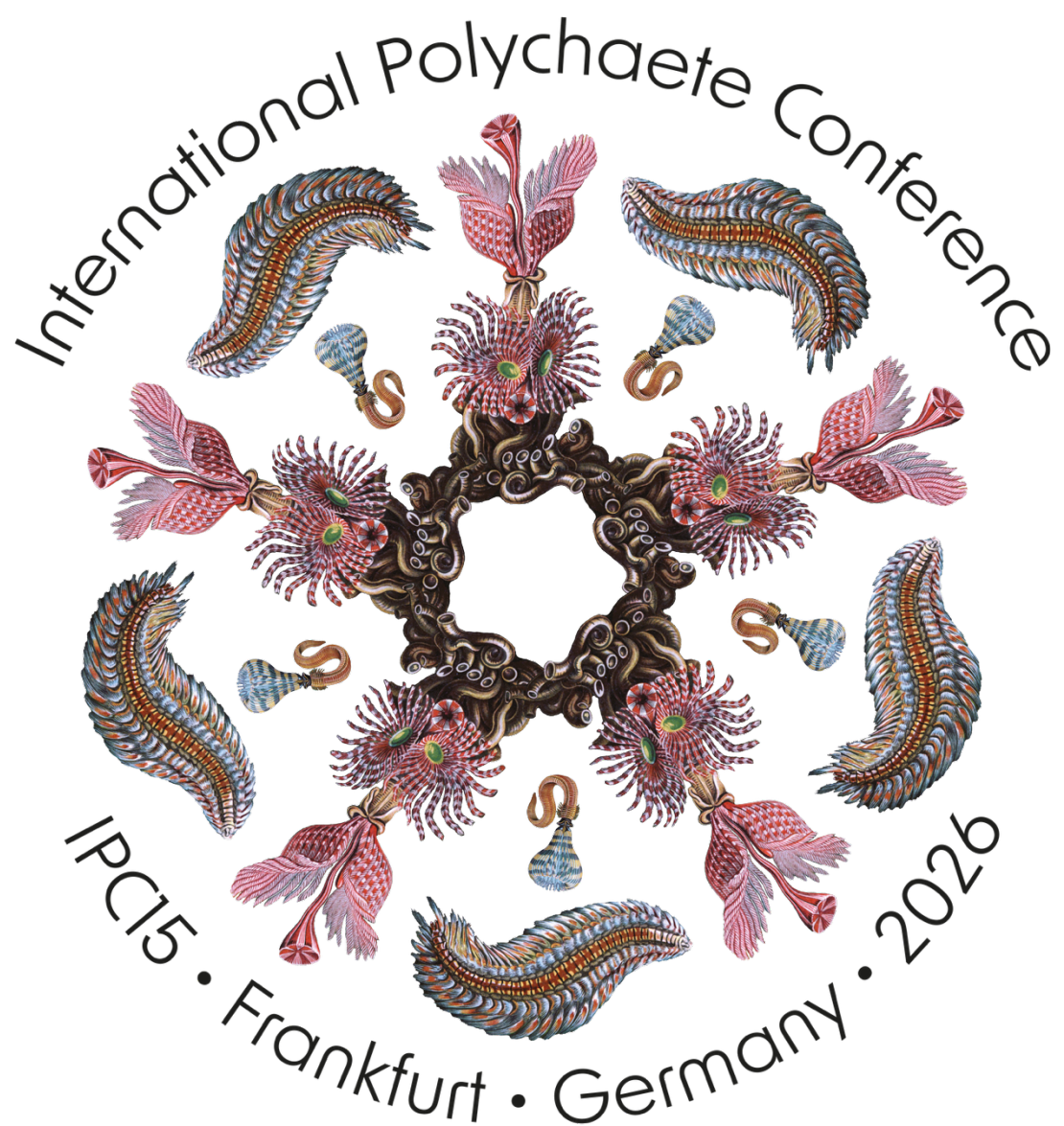




Programme • Abstracts

PROGRAMME OUTLINE

SUNDAY 26 July	MONDAY 27 July	TUESDAY 28 July	WEDNESDAY 29 July	THURSDAY 30 July	FRIDAY 31 July
17 ⁰⁰ - 20 ⁰⁰ Ice-Breaker	Morphology & Physiology	Taxonomy, Systematics & Phylogenomics	Mid-Conference Excursion	Ecology, Biodiversity & Conservation	EvoDevo & Genomics
	9 ⁰⁰ - 10 ⁰⁰ Welcome Session	9 ⁰⁰ - 10 ⁰⁰ Keynote: Joana Zanol		9 ⁰⁰ - 10 ⁰⁰ Keynote: Monika Bright	9 ⁰⁰ - 10 ⁰⁰ Keynote: Elaine Seaver
	10 ⁰⁰ - 11 ⁰⁰ Keynote: Thomas Bartolomaeus	10 ¹⁵ - 11 ¹⁵ Session 6 Taxonomy, Systematics & Phylogenomics		10 ¹⁵ - 11 ¹⁵ Session 12 Ecology, Biodiversity & Conservation	10 ¹⁵ - 11 ¹⁵ Session 18 EvoDevo & Genomics
	11 ¹⁵ - 12 ³⁰ Session 1 Morphology & Physiology	11 ³⁰ - 12 ⁴⁵ Session 7 Taxonomy, Systematics & Phylogenomics		11 ³⁰ - 12 ⁴⁵ Session 13 Ecology, Biodiversity & Conservation	11 ³⁰ - 12 ¹⁵ Invited Talk: Toru Miura
	Lunch Break 12 ³⁰ - 13 ³⁰	Lunch Break 12 ⁴⁵ - 13 ⁴⁵		Lunch Break 12 ⁴⁵ - 13 ⁴⁵	12 ¹⁵ - 13 ⁰⁰ Session 19 EvoDevo & Genomics
	13 ³⁰ - 14 ⁴⁵ Session 2 Morphology & Physiology	13 ⁴⁵ - 15 ⁰⁰ Session 8 Taxonomy, Systematics & Phylogenomics		13 ⁴⁵ - 15 ⁰⁰ Session 14 Ecology, Biodiversity & Conservation	Lunch Break 13 ⁰⁰ - 14 ⁰⁰
	15 ⁰⁰ - 16 ³⁰ Session 3 Morphology & Physiology	15 ¹⁵ - 16 ³⁰ Session 9 Taxonomy, Systematics & Phylogenomics		15 ¹⁵ - 16 ³⁰ Session 15 Ecology, Biodiversity & Conservation	14 ⁰⁰ - 15 ¹⁵ Session 20 Mitagenomics & Phylogenomics
	Session 4 Biodiversity Infrastructure				
	16 ³⁰ - 18 ⁰⁰ Poster Session 5 Posters - A1, B1, C1	16 ⁴⁵ - 17 ⁴⁵ Session 10 Taxonomy, Systematics & Phylogenomics			15 ³⁰ - 17 ⁰⁰ Obituaries General Assembly/Business Meeting
		17 ⁴⁵ - 19 ³⁰ Poster Session 11 Posters - A2, B2, C2	17 ³⁰ - 20 ³⁰ Evening Social & Dinner		
				16 ⁴⁵ - 17 ⁴⁵ Session 16 Taxonomy, Systematics & Phylogenomics	19 ⁰⁰ - 22 ⁰⁰ Conference Dinner

CONFERENCE VENUE

ARTHUR-VON-WEINBERG HAUS Robert-Mayer-Straße 2, 60325 Frankfurt am Main

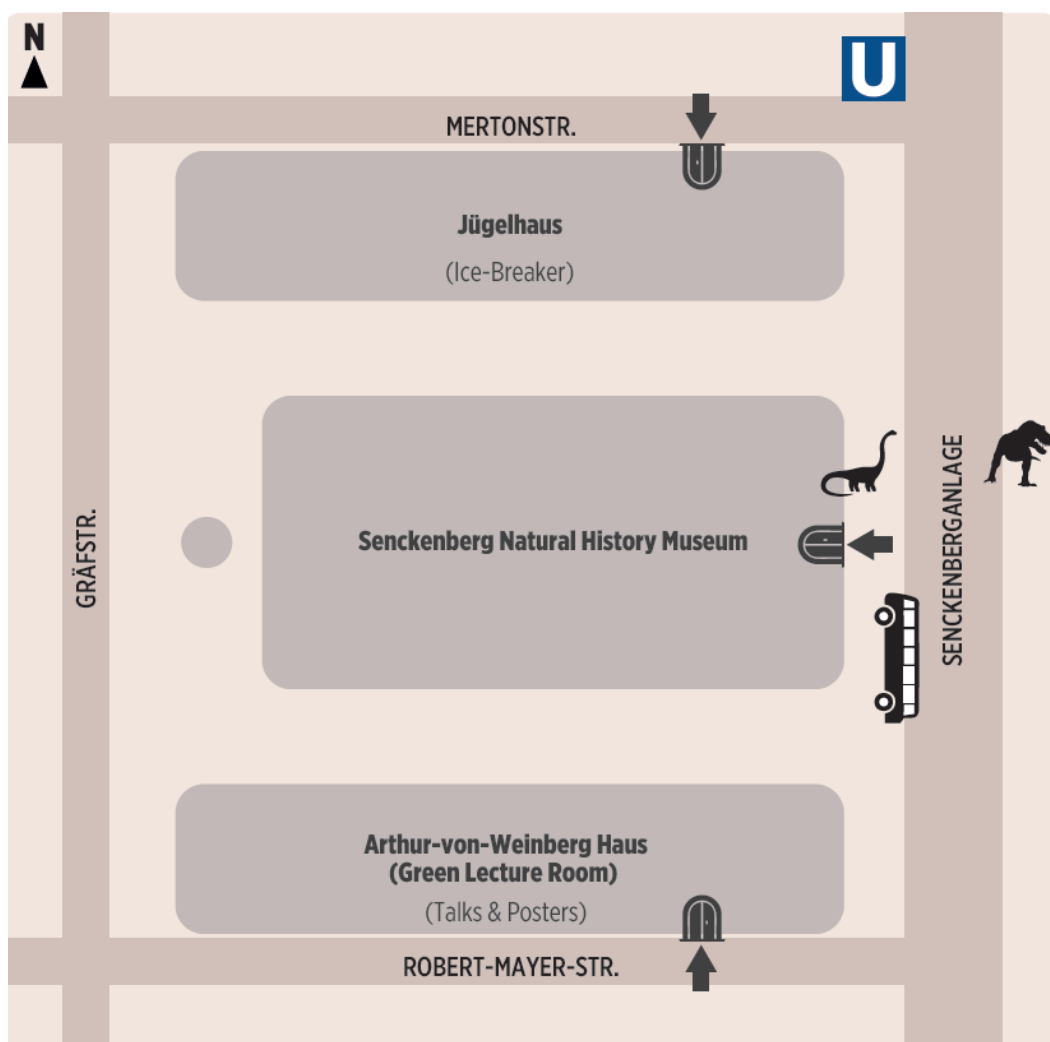
- IPC15 Conference (26th-31th July) – Green Lecture Room (1st Floor)
- Poster Sessions – Glass Bridge, 1st Floor, 2nd Floor

SENCKENBERG NATURAL HISTORY MUSEUM Senckenberganlage 25, 60325 Frankfurt am Main

- Conference Dinner (31th July) – Dinosaur/Elephant Hall
- Wednesday excursions (Messel & Dinner, 29th July) – Departure & Return point at main entrance

JÜGELHAUS Mertonstraße 17, 60325 Frankfurt am Main

- Icebreaker (26th) – Foyer



HOW TO GET HERE

- U-Bahn **U4, U5, U6, U7** from Frankfurt Hbf (main station) to Bockenheimer Warte
- S-Bahn **S3, S4, S5, S6** from Frankfurt Hbf (main station) to Frankfurt West
- Tram **16, 17** from Frankfurt Hbf (main station) to Bockenheimer Warte (16) / Varrentrappstraße (16,17)

PROGRAMME OF PRESENTATIONS

MONDAY 27th July 2026

WELCOME Chair: Ekin Tilic

09:00	0.1 Welcome to Senckenberg Julia Sigwart (Head of Department Senckenberg Marine Zoology)
09:15	0.2 The Polychaete Collections at Senckenberg Dieter Fiege , Ekin Tilic
09:30	0.3 The Senckenberg Ocean Species Alliance – joining forces to alleviate the taxonomic impediment Jan Steger , Torben Riehl, Julia D. Sigwart
09:45	0.4 Establishing a Polychaeta Specialist Group to Advance Global Marine Invertebrate Conservation Julia Silva Beneti , Anne Helene S. Tandberg, Julia D. Sigwart

10:00 **1.0 | KEYNOTE: Morphology**
Thomas **Bartolomaeus**

MORPHOLOGY & PHYSIOLOGY Chair: Katrine Worsaae

11:15	1.1 Ultrastructural 3D analysis of the photoreceptive structures in a basal branching annelid, <i>Psammodrilus balanoglossoides</i> (Psammodrilidae, Chaetoptera) Günter Purschke
11:30	1.2 Characterization of high-resolution tubular eyes in <i>Eupolyodontes</i> (Acoetidae) scale worms Brett C. Gonzalez , Michael Bok, Katrine Worsaae, Karen J. Osborn, Anders Garm
11:45	1.3 The secret(e) is out - Forays into understanding neuroglandular interactions in <i>Platynereis dumerilii</i> Alexandra Kerbl , Gáspár Jékely
12:00	1.4 * A bloody mystery – morphological investigations shed light on the function of the glycerid venom system (Glyceridae, Annelida) Antonia Dopp, Paul Ritter-Kalke, Jenna Moore, Patrick Beckers, Conrad Helm
12:15	1.5 * Differential Gene Expression analysis unravels different molecular basis of sex determination in three sexual systems in <i>Ophryotrocha</i> Jose María Lorente-Sorolla Pons , Sergi Taboada, Irene de Sosa, Ana Riesgo, Cristina Lorenzi

MORPHOLOGY & PHYSIOLOGY Chair: Glafira Kolbasova

13:30	2.1 <i>Ophryotrocha labronica</i> (Dorvilleidae) as a model annelid species for eco-evolutionary and ecotoxicology studies in a changing ocean Gloria Massamba N'Siala
13:45	2.2 From brackish origins to freshwater success: osmoregulation in <i>Hypania invalida</i> Serena Mucciolo , Maciej Studzian, Shrikant Vichare, Tomasz Mamos, Tomasz Rewicz, Łukasz Pułaski, José María Martín-Durán, Andrea Desiderato
14:00	2.3 * When Structure Is Not Enough: Absorption Shapes Color in Sea Mouse Bristles Carina Bittner , Alexander Kichigin, Benjamin Apeleo-Zubiri, Shosuke Ito, Kazumasa Wakamatsu, Ekin Tilic, Nicolas Vogel
14:15	2.4 Diversity and Development of the Prototroch in Polychaeta Jörn von Döhrn
14:30	2.5 * Feather-Dusters and Their “Feathers”: Novel Comprehensive Data on Anatomy Provide New Insights into Taxonomy, Function, and Evolution within Sabellidae Tim Sharet , Nadezhda Rims kaya-Korsakova

MORPHOLOGY & PHYSIOLOGY / BIODIVERSITY INFRASTRUCTURE Chair: Conrad Helm

15:00	3.1 Sclerolium tubeworms (Annelida, Siboglinidae) colonize degrading bones Nadezhda Rimskaya-Korsakova , Mari Heggernes
15:15	3.2 How to identify the ‘Freak’, or convergent evolution of head appendages in Scalibregmatidae Paul Kalke , Katrine Worsaae, Patrick Beckers, Alejandro Martinez Garcia, Conrad Helm
15:30	3.3 First Deep Learning approach to study the anatomy of Terebellidae Sars, 1835 (Annelida, Trichobranchidae) María Barroso , María Candás, Julio Parapar, Juan Moreira, Tomás Golomb Durán
15:45	3.4 * Quantifying disparity in annelid locomotion using discrete non-morphological characters Harry Savage , Russell Garwood, Jane Reeves, Tom Roper-Smith, Robert Sansom, William Sellers, Luke Parry
16:00	4.1 The National Polychaete Collection of Mexico, ICML-UNAM, a 48 years adventure Vivianne Solis-Weiss , Pablo Hernández-Alcántara
16:15	4.2 From Ecology to Omics: Dataset Publication and the Role of Research Infrastructures in Polychaete Biodiversity Science Christos Arvanitidis , Daniel Martin, Rafael Sardá

TUESDAY 28th July 2026

09:00 **6.0 | KEYNOTE: Taxonomy, Systematics & Phylogeny**
Joana Zanol

TAXONOMY, SYSTEMATICS & PHYLOGENY Chair: Jenna Moore

- 10:15 **6.1 | A paradox of *Ficopomatus*: a common but poorly known group of notorious estuarine biofoulers and bioinvaders**
Elena Kupriyanova, Ravil Abdriashitov, Simon Ho
- 10:30 **6.2 * | *Spirobranchus* revisited: Morphology and sequence data tell different tales**
Ivison Cordeiro Brandão, João Miguel de Matos Nogueira, Elena Kupriyanova
- 10:45 **6.3 | The Pandora' box reopened: the *Amphiglena* enigma**
Matteo Putignano, Mariana Strauss, Maria Cristina Gambi, Adriana Giangrande, María Capa, Ekin Tilic
- 11:00 **6.4 | Dusting off the arrangement of the flowers of the sea: Phylogeny and systematics of Sabellidae (Annelida) via targeted exon-capture and genome-skimming phylogenomics**
Ekin Tilic, María Ana Tovar-Hernández, Adriana Giangrande, Greg Rouse

TAXONOMY, SYSTEMATICS & PHYLOGENY Chair: Josefin Stiller

- 11:30 **7.1 | Revisiting the diversity of 'spaghetti worms' (Terebellidae, Polychaeta) from the French Southern and Antarctic Lands: new species, redescrptions and hidden synonymies**
Nicolas Lavesque, Yann Lelièvre, Thomas Saucède, Guillemine Daffe, Stéphane Hourdez, Pat Hutchings
- 11:45 **7.2 | The biodiversity and phylogeny of *Loimia* (Terebellidae) in China**
Yanjie Zhang, Deyuan Yang, Caifang He, Yanan Sun
- 12:00 **7.3 | Systematic Revision of *Eupolyornia* Verill, 1900 (Annelida, Terebellidae) in European waters**
Maël Grosse, Nicole Lidholm, Andrea Toso, Joachim Langeneck, Nicolas Lavesque, Daniel Martin, Arne Nygren
- 12:15 **7.4 | The discovery of Australian terebellids**
Pat Hutchings, Emily McLaren, Nicolas Lavesque
- 12:30 **7.5 | Phylogeny of the tribe Ampharetini Malmgren, 1866**
Yessica Chávez López

TAXONOMY, SYSTEMATICS & PHYLOGENY Chair: María Capa

- 13:45 **8.1 | Museomic insights into the evolutionary history and biogeography of ramified syllids**
Maria Teresa Aguado, Guillermo Ponz-Segrelles, Thilo Schulze, Naoto Jimi Toba, Ekin Tilic, Conrad Helm, Joelle Van der Sprong, Nicole de Voogd
- 14:00 **8.2 * | No Worm Without its Host: Museum-Based Phylogenomics of Sponges Hosting *Ramisyllis***
Joëlle van der Sprong, Thilo Schulze, Nicole J. De Voogd, Maria Teresa Aguado
- 14:15 **8.3 * | Rare Group in an Understudied Sea: New Insights into Autolytinae (Syllidae, Annelida) Systematics**
Duarte Martins, Marcos A. L. Teixeira, Gustav Paulay, Susana Carvalho, Patricia Álvarez-Campos
- 14:30 **8.4 | One ring to rule them out: integrative taxonomy clarifies the identity of the alleged *Nereis agulhana* Day, 1963 (Annelida: Nereididae) in the Mediterranean Sea**
Joachim Langeneck, Desirée Dimichele, Pero Ugarković, Maria Rousou, Jean-Georges Harmelin, Luigi Musco
- 14:45 **8.5 | New fashion trends unlocked: Undescribed Nereididae and Phyllodocidae (Annelida, Polychaeta) from the Red Sea, Arabian Gulf and Mediterranean Sea**
Marcos A. L. Teixeira, Vitaly Syomin Shirshov, Joachim Langeneck, Chloé Julie Lois Fourreau, Glafira D. Kolbasova, Arne Nygren, Eva Aylagas, Susana Carvalho

TAXONOMY, SYSTEMATICS & PHYLOGENY Chair: Brett Gonzalez

- 15:15 **9.1 | Bringing together international taxonomists to study the annelid fauna of the Aleutian Trench – Presentation of results from an almost finished project**
Karin Meißner, Nicolas Lavesque, Martin Schwentner
- 15:30 **9.2 | An integrative revision of *Eunoe*: implications for generic boundaries in Polynoidae**
Martha W. Everett, Anna Koroleva Lomonosov, Nicolas Straube, Nataliya Budaeva
- 15:45 **9.3 * | Rethinking *Bylgides* (Polynoidae): Integrating morphology and phylogeny**
Eva Samson, Martha W. Everett, Tom Alvestad, Nataliya Budaeva
- 16:00 **9.4 * | Freshwater colonization by a scaleless scale worm: *Pisone mizuchi* Shimooka & Jimi in Shimooka et al., 2026 (Sigalionidae)**
Satoshi Shimooka, Akihito Omori, Natsumi Hookabe, Yuma Fujino, Naoto Jimi
- 16:15 **9.5 | Fourteen Years in the Mud: Revisiting an Orbiniidae Taxonomic Thriller**
Paul Wolf

TAXONOMY, SYSTEMATICS & PHYLOGENY Chair: Nataliya Budaeva

- 16:45 **10.1 | Integrative taxonomy to resolve species complexes and genetic typification of original polychaete names from type localities**
Torkild Bakken, Jon Anders Kongsrud, Eivind Oug, Tom Alvestad, Maël Grosse, Arne Nygren, Nataliya Budaeva
- 17:00 **10.2 | Clarifying the presence of *Eunice kinbergi* Ehlers, 1868 and *Eunice aphroditois* (Pallas, 1788) in South Africa**
Jyothi Kara, Robin Lacey, Carol Simon
- 17:15 **10.3 * | Systematic revision of *Arabella iricolor* complex in Korean waters, with implications for Northeast Asian waters**
Seong-Hun Kang, Jin-Ho Park
- 17:30 **10.4 | The "Giant" in the State Museum of Natural History Karlsruhe - only another Bobbitt worm?**
Markus Böggemann

