stability. For example, silica matrices and clays are used to encapsulate and thus protect the organic dyes. Such hybrid pigments synthesized via sol-gel chemistry or solid-state grinding allow producing either mass-colored amorphous materials with high photo-stability or surface-colored crystalline pigments with poor photo-stability, respectively. Interestingly, adult sea urchins are able to produce mass-colored crystalline biominerals through the encapsulation within their mineralized spines of a family of secondary metabolites: the polyhydroxylated-naphthoquinone (PHNQ) pigments (Anderson *et al.*, 1969), whose colors resist intensive bleaching. In particular, spinochrome A, which is the most abundant PHNQ found in *Paracentrotus lividus* species from Atlantic Ocean, is responsible for the intense purple and green colors of their spines. Although little is known about mineral pigmentation, it likely takes place during calcite crystal growth (Towe, 1990) that occurs, in sea urchin spines, through the initial deposition of amorphous calcium carbonate (ACC) (Politi *et al.*, 2004).

Therefore, inspired by the formation of mass-colored sea urchin spines, we produced calcitic biohybrid pigments through the precipitation of ACC in the presence of biogenic PHNQs (spinochrome A, B and E). Although all pigments are initially reddish, we show that spinochrome A leads to intense purple calcite whereas spinochrome B and E lead to slightly yellowish calcite. These color changes, quantified by UV-visible measurements of both the titrant during CaCO₃ synthesis and the resulting hybrid pigments are likely due to pH variation during ACC precipitation and crystallization. SEM observations and HR-XRD measurements reveal that the morphology and the atomic structure of the hybrid pigments is the less affect by spinochrome A than spinochrome E and C. This suggests that the preferential incorporation of spinochrome A in *P. lividus* spines may be due to its smaller effect on the crystalline structure and morphology and its ability to yet provide intense color to the biominerals, suggested to act as UV-protectant (Brasseur *et al.*, 2017). In addition, we show that the encapsulation of PHNQs within CaCO₃ allow for color stability up to 400°C. Finally, the biohybrid pigments were subjected to textile finishing to test their ability to be used as chemical and photo-stable dyes for sustainable biocoloring.

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The taxonomic status of *Aporocidaris incerta* (Koehler, 1902): Such a long enigma for a common species

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Koehler (1902) described a new species, *Aporocidaris (Porocidaris) incerta* (Koehler, 1902), based on six small specimens dredged in the Bellingshausen Sea (Antarctica) during the Belgica expedition (1897-1899). However, considering the small size of the poorly preserved specimens, he recognized that the taxonomic assignment of specimens remained uncertain, thereof the epithet "*incerta*" (uncertain in Latin). The new species was subsequently transferred to the genus *Aporocidaris* Agassiz & Clark, 1907 by Mortensen (1928), who believed it closely related to *Aporocidaris (Porocidaris) milleri* (Agassiz, 1898) based on primary spines and tubercles morphology. Until new material is collected, he considered the species assignment to *Aporocidaris* was the most probable, a position also followed by David *et al.* (2005). Surprisingly, the description of specimens clearly differs from *Aporocidaris* by several diagnostic characters as later noticed by Lockhart (2006), who proposed its assignment to a new genus, *Miracidaris* Lockhart, 2006, a nomen nudum (Kroh & Mooi 2023) for which *Miracidaris incerta* was designated as type species. The fact that the species has never been collected since its discovery, despite the numerous cruises undertaken in this part of the Southern Ocean over the last century (David *et al.*, 2005) remains an enigma, unless taxonomic confusion and the lack of knowledge of Antarctic marine life made us miss the obvious.

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Treatise on Invertebrate Paleontology, Part U, Echinodermata 3, Asterozoa - Echinozoa: Last updates and perspectives for the future

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Echinoderm taxonomy and classification presented in the current version of the *Treatise on Invertebrate Paleontology* (published in 1966) have largely been revised over the last decades. Advances are due to the amazing development of molecular methods and also to many novel findings, both extant and fossil, and their in-depth examination using new morphological analyses. After a promising first *Treatise* workshop (S-T-U volumes) organized during the 16th IEC in Nagoya (2018), a second meeting was held on the occasion of the 10th European Conference on Echinoderms at the Borissiak Paleontological Institute RAS, in Moscow, in 2019.

Main points addressed were the presentation of most recent scientific advances (mostly classification), the list of potential contributors, and main outlines of chapters including introduction, general features of each class, and systematics sections. A review of the state of progress indicated that all chapters of volume U were starting, with some significant advances for some of them. Volume S will also include a section common to all volumes presenting the general features of all Echinodermata.

An important point was also addressed during discussions concerning the writing of a general glossary common to all volumes, as well as the outlines of individual chapter glossaries. Illustrations were another important concern. To make the revised version of the *Treatise* more attractive and above all, useful to a wider audience (not only a handful of experts), it was stressed that clear illustrations of well-preserved, real specimens, including color plates, should be provided and preferred over type specimens (generic types) when badly preserved or broken. Several views and combined LM/SEM/microCT images are very welcome when possible.

After the pandemic, and four years later, the 11th European Conference on Echinoderms will be the opportunity for the community to meet again and discuss in person, during a dedicated *Treatise* session most recent advances and updates on the taxonomy and classification of post-Paleozoic echinoderms. A round-table discussion will also help identify the next steps in the revision of part U of the *Treatise*.

Global trends of echinoid mass mortalities – insights from *Echinocardium* from the Eastern Mediterranean Sea

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Mass mortality events (MMEs) have been occurring since the dawn of time. However, in contrast to terrestrial events, most marine MMEs remain undetected due to the inaccessibility of many marine environments. One of the most notorious marine MMEs is the population collapse of *Diadema antillarum* in the Caribbean during the early '80s which triggered a catastrophic phase shift in local benthic communities – from which the region never fully recovered.

Here we present a systematic review of global echinoid MMEs including scientific literature and grey literature dating back to 1888. We then provide the first reports of echinoid MMEs in the Eastern Mediterranean, compiling *in situ* observations, molecular, morphological, and environmental data, to illustrate a decade-long history of ongoing localized MMEs in the region. We formulate five potential mechanisms driving echinoid MMEs and calculate their relative abundance: 1) catastrophic events (22%), 2) harmful algal blooms (12%), 3) pathogenic activity (25%), 4) temperature and tides (33%) and 5) human activity (8%). Along the Israeli Mediterranean coastline, four MMEs of irregular echinoids of the genus *Echinocardium* are reported between 2011 and 2020. Using the Israeli MMEs as a case study to scrutinize the abovementioned mechanisms, we analysed skeletal remains collected during one of the MMEs, as well as meteorological and remote-sensed environmental data (Chlorophyll *a*, sea surface temperatures, and precipitation) collected during the weeks prior to the MMEs. While none of the environmental parameters alone could be identified as the sole contributor of the Israeli MMEs, the mortality events were always recorded near the outlet of polluted rivers or adjacent to major power stations – suggesting pollution from human activity as the main source of these mortalities. Observations from the warm Eastern Mediterranean may predict the future of western more parts of the Mediterranean as global warming accelerates and human activity intensifies.

First record of the echinid *Echinus melo* Lamarck, 1816 on the west coast of Algeria (Sidi-Madjdoub, Mostaganem)

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Echinoids are an important group of echinoderms that are represented by several genera, among them the genus *Echinus*. This genus is characterized by a more or less globular bulging test, large in size in adult forms compared to the other genera of echinoids. In the Mediterranean, the genus *Echinus* is represented by only one species, *Echinus melo* (Lamarck, 1816), which is very rarely found in the Mediterranean Sea and is often confused with *Gracilechinus acutus* (Lamarck, 1816).

An individual of *Echinus melo* was found in a batch collected as by-catch from artisanal fisheries in April 2022 in the Sidi-Medjdoub region (Mostaganem, Algeria) at a depth of 74 m. The detailed study of morphological characters allowed us to identify it and to report it for the first time on the west coast of Algeria, which is considered as one of the hotspots of biodiversity in Algeria.

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Novel 3D quantification of plate and needle/prism dimensions in teeth of the Odontophora (Echinoidea: Camarodonta)

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Sea urchin teeth form in two stages. The first stage of biomineral formation consists of arrays of curving plates of different types and of rod-like structures termed needles when they have smaller diameters and prisms when their diameters increase. Then, second stage Mg-enriched calcite cements the first stage plates and needle/prisms together. This paper reports novel high-resolution synchrotron microComputed Tomography (microCT) imaging of teeth from multiple species of superfamily Odontophora Kroh & Smith, 2010. The reconstructed volume elements (voxels) are smaller than 1.3 μm , and this permits true 3D quantification of plate thicknesses and needle/prism diameters in Odontophora teeth. Mean values and their standard deviations are reported although the main focus is on the spatial variation of thickness within single carinar process plates and of diameter along selected prisms' lengths. Measurements for species within the three families of the Odontophora are compared as are the functional consequences of variations. Finally, prospects for extending the study to higher resolutions are discussed.

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Genital plates and associated structures in Ophiuroidea – morphology and phylogenetic implications

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Recent progress in ophiuroid morphology has greatly improved the understanding of various skeletal parts (e.g., lateral arm plates, oral elements). This has led to a revised phylogeny and classification with good congruence between molecular and morphological data. The morphological dataset is still rather small though and additional characters are needed to expand the number of taxa for a better resolution of the tree. Genital plates have received comparatively little attention so far. They are found inside the disc, two often elongated ossicles positioned laterally at the arm vertebrae, with the bursal slit opening between them. The adradial genital plate (adGP) articulates with the radial shield from below, the abradial genital (abGP) plate articulates with the adradial one. Previous studies examined the articular structures of adGP and radial shield, described as condyles and grooves, but the overall shape of these highly non-symmetric ossicles was mostly neglected. Here, I examined about 60 species from 28 families, by SEM and micro-CT. The overall shape of genital plates and inner aspects of radial shields, as well as the articular structures, were assessed and described. A third genital plate was (re-) discovered, previously only mentioned by few authors and never studied in morphological detail. Since this plate sits at the oral shield, this and the inner side of the madreporite were also included. The third genital plate was found absent in Euryophiurida, but present in Ophintegrida. It showed a surprising morphological diversity and appears to hold a phylogenetic signal. The shapes of the adGP were here described as bar-like, cleaver-, wrench- or cup-shaped, multi-layered, stout or inflated. The abGP was classified as flat curved scale, sabre- or sickle-shaped, twisted, triangular to pear-shaped, blade-like, scoop- or cup-shaped. The previous character matrix was updated with new characters, incorporating also data from recent advancements in oral structures, and a Bayesian analysis was performed. The resulting tree recovers most of the same clades as the latest molecular tree, with some differences.

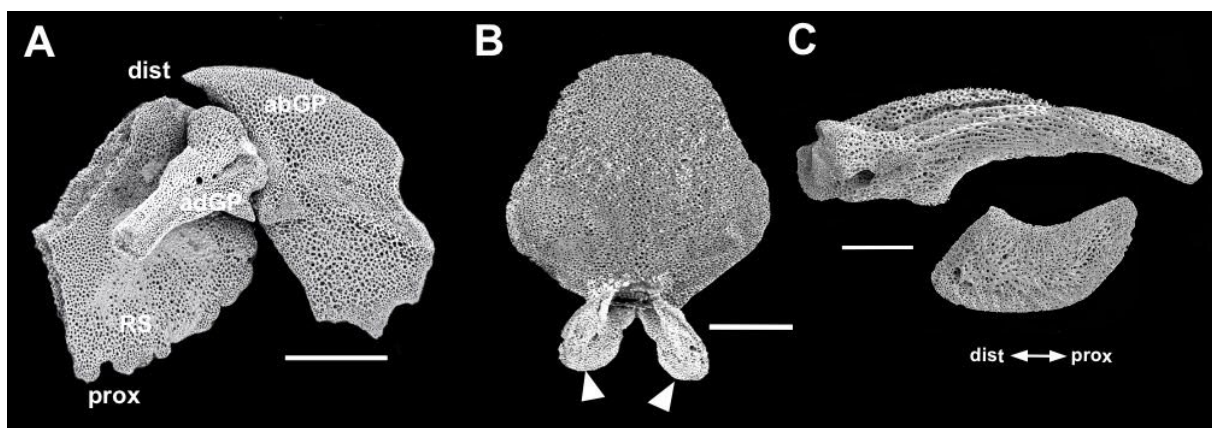


Fig. 1. A, *Ophiura*, bar-like inflated adGp, cup-shaped abGP, articulated with radial shield. B, *Ophiocoma*, oral shield inner aspect with attached genital plates (arrowheads). C, *Ophiacantha*, bar-like adGP and flat curved scale abGP. Scale bars 0.5 mm.

A revised classification for Edrioasteroidea

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Edrioasteroids are a medium-sized group of Paleozoic echinoderms that persisted minimally between the Middle Cambrian through Late Permian. The peristomial border consisting of some combination of oral and oral frame plates and ambulacra bearing a food groove covered by ambulacral cover plates, suggest that they have close affinities with blastozoans rather than echinozoans as they have traditionally been assigned. A phylogenetic classification has recently been proposed in *Phylonyms: a companion to the Phylocode*, providing formal definitions to existing clades, as well as adding a few new clade names. No formal definition for Edrioasteroidea was given as it is unclear whether isorophids and edrioasterids are sister taxa although it seems likely. Earlier taxa, such as *Kailidiscus*, *Stromatocystites*, *Cambraster* and associated taxa, lie as stem lineages outside this more restricted group. Edrioasterida is defined as the node-based clade descended from the last common ancestor of edrioasterids (*Edrioaster bigsbyi*), cyathocystids (*Cyathotheca suecia*), edrioblastoids (*Lampteroblastus hintzei*), and rhenopyrgids (*Rhenopyrgus piojoensis*). This clade includes taxa with biserial floor plates bearing podial pores and broadly exposed abradial floor plates. This clade has a known range of Late Cambrian to middle Devonian. Isorophida is defined as the node-based clade descended from the last common ancestor of Pyrgocystidae (*Streptaster vorticellatus* and *Argodiscus espilezorum*), Carneyellidae (*Carneyella pilea*) and Isorophinae (*Agelacrinites hamiltonensis*). Isorophids share uniserial adradial floor plates, hydropore and gonopore united into a shared hydro-gonopore along ambulacrum C, and cover plates with intrathecal extensions plesiomorphically. This clade has a known range of Late Cambrian through Late Permian. Isorophina is defined as the node-based clade descended from the last common ancestor of Isorophidae (*Isorophus cincinnatiensis*) and Agelacrinitidae (*Agelacrinites hamiltonensis* and *Hypsioclavus huntsvillensis*). The clade Isorophina includes forms with secondary ambulacral cover plates, valvular anal structure, and cover plates with intrambulacral extensions. It has a known range of Early Ordovician through Late Permian. Agelacrinitidae is defined as the node-based clade descended from the last common ancestor of agelacrinitids (*Agelacrinites hamiltonensis*) Lepidodiscina (*Lepidodiscus squamosus*) and Discocystina (*Hypsioclavus huntsvillensis*). Agelacrinitids are diagnosed by a lack of differentiation of the primary peristomial cover plates, offset of the hydro-gonopore rise from the peristome, loss of intrathecal extensions on the ambulacral cover plates and cover plates formed into cycles. This clade has a known range of Middle Silurian through Late Permian. Lepidodiscina is defined as the node-based clade descended from the last common ancestor of *Lepidodiscus squamosus*, *Ulrichidiscus pulaskiensis* and Discocystinae (*Hypsioclavus huntsvillensis*). The clade Lepidodiscina is diagnosed by three or more sets of shared cover plates, floor plates with lateral extensions, a complex hydro-gonopore, and a great expansion of the pedunculate zone. It has a known range of Middle Devonian through Late Pennsylvanian. Discocystinae is defined as the node-based clade descended from the last common ancestor of *Discocystis kaskaskiensis*, *Clavidiscus laudoni*, *Hypsioclavus huntsvillensis* and *Giganticlavus bennisoni*. It is characterized by adjacent interambulacral plating, plating of the pedunculate zone organized into columns, thick floor plates and a peripheral rim much smaller than the thecal diameter. This clade has a known range of Late Devonian through Late Permian.

A new understanding of North American, Late Paleozoic brittle star faunas based on microfossils

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It is generally believed that ophiuroids are rare components of Late Paleozoic faunas and to date, few specimens have been described. This has led to the inference that a diverse Early and Middle Paleozoic ophiuroid fauna was decimated by the Late Devonian biodiversity crisis, barely surviving into the Late Paleozoic. Notionally, the end Permian Mass Extinction eliminated the remaining archaic taxa and the modern brittle star fauna diversified in the Mesozoic. New data from Late Paleozoic ophiuroid microfossils from North America show this to be untrue. Middle to late Mississippian faunas are richly diverse despite the rarity of preserved articulated skeletons with faunas having between 8 and 15 species. Early – late Viséan faunas are dominated by protasterids, furcasterids and *Onychaster*. Present in lower numbers are cheiroptasterids, stenuroids and modern clade ophiuroids. These faunal compositions and abundances are consistent with Middle Paleozoic faunas and show that there is little change following the Devonian biodiversity crisis. This pattern continues into the late Viséan where *Cholaster* is first sampled. In the Pennsylvanian of North America, Serpukhovian faunas have yet to be sampled as microfossils. By the Moscovian, a major faunal turnover has occurred, and faunas are somewhat lower in diversity typically with 5-11 species. Modern-type brittle stars, including up to three genera, compose between 78-99 percent of brittle star microfossils in some late Pennsylvanian - Early Permian samples. Furthermore, these faunas are at times highly abundant with up to 640 lateral arm plates per gram of fossil residues in the 250 – 500-micron size fraction. Archaic taxa including protasterids, furcasterids, cheiroptasterids, and stenuroids persist and are at times common, but never again dominate samples. These faunas also show consistent compositional patterns among different samples from the same rock units.

The turnover in ophiuroid faunas mirrors turnovers in crinoid faunas as Carboniferous glaciation begins in North America. At this time, North American paleoenvironments change from warm tropical carbonate banks and ramps to cooler water environments dominated by siliciclastic sediments. It is thought that this environmental transition led to the rise of the modern brittle star fauna rather than the recovery from the Permian Mass extinction. It is unknown when the archaic brittle star clades went extinct, but the major lineages minimally extend into the Early Permian.

Origin and evolution of echinozoan body plans

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Echinozoans, the group of animals including echinoids (sea urchins) and holothurians (sea cucumbers) is a diverse clade occupying a range of ecologies and habitats in today's oceans. Modern echinozoans exhibit a disparate range of body plans, from the soft-bodied vermiform holothurians to the multi-plated globular echinoids. Echinozoans are first known from the Ordovician period, and despite their well-characterized body plans in modern ecosystems, little is known of the morphological characterization of their earliest representatives. To better understand this, we first carried out micro-CT scanning of various basal taxa, which clarifies the morphological transitions characterizing the early evolution of their body plans and reveals a number of new, transitional, morphologies. We then constructed a character matrix encompassing numerous Palaeozoic and non-Palaeozoic echinozoans, along with other echinoderm outgroups, to phylogenetically understand the inter-relationships of echinozoan classes, and their relationships to other eleutherozoans (including asteroids, ophiuroids, and edrioasteroids, and other Cambrian echinoderms) using morphological and molecular data. We then analyzed changes in disparity, leading from the earliest members of the Echinozoa to those of the crown group, which revealed contrasting evolutionary histories in body plan diversification amongst the echinoids and holothurians. This sheds new light on the origin of the echinozoan body plans and their evolutionary histories from their Palaeozoic origins to the modern.

Was the Triassic ophiuroid radiation triggered by the Carnian Pluvial Event?

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The Ophiuroidea have a long and complex evolutionary history dating back at least into the Ordovician. Recent advances in the understanding of ophiuroid skeletal morphology and its connection with phylogenomics have profoundly changed our view of how the group evolved during Earth history. Between the Silurian origin of the modern clade and the development of the first modern-type ophiuroid communities in the Cretaceous, the class underwent significant evolutionary change that has been difficult to disentangle mostly due to patchy fossil sampling and an insufficient understanding of extinct taxa. While the previously hypothesised drastic evolutionary bottleneck coinciding with the end-Permian mass extinction was recently refuted, it seems clear that the class underwent a major diversification during the early Mesozoic. However, neither the timing nor any potential connection with Earth history events have been substantiated.

With the latest insights on ophiuroid morphological phylogenetics at hand, we explore the Triassic fossil record of ophiuroids including many previously unpublished occurrences in order to refine the early diversification of the modern clades. While our work is still in progress, there is growing evidence that the vast majority of extant family-level clades originations during the Triassic coincide with a global climate change event called the Carnian Pluvial Event (CPE). Associated with substantial volcanism, the CPE triggered significant biological turnover, including a mass extinction but also the rise of the first scleractinian coral reefs and the first rock-forming calcareous nannoplankton. We hypothesise that these environmental changes and/or their biotic effects triggered the ophiuroid radiation during the Triassic. Interestingly, innovation rates seem to be highest in clades living in deep shelf to upper slope settings during the CPE, suggesting that a turnover in trophic structure via increased continental runoff and/or the rise of nannoplankton was among the driving factors of the ophiuroid radiation.

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Each with its own specialities, the three marine stations at Banyuls-sur-mer (Observatoire Océanologique de Banyuls-sur-Mer - OOB), Roscoff (Station Biologique de Roscoff - SBR) and Villefranche-sur-Mer (Institut de la Mer de Villefranche - IMEV), under the joint supervision of Sorbonne University (SU) and the CNRS have joined forces to form the French National Marine Biological Resource Centre, EMBRC-France. Being the entry point for the exploration of marine bio-resources in France, EMBRC-France benefits from the support of the "Investissements d'avenir" programme and the strong involvement of the Brittany, PACA and Languedoc Roussillon regions and the Mer Bretagne Atlantique and Mer Méditerranée competitiveness clusters in its governance. EMBRC-France is the French node of the European Research Infrastructure Consortium "European Marine Biological Resource Centre" (EMBRC-ERIC).

As a multi-site IR, EMBRC-France (<https://www.embrc-france.fr>) provides access to more than 20 platforms and services distributed across the three SU/CNRS marine stations.

The main objective of EMBRC-France is to serve the community of public and private researchers by supporting research projects on marine organisms and ecosystems, while promoting their sustainable exploration (biodiversity), exploitation and exploitation, and is in line with SDG14 Aquatic Life - to conserve and sustainably use the oceans, seas and marine resources for sustainable development. Its scientific fields are marine biology, marine ecology and biological oceanography. Its mission is to offer and facilitate access to marine ecosystems and their biological resources, as well as to a high-level technological environment of local technological platforms open to the academic and industrial communities, to support research projects of excellence from the entire French community. The know-how, equipment and resources are at the service of scientists from all disciplines (marine, agri-food, health, etc.).

Among studies carried out by EMBRC-France, several projects focus on increasing our knowledge of the biodiversity, using a wide variety of marine organisms, meaning optimising culture conditions, deseasonalisation of the reproduction period or cryopreservation. The model organisms studied include sea urchins (*Paracentrotus*), organisms used for characterising the molecular interrelationships between the regulation of gene expression and embryonic development (fertilisation, cell cycle, embryogenesis, metamorphosis and the appearance of pentaradiary symmetry), as their life cycle has now well mastered.

Sea star (Asteroidea) diversity in the Magellanic region (south-Chile) and their affinities within the Southern Ocean

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Sea stars are a diverse and important component of the Southern Ocean benthos. However, only scarce information is available regarding their diversity and evolution, and taxonomic revisions are required. The Magellanic region (south of Chile) remains under-sampled despite its pivotal position for species richness and distribution, being located at the crossroad of three ocean basins. In the presented work, we assessed sea star biodiversity in the Magellanic region and their faunal affinities within the Southern Ocean. An integrative approach combining morphological identification with DNA barcoding has been implemented to highlight taxonomic discrepancies such as synonymous species and unrecognised diversity. We assembled a DNA barcode library of more than 200 COI sequences to aid future genetic identifications. We identified 15 sea star species from the Magellanic region and reported the occurrence of *Cycethra frigida* for the first time in the area. The distribution of these 15 species ranged from endemic to the Magellanic Region to circumpolar, bipolar or possibly cosmopolitan. We also discussed the role of developmental mode in shaping biogeographical patterns. Relying on this trait alone is insufficient and other life history traits (e.g. physiological constraints, competition, bathymetrical range, and the possibility of passively rafting on kelp) are suggested to be at least equally important. Finally, we highlight the possible synonymy between two species pairs within the *Anasterias* and *Odontaster* genera.

This preliminary biodiversity assessment forms an important baseline for monitoring and conservation purposes, especially in the face of distribution shifts as a response to climate changes and the increased risk of invasions in the Southern Ocean.

The internal anatomy of Middle Jurassic comatulid cups (Comatulida, Articulata, Crinoidea), as revealed by X-ray microtomography, and its implications for the radiation of comatulid crinoids

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True comatulid crinoids (Comatulida, Articulata, Crinoidea) are the only crinoids commonly seen in modern shallow marine (<100m) ecosystems and first appeared during the Lower Jurassic. They were traditionally thought to have evolved slowly throughout the Jurassic, before radiating rapidly in the Lower Cretaceous, where they are first known to dominate shallow sea floor communities. More recently, X-ray microtomography (microCT) of modern and some Cretaceous fossil comatulids has suggested that internal structures of the cup, related to the circulation of celom, are phylogenetically significant. Furthermore, these phylogenetic studies suggest that evolution occurred more rapidly than is currently evidenced by the fossil record. The discovery of a new Bathonian (Middle Jurassic) lagerstätte in Wiltshire, UK, has produced over 3000 isolated cups and 300 articulated individuals of the comatulid *Andymetra* sp. This new material, along with historically collected articulated comatulid fossils from the Middle Jurassic of the UK (*Solenocrinites* and *Palaeocomaster*), provides the taxonomic coverage of all currently known generic diversity of Middle Jurassic comatulids. These have been examined using microCT for the first time. The celomic structures of the Jurassic species vary distinctly from one another but are consistent with predictions of recently published phylogenies. This is consistent with recent findings suggesting that comatulids diversified rapidly during the Jurassic and that significant diversity is currently unrecognised in the Jurassic fossil record. Furthermore, despite stalkless crinoids existing in large numbers at various locations during the Jurassic, the Bathonian Wiltshire Lagerstätte is the earliest incidence of true comatulids dominating a shallow sea floor community, pushing back this phenomenon, which is an important contribution to biomass in some modern shallow marine settings, by some 25 million years.

Chemical composition and distribution in sea urchin teeth using synchrotron X-ray fluorescence

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Sea urchin teeth grow continuously throughout the life of the organism, with a self-sharpening mechanism maintaining the sharp cutting edge of the tooth tip. They are composed of long single crystalline rods within a polycrystalline matrix, and their structure and composition lend them strength to suit their function. Their complex hierarchical structure is challenging to unpick as it varies between different features that occur in the same location, as well as changing in composition as it grows, getting progressively more mineralized. This high strength and complex structure that continuously grows make it a useful model system for investigating biomineralization processes, as well as inspiration for synthetic materials design.

In this work we investigate how chemical composition and distribution vary in adult sea urchin teeth, within a cross-section as well as at different stages of development. Focusing on the relatively unstudied species *Mespilia globulus*, we demonstrate the heterogeneity of the chemical make-up of different regions of the tooth using nanofocus X-ray fluorescence, and reveal structural features in the stone part. We describe how these characteristics develop over the length of the tooth.

Divergent function between perivisceral fluid and hydrovascular fluid under immunological stress in sea cucumbers (*Holothuria forskali*)

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Echinoderms have two main coelomic cavities in their body plan: the general perivisceral cavity containing the different organs and the hydrovascular cavity constituting a unique vascular system also known as the water vascular system. These two cavities are filled with a fluid whose composition is close to that of seawater, but which contains a large amount of metabolites and cells. These cells are called coelomocytes and constitute the main actor of echinoderm immunity. Different cell types have been described based on morphological criteria; it appears that sea cucumbers show the greatest diversity among the five classes of echinoderms at six to seven different types. While the immune response of perivisceral coelomocytes has already been studied in different species, the immune response of hydrovascular coelomocytes remains understudied and the differences in their immune response have not been investigated yet. In the present study, we investigated the transcriptomic response of coelomocytes to injections of lipopolysaccharide (LPS) – a molecule that mimics a bacterial infection – in the sea cucumber *Holothuria forskali*. Coelomocytes from both fluids were studied distinctly to compare their immune response. In addition, we attempted to correlate gene expression with the proportion of different coelomocyte types in each fluid by counting the cells (Fig. 1). Our results revealed 17,646 differentially expressed genes (DEGs) between control and LPS-injected individuals (by considering both fluids) and 5524 and 6420 DEGs specific to the perivisceral and hydrovascular fluid, respectively. Regarding the comparison of the two fluids, 2853 genes were DEGs when considering all individuals (*i.e.*, control and LPS-injected individuals). Interestingly, the same analysis resulted in only 179 DEGs in control individuals but in 2773 DEGs in stressed individuals. These results suggest that in immunoquiescent conditions, the coelomocytes from both fluids have a similar function but that this function tends to change following the immunological stress. Furthermore, this change coincides with an increase in the concentration of hemocytes as a result of immunological stress that occurs only in the hydrovascular fluid. Finally, the functional annotation of DEGs offers precious information about the specific functions of coelomocytes in both fluids. This research raises interesting questions about the function of the hydrovascular system and coelomocytes and provides valuable data for comparative immunology.

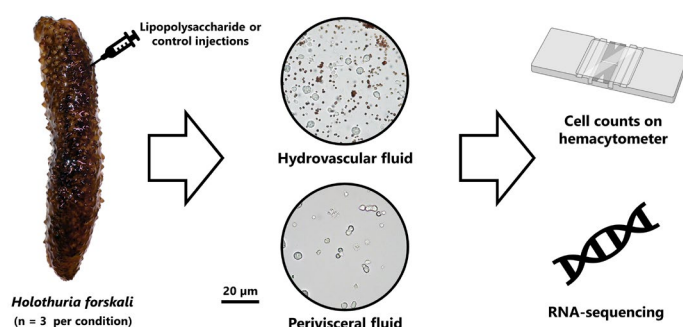


Fig. 1. Experimental design: 6 specimens were selected (3 control injection individuals and 3 lipopolysaccharide injection individuals); their hydrovascular fluid and perivisceral fluid were harvested; coelomocytes were counted on a hemacytometer before performing the RNA-sequencing analysis.

Behavioural responses of juvenile Crown of Thorns Starfish (*Acanthaster* sp.) to flow and chemosensory cues from coralline algae, coral, and adult conspecifics

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The accumulation of juvenile Crown of Thorns Starfish (COTS; *Acanthaster* species complex) hidden within the reef rubble is a potential source of population outbreaks of this species which devastate coral reefs across the Indo-Pacific. Whilst expansive research has investigated the larval and adult life stages, our understanding of the early herbivorous juvenile stage of COTS is poor. The behavioural responses of the juveniles COTS were investigated to identify the potential that semiochemical cues may be associated with the ontogenetic diet transition from a herbivorous crustose coralline algae (CCA) diet to coral predation. Juvenile COTS (5-20 mm diameter) that were ready to undergo the diet transition (juveniles in waiting) were exposed to cues from CCA, corals and adult COTS in y-maze flow-through choice chambers to determine if waterborne chemical cues influence directional movement and decision making. The juveniles demonstrated positive rheotaxis moving upstream. When exposed to CCA, and coral as single cues, the juveniles demonstrated attraction and directional movement towards the source of these cues. However, when exposed to adult COTS, the juveniles demonstrated a fleeing avoidance response. When exposed to cues from coral or CCA simultaneously originating from different flow, the juveniles showed a preference for coral. When exposed to cues from a food source (live coral or CCA) and adult COTS they displayed equivocal behaviour with great variation between individuals in their responses. These results indicate the potential for adult density dependant interactions, whereby the abundance of adults deters the herbivorous juveniles from making the diet switch to corallivory supporting the juvenile in waiting hypothesis.

Bonding with sea cucumbers: Identification of tube foot adhesive proteins from transcriptomic data

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Many marine invertebrates produce adhesives that act in the presence of water, and this has raised growing scientific interest because of the potential to mimic such adhesives for use in human medicine and dentistry. In echinoderms, adhesive secretions are mostly within the tube feet, which are the external appendages of the water-vascular system, a distinctive feature of the phylum (Flammang *et al.*, 2016). Tube feet are involved in tasks that require temporary adhesion underwater, such as locomotion, maintenance of position, and feeding. Although tube feet are present in every extant echinoderm species, adhesion has only been studied in detail in asteroids and regular echinoids. Within the tube feet, duo-gland adhesive systems release proteinaceous secretions from adhesive cells, while de-adhesive cell secretion allows detachment.

In our laboratory, we have been studying tube foot adhesion in echinoderms for many years. However, it is only recently that some adhesive proteins have been characterized in the sea urchin *Paracentrotus lividus* (Pjeta *et al.*, 2020) and in the sea star *Asterias rubens* (Algrain *et al.*, 2022). In contrast, very little information is available on adhesive proteins produced by sea cucumber tube feet. Taking a bioinformatics approach, we have utilised existing transcriptome data and knowledge of adhesive protein attributes in other echinoderms to identify key proteins involved in adhesion in the sea cucumber, *Holothuria forskali*. More specifically, Blast searches were used to identify proteins similar to adhesive proteins from *P. lividus* and *A. rubens* in the body wall transcriptome of *H. forskali*. The list of candidate proteins was further refined by differential transcriptomics, comparing the expression levels of their coding mRNAs in the ventral (with tube feet) and dorsal (without tube feet) body wall. This allowed us to establish a short list of about 10 adhesive protein candidates which were then further validated by confirming they are expressed in tube feet but not in other organs using PCR. Once fully characterized, these proteins could offer novel features and/or performance characteristics for applications in wet environment adhesion.

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Integrative taxonomy of the order Euryalida (Echinodermata, Ophiuroidea) from the West Pacific

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Among numerous hypotheses on phylogenetic relationships within the order *Euryalida*, the most convincing hypothesis has proposed three families, the Euryalidae, Asteronychidae, and Gorgonocephalidae (O'Hara *et al.*, 2017). The order Euryalida contains 48 genera (Stöhr *et al.* 2023). The genus-level relationships have remained unresolved due to inadequate taxon sampling and insufficient molecular markers. We attempt to present a more complete genus-level revision of the order Euryalida based on more species and sequences from nuclear genes and mitochondrial genes.

Especially, we put extra focus on the relationship between the genera *Asteroschema* and *Ophiocreas*, which are currently mixed in the same clade, making them polyphyletic. The two genera have high similarities in morphology, and the absence/presence of external ossicles is their main diagnostic characteristic. We examined specimens of these two genera, and revised the tabular key of all their species. We collected nuclear genes and mitochondrial genes of the two genera to figure out the phylogenetic relationship between them.

Several new species were found in the genus *Astrodia* (Asteronychidae, Euryalida) and in genus *Asteroschema* (Euryalidae, Euryalida). Comprehensive descriptions of morphological features are provided, including characteristics of the arm skeleton, as well as a phylogenetic analysis based on sequences from nuclear and mitochondrial genes.

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The oldest record of stylophorans

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Styolophorans (cornutes and mitrates) constitute a bizarre clade of exclusively Palaeozoic primitive echinoderms that expanded from the Cambrian to the Carboniferous. They are characterized by an asymmetric to symmetrical body (theca) and a single tripartite appendage which is constructed by a proximal polyplated flexible part, a characteristic cone-shaped intermediate plate called stylocone and a distal more stiff uniserial part which is covered dorsally by mobile cover plates. The phylogenetic position of stylophorans within deuterostomes has been highly controversial with different interpretations considering them as plesiomorphic chordates (calcicordate theory), plesiomorphic echinoderms or derived echinoderms. The earliest record of the group is patchy with earliest members reported from the Wuliuan of West Gondwana and Baltica assigned to *Ceratocystis*; and from the Drumian of Laurentia described as *Archaeocothurnus*. Herein I present a new stylophoran from the Anti-Atlas (Morocco) collected in the Wuliuan, Jbel Wawrmast Formation at several localities. It is represented by about ten well-preserved, fully articulated specimens providing information about dorsal and ventral surfaces, plus well preserved aulacophore. This find might represent the oldest report of stylophorans worldwide and its characteristics provide information on the plesiomorphic condition of the group and possible relationships with other echinoderm classes.

An overview of cinctans and ctenocystoids (stem-echinoderms)

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Cinctans and Ctenocystoids represent two different groups of closely related echinoderms that are considered as the most primitive echinoderms (Zamora & Rahman, 2014) or as a derived group of echinoderms (David *et al.*, 2000). While the study of cinctans have received important advances in the last decade in terms of their systematics, distribution, phylogeny, and palaeobiology, ctenocystoids have remained unstudied since the last century with only few papers focusing on the description of new occurrences. Herein we update information about the two groups and recognize gaps that should be filled in the next years. New species of ctenocystoids from Morocco, Spain, and Bohemia provide important information about the systematics and functional morphology of the group. The genus of ctenocystoids *Courtessolea*, originally described in France, represents the plesiomorphic condition of the group with new species to be described from Spain and Morocco. The presence of a single marginal ring, position of the anus in the upper integument and anatomy of the feeding apparatus (ctenidium) provide shared characteristics with cinctans and inform about the condition of the common ancestor of cinctans + ctenocystoids.