THURSDAY 30th July 2026

09:00	12.0 KEYNOTE: Ecology, Biodiversity & Conservation Monika Bright
ECOLOGY, BIODIVERSITY & CONSERVATION Chair: Christoph Bleidorn	
10:15	12.1 Polychaete Diversity Through the Lens of iNaturalist Andrew Davinack , Leslie Harris
10:30	12.2 Distribution of Paraonidae Species (Annelida: Polychaeta) Along the Aegean and Levantine Seas (Eastern Mediterranean) Deniz Erdoğan Dereli , Melih Ertan Cinar
10:45	12.3 Temporal changes in soft-bottom polychaete assemblages of the Bay of Biscay (NE Atlantic) Maxime Cottin-Bournois, Lise Bacouillard, Salomé Coignard, Louise Lanrivain, Esteban Toribio, Yann Patry, Thomas Pommier, Philippe Bornens, Paulo Bonifácio
11:00	12.4 Current Status of Benthic Polychaeta in ASEAN Countries Izwandy Idris , Jonathan Anticamara, Joko Pamungkas, Itchika Sivaipram, Aqilah Syahirah Mohd-Azhar, Nur Asha Shahira Zamri, Zainul Abid Puthiyaveetille-Manningayil, Abigail Garcia, Audrey Marie Atienza, Mark Lester Geonzon, Marlon Gutierrez, Worrawit Boonrit
ECOLOGY, BIODIVERSITY & CONSERVATION Chair: Carol Simon	
11:30	13.1 Microbes Are Everywhere, but Whose Are They? Robust Workflows and Host Filtering in the <i>Ramissyllis</i> – <i>Petrosia</i> Nested Holobiont Theda U.P. Bartolomeaus , Joëlle van der Sprong, Maria Teresa Aguado
11:45	13.2 A multi-trait phylogenetic roadmap to predict venom evolution in Polychaeta: Integrating ecological traits for systematic bioprospecting Ana P. Rodrigo , Carolina Madeira, Cátia Gonçalves, Jorge Lobo-Arteaga, Ana Rita Grosso, Pedro M. Costa
12:00	13.3 From host species to oceanic regions: multiscale structuring of Syllidae microbiomes Patricia Alvarez-Campos , Pau Bernadó, Almudena Álvarez-Fernandez, Ana Riesgo, Cristina Díez-Vives
12:15	13.4 Fields of worms: distribution, population dynamics and unresolved taxonomy of massive <i>Bispira</i> aggregations in the Mediterranean Sarah Faulwetter , Capa María Capa, Evangelos Tzanatos, Alexis Ramfos, Matteo Putignano
12:30	13.5 EuroWorm: Accelerating global marine annelid biodiversity research with open genomic data for European species Jenna Moore , Maria Teresa Aguado, Christoph Bleidorn, Cristina Garilao, Carola Greve, Conrad Helm, Sarah Lemer, Karin Meißner, Alexander Sang-Yae Suh, Ekin Tilic
ECOLOGY, BIODIVERSITY & CONSERVATION Chair: Barbara Mikac	
13:45	14.1 Cave dwelling polychaetes from the Balearic Islands María Capa , Alejandro Martínez, Eva Mangado-Mier, Shantika M. Sastraprawira, Francesc Gràcia, Daniel Martin
14:00	14.2 Four Decades Underappreciated: Annelid Genetic Diversity and Connectivity from the Porcupine Abyssal Plain Sustained Observatory, Northeast Atlantic Laetitia Guntón , Amanda Serpell-Stevens, Tammy Horton
14:15	14.3 Towards understanding high Arctic deep-sea annelid diversity and connectivity Nataliya Budaeva , Tom Alvestad, Carolin Uhler, Andrey Vedenin
14:30	14.4 * Population structure of <i>Lamelligibrachia barhami</i> (Siboglinidae) across the Eastern Pacific methane seeps Marharyta Abashkina , Josefin Stiller, Marina McCowin, Greg Rouse
14:45	14.5 Population connectivity of vent scale worms along Indian Ocean ridges Yadong Zhou , Xi Chen, Terue C. Kihara, Sook-Jin Jang, Jin Sun
ECOLOGY, BIODIVERSITY & CONSERVATION Chair: Sarah Faulwetter	
15:15	15.1 Arrive, survive, and (sometimes) thrive: Invasion of Galveston Bay, TX by <i>Ficopomatus</i> spp. (Annelida: Serpulidae) Vanessa Fernandez-Rodriguez, Anja Schulze
15:30	15.2 Stowaways on molluscs: unveiling non-native polydorin pests in Adriatic oyster aquaculture Barbara Mikac , Eugenio Fossi, Marina Antonia Colangelo, Sara Dessì, Giuseppe Prioli, Marijana Pećarević, Krno Bonačić, Borut Mavrič, Valentina Pitacco, Federica Costantini
15:45	15.3 Annotated Checklist of Polychaeta from Namibia with Updated Synonymy, Distribution, and Systematic Notes Amoré Malan , Carol Simon, Jyothi Kara, Dylan Clarke, Mayday Haulofu, Robyn Payne, James Cook, Gerhard de Jager, Kevin Schmidt, Aiden Biccard
16:00	15.4 Habitat preference and life-history traits of polydorid species (Annelida: Spionidae) inhabiting farmed and wild molluscan shells in France and South Africa Yuki Nagai , Jean-Claude Dauvin, Carol A. Simon, Kenji Okoshi, Waka Sato-Okoshi
16:15	15.5 DNA Metabarcoding the gut-contents of alien tubeworm, <i>Diopatra aciculata</i> (Annelida: Onuphidae) suggests scavenging in two estuaries in South Africa Carol Simon , Hendre van Rensburg & Conrad Matthee
ECOLOGY, BIODIVERSITY & CONSERVATION Chair: Elena Kupriyanova	
16:45	16.1 * Hidden Diversity in Rock-Boring Phascolosoma (Phascolosomatidae: Sipuncula) Structured by Latitude and Substrate, with Implications for Cosmopolitan Distribution Chiharu Shinomiyai , Luna Yamamori, Takahiro Sugiyama, Hiroshi Kajihara, Naoto Jimi, Genki Kobayashi, Akira Asakura, Michitaka Shimomura, Ryutaro Goto
17:00	16.2 Host-associated camouflage without genetic differentiation in a holothurian-ectoparasitic scale worm Takahiro Sugiyama, Genki Kobayashi, Chloé Julie Lois Fourreau, Kohei Hamamoto, James Davis Reimer, Michitaka Shimomura, Akira Asakura, Ryutaro Goto
17:15	16.3 Diversity, connectivity and microbial composition in Iberian <i>Osedax</i> : Insights from newly discovered species Teresa Alonso-Hartanyil , Andrea Corral-Lou, Marta Turon, Carlota Gracia-Sancha, Almudena Álvarez-Fernández, Javier Cristobo, Pilar Ríos, Cristina Boza, Alejandra Calvo-Díaz, César González-Pola, Eneko Aierbe, Francisco Baldó, Ricardo Sánchez-Leal, Teresa Montañó, Sergi Taboada
17:30	16.4 * How does annelid fauna respond to the Atlantification of an Arctic fjord in western Svalbard? Zofia Maurer , Tom Alvestad & Nataliya Budaeva

FRIDAY 31th July 2026

09:00 **18.0 | KEYNOTE: EvoDevo & Genomics**
Elaine **Seaver**

EVODEVO & GENOMICS Chair: Allan Carrillo-Baltodano

- 10:15 **18.1 |** Syntenic Constraints and the Biocementation Toolkit: Integrating Functional Genomics in the Mediterranean Reef-Building Sabellaria (Annelida: Sabellariidae)
Shrikant Vichare, Serena Mucciolo, Antony Paul Chakkiath, Tomasz Rewicz, Tomasz Mamos, Andrea **Desiderato**
- 10:30 **18.2 |** Cell-by-cell reconstruction of a polychaete: the developmental cell lineage of *Platynereis dumerilii* revealed by light-sheet microscopy
Mette **Handberg-Thorsager**, Beke Lohmann, Detlev Arendt, Philipp Keller, Jan Huiskens
- 10:45 **18.3 |** A first look at the Charlie-Chaplin-Worm genome
Josefin **Stiller**, Tillman Schell, Alexander Ben Hamadou, Carola Greve, & Ekin Tilic
- 11:00 **18.4 |** How to Build a Worm—Studies on *Ophryotrocha labronica* (Eunicida, Dorvilleidae)
Meghan **Yap-Chiongco**, Éloïse Defourneaux, Alessandro Formaggioni, Madeleine Aase-Remedios, Shoyo Sato, Katrine Worsaae

EVODEVO & GENOMICS Chair: Maria Teresa Aguado

- 11:30 **19.0 | Invited Talk: EvoDevo & Genomics**
Toru **Miura**
- 12:15 **19.1 |** Smaller but faster: heterochronic shift in gene expression leads to larval onset of spermatogenesis and miniaturised males
Katrine **Worsaae**, Alice Rouan, Madeleine Aase-Remedios, Norio Miyamoto
- 12:30 **19.2 * |** Evolutionary routes to miniaturization: Hox gene evolution and patterning in Annelida
Éloïse **Defourneaux**, Meghan Yap-Chiongco, Madeleine Aase-Remedios, Alice Rouan, Alessandro Formaggioni, José-Maria Martín-Durán, Katrine Worsaae
- 12:45 **19.3 |** The evolution of developmental system drift in axial specification in Annelida
Allan **Carrillo-Baltodano**, Emmanuel Haillot, Steffanie Mutiara, Jimena Montagne, Yun-Ju Lee, Tsai-Ming Lu, David Ferrier, Artenis Pashaj, Imran Luqman, Stephan Schneider, Jose Martin-Duran

MITOGENOMICS & PHYLOGENOMICS Chair: Mette Handberg-Thorsager

- 14:00 **20.1 |** Intron group II in annelid mitochondrial genome: not so rare as previously thought. A case of *Sagitella kowalewskii* Wagner, 1879 (Typhloscolecidae)
Glafira **Kolbasova**, Tatyana Neretina, Alexandra Bezmenova, Margarita Ezhova
- 14:15 **20.2 * |** Mitochondrial genomes provide insights into the genetic diversity and evolution of *Dodecaceria*
Thilo **Schulze**, Mateo Carvajal, Melina Möller, Maria Teresa Aguado, Conrad Helm & Christoph Bleidorn
- 14:30 **20.3 |** Evolutionary relationships and mitochondrial genome diversity in Spionidae (Annelida)
Viktoria **Bogantes**, Ana Kathyren Bracken, Damien S. Waits, Karin Meißner, Kenneth M. Halanych
- 14:45 **20.4 |** Genomic insights into calcareous tubeworm phylogeny: Development and application of a Polychaete-specific UCE probe set
Yanan **Sun**, Qinghua Bao & Elena Kupriyanova
- 15:00 **20.5 |** One species, two mitochondrial genomes: extreme heteroplasmy and its implications for annelid molecular inference
Sam **Pazoki** & Torsten Struck

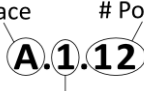
OBITUARIES Chair: Ekin Tilic

- 15:30 **21.0 |** Gérard Bellan (1934–2026): a polychaete taxonomist and benthic ecologist whose scientific excellence stood alongside his good humor and warmth
Paulo **Bonifácio**
- 15:45 **21.1 |** David George (1938–2024)
Pat **Hutchings**

INTERNATIONAL POLYCHAETOLOGY ASSOCIATION

- 16:00 **22.0 |** International Polychaetology Association Meeting

LIST OF POSTERS

Place # Poster

 # Poster Session

A = Glass Bridge
B = 1st Floor
C = 2nd Floor

1 = Monday 27th July
2 = Tuesday 28th July
3 = Thursday 30th July

- A.1.1** Inventory, mapping and revision of Swedish Terebellidae through large scale megabarcoding using oxford nanopore technology (ONT)
 Maël **Grosse** & Arne Nygren
- A.1.2** Between a rock and a holdfast: polychaete diversity in *Ecklonia maxima* holdfasts from the Cape Peninsula, South Africa
 Courtney Bailey, Zeane Nel, Nasreen Peer & Carol **Simon**
- A.1.3** Opening a can of worms from the Discovery collections: Annelids from the Porcupine Abyssal Plain Sustained Observatory (PAP-SO) Northeast Atlantic
 Amanda **Serpell-Stevens**, Laetitia Gunton & Tammy Horton
- A.1.4** New records of Dorvilleidae (Annelida: Eunicida) from the Romanian Black Sea coast, including the first record of *Protodorvillea artemidis* for the Black Sea
 Mihaela Cosmina **Teodorof**, Victor Surugiu, Camelia Dumitrache, Adrian Filimon, Valeria Abaza, Raluca Băncilă & Raluca Băncilă
- A.1.5** High dominance of polychaetes in terms of abundance and species richness and their relationship with the seasonal variability of a macroinfaunal community in the Quintupeu fjord, Northern Patagonia, Chile
 Eulogio **Soto** & Diego Droguett
- A.1.6** New records of *Terebellides* species from the British Isles and nearby waters
 Teresa **Darbyshire** & Michael Harrison
- A.1.7** First record of boring spionid species on European flat oyster *Ostrea edulis* in Japan
 Maho **Taniguchi**, Sayaka Teramoto & Waka Sato-Okoshi
- A.1.8** Biodiversity of polychaetes in oyster reefs of the northern South China Sea
 Jinghuai **Zhang**, Yaohui Chen, Xiaomin Li & Xiaokang Ji
- A.1.9** Fauna D'Italia – Sabellida: a new comprehensive guide to the European Fan Worms species
 Adriana Giangrande, Cinzia Gravili & Matteo **Putignano**
- A.1.10** Gateways of invasion: unveiling Polychaeta diversity in Tunisian ports
 Yann **Toso**, Joachim Langeneck, Desirée Dimichele, Kawther Kaziz, Luigi Musco, Stefano Piraino, Mohamed Banni & Maria Giovanna Parisi
- A.1.11** Scaling up polychaete community assembly: scale-dependent environmental filtering, distance decay and upwelling effects
 Manoela C Abreu, Gustavo Mattos, Paulo C Paiva & Rodolfo L **Nascimento**
- A.1.12** When space gives way to time: global latitudinal patterns in polychaete β -diversity
 Luiza R Souza, Janne Soininen, Paulo C Paiva & Rodolfo L **Nascimento**
- A.1.13** Diversity and distributional patterns of soft-bottom polychaetes in Slovenian waters
 Valentina **Pitacco**, Lisa Sandri, Federica Nasi & Borut Mavrič
- A.1.14** Hidden bristles revealed; the potential for extension of Polychaeta knowledge in Aotearoa New Zealand via a citizen-naturalist social-network of observers.
 Fiona **MacLean** & Geoffrey Read
- A.2.15** Unravelling the fatty acid profiles of different polychaete species influenced by river run-off
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- A.3.40** Assessing the biodiversity of intertidal annelids across the European North Atlantic coastline through morphological and molecular approaches
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Brice **Morhain**, Sarah Samadi & Stéphane Hourdez
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Alvin **Han**, Rike Schwanke, Leslie Pan, Victoria Witte, Elizabeth Hambleton, Giulia Ghisleni & Detlev Arendt
- B.1.43** Multi-loci high-throughput genotyping of the *Platynereis dumerilii* species complex along European Coastlines
Rike **Schwanke**, Leslie Pan, Alvin Han, Victoria Witte, Julika WeiB, Christoph Bleidorn & Detlev Arendt
- B.1.44** A multiomic perspective on the invasive polychaete – *Hypania invalida* (Grube, 1860)
Shrikant Vichare, Tomasz Rewicz, Tomasz Mamos & Andrea **Desiderato**
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Paul **Wolf**
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Pablo Palau, Rannyele Passos Ribeiro, Félix Sánchez-Valverde, Conrad Helm, Yolanda Leon, Marta Magariños & **Maria Teresa Aguado**
- B.1.47** Towards the connectome of the 6-day-old *Platynereis dumerilii* larva
Kata **Szabó**, Karel Mocaer, Alexandra Kerbl & Gáspár Jékely
- B.1.48** Genomic Underpinnings of Miniaturised Annelids
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Jane **Reeves**, Russell Garwood, Luke Parry & William Sellers
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Pablo Hernández-Alcántara, Vivianne **Solis-Weiss** & Rosario Mateos-Valdez
- B.2.52** Revision of *Euphionella* Monro, 1936 and *Dilepidonotus* Hartman, 1967 (Polychaeta, Polynoidae, Lepidonotinae)
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- B.2.53** Life on the back end: a new genus of epibiotic serpulids from deep-sea wood-fall chitons
Louka **Wijnmaalen**, Elena Kupriyanova, Nataliya Budaeva, Julia Sigwart¹ & Ekin Tilic
- B.2.54** Long Hidden in Tubes: First Steps Towards Resolving the *Filograna/Salmacina* (Serpulidae)
Hannah Annika **Cremer**, Elena Kupriyanova, Christina Sagorny, Yanan Sun & Ekin Tilic
- B.2.55** Splitting more: cryptic diversity within *Scolecopsis squamata* species complex (Annelida: Spionidae) reveals a new species of *Scolecopsis* from the Black Sea
Victor **Surugiu** & Oana Paula Popa

- B.2.56** What's in a Name? Gender Representation in Polychaete Eponyms
Damhnait **McHugh** & Payton Gore
- B.2.57** Deep-sea polynoid scale worms from the western Pacific: hidden diversity, phylogenetic instability, and morphological character evolution
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- B.2.58** Molecular analyses detect depth-structured diversity in *Phylo norvegica* (Annelida, Orbiniidae) in Norwegian waters
Miguel A. **Meca**, Tom Alvestad, Luis Martell & Nataliya Budaeva
- B.2.59** First integrative approach to *Theodisca laevigata* (Grube, 1855) complex with the reinstatement of *Theodisca anserina*
Ricardo Ignacio Castro **Álvarez**, Joachim Langeneck, Isabel Carmona & Nataliya Budaeva
- B.2.60** Demystifying the *Leitoscoloplos robustus* and *Leitoscoloplos fragilis* complexes (Annelida: Orbiniidae) in the Southwestern Atlantic: an integrative taxonomic approach
Ricardo Ignacio Castro **Álvarez**, Nataliya Budaeva, Miguel A. Meca, Erica Keppel, André Garraffoni & A. Cecília Amaral
- B.2.61** New species of *Prionospio* (Annelida: Spionidae) from Guanabara Bay, Brazil (Southeast Atlantic Ocean)
Gabriela Baluardo Tristão Gomes, Joana Zanol, Antônio Peixoto, Vitória Reis, Paulo C. Paiva & Ricardo Ignacio Castro **Álvarez**
- B.2.62** An undescribed genus and two undescribed species of Acrocirridae from the western Pacific
Naoto **Jimi**, Satoshi Shimooka, Chong Chen & Natsumi Hookabe
- B.3.63** Magelonidae Cunningham & Ramage, 1888 – an update on key morphological characters
Katie **Mortimer-Jones**
- B.3.64** Revision of the family Phascolosomatidae Stephen & Edmonds, 1972 (Sipuncula)
Julio **Gómez-Vásquez**
- B.3.65** A first assessment of polychaetes diversity in the North Adriatic Sea using DNA barcoding
Lisa **Sandri**, Federica Nasi, Elisa Banchi & Tamara Cibic
- B.3.66** Molecular phylogenetic hypothesis of *Leodice* Lamarck, 1818 (Annelida: Eunicidae)
Thais Kananda Silva Souza, Ricardo Álvarez, Ha-Eun Lee, Gi-Sik Min, Nataliya Budaeva & Joana **Zanol**
- B.3.67** Digital collections of annelids: defining priorities for the digitalization of different taxa
Camila Simões, Eduardo Dalcin & Joana **Zanol**
- B.3.68** Species delimitation of *Oenone fulgida* (Lamarck, 1818) (Oeononidae: Eunicida)
Matheus Vianna, Cinthya S. G. Santos & Joana **Zanol**
- B.3.69** New species of *Acoetes* and *Euarche* (Aphroditiformia: Acoetidae) from Brazilian coast
Namy Ogawa, Helena Lavrado & Alexandra **Rizzo**
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- B.3.71** Genetic differentiation between *Spirobranchus akitsushima* and *Spirobranchus* sp. 6 based on genome-wide SNPs
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- B.3.73** *Lagis depende* a new member of the Pectinariidae
Mária **Barroso**, Mária Capa, Ascensão Ravara, Juan Moreira & Julio Parapar
- C.1.74** New bathyal Terebelliformia (Annelida) from the Brazilian continental slope: hidden diversity and wide-distribution signals in the South Atlantic
Orlemir Carrerette, João Gabriel **Rebello** & João Miguel de Matos Nogueira
- C.1.75** A Caribbean Anamobaea in taxonomic limbo: Reassessment of a long-recognized undescribed species
João Gabriel **Rebello**, Mária Ana Tovar-Hernández & Orlemir Carrerette
- C.1.76** Phylogeography and Biogeography of Phyllodocida Dales, 1962 (Annelida): A Systematic Review
Leticia M. Ferreira, Victor Corrêa Seixas, Tulio F. Villalobos-Guerrero & Cinthya S. G. **Santos**

- C.1.77** Uncovering intraspecific morphological variation in *Poecilochaetus australis* Nonato, 1963 (Spionidae, Annelida)
Cinthya S. G. **Santos**, Vitória Reis, Ricardo Ignacio Castro Álvarez, Leonardo Santi, Paulo C. Paiva & Joana Zanol
- C.1.78** Resolving species complexes among early described polychaetes – tracing the footprints of O.F. Müller (1776)
Eivind **Oug**, Torkild Bakken, Jon Anders Kongsrud, Arne Nygren & Maël Grosse
- C.1.79** An unusual behavior of epibenthic tube-dwelling *Hyalinoecia* (Hyalinoeciinae, Onuphidae) in Amami-Oshima, Japan
Luna Yamamori & Nataliya **Budaeva**
- C.1.80** Old synonyms getting a second wind: integrative taxonomy to the rescue of Alciopini (Annelida, Phyllodocidae)
Glafira **Kolbasova**, Vitaly Syomin & Tatyana Neretina
- C.1.81** Aphroditiformia (Annelida) of the Aleutian Trench & Bering Sea (NE Pacific)
Paulo **Bonifácio** & Dieter Fiege
- C.1.82** Biogeography of polychaetes (Annelida) in the Bay of Biscay (NE Atlantic): new records and distribution patterns
Louise Lanrivain, Lise Bacouillard, Salomé Coignard, Maxime Cottin-Bournois, Esteban Toribio, Yann Patry, Thomas Pommier, Philippe Bornens & Paulo **Bonifácio**
- C.1.83** *Flabelligera* (Annelida) in Norwegian waters reveals hidden diversity
Ellisiv Tomasgard Raffevold, Jon Anders Kongsrud & Torkild **Bakken**
- C.1.84** Uncovering hidden diversity in *Amphicteis gunneri* (Ampharetidae)
Tom **Alvestad**, Jon Anders Kongsrud, Katrine Kongshavn & Nataliya Budaeva
- C.2.85** Comparative analyses of mitogenomes in Eunicidae Berthold, 1827 (Annelida)
Tatiane Lima, Vitória Reis, Matheus Vianna, Paulo Cesar Paiva, Ricardo Álvarez, Anja Schulze, Victor Corrêa Seixas & Joana **Zanol**
- C.2.86** Species delimitation of epitokous *Eunice* sp. (Eunicidae, Annelida) from East Timor
Tatiane Lima, Anja Schulze, Victor Corrêa Seixas & Joana **Zanol**
- C.2.87** Polychaete diversity from La Caleta (Cádiz, southern Iberian Peninsula) reveals putatively undescribed lineages of Nereididae
Mateo Almodóvar **de Haro**, María del Rosario Martín-Hervás Santos, Marcos A.L. Teixeira, Juan Lucas Cervera Currado & Patricia Álvarez Campos
- C.2.88** A new 518-million-year-old stem annelid illuminates the ancestral body plan of Annelida
Luoyang **Li**
- C.2.89** One species, many faces: integrative taxonomy uncovers the Mediterranean expansion of the Lessepsian polychaete *Syllis crassiacirrata*
Desirée **Dimichele**, Joachim Langeneck, Yann Toso, Georgios Chatzigeorgiou & Luigi Musco
- C.2.90** Mitochondrial genome of *Chitinopoma serrula* (Filograninae, Serpulidae, Annelida)
Alexandra Bezmenova, Margarita Ezhova, Glafira Kolbasova, Elena Kupriyana, Tatiana Neretina & Alexander **Tzetlin**
- C.2.91** A new species of *Levinsenia* Mesnil, 1897 (Paraonidae) from the White Sea
Anna Zhadan & Alexander **Tzetlin**
- C.2.92** A novel *Phyllochaetopterus* Grube, 1863 (Annelida: Chaetopteridae) from Northeastern Brazilian waters
Layla Fontão & Wagner **Magalhães**
- C.2.93** Two new species of Phyllodocidae Örsted, 1843 from Northeastern Brazil
Gabriel Santos Sueira de Jesus, Verônica Maria de Oliveira & Wagner **Magalhães**
- C.2.94** A new species of *Syllidia* Quatrefages, 1866 (Annelida: Hesionidae) from Brazil
Danilo Cerqueira, Elizabeth Neves, Rodrigo Johnsson & Wagner **Magalhães**
- C.3.95** Deep-sea and coastal Cirratulidae (Annelida) from the Southwestern Atlantic: advances in systematics and diversity
Roberta Freitas, Meriane **Paula**, Lucas Fonseca, Carolina Moraes, Julia Ramos, Ana Cassiano, Yasmin Sysak & Christine Ruta
- C.3.96** Taxonomic contributions to Hesionidae (Annelida) along the Brazilian coast
Victor Hugo Marques, Roberta Freitas, Meriane **Paula**, Lucas Fonseca, Yasmin Sysak, Carolina Moraes, Julia Ramos & Christine Ruta

- C.3.97** Climate change responses across the life cycle of *Platynereis dumerilii*: insights from the first Southern Hemisphere culture
Lucas Fonseca, Meriane **Paula**, Roberta Freitas, Júlia Carolina Ramos, Carolina Moraes, Ana Cassiano, Jhenifer Lima, Yasmin Sysak & Christine Ruta
- C.3.98** Reassessing Central Pacific Eunicidae: Diversity and Discovery from the Remote Palmyra Atoll
Abbie **Taylor**, Kate Mortimer, Miguel Muñoz-Hurtado, Richard Johnston & Craig Robertson
- C.3.99** Re-building the Syllid Tree: Phylogenomics, mitochondrial gene-order shifts, and genome-size dynamics
Mateo Carvajal **Calero**, Thilo Schulze & Maria Teresa Aguado
- C.3.100** Several new species of the deep-sea genus *Anguillostylis* Day, 1963 (Annelida, Syllidae) from the Aleutian Trench
Chris Joel Roland **Springer**, Lenka Neal, Katharina Henze & Maria Teresa Aguado
- C.3.101** Taxonomical and Ecological Features of Glyceridae and Goniadidae (Polychaeta) Species Distributed Along the Coasts of Türkiye
Sevgi **Kus**, Güley Kurt & Melih Ertan Çınar
- C.3.102** Small adult body size and intratubular brooding in a new cryptogenic species of *Protula* from southern California
Bruno Pernet, Leslie **Harris** & Rolando Bastida-Zavala
- C.3.103** Polychaete (Annelida) diversity in the impacted Berg River Estuary, South Africa
Carol A. Simon, D Pretorius, Robin S. Lacey, A April, Stephanie Shoeman & Jyothi **Kara**
- C.3.104** Occurrence and establishment of the alien *Alitta succinea* (Annelida: Nereididae) along the southern French Mediterranean coast
Yolanda Lucas, Paola Mura, Miguel A. Meca, João Gil, Sébastien Thorin & Daniel **Martin**
- C.3.105** Diversity of symbionts within Chaetopteridae (Polychaeta), with description of a Vietnamese *Chaetopterus*-associated member of the *Hololepidella nigropunctata* species-complex (Polynoidae)
Daniel Martin & Temir Britayev

INVITED SPEAKERS**1.0 | KEYNOTE: Morphology****Thomas Bartolomaeus**

University of Bonn, Bonn, Germany

Thomas Bartolomaeus served as Professor for Zoology and Evolutionary Biology at the University of Bonn from 2008 until his retirement in 2025, where he also headed the Bonn Institute of Organismic Biology. He studied biology, chemistry, and physics at the University of Göttingen, completing his doctorate there in 1987 and his habilitation in 1993 on the evolution and development of body cavities and nephridial organs in Bilateria. He held professorships at the University of Bielefeld and the Freie Universität Berlin before moving to Bonn in 2008. His research centers on comparative morphology and ultrastructure to reconstruct the phylogeny of the Metazoa. Within polychaetes, Bartolomaeus is especially recognized for his comparative ultrastructural work on the nervous system, chaetae, and larval sense and excretory organs, using electron microscopy, histology, and laser scanning microscopy to distinguish shared ancestry from convergent evolution.