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Systematics of deep-sea starfish order Brisingida (Echinodermata: Asteroidea), with revised classification and remarks on character evolution

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Brisingida Fisher, 1928, as one of the most enigmatic starfish orders, possesses 6–20 long arms and lives almost exclusively in the deep ocean. As widespread and endangered as species of this group are, the lack of systematic studies on this order of echinoderms has for years impeded our understanding of their global diversity and evolution. We present the first comprehensive phylogenetic study on Brisingida, which encompasses the highest taxonomic diversity (15 of 17 genera) to date. DNA barcodes (*COI*, *16S*, *12S* and *28S*) were obtained from 225 specimens collected from various habitats around the world ocean. Maximum likelihood and Bayesian analyses yielded congruent tree topology, which revealed polyphyletic families and genera within the current classification scheme. Sixteen morphological key characters and their states were mapped onto the tree and their phylogenetic values were assessed. A series of pedomorphic characters were found in several genera and species, which has led to a high degree of homoplasy across phylogenetically distant groups. A novel classification of the order, consisting of 5 families and 17 genera, is proposed based on molecular and morphological evidence. Families Odinellidae, Brisingasteridae and Novodiniidae (*sensu* Clark & Mah, 2001) were resurrected to encompass the genera *Odinella*, *Brisingaster* and *Novodinia*. Brisingidae and Freyellidae were further revised to include 11 and 3 genera, respectively. A new genus and species as well as two new subgenera will be proposed and described in the near future. The resolved phylogeny and revised classification of Brisingida will provide baseline data on deep-sea biodiversity, which is an essential index used for conservation and restoration of marine ecosystems.

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Virtual reconstruction and analysis of a new, exceptionally preserved Silurian cyclocystoid provides insights into soft tissue structures and the mode of life of an enigmatic extinct class

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Cyclocystoids are a rare and enigmatic extinct class of disc-shaped echinoderms, with considerable uncertainty surrounding their affinities and ecology. Key features, such as the mouth frame, location and structure of the anus, and the form and function of the ambulacral system, remain poorly understood, despite the group's extensive fossil record (Ordovician to Carboniferous) and several detailed studies. To address this, exceptionally preserved cyclocystoid fossils (*Apynodiscus williamsi* n. sp.), recently donated to the Natural History Museum, London, from the Silurian of Shropshire, UK, and other well-preserved historical specimens (*Polytryphocycloides grandis*, *Apynodiscus decussatum* and *Zygocycloides variabilis*), were imaged using X-ray microtomography (microCT). This revealed the detailed structure of the oral surface, particularly the location of sutural pores between ray and inter-ray plates on the oral surface. These pores are significant as they have been hypothesized to be the location of the tube feet, thus suggesting the structure and location of the hydrovascular system and possible means of food acquisition or locomotion. It was found that the position of these pores varied widely between genera, appearing to be unpaired in *Zygocycloides*, paired and more closely associated with the ray plates of *Polytryphocycloides* and paired, but associated with the inter-ray plates in *Apynodiscus*. Significantly, in one specimen of *Apynodiscus* sp. nov., short, paired, finger-like extensions were seen arising from these pores. The fact that these paired finger-like extensions are situated within the inter-ray areas of the oral surface precludes them being cover plates or tube feet and instead are postulated as papulae with possibly the same function as in today's asteroids. The accurate virtual reconstruction of cyclocystoid morphology generated from our microCT scans also formed the basis for an analysis of their life orientation using computer simulations of fluid flow (computational fluid dynamics).



POSTERS

POSTERS

Exploring the effects of neurotransmitters and neuropeptides on the swimming behaviour of crinoid larvae

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The doliolaria larvae of most crinoids are lecithotrophic larvae that, before settlement and metamorphosis, disperse in the water column, using ciliary bands for swimming. However, the precise modulation of this behaviour remains elusive. Recent studies have identified the expression of various neurotransmitters, including monoamines and neuropeptides, in this larval stage (Mercurio *et al.*, 2019; Aleotti *et al.*, 2022). These molecules are potential regulators of swimming behaviour in doliolaria larvae. To address this issue, we have established a specific behavioural assay to assess the effects of neurotransmitters / neuropeptides on swimming activity of doliolaria of *Antedon mediterranea*. Larvae were placed in 24-well plates containing filtered artificial sea water, and their baseline behaviour was video recorded under a stereomicroscope for two minutes. Subsequently, a neurotransmitter/neuropeptide was introduced, allowing one minute for dispersion and absorption by the larvae. The larvae were then recorded for an additional two minutes. Ongoing work with the video tracking package trackR aims to characterise parameters such as overall distance, speed, and path type (straight or curved) to identify potential differences in larval movement pre- and post- treatment and also among different neurotransmitters. Investigation of the modulation of doliolaria swimming by neurotransmitters and neuropeptides may enhance our understanding of this crucial stage in crinoids, wherein the larvae must disperse before settling to the substrate and transitioning to the sessile pentacrinoid stage. Moreover, our findings could have broader implications for understanding crinoid nervous system development, providing a valuable baseline for comparative studies among echinoderms.

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Exploring the impact of climate change on trophic plasticity and gut microbiome variability: Insights from a southern ocean sea urchin species

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Sterechinus neumayeri (Meissner, 1900) is an endemic and abundant sea urchin species of Antarctica, generally considered as a keystone species in nearshore marine ecosystems. This sea urchin is omnivorous, feeding on detritus, algae, and various invertebrates.

Like many other Antarctic species, *S. neumayeri* is potentially vulnerable to fast-paced environmental shifts, materializing as increased seawater temperatures and changes in sea-ice dynamics. The subsequent alterations of the community structures, of species interactions, and of the availability and abundance of food, might threaten the sea urchin's scope for survival by disrupting its feeding habits. Additionally, the potential alterations of its gut microbiome due to habitat and dietary changes might represent another related threat. Indeed, the emerging understanding of the close relationships between diet and gut microbiome composition and functionalities highlights the gut microbiome's role in digestion, nutrient assimilation, and pathogen resistance, thereby influencing the host's overall health.

Today, limited knowledge exists on the trophic plasticity of Southern Ocean sea urchins, i.e., its ability to shift from one food source to another, and even less is known on their gut microbiome composition, functions, and variability.

In this context, the present study addresses the trophic plasticity and gut microbiome as a dynamic association to assess the potential acclimation of *Sterechinus neumayeri* to changes in its trophic ecology. We present first insights arising from a recent field survey (TANGO1) conducted in the western Antarctic Peninsula (WAP), encompassing different sites displaying environmental gradients. Stable isotope analyses were used to characterize the trophic niche of *S. neumayeri* and identify the diversity of food sources in different environmental conditions. Besides, metabarcoding was used to gain insights into the sea urchins diet, and into the diversity, composition, and potential functions of gut microbial communities.

Nutritional quality and culinary and nutraceutical valorization of sea cucumbers from the Mostaganem region (Algeria)

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Sea cucumbers have a high level of proteins including collagen and a low lipid level represented by unsaturated fatty acids (omega-3, omega-6) thus constituting a perfect combination for human consumption in addition to their high level of vitamins and minerals. In addition, numerous species of the Holothuroidea contain many bioactive molecules such as saponins that have a wide range of biological activities (anticancer, antiviral, antifungal, ...).

Our work focuses on the valorization of "sea cucumbers" from the Mostaganem region (Algeria), which is a resource caught illegally and exported abroad via intermediaries at very low prices. In this study, we propose processing of fresh "sea cucumbers" into dry products called "bêche-de-mer" that we valued in two ways: 1) Culinary valorization imitating the recipes of various dishes commonly consumed in Algerian cuisine ["bourek" (very fine paste composed of wheat flour filled with the stuffing of chopped sea cucumber), "sea cucumber with white sauce and mushrooms", "sausages" and "marinated sea cucumber salad"] and 2) Nutraceutical valorization in the form of powder and food supplement.

Through this study, we aim to contribute to food security with a product rich in protein and which enters the purchasing power of the Algerian population, especially since its manufacturing process is not very expensive.

Insights into stylophoran anatomy and taphonomy based on an exceptionally preserved mitrate from the Lorraine Group (Upper Ordovician) of New York, USA

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Several levels of the Lorraine Group (Upper Ordovician) in upstate New York (USA) have yielded low-diversity, exceptionally preserved, pyritized invertebrate assemblages dominated by the trilobite *Triarthrus eatoni*. Sedimentological and taphonomic features suggest dysoxic bottom-water conditions, with limited transport and rapid burial by distal turbidites (Farrell *et al.*, 2009, 2011). Echinoderms are extremely rare in these strata. Here we report, for the first time, the occurrence of the anomalocystitid mitrate *Enoploura* in the Konservat-Lagerstätte of Beecher's Trilobite Bed. A pyritized specimen of this stylophoran was CT-scanned and three-dimensionally reconstructed. The mitrate is laterally compressed, but its 3D-rendering provided several insights into its internal anatomy and taphonomy. The recurved position of the single feeding appendage (aulacophore) probably results from ligament-induced, post mortem contraction. This posture and the collapse of one lateral series of cover plates indicate that the individual was probably not buried alive. Nevertheless, a portion of the distal aulacophore shows clear evidence of exceptionally preserved soft parts (ambulacral system) in between two sets of slightly open cover plates and the underlying ossicles. One of the most intriguing features of this specimen is its close association with a sinuous, elongated, pyritized trace fossil, which enters the stylophoran through the mouth and disappears into the proximal aulacophore. In marked contrast with other skeletal parts of the specimen (theca and distal part of the aulacophore), the proximal rings of the aulacophore are heavily disrupted and disarticulated. Proximal rings are usually the most decay-resistant skeletal regions in stylophorans (Saleh *et al.*, in press). Therefore, close association of this disrupted region with a trace fossil that penetrates it suggests the action of an unknown infaunal scavenger. Proximal rings of the aulacophore, which housed powerful muscles in life, were likely very attractive to scavengers who could detect freshly killed benthos in the first stages of decay.

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Preliminary results of the study of the echinoids of the Scotia Arc (Antarctica)

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The Scotia Arc is an interesting region to investigate in biogeography as it constitutes a natural “bridge” or “stepping stone” area made of a discontinuous chain of sub-Antarctic islands and archipelagoes that stretch from southern South America in the north to the Antarctic Peninsula in the south (Longhurst, 2007; Griffiths *et al.*, 2009; Briggs & Bowen, 2012; Martin-Ledo & Lopez Gonzalez, 2014; Moreau *et al.*, 2017, among others). Among the main biogeographic issues to investigate one is to test whether (1) the Scotia Arc may constitute a single biogeographical entity on its own, or (2) may be separated into different biogeographical sub-units. Results of our study supports the first hypothesis. Based on species occurrence data obtained from identified specimens sampled during past Spanish oceanographic campaigns (ANTARTIDA 8611, ANTARTIDA 9101, BENTART-94, BENTART-95), our results show that no species new to science was discovered but the new records extend our knowledge of some species distribution ranges that were formerly unknown from the Scotia Arc region, as it is the case for the cidaroid *Notocidaris gaussensis* off the Sandwich Islands or species of the spatangoid genus *Amphipneustes*. Comparing our data with records available from online public databases (OBIS and SCAR), we identified many unreliable records, as well as a lack of data for the South Sandwich Islands, one archipelago of the Scotia Arc region, which makes robust biogeographic analyses impossible. It is therefore recommended to check for the reliability of these records before analyses and to improve sampling effort around the South Sandwich Islands in the future.

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Diversity in the deep sea: A case study of the Pterasteridae (Echinodermata: Asteroidea)

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An essential step in deepening our knowledge of biodiversity is the ability to delimit and classify species. To achieve this, integrative taxonomy, which according to Dayrat (2005) allows to «delimit the units of life's diversity from multiple and complementary perspectives (phylogeography, comparative morphology, population genetics, ecology, development, behaviour, etc.)», seems to be a real asset. A recent study of the diversity of the sea star family Pterasteridae in the Southern Ocean (Jossart *et al.*, 2021) underlined the importance of using an integrative approach (combining morphology and genetics) and enabled us to investigate their diversity and reassess their taxonomy. Those primarily deep-sea sea stars present a particularly modified morphology, with some anatomical structures usually used for taxonomy being reduced or absent. In addition, the remaining characters are often fragile and can therefore be potentially damaged during sampling or preservation. This study follows on from the work of Jossart *et al.* (2021), with an increase in taxonomic and geographic coverage by including new specimens. The molecular (COI mitochondrial fragment) and morphological identification of 128 specimens from seven genera (*Amembranaster* Golotsvan, 1998, *Benthaster* Sladen, 1882, *Calyptaster* Sladen, 1882, *Diplopteraster* Verrill, 1880, *Euretaster* Fisher, 1940, *Hymenaster* Wyville Thomson, 1873 and *Pteraster* Müller & Troschel, 1842) and the compilation of all available online genetic data represents a final barcode library of 583 entries. Samples collected from other ocean basins (North Atlantic, North Pacific, Indo-Pacific) have given the opportunity to explore biogeographic patterns on a global scale, as suggested by Jossart *et al.* (2021). The taxonomic position of some groups is also discussed, highlighting the need to re-evaluate the taxonomy at both genus and species levels.

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Distributional congruence and species richness of echinoderms in the East Pacific

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The biogeographic patterns of echinoderms throughout the eastern Pacific have not been well documented. In this work, more than 100,000 records contained in the Global Biodiversity Information Facility (GBIF) repository databases were analyzed and validated in order to identify the distributional congruence and record the areas with highest specific richness. A total of 893 species of echinoderms distributed in the region were recorded for the first time. Five areas with the highest richness were located: 1) the Gulf of California; 2) the Bay of Panama, including the Malpelo and del Coco Islands; 3) the Galapagos Islands; and finally, near the Strait of Magellan, 4) the Chilean Fjords. Separately, changes in latitudinal gradient were identified, one in a hot zone, another in a temperate zone and finally in a cold zone, each area with the corresponding endemic species were mapped. Fourteen consensus areas were identified, which show the distributional congruence of the species; each area was assigned to each identified pattern, as well as the species that support the area and their percentage of species richness. The patterns were: Bering Strait, British Columbia nested with California (USA), Gulf of California, Panama Bay, Galapagos Islands and the Chilean-Patagonian region. It is necessary to continue with the analyses of the biogeographic patterns of the area to evaluate the possible common histories of the biota and the ecological processes that could be involved.

Skeleton structure of *Nidorellia armata* (Gray, 1840) (Echinodermata: Asteroidea) as archaeological evidence of its presence in the offerings of Templo Mayor, Mexico

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During the last two seasons of excavations of the Templo Mayor Project in Mexico, carried out between 2007 and 2018, at the foot of the main pyramid tens of thousands of archaeological remains of animal origin have been recovered; among them 65,640 plates of starfish in Mexica ritual deposits. In these deposits, disarticulated concentrations of whitish calcareous plates of various shapes were observed, resulting from the decomposition process and the loss of skin and organic tissues that connect the skeletal plates. So far, seven species of starfish have been identified from these plates, one of them distributed in the Atlantic Ocean (Zuñiga-Arellano *et al.*, 2019). *Nidorellia armata* (distributed in the Pacific Ocean) is the most represented. A complete comparative study of the structural components of the *Nidorellia armata* skeleton of modern specimens from the National Collection of Echinoderms "Dra. María Elena Caso Muñoz" (ICML-UNAM) and of the archaeological pieces found in the offerings was made, in order to confirm its presence in the offerings of the Templo Mayor, and to identify the approximate number of individuals that were buried. The actinal, abactinal, adambulacral, ambulacral, carinal, madreporic, marginal, odontophore and mouth plates were analyzed with photography and multifocal microscopy. It was found that the plates are of various shapes and have a size between 3 and 17 mm, presence of conical spines, the lateral ones are robust and large, the actinal ones are small and square and the ambulacral plates are elongated and compressed. We analyzed a total of 124,940 plates that make up the endoskeleton. It is possible to estimate that a minimum of 160 individuals were buried in one offering of the most recent excavation. The size of some of the skeletal plates led us to believe that this species remains correspond to organisms of much greater sizes than those found on our shores today; the size of the biggest mouth plates of the specimen originally buried was 16.57 mm, which corresponds to R=135.99 mm. This is surprisingly big in comparison with specimens held at the ICML whose R value does not exceed 87 mm.

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Echinodermata assemblages from northern Tunisia (Central Mediterranean Sea)

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Faunal and/or floral studies on the composition of marine biodiversity are essential to understand the ecological patterns of species distribution. The phylum Echinodermata, which is well known by its adaptability and plasticity to various environmental conditions, is one of the most dominant and diverse components of marine communities. The present work aims to understand the distribution and the assemblages of the echinoderms in northern Tunisia by quantifying and qualifying their faunal composition from the shallow water (0 m) to bathyal level (up to 100 m). Sampling was carried out along the northern coasts of Tunisia, from the Algerian border till the Cape-Bon peninsula. Several sampling methods were used, hand collection with quadrat for bottoms less than 1 m depth, experimental dredging for shallow waters less than 50 m depth, and benthic fishing trawls for depths exceeding 50 m. Also, scuba diving was employed for restricted places with hard bottoms. After collection, the specimens were sorted, identified and preserved in ethanol. Multivariate Analysis of Ordination such as multidimensional scaling (MDS) and similarity percentage analysis (SIMPER) were performed using the statistical package Primer-E v6. In addition, species and classes distribution were evaluated according to the horizontal marine zonation described by Pérès (1967) for the Mediterranean. A total of 1430 specimens from the five living classes Echinodermata were collected and 45 species were identified. MDS analysis detected no difference between the three studied sectors but between localities nested sectors. Same results were also confirmed by pairwise testing. However, SIMPER analysis revealed a significant difference between localities from sector 1 (S1) and no differences between the localities from sector 2 (S2). Otherwise, the distribution of the classes along the different bathymetric levels shows an increasing of Asteroidea and the decreasing of Holothuroidea from the upper to the lower levels. In contrast, Crinoidea and Ophiuroidea were absent or very scarce in shallow water. Finally, the knowledge of marine biodiversity and, specifically, that of a group as important as echinoderms, is very useful for the management of marine ecosystem and so for identifying conservation priorities.

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Echinoderms (Echinodermata) from marine protected areas of Central Chile coast

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The Chilean coast is one of the most remote marine areas in Latin America. It encompasses an important number of islands most of them are recognized as Multi-Use Marine Coastal Protected Area (MU-MCPA). The central Chilean continental fringe holds a significant amount of marine species mainly are algae, mollusks and fish. Despite the relevance of the phylum Echinodermata to coastal and marine ecosystems management, studies on its community structure and distribution pattern are scarce and poorly understood in Chile. Here we explore the faunal diversity of the echinoderms from intertidal and subtidal zones of marine protected areas (MPAs) of central Chile. The studied area extends from 27°S, 70°W (on the north) to 34°S, 72°W (on the south) central Chilean coast and it comprise three main MPAs: Las Cruces coastal reserve, Isla Grande of Atacama and Isla Chañaral-la Higuera reserve. The echinoderm fauna studied in this work comes from the existing database collected from the available articles, catalogs, checklists and reports. These are dating from 1978 to 2011. Several sampling methods were used to cover the tidal shoreline such as, hand collection, quadrat and Beam trawling. Echinoderms found here are 15 species belonging to three living classes and comprising 11 Asteroidea, 3 Echinoidea and only one Ophiuroidea (*Amphipholis squamata* (Chiaje, 1829). According to available data of central Chile, crinoids were totally absent from intertidal and subtidal zones however, the holothurian appears only from benthic level. The generated statistical analysis revealed that the sea star *Heliaster helianthus* (Lamarck, 1816) was the most abundant and frequented species in intertidal zone with over 67% of the total specimens. Same species is considered as a keystone predator at rocky intertidal sites in central Chile. Indeed, the sea urchin *Loxechinus albus* (Molina, 1782) characterized the subtidal sites with 20% of the total material. Same analysis pointed out large echinoderms diversity in subtidal zone with the presence of ten species against only four intertidal taxa. This could be attributed to the stability of the physiochemical parameters and the consistence submergence of subtidal areas. The number of the echinoderms that occur in shallow marine protected areas of central Chile is mostly related to both sampling effort and environmental characteristics that promote their biodiversity in such area.