Polychaete Morphology: Coordination matters

Timing and coordination of morphogenetic processes drives morphological evolution. The processes can be studied in polychaetes during embryogenesis and postlarval segment addition. The order, timing, and interaction of developing structures generate differences in the spatiotemporal coordination of morphogenesis that explain much of the morphological diversity in polychaetes. Examples from chaetogenesis, nephridiogenesis, and coelomogenesis illustrate how changes in the onset, duration, or termination of morphogenetic processes generate morphological diversity. Chaetae are external chitinous structures that serve in locomotion, defense, and attachment. They are shaped by cellular dynamics within an ectodermal follicle. Changes in their arrangement result from truncated or extended chaetogenesis and correlate with different lifestyles. Nephridia eliminate nitrogenous wastes by ultrafiltration and subsequent modification. Protonephridia combine both processes in a single organ suited to the acoelomate organization of larvae. In metanephridial systems both processes are spatially separated by a coelom, characteristic of segmented developmental stages. Protonephridia in adults, however, result from truncated nephridial development and evolve repeatedly among annelids. Coelomic cavities are formed from a terminal growth zone with high mitotic activity. Timing and duration of coelomogenesis correlate with body size; truncated coelomogenesis may cause secondary acoelomate conditions in annelids or extremely reduced numbers of segments. These examples illustrate that heterochrony acts primarily at the level of developmental modules or organ systems, providing a mechanistic framework for understanding annelid morphological evolution.

6.0 | KEYNOTE: Taxonomy, Systematics & Phylogeny

Joana Zanol

Museu Nacional, Universidade Federal Rural do Rio de Janeiro (UFRRJ), Brazil

Joana Zanol is Associate Professor at the National Museum, Federal University of Rio de Janeiro, where she also curates the Annelida Collection. She earned her MSc at the Federal University of Rio de Janeiro and her PhD at The George Washington working on the phylogeny of the family Eunicidae. Her research centers on the systematics and evolution of marine annelids, combining molecular and morphological data to resolve relationships within Eunicida, with a particular focus on the genera *Eunice*, *Marphysa*, and their relatives across the Atlantic, Pacific, and Indian Oceans. Zanol has described numerous new species from Brazil, Australia, and beyond, and co-authored the Eunicida and Eunicidae chapters of the Handbook of Zoology Annelida. Beyond her taxonomic work, she leads projects on the digitization and molecular characterization of the National Museum's annelid collection and mentors a large cohort of graduate and undergraduate students in molecular systematics and species delimitation. She is active in science outreach, bringing marine invertebrate biodiversity to schools and the general public, and her research on eunicids has been featured in international media, such as BBC's Blue Planet II.

Combining Taxonomy and Systematics to bridge knowledge gaps in Eunicida: Tales of Rare Families and Giant Polychaetes

Eunicida is one of the most morphologically distinctive annelid groups, characterized by a unique maxillary apparatus. The plates that make up the maxillae constitute the main annelid fossil record, while fossil records of the order also include ichnofossils of giant worm tubes. Thus, understanding of the evolution of maxillary plates and giant species allows connecting information from both extinct and extant taxa. Yet fundamental questions regarding family relationships, jaw evolution and body-size evolution remain unresolved. The only consistent relationship recovered in previous molecular phylogenetic analyses of the order is the sister-group relationship between Eunicidae and Onuphidae (Eunicoidea), whereas the rare family Hartmaniellidae has remained unsampled in molecular datasets. The discovery of two undescribed Hartmaniellidae species, suitable for molecular analyses, has enabled their inclusion, for the first time, in the phylogenetic framework of the order. Their inclusion consistently recovered Hartmaniellidae as sister to Eunicoidea, regardless of the relationships among the remaining families, and supports a single origin of the asymmetric maxillae shared by these groups. The same phylogenetic perspective used to reconstruct jaw evolution also provides a basis for investigating the evolution of gigantism in Eunicida. Among extant Eunicida, giant worms — here defined as species exceeding one meter in length and one centimeter in width — are mainly known from the currently polyphyletic genus *Eunice*, the type genus of Eunicidae. The existing phylogenetic hypothesis for the family Eunicidae, which has led to a reassessment of generic boundaries within the family, provides the necessary framework to understand the evolution of giant species. Including most valid giant species and an undescribed giant species from the Brazilian coast within this framework supports at least two origins of gigantism within the family. These two lineages also appear to have different habitats and feeding modes. The recent discovery of undescribed giant species suggests that, despite their remarkable size, these animals may remain undetected even in well-studied regions, often concealed under the broadly applied name *Eunice aphroditois*. New species, rare lineages, and overlooked giants show that our understanding of Eunicida evolution depends on integrating taxonomy, morphology, fossils, and molecular phylogenetics. Taxonomy provides the foundation upon which evolutionary hypotheses are built, and phylogenetic systematics, in turn, allows taxonomic classifications to be evaluated, refined, and made evolutionarily meaningful.

12.0 | KEYNOTE: Ecology, Biodiversity & Conservation**Monika Bright**

University of Vienna, Vienna, Austria

Monika Bright is University Professor and Vice Head of the Department of Functional and Evolutionary Ecology at the University of Vienna. She completed her doctorate in zoology and paleontology at the University of Vienna, followed by postdoctoral stays in Tübingen, Miami, Penn State, and Vienna, before rising through the professorial ranks at her home institution since 1998. Her research explores the ecology and evolution of symbiotic mutualisms, with a particular focus on the giant tubeworm *Riftia pachyptila* and its bacterial symbionts at deep-sea hydrothermal vents, as well as thiotrophic ciliate symbioses and deep-sea hydrothermal vent and cold seep as well as shallow-water wood-fall communities. Bright has taken part in numerous oceanographic cruises and submersible dives, including thirteen dives aboard HOV Alvin, and served as chief scientist on a 2023 Schmidt Ocean Institute research cruise. She has secured extensive competitive funding from the Austrian Science Fund over more than two decades and mentored dozens of graduate students and postdoctoral researchers. In 2025 she received the Eunice Newton Foote Medal for Earth-Life Science from the American Geophysical Union, and in 2015 she founded the Women in Biology Initiative at the University of Vienna.

The Giant Tubeworm *Riftia pachyptila* in Underworld of Hydrothermal Vents

The giant tubeworm *Riftia pachyptila* (Vestimentifera, Siboglinidae) was the first animal discovered over 40 years ago at the deep-sea hydrothermal vents of the Galapagos Spreading Center. Hundreds of publications attest to the continued high level of scientific interest in this symbiotic dual-partner mutualism. As adults, these animals lack a digestive system and are fed by their chemotrophic bacterial symbionts *Candidatus Endoriftia persephone*. Twenty years ago, we were able to show that a few symbiotic bacteria infect host larvae and proliferate as endosymbionts to large populations within a complex, mesodermal symbiont-hosting organ, the trophosome. Ten years later, experiments conducted in high-pressure vessels revealed that some of the symbionts leave their host after its death. These infection cycles of the horizontally transmitted, facultative symbiont and its escape from the host to enrich the free-living population are crucial for the host's survival across generations. The life cycle of the obligate, benthic host and its aposymbiotic, pelagic larvae is not yet fully understood. They are thought to disperse in the water column, although they have never been observed there. We hypothesized that these animals not only rely on the open ocean to disperse their offspring but also migrate through the Earth's crust and colonize hydrothermal fluids at the seafloor. During a Schmidt Ocean Institute-funded oceanographic expedition to the East Pacific Rise in 2023, we uplifted lobed lava shelves and discovered cavities in the seabed that revealed not only a known subseafloor microbial community but also a community of tubeworms and other vent animals. The presence of tubeworms in these subseafloor cavities, along with their free-living symbionts, suggests larval dispersal through the recharge zone of the hydrothermal circulation system. These larval populations not only colonize, mature into adults, and reproduce there, but they could also serve as a source of tubeworms on the seabed. The finding of animals below the visible seabed in the 'underworld' of hydrothermal vents demonstrates the interconnectedness of seafloor and subsurface communities, but with this discovery the study of the subseafloor biosphere for animal life just begun.

18.0 | KEYNOTE: EvoDevo & Genomics**Elaine Seaver**

Whitney Laboratory for Marine Bioscience, University of Florida, Florida, USA

Elaine Seaver is a Professor of Biology at the Whitney Laboratory for Marine Bioscience, University of Florida, where she is also Graduate Faculty in the Department of Biology and a member of the University of Florida Genetics Institute. She earned her PhD at the University of Utah, working on neurogenesis in grasshoppers, before postdoctoral training in leech development at the University of Texas at Austin and polychaetes at the Kewalo Marine Laboratory, University of Hawaii, where she later held faculty positions for over a decade prior to moving to Florida in 2012. Her research uses the annelid *Capitella teleta* as a study animal to investigate the molecular and cellular basis of development, neurogenesis, axis formation, and regeneration, helping establish *Capitella* as a key model for comparative studies of spiralian development. She has been continuously funded by the NSF for over two decades, including her current work on stem cell niches underlying regeneration, and has trained a large number of undergraduate, graduate, and postdoctoral researchers, including through her long-running NSF-funded Research Experience for Undergraduates program at the Whitney Laboratory. Seaver has served on the editorial boards of several major journals, including BMC Evolutionary Biology and EvoDevo, and has taught in the Embryology course at the Marine Biological Laboratory, Woods Hole, for over a decade.

Evo Devo approaches in annelids: elucidating the rules of successful regeneration in *Capitella teleta*

The field of Evo Devo (Evolution of Development) brings a powerful approach towards building an understanding of the evolutionary processes that generated the wide range of extant animal diversity. Further, the fact that many animals undergo sexual reproduction provides a challenge to understand the role of embryogenesis in body plan evolution. Recent advances in comparative and functional genomics, as well as live-cell imaging approaches make it an exciting and opportunistic time to investigate animal diversity. Annelids display a range of favorable properties for such investigations, including: a highly stereotyped embryonic cell cleavage pattern called “spiral cleavage, a wide range of life history modes, including asexual reproduction and variable adult postembryonic development and regeneration abilities. *Capitella teleta* is a capitellid annelid that has robust posterior regeneration abilities, reforming multiple organs following transection along the main body axis but lacks anterior regeneration abilities. Interestingly, the regeneration response of *C. teleta* also varies across the life cycle (temporal) and at different spatial sites along the anterior-posterior axis. This provides a unique opportunity to compare the regenerative responses between body fragments that differ in their regeneration abilities within the same genome (vs. comparing different species). Furthermore, *C. teleta* has several advantageous characteristics for in vivo studies of regeneration and stem cell biology, including availability of functional genomic tools, a stereotypic embryonic cleavage program and associated fate map, along with a sequenced genome. I will discuss ongoing work on regeneration patterns and processes in *C. teleta*, including our ability to partially rescue anterior regeneration following perturbation of cell signaling pathways. Thus, annelids provide a rich and underexplored source of material for exploring diverse species-specific differences that can be experimentally manipulated. Comparing tissues with different pre- and post-embryonic patterning abilities within an individual organism can elucidate mechanisms underlying regeneration regulation, thereby enabling the prospect of rescuing or increasing regeneration ability in regeneration-deficient tissues.

19.0 | INVITED TALK: EvoDevo & Genomics

Toru Miura

Misaki Marine Biological Station, School of Science, The University of Tokyo

Toru Miura is Professor and Director of the Misaki Marine Biological Station, School of Science, The University of Tokyo. He completed his undergraduate, master's, and doctoral training at the University of Tokyo before taking up an assistant professorship there, followed by an associate professorship at Hokkaido University, and returning to Misaki as professor in 2017. While his research is best known for work on developmental plasticity in arthropods, including caste differentiation in termites, life-history polyphenisms in aphids, and mandibular development in stag beetles, his laboratory has increasingly turned to syllid annelids as a model for studying developmental underpinnings of body plan evolution, extending his broader interest in segmentation, appendage differentiation, and trunk reorganization in polychaetes. His work integrates detailed morphological analysis with comparative developmental approaches across a wide range of taxa, including echinoderms, cnidarians, bryozoans, and vertebrates, in pursuit of larger evolutionary questions about sociality, coloniality, and what constitutes an "individual" in animals. He has received several honors from the Zoological Society of Japan, including its Award for Young Scientists in 2011 and its main Society Award in 2021.

Stolonization as a developmental innovation: Localized axial re-patterning and cyclic sex differentiation in the syllid *Megasyllis nipponica*

Toru Miura, Daisuke S. Sato, Kohei Oguchi

Misaki Marine Biological Station, School of Science, The University of Tokyo

To elucidate the developmental and evolutionary mechanisms underlying stolonization, we established *Megasyllis nipponica* as an evo-devo model and applied a combination of histology, transcriptomics, and molecular approaches. During stolonization, secondary head and tail formation differs histologically from regeneration. For example, segmental nerve rings are reorganized into a brain-like nervous system, rather than regenerating a new brain from the severed end of the ventral nerve cord. Likewise, secondary-tail formation lacks several regeneration-specific processes and instead proceeds through stolonization-specific processes, such as the fusion of paired half-tail buds and the early formation of muscle and nerve branches before stolon detachment. Analyses of Hox and Wnt gene expression showed that stolonization partially utilizes conserved tail-patterning mechanisms while lacking several regeneration-associated Wnt programs. RNA-seq analyses further demonstrated that only a subset of head-patterning genes, including Otx, Six3, and Pax6, are activated during secondary-head formation, suggesting that local activation of head or tail identity within individual segments is sufficient to transform trunk segments without global axial re-patterning. In addition, rearing experiments examining sexual differentiation during repeated stolonization cycles demonstrated bidirectional sex changes, while histological and transcriptomic analyses showed that pre-stolon tissues lack sexually differentiated gonads and remain transcriptionally similar regardless of the sex of the previously produced stolon. Sex-specific gene expression and gonadal differentiation are newly activated during each stolonization cycle, indicating repeated de novo sexual differentiation. Together, these findings suggest that syllids evolved a unique post-embryonic developmental program that combines localized body-axis re-patterning, partial co-option of regenerative mechanisms, and repeated de novo sexual differentiation, thereby enabling the repeated production of reproductive individuals within a single animal body.

TALKS

0.2 | The Polychaete Collections at Senckenberg

Dieter Fiege & Ekin Tilic

Senckenberg Research Institute and Natural History Museum Frankfurt, Germany

Soon after the foundation of the Senckenberg Naturforschende Gesellschaft in 1817, studies on marine zoology started with naturalist Eduard Rüppell. Among the earliest specimens present in the collection is the holotype of *Polyodontes gulo* (Grube, 1855) collected by Rüppell in 1827 near Suez in the northern Red Sea. However, it was only in 1990 that taxonomy and systematics of polychaetes became a research focus of the section Marine Invertebrates II. Resulting from research projects and participations in expeditions from coastal areas to the deep sea, and depositions from international researchers the collections have grown to about 25.000 registered lots, accessible through the online database 'search.senckenberg.de'. The collection currently includes 135 name-bearing types as well as several thousand additional lots of specimens from all over the world awaiting identification and further study. With regard to specimens and taxon numbers, collections from the North Sea, Mediterranean Sea, Red Sea, Persian Gulf and South China Sea are of international importance. Taxonomic groups best represented comprise the Aphroditoidea, Glyceridae, Eunicida, Terebellomorpha, and Serpulidae. The latter includes the unique collection of Helmut Zibrowius (Marseille). The section library serves as an important research tool with currently more than 15.000 papers. It includes the libraries of Gesa Hartmann-Schröder (Hamburg) and Volker Storch (Heidelberg), as well as an extensive card catalogue (> 4.000 cards) containing information on polychaete taxa compiled by the late Gesa Hartmann-Schröder. This catalogue has recently been digitised and will be made available online. Research on annelids at Senckenberg has entered a new phase since 2023 with Ekin Tilic as the new curator, with an increased focus on integrative taxonomy, phylogenomics, genomics, and the application of modern imaging techniques such as μ -CT.

0.3 | The Senckenberg Ocean Species Alliance – joining forces to alleviate the taxonomic impediment

Jan Steger, Torben Riehl & Julia D. Sigwart

Senckenberg Research Institute and Natural History Museum Frankfurt, Germany

Polychaetes are an integral component of marine ecosystems from coastal areas to deep-sea trenches, yet numerous species are still unknown to science. Ambitious field campaigns, museomics, modern sampling technology, and increasingly sophisticated molecular approaches have resulted in a surge of exciting discoveries worldwide. However, limited time, financial and technical constraints, and modest academic reward for alpha-taxonomic work continue to be major bottlenecks to these species' timely formal description, impeding downstream phylogenetic and ecological studies, informed marine policy, and conservation action that all rely on scientific names as indispensable currency for effective communication. The Senckenberg Ocean Species Alliance (SOSA) initiative is an open international network of researchers, conservationists and science communicators that aims at alleviating these constraints. Together with the marine taxonomist community, we have tested and deployed collaborative and streamlined taxonomic workflows, implemented by the world's first philanthropically funded lab facility supporting researchers describing new invertebrates. With a specialized technical team, the lab performs a wide range of morphological analyses on specimens free of charge, providing high-quality data through photography, specimen preparation, light and electron microscopy, morphometry, technical drawings, CT scanning and DNA barcoding, thereby facilitating integrative description projects. Complementing its technical support portfolio, SOSA maintains the taxonomy-focused peer-reviewed open-access article series Ocean Species Discoveries in Biodiversity Data Journal to accelerate the publication of species descriptions, increase their visibility, and maximise the academic reward for contributing authors. Besides directly benefitting individual researchers and the scientific community as a whole, the numerous interactions with international taxonomists of all career stages, involvement in more than 160 taxonomically diverse description projects, as well as mutual knowledge exchange have empowered SOSA to develop an increasingly efficient, flexible and scalable model that is transferrable also to other geographical and institutional settings, inspiring a more collaborative, faster, and equitable approach to global invertebrate taxonomy.

0.4 | Establishing a Polychaeta Specialist Group to Advance Global Marine Invertebrate Conservation

Julia Silva Beneti¹, Anne Helene S. Tandberg^{1,2} & Julia D. Sigwart¹

¹ Senckenberg Research Institute and Natural History Museum Frankfurt, Germany

² University Museum of Bergen, University of Bergen, Bergen, Norway

The International Union for Conservation of Nature (IUCN) Species Survival Commission (SSC) Specialist Groups are global networks of volunteer experts—including scientists, researchers, and conservation practitioners—who collaborate to assess species' conservation status and advance biodiversity protection. As part of the SSC, the Specialist Groups provide technical expertise, contribute to the IUCN Red List of Threatened Species, and develop evidence-based strategies and action plans to safeguard species at risk. Their work follows the SSC's Assess–Plan–Act framework, which integrates extinction-risk assessments, conservation planning, and implementation of targeted conservation actions. Through this approach, Specialist Groups gather robust scientific knowledge that strengthens conservation practice, informs policy, and supports international biodiversity targets. Despite these efforts, many invertebrate taxa remain underrepresented within the IUCN system. Polychaetes (Annelida) are among the most diverse and ecologically significant marine invertebrates, playing essential roles in benthic ecosystem functioning, nutrient cycling, and habitat structuring. However, their conservation status is currently unrepresented on the IUCN Red List website, and there are no species-focused conservation initiatives directed at this group. We therefore propose establishing a Polychaeta Specialist Group within the IUCN SSC to address this gap. The formation of this group will be supported by the IUCN SSC Marine Invertebrates Red List Authority (MIRLA), established by the Red List Unit of the Senckenberg Ocean Species Alliance (SOSA), and by the IUCN SSC Marine Conservation Committee. This initiative represents an opportunity to coordinate global expertise, accelerate Red List assessments, and strengthen conservation actions for polychaetes. We invite researchers to join this collaborative effort to enhance the recognition and protection of these important but often overlooked species.

1.1 | Ultrastructural 3D analysis of the photoreceptive structures in a basal branching annelid, *Psammodrilus balanoglossoides* (Psammodrilidae, Chaetopterida)

Günter Purschke

University of Osnabrueck, Germany

Annelids, and polychaetes in particular, show a great diversity of photoreceptor structures and eyes. However, pigmented eyes occur rarely in members of the so-called basal radiation and our knowledge on the occurrence of unpigmented, and as such usually invisible, photosensory structures is limited. Psammodrilidae belong to the second lineage branching off in the annelid phylogenetic tree and have been described to possess phaosomes. Such structures are formed by a single cell and represent entirely closed invaginations of the cell apex bearing the sensitive processes which are either microvilli or cilia. However, the origin of the sensory processes inside this vacuole and their nature was unknown so far. Since phaosomes are extremely rare in annelids, their presence in members of the basal radiation would imply that they evolved early during annelid evolution. We investigated these sensory structures by analyzing serial sections with conventional transmission electron microscopy as well as with serial block face imaging. Our results reveal that these annelids don't possess phaosomes rather than a specific unpigmented photoreceptor structure comprising two cells: a supportive cell and a ciliary photoreceptor cell. The supportive cell forms the cavity into which the branching cilium of the adjacent photoreceptor cell projects. Both cells are integrative part of the epidermis. Moreover, the supportive cell is structurally almost indistinguishable from typical ciliated epidermal cells. As will be discussed in more detail, these findings further elucidate the evolutionary history of photoreceptive structures in Annelida.