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The echinoderm collection of the Biologiezentrum (OÖ Landes-Kultur GmbH), Linz, Austria

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The Biologiezentrum (OÖ Landes-Kultur GmbH) in Linz holds the second largest natural history collections in Austria with over 9.000.000 objects. Numerically the largest collections are those of the Mollusca and Protista, however collections span throughout the animal kingdom including Echinodermata. The echinoderm collection dates back to the middle of the 18th century. By the 19th century the collection increased significantly mainly due to material collected by F. Fridrich, A. Hauser, J. Klimesh, B.M. Klein from the Mediterranean Sea and the North Sea. The collection continued increasing through new sampling expeditions and donations and today it numbers over 300 dry and wet specimens from throughout the world that can be allocated to over 50 species.

A possible peltocystid mitrate (*Stylophora*) in a new Praguian (Early Devonian) Konservat-Lagerstätte from Belgium

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Peltocystid mitrates are the most long-ranging clade of stylophorans, with representatives known from the Tremadocian (Early Ordovician) to the Bashkirian (Early Pennsylvanian). They are characterized by the possession of a single posterior spine (glossal) and two particularly large adorals extending on most of (Peltocystidae) or on the entire upper thecal surface (Jaekelocarpidae and Kirkocystidae). Although peltocystids were highly diverse and palaeogeographically widespread in the Ordovician, their younger record is particularly cryptic (Lefebvre, 2007). They are so far undocumented in the Silurian, and are known from only two later occurrences: in the Lower Devonian Hunsrück Slate of Germany ("*Mitrocystites*" *styloideus*; Dehm, 1934) and the Upper Carboniferous Gene Autry Shale Formation of Oklahoma (*Jaekelocarpus oklahomaensis*; Kolata *et al.*, 1991).

A third possible occurrence of post-Ordovician peltocystids is reported here from a new Konservat-Lagerstätte in the Praguian (Lower Devonian) of southern Belgium that was discovered thanks to the BRAIN-be project B2/202/P1/VERTIGO of Belspo. In 2021 and 2022, two field campaigns in the Neufchâteau Synclinorium yielded several hundreds of fossils, some of which preserving soft parts. This particularly diverse marine assemblage comprises arthropods, molluscs, priapulians, as well as putative *Pikaia*-like cephalochordates. A wide range of techniques have been used (e.g. X-ray elemental mapping, CT-scan, energy-dispersive X-ray spectroscopy) to reveal the morphology and, in some cases, the internal anatomy of these fossils. One of the fossils is morphologically very similar to "*Mitrocystites*" *styloideus* and other as yet undescribed peltocystids from the Devonian of Germany (Haude, 1983). Although its posterior spine is apparently absent, the specimen is remarkably well preserved, with a fully articulated theca and a relatively long appendage (aulacophore?) preserved in extended (feeding) position.

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Quantifying *in situ* growth rates in the New Zealand sea star *Coscinasterias muricata* using tetracycline tag-recapture methods

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Determining growth patterns is key in understanding a species' ecology and population biology. However, growth patterns in sea stars are still poorly understood, despite their position as globally important predators that play a key role in structuring invertebrate communities. Determining growth in sea stars is problematic, since most species lack obvious growth markers such as bands or lines on their skeletal elements. Previous studies on sea star growth and population structure have generally focused on analysis of size-frequency distributions and progression of cohorts within populations. This method, while useful, is inherently inexact, given that it requires validation of the age of cohorts. It also works entirely with population averages, not returning growth measurements for any individual subject.

Using the tetracycline tag-recapture method widely applied to echinoids, we aim to accurately determine the growth patterns of a sea star. Our study focuses on a population of the eleven-armed sea star *Coscinasterias muricata* in Doubtful Sound, one of the fiords of southwestern New Zealand. Using this method, we first established a strong allometric relationship between ambulacral ossicle length and body size in *C. muricata*. Laboratory and field trials indicate the ossicles incorporate tetracycline in their calcite matrix, visually marking the size of the plate at the time of tagging, and therefore allowing us to estimate any increase in size when the animal is recaptured. The ossicle size change can then be converted to overall body size change, allowing an estimate of individual growth.

In December 2022, we tagged 260 in our *C. muricata* population with tetracycline. A preliminary sample taken in May 2023 showed 20% of recovered animals had visible tetracycline tags. In December 2023, a larger sample of animals will be recovered from this population, and tags will be analysed to determine the increase in size of the ambulacral ossicles. These will then be related to the overall size of the animal by the previously calculated morphometric relationships, allowing estimation of the increase in size of each individual sea star.

Quantifying tiering of crinoid communities using a new echinoderm Lagerstätte from the Jurassic of Wiltshire, UK

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Marine animal forests have been a vital component of oceanic ecosystems since the appearance of the first large and morphologically complex organisms over half a billion years ago. They comprise communities of benthic suspension feeding animals, such as crinoids, which can be tiered to reduce vertical competition for resources in the water column. Tiering is thought to have played an important role in generating evolutionary and ecological variation but limited work has been done to quantify its role in structuring ecosystems in past and present oceans. Owing to their extensive fossil record, which stretches back to the Ordovician (~480 Ma), crinoids are potentially an ideal group with which to study tiering. However, because their plates are held together in life by soft connective tissues, crinoid fossils are often found partly disarticulated and/or incomplete. This hinders our ability to reconstruct their heights and level of tiering.

A new Middle Jurassic (Bathonian) echinoderm Lagerstätte from Wiltshire, UK, provides an ideal opportunity to address this issue. Discovered in 2021, this site is considered one of the best Jurassic echinoderm localities worldwide. It is interpreted as a shallow marine crinoid ‘meadow’, dominated by the comatulid *Andymetra* sp. and the isocrinid *Isocrinus nicoleti*. It is believed that at least two storm-generated muddy debris flows rapidly buried the meadow. As a result, the assemblage contains abundant and near-complete in-situ crinoid specimens, many of which preserve the crown and stalk.

Our goal is to use this exceptional fossil material to develop a new method to infer the height of crinoids and thereby reconstruct tiering of their communities through time. To achieve this, we are measuring key morphological features of complete and incomplete fossils from the Wiltshire site. We have digitized fossil slabs using different surface-based techniques (photogrammetry, laser scanning and structured light scanning) to determine the most accurate approach for capturing morphological information.

Preliminary results suggest photogrammetry provides the best balance between ease of use and accuracy of 3D measurements, with deviations of only 0.1mm from measurements taken directly from the fossils with digital callipers. These data are being analysed with general linear regressions to determine if there are any relationships between stalk length and dimensions of the crown, which would allow us to reconstruct heights for partial fossil specimens. We anticipate that this project will deliver a powerful new method for inferring the height of incomplete crinoid fossils. This will allow us to expand studies of tiering to a wider range of fossil material, including incomplete specimens. Ultimately, this will enable us to develop new metrics to quantify tiering and its effects on co-evolutionary dynamics.

Can holothurians from the deep-sea of New Caledonia be used to monitor microplastic pollution?

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Plastic production has risen exponentially since the early 1950s. Plastics represent the vast majority of total marine litter, while they mostly stem from mismanaged land-based litter. Most of the plastic pollution is today believed to be due to microplastics, microparticles resulting from the weathering and breakdown of larger plastics. Microplastics display a wide variety of toxicity, and can easily be ingested by a broad range of organisms. Moreover, microplastics can sink onto the seafloor due to their density or to biofouling or marine snow. As such, several studies have shown that microplastics can accumulate in the sediments, and that the deep-seafloor could constitute a major microplastic sink, rendering them bioavailable to benthic organisms.

Most holothurian species are benthic organisms present at all depths and latitudes. A vast majority of species are deposit-feeders, with high bioturbation and sediment-filtering rates, comprised between 9 and 82 kg per individual per year. Hence, we hypothesise that holothurians could be a relevant model organism to study microplastics pollution. Research in shallow water ecosystems has already demonstrated the presence of microplastics in several families of holothurians.

In this project, we will investigate microplastic pollution temporal trends, using a time-series collection of deep-sea New Caledonia holothurians of the *Muséum National d'Histoire Naturelle*. The sampling strategy of the collection specimens will be presented, as well as preliminary analyses of microplastic contents found in holothurians. This project also ambitions to determine the potential uptake and biodistribution of microplastics by holothurians, and investigate microplastics ingestion physiological consequences. Altogether, these experiments will enable to obtain a better understanding of the impact of microplastic pollution on holothurians, an important ecological and economical class of organisms.

***Ophiotholia saskia*: a new brittle star from the Clarion Clipperton Zone**

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The Clarion-Clipperton Zone (CCZ) in the Northeast Pacific hosts the largest deposits of polymetallic nodules at abyssal depths. These nodules are rock formations that contain valuable metals and minerals and are intended to be mined. They also provide a diverse habitat for many deep-sea species. To date, little is known about the taxonomy, history and biogeography of deep-sea fauna, but this is essential for an accurate assessment of the risk of species extinction from large-scale mining. One of the most common megafauna taxa in the CCZ are brittle stars (Ophiuroidea), among which the genus *Ophiotholia* Lyman, 1880 shows increased abundance in the CCZ. In general, the genus *Ophiotholia* is distributed worldwide and currently comprises six species. The material collected on seven scientific expeditions in the CCZ was examined morphologically together with comparative material of all known species. Due to the small body size and the damage caused during sampling, morphological identification was often not possible, so the specimens were genetically analysed using a fragment of the mitochondrial COI gene. Scanning electron micrographs of the most important microstructural features were taken with selected specimens from the CCZ as well as the comparison material. One morphotype from the CCZ was identified as the described species *Ophiotholia supplicans* Lyman, 1880, while the second morphotype was recently described as *Ophiotholia saskiae* Eichsteller *et al.*, 2023. The identification and description of such a poorly known genus improves the assessment of species diversity not only in the CCZ, but also in the entire deep sea.

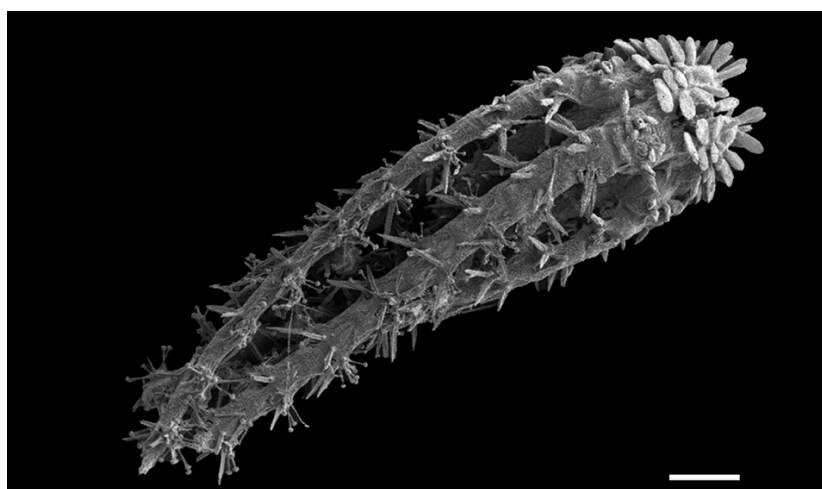


Fig. 1. Habitus of *Ophiotholia saskiae*, scanning electron micrograph. Scale = 0.5 cm

Revision of the genus *Benthogenia* Fisher, 1911, with description of a new species, and detailed ossicle anatomy

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Porcellanasteridae Sladen, 1883 is a family of mud-dwelling sea stars, living in bathyal and abyssal environments. Among the twelve currently recognized genera of porcellanasterids (Mah, 2023), the genus *Benthogenia* Fisher, 1911 is the only one known to occur at depths shallower than 1000 meters (Mironov *et al.*, 2016) and differs from all other porcellanasterids by having cribriform organs between all its marginals, from the disc to the tip of the arms. Here is reported an occurrence of *Benthogenia cribellosa* as shallow as 111 meters, and a new species, *Benthogenia* n. sp., is described from material housed in the Muséum national d'Histoire naturelle, Paris (MNHN). *Benthogenia* n. sp. is represented by twelve specimens, collected at depths ranging from 400 meters to 1200 meters during four different expeditions. *B. cribellosa* is represented by two specimens from the MNHN, plus the holotype and two specimens from the National Museum of Natural History, Washington DC. *Benthogenia* n. sp. differs from *B. cribellosa* mostly by having more robust arms, fewer oral and adambulacral spines, and by the cribriform organs not covering the entire surface of the superomarginals of the disc. Molecular data (16S) were also used as an independent dataset to test for the monophyly of the new species. Geographic distribution data show that *Benthogenia* n. sp. occurs in New Caledonia, Solomon Islands and Vanuatu, whereas *B. cribellosa* is only known from the Philippines. Detailed descriptions of both species are provided, as well as a detailed description of the skeleton of the new species.

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Effect of acidification on populations of the sea urchin *Paracentrotus lividus* (Lamarck, 1816) using natural gradients

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Ocean acidification caused by the increasing atmospheric CO₂ that is partially absorbed by the oceans stands out as one of the main threats to marine ecosystems (Hoegh-Guldberg & Bruno, 2010). Under current conditions, it is projected that the pH of the oceans will decrease by 0.3 units compared to the current values by the end of the 21st century. This decrease in pH leads to a reduction in the availability of carbonate ions, which are essential for the formation of calcareous skeletons and the synthesis of carbonate biostructures in echinoderms and other invertebrates (Byrne & Fitzer, 2019). Species with broad distribution along natural environmental gradients in the present ocean offer the opportunity to interpret their adaptability to climate change. Herein, we expose the effect of acidification on the metabolic rates of the sea urchin *Paracentrotus lividus* along a natural pH gradient generated by a shallow CO₂ vent located in the Canary Islands, Spain (Fig. 1A). Populations of *P. lividus* across this vent experience pH values from 8.2 at the control sites to 7.2 at the vent sites. Our preliminary results reveal significant differences in basal metabolism between populations from the control and vent sites. Individuals from the vent sites displayed lower metabolic rates and oxygen consumption compared to those from the control sites. Additionally, we demonstrated the plasticity of this trait, as individuals collected from control sites reduce their metabolism when exposed to low pH values in aquarium conditions (Fig. 1B).

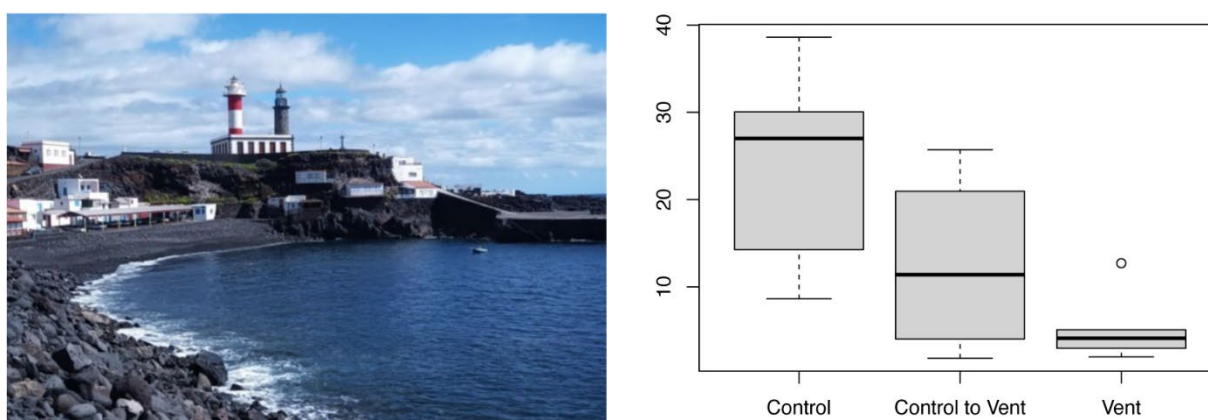


Fig. 1. A - CO₂ vent located in La Palma, Canary Islands. B - Basal metabolism between *P. lividus* populations from controls and vent sites.

The type material of the iconic Muschelkalk ‘stone lily’ *Encrinus liliiformis* Lamarck, 1801 (Triassic Crinoidea)

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Fossil and present-day crinoids have attracted observant and interested people, not only naturalists and scientists, for centuries. These included finds from the ‘Muschelkalk’ (Triassic: Anisian/Ladinian) of Germany, which were later described under the scientific name *Encrinus liliiformis*. Due to the wide distribution of these fossils, not only in Germany and France, as well as the long history of research, including: Friedrich Lachmunds “OPYKTOΓPAΦIA Hildesheimensis” (1669), Michael Reinhold Rosinus’ “Tentaminis de Lithozois ac Lithophytis...” (1719), Gottfried Wilhelm Leibniz’ “Protogaea...” (posthumously published in 1749), John Ellis’ “An Essay towards a Natural History of the Corallines” (1755), Jean-Étienne Guettards “Memoires sur les Encrinites...” (1755), Georg Wolfgang Knorrs “Sammlung von Merckwürdigkeiten der Natur und Alterthümer des Erdbodens...” (1755), Christian Friedrich Schulze “Betrachtung der versteinerten Seesterne...” (1760), J. E. Immanuel Walchs “Die Naturgeschichte der Versteinerungen...” (1773), and many others with short or detailed descriptions, illustrations or repeated illustrations by earlier descriptors, *Encrinus liliiformis* acquired an iconic status.

Jean Baptiste de Lamarck established the valid name *Encrinus liliiformis* for the well-known Muschelkalk ‘stone lily’. In 1801 he designated two syntypes, which, however, were regarded as missing or forgotten since the late 1760s. One of these syntypes was recently rediscovered at the Bergakademie in Freiberg/Saxony, after being forgotten for more than 250 years (Hagdorn *et al.*, 2023).

Here we present and outline the complex finding history of this single syntype, which will be declared as the lectotype of *Encrinus liliiformis* in a future work.

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[therein also all papers cited here]

Ecological niche evolution within the echinoid genus *Arbacia* Gray, 1835

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The biogeographic distribution of species is not random, it is conditioned by species ecological niches, ecological factors, Earth and evolutionary histories. Hutchinson (1957) defined the species ecological niche as a multidimensional space in which dimensions are environmental factors. He also defined the species fundamental niche as all suitable environmental conditions allowing the species to reproduce and survive. The realized niche, which is a subset of the fundamental niche corresponds to the species occupied niche as a result of biotic interactions and dispersal limitations. Species Distribution Modeling (SDM) allows the study of species distribution and determine environmental factors that impact their distribution by correlating species occurrences and their ecology with existing environmental conditions. SDM can infer the species niche based on actual occurrences and environmental data because if a population is reported in an area, this area is considered as suitable to the species reproduction and surviving. Species distribution changes through time as a function of environmental changes, the dynamics of physicochemical barriers to dispersal, and the evolution of the species fundamental niche. Biogeographic events and niche evolution control the diversity and distribution of species. Studying the species niche evolution allows understanding the geographical evolution of clades and infer the associated speciation processes. In the present work, SDM were performed for species of the echinoid genus *Arbacia* Gray, 1835 which is widely distributed along the Pacific coasts of North and South America, in the Atlantic Ocean and the Mediterranean Sea. SDM were compared between species to check for ecological conservatism with regards to their phylogeny and fossil data.

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Molecular phylogeny of Neoasteroidea (Asteroidea) based on mitochondrial genome

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The systematic interrelationships among extant members of the crown group Neoasteroidea remain controversial, even when fossil species with taxonomic inconsistencies are excluded (Mah & Blake, 2012). Molecular phylogenetic analyses have showed that Valvatida, which is the largest group in Neoasteroidea, is polyphyletic (Mah & Foltz, 2011).

Recently, phylogenetic analyses using multiple molecular markers, including full mitochondrial genomes, have become more accessible (e.g., Mu *et al.*, 2018; Inoue *et al.*, 2020). This has allowed questions pertaining to deep phylogeny and higher taxonomy to be addressed. In this study, we determined the mitochondrial genomes of 33 starfishes by shotgun sequencing using an Illumina next generation sequencing platform. Phylogenetic inferences were conducted using 13 mitochondrial protein-coding genes (PCGs) from 50 species, including 17 available sequences in GenBank, and thus covering all three superorders of Neoasteroidea (Forcipulatacea, Spinulosacea, and Valvatacea).

The resulting phylogeny recovered all three superorders, strongly supporting the monophyly of Forcipulatacea. Although the monophylies of the remaining two superorders were recovered, Spinulosacea was found to be nested within Valvatacea. Spinulosacea was paraphyletic if Mithrodiidae was excluded. Interestingly, Blake (1987) moved Mithrodiidae from Spinulosida to Valvatida based on morphology. Our result thus suggests that the family should be reclassified under Spinulosida. Valvatida are polyphyletic, which agrees with Mah & Foltz (2011). We also found Spinulosida (of Spinulosacea) and Paxillosida (of Valvatacea) to be well-supported. Our findings highlight the need to re-examine the taxonomy of Neoasteroidea, including Spinulosacea and Valvatacea. Such revision will require future taxonomic studies with detailed morphological observations and molecular analyses.

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Scientific diving in France: an overview of the current practices in science

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The French National Committee for Scientific Diving (CNPS) takes on different tasks including acting as an observatory of occupational scientific diving practices and innovations. Since 1991 in France, scientific diving has been recognized by law as an occupational sector and is therefore regulated with the aim to reduce the hyperbaric risk. Currently, French scientific diving encompasses many fields such as life sciences and ecology, geosciences, social & cultural sciences including archeology, health & food, engineering sciences, and energy industry... Due to the existence of overseas territories - with France's maritime spaces representing the world's second largest exclusive economic zone - French territories display an extensive variety of submarine habitats. Furthermore, the historical richness of scientific diving in France has led the French scientific diving community to be involved in all oceans worldwide. All subaquatic ecosystems, from the polar regions to the tropical belt, from drowned karsts to freshwater and high-altitude lakes, including mesocosms and artificial structures are studied by diving scientists. On top of the traditional diving methods (apnea, open circuit and hookah) scientific diving benefits in recent years from the use of closed-circuit rebreathers (CCR) but also from combining CCR and saturation methods, which greatly enhanced the study of the mesophotic zones. In light of the diversity of environments, disciplines and scientific issues, scientific divers are continuously innovating to perform outstanding research. This poster outlines the recent work of the last decade highlighting the importance of scientific diving in science (with a focus on France).

This poster has been presented at the 7th European Scientific Diving Conference, 2023 May 14-18th, Roscoff, France, doi: 10.23708/fdi:010087876

***Amphipholis squamata* is an allopolyploid swarm**Andrew HUGALL¹, Maria BYRNE² & Timothy D. O'HARA¹¹ Museums Victoria, Melbourne, Australia. ahugall@museum.vic.gov.au² University of Sydney, Sydney, Australia. maria.byrne@sydney.edu.au

Amphipholis squamata is one of the most widespread and abundant of all brittle-stars and has been the focus of much ecological, life history, demographic, and physiological research. Our next generation DNA sequencing data revealed nuclear exons within this taxon having numerous divergent alleles indicative of elevated levels of ploidy and hybrid origins. Transcriptome data show that multiple alleles are expressed and are not pseudogenes. Genetic composition is very variable across samples, signifying multiple hybridisation events and variable ploidy, characteristic of an ancient polyploid swarm. Moreover, this complex is polyphyletic, with several diploid clades embedded within it, including dioecious sexually-dimorphic *Ophiodaphne-Ophiosphaera* species that are commensal with sea urchins. We hypothesise that the genetic variability, high dispersal capability, and ability to generate parthenogenetic offspring have contributed its long-term evolutionary success.

Environmental control on the structure of asteroid assemblages in the Patagonia Argentine

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From October 2007 to April 2010, the Atlantis project was carried out in the Patagonia Argentine, with the main objective to identify and analyze Vulnerable Marine Ecosystems (VMEs), as well as their relationship with fishing activity (del Río *et al.*, 2012). The present work characterizes the structure and spatial distribution of asteroid species (Hurtado-García & Manjón-Cabeza, 2022), as well as the identification of the environmental factors that determine the structure of the community. Asteroids were collected at 296 sampling stations (107- 2063 m) and a total of 44 species were found, of which *Ctenodiscus australis* Loven in Lütken, 1871 was the most abundant (38.96%) and occurring species (53.37%). The study was divided into three subareas (platform, slope, and submarine canyons); 29.55% of the species are present in the whole area, constituting the general taxocenosis. There are three habitats associated with each subarea: (1) aggregations of Demospongiae and Ascidiae on the platform; (2) funds richer in mud with aggregates of sponges, gorgonians, and pennatulaceans on the slope; (3) coral gardens with patches of other types of bioconstructive benthic biota in submarine canyons. However, these habitats do not conform to the different taxocenosis found. In some cases, they present specific associations or a certain dependence on specific substrates that would be distributed in isolated small patches. The taxocenosis found are: (1) taxocenosis of *Henricia studei* (Perrier, 1891); (2) taxocenosis of *Lethasterias australis* Fisher, 1940; (3) taxocenosis of *Cheiraster planeta* (Sladen, 1889); (4) taxocenosis of *Pillsburiaster calvus* Mah, 2011; (5) taxocenosis of *Smilasterias scalprifera* (Sladen, 1889); (6) taxocenosis of *Labidiaster radiosus* Loven in Lütken, 1871; (7) Rocky bottoms of the platform; (8) bottoms of deep pennatulaceans; (9) shallow coral bottoms; (10) bottoms of deep coral gardens.

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Exceptionally well preserved *Stegophiura* (Echinodermata, Ophiuroidea) fossils from the Pliocene of central Japan

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Three well-preserved articulated ophiuroids were found in the Pliocene Hatsuzaki Formation of Ibaraki, central Japan. The specimens are assigned to the genus *Stegophiura* on account of the large swollen disk scales, dorsal arm plates with a high ridge, tiny squarish scales and short spines. Among the sixteen congeneric extant species, the present species is most similar to *Stegophiura ponderosa* in having swollen disk scales and high arms. However, the present species differs from *S. ponderosa* in having larger disk scales and radial shields abutting in their central part. In addition, the dissociated lateral arm plates of the Pliocene species have eight or nine spurs, whereas those of *S. ponderosa* only have six. The Pliocene species differs from the only known fossil species assigned to *Stegophiura*, *S. miyazakii* from the middle to upper Cenomanian of Japan, in lacking small granules along the disk edge and having shorter arm spines. We therefore established a new species *S. takaisoensis* (Ishida *et al.*, 2023; Fig. 1) for the Pliocene material, representing the second and youngest extinct representative of *Stegophiura*.

The three specimens have the disk and long arms with tiny arm spines, scales and papillae all in their anatomical position. In particular, one specimen was found parallel to the bedding plane with the mouth facing down and arms extending radially. We therefore assume that the specimens were buried alive by rapid channel fill deposits with no or very little transport.

Based on bivalve and sedimentological evidence, we assume that the new species lived in lower shelf to upper bathyal settings, in line with the present-day bathymetric distribution of the genus.

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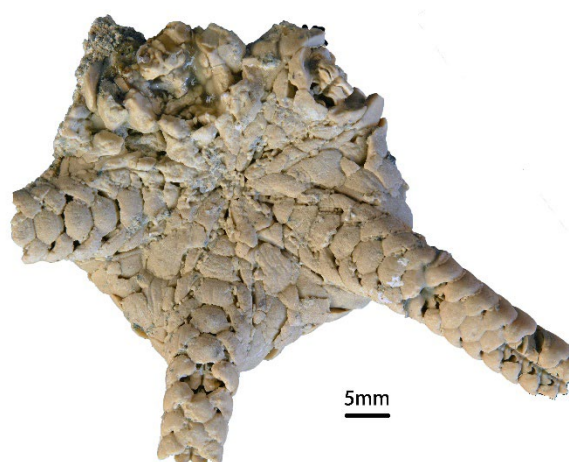


Fig. 1. *Stegophiura takaisoensis* (ventral side)

Autotomy in the apodid sea cucumber *Chiridota laevis*

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This study characterizes the autotomic ability in the apodid sea cucumber *Chiridota laevis*. Although this species has been documented in temperate benthic marine environments for over a century, basic information regarding its regenerative capacity is absent from the literature. Our initial investigations of *C. laevis* demonstrated that it can undergo remarkably rapid transversal fission. This unique behaviour and its relationship to various triggers were investigated from ecological and evolutionary perspectives. Experimental results confirmed that this mid-body splitting behaviour is indeed true autotomy (i.e. an active defense mechanism in response to physical stimuli) as opposed to reproduction through fission. Physical triggers were explored, along with the autotomic breakage planes and kinetics of the healing process post splitting. Preliminary results suggest that autotomy is closely linked with season and possibly ontogeny and reproductive maturity. The findings will directly address knowledge gaps in the field of regenerative biology, while providing useful information about an interesting and valuable model organism for evolutionary biology research.

Sea star mitogenomes: Characterization and utility for phylogenetics

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Despite the high diversity and ecological importance of Asteroidea (sea stars), the phylogenetic relationships within the class have been controversial for more than 100 years and are still subject to discussions and debates at different taxonomic levels. Some uncertainties remain regarding basal relationships (among orders) as well as several intra-ordinal relationships. The interest of mitochondrial genomes (mitogenomes) in phylogenetics has been highlighted in various taxa during the last twenty years. They still represent powerful and independent markers to confront the patterns observed from nuclear data. Currently, the complete mitogenomes of 31 sea star species have been released, representing 18 different families. Nevertheless, there is no representative mitogenome for 20 of the 38 families and some orders remain particularly under-represented (e.g., Velatida: two species, Spinulosida: one species). In the present study, we used two methods alongside (long-range PCR approach and low coverage skimming sequencing) to characterize new mitochondrial genomes for 16 species. This includes newly characterized mitogenomes for five families (Ganeriidae, Odontasteridae, Poraniidae, Solasteridae and Stichasteridae) and represents a major addition for the Velatida order (from two to six species), the Spinulosida order (from one to three species) and the Southern Ocean taxa (from two to sixteen species, including *Odontaster validus*, one of the most abundant and important benthic animals in Antarctica). By combining these newly characterized mitogenomes with the ones previously available on GenBank, we evaluated the mitogenomic variation within the Asteroidea class by addressing two main goals: 1) Verify how the organization of the mitogenomes (size of the whole genome, length of each gene, gene orders) is consistent across the class. 2) Assess the relationships at both the inter-ordinal and intra-ordinal levels, considering that the data from the present study represent the most exhaustive molecular data available for multiple taxa.

Molecular diversity and structure-activity relationship of saponin in Indo-Pacific sea cucumber *Bohadschia argus*

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Sea cucumbers are slow moving benthic invertebrates that contain triterpenoid saponin glycosides in abundance (Kamyab *et al.*, 2020). Sea cucumber saponins are chemically highly diverse with variations in their aglycones or sugar moieties (Popov, 2002; Kalinin *et al.*, 2008). In this study, we investigated the chemical structure and bioactivity of different saponin glycosides isolated from Indo-Pacific sea cucumber species, *Bohadschia argus* which appeared to be highly active in initial bioactivity screening. Using Feature-Based Molecular Networking (FBMN), we first identified the major saponin compounds present both in the whole organism as well as in its Cuvierian tubules (CTs, specialized structure that often accumulates a cocktail of saponins). In addition, four already identified saponin compounds were isolated and their structures were elucidated as bivittosides C, D and argusides B and C by high-resolution MS and MS/MS experiments combined with nuclear magnetic resonance (NMR) spectroscopy. Finally, we were able to draw structure-activity relationships between different saponins and their antibacterial, antifungal, anti-viral, and anticancer activities. It showed that the observed bioactivities were influenced by the presence or absence of hydroxyl groups at C-12 and C-17 in the aglycone moiety, as well as by changes in the sugar moiety specifically in the second sugar unit of the saponins. In conclusion, we revealed that *B. argus* contains structurally diverse saponins, with specific structural features being correlated to different bioactivities. This highlights the importance of studying the structural characteristics and the biological activities of saponins to identify the main bioactive moieties of the molecules useful for possible industrial productions.

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IceDivA Project: The study of diversity of deep-sea holothurians in the North Atlantic Ocean using molecular approaches

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Monitoring the unexplored diversity of deep-sea marine ecosystems has been challenging due to the limited accessibility and size variety of organisms from different taxa. During the IceDivA expeditions (Icelandic marine Animals meets Diversity along latitudinal gradients in the deep sea of the Atlantic Ocean; SO280 and 286), we assessed deep-sea planktonic and benthic fauna presented in abyssal plains east and west of the Mid-Atlantic Ridge. Within IceDivA, we identified sea cucumbers using targeted sanger-sequencing (COI barcoding) as well as, for the first time, proteomic fingerprinting using MALDI-TOF MS analysis for holothurians. The preliminary results related to holothurian identification showed that sea cucumbers have a patchy distribution along deep-sea basins. Moreover, initial morphological observations and comparison of our sequences to public DNA repositories (i.e., BOLD and NCBI) showed that among 28 specimens, most of the samples belonged to the order *Elasipodida*. In parallel, MALDI-TOF MS analysis was able to differentiate between the proteomic fingerprints of most of the species in correspondence to the COI barcodes. Finally, in order to complete the assignment and provide accurate identifications at species level, a combination of molecular methodologies with classical taxonomic identifications is necessary.

Taxonomical revision of *Ophiopholis aculeata* and *O. japonica* based on the mitochondrial COI and morphological analysis

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The genus *Ophiopholis*, belonging to the family Ophiophilidae and the order Amphilepidida (Stöhr *et al.*, 2023), comprises eight species with notable intraspecific morphological variations. These variations present challenges in establishing definitive species characteristics within the genus. Currently, the Korean marine fauna has reported four species of *Ophiopholis*: *O. aculeata*, *O. brachyactis*, *O. japonica*, and *O. mirabilis* (Shin, 2012). However, distinguishing between *O. aculeata* and *O. japonica* based on morphological features has proven to be problematic.

In this study, we conducted a comprehensive re-examination of specimens collected in Korea that were initially identified as *O. aculeata*. Morphological and molecular analyses in this study revealed that all previously collected samples identified as *O. aculeata* in Korea were, in fact, misidentified as *O. japonica* due to the similarity of their morphological characteristics. To further support these findings, we reanalyzed the COI data of *Ophiopholis* species available in the NCBI library and identified one misidentified species.

These results highlight the inherent difficulties associated with accurate species identification within the genus *Ophiopholis* and underscore the importance of integrating morphological and molecular approaches in taxonomic studies.

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Comparative taxonomic analysis of *Holothuria (Thymiosycia) decorata* and *H. (Mertensiothuria) hilla*

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Holothuria (Mertensiothuria) hilla is a common sea cucumber in the northwest Pacific, and it extends its reach to regions such as Korea, Japan, Hawaii, the Indo-Pacific, Australia, and Zanzibar in East Africa. Several species have been synonymized with *H. (M.) hilla*. However, *H. (M.) hilla* collected from the northwest Pacific, particularly the adjacent waters of Korea and Japan, exhibit distinct morphological differences compared to specimens from the Indo-Pacific region.

In this study, we conducted a comprehensive investigation into the species history based on previous articles and analyzed their morphological characteristics. Additionally, we obtained DNA barcoding sequences from both *H. (M.) hilla* and *H. (Thymiosycia) decorata*. The results of this study revealed significant differences in the morphological characteristics of ossicles between these two species. Furthermore, the DNA barcoding analysis clearly indicates that *H. (M.) hilla* and *H. (T.) decorata* are different at the species level. Based on the results in this study, we suggest recognizing *H. (T.) decorata* as a separate species.

Late Ordovician echinoderms from the Brabant Massif (Belgium): Taxonomic revision, palaeoecology and palaeobiogeographic implications

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In the Ordovician, the Brabant Massif (Belgium) was situated in the eastern part of the Avalonia microcontinent, which then also comprised eastern Newfoundland, southern Ireland, Wales, England, the Netherlands, southern Denmark and northwestern Germany. With the exception of the British Isles, which yielded a more or less continuous fossil record of the diversification of echinoderms from Cambrian Series 2 (Stage 3) to the Late Ordovician (Hirnantian), data are scarcer in most other Avalonian regions.

First documented by Malaise (1873) and thoroughly investigated by Regnéll (1951), the echinoderm faunas from the Huet Formation (middle Katian, Upper Ordovician) represent the earliest record of the phylum not only in the Brabant Massif, but also in modern Belgium. Their recent taxonomic revision has largely confirmed the validity of Regnéll's (1951) identifications, and has also made it possible to assign to *Haplosphaeronis proiciens* most of the diploporitan taxa left in open nomenclature (sphaeronitid gen. and sp. indet. 3, 4 and 5). Interestingly, two distinct coeval echinoderm assemblages could be evidenced within the Huet Formation. The first one is dominated by sphaeronitids (*H. proiciens*), associated to rhombiferans (*Echinosphaerites belgicus*) and rare cyclocystoids (Fauquez area), whereas the second one is dominated by rhombiferans (*E. belgicus* and *Heliocrinites malaisei*), associated to sphaeronitids indet. and rare specimens of *H. proiciens* (Gembloux area). Future investigations will determine whether the same pattern, which documents the existence of different environmental conditions in the two areas, can be also evidenced for other groups of benthic invertebrates (e.g. brachiopods, trilobites). In the Gembloux area, a relatively diverse younger echinoderm fauna comprising *Heliocrinites* and sphaeronitids was documented for the first time and may originate from the Madot Formation (upper Katian, Upper Ordovician).