1.2 | Characterization of high-resolution tubular eyes in *Eupolyodontes* (Acoetidae) scale worms

Brett C. Gonzalez¹, Michael Bok², Katrine Worsaae³, Karen J. Osborn⁴ & Anders Garm³

¹The University of Western Australia, Australia

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Aphroditiformia (scale worms) comprises nearly 2,000 species and includes morphologically and ecologically diverse annelids occupying marine habitats from the intertidal to the deep sea. Among their sensory systems, eyes are particularly variable, ranging from complete absence to elaborate image-forming structures. Within Aphroditiformia, Acoetidae is especially notable for the diversity and complexity of its visual structures, particularly in the genus *Eupolyodontes*. This genus includes shallow-water, tube-dwelling predators that can exceed one metre in length and capture large mobile prey, including fish, making it an excellent system for examining whether rapid, independent evolution within annelids has produced a visual system approaching the functional complexity of other high-performance bilaterian eyes. Here we present preliminary results from an integrative investigation of eye evolution in Acoetidae, combining morphology, physiology, behaviour, and transcriptomics. Our preliminary morphological data indicate that *Eupolyodontes* possesses one of the most elaborate eyes yet described in Annelida, including large tubular eyes with a well-developed lens and ocular architecture consistent with high-resolution vision. Complementary physiological and molecular data further suggest the use of a single visual opsin with peak sensitivity around 470–472 nm and high temporal resolution, consistent with rapid detection of moving prey overhead. However, equally elaborate eye morphology is not shared uniformly across Acoetidae, suggesting that tube dwelling and ambush predation alone do not explain the evolution of visual complexity in the group.

1.3 | The secret(e) is out - Forays into understanding neuroglandular interactions in *Platynereis dumerilii*

Alexandra Kerbl & Gáspár Jékely

Heidelberg University, Germany

Developments in the fields of single cell transcriptomics and volume electron microscopy have granted insight into neural circuits, i.e., the connection between neurons and between neurons and their effector cells, in unprecedented detail in the small marine larva of *Platynereis dumerilii* (Audouin & Milne Edwards, 1833). While the circuits controlling muscles and cilia have been mapped and analysed in previous studies, the neuronal control of secretory glands is less well understood. Exocrine glands have a variety of functions in animals, including the protection of the body from dehydration, the secretion of material to build brooding or protective structures or the lubrication of locomotor cilia. We will focus on the neural control of the so-called spinning glands, which are suggested to produce the mucous tubes juvenile worms can retreat in between settling for a benthic lifestyle and swimming to the surface as mature adults. Using an integrated approach of behavioural and morphological analyses we characterize the function and development of these glands and their underlying circuit in detail. We will thereby deliver circuit maps at synaptic resolution, which will further our functional understanding of the control of an excretory gland in an emerging model organism.

1.4 * | A bloody mystery – morphological investigations shed light on the function of the glycerid venom system (Glyceridae, Annelida)

Antonia Dopp¹, Paul Ritter-Kalke¹, Jenna Moore², Patrick Beckers³ & Conrad Helm¹

¹Georg-August-Universität Göttingen, Germany

²Museum of Nature Hamburg, Germany

³University of Bonn, Germany

Glyceridae are venomous annelids living in various marine environments. They possess an eversible proboscis with four terminally situated jaws to grab their prey and produce a distinct venom to paralyze the latter. For decades it was assumed that putative venom glands that are associated with the jaws produce the venom. However, immunohistochemical analyses and in-situ hybridization approaches indicated that the venom is produced in another morphologically distinct area, named as pharyngeal

* Denotes a student contribution eligible for a prize.

Presenting author shown in **bold**.

lobes. Due to lacking investigations, most of the existing morphological studies investigated the venom system of Glyceridae based on the assumption that the putative venom glands produce the venom and therefore did not consider to investigate other structures associated with the jaw apparatus. Hence, a detailed morphological investigation of the venom system including the pharyngeal lobes is still lacking. Therefore, we used an integrative morphological approach including scanning electron microscopy (SEM), immunohistochemistry as well as histological azan serial sections to reconstruct the venom system of *Glycera* sp. nov.. Our investigations represent the first comprehensive morphological analysis of the glycerid venom apparatus and provide a detailed picture of the putative venom glands as well as the pharyngeal lobes. Hence, the entire system is embedded in a dense scaffold of differently orientated muscles and innervated by a dense meshwork of distinct neurite bundles. Furthermore, the putative venom glands – presumably used for storage of the venom cocktail – are directly connected to the jaws via a prominent duct. Our investigations provide a detailed view on the different substructures of the venom system in *Glycera* sp. nov. and represent an important overview necessary for further investigations dealing with the assignment of functions for respective parts of the glycerid venom system.

1.5 * | Differential Gene Expression analysis unravels different molecular basis of sex determination in three sexual systems in *Ophryotrocha*

Jose María Lorente-Sorolla Pons, Sergi Taboada, Irene de Sosa, Ana Riesgo & Cristina Lorenzi

Museo Nacional de Ciencias Naturales, Spain

Species of the genus *Ophryotrocha* are marine annelids widely used as experimental model species due to their tolerance to stress, high fecundity, and the diverse sexual systems they present, which include simultaneous and sequential hermaphroditism as well as gonochorism. Despite the attention that these organisms have garnered, they have been barely studied under a genomic point of view. In this study, we analyzed differential gene expression in the transcriptomes of three *Ophryotrocha* species: *Ophryotrocha diadema* (simultaneous hermaphrodite), *Ophryotrocha puerilis* (sequential hermaphrodite), and *Ophryotrocha japonica* (gonochoristic), with the aim to identify genes and molecular pathways involved in sex determination. By comparing gene expression between sexes and between reproductive and non-reproductive individuals, we detected significant differences in the expression of genes related to sex hormones, methylation/demethylation processes, germline maintenance, sex determination, and gametogenesis. Notably, we found differential expression in well-known genes such as DMRT2 involved in sex determination in *Drosophila* and YX sex reversal in humans and FGFR2, which regulates proliferation and Sertoli differentiation during male sex determination in mice, suggesting their potential role in the regulation of sex determination in *Ophryotrocha*. Importantly, we detected Single Nucleotide Variants (SNVs) when analysing the transcriptomes of females and males for *O. japonica*, the gonochoristic species, with several of them producing non-synonymous changes of aminoacids. In particular for DMRT we identified changes having an effect on the tridimensional conformation of the DM domain, which might explain the differences observed at the transcriptional level when comparing both sexes. Our study sheds light into the molecular basis of sex determination in annelids, a group of marine invertebrates that has barely been studied to this respect.

2.1 | *Ophryotrocha labronica* (Dorvilleidae) as a model annelid species for eco-evolutionary and ecotoxicology studies in a changing ocean

Gloria Massamba N'Siala

Old Dominion University, USA

Climate change and coastal pollution are impacting coastal marine environments through increasingly complex, interacting stressors. Extreme fluctuations in seawater salinity and temperature are projected to become more frequent and intense, while contaminants simultaneously accumulate in coastal ecosystems. Understanding how marine organisms respond to combined stressors is essential for predicting species persistence and ecosystem resilience. Here, we highlight the marine benthic annelid *Ophryotrocha labronica* (Dorvilleidae) as a promising model species for studying ecological, evolutionary, and ecotoxicological responses to ocean change. In a first experiment, we investigated how acclimation to a salinity gradient (12–50 psu) influences thermal tolerance. Results showed that only low, sub-optimal salinities reduced heat tolerance, although survival remained high and no clear life-history trade-offs were detected across treatments. In a second experiment, we examined the combined effects of salinity (22, 27, 32 psu) and zinc exposure (0, 50, 100 µg/L) on survival, growth, and fecundity across multiple life stages of *O. labronica*. Zinc reduced survival and growth at the highest concentration regardless of salinity, life stage, or sex, while fecundity remained unaffected. Interactive effects between salinity and zinc were minimal, indicating that zinc toxicity can dominate organismal responses under environmentally realistic conditions. These studies demonstrate the versatility of *O. labronica* as an

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experimental system for investigating physiological and life-history plasticity, or robustness under combined ocean changes, providing opportunities to bridge ecology, evolution, and ecotoxicology in marine research.

2.2 | From brackish origins to freshwater success: osmoregulation in *Hypania invalida*

Serena Mucciolo¹, Maciej Studzian¹, Shrikant Vichare¹, Tomasz Mamos¹, Tomasz Rewicz¹, Łukasz Pułaski¹, José María Martín-Durán² & Andrea Desiderato¹

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Osmotic stress is a major factor limiting species distribution in aquatic environments, and tolerance to varying salinity is a common trait among successful non-indigenous species (NIS). In Europe, many freshwater NIS originate from the Ponto-Caspian region, where fluctuating environmental conditions have driven the evolution of broad physiological tolerances, enabling species to cope effectively with osmotic stress. At the cellular level, osmoregulation depends on membrane proteins that maintain cell volume and ionic balance. Aquaporins (AQPs) are particularly important, as they facilitate the transport of water and small solutes across cell membranes in both vertebrates and invertebrates. Among Ponto-Caspian taxa, the ampharetid *Hypania invalida* (Grube, 1860) stands out as a particularly successful invader, having spread widely across European freshwater systems in recent decades. Despite its ecological relevance, data on its ecophysiology remain limited. This study adopts a multi-level approach, integrating experimental, molecular, and microscopy analyses to investigate the species' responses to osmotic stress. Osmotic tolerance experiments were conducted, alongside *in silico* and experimental analyses of AQP expression following salinity exposure. Results indicate that *H. invalida* exhibits osmoregulatory behavior at low salinities and shifts toward osmoconformity at higher salinities. Multiple AQP paralogs were identified *in silico*, clustering into four main clades: orthodox, aquaglyceroporins, ammonioporin, and unorthodox AQP. Experimentally, the expression of orthodox aquaporins and aquaglyceroporins increased under higher osmotic stress, aligning with osmoconforming conditions. Overall, this study provides the first experimental evidence of aquaporin involvement in osmoregulation in annelids, suggesting that their modulation under osmotic stress may play a key role in the physiological plasticity underpinning the invasion success of *H. invalida*.

2.3 * | When Structure Is Not Enough: Absorption Shapes Color in Sea Mouse Bristles

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The marine polychaete *Aphrodita aculeata* (sea mouse) exhibits two distinct bristle types with structural coloration: highly conspicuous, strongly iridescent capillary notochaetae and dark red to nearly black acicular chaetae (including acicular noto- and neurochaetae), which exhibit iridescence only under direct illumination. The origin of this optical contrast remains unresolved. Here, we investigate the structural and compositional basis of both bristle types to elucidate the mechanisms governing their optical response. Using light microscopy, reflectance spectroscopy, and electron microscopy. Surprisingly, we find that both share a comparable photonic architecture, yet exhibit fundamentally different macroscopic optical properties. We demonstrate that this difference cannot be explained by structure alone, but arises from the incorporation of absorbers within the photonic system. These absorbers attenuate and modify the reflected signal, leading to the darkened appearance of the acicular chaetae. Our results suggest that optical functionality in sea mouse bristles arises from the interplay of structure and absorption. For the acicular chaetae, the pronounced darkening indicates that this system is not optimized for maximal color intensity, but instead could reflect a function-driven design in which mechanical stability is prioritized, with structural coloration emerging as a secondary consequence, similar to the pearlescent properties of nacre.

2.4 | Diversity and Development of the Prototroch in Polychaeta

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The prototroch, a preoral ring of ciliated cells used for swimming and feeding, is the eponymous structure of the trochophore, the iconic larva of Polychaeta. The cell-lineage of the cells constituting the prototroch, the trochoblasts seems to show a stereotypic pattern in nearly all investigated species. The trochoblasts cease to divide already early during embryogenesis and start to develop cilia, making the resulting prototroch the first differentiated structure in the trochophore. As a strictly larval structure, the prototroch is restricted to the larval phase of the polychaete life-cycle. Although the prototroch has been in the focus of investigations for more than 100 years, there are still open questions regarding (1) the exact composition of the prototroch in different polychaete lineages, (2) the maintenance of prototroch cells during larval development, and (3) the fate of the prototroch cells during metamorphosis of the trochophore to the juvenile. These questions are addressed using different stains and detection with CLSM in several polychaete species. The results show that the prototroch is a structure that has diversified considerably during the evolution of its bearers.

2.5 * | Feather-Dusters and Their “Feathers”: Novel Comprehensive Data on Anatomy Provide New Insights into Taxonomy, Function, and Evolution within Sabellidae

Tim Sharett¹ & Nadezhda Rimsakova-Korsakova²

¹ Tel Aviv University, Israel

² Friedrich Schiller University Jena, Germany

Magnificent worms with a plume of feathery tentacles, Sabellidae are highly adaptive, diverse, and widespread annelids inhabiting marine and freshwater environments, as well as living in association with other animal species. Their success is, inter alia, facilitated by their radiolar crown, while the entire anterior end plays a crucial role in the evolution of the group. We reinvestigated the head region anatomy of five sabellid species using classical histology and 3D modelling to trace with precision the interdependence of the radiolar crown and other organ systems. The selected species represent typical forms of the main lineages within the family. Combining high-quality serial histology with modern tracing techniques, we identified a previously undescribed set of features in the innervation, branchial skeleton, mouth cavity, and dorsal pit. Our data suggest that differences between the Sabellinae and Myxiolellinae subfamilies are more fundamental than previously assumed and involve deep anatomical modifications. These findings may affect current taxonomic and cladistic approaches and facilitate identification of the phylogenetic position of problematic genera based on anatomy in the absence of genetic data. Our results provide a new perspective on key adaptations in each investigated genus and subfamily, as well as insights into variation in feeding mechanisms across lineages. Moreover, they may reveal broader patterns relevant to the evolution of the order Sabellida and to common factors underlying suspension feeding in worm-bodied invertebrates.

3.1 | *Sclerolinum* tubeworms (Annelida, Siboglinidae) colonize degrading bones

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Tubeworms of the genus *Sclerolinum* — the smallest and least-studied siboglinid clade — are known from cold seeps, hydrothermal vents and reduced sediments, often associated with decaying substrates such as wood, rope and leather. Here we report that two *Sclerolinum* species can also colonize degrading vertebrate bones, both in long-term laboratory aquaria and in the deep sea. *Sclerolinum brattstromi* inhabits cow bone in three long-term aquarium colonies with continuous occupancy on the same substrate for over six years. Histological evaluation revealed only spermatogenesis and no oocytes across all three colonies, indicating a clonal, all-male lineage maintained through asexual reproduction. *Sclerolinum contortum* was once independently sampled from a whale skull at ~1000 m on the Arctic Mid-Ocean Ridge, where collected specimens showed gonochoristic sexual reproduction. On both substrates, *Sclerolinum* settled after prior colonization by *Osedax*. Species identity of the worms was confirmed using DNA barcoding (COI and 16S rRNA), and the symbiont was identified via bacterial 16S rRNA gene analysis. Transmission electron microscopy of *S. brattstromi* from bones showed retention of the typical trophosome ultrastructure with intracellular bacterial

* Denotes a student contribution eligible for a prize.

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symbionts of the recently described genus *Candidatus Vondammii*. Synchrotron X-ray micro-CT revealed worms occupying pre-existing cavities within the porous bone matrix. Our findings extend the known substrate range of *Sclerolium* to vertebrate bones — a habitat type previously documented only for the siboglinids *Osedax* and vestimentiferans. We also raise the possibility that *Sclerolium* colonizes Arctic bone-falls after *Osedax* and establish a stable laboratory culture — opening this clade to experimental investigation of host-symbiont interactions, reproductive plasticity, and chemosynthetic ecology.

3.2 | How to identify the ‘Freak’, or convergent evolution of head appendages in Scalibregmatidae

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The evolution of palps in Annelida remains strongly debated, although their conserved dual-root innervation pattern across all major lineages studied so far is widely recognized as a key feature of their homology. At the same time, their repeated reduction—and possible re-evolution—continues to raise fundamental questions about the evolutionary stability of complex morphological structures. Within the sedentary Scalibregmatidae, most species are burrowing deposit feeders that lack anterior appendages entirely. However, the derived *Axiokebuita*–*Speleobregma* clade bears prominent palp-like head appendages, raising the question whether these structures are homologous to annelid palps or represent a case of convergent evolution. To address this, we compared three taxa representing successive morphological conditions: *Travisia* sp. (smooth prostomium without appendages), *Scalibregma celticum* (short lateral prostomial horns), and *Axiokebuita cavernicola* (elongated, densely ciliated palp-like appendages). We combined immunohistochemistry, confocal laser scanning microscopy, azan-stained histology, and 3D reconstruction to analyze both neuronal innervation and muscular architecture of these anterior structures. To assess homology versus convergence, we integrated our morphological data within the comparative framework of Remane’s three criteria: position, special quality, and continuity. Our results show that *Travisia* lacks any neural or muscular remnants of head appendage innervation. In *Scalibregma*, the prostomial horns exhibit diffuse neuronal and muscular innervation. In *Axiokebuita*, five distinct appendage nerves arise exclusively from the dorsal root of the circumoesophageal connectives, while the musculature and positional relationships fail to meet the criteria for palp homology. Instead, the integrated evidence supports independent evolutionary re-emergence of palp-like structures, representing a striking case of convergent evolution in a character complex previously considered as being deeply homologous.

3.3 | First Deep Learning approach to study the anatomy of *Terebellides* Sars, 1835 (Annelida, Trichobranchidae)

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Deep Learning (DL), the branch of Artificial Intelligence that uses neural networks to automatically learn complex patterns from data, is currently being applied in biology to accelerate species identification and process DNA sequence data. However, its application for polychaetes remains poorly explored. There is also a gap in the use of DL to automate anatomical segmentation, the recognition of anatomical structures and the generation of 2D representations. This study presents an initial approach using DL to segment anatomical structures within the genus *Terebellides* Sars, 1835, focusing on the digestive system. The main aim is to train a model to demonstrate high predictive accuracy and generate reliable segmentations on previously unseen images. To ensure high quality in training data, an inter-annotator agreement protocol was developed to refine and validate the annotation guidelines. Subsequently, a novel gold standard dataset was defined, the reference for the model to follow. It comprises 200 transversal micro-computed tomography 2D images, manually annotated by experts. Software and libraries widely used in medicine for segmenting anatomical elements, such as 3D Slicer and MONAI, were implemented. The technical framework utilises a U-Net architecture implemented in a Google Colab environment. In addition to automating the segmentation, the model is being designed to extract morphometric data, such as the maximum and minimum thickness of each predicted layer. This model increases segmentation

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speed, reducing the time required from hours or days to just a few minutes. Furthermore, the model exports a CSV file containing layer measurements for all images in the dataset. In conclusion, this initial step aims to highlight and develop the potential of deep learning applications in anatomical studies of polychaetes. This first approach could be adapted to other taxonomic groups, including other polychaete families and other invertebrate phyla.

3.4 * | Quantifying disparity in annelid locomotion using discrete non-morphological characters

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Locomotion is a set of behavioural traits that is fundamental to how annelids interact with their environment, often playing a major role in feeding, dispersal, mating, and survival strategies. Annelid locomotion strategies are highly diverse, generally thought to represent adaptations for life in specific habitats that have coevolved with morphology. This diversity is evident when comparing the two major annelid subclasses, Errantia and Sedentaria, which generally occupy different ecological niches and can be characterised by their locomotory strategies. To examine the drivers behind differing locomotion strategies, we use a suite of discrete non-morphological characters to capture the similarities and differences between the locomotion strategies of all major annelid groups, and define an annelid 'locomotion space' within which the locomotory disparity of phylogenetic and functional groups can be compared. We find that annelid locomotion can be broadly divided into two types: appendage-using and non-appendage-using, which broadly align with the Errantia and Sedentaria respectively. This novel approach: demonstrates that there is loose phylogenetic constraint over annelid locomotion strategy; uncovers an overall correlation between locomotion and ecology; and indicates that the variance in locomotion strategy is better explained by certain ecological variables than by phylogeny. In addition, using a co-opted morphological phylogenetic dataset, we quantify annelid morphological disparity and demonstrate a decoupling between morphology and locomotion. Our results suggest that the evolution of annelid locomotion has been shaped by the adaptability of the annelid bauplan, coupled with the acquisition of functional locomotory anatomical and neurological traits in the annelid stem-group. These factors enabled rapid diversification of locomotion strategy with only weak phylogenetic constraints, permitting the decoupling of morphology and locomotion. Overall, our results reveal that the evolution of annelid locomotion is governed less by anatomical and developmental constraints, and more by the demands of ecology and the environment.

4.1 | The National Polychaete Collection of Mexico, ICML-UNAM, a 48 years adventure

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The National Polychaete Collection of Mexico, the oldest and largest of Polychaetes from Mexico worldwide, is the result of VSW 48 research years in the ICML-UNAM. Previously, Rioja had created a collection which disappeared in 1963, following his death, never to be found again and polychaete research died with him, until VSW was hired. Nowadays, several collections exist in Mexico, (De León, Salazar, Bastida...), but the National Collection is housed in our lab and under our custody as curators. Started with the first samplings VSW performed in Mexico, and with all specimens personally collected by us, the master database holds 9077 entries, more than 25000 specimens, and around 800 catalogued species from 47 families, representing all the ecological marine and estuarine ecosystems in Mexico (from shallow to more than 4000m depth). Unusual new species described include nereidids from a high cave in Mexico's southwestern mountains, parasitic polychaetes inside other polychaetes, hydrothermal vents' alvinellids. Unusual collecting sites include cenotes or Clipperton Atoll. We hold currently 42 holotypes (17 families) and 52 paratypes (18 families); twenty-six holotypes were either deposited in the Natural History Museum, Smithsonian Institution, Washington, DC (Fauchald's recommendation then) or, much later, in the Collection of Nuevo León University, because De León González was first author of these joint descriptions. We have used our Collection for research and teaching: 98 research publications in peer reviewed Journals, 36 book chapters, 281 congress presentations, in four languages and have some outstanding discoveries, such as marine zoophilous pollination by polychaetes, two parasites of other polychaetes in coralline environments, Trochochaetidae's first records for Mexico, Trichobranchidae's unexplained beachings, and new species from hydrothermal vents.

Forty-five students have obtained their degree (BSc:30, MC:10, PhD:5). Despite such important results, we really fear that the same fate of Rioja's collection could happen to this collection when we retire.

4.2 | From Ecology to Omics: Dataset Publication and the Role of Research Infrastructures in Polychaete Biodiversity Science

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The rapid expansion of biodiversity data infrastructures and molecular repositories is transforming the way marine biodiversity knowledge is produced, disseminated, and reused. Polychaete research provides an ideal model to investigate these dynamics because it bridges long-established taxonomic and ecological traditions with rapidly growing genetic/genomic approaches. In this study, we first examined the temporal trends in conventional ecological and genetic/genomic polychaete datasets and scientific publications within the Spanish research community from the 1980s to the present. Data were compiled from major biodiversity repositories and infrastructures, including OBIS, GBIF, GenBank, ENA, BOLD, and LifeWatch ERIC-enabled resources. In parallel, publication trends were reconstructed through bibliographic analyses spanning ecological and molecular research domains. Our comparative analyses reveal that genetic/genomic datasets are associated with substantially higher publication growth rates than conventional ecological datasets, particularly since the 2000s. These patterns suggest that properly published, standardized, interoperable, and reusable datasets have stronger scientific amplification potential, contributing disproportionately to knowledge production over time. We then extended the analyses to the global polychaete research landscape and identified trends consistent with those in the Spanish case study. This finding indicates that the shift from ecology-based approaches to omics-driven research is a widespread international trend rather than a geographically restricted phenomenon. Importantly the observed differences cannot be attributed solely to advances in molecular technologies. Our results highlight that data accessibility, semantic harmonisation, interoperability, and FAIR-compliant publication practices play a key role in enabling long-term scientific reuse of biodiversity datasets. In this context, Research Infrastructures, and particularly LifeWatch ERIC, are central to facilitating data integration, discoverability, virtual analytical environments, and cross-domain interoperability. These services help accelerate scientific workflows, increase dataset reuse, strengthen collaboration networks, and ultimately enhance researcher productivity across biodiversity disciplines. By linking scientometric patterns with biodiversity cyberinfrastructure development, this study highlights the strategic importance of Research Infrastructures in shaping the future of marine biodiversity science. Ultimately, the transition from isolated datasets to interoperable digital ecosystems may be just as influential for scientific progress as the shift from ecology to omics itself.

6.1 | A paradox of *Ficopomatus*: a common but poorly known group of notorious estuarine biofoulers and bioinvasers

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Ficopomatus is a serpulid genus currently containing six species found in estuarine localities world-wide. Two of them, warm-temperate *Ficopomatus enigmaticus* and tropical *F. uschakovi*, are reported as notorious biofouling and invasive reef-building species. Paradoxically, whereas hundreds of studies examined ecology of *Ficopomatus*, the only taxonomic revision of the genus dates to 1978 and only a handful of publications report any DNA data. As a result, generic biodiversity is underestimated, species delimitations are still based on morphology alone and reported native and invasive ranges are speculative. Recent genetic studies showed the existence of cryptic species in *F. enigmaticus*, but the taxonomic status of other congeners remains uncertain. We conducted a pilot phylogenetic study within *Ficopomatus* using sequences of mitochondrial cytochrome b (cytb) and nuclear ribosomal (18S) genes. The results recovered *F. uschakovi* as a monophyletic group of morphologically similar, but genetically distinct species, some of which are invasive. We plan a modern integrative revision of the genus that would uncover cryptic biodiversity and examine biogeographic patterns shaped by evolutionary history and anthropogenic transport. We will integrate morphology with modern genomic data to build a robust phylogeny of the genus, examine invasion pathways, and provide molecular tools for recognition of potential invaders.