From a palaeobiogeographic point of view, the blastozoans of the Huet Formation (diploporitans and rhombiferans) indicate relatively strong affinities with Late Ordovician assemblages from other Avalonian areas and Baltica, but also with late Katian faunas from the higher latitude Mediterranean Province (Boda Event). On the other hand, the cyclocystoids rather suggest affinities with Laurentia (Scotland).

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Taxonomic revision of the first described stylophoran echinoderm: *Ateleocystites huxleyi* Billings, 1858

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The mitrate stylophoran *Ateleocystites huxleyi* was originally described based on four incomplete specimens collected in the Trenton Group (Hull Beds), Quebec, Canada (Billings, 1858; Wilson, 1946). Additional and better preserved material from the Guttenberg Formation (lower Katian, Upper Ordovician) of Illinois, Missouri and Wisconsin was subsequently assigned by Kolata & Jollie (1982) to a distinct species of the same genus: *A. guttenbergensis*. In the past twenty years, several new specimens of *Ateleocystites* were collected in the lower Katian (Upper Ordovician) of the Québec City area (Neuville Formation) and on the island of Montréal (Rosemont Member, Montréal Formation) and Ontario, Canada (Brechtin Lagerstätte: Kirkfield and Verulam formations), as well as in coeval rocks of New York State, USA (Rust Formation).

The reexamination of the type material of *A. guttenbergensis* and *A. huxleyi*, along with the observation of the new specimens, largely confirms the validity of previous descriptions. However, an unexpected morphological variability is evidenced in the arrangement and number of imbricate supracentral elements forming the posterior half of the upper thecal surface of *A. huxleyi*. Examination of a larger number of specimens also indicates that all other characters supposedly diagnostic of *A. guttenbergensis* fall within the range of variation observed in *A. huxleyi*. This implies that *A. guttenbergensis* represents a junior synonym of *A. huxleyi*. This anomalocystitid mitrate was thus palaeobiogeographically widespread in Laurentia, though within an apparently short time interval bracketed in the early Katian. Several aspects of its morphology remain poorly documented, in particular the morphology of its two posterior spines. Their presence has been so far only deduced from the observation of 'sockets' for their articulation onto the postero-lateral corners of the marginal frame.

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An investigation of the molecular and structural properties of the mutable collagenous tissue in the European sea cucumber *Holothuria forskali*

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The mutable collagenous tissue (MCT) found in echinoderms, including sea cucumbers, is a unique connective tissue that can rapidly change its mechanical properties in response to certain stimuli. This tissue is constantly switching between different stiffness states! In sea cucumbers, the tissue properties are modulated by the release of molecular factors in the extracellular matrix, leading to the formation of transient cross-bridges between collagen fibrils. Surprisingly, despite this unique ability, there have been relatively few studies on the molecular and structural characteristics of MCT compared to other collagen-based connective tissues.

The present project aims to explore the molecular composition and the structure of the MCT constituting the dermis of the European sea cucumber *Holothuria forskali*. Proteomic analyses coupled to transcriptomics allowed to investigate the specific molecular components of the MCT. Obtained results showed an interesting combination of alpha 1, 2 and 5 chains in purified collagen fibrils. Furthermore, Raman and ATR-FTIR spectroscopy showed bands consistent with type I collagen, corroborating SEM observations of the fibrils. Additionally, characterization of the collagen structure and organization in the dermis of *H. forskali* was performed using polarized light microscopy and X-ray diffraction in comparison with another species, *Cucumaria frondosa*. Preliminary data seem to indicate a species-specific preferential alignment of collagen in holothuroids. Understanding the molecular and structural properties of MCT could have potential applications in the medical and engineering fields as an inspiration for memory-shaped material with reversible viscoelastic state.

First observations and morphological descriptions of biogenic calcareous microcrystalline structures in an echinoderm

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Biogenic calcareous microcrystalline structures (or microcrystals) have been observed in many animal taxa, including Porifera, Anthropoda, Mollusca, and Chordata (from Tunicata to Mammalia). In mammals, these microcrystals and other types of urinary crystals are morphologically complex and often associated with urine as a by-product of metabolism. In this study, different tissues (e.g., skin, muscles, intestine, gonad) of the holothuroid *Cucumaria frondosa* were analysed to isolate calcium-based microcrystals. We found microcrystals—classified as calcium carbonate or calcium oxalate dihydrate—from the circular muscle, the cloaca, the Polian vesicle, the respiratory tree, the retractor muscle, the skin, or the tentacle in all examined individuals. Notably, they were absent from the ampulla, genital papilla, the gonad, the intestine, longitudinal muscle, and the stomach. Calcium carbonate microcrystals varied in shape and size: rhombohedral (20 to 50 µm) or barrel-shaped (12 to 142 µm). While calcium oxalate dihydrate were either octahedral (5 to 50 µm) or dodecahedral in shape (12 to 70 µm). We suspect that the accumulation of these microcrystals in tissues of holothuroids could be related to tissue fatigue and, as is the case for mammals, a method to diagnose disease, which could make echinoderms a new model taxon to study the evolution and function of biogenic microcrystals.

Ophiuroidea of the Avilés Canyons System (INDEMARES + LIFE Project)

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The Avilés Canyons System (ACS) is located in the Cantabrian Sea (Bay of Biscay) and is composed of three canyons. It was declared Site of Community Importance (SCI: C ESZZ12003) within the Natura 2000 Network (Ministry of Agriculture, Food and Environment, 2014) due to their diversity of species and vulnerable habitats (Sánchez *et.al.*, 2014). During the years 2010 - 2012 several campaigns of the INDEMARES LIFE - ACS project were carried out. This study includes the zone that goes from the beginning of the continental slope to the maximum depth sampled in the bathyal zone (depth range between 266 and 2291 m). A total of 7413 specimens which correspond to 48 species, were collected from 50 stations. The most abundant species were *Ophiocten affinis* (Lütken, 1858) with 4092 specimens and *Ophiothamnus affinis* Ljungman, 1872 with 1842. The most frequent ones were *Ophiactis abyssicola* (M. Sars, 1861) and *Ophiacantha bidentata* (Bruzellius, 1805) present in 48% and 26% of stations respectively. Comparing our species with public databases (OBIS, GBIF) and the bibliography, five potential new records have been found for the Cantabrian Sea, part of the North-Atlantic Marine Subdivision (Lavín *et. al.*, 2012).

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Adaptation and divergence patterns in the spiny sea star *Marthasterias glacialis*

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Marthasterias glacialis is a voracious sea star, with Atlantic-Mediterranean distribution. Previous studies on this species demonstrated the existence of two mitochondrial lineages (Pérez-Portela *et al.*, 2010, 2017) one with Atlantic-Mediterranean distribution and the other one endemic to the Mediterranean basin. To date, the limited nuclear information available for this species has impeded the elucidation whether these two lineages may correspond to two isolated species or lineages from the same species. Additionally, no clear information about gene flow or local adaptation patterns exist for a species distributed from the cold waters of Norway to the warm Eastern Mediterranean. To clarify these questions, we generated double digested Restriction-site Associated DNA sequencing (ddRAD-Seq) data for 258 individuals collected in 19 localities from the north-east Atlantic to the western Mediterranean coasts. We identified 18,589 Single Nucleotide Polymorphisms (SNPs) or genomic markers suitable for population genomics and adaptation analyses. All results demonstrated absence of divergence between the mitochondrial lineages but significant differences among populations and three main geographical areas: the continental Atlantic, the Azores, and the Western Mediterranean, due to isolation by distances. Local adaptation was also detected to two major environmental parameters: temperature and salinity, and at least, 1,789 SNPs seemed to be under selection of these variables. Nuclear and mitochondrial data showed a divergent history, likely related to the isolation of lineages during a glacial period of the Pleistocene. During glacial periods, interruptions in gene flow between the Atlantic and Mediterranean basins could have promoted divergence between nuclear and mitochondrial lineages, with a posterior secondary contact that would have allowed the Atlantic newly created lineage to colonise the Mediterranean, following the main current system in this area. An incomplete lineage sorting would have allowed nuclear lineages mixing again, whereas the mitochondrial ones would have persisted over time due to the absence of recombination.

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Long term stability of *Centrostephanus* populations in coral associated habitat despite other sea urchin populations declining in the subtropical-to-temperate transition zone of east Australia.

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Tropical-to-temperate transition zones are the dynamic ecotone between tropical and temperate systems that host a mix of tropical, subtropical, and temperate species. As the oceans warm, tropical species are expected to increase while temperate species are predicted to decrease in these habitats. These ecotones provide a window into the future of species assemblages as species migrate poleward. *Centrostephanus rodgersii* populations in the east Australia's subtropical-to-temperate transition zone, a significant high biodiversity region, were investigated in coral associated habitat over a 10-years (2010 – 2019) across ~3° of latitude, during a time of significant warming and heatwaves. Despite predictions that the temperate species *C. rodgersii* may decline due to warming, the populations showed stable density and size structure through time. In contrast, warm range edge subtropical (*Tripneustes kermadecensis*) and tropical (*Diadema spp.*) species declined through the study. In its coral association we suggest that herbivory by *C. rodgersii* may facilitate the success of corals in the region by preventing overgrowth of macroalgae. This study of the population dynamics of sea urchins in the subtropical-to-temperate transition zone of east Australia contributes critical information for conservation and management of this unique ecosystem.

Investigating the mystery of beaching events involving sea cucumbers

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Most reports of stranding in echinoderms relate to mass mortalities of sea stars and sea urchins, while documentation of sea cucumber beaching events (i.e. wash-ups of live or dead individuals along the shores) have received less attention. The present study compiles and analyses the reported cases of sea cucumbers washing up on shores around the world over the past century. Although they are still mostly anecdotal, being issued by the general public, media, and research scientists alike, they appear to have increased in frequency, particularly over the last decade. The details and magnitude of documented stranding events were examined in an attempt to draw some preliminary interpretations regarding their potential causes and ecological significance. While parallels can be drawn across events, taxa-specific ecophysiological aspects also seem to be emerging, pointing to a diversity of mechanisms. As our understanding of sea cucumbers and other echinoderms grows, we can start to define with a little more certainty the potential triggers leading to this sometimes sad finality and be on the look-out for an intensification of certain types of beaching events under the influence of climate change.

Systematic revision of *Ctenodiscus* (Asteroidea, Paxilloidea) in Japanese waters

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The mud star genus *Ctenodiscus* Müller & Troschel, 1842 currently consists of five valid species. Of these, *C. crispatus* (Bruzelius, 1805) is considered the most dominant, widely distributed species on the subtidal and bathyal muddy floors from arctic to temperate regions in the northern hemisphere. It is the only species of the genus so far recorded from Japanese waters, whereas morphological differences have been pointed out between the Sea of Japan and Pacific populations. In this study, we conducted molecular and morphological analyses to understand the actual diversity of *Ctenodiscus* in this region.

Our analyses with the nuclear ITS2 and mitochondrial COI sequences revealed three genetic groups in Japanese *Ctenodiscus* with parapatric geographic distributions, namely Group I from southern Japan, Group II from the Sea of Japan, and Group III from the Pacific coasts of northern Japan. Group I, lacking any similar sequence in the public databases, was distantly related to the northern Groups II and III, which were reciprocally monophyletic in our ITS2 tree with no gene flow detected in either gene. A majority of Group II was identical to *C. crispatus* from North America in the COI comparison. Contrarily, the COI of Group III was closest to *C. australis* Loven in Lütken, 1871 from the southwestern Atlantic.

The three groups were also distinguished morphologically. Group I, characterized by its slender, pointed arm and predominantly undeveloped inferomarginal spines, could be identified as *C. crispatus* with literature information on its holotype from the Indian Ocean, as a senior synonym of *C. orientalis* Fisher, 1913. Group II was distinguished from Group III by its significantly shorter arms and more numerous paxillar spinelets than Group III. The shorter arm as well as its obvious madreporite and well-developed inferomarginal spines were consistent with *C. polaris* (Sabine, 1842) from Arctic Canada, which are currently synonymised under *C. crispatus*. With the paxillar column narrowed in the middle, Group III resembled *C. procurator* Sladen, 1889 from the southeastern Pacific.

Groups I and II were therefore identified as *C. crispatus* and *C. polaris*, respectively. The species name for Group III remains yet to be determined with nuclear DNA data from *C. australis* and *C. procurator*.

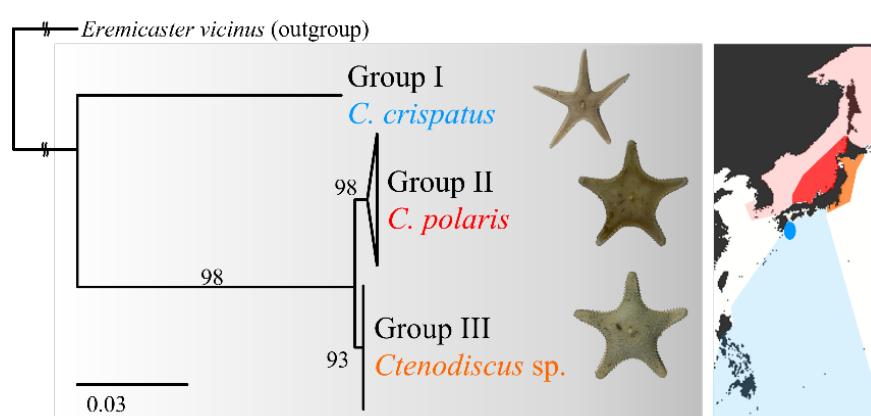


Fig. 1. Maximum likelihood tree of *Ctenodiscus* species from Japanese waters based on the nuclear ITS2 (414 bp). Numbers on branches are bootstrap values (%). Distribution ranges are shown in blue (*C. crispatus*), red (*C. polaris*) and orange (*C. sp.*); localities of the molecular material are highlighted with darker colours.

Echinoderm diversity in the northeastern Aleutian Trench

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The AleutBio (Aleutian Trench Biodiversity Studies; SO293) expedition, onboard RV SONNE, took place from July to September 2022 around the Bering Sea and the Aleutian Trench in the Northeast Pacific. The objectives of this expedition were to survey biodiversity and biogeography of benthic organisms from bathyal to hadal ecosystems (3500 to 7000 m). Ultimately, this approach will allow a comparative work with previous Russian expeditions performed around the Kuril-Kamchatka Trench in the Northwest Pacific. For this purpose, a set of complementary sampling gears was used (MUC: multi corer; AGT: Agassiz trawl; BC: box corer; EBS: epibenthic sledge) to collect meio-, macro-, and megafauna.

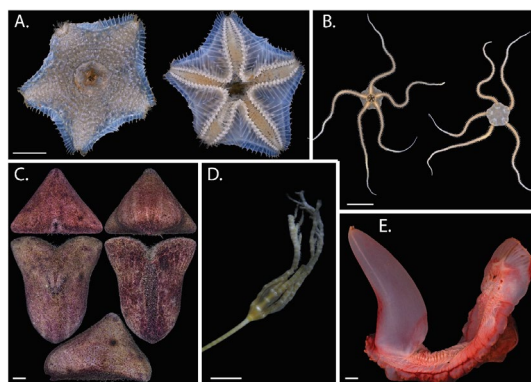


Fig. 1. Examples of echinoderms collected during the SO293 expedition. A. *Hymenaster* sp., scale: 10 mm; B. *Silax* cf. *daleus*, scale: 10 mm; C. *Echinocrepis rostrata*, scale: 5 mm; D. *Bathycrinus* sp., scale: 5 mm; E. *Psychropotes* sp., scale: 10 mm. Photo credits: Chong Chen (A, B, C, E) & Camille Moreau (D).

One of the most dominant megafaunal taxa sampled was the Phylum Echinodermata (Fig. 1), representing ~50% of organisms captured by some gears. More than 7000 specimens (work still in progress) belonging to the five extant classes (Asteroidea (303), Crinoidea (6), Echinoidea (151), Holothuroidea (1346), and Ophiuroidea (5566) were sorted and morphotyped onboard.

Genetic (COI barcoding) and morphological analyses were used to characterise the collected diversity within each class and provide a baseline for future reference. Biogeographical and phylogeographical analyses will follow, allowing comparisons with results from other deep-sea basins and trenches (e.g. Kuril-Kamchatka Trench, Iceland, Clarion-Clipperton Zone) and a better understanding of the global distribution of echinoderms.

Systematics of the urchin *Ctenocidaris (Eurocidaris) nutrix* (Thomson, 1876)

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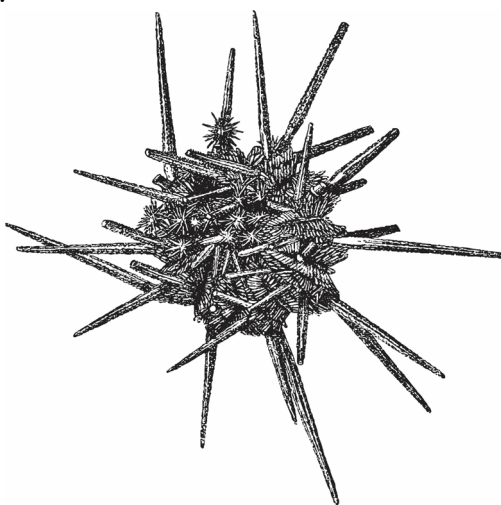
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The cidaroid sea urchin *Ctenocidaris (Eurocidaris) nutrix* (Thomson, 1876) was initially described from the remote Kerguelen archipelago where it is common on the shoreline and across the surrounding oceanic plateau. It was mentioned with both Antarctic and sub-Antarctic distributions and two distinct morphologies: the longispina and nutrix forms. The monospecific status of *Eurocidaris* is however questioned, together with its wide Antarctic and sub-Antarctic distribution. Here we review the genetic and morphological diversity of the species along with the revision of its taxonomy.

Morphological variations (relative length of primary spines, apex relative diameter, gonad biomass) were analysed and no correlations with genetic data were found. Only one haplotype was found on the Kerguelen Plateau regardless of depth or location, suggesting a recent colonisation followed by isolation. Populations of two shallow sites of the Kerguelen archipelago showed differences in relative spine length and gonad biomass that are likely the result of contrasting habitats, ecophenotypy and/or ecological plasticity.

Some doubts about the distribution of the species due to misidentifications of the morphologically close species *Ctenocidaris rugosa* and ‘*Miracidaris incerta*’ are expressed. The species is undoubtedly recorded in the sub-Antarctic region, from the Diego Ramirez island (this study) to Crozet and the Kerguelen Plateau. Because the species is very common in the sub-Antarctic Islands, and absent from the Scotia Arc region, its occurrence along the coasts of Antarctica can be questioned.



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Phylogeography of the deep-sea benthos: Results from the abyssal sea star family Porcellanasteridae (Asteroidea, Echinodermata)

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Despite being the largest biome on our planet, representing 65% of the Earth's surface, deep-sea ecosystems (below 200 m) remain subject to comparatively few investigations. The ecology and evolution of deep-sea benthos in particular has been scarcely studied over the past decades, generating hypotheses that are now being challenged.

To date, over 25,000 described species are known from the deep sea, although recent estimates suggest that the true richness could be at least ten times higher. Such a lack of knowledge about the biodiversity of Earth's largest biome can straightforwardly be attributed to logistical and financial constraints of deep-sea sampling. Expanding our knowledge of deep-sea biology is fundamental to assess global biogeographic processes. Indeed, deep-sea benthic areas lack obvious isolating barriers, raising intriguing questions about how and where new species evolve in these vast, distant, and complex environments. Moreover, their role as a source of diversity towards other shallower biomes has been discussed at geological time scales but also as an ongoing process. This suggests a pivotal function of deep-sea environments for the entire marine biodiversity. At a time of intense geopolitical and economic interests, it is primordial to evaluate ecosystems' resilience and to identify comprehensive and optimal strategies for their conservation.

In the preliminary results presented here, we use the sea star family Porcellanasteridae Wyville Thomson, 1878 as a model to understand the deep-sea evolutionary history of benthic organisms. We gathered samples from various collections to obtain a wide sampling area covering the World Ocean. Mitochondrial gene COI sequences of hundreds of specimens were used to understand the relationships amongst the different taxa and oceanic basins.

While some lineages show very little genetic differentiation suggesting the presence of widespread populations (especially when considering the sampling bias) other exhibit more complex patterns. These results lay the foundation for further integrated analyses using morphology and genomics.

Accelerated and variable evolution rates of Ophiuroidea based on a comparison of the mitochondrial genome

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The mitochondrial genome (mitogenome) architecture of Ophiuroidea suggests a higher rate of evolution compared to other echinoderms, but absolute rates of evolution in ophiuroid groups are unknown, and the factors causing differences in evolution rates are unclear. To investigate these issues, we compared 21 newly published mitogenomes of Ophiuroidea in combination with 26 previously reported ones. We proposed that PRT8 is the ancestral gene order. We found that gene rearrangement and evolution rates are unevenly distributed across orders, with Ophiacanthida experiencing dramatic evolutionary changes, exhibiting extensive gene order rearrangement at species level, and rapidly evolving in PCGs, demonstrating the fastest evolutionary rate. They are followed by Amphilepidida and Ophiurida, with Euryalida having the slowest evolutionary rate. Within Ophiacanthida, Ophiacanthidae showed the MGO "hot spots" that have the most complex rearrangement, indicating it may evolve faster than other families. Our analysis suggests that the accelerated evolution rate in Ophiuroidea is mainly due to the increase of diverse habitats, with organisms needing to accumulate more beneficial mutation to adapt to variable environmental factors and survive in a highly variable environment. Further studies are needed to fully understand the evolutionary history of Ophiuroidea, the effects of selection pressure on habitat, and the factors affecting evolutionary rates in ophiuroids.

Cambrian gogiid eocrinoids from the Barrandian area: Re-evaluation of their diversity

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The Cambrian is an important period for the phylum Echinodermata as they first appeared in the fossil record and underwent the initial diversification. The Barrandian area (Czech Republic) is well known for its Cambrian echinoderm fossil record. Echinoderms show a notable diversity in Czech Cambrian (Miaolingian) deposits where eight distinct echinoderms group were reported: lepidocystids, felbabkacystids, gogiid eocrinoids, rhombiferans, cinctans, ctenocystoids, edrioasteoids and stylophorans. This contribution focusses on the most diverse group of echinoderms from the Příbram-Jince Basin - on gogiid eocrinoids represented by four genera. Three gogiid genera *Acanthocystites* Barrande, 1887; *Akadocrinus* Prokop, 1962 and *Luhocrinus* Prokop and Fatka, 1985 share common morphological features: straight biserial brachioles, theca consisting of polygonal plates (with/without epispire) and holomeric stem. The goal of this study is to conduct a taxonomic re-evaluation based on the detailed morphological description and generate revised data concerning diversity. In the genus *Akadocrinus*, three species were originally described – *A. jani* Prokop, 1962; *A. nuntius* Prokop, 1962 and *A. knizeki* Fatka & Kordule, 1991. The first two species are considered to be synonyms. The third species is very likely also a synonym, but official confirmation is needed in this regard. The differences between these echinoderms could be caused by different ontogenetic stages or taphonomic processes. It is probable that the *Akadocrinus* represents distinct growth stages of *Acanthocystites*.

First results of the revision of the eublastoids (Echinodermata) from the Devonian of the Armorican Massif (NW France)

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Eublastoids are an extinct clade of worldwide distributed echinoderms (except Antarctica) known in marine sediments from the Middle Silurian to the Middle Permian (Waters *et al.*, 1990; Bauer *et al.*, 2019). Their theca is characterized by 17 major plates (3 basals, 5 radials, 4 deltoids and 5 lancets beneath the ambulacra) and tens of thousands of rarely preserved smaller plates. Eublastoids respired with internal structures, the hydrospires (Bauer *et al.*, 2019). In the Armorican Massif, eublastoids were first described in 1876. However, they remain poorly studied with no new publications in the last 50 years. The literature reports the existence of several taxa in the Lower and Middle Devonian (412–383 Ma) of the Armorican Massif: *Belocrinus cottaldi*, *Cordyloblastus clavatus*, *C. eifeliensis*, Eublastoidea indet. (Brest area), *B. cottaldi* (Ménez-Bélair and Laval synclines) and Eublastoidea indet. (Normandy). Since the publication of the S volume of the *Treatise on Invertebrate Paleontology*, many new eublastoids have been described worldwide, and several new Armorican specimens have been discovered.

The aim of this study is to provide preliminary results on the ongoing revision of eublastoids from NW France. The genus *Cordyloblastus* is considered as a junior synonym of *Hyperoblastus*. Thus, two families are identified so far: hyperblastids and troosticrinids. The biostratigraphic range of taxa and their associated paleoenvironments are re-evaluated, while their paleobiogeography is investigated. In the Early (Pragian–Emsian, 412–406 Ma) and Middle Devonian (Givetian, 385–379 Ma), they are found in a wide range of settings, from the intertidal zone to the storm wave base. However, most taxa seem to be restricted to relatively quiet, low energy environments. Finally, some of them lived in restricted and slightly reducing settings and/or in waters with moderately low oxygen concentrations highlighting their adaptability. The oldest known troosticrinids are from the Silurian (~430 Ma) of Laurussia (NE USA), where they possibly originated, before crossing southwards the Rheic Ocean and eventually reaching North Gondwana, as indicated by the presence of *B. cottaldi* (single troosticrinid known from Gondwana). Meanwhile, the oldest hyperblastids are from the Emsian of North Gondwana (Spain). They then spread into other peri-Gondwanan areas such as Bolivia (Eifelian), NW France and Morocco, but also to China, which was then part of another continent (Givetian).

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Unexpected brittle-star diversity in the Carnian (Upper Triassic) of SW-China and Japan

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Knowledge of the Triassic fossil record of the Ophiuroidea is still very patchy, with the vast majority of occurrences reported from the Middle Triassic Muschelkalk strata. Brittle-star fossils from other Triassic deposits, especially from outside Europe, have received comparatively little attention, with few exceptions. Among these are exceptionally preserved, articulated ophiuroids from the Carnian of Yamaguchi, Japan, and dissociated lateral arm plates from the Carnian of Sichuan, China. Previous studies on these two occurrences described one new ophiacanthid taxon for each locality (Thuy *et al.*, 2013; Thuy, 2013). We here present the first results of a more thorough analysis of the two ophiuroid assemblages, revealing a much higher diversity and, surprisingly, a number of species that are found at both localities. The Sichuan assemblage is well-constrained in terms of age and depositional setting, representing a Tuvalian (Late Carnian) outer shelf to upper slope setting (Forel *et al.*, 2019). The high number of shared species with the Japanese assemblage suggests that the latter has a similar age and palaeobathymetric context. The new insights prove highly relevant for the assessment of the early Mesozoic ophiuroid radiation since several of the taxa identified represent the oldest known members of extant family-level clades, in particular the Ophiocamacidae, Ophionereididae and Ophiosphalmidae.

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Expression of glia transporters GLAST and GLT-1 in the Mexican Pacific sea biscuit *Dendraster excentricus*

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Echinoderms are strategic models for neurosciences due their close phylogenetic relationship with chordates. Invertebrates and vertebrates' nervous systems are mainly made up of neurons and glia cells, which have similarities in their biochemistry and functionality. In few echinoderm species the presence of glial cells has been demonstrated (Mashanov *et al.*, 2010; Viehweg *et al.*, 1998). In the present work we are reporting gene expression of glutamate transporter GLAST in adults, larvae and post-larvae of the Mexican Pacific sea biscuit *Dendraster excentricus*. Echinoderm adult organisms were collected from the Punta Banda Bay in Baja California, Mexico. *Dendraster excentricus* larvae and post-larvae cultures were carried under laboratory conditions (Olivares-Bañuelos *et al.*, 2012). Quantitative PCR was carried out by triplicate to measure *GLAST* and *GLT-1* gene expression; *Ribosomal 18S*, *Actin*, and *Polyubiquitin-C* housekeeping genes expression were measured too as internal controls. Sequencing of expressed glutamate transporters genes was done to verify the amplicon. Results showed statistically significant differences in GLAST expression between adults, larvae and post-larvae of *D. excentricus*. As expected, adult echinoderms presented the higher relative expression of GLAST and GLT-1 genes. Results showed us that functional glia cells are present in *D. excentricus*. The fact that echinoderms have a simpler nervous system than chordates, together with our results, strengthens their use as an important animal model for neuroscience and for the search for therapies that help in the treatment of neurodegenerative diseases.

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A new echinoid fauna from the Famennian of Velbert (W Germany) and its implications for Late Devonian evolution of sea urchins

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Despite the limited fossil record and presumably low diversity of Paleozoic echinoids, a short-lived radiation of stem-lineage members during the Early Carboniferous can be identified. Dominant echinoid groups of the Carboniferous are quite different from those present in the Devonian, thus implying that important changes in the composition of echinoid faunas took place during the Late Devonian. The role of the various biotic crises of the Late Devonian in these changes, particularly those at the Frasnian/Famennian and Famennian/Tournaisian boundaries, is currently poorly known.

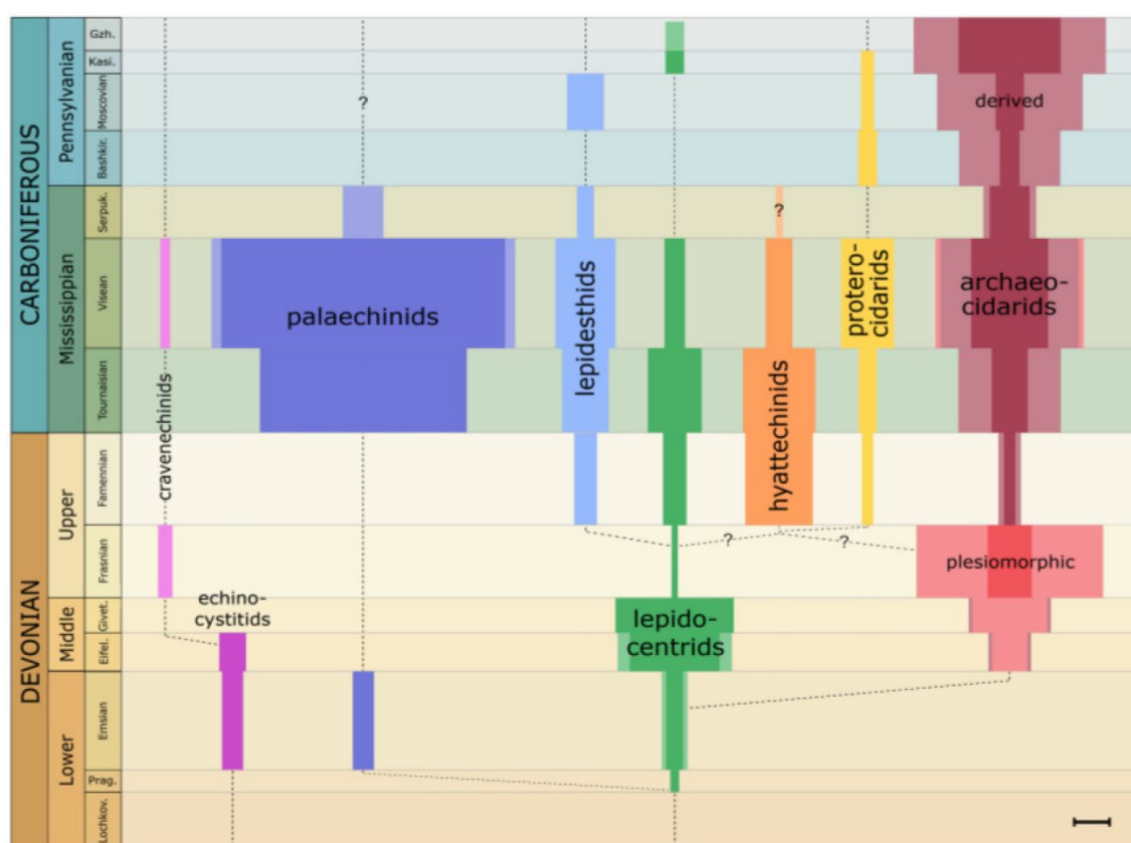


Fig. 1. Diversity of echinoids during the Devonian/Carboniferous interval. Scale bar represents one species per Ma.

This study describes hundreds of echinoid fossils from layers of the middle to upper Famennian at Velbert near Düsseldorf, Germany. They are excellently preserved as external and internal molds within tempestitic claystone and siltstone layers and include preservation of complete tests with intact spines as well as lanterns, apical disks and even pedicellariae. Five new species belonging to four families are present: one species of the lepidocentrid *Lepidechinoides*, two of the hyattechinid *Hyattechinus*, one new genus and species belonging to the Proterocidaridae which represents the oldest and first pre-Carboniferous member of the

family, and one new genus and species of archaeocidarids with strong similarities to its more derived relatives from the Carboniferous. Furthermore, new morphological data now strongly supports a close relationship between hyattechinids and proterocidarids. Analysis of a dataset of all confirmed echinoid species from the Devonian and Carboniferous including the new species show little quantitative, but strong qualitative change in echinoid faunas from the Frasnian to the Famennian. Most significantly, plesiomorphic archaeocidarids seem to have disappeared at the F/F boundary and several lineages that would become important in the Carboniferous first appeared during the Famennian. These changes might be linked to the extinctions around the F/F boundary, particularly the global collapse of metazoan reef systems. The Famennian/Tournaisian extinction seems to have had little negative impact on echinoid diversity and was followed by the known strong radiation in the Tournaisian and Viséan which can largely be attributed to the diversification of the family Palaechinidae.

A new multiarmed asteroid from the Lower Devonian of Morocco

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Deviation from the classical pentameral symmetry through the possession of supernumerary arms and associated ambulacra is relatively common in extant Asteroidea: five families (out of 34) are exclusively multiarmed, and nine include both multiarmed and five-armed taxa (Hotchkiss, 2000). In contrast, Palaeozoic multiarmed asteroids are rare, with only 11 occurrences reported so far (Herringshaw *et al.*, 2007a). Their earliest occurrences include *Lepidaster grayi* from the Wenlock of England, an undescribed starfish from the Ludlow of Australia (Herringshaw *et al.*, 2007a), and two Emsian taxa from the Hunsrück Shale of Germany (*Helianthaster rhenanus* and *Palaeosolaster gregoryi*; Blake, 2009).

Here, we report a new occurrence of multiarmed asteroid, based on about half of the oral surface of a single specimen from the Emsian of the Erfoud area (eastern Anti-Atlas, Morocco). Although incomplete and weathered, the morphology of this specimen, which originally possessed approximately 20 elongate arms, departs from that of coeval forms from the Emsian of Germany. The new Moroccan asteroid is tentatively assigned to the family Lepidasteridae, which includes the two multiarmed genera *Lepidaster* (Silurian of England) and *Michiganaster* (Middle Devonian of Michigan), as well as the five-armed *Lepidactis* (Silurian of England and, possibly, Middle Ordovician of western France) (Herringshaw *et al.*, 2007a, 2007b; Blake *et al.*, 2016).

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Anal teeth in modern and fossil holothuriid sea cucumbers (Echinodermata: Holothuroidea: Actinopoda)

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The Holothuroidea are probably the most morphologically diverse, but also the least understood clade of the present-day echinoderms. This concerns not only the size of adults or their mode of life, but also their hard part morphology. The calcareous ring surrounding the pharynx in the mouth area and the ossicles of the body wall are functionally almost indispensable and, with a few exceptions, present in all species. An additional rigid test or anal teeth, as well as phosphatic deposits in the body wall, in contrast, are limited to some holothuroid groups; chitinous tentacle-sheaths have so far only been recorded from one species.

The five anal teeth or the plates that surround the anus ring-like also belong to the morphologically almost unknown and rarely studied hard part structures of sea cucumbers. Although first mentioned in the 18th century, the knowledge about this distinct morphological structure in terms of anatomy, stereom differentiation, function etc. is insufficient. The taxonomic distribution of those calcareous elements is variable and particularly well developed in a few clades of actinopodid sea cucumbers (Holothuriida, Molpadida, Dendrochirotida), but unknown in detail.

Our study presents for the first time an overview of the anal teeth of various members of the Holothuriidae — *Actinopyga*, *Holothuria* (*Microthele*), *Holothuria* (*Platyperona*) — obtained by light, laser scanning and scanning electron microscopy, as well as x-ray computed tomography. The modern examples are compared with the only distinct fossil anal teeth known so far (from the Middle Triassic/Anisian ‘Muschelkalk’ of southern Germany). The latter finds confirm that anal teeth have been present in Holothuriida (clade Pneumonophora) for at least 243 million years.