6.2 * | *Spirobranchus* revisited: Morphology and sequence data tell different tales

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Spirobranchus Blainville, 1818 is a genus within Serpulidae Rafinesque, 1815, defined by a calcareous opercular endplate lacking movable parts, together with the presence of peduncular distal wings and collar tonguelets. Traditionally associated with the iconic “Christmas tree worms”, 44 of *Spirobranchus* species are currently recognized, 33 of which result from the synonymization of former *Pomatostegus latiscapus*, *Pomatoleios kraussii* and *Pomatoceros* species. Consequently, *Spirobranchus* inherited their complex taxonomic history, including reports of some widely distributed species, largely due to high interspecific morphological similarity, which encouraged the assumption that single species could occupy vast geographic ranges far beyond their type localities. As these broad distributions were increasingly questioned, DNA sequence evidences demonstrate that *S. kraussii* represents a complex of regionally restricted undescribed species, while the wide distribution attributed to *S. tetraceros* results from the synonymization of multiple distinct taxa. Complexes such as *S. giganteus* sensu lato and *S. latiscapus* remain unsolved. Here, we present the first comprehensive phylogenetic analysis of *Spirobranchus* integrating morphological and molecular data. A dataset of 88 morphological characters across 47 taxa was analyzed under maximum parsimony. The resulting hypothesis was compared with a molecular phylogeny inferred from nuclear 18S and mitochondrial cytb markers, enabling the identification of synapomorphies supporting major clades. Both approaches recovered the *S. kraussii* complex as a monophyletic group, supported by a funnel-shaped opercular ampulla without thorns. In contrast, the *S. polytrema* and *S. latiscapus* complexes are only supported morphologically, while molecular data disperse the taxa across the topology. Similarly, *S. tetraceros* and *S. giganteus* sensu lato complexes form monophyletic groups according to morphology, which are recovered as polyphyletic and paraphyletic, respectively, by molecular data. These results suggest strong influence of ecological convergence on character evolution in species of *Spirobranchus*, emphasizing the need for integrative approaches to solve the evolutionary history within this genus.

6.3 | The Pandora’ box reopened: the *Amphiglena* enigma

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Amphiglena Claparède, 1864 is a genus of sabellids typically not exceeding a few millimetres in length, that dwell within photophilic algae and coarse sand across shallow temperate and tropical waters. *Amphiglena mediterranea* (Leydig, 1851) was historically regarded as the single representative of the genus in the Mediterranean Sea. *Amphiglena* show parental care, brooding their eggs and their larvae inside their tube, suggesting a relatively short dispersal potential. Recent molecular and morphological studies suggest that multiple *Amphiglena* species coexist in the Mediterranean, indicating a complex of potentially cryptic diversity within what has traditionally been considered *A. mediterranea*. To date, the link between the genetic data and available species names is still missing, and the diversity of *Amphiglena* in the Mediterranean Sea remains understudied. Following an extensive sampling that allowed us to obtain material from several areas across the Mediterranean and selected adjacent Atlantic localities, we present an integrative taxonomic revision of Mediterranean *Amphiglena*. Our aim is to contribute to stabilizing the taxonomy of this group by providing molecular diagnoses for both historically and recent available names (i.e., *Amphiglena armandi* Claparède, 1864, *A. mediterranea* and *Amphiglena gravinae* Giangrande, Putignano, Licciano & Gambi, 2021), reassessing species diversity patterns and testing the traditional diagnostic characters employed for species distinction.

6.4 | Dusting off the arrangement of the flowers of the sea: Phylogeny and systematics of Sabellidae (Annelida) via targeted exon-capture and genome-skimming phylogenomics

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Sabellidae is a diverse clade of annelids with ~600 accepted species taxa whose internal relationships have remained poorly resolved despite recent phylogenomic advances. Here, we present a densely sampled phylogenomic framework for Sabellidae based on targeted exon capture, low-coverage genome skimming, and transcriptomic data. Across 83 terminals, we recovered up to 134 loci per sample and constructed occupancy-filtered supermatrices to infer phylogenetic relationships. Our analyses recover two deeply divergent and well-supported subfamilies, Sabellinae and Myxicolinae, consistent with previous transcriptomic studies. Within these, we identify four principal lineages corresponding to the tribes Sabellini, Hysicomini, Myxicolini, and Amphiglenini. Several genera were recovered as paraphyletic, highlighting the need for future taxonomic revision. In addition to resolving relationships, the dataset established here provides a scalable framework for the integration of future genomic data across Sabellidae. We further evaluate the complementary performance of sequencing approaches, showing that exon-capture yields the highest locus completeness, while genome skimming substantially increases taxon sampling at much lower cost. Together, our results provide a robust phylogenomic backbone for Sabellidae, establish a stable higher-level classification and demonstrate the complementary strengths of exon-capture and genome skimming for scaling phylogenomic studies in non-model taxa.

7.1 | Revisiting the diversity of ‘spaghetti worms’ (Terebellidae, Polychaeta) from the French Southern and Antarctic Lands: new species, redescrptions and hidden synonymies

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The French Southern and Antarctic Lands (TAAF)—including Kerguelen Islands, Crozet Islands, and Antarctic Station of Dumont d’Urville—host a unique benthic fauna. Among the most emblematic groups are the ‘spaghetti worms’ (Terebellidae sensu lato), known both for their ecological importance and complex taxonomy. This study presents the first comprehensive taxonomic revision of TAAF terebellids, combining new species descriptions, redescrptions of historical species, and resolution of long-standing synonymies. Using historical type specimens from diverse museums (Paris, London, Washington, Stockholm), as well as specimens collected during recent oceanographic expeditions, we analysed morphological and genetic data to clarify the status of problematic species. Notably, several species of *Thelepus* previously described multiple times under different names are here recognized as single species, while others species are identified as new to science. Our findings highlight the importance of integrating type material examination and modern imaging techniques (e.g., SEM, DNA) to resolve taxonomic ambiguities in polar environments. This work not only advances our understanding of TAAF biodiversity but also provides a taxonomic framework for future ecological and biogeographical studies in the Southern Ocean. This is all the more important for these fragile ecosystems that are on the front line in facing the effects of global warming.

7.2 | The biodiversity and phylogeny of *Loimia* (Terebellidae) in China

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Hainan University, China

The genus *Loimia* Malmgren, 1866 is a globally distributed group within the terebellid family, characterized by enlarged lateral lobes on anterior segments and monopectinate uncini. Most of the 34 recognized species inhabit tropical and subtropical intertidal or coastal areas. Identifying *Loimia* species remains challenging due to highly similar morphological traits, with key diagnostic characters (e.g., lateral lobe shape, uncini teeth number, ventral pads) sometimes changing during growth. Limited molecular data and quantitative morphometric studies hinder an integrated taxonomic revision. Molecular resources for *Loimia* are scarce, comprising a few standard markers (e.g., *cox1*, 16S, 28S, 18S), two transcriptome datasets, and two mitochondrial genomes. Integrated morphological–molecular approaches are essential to resolve the taxonomic status of *Loimia* and improve species

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identification. In this work, *Loimia* from China will be reviewed and phylogeny will be constructed using different datasets, including concatenated standard markers (e.g., *cox1*, 16S, 28S, 18S), mitochondrial genome or transcriptome datasets. This work will contribute to further exploring the biodiversity of *Loimia* in China.

7.3 | Systematic Revision of *Eupolyornia* Verill, 1900 (Annelida, Terebellidae) in European waters

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For over a hundred years, since the last revision of the group in 1917 (Hessle 1917) and until the description of three new species in 2021, only two species of *Eupolyornia* Verrill, 1900 (Annelida, Terebellidae) were known in Europe. *Eupolyornia nebulosa* (Montagu, 1818) and *Eupolyornia nesidensis* (Delle Chiaiei, 1828). As is often the case with early-described polychaete species, the descriptions of each taxon lacks details, no type material exists and the locations of the type localities are vague. However, recent molecular analyses revealed the presence of other species of *Eupolyornia* in European waters, several of which were described as new (Lavesque et al. 2021). Yet, neither *E. nebulosa* nor *E. nesidensis* were re-described, which was an obstacle to further systematic investigation of the genus. This paper presents a complete systematic revision of the genus *Eupolyornia* in Europe. Based on a large sampling effort including Norway, Sweden, the United-Kingdom, Ireland, France, Spain, Italy and Greece, a collection of over 220 specimens was assembled. Extensive phylogenetic analyses (Maximum Likelihood and Bayesian Inference), species delimitation analyses (ASAP, sPTP, mPTP, GMYC, STACEY) and haplotype network analyses were performed on a dataset comprising two mitochondrial and four nuclear molecular markers: *COI*, 16S, 18S, *ITS1*, *ITS2* and 28SD1–D2. A total of 10 species were found. Four species are described as new. *Eupolyornia debilis* (Malmgren, 1966) and *Eupolyornia danielsseni* (Malmgren, 1866) are reinstated as valid species. *Eupolyornia gili* Lavesque et al. 2021 is synonymized to *E. nebulosa*. Neotypes are designated for *E. nebulosa* and *E. nesidensis*. Each species is described in details and extensively illustrated with macro-photographs, micro-photographs and scanning electron microscopy images.

7.4 | The discovery of Australian terebellids

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Australia has a very large EEZ from the tropics to the subantarctic and from shallow to abyssal depths, and we suggest that many more species remain to be described. Terebellidae are one of the largest polychaete families with 60 genera and 645 species, and in Australia we currently have 34 genera and 93 species recorded, with the first species with recorded in 1861 by Schmarda from Twofold Bay, NSW. Over the next 100 years or so, numerous oceanographic expeditions collected benthic samples which were taken back to Europe for identification. The check list of Australian polychaetes by Day & Hutchings (1979) listed 78 species belonging to 27 genera, which included 17 described from outside Australian waters. Over time, all of these non-Australian species were found to represent new species. Plotting the type localities of the 93 Australian species reveals the regions of Australia poorly sampled which includes many offshore areas, and areas in Northern and Southern Australia, notably around the Great Australia Bight. While some species are known only from their type locality, others are more widely distributed including some also occurring in PNG, New Caledonia. Of the 93 species, only the recently described (from 1995 onwards) ones have molecular data as well as morphology, and we suggest that as more molecular data becomes available some of these apparently widely spread species will be found to represent cryptic species. These include six species with type localities in the Philippines which have poorly preserved type material and have been recorded from Australia based purely on morphology. Recent oceanographic cruises to various Australian bioregions as well as dedicated workshops have shown how much is still unknown. Some attempts are made to compare the Australian terebellid diversity with other regions of the world.

* Denotes a student contribution eligible for a prize.

Presenting author shown in **bold**.

7.5 | Phylogeny of the tribe Ampharetini Malmgren, 1866

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The family Ampharetidae comprises small benthic and tubicolous marine annelids, particularly abundant in sublittoral soft bottoms. The tribe Ampharetini stands out in the family because the 54 valid species are classified into only two genera: *Ampharete* and *Neosabellides*, while other genera in the tribe have been treated as minor synonyms (i.e., *Asabellides*, *Branchiosabella*, *Heterobranchus*, *Pavelius*, *Pseudosabellides*, *Pterampharete*, and *Sabellides*). Although the monophyly of Ampharetini has been confirmed, the phylogenetic relationships within the tribe remain poorly understood, as most characters are considered ambiguous, including commonly used taxonomic characters. Therefore, the main objective of this research was to evaluate the systematics of Ampharetini through phylogenetic analyses using separated cladistic analyses based on external morphological characters and molecular phylogenetic analysis of multiple genes. Two separate analyses were conducted to assess the relationships within Ampharetini: (1) a cladistic analysis based on 51 species and 74 morphological characters and (2) a combined analyses based on 30 species, five genes (COI, 16S, 18S, 28S, and H3), and 81 morphological characters. Ampharetini was monophyletic in both morphological and combined phylogeny, defined by the synapomorphies of pinnate buccal tentacles, notochaetae on segment II, and an achaetous segment III. In contrast, *Ampharete* and *Neosabellides* were polyphyletic as currently defined. In morphological phylogeny, *Ampharete* species were grouped in six principal separated clades, while the position of other eight species remained uncertain. The *Pavelius* species, previously considered in *Neosabellides*, were grouped out from both *Neosabellides* and Ampharetini. Meanwhile, the remaining four species of *Neosabellides* formed two clades: *Neosabellides* sensu stricto and another unnamed clade. Sequence data supported *Ampharete* s. s., *Neosabellides* s. s., and *Pavelius* as well-supported clades, and *Sabellides octocirrata* and *Neosabellides lizae* as separated branches from *Ampharete* s.s. and *Neosabellides* s.s. respectively. Based on all available information, a different classification of Ampharetini is proposed.

8.1 | Museomic insights into the evolutionary history and biogeography of ramified syllids

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Ramified syllids are marine annelids that possess a single head and a series of posterior branches, representing a remarkable case of morphological and ecological specialization. This talk examines the systematics, distribution, and evolutionary origins of the only currently-known branching taxa: *Syllis ramosa*, originally described from the Indo Pacific, and the recently discovered members of the genus *Ramisyllis* from Australia and Japan. Genome skimming of historic museum specimens, together with newly collected field samples, produced robust phylogenomic datasets that, when combined with detailed morphology, resolved long standing taxonomic ambiguities. The resulting phylogeny recovered a well-supported monophyletic clade comprising two major lineages. Ecological divergence between these lineages appears to have driven the primary split, whereas diversification within each lineage indicates host specific, fine scale radiation. All newly recognized *Ramisyllis* species were identified from museum collections, expanding the genus' diversity without additional field effort. In parallel, two deep sea specimens that closely resemble *S. ramosa* were freshly collected from bathyal habitats, and a series of historic museum samples (collected from 1914 onward) were reexamined. Nondestructive micro CT scanning was employed to visualize the worms within the sponge matrices, allowing detection of the symbionts and extraction of small tissue fragments for molecular and morphological analyses without damaging the valuable historical material. This work underscores the untapped potential of museum collections to uncover hidden biodiversity and to reconstruct the evolutionary histories of rare, morphologically exceptional marine organisms.

8.2 * | No Worm Without its Host: Museum-Based Phylogenomics of Sponges Hosting *Ramissyllis*

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Polychaetes are well known for their close associations with various marine invertebrate hosts, ranging from commensalism to obligate endosymbiosis. A particular curious example is the branching syllid *Ramissyllis*. This species lives inside multiple sponge species within the *Petrosia* genus for its entire life, with its body branching throughout the canal system. Such an intimate lifestyle raises questions about the evolutionary mechanisms that shape and sustain it. Insight into the evolutionary history of the host is required to understand the origin and nature of this association, yet this has long remained elusive due to the notoriously complex systematics of *Petrosia* and its order, Haplosclerida. Both are plagued by pervasive para- and polyphyly under current morphology-based classification. Here, we used target enrichment of nuclear exon loci from museum-preserved *Petrosia* specimens associated with *Ramissyllis* from across the Indo-Pacific to generate a robust phylogenomic framework for the host sponges. Despite the taxonomic complexity of this order, all specimens harbouring this branching syllid form a single, well-supported, monophyletic clade within Haplosclerida. This suggests that the capacity to harbour *Ramissyllis* is a derived, shared character of this poriferan lineage. Comparing this with an existing *Ramissyllis* phylogeny reveals broadly congruent patterns. This provides, for the first time, a phylogenetic framework within which questions about the shared evolutionary history of the worm and its host can be meaningfully addressed. Sponges and syllids are both marine invertebrate groups whose evolutionary histories are still poorly understood, making this obligate endosymbiosis a compelling system for investigating the origin, persistence and diversification of intimate associations between these groups over time.

8.3 * | Rare Group in an Understudied Sea: New Insights into Autolytinae (Syllidae, Annelida) Systematics

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Autolytinae is a well-established monophyletic subfamily within Syllidae, characterised by a carnivorous lifestyle and association with benthic invertebrates. Despite this, the group remains poorly represented in benthic surveys, with many of its 124 described species known from single specimens. In addition, taxonomy within Autolytinae is particularly challenging due to the strong reliance on reproductive biology and live colouration, traits that are often unseen or lost during sampling and preservation. The Red Sea represents a largely understudied region for this subfamily, with only 13 species reported to date. Specimens recently collected during a BioBlitz effort in coral reef habitats along the northern Saudi Arabian coast were analysed using an integrative taxonomic approach combining both morphological and molecular data. Our results reveal a new monotypic genus and three new species, significantly expanding the known diversity of the group in the region. These findings provide new insights into the systematics of Autolytinae and highlight the limitations of current knowledge based on sparse sampling and traditional taxonomy alone. More broadly, this study underscores the Red Sea's potential as a reservoir of previously undocumented diversity and emphasises the need for integrated approaches to resolve the taxonomy of elusive and understudied annelid groups.

8.4 | One ring to rule them out: integrative taxonomy clarifies the identity of the alleged *Nereis agulhana* Day, 1963 (Annelida: Nereididae) in the Mediterranean Sea

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Nereis agulhana Day, 1963 is a small Nereididae originally described from South Africa, characterised by a peculiar, contrasted live colour pattern that is often maintained in preserved individuals. Starting from the 1960s, individuals morphologically close to this

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species were reported from several areas across the Mediterranean Sea, and the species was considered non-indigenous in the region, despite the differences reported between Mediterranean material and the original description. A re-examination of several individuals from France, Italy, Croatia, Cyprus and Lebanon based on morphological characters as well as DNA sequence data highlighted the occurrence of two different morphotypes, overall sharing the same live colour pattern, but clearly different when taking into account chaetal and pharyngeal features, not closely related, and both showing differences towards *N. agulhana*. One morphotype, occurring in seagrass meadows in France and Italy, is devoid of notopodial homogomph falcigers and characterised by a paragnath arrangement unique among Mediterranean Nereididae; it includes a single molecular lineage and is tentatively assigned to the genus *Neanthes*. The other morphotype, provided with notopodial homogomph falcigers and showing some similarities with *Nereis rava* Ehlers, 1868, is widespread on both seagrass meadows and soft bottoms down to 50 m depth, and includes three molecular lineages structuring a clade, with distributions coarsely corresponding to Mediterranean sub-basins (Tyrrhenian, Ionian+Adriatic, Levantine Seas). The genetic structuring within the Mediterranean Sea supports the hypothesis of a native lineage at least for the second morphotype, seemingly the one morphologically closer to *N. agulhana*, allowing us to disprove the occurrence of this latter species in the Mediterranean Sea.

8.5 | New fashion trends unlocked: Undescribed Nereididae and Phyllodocidae (Annelida, Polychaeta) from the Red Sea, Arabian Gulf and Mediterranean Sea

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Recent efforts to document marine biodiversity in the Kingdom of Saudi Arabia increasingly integrate morphological taxonomy with DNA barcoding. This combined approach establishes robust baselines for species identification, supporting long-term monitoring and early detection of non-indigenous species. Despite their ecological importance, marine annelids along the Arabian Peninsula remain poorly studied due to outdated taxonomy and limited molecular data. This gap is particularly relevant given the continued discovery of new species, even in well-studied regions. In this study, we investigate the diversity of polychaetes within the families Nereididae and Phyllodocidae from the Saudi Red Sea and Arabian Gulf, complemented by comparative material from the Mediterranean. Specimens in Saudi waters were collected from coral reefs, intertidal zones, and artificial substrates deployed in ports and marinas. More than 1,200 DNA barcodes were generated, resulting in over 95 Barcode Index Numbers (BINs). From those BINs, only 24 could be assigned to species-level, with most resolved to genus. Our results reveal substantial previously overlooked diversity, particularly within the nereidid genera *Ceratonereis*, *Nereis*, *Perinereis* and *Pseudonereis*, and the phyllodocid genera *Nereiphylla* and *Phyllodoce*. As the most notable examples, the species *Ceratonereis mirabilis* Kinberg, 1865 and *Nereiphylla castanea* (Marenzeller, 1879) have been previously reported from the Arabian Peninsula as the single representatives of each respective genus. Yet, our collections identified at least nine distinct *Ceratonereis* species and four *Nereiphylla* species. Additional analyses of European material further uncovered five cryptic lineages within the *Nereiphylla rubiginosa* (Saint-Joseph, 1888) complex. These taxa are delineated using multiple genetic markers and diagnostic morphological features, including pigmentation patterns, chaetal morphology, parapodial structures, and jaw canals. This study underscores the prevalence of both cryptic speciation and regional limited representation of polychaetes and highlights the urgent need for systematic biodiversity baselines in the face of environmental change and increasing biotic exchange among marine ecoregions.

9.1 | Bringing together international taxonomists to study the annelid fauna of the Aleutian Trench – Presentation of results from an almost finished project

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In July 2022 the research vessel 'SONNE' started its cruise SO293 to the NW Pacific Ocean. The aim was to study the benthic fauna of all size classes from protists to megafauna in abyssal and hadal depths of the Aleutian Trench, and also the adjacent Bering Sea. The benthic fauna of the Aleutian Trench was a priori regarded as virtually unknown since only a single box core had been realized in the 1970s (Jumars & Hessler 1976). The recent collection of samples was now undertaken by deploying various sampling gear, as e.g. different cores and sledges. Already during sample management on board, the benthic fauna turned out to be very diverse and annelids seemed to be the prevailing group among all macrofaunal taxa. Succeeding sample sorting in the lab proved this observation correct, with annelids being the dominating macrofaunal taxon. The number of collected polychaetes was nearly 3.000 for the box core but almost 12.000 for the epibenthic sledge, belonging to 40 different 'families'. Being aware of this high taxonomic diversity and the great value of the material preserved for both morphological and molecular studies, the greatest success for elucidating the composition of the polychaete fauna seemed only achievable by involving experts for the different taxa, and work jointly. In September 2024, 19 polychaete taxonomists, from 13 institutions across Europe and the U.S., gathered at Station Biologique de Roscoff (France). During this workshop it was agreed to publish a special volume on the annelid fauna of the Aleutian Trench as a compilation of taxonomic papers and associated contents. Another identified goal was the establishment of a barcode reference library for the area. During the 15th IPC first results of the discoveries are presented in a generalized format, and for some spionid taxa selected findings and achievements also in more detail.

9.2 | An integrative revision of *Eunoe*: implications for generic boundaries in Polynoidae

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Generic diagnoses in Polynoidae have traditionally relied on external morphological characters that are easy to observe but difficult to interpret phylogenetically. An integrative revision of *Eunoe*, based on morphology, multilocus DNA data (COI, 16S rRNA, ITS2, and 28S rRNA), and museomic sequences from the lectotype of *E. oerstedii*, recovered *Eunoe* sensu lato as polyphyletic and restricted *Eunoe* sensu stricto to a clade of six species: *E. nodosa* (the type species), *E. oerstedii*, *E. cf. oerstedii* CMC01, *E. ciliata* comb. nov., *E. shirikishinai*, and *E. spinicirris*. Fifteen species currently assigned to *Eunoe* were recovered outside *Eunoe* s. str., scattered across several clades and often associated with other polynoid genera, including *Harmothoe*.

These results indicate that traditional characters used for generic diagnoses in Polynoidae may be homoplastic. In particular, the placement of *E. ciliata* comb. nov., formerly *Gattyana ciliata*, within *Eunoe* s. str. shows that notochaetal morphology does not effectively separate *Eunoe* from *Gattyana*. By contrast, ventral anterior eyes appear informative for delimiting *Gattyana* s. str., indicating that some characters remain useful for generic diagnoses. *Eunoe* s. str., however, is currently characterized by a non-exclusive combination of dorsal or dorsolateral anterior eyes and elytral macrotubercles, a "*Eunoe*-like" morphology also observed in unrelated lineages. Therefore, morphology remains important for polynoid taxonomy, but commonly used generic characters, especially chaetal and elytral characters, should be re-evaluated in a phylogenetic context.

9.3 * | Rethinking *Bylgides* (Polynoidae): Integrating morphology and phylogeny

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The genus *Bylgides* (Polynoidae, Annelida) currently comprises nine species and was last revised by Pettibone (1993). Like many polynoid genera, the taxonomic history of *Bylgides* is complex, and species identification based on morphology remains difficult. Furthermore, there are no molecular studies focusing on *Bylgides* and the attribution of species names to sequences is often erroneous. We found *Bylgides* to be polyphyletic based on multiple loci phylogeny combining newly obtained sequences (COI, 16S, 28S) from the material from the University Museum of Bergen with public data from BOLD and GenBank. *Bylgides* sensu stricto contains five species, including the type species *B. elegans*, and is defined by the presence of 14–15 pairs of elytra, coarse and stout notochaetae, and more delicate, unidentate neurochaetae of which most or all taper into hair-like tips distally. Additionally, we suggest short lateral antennae and small eyes, both anterior and posterior, to be diagnostic characters of the newly delimited genus. Three species, *B. acutisetis*, *B. macrolepidus* and *Bylgides* sp. were recovered outside the *Bylgides* sensu stricto clade, however their placement within the system of Polynoidae requires further study. Five species of *Bylgides* were well delimited and redescribed based on the type and non-type material. However, the morphological distinction between *B. elegans* and *B. sarsi*, recovered in separate clades in phylogenetic analyses, remains ambiguous. Distribution maps revealed an Arctic distribution of *Bylgides* sensu stricto with few records from boreal regions and the Baltic Sea.

9.4 * | Freshwater colonization by a scaleless scale worm: *Pisone mizuchi* Shimooka & Jimi in Shimooka et al., 2026 (Sigalionidae)

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Annelids excluding earthworms and leeches that inhabit freshwater account for less than 2% of all known species (Glasby and Timm, 2008). To survive in freshwater environments, annelids must develop effective osmoregulatory systems. In particular, reproductive adaptations to unidirectional flow are required in riverine habitats (Kuo, 2017; Glasby et al., 2021). We described the second freshwater scale worm species, *Pisone mizuchi* Shimooka and Jimi in Shimooka et al. 2026, from shallow freshwater environments in the downstream sections of three river on Sado Island, Japan. Phylogenetic analyses indicate that this species represents a lineage that independently colonized freshwater from among marine *Pisone* species. Subsequent investigations revealed additional populations not only from the type locality on Sado Island but also from the southern part of the Japanese main island. Although the reproductive mode of this species was reported as unknown in Shimooka et al. (2026), these findings suggest that it disperses via planktonic larvae transported by marine currents, such as the Kuroshio Current.

9.5 | Fourteen Years in the Mud: Revisiting an Orbiniidae Taxonomic Thriller

Paul Wolf

Ocean Wolf. New Zealand

More than fourteen years ago, at the University of Rostock, I embarked on a journey into the mud to uncover the story of a worm. This tale began in 1776 when Müller described *Lumbricus armiger* from Norway. Since then, this species has been relocated, renamed, reclassified, synonymised, and identified globally as the supposedly cosmopolitan *Scoloplos armiger*. My Diplomarbeit aimed to clarify a small part of this extensive history. Analysing material from Kindo in the White Sea and Sylt in the North Sea, I integrated morphological data with mitochondrial NAD6 and nuclear 18S sequences. Instead of identifying a single familiar species, the specimens revealed at least three distinct lineages: *S. armiger* sensu stricto, a White Sea *Scoloplos* lineage, and a North Sea

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Scoloplos lineage. The most significant insights emerged not from isolated "magic" characters but from combinations of uncini distribution, thoracic segmentation, and parapodial features. At times, morphology and genetics aligned; at other moments, they seemed to diverge. Returning to Germany—and to Frankfurt, within the broader Senckenberg community linked to collections that shaped my early training—feels like reopening an old case file. This is not the concluding chapter of the Orbiniidae thriller but an invitation to further the investigation with additional material, colleagues, and unexpected discoveries hidden within the sediment.

10.1 | Integrative taxonomy to resolve species complexes and genetic typification of original polychaete names from type localities

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Integrative taxonomy demonstrates a large hidden diversity among polychaetes. In Norway named species has increased from around 600 to more than 800 the last 20 years. Sequencing well-known species (e.g. *Scalibregma inflatum*, *Amphiteis gunneri*) cluster into multiple groups representing putative species. From extensive sampling in Norwegian waters, more than 4000 DNA barcodes (CO1, 16S, 28S) of more than 500 named species have resulted in more than 700 BINs. Consequently, polychaete species numbers are estimated to be 30-40% higher than presently known for the region. Multiple BINs, documenting complexes of confused species, seem particularly common among early described species, for which present descriptions and names may confound characters and lead to incorrectly reported species distributions. Original species descriptions from the 18th and 19th century were generally short and little specific, often in Latin or a Scandinavian language, and from localities with place names not found in today's maps. In a new Norwegian project – PolyType – aimed at resolving species complexes, samples from original sampling localities (type localities) will be basis for genetic characterisation and morphological redescrptions. This to anchor original species name with the 'correct' genetic clade in well-documented species complexes. The potential of eDNA and metabarcoding for biodiversity assessments will rely heavily on quality-assured sequence libraries. Similarly, international initiatives to obtain species genomes rely on sequencing the 'correct' genetic clade to establish a reference genome to a species name. This can only be obtained through critical taxonomic work based on curated sequence libraries and museum voucher specimens. Unravelling species group diversity across geographic regions and for widely distributed species in general will contribute to resolve hidden diversity and document the real distribution of confused species. Coordination and collaborative work are necessary to understand biological diversity in a world facing rapid nature loss.

10.2 | Clarifying the presence of *Eunice kinbergi* Ehlers, 1868 and *Eunice aphroditois* (Pallas, 1788) in South Africa.

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Genus *Eunice* Cuvier, 1817 is ranked 2nd highest priority in need of taxonomic and genetic revision in South Africa. Among these, indigenous *Eunice kinbergi* Ehler, 1868 has a confusing taxonomic history. The species was originally described from the Cape of Good Hope, South Africa. Day (1967) synonymised *E. kinbergi* with *Eunice aphroditois* (Pallas, 1788) from Sri Lanka without justification and reported a widespread local distribution from Namibia (southwest coast of Africa) to KwaZulu-Natal (east coast of South Africa) and a cosmopolitan distribution globally. Fauchald (1992) reviewed the syntype material of *E. kinbergi* and deemed it independent from *E. aphroditois* based on its articulated notopodial cirri and ceratostyles, in the former, although the species are very similar morphologically. In South Africa, '*E. aphroditois*' is the popular bait, the giant wonderworm, so it is important to clarify its taxonomic identity as additional material collected locally have not been taxonomically examined since Fauchald (1992). We examined fresh specimens of *Eunice* from Sea Point, Strand and Knysna (i.e., within its distribution range), and specimens determined by Day (1967), lodged at the Iziko Museum. Examination of specimens determined by Day from False Bay revealed inconsistencies with the description of *E. aphroditois* in Day (1967), including shape of branchiae base and filament number and variation in teeth numbers on MXII, while specimens match the description of *E. kinbergi* by Fauchald (1992) more closely. COI sequences generated from fresh material revealed a strongly supported monophyletic clade from South Africa that was

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independent to *E. aphroditois* from Japan and Portugal which differed genetically by 22%. As such, the current study provides an updated description of *E. kinbergi* from South Africa with genetic sequences. Additional taxonomic and genetic comparisons are warranted for specimens from Namibia and KwaZulu-Natal to confirm the identity and distribution limits of the species, regionally.

10.3 * | Systematic revision of *Arabella iricolor* complex in Korean waters, with implications for Northeast Asian waters

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The *Arabella iricolor* species complex has long been considered taxonomically problematic due to incomplete original descriptions and morphological similarity among congeners. In Northeast Asian waters, records assigned to *Arabella iricolor* have not been comprehensively re-evaluated in light of recent type-locality-based concepts of *A. iricolor* sensu stricto. This study provides a systematic revision of *Arabella iricolor* species complex from Korean waters, based on extensive sampling across 42 localities detailed morphological examination, and DNA barcoding (COI and 16S rRNA). Four species are recognized, including *Arabella turbidicolor*, which is redescribed, and three species newly described herein. The examined taxa are distinguished by a combination of diagnostic morphological characters, including: 1) prostomium length-to-width ratio; 2) mandible cutting plate morphology (V-shaped vs. U-shaped); 3) relative length of mandible cutting plates and carriers; 4) relative length and shape of maxillary dorsal and ventral carriers; 5) symmetry of maxilla II; 6) development of anterior notopodial cirri; 7) pygidial structure (two lobes vs. four cirri). Molecular analyses indicate that none of the Korean specimens examined are conspecific with *A. iricolor* sensu stricto. Phylogenetic results further show that sequences previously identified as *A. iricolor* from Japan and China cluster within these Northeast Asian lineages. These findings suggest that the records of *A. iricolor* sensu stricto in Northeast Asia require taxonomic re-evaluation. Analysis of distributional patterns of the *A. iricolor* species complex revealed geographically structured distributions within Korean waters. A distinct lineage was restricted to the Yellow Sea, whereas others were distributed across the East and South Seas of Korea. These patterns suggest regional differentiation among lineages, potentially associated with oceanographic boundaries. Here, we provide morphological diagnoses, DNA barcoding data, and distributional information for the Korean *A. iricolor* species complex to facilitate accurate identification and support future research.

10.4 | The “Giant” in the State Museum of Natural History Karlsruhe - only another Bobbitt worm?

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An approximately 1,5-meter-long fragment of an Eunicidae (Annelida: “Polychaeta”) is described from one of the largest aquariums in Germany, where it lived more or less undetected for almost ten years, only occasionally nibbling on corals and leaving slime tubes. Originally it seems to be from Indonesia and apparently arrived at the State Museum of Natural History Karlsruhe via live rocks. For a polychaetologist a fascinating animal, for an aquarist, however, an unwanted parasite and the cause of sleepless nights. By using various forensic methods, several questions should be answered: What species is it? How large was the animal originally? What parts of it are missing and why? What did it feed on? Why did it appear? And did the head survive? We can no say a little more about one particular specimen (“Walter” as his fans have named him). However, it is a shame that we know so little about such a “well-known” species (or probably species complex) which is of interest even to laypeople.

12.1 | Polychaete Diversity Through the Lens of iNaturalist

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Community-science platforms are transforming how biodiversity is documented, yet their performance for taxonomically complex marine invertebrates remains largely untested. Despite their ubiquity, polychaetes have rarely been examined through the lens of large-scale community-science datasets. Here we evaluate whether research-grade iNaturalist observations can be used to characterize broad patterns of polychaete diversity across United States coastlines. We compiled a nationwide dataset of georeferenced, community-verified polychaete observations spanning more than a decade and standardized all taxonomic

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identifications against an authoritative marine taxonomy framework (WoRMS). Observations were classified into major coastal regions and analyzed to assess regional richness patterns, taxonomic composition, sampling structure, and observation-based community distributions. Effort-standardized approaches, including rarefaction and rank-abundance analyses, were used to distinguish sampling effects from emergent diversity patterns. Our results reveal strong spatial structure in observation-derived assemblages and highlight how community-generated data capture both biologically meaningful signals and systematic sampling biases. Patterns recovered from the dataset are consistent with established marine biogeographic expectations while simultaneously exposing substantial gaps in regional coverage and taxonomic representation. Interpretation of species-level patterns must be framed within current taxonomic knowledge, as several frequently observed taxa belong to unresolved species complexes known to contain undescribed cryptic diversity that cannot be reliably distinguished from photographic records alone. This study establishes the first large-scale baseline assessment of polychaete diversity in North America as represented in a global community-science archive and provides a model for integrating opportunistic observational data into marine biodiversity research. As marine ecosystems face accelerating environmental change, leveraging public data streams alongside traditional surveys may be critical for documenting shifting species distributions and prioritizing future taxonomic effort.

12.2 | Distribution of Paraonidae Species (Annelida: Polychaeta) Along the Aegean and Levantine Seas (Eastern Mediterranean)

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This study presents the first large-scale taxonomic and ecological analysis of Paraonidae species in the eastern Mediterranean Sea, based on long-term benthic monitoring data collected between 2015 and 2024 under the National Integrated Marine Pollution Monitoring Program (DEN-IZ). A total of 705 samples were collected from 46 soft-substrata stations, with depths ranging from 7 to 702 m, across the Aegean (25 stations) and Levantine (21 stations) coasts of Türkiye. A total of 16,178 individuals belonging to five genera (*Aricidea*, *Cirrophorus*, *Levinsonia*, *Paradoneis* and *Paraonis*) and 35 species were identified. Among these, *Levinsonia* (46%) was the most dominant genus, and *L. demiri* was the most dominant species (43.5%), while *Aricidea claudiae* (34%) and *L. demiri* (34%) exhibited the highest frequency of occurrence. Furthermore, *L. demiri* and *Paradoneis* sp. showed the widest bathymetric distribution. In the Aegean Sea, a total of 15,398 individuals belonging to five genera and 35 species were recorded, with *L. demiri* (42%) and *A. claudiae* (23%) being the most dominant. The number of species per sample ranged from 1 to 12, while the paraonid density varied between 10 ind.m⁻² and 6,370 ind.m⁻². In the Levantine Sea, a total of 780 individuals belonging to 26 species were identified. In this region, *L. demiri* and *A. claudiae* were the most frequent and dominant species. The number of species per sample ranged from 1 to 6, and the paraonid density varied between 10 ind.m⁻² and 6,420 ind.m⁻². *Aricidea fragilis* and *A. bulbosa* were recorded as alien species in the regions. While *A. bulbosa* was recorded exclusively in the Levantine Sea, *A. fragilis* was present in both regions. *Aricidea fragilis* accounted for 3.6% and 7.8% of total paraonid abundance in the Aegean and Levantine Seas, respectively. *Aricidea bulbosa* comprised only 0.1% of total paraonid abundance in the Aegean Sea.

12.3 | Temporal changes in soft-bottom polychaete assemblages of the Bay of Biscay (NE Atlantic)

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Within the French energy transition framework, offshore wind farms are being deployed, particularly at the Bay of Biscay because its strong winds and expansive continental shelf. Establishing an environmental baseline by studying soft-bottom benthic macrofauna particularly polychaetes is essential for evaluating the ecological impact of these wind farms, but also for understanding natural changes. In order to evaluate spatio-temporal changes in these assemblages a two-year survey (2023–2024), at Oléron 1 & 2 parcs over 430 km², took place by sampling 444 stations across four campaigns (conducted in late summer and late winter) and using a 0.1 m² Day grab (five replicates per station). A total of 50,095 individuals were sampled belonging to at least 272 species. Values of species abundance and richness did not show a trend over time. Whereas Autumn (2023 vs. 2024) sampling showed significantly contrasting values of species abundance and richness, Spring (2024 vs. 2025) sampling were more similar. Scalibregmatids were responsible for higher abundances values in Autumn 2023 while spionids and lumbrinerids contributed the most for the subsequent sampling periods. Four assemblages were found (cluster, nMDS) mostly associated with

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sediment granulometry. Assemblage I contained 66 stations distributed predominantly in muddy sediments in the east. Assemblage II contained 211 stations distributed predominantly in sandy sediments in the south. Assemblage III contained 165 stations distributed predominantly in coarse, gravelly sediments in the north. Assemblage IV included 2 stations in an artificial group. Rarefaction curves indicated that assemblages I and III were more diverse than assemblage II and did not reach asymptotes at local scale. While seasonal descriptors of polychaetes fluctuated, the underlying species composition structure remained stable and closely tied to sediment characteristics, offering a robust baseline for future environmental assessments in the bay. However, regional hydrodynamics and climate still need to be considered.

12.4 | Current Status of Benthic Polychaeta in ASEAN Countries

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Benthic marine Polychaeta (Annelida) are foundational components of Southeast Asian marine ecosystems. They are increasingly valued not only for their conventional uses in aquaculture and recreational fishing but also for non-conventional applications in nanomaterial production and health, such as acute wound healing. Despite their ecological and economic importance, comprehensive knowledge of polychaete diversity in the region remains heavily fragmented. The study evaluates the current identification status and taxonomic research capacity for benthic Polychaeta across ASEAN nations. Regional occurrence data and researcher demographics were compiled from published scientific literature, reports, and government databases spanning over the past two decades. Species names were validated for accuracy using the World Register of Marine Species (WoRMS). A heatmap analysis was applied to reveal the pattern of polychaete species discovery across the ASEAN. We found a total of 1,119 valid benthic polychaete species documented across the ASEAN region. Species distribution is highly uneven across the nations. Indonesia records the highest regional diversity with 456 species (~35.4% of total identified species). Followed by Thailand and the Philippines with 353 and 250 species, respectively. Interestingly, Cambodia currently has no identified marine Annelida species. An overwhelming 947 species (84.63%) are recorded in only a single country, suggesting severe sampling gaps with other countries in the same region. The highest species similarity occurs between Indonesia and the Philippines (51 shared species). Furthermore, the data exposes a critical "taxonomic impediment" driven by a shortage of local experts. Lack of funds, absence of physical infrastructures (repositories) and bureaucratic further delayed the progress of polychaete research in ASEAN. The profound disparities in species records reflect significant sampling biases rather than true ecological endemism. ASEAN nations must prioritise local taxonomic capacity building, strengthen national natural history repositories, and foster cooperative cross-border marine assessments.

13.1 | Microbes Are Everywhere, but Whose Are They? Robust Workflows and Host Filtering in the *Ramissyllis-Petrosia* Nested Holobiont

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Microbes are the invisible majority of life: they built Earth's biosphere and are now recognised as integral partners of the animals they inhabit. Host microbiomes are not random assemblages, their composition reflecting which microbes disperse in, which pass host physiological filters, and which adapt to the host; across many animals, microbial communities mirror host evolutionary relationships, a pattern termed phyllosymbiosis. Yet recovering trustworthy host-associated signal is hard precisely because microbes are everywhere. Robust microbiome research therefore depends on established, standardised workflows: DNA extraction choices alone can shift apparent diversity and composition, host-derived reads are easily misclassified as bacteria in 16S data, and reagent or cross-system contamination readily generates artefacts. Even a carefully controlled pipeline is not enough, detected taxa must be scrutinised for biological plausibility, since cosmopolitan organisms such as *Pseudomonas*, abundant in sediments,

* Denotes a student contribution eligible for a prize.

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seawater and reagents, can masquerade as genuine host signal. Together, established protocols and critical, sanity-checked interpretation now make it possible to study microbiomes in diverse, non-model environments. We apply this framework to the *Ramissyllis kingghidorahi*–*Petrosia* sp. association, a nested holobiont in which a branching syllid lives permanently inside the canal system of its sponge host, so two phylogenetically distant animals share one microbial environment, a natural test of host filtering. Using paired 16S rRNA amplicon sequencing and PICRUST2 functional inference across three Japanese islands, with explicit host-read screening and reagent-contaminant removal, we find host-derived sequences negligible and sponge and worm maintaining distinct, host-specific microbiomes: *Petrosia* shows the canonical *Chloroflexota*-dominated high-microbial-abundance phenotype, the worm a more variable, copiotroph-enriched community. Even under shared exposure, host identity filters the microbiome, establishing this nested holobiont as a robust model for how animals shape their microbial partners.

13.2 | A multi-trait phylogenetic roadmap to predict venom evolution in Polychaeta: Integrating ecological traits for systematic bioprospecting

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Polychaetes are fundamental organisms of marine benthic communities, occupying diverse ecological niches from stable estuarine mudflats to high-energy intertidal rocky platforms. These varied environments impose distinct selective pressures on feeding strategies and defense mechanisms, driving the evolution of specialized bioactive compounds. Despite this rich functional diversity, the discovery of marine toxins remains largely on organisms with nefarious human interaction. Thus, this study addresses this gap by integrating evolutionary ecology with bioinformatic modeling to identify toxin-bearing taxa. Using *Eulalia clavigera* and other intertidal polychaetes from the Portuguese coast as a case study, we investigated how environmental positioning and trophic ecology influence the emergence of venom systems. We employed Bayesian inference-based phylogenetics, combining molecular systematics (COI-5P) with foregut morphoanatomy and physiological traits. Building upon the framework used for *Eulalia clavigera*, our research constructed a multi-trait roadmap to predict the occurrence of venomous and toxungenous systems. The results demonstrate that DNA sequences, the presence of specialized jaws, and predatory life-history traits are primary indicators of venom evolution. We successfully mapped high-priority targets within the Order Phyllodocida, including *Glycera alba* (Glyceridae), *Mysta picta* and *Eulalia clavigera* (Phyllodocidae), *Nephtys hombergii* (Nephtyidae) and *Hediste diversicolor* (Nereididae). These species have evolved sophisticated delivery systems as a specialized predation strategy, making them ideal candidates for downstream venomomics studies. By shifting from random sampling to a phylogenetically-informed, ecological screening process, this approach provides a powerful tool for systematic biotechnological development and enhances our understanding of the evolutionary drivers behind annelid chemical weaponry.

13.3 | From host species to oceanic regions: multiscale structuring of Syllidae microbiomes

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The microbiome is increasingly recognized as a key component of host evolutionary success, often exhibiting strong host-specific associations. However, the microbial communities associated with Syllidae polychaete annelids remain largely unexplored, with current knowledge restricted mainly to the sponge-symbiotic genus *Haplosyllis*. In addition, the relative contribution of host identity and geographic factors in shaping Syllidae-associated microbiomes is still poorly understood. To investigate patterns of microbiome diversity and specificity in this family, we analyzed bacterial communities associated with 21 host species collected across the Mediterranean Sea and the Atlantic and Pacific Oceans using 16S rRNA gene amplicon sequencing. Across our 136 samples, we detected 50 bacterial phyla, 293 orders, 630 families and 1,743 genera, revealing a highly diverse bacterial assemblage associated with syllid hosts. Our results demonstrate that host genus and species are the primary drivers of microbiome diversity and community structure, supporting a strong degree of host specificity in Syllidae-associated bacterial assemblages. Oceanic region also contributed significantly to microbiome structuring, although its effect was secondary to host identity. At a finer spatial scale, locality explained additional variation within oceanic regions, revealing geographically structured microbiomes even among nearby populations. Shared bacterial taxa were detected among hosts, but each species maintained a distinct microbial signature.

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Overall, this study provides the first broad-scale characterization of microbiomes across multiple Syllidae taxa and geographic regions, highlighting the hierarchical influence of host phylogeny and spatial scale on the assembly of marine annelid-associated microbial communities.

13.4 | Fields of worms: distribution, population dynamics and unresolved taxonomy of massive *Bispira* aggregations in the Mediterranean

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Dense aggregations of *Bispira* have recently been reported in the Mediterranean coastal habitats forming extensive fields spanning hundreds to thousands of square metres at depths of 15 to 80 m in Greece, Italy and along the Spanish coast. They are composed of either of two morphotypes: a small form with thin, coiled tubes, and a large form with thick, upright tubes. Despite their conspicuous nature, the taxonomic identity of the species involved remains unresolved. Three Mediterranean species are currently recognised within the *Bispira viola* group (*B. viola*, *B. riccardi* and *B. causioi*), although morphological differences among some of them are subtle. To investigate species boundaries and population structure, we analysed COI barcode sequences from specimens collected in Catalonia (Spain) and the Gulf of Corinth (Greece), together with unpublished and published Mediterranean *Bispira* sequences. Results suggest that specimens previously assigned to different nominal species, including individuals forming dense aggregations, may belong to a single evolutionary lineage. However, genetic divergence within this broader clade reached up to 9.8%, indicating substantial hidden diversity or a complex of cryptic taxa. Monthly ecological monitoring of a small-morphotype aggregation in Greece since September 2025 revealed densities peaking at 6700 ind/m² in late summer and decreasing to 1300 ind/m² in winter. Body size increased over winter (median length from 9.5 mm to 18 mm in April, with a maximum size of 41mm). Sexually mature animals were present from March while asexual fission was observed in up to 28% of individuals during winter months. What drives underlying the formation and apparent spread of these dense *Bispira* aggregations remain unclear. Resolving the taxonomy of the *B. viola* group is essential for understanding the ecological role, origin (native outbreak, cryptic introduction or native invasion) and conservation implications of these previously overlooked benthic habitats.