Deciphering evolutionary patterns in the fossil *Metopaster* (Valvatida, Asteroidea) using 3D geometric morphometrics on ultimate superomarginal ossicles

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Metopaster is an extinct genus of goniasterid sea stars comprising about 45 species, mostly found in the Late Cretaceous and Paleogene of Europe. Due to their articulated body structure, sea stars are rapidly split in a jumble of isolated ossicles after death. Thus, isolated ossicles are far more common than complete or almost complete specimens in the fossil record. The marginal ossicles of Goniasteridae are often larger and more robust than any other ossicles, and preserve well. In the case of *Metopaster*, isolated marginal ossicles can bear sufficient morphologic features to be species-specific. In the *Metopaster* species and several other Goniasteridae, the distalmost superomarginal pair of the arms are enlarged. They are called the ultimate superomarginal (USM) and are commonly used for species definition. Based on the anatomy of the USM, Breton (1997) recognized several species in the Late Cretaceous of western France (*M. loirensis*, *M. trichilae*, *M. chilipora* and *M. hypertelicus*) organized in a 10 million years lineage evolving through peramorphosis. In order to investigate Breton's hypothesis, we used 129 USM representing ontogenetic series of 12 *Metopaster* species occurring in the Santonian and Campanian of Charentes (Western France). We used 3D geometric morphometric methods to describe shape variations, setting up a combination of anatomical landmarks, curves and surfaces sliding semi-landmarks. We performed a PCA and we observed that the main axis of shape variations is linked to size and defined by a lengthening and a thickset shape in the extremes. A discriminant analysis confirmed that the USM studied are morphologically distinct and allow for species level identifications. We showed a progressive increasing of the size and of the relative height of the USM during the Campanian. The juvenile of a specie is similar to the adult shape of an older species. Thus, our results show that heterochronies have played an important role in the species evolution. The results are consistent with the initial hypothesis raised by Breton. However, all changes cannot be summarized in a simple peramorphosis trend. At least two species evolved through size decrease. The morphology of the USM were set in distinct modules each accommodating specific functional constraints or level of integration. Evolution of all individual modules followed the same main trend but were modulated by specific constraints.

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Focus on the morphology of *Ophioderma* Müller & Troschel, 1840 from the Algerian west coast

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Brittle stars are a very common species in the Mediterranean Sea, especially on the west Algerian coast. However, studies on these species are very limited. The aim of this study is to discuss the morphology of *Ophioderma* complex species found at the Algerian west coast, using morphological, morphometric and genetic analysis. Individuals found under rocks and stones were collected by scuba diving from three stations at the Mostaganem shallow water coast during a period from November 2020 to September 2021. Our results showed a strong variability between individuals. Most of the studied individuals resembled *O. hybridum* Stöhr, Weber, Boissin & Chenuil, 2020, others *O. zibrowii* Stöhr, Weber, Boissin & Chenuil, 2020 and some *O. longicaudum* (Bruzelius, 1805). The morphometric study displayed a locality effect defined by several variables such as arm length, arm width and interradius length.

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Récolnat: a digital platform for the promotion of 350 years of natural history collections

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The national network of naturalist collections (Récolnat) is a Research Infrastructure (RI) whose scope concerns all natural history collections and their enhancement through research. Récolnat has been on the infrastructure roadmap of the French Ministry of Research (MESR) since 2016 (MENESR, 2016). At the heart of its missions are the production and provision of a corpus of data for the study of current and past biodiversity.

Initiated in 2013 through the e-Récolnat future investment program (ANR-11-INBS-0004), the RI offers a portal giving access to nearly 11 million images and their ancillary data from more than 80 institutions in France (mainland and overseas).

Since 2020, the national network of naturalist collections has consolidated its foundation and scope with the ambition of structuring natural history communities in France. In the form of a scientific interest group (GIS), Récolnat's ambition is to constitute a network of scientific excellence by bringing together professionals and harmonizing practices related to naturalist collections. Museums, universities and research institutions work together to offer increased and privileged access to naturalist collections and their data. In this sense, Récolnat is part of the open data policy and the FAIR principles (findable, accessible, interoperable, reusable). Led by the National Museum of Natural History, Récolnat is also the French hub of the European mirror infrastructure DiSSCo (Distributed System of Scientific Collections).

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Accretionary skeletal growth in post-metamorphic *Paracentrotus lividus* (Echinodermata: Echinoidea)

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While the mechanisms of skeletal growth and development in larval and embryonic sea urchins are well-characterized, the mechanisms underlying skeletal growth in post-metamorphic sea urchins are comparatively more poorly understood. We herein characterize one mode of growth operating in post-metamorphic echinoids: accretionary skeletal growth. We use high-resolution micro-CT scanning to characterize morphological changes taking place in the biomineralized skeleton of the regular euechinoid *Paracentrotus lividus* across a few stages of post-metamorphic growth (from the J2 stage of juvenile development up to small adults). By using micron to sub-micron resolution, we are able to identify and characterize not only different types of stereomic microstructure, but also distinct pulses of growth in the interambulacral and ambulacral plates of the studied individuals. This confirms that accretionary growth in echinoids is non-isometric and that different plates grow at different times during development. To understand the molecular basis for accretionary skeletal growth in these animals, we subsequently used immunohistochemistry and Hybridisation chain reaction RNA-FISH to assay the spatial expression of a number of genes whose activity is known to be involved in elongation of the echinoid larval skeleton. We find that a number of these genes, including *Alx1*, *Jun*, and *Sm50* are expressed during accretionary growth, which implies a similarity of skeletal growth mechanisms across life history stages in echinoids.

Molecular investigations into the basis and role of colouration in the sea star *Linckia laevigata*

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Linckia laevigata is a sea star commonly appearing throughout the Indian and Pacific Oceans. *L. laevigata* display an array of colour morphs, but the biological factors driving their colour diversity remain largely unexplained. In some shallow-water locations (less than one metre deep), *L. laevigata* appear to exist almost exclusively as the royal blue colour morph. This has sparked scientific interest due to *L. laevigata*'s blue pigmentation potentially aiding survival in high temperature and UV environments.

Our current research is investigating the biochemical basis of *L. laevigata* colouration, building upon preliminary sequence data for a pigment-associated protein (informally dubbed the 'colour' gene). In combination with a subset of carotenoids, the 'colour' protein forms the basis of the colours seen with the naked eye. The sequence of this protein seems to differ consistently between royal blue individuals and those with other colours. Furthermore, previous research suggests that *L. laevigata* utilize a range of *colour* gene loci to elicit different colour morphs, with differential expression of these loci being a deciding factor in the overall colour of the animal.

We aim to confirm whether these factors underpin colour differences among *L. laevigata* colour morphs. Using transcriptomic data to inform a range of techniques in protein biochemistry, we are investigating how changes in this gene's sequence affect the structure of the resulting protein, and if this links through to the biology of *L. laevigata* and other sea stars. Future research will use field sampling to determine whether these pigments play a role in altering the colour, physiology and behaviour of *L. laevigata* in the wild.

Glycoproteins: Are they involved in sea urchin adhesion?

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Biomedical adhesives have been increasingly used over the past years, exhibiting attractive features for an array of medical applications. However, achieving strong adhesion in wet environments is still a technological challenge. In this context, biological adhesives secreted by marine invertebrates have three appealing characteristics to incorporate into new underwater biomimetic adhesives: water resistance, nontoxicity and biodegradability. Nevertheless, only a very limited number of marine invertebrates have been used as models.

Up to date, most biomimetic adhesives developed rely on Dopa (3,4-dihydroxylphenylalanine), a post-translationally modified amino acid found in abundance in mussel adhesive proteins. With an important interfacial adhesive and bulk cohesive role, DOPA requires a specific redox environment to function, a feature that limits its biotechnological potential. However, other organisms, with permanent and temporary adhesion, are starting to be used as models, since their adhesive protein sequences have become recently available. Several of these adhesive protein candidates have been pinpointed as glycoproteins.

However, little is still known about temporary adhesion. A transcriptomic differential analysis of sea urchin *Paracentrotus lividus* tube feet identified 16 adhesive/cohesive protein candidates (Pjeta *et al.*, 2020). Additionally, our lab demonstrated that the adhesive secreted by this species is composed of high molecular weight proteins associated with Nacetylglucosamine in a specific chitobiose arrangement (Simão *et al.*, 2020). Taking advantage of adhesion related glycobiology, we aimed to investigate which of these adhesive/cohesive protein candidates were glycosylated through lectin pulldowns, protein identification by mass spectrometry and *in silico* characterization. We demonstrated that at least five of the previously identified protein adhesive/cohesive candidates are glycoproteins (Ventura *et al.*, 2023).

By providing a deeper characterization of these adhesive/cohesive glycoproteins, this work (Fig. 1) provided insights regarding temporary adhesion building blocks and advances our understanding of the key features that should be replicated in future sea urchin-inspired bioadhesives.

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An updated model for sea urchin adhesion

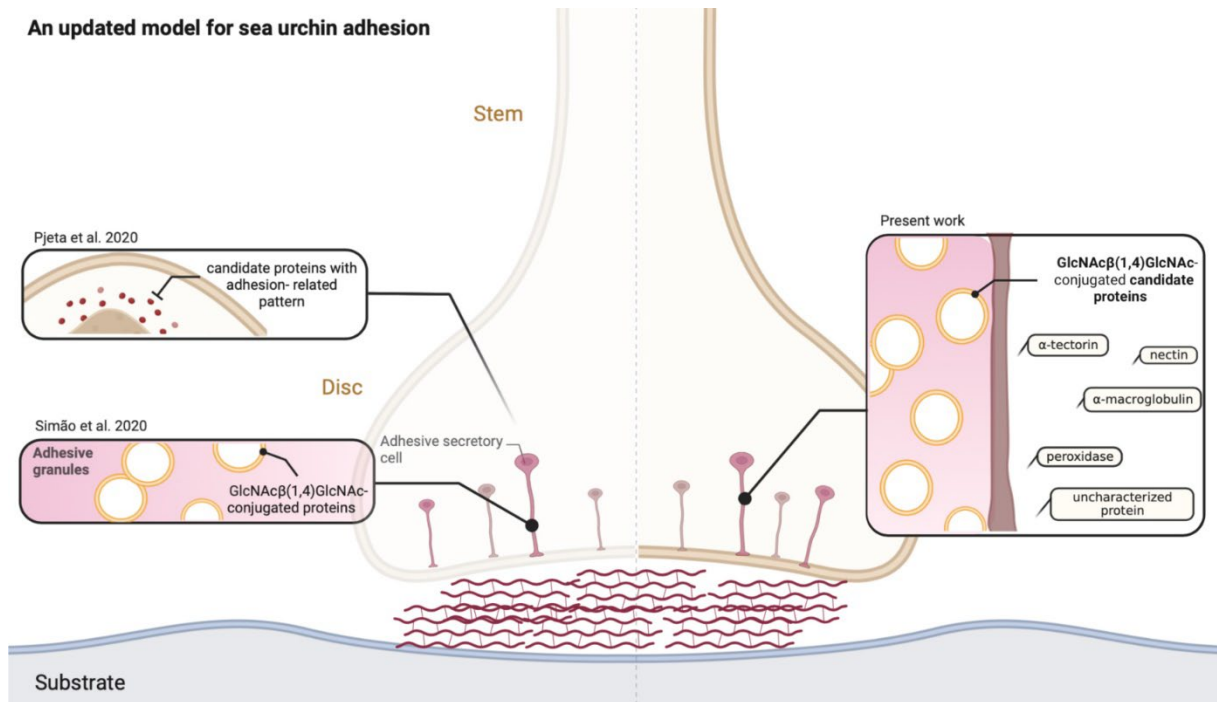


Fig. 1. An updated model for sea urchin temporary adhesion.

Genetic control of blue colour in tropical starfish *Linckia laevigata*

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Heritable colour polymorphisms (CPs), where alternate colour morphs occur within a single species and are genetically controlled, provide an unparalleled opportunity to rigorously assess the role colour plays in the evolution of species. However, until now there was little possibility of investigating CP in marine invertebrates as the pigments responsible for colours in this group are rarely known and even less is known about their synthesis or inheritance.

The iconic seastar *Linckia laevigata* is a rare exception to this rule. This seastar with its attractive appearance and rainbow of colour morphs is a ‘poster child’ for tropical reefs in the Indian and Pacific Oceans. It occurs as a variety of colours including yellow, orange, grey and purple but is best known for its royal-blue morph. Blue pigments are extremely rare in the animal kingdom, and as a result this species is prized by the aquarium trade and is in the top ten most traded marine invertebrates. Exceptionally the pigments responsible for the iconic blue coloration of the seastar *Linckia laevigata* have not only been identified as carotenoproteins, but we have obtained full-length sequences of the gene responsible for the protein moiety.

Here we present the first data to show whether there is a link between variation in the colour gene and visible colour. We also present the first draft genome for this species, which is also the first for the family Ophidiasteridae and show how the ‘colour’ gene has evolved in echinoderms. Our data will provide the opportunity to further investigate the effect of colour on adaptation, ecology, geographical range and speciation in *Linckia* and more widely in other species.

Morphological and molecular phylogenetic analysis of sea cucumbers (Holothuroidea) collected on the Kyushu-Palau ridge

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In contrast to other echinoderms that can be more readily collected, members of the class Holothuroidea present challenges in preservation due to their susceptibility to damage and difficulty in preservation. Despite their broad distribution, there remains a paucity of DNA molecular data for sea cucumbers. Further research employing morphological and molecular phylogenetic identification techniques is necessary to address this deficiency.

During the DY68 voyage, multiple sea cucumber samples were collected in the Kyushu-Palau Sea area. After morphological identification and molecular phylogenetic analysis, 14 sea cucumber species of the Psychropotidae family of the Elasipodida order were found, including 9 known *Benthodytes* species and 1 new species, and 5 *Psychropotes* species. Based on the results of molecular phylogenetic analysis using COI and 16S, we found that the branches of the *Benthodytes* genus were inlaid by the branches of the *Psychropotes* genus to form a paraphyletic group, suggesting that the *Benthodytes* genus can be further divided into two genera. In addition, based on the results of morphological identification, we found that the presence or absence of dorsal appendages cannot be used as a basis for classification, suggesting that the classification of the Psychropotidae family requires other morphological evidence.

The findings of this study will augment the currently limited sea cucumber DNA molecular database, facilitating future taxonomic efforts.

ADRIEN Jérôme 132, P2_50
AGUERA Antonio 67, S5_13
ALBERIC Marie 27, 104, S7_01, S12_04
ALDEA Cristian 138, P1_07
ALEOTTI Alessandra 129, P1_01
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CABROL Léa 44, S6_01
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CANDELA Yves 161, P2_46
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COAKLEY Jack 142, P2_37
COCHRAN J. Kirk 90, S14_03
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CONAND Chantal 37, S11_02
CONEJEROS-VARGAS Carlos A. 136, P1_27
CORBISIER Guillaume 38, S13_01
CORMIER Patrick 39, S1_04
COUBRIS Constance 29, 40, S2_01, S2_05
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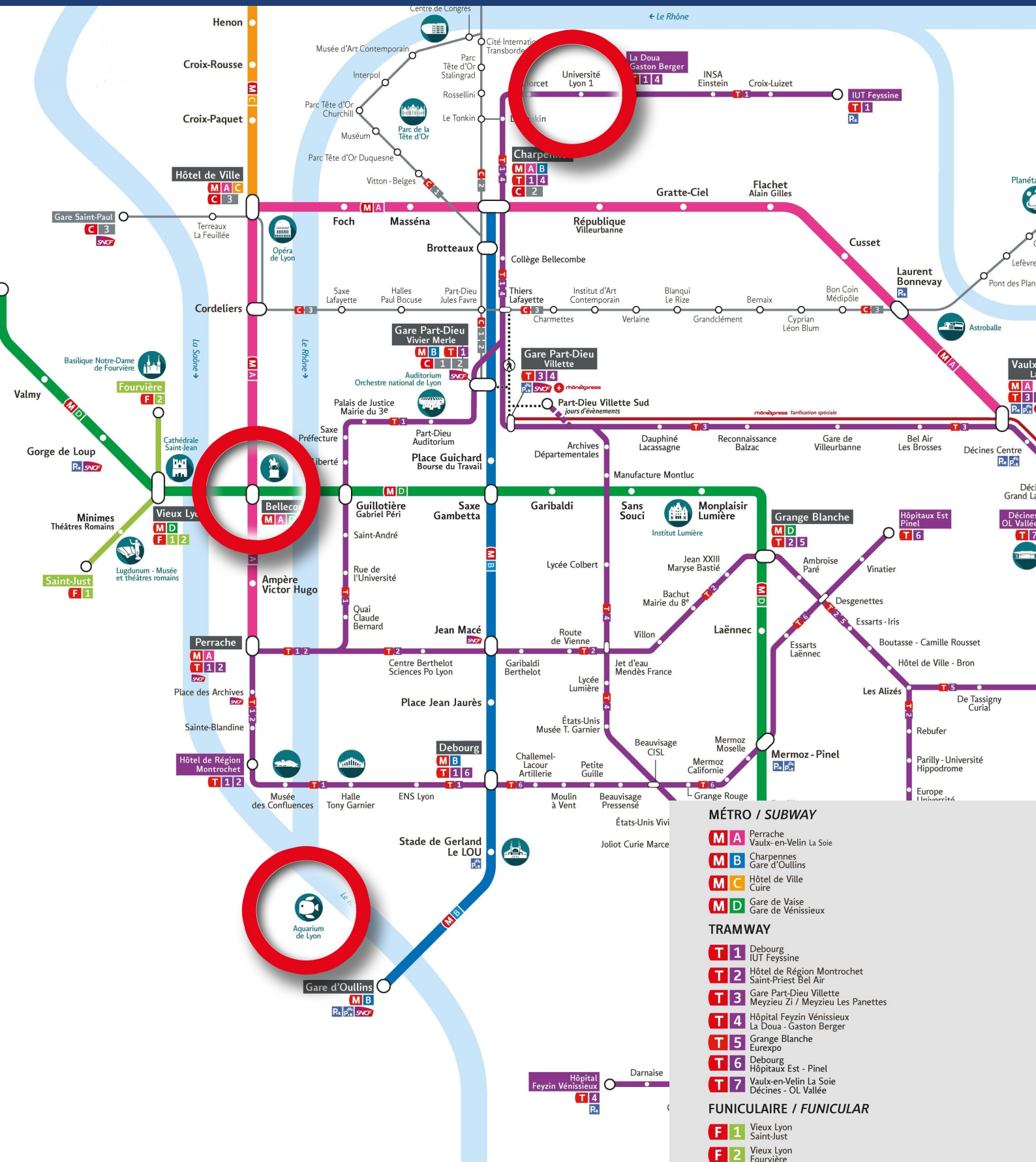
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PUBLIC TRANSPORT MAP



MÉTRO / SUBWAY

- M A** Perrache
Vaulx-en-Velin La Soie
- M B** Charpenne
Gare d'Oullins
- M C** Hôtel de Ville
Cuire
- M D** Gare de Vaise
Gare de Vénissieux

TRAMWAY

- T 1** Debourg
IUT Feysine
- T 2** Hôtel de Région Monrochet
Saint-Priest Bel Air
- T 3** Gare Part-Dieu Villerette
Meyzieu Zi / Meyzieu Les Panettes
- T 4** Hôpital Feyzin Vénissieux
La Doua - Gaston Berger
- T 5** Grange Blanche
Eurexpo
- T 6** Debourg
Hôpital Est - Pinel
- T 7** Vaulx-en-Velin La Soie
Décines - OL Vallée

FUNICULAIRE / FUNICULAR

- F 1** Vieux Lyon
Saint-Just
- F 2** Vieux Lyon
Fourvière

LIGNE DE BUS MAJEURE / TRUNK ROUTE

- C 1** Gare Part-Dieu - Vivier Merle
Cuire
- C 2** Gare Part-Dieu - Vivier Merle
Rillieux Semallès
- C 3** Gare Saint-Paul
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