13.5 | EuroWorm: Accelerating global marine annelid biodiversity research with open genomic data for European species

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The modern practice of taxonomy began in 18th century Europe; however, the designation and deposition of type specimens in scientific collections only became standard in 1961. Many early type specimens were therefore never deposited in museum collections, were subsequently lost, or remain undiscovered in European collections. The early taxonomic descriptions of the European fauna also lacked sufficient context and detail to adequately differentiate closely related species in other parts of the world. Compounding the problem, the cosmopolitan marine species paradigm which dominated taxonomic theory in the 20th century led to the application of European names in distant localities around the world. These factors have resulted in a poorly characterized European fauna with inaccessible reference specimens, severely limiting global efforts to characterize and quantify marine biodiversity. We introduce the EuroWorm project: a collaborative effort joining annelid taxonomists, morphologists, and genomics experts across Europe to create openly accessible data on the European annelid fauna. EuroWorm will re-collect topotypic specimens from historically important marine type localities in Europe, and create accessible museum voucher collections with live photographs and curated genetic data for commonly used markers. The project will generate reference genomes for select taxa to enable comparative genomic analyses of evolutionary innovations and lineage-specific adaptations, while low-coverage genome-scale data will provide an expanded phylogenomic framework for investigating the placement of challenging annelid taxa. The ultimate goals of the project are to unlock European biodiversity information with modern

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techniques, accelerate biodiversity discovery worldwide with openly accessible museum data, and unravel the evolutionary history of the phylum Annelida, a diverse, ecologically important, and ubiquitous, yet neglected group.

14.1 | Cave dwelling polychaetes from the Balearic Islands

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Submarine coastal caves host specialized and still poorly known annelid assemblages. Recent surveys conducted in Mallorca considerably increased the number of polychaete species recorded from these ecosystems, revealing unexpectedly high diversity and endemism. Several taxa appear restricted to single cave systems, whereas others are shared among different caves and open sea sciaphilous habitats. Our surveys resulted in the description of new species, including *Pollentia perezi* and *Polycirrus burballes*, species to be described, and new records, highlighting the importance of submarine caves as overlooked hotspots of annelid diversity and speciation. The fauna recorded to date includes representatives of at least Terebellidae, Sabellidae, Serpulidae, Syllidae, and Polynoidae, substantially expanding current knowledge of Mediterranean cave-dwelling polychaetes. To place these findings in a broader context, we also compiled an updated checklist of cavernicolous polychaetes from the Balearic Islands, providing new insights into regional diversity patterns, endemism, and major knowledge gaps. Altogether, our results emphasize the ecological singularity and vulnerability of submarine cave ecosystems and reinforce their relevance for studying isolation, adaptation, and evolution in extreme marine environments.

14.2 | Four Decades Underappreciated: Annelid Genetic Diversity and Connectivity from the Porcupine Abyssal Plain Sustained Observatory, Northeast Atlantic

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The Porcupine Abyssal Plain Sustained Observatory (PAP-SO) in the northeast Atlantic (48°50'N, 16°30'W; 4850 m depth) is the longest running abyssal time series site in the world, with over 40 years of data collected. There have been numerous ecological studies on larger megafauna from the site, yet little research has been performed on the smaller annelid fauna. Historically, material collected from the PAP-SO was fixed in formalin, limiting analyses to morphological studies. However, for the first time, in 2023 and 2024, trawled material was fixed in ethanol allowing the possibility of molecular studies on specimens. Using genetic data (COI, 16S gene fragments), we present novel findings on the annelid fauna from PAP-SO. Our results indicate at least 13 potentially new species. Interestingly, at least two species present at PAP-SO are genetically identical to species described from different ocean basins; *Laetmonice murrayae* and *Neanthes goodayi* described from deep Australian waters and from Clarion Clipperton Zone, Pacific Ocean, respectively. Our findings highlight high levels of genetic connectivity within one of the most intensively studied areas of the deep-sea floor.

14.3 | Towards understanding high Arctic deep-sea annelid diversity and connectivity

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Abyssal Arctic annelid fauna is practically unknown, with a few species recorded from waters below 3000 m depth and extremely scarce molecular data. This study presents some of the first results of DNA barcoding of high-Arctic deep-sea polychaetous annelids collected from the Nansen and Amundsen basins, including the North Pole, at depths of 3700–4400 m. The material was collected during the RV Polarstern ArcWatch expedition in 2023 using an epibenthic sledge and a box corer. Representatives of all

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morphotypes were barcoded (COI and 16S rRNA), and the obtained sequences were compared with publicly available data. Twenty-two lineages, provisionally identified as species from 15 annelid families, were recovered, the majority of which are potentially undescribed. Only four lineages could be confidently identified to species level: *Anobothrus laubieri*, *Ophelina opisthobranchiata*, *Terebellides irinae*, and *Ymerana pteropoda*. Several lineages were nearly identical to those from the Clarion–Clipperton Fracture Zone, indicating a high degree of connectivity between the deep Arctic and the eastern Pacific, and increasing the number of molecularly confirmed, widely distributed annelid species in the deep sea. Connectivity with the deep northern Atlantic was reported for a single lineage, however this might be due to lack of comparative data.

14.4 * | Population structure of *Lamellibrachia barhami* (Siboglinidae) across the Eastern Pacific methane seeps

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Deep-sea vestimentiferan tubeworms represent an extraordinary clade of annelids adapted to chemosynthetic environments such as methane seeps and hydrothermal vents. *Lamellibrachia* Webb, 1969 is one of the few vestimentiferan genera showing a wide geographic and habitat distribution, with species reported from seeps, vents, whale falls and ship wrecks in the Pacific, Atlantic oceans and the Caribbean and Mediterranean Seas. One species *L. columna* Southward, 1991 has been inferred to range across an extensive area of the western Pacific, though only via mitochondrial data.

Lamellibrachia barhami, Webb, 1969 was the first named member of Vestimentifera, found at methane seeps near California. It has since been recorded off Canada and northern Chile (ranging over 11,000 km), though again based on mitochondrial data. This wide geographic distribution raises the interest in the dispersal potential of such deep-sea fauna and whether one species can indeed populate such a substantial distance. Here we report a further range extension for *L. barhami* from the Aleutians (Alaska) to central Chile (~16,000 km). Using over 100 *L. barhami* individuals collected across 9 geographic locations across the range, we analyze full mitochondrial genomes and millions of nuclear genomic variants from whole genome sequencing to study the population structure and genetic diversity. Our results support the hypothesis that *L. barhami* is a single species, with surprisingly low genetic differentiation among populations, indicating genetic connectivity over vast geographic distances. Low levels of population differentiation exist between northern and southern populations. We interpret these findings in context to vestimentiferan larval biology and life-history traits.

14.5 | Population connectivity of vent scale worms along Indian Ocean ridges

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Indian Ocean hosts four mid-ocean ridges, which harbor multiple hydrothermal vent fields and distinct and diversified vent fauna. Given that five exploration contract areas for sulphides are located surrounding those vent fields, population connectivity of their associated vent fauna are important to inform the environmental management. However, very few species were characterized in population genetics over the whole geographic range. The deep-sea scale worm *Branchipolynoe longqiensis*, commensal within the Bathymodiolin mussel and widespread along the Indian Ocean ridges, provides an opportunity to test population connectivity across all five contract areas. By analyzing 102 individuals from 13 hydrothermal vents using 11 million single-nucleotide polymorphisms, we identify two genetic groups, with one corresponding to populations on the Southwest Indian Ridge (SWIR), Southeast Indian Ridge (SEIR) and the southern Central Indian Ridge (sCIR), and the other to Carlsberg Ridge (CR) and northern Central Indian Ridge (nCIR). However, the nCIR also show genetic signals from the southern sites. Slight genetic divergence was observed between CR and nCIR, while there is no significant genetic differences among populations harboring the extensive area from SWIR to SEIR, suggesting that the dispersal range of the polychaete might be very extensive, in accordance with its host *Bathymodiolus septemdirum*. Geneflow analysis shows net northward geneflow from SWIR/SEIR/sCIR to nCIR, which, however, is blocked between nCIR and CR. Historical demography support nCIR as a sink receiving inputs from its

both north and south sides.

15.1 | Arrive, survive, and (sometimes) thrive: Invasion of Galveston Bay, TX by *Ficopomatus* spp. (Annelida: Serpulidae)

Vanessa Fernandez-Rodriguez¹ & **Anja Schulze**¹

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Galveston Bay (GB), Texas (USA) is home to three major ports and the Houston Ship Channel, with abundant transport opportunities for non-native species in hull fouling communities and ballast water of vessels from global locations. The non-native *Ficopomatus enigmaticus* was first reported in GB in 2003. Since seasonal monitoring started in 2019, the species was regularly recovered on settlement plates deployed at marinas in a range of salinities. In 2023 and 2024, *F. enigmaticus* had unprecedented, but localized and short-lived, population outbreaks with significant reef formation in a single marina in mesohaline conditions. Smaller aggregations of a second species, *Ficopomatus* cf. *uschakovi*, appeared at a single low-salinity station after the landfall of Hurricane Beryl in August 2024 and subsequent continued heavy rainfalls. This study investigates the genetic diversity of *F. enigmaticus* and *F. cf. uschakovi* in GB and in a global context, based on the mitochondrial marker cytochrome b. *F. cf. uschakovi* from GB is genetically highly similar to *F. cf. uschakovi* from both coasts of Mexico and from Thailand. *F. enigmaticus*, which was sampled seasonally over a two-year period, shows high haplotype diversity in GB and shared haplotypes with California, New Zealand, Australia, Japan, the Mediterranean, and Eastern Atlantic. The presence of unique haplotypes in GB, which are closely related to dominant widespread haplotypes, may indicate that they originated locally. The *F. enigmaticus* population in GB appears panmictic, without any differentiation between outbreaks vs. no outbreaks, among stations, seasons, or years. To investigate the environmental conditions and genetic pathways which trigger outbreaks, we have conducted experiments on larval survival and tube grow at different temperatures and have generated a high-quality transcriptome as a basis for future differential gene expression studies. We are currently examining how ocean acidification affects formation and microstructure of *Ficopomatus* tubes.

15.2 | Stowaways on molluscs: unveiling non-native polydorin pests in Adriatic oyster aquaculture

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Polydorini (Annelida: Spionidae) are well-known mollusc pests that are transported as hitchhikers through the movement of farmed species between mariculture sites, invading new locations worldwide and causing significant economic losses to the aquaculture industry. Our analyses of farmers' Local Ecological Knowledge revealed that polydorin infestations have become an increasing problem in Italian oyster aquaculture in recent years, and that frequent transfers of juvenile and adult oysters and mussels occur among farms in Italy, Croatia, Slovenia, Greece, France, and Spain, both within and beyond the Mediterranean basin. Here, we present the results of the first coordinated assessment of polydorin infestations in Pacific and European oyster farms across the Adriatic Sea. Morphological and molecular analysis identified five non-native species: *Dipolydora giardi* in Slovenia and Croatia, *Polydora caeca* in Slovenia and Italy, *P. hoplura* in all three countries, and *P. websteri* and *P. cornuta* exclusively in Italy. The prevalence of overall infestation ranged from 13% and 93% depending on the farm. Infestation intensity was also remarkable, reaching up to 62 individuals per oyster for *P. websteri* in Italy and 32 individuals per oyster for *P. hoplura* in Croatia. Population genetic analyses of these two species are ongoing and, together with analyses of mollusc transfers, aim to provide insights into their invasion pathways. Overall, our results suggest that polydorin invasions represent an imminent threat to the Mediterranean oyster industry and highlight the need for coordinated international actions involving interdisciplinary approaches and multiple stakeholders to address this growing environmental issue. In this context, the new PolyFREE project, involving the University of Bologna and stakeholders from the aquaculture sector, is currently testing treatment methods for the effective reduction of *Polydora* infestations in oyster farms.

15.3 | Annotated Checklist of Polychaeta from Namibia with Updated Synonymy, Distribution, and Systematic Notes

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To date, no comprehensive annotated checklist of Namibian marine polychaete taxa is available. Here, we present the first specimen-based checklist from material collected from intertidal to continental shelf habitats along the Namibian coast. The checklist integrates curated collections and verified occurrence records, with synonymies validated against the World Polychaete Database. Each taxon is accompanied by key metadata, including biogeographic status (indigenous, alien, or unresolved cosmopolitan), type locality, habitat, and depth distribution, as well as notes on taxonomic uncertainty. This synthesis refines regional biogeographic patterns through a high-resolution (10 km grid) distribution map of occurrence records along the Namibian coastline. A supplementary dataset further documents specimen availability, highlighting material suitable for morphological re-examination and molecular analyses. New DNA sequences are further provided for selected taxa to support the resolution of taxonomic uncertainties and to strengthen molecular reference libraries for this understudied region. By consolidating accessible collections and identifying priority taxa and knowledge gaps, this work establishes a baseline for future taxonomic revision and biodiversity assessment. It also promotes collaboration, student training, and capacity development by facilitating access to material and outlining opportunities for targeted research and funding. We invite regional and international partnerships to address outstanding taxonomic and biogeographic questions in this understudied yet ecologically significant fauna.

15.4 | Habitat preference and life-history traits of polydorid species (Annelida: Spionidae) inhabiting farmed and wild molluscan shells in France and South Africa

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Many polydorid polychaetes (Annelida: Spionidae) bore into molluscan shells, causing significant impacts on their hosts. Their infestations have become a serious concern, as the global trade of commercially important molluscs facilitates the unintentional anthropogenic dispersal of polydorid species. This study investigated polydorid infestations in molluscan aquaculture and adjacent wild habitats in France and South Africa, focusing on species distribution, habitat preferences, and larval development. Sampling was conducted at 21 sites in France (Mediterranean Sea, Atlantic, English Channel and North Sea) and 8 sites in South Africa (Indian and Atlantic coast) during 2023 and 2024. Cultured oysters (*Magallana gigas*, *Ostrea edulis*) and abalones (*Haliotis midae*) were collected from intertidal, offshore, and onshore farms and polydorid worms were extracted from the shells. Wild substrates including oysters, mussels, turban snails, limpets, coralline algae, chalk, and sandstones, were also sampled from surrounding natural habitats. A total of nine species (5 *Polydora*, 1 *Dipolydora*, 2 *Boccardia*, and 1 *Boccardiella*) were recorded in France, and ten species (4 *Polydora*, 2 *Dipolydora*, 3 *Boccardia*, and 1 *Pseudopolydora*) in South Africa. Species distribution was mainly influenced by host species, sediment type, and water depth, although some species inhabited multiple habitat types. Particularly, *Polydora onagawaensis* exhibited broad substrate use in France, boring into oyster shells, limpet shells, chalk, and sandstones. Five species were recorded in both countries, among which *Polydora hoplura* and *Polydora websteri* frequently dominated aquaculture environments. Both species exhibit poecilogony in their larval development, producing adelphophagic larvae that may facilitate local retention, as well as planktotrophic larvae that enable long-distance dispersal within and between populations. This dual larval strategy is likely a key factor promoting successful establishment across diverse marine environments worldwide. These findings highlight key invasive species and their unique biological traits, emphasizing the importance of integrating species-specific traits into the effective management of polydorid infestations.

* Denotes a student contribution eligible for a prize.

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15.5 | DNA Metabarcoding the gut-contents of alien tubeworm, *Diopatra aciculata* (Annelida: Onuphidae) suggests scavenging in two estuaries in South Africa.

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Stable isotope analyses classified Australian onuphid polychaete, *Diopatra aciculata*, as a facultative carnivore occupying a high trophic position among macrobenthic estuarine invertebrates. In South Africa, this worm has invaded estuaries that harbour rare mollusc and fish species and provide nursery sites for economically important fish and invertebrates. It is therefore important to understand what they are eating, to better understand their trophic impact in our estuaries. Using DNA metabarcoding, we retrieved 78 operational taxonomic units (OTUs) for Animalia in the guts of *D. aciculata* from four sampling areas in two closely situated estuaries on the south coast. Phyla with highest relative frequency of occurrence (RFocc) were Arthropoda (46 – 49%), Chordata (fish: 31 – 40%) and Mollusca (10 – 18%). PERMANOVA and PERMDISP analyses show that gut contents of worms overlap significantly in the two estuaries at the three sites closest to the mouths, and that individuals were highly variable. By contrast, gut contents of worms from the site under most freshwater influence was significantly different from at the other sites, and more similar to each other. These results reinforce the generalist nature of *D. aciculata*'s diet, exploiting available resources within its restricted range of movement, and varying according to diversity of local prey at the different sites. The high RFocc of economically important fish and endangered Syngnathidae (either Knysna seahorse or pipefish) suggests that *D. aciculata* may exert significant negative impacts on diversity in the estuaries. However, because DNA metabarcoding cannot distinguish between larvae and adults, we don't know the life stage of ingested fish. Based on similar studies on crabs and *Aphrodita aculeata*, *D. aciculata* are probably scavenging dead fish or viscera discarded by anglers. Thus, impact of the worm may be indirect, through removing high quality detrital matter from the system, rather than through direct predation.

16.1 * | Hidden Diversity in Rock-Boring *Phascolosoma* (Phascolosomatidae: Sipuncula) Structured by Latitude and Substrate, with Implications for Cosmopolitan Distribution

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Sipunculans inhabit a wide range of environments, from muddy bottoms to rocky shores. The genus *Phascolosoma* (Sipuncula: Phascolosomatidae) includes species that bore into hard substrates and play an important role in bioerosion. In Japan, six species of this genus have been reported. However, species diversity within this genus remains poorly understood due to the difficulty of morphology-based taxonomy. In this study, we investigated species diversity in Japanese *Phascolosoma* with a focus on variation associated with latitude and hard-substrate environments, using a combination of DNA barcoding and morphological observations. *Phascolosoma* spp. were collected from rocky substrates (coral rocks and mudstones) at 17 sites ranging from the cold-temperate to the subtropical zone. Specimens were examined for external morphology. DNA barcoding and species delimitation based on the COI gene was conducted. For selected representative specimens from each OTU, phylogenetic analyses were conducted based on four genes (COI, 16S, 28S, and H3). In this study, we recovered three lineages from temperate and cold-temperate Japanese regions and ten from the subtropical Ryukyu Archipelago. Each clade shows a high degree of genetic distinctiveness, warranting their recognition as independent species. Although no species were distributed across both the Pacific and Atlantic Oceans, two species, *P. stephensoni* and *P. perlucens*, exhibit a broad distribution ranging from Japan to South Africa. (COI: K2P < 1%). Within *P. nigrescens*, four distinct lineages were detected, two of which were found in both coral rocks and mudstones. In contrast, the two lineages within *P. perlucens* showed clear substrate differentiation between coral- and mud-rocks. These results suggest that species diversity of *Phascolosoma* in Japan is markedly higher in the subtropical zone and decreases toward higher latitudes. Furthermore, the restriction of certain species to specific hard substrates suggests that substrate type may influence species diversity.

16.2 | Host-associated camouflage without genetic differentiation in a holothurian-ectoparasitic scale worm

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Striking host-associated phenotypes in parasitic organisms are often interpreted as evidence of host-associated divergence or incipient speciation. However, visually host-specific traits may arise without underlying genetic differentiation. Here, we assess whether phenotypic variation reflects underlying genetic differentiation in the scale worm *Gastrolepidia clavigera*, a widespread ectoparasite of holothuroid sea cucumbers. Across the Ryukyu Archipelago (southern Japan), *G. clavigera* exhibits remarkable host-associated camouflage; individuals closely resemble the color and pattern of their hosts, including black, brown, white, and previously undocumented striped morphs. We sampled worms from 14 host species, including six newly recorded associations, to evaluate whether this apparent host specificity reflects host-species-associated genetic structure. We analyzed mitochondrial COI sequences and genome-wide SNPs (MIG-seq) to assess population differentiation. Neither dataset revealed genetic structuring associated with host species or color morph. Although genome-wide SNPs detected two minor genetic clusters, these showed no correspondence with host use or phenotype. These results demonstrate that the apparently host-specific camouflage of *G. clavigera* arises independently of genetic divergence. Instead, this phenotype is consistent with intraspecific phenotypic plasticity, potentially in response to host environments. However, how *G. clavigera*, which appears to have limited visual capacity, achieves such precise host-matching coloration remains an open question.

16.3 | Diversity, connectivity and microbial composition in Iberian *Osedax*: Insights from newly discovered species

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Annelid worms of the genus *Osedax* (Family Siboglinidae), commonly known as 'bone-eating worms', are specialized colonizers of vertebrate remains on the seafloor. They lack mouth, gut and anus and rely on an obligate symbiosis with rich and diverse bacterial communities capable of digesting the organic matter retained inside the bones. Since their discovery almost two decades ago, 34 different species have been described, occurring worldwide across all oceans. However, the diversity, connectivity, and microbial associations of *Osedax* in the Atlanto-Mediterranean region remain poorly understood. In this study we used cow and pig bones experimentally deployed at different depths (90-1,200 m) around the Iberian Peninsula to investigate the presence of *Osedax* worms. Using an integrated morphological and phylogenetic approach we report the existence of three new species to science: *Osedax emmae* sp. nov., *Osedax martini* sp. nov. and *Osedax teoi* sp. nov. We performed population genetics analyses to assess the genetic connectivity between populations of two of these species showcasing very different patterns: exceptionally high haplotype diversity at a single locality in *O. emmae* sp. nov. and broad Atlanto-Mediterranean genetic homogeneity in *O. martini* sp. nov. To characterize the microbial communities associated with the three Iberian species, we produced new data using 16S rRNA amplicon sequencing, finding no species-specific communities among species. Nevertheless, we found four core microbes present not only across these three Iberian species but also in the Antarctic *Osedax deceptionensis*. Altogether, our findings substantially expand current knowledge of this group of marine invertebrates in Atlanto-Mediterranean deep-water habitats.

16.4 * | How does annelid fauna respond to the Atlantification of an Arctic fjord in western Svalbard?

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Despite being frequently sampled, Isfjorden fauna remains poorly understood. Exposed to both Atlantic warm-water West Spitsbergen Current and Arctic cold-water East Spitsbergen Current, annelids of Isfjorden exhibit diverse biogeographical patterns. This study is part of Marine Annelid Diversity in Arctic Norway (MANDArIN) project funded by the Norwegian Biodiversity Information Centre and aims to shed some light on the taxonomical status and biogeography of Annelida within Isfjorden. We used an integrative taxonomical approach, combining morphological identification methods with molecular ones, to pick up on the cryptic diversity, increase the general reliability of species ID's and assess accurate biogeographical ranges. The material was collected in July-August 2024 using a Van Veen grab from 30 stations at 9–266 m depths. COI DNA barcoding was performed on 200 specimens corresponding to 70 genetic lineages, 21 more lineages previously found in Isfjorden were retrieved from BOLD. Only around a third of taxa confirmed with molecular methods had a clear taxonomical status. The remaining taxa were the members of species complexes, potentially new undescribed species, or could not be identified to species level with certainty. Ranges of all species were assessed based on newly obtained and public records with associated molecular data by matching to a BIN number in BOLD (>98% similarity). In contrast to previous studies reporting the prevalence of the species with Arcto-Boreal distributions, our data show that half of the annelid species in Isfjorden were restricted to the Arctic region, while less than a third were Arcto-Atlantic, about 10% were Arcto-Pacific and 11% were Arcto-Atlanto-Pacific. This study highlights the importance of molecular data in diversity and biogeography assessments. Moreover, our dataset can serve as a starting reference point for evaluating long-term Arctic faunal shifts due to climate changes.

18.1 | Syntenic Constraints and the Biocementation Toolkit: Integrating Functional Genomics in the Mediterranean Reef-Building *Sabellaria* (Annelida: Sabellariidae)

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Biogenic reefs constructed by the genus *Sabellaria* represent some of the most complex structural habitats in the Mediterranean Sea, providing essential ecosystem services including coastal protection and niche provision for diverse marine assemblages. In the Mediterranean Sea, these reefs face increasing pressure from environmental stochasticity and anthropogenic shifts, yet the molecular mechanisms underlying their specialized biocementation and evolutionary success remain poorly characterized. Leveraging Oxford Nanopore Technologies (ONT), we assembled the first reference-level mitogenomes for the Mediterranean ecosystem engineers *Sabellaria alveolata* and *Sabellaria cf. taurica*. Our analysis reveals a conserved mitochondrial gene order across the nad4l-nad4 bicistron. However, this architectural stability appears to impose a functional trade-off: a truncated NAD4 protein sequence, seemingly sacrificed to accommodate the downstream trnC gene. This structural constraint, conserved across both species, suggests that mitogenomic synteny in sabellariids is maintained under evolutionary pressure, potentially impacting the C-terminal domain of the respiratory Complex I. To investigate the broader physiological context of these reef-builders, we utilized a somatic transcriptome to profile the biocementation machinery of *S. cf. taurica*. We identified a suite of highly basic "sand-castle proteins" (Scps) and performed comparative analyses to assess their orthology with other Sabellariidae. Our results suggest that the mitochondrial "simplification" of the NAD4 subunit may reflect an evolutionary strategy for metabolic optimization, balanced against the high energetic demands of biocementation. By linking structural mitogenomics with the functional adhesive toolkit, this study provides a new genomic framework for understanding the evolution and metabolic constraints of Mediterranean *Sabellaria* reefs.

18.2 | Cell-by-cell reconstruction of a polychaete: the developmental cell lineage of *Platynereis dumerillii* revealed by light sheet microscopy

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Spiralian development, characterised by spiral cleavage and early cell fate specification, is ancestral to annelids and other spiralian. Although annelid development has been extensively described at both the morphological and molecular levels, the dynamic cellular processes underlying embryo and larval formation remain poorly understood. In this study, we utilize the polychaete *Platynereis dumerillii* (Nereididae) to reconstruct development at single-cell resolution. *P. dumerillii* is especially suitable for long-term live imaging because its embryos are transparent, zygotic microinjection is feasible, embryos can be immobilised for imaging, and larvae develop without external feeding until the late nectochaete stage. We injected mRNAs encoding fluorescent nuclei and membrane markers into zygotes and recorded time-lapse movies using light sheet microscopes, including the portable Flamingo microscope designed in our lab. Semi-automated tracking of fluorescently labeled nuclei enabled reconstruction of the complete developmental lineage up to the one-day-old larval stage, comprising approximately 1200 cells. Membrane labeling additionally revealed cell division dynamics throughout development. In this talk, I will show how individual cells contribute to the formation of the bilaterally symmetric larval body plan, together with asymmetries revealed by comparisons between corresponding left-right cell lineages. We are also integrating anatomical data into the lineage reconstruction to track the development of specific structures, including the nervous system. These data offer new insights into lineage relationships, cell behavior, division patterns, and migration during the formation of the *Platynereis* body plan. More broadly, this work establishes an approach for comparative live imaging and cellular-resolution lineage reconstruction in spiralian embryos.

18.3 | A first look at the Charlie Chaplin worm genome

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Histiobdella homari is a minute annelid that is sometimes referred to as the “Charlie Chaplin worm” because of its distinctive mode of locomotion. As an inhabitant of the gills of lobsters, it is characterized by a derived morphology and because of its uncertain phylogenetic placement, this species represents one of the more enigmatic annelid lineages. Its small size and host-associated lifestyle have limited the development of genomic resources. Here, we present a draft genome assembly generated using PacBio long-read sequencing together with a genome annotation supported by transcriptomic and homology-based evidence. Comparative analyses with other annelids provide a first view of the genomic architecture of this lineage. This resource provides a foundation for investigating the genomic basis of ecological specialization and host-associated lifestyles in Annelida, while offering new perspectives on the evolution of this distinctive species.

18.4 | How to Build a Worm—Studies on *Ophryotrocha labronica* (Eunicida, Dorvilleidae)

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Decreases in body size over time may occur through stepwise processes of gains, losses, and mutations or through evolutionary “shortcuts” such as heterochrony (i.e. pedomorphosis). However, we know relatively little about the genomic changes underpinning miniaturization. To further tease apart these processes we have generated long-read and Hi-C data to produce a contiguous assembly of *Ophryotrocha labronica* (Eunicida, Dorvilleidae). As a secondarily small species with slight sexual dimorphism, *O. labronica* is an excellent model to investigate the evolutionary underpinnings of miniaturization on both macro- and microevolutionary time scales. Using this resource we have begun to look at potential drivers of miniaturization including differential expression of key developmental genes, gain/loss in key pathways, and DNA methylation. In comparison to the miniaturized annelid *Dimorphilus gyrociliatus*, *O. labronica* has a relatively large genome (~1.2 Gb) that displays characteristic signals of DNA methylation and retains a complete repertoire of the core methyltransferase genes. Blocking of methylation in early

* Denotes a student contribution eligible for a prize.

Presenting author shown in **bold**.

stages with demethylating agents shows similar patterns to other annelids where early developmental methylation levels seem to be necessary for proper growth and development. Together with future in situ expression studies of methylation genes and base-resolution methylome sequencing, we aim to elucidate methylation as a regulator of developmental plasticity and its relationship to miniaturization.

19.1 | Smaller but faster: heterochronic shift in gene expression leads to larval onset of spermatogenesis and miniaturised males

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Many microscopic animal lineages (meiofauna) are hypothesised to have evolved from macroscopic ancestors, yet direct evidence for the genomic and developmental mechanisms underlying such extreme miniaturisation remains limited. One prominent hypothesis invokes heterochrony—evolutionary shifts in the timing of developmental events—which can lead to truncated or paedomorphic body plans. In this study, we investigate the molecular developmental basis of the microscopic, paedomorphic males of the annelid *Osedax japonicus*, a species in which non-feeding dwarf males coexist with large, bone-eating females. We show that males initiate sexual maturation exceptionally early, with reproductive tissue already forming during the larval stage, and cease their somatic growth shortly after metamorphosis. Gene expression analyses reveal heterochronic shifts that underpin this paedomorphic phenotype, including the precocious activation of germline development, sexual determination, and maturation, coupled with an early termination of somatic growth programs. Together, these findings provide direct developmental evidence linking heterochrony to extreme miniaturisation and offer new insights into the evolutionary pathways that may have given rise to the many microscopic animal lineages.

19.2 * | Evolutionary routes to miniaturization: Hox gene evolution and patterning in Annelida

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Miniaturization, or the evolution of extremely small body size, is an important evolutionary process often accompanied by reduction, simplification, and loss of morphological characters. While some microscopic animal lineages are ancestrally small, many others have become small secondarily, a process particularly common within Annelida. It has been hypothesized that miniaturization may occur through a combination of mechanisms including gene loss and shifts in developmental timing (i.e. heterochrony). Hox genes play a fundamental role in anterior-posterior patterning during early development. Therefore, changes in their repertoire and expression patterns may influence body plan and life-history evolution. For example, the divergent larvae of *Owenia fusiformis* exhibit delayed trunk development and in turn, show a later onset of Hox gene expression. Losses within the Hox repertoire are exemplified by *Dimorphilus gyrotilatus*, a miniaturized species whose reduced segmentation and loss of chaetae is thought to be associated with the loss of Post1 and Lox2. *Ophryotrocha labronica* is a miniaturized annelid easily kept in cultures, making it a highly suitable species for experimental studies. With its development recently characterized and a chromosome-level genome assembly underway, *O. labronica* is emerging as a model organism within Annelida. Our findings indicate that *O. labronica* possesses an incomplete Hox gene set with loss of Hox7 and Lox2, which may represent a recurrent evolutionary feature associated with miniaturization in annelids. To further investigate the role of Hox genes during *O. labronica* development, we sequenced transcriptomes from ten developmental stages, spanning early embryos to juveniles and adults. Spatial and temporal expression patterns of Hox genes were analyzed using differential gene expression and in situ Hybridization Chain Reaction. Our ongoing analyses will detect any heterochronic changes in Hox gene expression in this miniaturized species and provide new insights into the evolutionary origins of microscopic animal lineages.

19.3 | The evolution of developmental system drift in axial specification in Annelida

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Spiral cleavage is a highly stereotypical early programme of zygotic divisions ancestral to a large animal clade, the Spiralia, which includes nearly half of the animal kingdom, including snails and segmented worms (i.e., annelids). Within spiralian, those that have early equal cleavage rely on a conditional mechanism to specify the dorsoventral axis, while those that undergo unequal cleavage rely on maternal determinants. Using the equal cleaver annelids *Owenia fusiformis* and *Spirobranchus lamarcki*, here I show that ERK1/2 and BMP signalling are the ancestral upstream mechanisms specifying the embryonic organiser and setting up the dorsoventral polarity in annelids, respectively. Despite the conservation of this cleavage mode and the ancestral patterning role of ERK1/2 and BMP in other spiralian, the mechanisms that control axial specification in annelids vary dramatically. Unlike *O. fusiformis* and *S. lamarcki*, the unequal cleaver *Capitella teleta* relies on Activin/Nodal to specify their dorsoventral axes. In contrast, the unequal cleaver *Platynereis dumerilii* only relies on BMP for the DV axis in the head. Therefore, axial patterning, particularly the dorsoventral axis — a homologous trait in all bilaterally symmetrical animals — develops through different lineage-specific upstream regulators, even between species of the same phylum that share similar cleavage patterns. This is a striking case of developmental systems drift that affects upstream signals in GRNs at one of the earliest and most critical phases in animal embryogenesis.

20.1 | Intron group II in annelid mitochondrial genome: not so rare as previously thought. A case of *Sagitella kowalewskii* Wagner, 1879 (Typhloscolecidae)

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Typhloscolecidae Uljanin, 1878 are a small holopelagic family of annelids. Their bizarre appearance makes them easily recognizable, but morphological features are quite uniform across the family and few are suitable for species delimitation. This makes typhloscolecid species difficult to distinguish from one another. Currently, only 16 species belonging to three genera are known. However, molecular barcoding suggests that the true diversity of typhloscolecids is much greater. Its reliable assessment is only possible using molecular genetic methods. In most cases, nuclear markers have been used in this group, as the use of standard primers for mitochondrial markers (CO1, 16S) often fails or leads to amplification of NUMTs. We obtained the complete genome and transcriptome of *Sagitella kowalewskii*, which allowed us to assemble nearly the entire sequence of its mitochondrial genome. The mitochondrion of *S. kowalewskii* is approximately 19,000 bp in length ($\geq 18,751$ bp); its GC content is 22.7%, and GC skew $((G - C)/(G + C))$ is 0.147. The minimum and mean coverage depths of the assembly by raw reads were 40x and 611x, respectively. All standard mitochondrial genes were annotated in the genome: 13 protein-coding genes (PCGs), 22 tRNAs, and 2 rRNAs. Between the tRNA-Val and tRNA-Pro genes, there is an AT-rich non-coding region of about 1,500 bp (neighboring PCGs are *cox1* and *nad1*); this region also exhibits negative GC skew. A type II intron of 2,466 bp was found in the *cox1* gene. A group II intron in the mitochondrial genome has been found in annelids before in such taxa as *Nephtys* sp. (Nephtyidae), *Endomyzostoma* sp. (Myzostomida), *Glycera* spp. (Glyceridae), *Decemunciger* sp. (Ampharetidae), and *Travisia* spp. (Flabelligeridae).

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20.2 * | Mitochondrial genomes provide insights into the genetic diversity and evolution of *Dodecaceria*

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The genus *Dodecaceria* comprises a group of over 20 species within Cirratulidae. These benthic organisms are typically found inhabiting tunnels within the crustose layer of the calcareous alga Lithothamnion. *Dodecaceria* can be found across a wide geographic margin spanning most continents. Despite this wide distribution, members of the genus exhibit relatively limited morphological differentiation, making species identification and delineation challenging. In contrast, *Dodecaceria* displays remarkable diversity in reproductive strategies, including parthenogenesis (absence of males), as well as sexual and asexual reproduction through architomy (fragmentation followed by regeneration). These reproductive differences have therefore become important criteria for species delimitation. Nevertheless, the genus remains characterized by a long and complex taxonomic history. Here we use genetic data to further characterize several species. A particular focus is set on *D. concharum* and *D. ater*, which occur sympatrically in the UK. Genome assemblies for these and additional *Dodecaceria* species were generated from short-read sequencing data. Complete mitochondrial genomes were recovered, and phylogenetic analyses reveal substantial genetic divergence despite the strong morphological similarity between species. Differences in mitochondrial gene order provide additional criteria for species identification. Finally, flow cytometry was used to compare cellular DNA content between the two focal species. Our results provide a phylogenetic framework for *Dodecaceria*, while mitochondrial gene order variation represents an additional genetic character for distinguishing species and investigating the evolutionary history of the genus. This study establishes an important foundation for future genetic research on *Dodecaceria*.

20.3 | Evolutionary relationships and mitochondrial genome diversity in Spionidae (Annelida)

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Spionidae is one of the most diverse and ecologically important families of annelids, occupying habitats from intertidal sediments to the deep sea and including several globally invasive species. Despite their ecological importance and remarkable diversity, a comprehensive phylogenetic reconstruction of Spionidae is still needed. However, phylogenomic and mitochondrial genome analyses are beginning to provide new insights into relationships among major spionid lineages and patterns of genome evolution within the family. Here, we present results from these ongoing studies using a broad phylogenomic framework supplemented with comparative mitochondrial genome analyses. Phylogenomic analyses recovered a monophyletic Spionidae composed of two major clades. One clade included the *Polydora*-complex together with *Pygospio*, *Spio*, *Marenzelleria*, *Scolecopsis*, *Dispio*, *Lindaspio*, and *Rhynchospio*, while the second included the *Prionospio*-complex, *Streblospio*, *Laonice*, *Aonides*, and *Spiophanes*. The *Polydora*-complex was consistently recovered as a strongly supported lineage, with *Pygospio elegans* as its sister taxon, supporting previous suggestions of close evolutionary affinity between these groups. The analyses further support the monophyly of Spionidae without inclusion of Trochochaetidae and indicate that several traditional morphological characters used in spionid systematics may represent ancestral conditions rather than synapomorphies. Comparative analyses of 19 mitochondrial genomes revealed substantial variation in genome organization within Spionidae, including five distinct mitochondrial gene arrangements. The greatest degree of rearrangement was concentrated within the *Polydora*-complex + *Pygospio* clade, with tandem duplication-random loss events and transpositions appearing to be major drivers of mitochondrial genome evolution in these taxa. All species retained the full complement of mitochondrial genes, including a highly divergent *atp8* gene that had previously been considered absent in several polydorids. These patterns suggest that mitochondrial gene arrangements within the *Polydora*-complex + *Pygospio* clade represent more derived character states relative to the more conserved architectures observed in other spionids and provide additional insight into evolutionary diversification within the family.

20.4 | Genomic insights into calcareous tubeworm phylogeny: Development and application of a Polychaete-specific UCE probe set

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Serpulidae Rafinesque, 1815 is a distinctive group of polychaetes that inhabit calcareous tubes, including approximately 576 accepted species in 69 genera. A recent revision of the family has reclassified the genera into Serpulinae (with tribes Serpulini and Ficopomatini), Spirorbinae, and Filograninae. However, previous efforts based on morphology or limited gene sets have failed to resolve phylogenetic relationships among most genera. To obtain a robust and well-supported phylogeny, we conducted a large-scale phylogenomic analysis using matrices derived from ultraconserved elements (UCEs) specifically designed for polychaetes. The new probe set (Polychaeta UCE v1) was designed and optimized from 13 available polychaete genomic resources, consisting of 19,839 probes covering 1,865 UCE loci, of which 90.8% are located in exonic regions. Using this probe set, we performed target capture sequencing on 35 representative species spanning 21 serpulid genera, resulting in a high-quality phylogenetic matrix comprising 1,427 UCE loci. Phylogenetic analyses yielded a stable topology with high support values. Our results robustly recover the monophyly of Serpulinae, Spirorbinae, and Filograninae, with Serpulinae and Spirorbinae forming a sister clade. Overall, our findings provide critical insights into the phylogeny of Serpulidae and demonstrate that target enrichment sequencing of UCEs can be broadly applied to polychaete phylogenetics.

20.5 | One species, two mitochondrial genomes: extreme heteroplasmy and its implications for annelid molecular inference

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Mitochondrial genes and genomes have long served as markers for species identification, species delimitation and phylogenetic inference, yet their reliability depends on the assumption of within-species homogeneity. Recent analyses, however, revealed a remarkable and previously overlooked mitochondrial system in the globally distributed biofouling serpulid *Hydroides elegans* (Haswell, 1883) consisting of possibly two divergent mitochondrial genomes within single individuals, a phenomenon known as heteroplasmy. Here, using population-scale genomic analyses, we move beyond suspicion to confirm the first case of mitochondrial heteroplasmy in annelids. We detected the coexistence within individuals of two deeply divergent circular mitochondrial genomes with 29.8% sequence divergence. This represents one of the most extreme cases of heteroplasmy reported in Metazoa. The pattern was repeatedly detected across 70 individuals from 17 geographically distinct populations, indicating that it is far from a transient or isolated phenomenon. Despite the coexistence of such highly divergent mitochondrial genomes, *Hydroides elegans* remains globally successful and ecologically resilient across fluctuating marine environments, suggesting that this unusual mitochondrial system is biologically stable and evolutionarily persistent. Its stability raises fundamental questions about mitochondrial inheritance, compatibility, and the potential adaptive significance of mitotype coexistence in marine invertebrates. Beyond their evolutionary significance, these findings expose limitations of certain mitochondrial-only approaches in annelids. If undetected and unaccounted for, heteroplasmy of this magnitude can influence estimates of cryptic diversity, distort phylogenetic structure, and yield possible incorrect evolutionary inferences. This study highlights the need for caution when interpreting evolutionary relationships from mitochondrial markers alone and emphasizes the value of integrating nuclear genomic data in annelid molecular inference.

POSTERS

A.1.1| Inventory, mapping and revision of Swedish Terebellidae through large scale megabarcoding using oxford nanopore technology (ONT)

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In Sweden, 59 species of Terebellidae are currently listed. However, many lines of evidence point towards this list being very inaccurate, and our knowledge of the true diversity of this group very poor. In particular, the systematics for this group in Scandinavia are outdated and our own preliminary studies based on molecular data show an important underestimation of its diversity. This project is part of a national effort dedicated to discover, list and map all the multicellular fauna and flora of Sweden. We aim to produce an updated checklist of all species present in Sweden, revise groups in need of revision, describe new species, produce identification resources, create a reference collection of specimens and publish a reference barcode database. Through ongoing monitoring programs and dedicated fieldwork we have gathered a collection of several hundreds of specimens from various habitats along the Swedish coast. Because of cryptic diversity, the likely presence of undescribed species, and the general need for a global revision, molecular data is fundamental and at the core of the project. In order to be able to sequence several markers for every single specimen available, we use a novel megabarcoding technique based using Oxford Nanopore Technology (ONT). This technique relies on using unique combinations of tagged primers during PCR in order to multiplex products during sequencing. During a pilot study on 521 specimens of the genus *Terebellides*, a total of 191 COI sequences were obtained with Sanger sequencing and 413 COI sequences with ONT. Sequences were obtained with both sequencing methods for 174 specimens, where 17 specimens could be sequenced only with Sanger, while 239 specimens could be sequenced only with ONT, demonstrating the advantage of the latter method for this type of dataset and its ability to alleviate the primer bias that is often problematic in polychaetes.

A.1.2 | Between a rock and a holdfast: polychaete diversity in *Ecklonia maxima* holdfasts from the Cape Peninsula, South Africa

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Kelp forests are highly productive ecosystems usually distributed in regions with cooler waters. Kelp also provides habitats for many invertebrates, with holdfasts supporting very diverse macroinvertebrate assemblages. Previous studies found that polychaetes are one of the most abundant taxa in holdfasts, although few identified worms beyond family level, or explored their functional diversity. Furthermore, these studies found comparatively fewer representatives of Sedentaria than Errantia, suggesting that standard sampling by shaking animals from pieces of holdfasts may be favouring the latter. This study focused on polychaete diversity in *Ecklonia maxima* holdfasts from the eastern (Miller's Point, n = 7) and western (Oudekraal, n = 9) shores of the Cape Peninsula. Holdfasts were subdivided, with fragments processed following the standard procedure, and others processed by removing worms individually while examining under dissecting microscope. A total of 103 species, in 21 families, and 17 functional groups were documented. A PERMANOVA showed that site had a significant effect on species and functional group community structure. Holdfasts at Miller's Point hosted more individuals and species than at Oudekraal, with families Polynoidae and Chaetopteridae present only at the former. By contrast, relative abundance of Nereididae and Onuphidae was greater at Oudekraal. Small microphagous taxa, irrespective of mobility, contributed most to differences between communities. There was a non-significant trend for samples processed using the refined method to host proportionally more sessile functional groups than those processed with the standard method, although samples were generally dominated by Errantia. Differences in water temperature and wave exposure may be responsible for differences noted.

A.1.3 | Opening a can of worms from the Discovery collections: Annelids from the Porcupine Abyssal Plain Sustained Observatory (PAP-SO) Northeast Atlantic

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The Porcupine Abyssal Plain Sustained Observatory (PAP-SO) in the NE Atlantic (48°50'N, 16°30'W) 4,850 m depth is the longest running abyssal time series site in the world, with 40 years of data collected. Yet much of the smaller invertebrate fauna from the site is poorly characterised at the species level, including the annelid worms. We provide the first species-level checklist of annelids recovered using trawls from the PAP-SO (2013-2024) accompanied with morphological diagnoses, taxonomic remarks, light photograph images, molecular data (COI, 16S gene fragments) including GenBank records, and links to vouchered specimen material housed in The Discovery Collections, National Oceanography Centre, Southampton, UK. More than 2,830 annelid specimens from 11 families have been recovered from trawls. Over 20 species are reported with 13 species potentially new to science. Interestingly, *Laetmonice* specimens recovered are morphologically and genetically identical to *Laetmonice murrayae* described from deep Australian waters. Furthermore, we extend the range of *Glycera* aff. *southeastatlantica* and *Neanthes goodayi*, reported from the Angola, Cape, and Guinea Basins, Atlantic Ocean; and the Clarion Clipperton Zone, Pacific Ocean respectively. This work provides critical baseline biodiversity data on an important group of invertebrates and will act as a springboard for future taxonomic and biogeographical studies in the area.

A.1.4 * | New records of Dorvilleidae (Annelida: Eunicida) from the Romanian Black Sea coast, including the first record of *Protodorvillea artemidis* for the Black Sea

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The family Dorvilleidae comprises the most primitive representatives within Eunicida, that are uniquely characterized by a complex maxillary apparatus, formed by paired rows of fused and free maxillary plates. The dorvilleids are further distinguished by their remarkable reproductive plasticity and opportunistic life-history strategies, often reaching high densities in organically enriched environments. Dorvilleidae presents a very intricate taxonomic history. Many early described species lack adequate morphological details, which has contributed to their apparently ‘cosmopolitan’ distribution. Although recently described dorvilleids integrate molecular data (i.e. gene sequences) with detailed morphological characterizations, this approach remains unavailable for many historically described species. In the Black Sea, dorvilleids are considered rare and exhibit low species diversity, with only four taxa reported to date: *Protodorvillea kefersteini* (McIntosh, 1869), *Dorvillea rubrovittata* (Grube, 1855), *Schistomeringos rudolphi* (delle Chiaje, 1828), and *Schistomeringos neglecta* (Fauvel, 1923), the latter being restricted to the Prebosphoric region. Out of these four dorvilleid species, only *Protodorvillea kefersteini* was previously reported along the Romanian coast of the Black Sea. The aim of this study was to reassess the taxonomical status of dorvilleids from the Black Sea. Our study reports *Schistomeringos rudolphi* and *Dorvillea rubrovittata* as new records for the Romanian Black Sea coast, along with the first record of *Protodorvillea artemidis* for the Black Sea basin. Our findings highlight the urgent need for taxonomic revision of early described species, integrating detailed morphological redescriptions with molecular data, especially from type localities. Such efforts could resolve longstanding taxonomic uncertainties and reveal potentially overlooked cryptic diversity within the family.

A.1.5 | High dominance of polychaetes in terms of abundance and species richness and their relationship with the seasonal variability of a macroinfaunal community in the Quintupeu fjord, Northern Patagonia, Chile

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This study aimed to describe the community structure of soft-bottom macroinfaunal organisms in the Quintupeu Fjord (42°S, 72°W), southern Chile. Seasonal samplings were conducted during four campaigns between September 2022 and October 2023. Sediment samples were collected using Van Veen grab (0.01m²) on each site, to study composition, abundance, diversity and abiotic variables. A total of 93 species were identified with a total of 1,169 individuals collected. The species composition was dominated by polychaetes with 43%, followed by crustaceans (33%) and mollusks (18%). The total abundance was 46,760 ind m⁻², with a clear dominance of Polychaeta, exhibiting the highest abundance and species richness. The polychaetes were predominantly represented by the families: Paraonidae (5,240 ind m⁻²), Cirratulidae (2,760 ind m⁻²), Nephtyidae (2,120 ind m⁻²), Dorvilleidae (1,800 ind m⁻²), and Capitellidae (1,520 ind m⁻²). In terms of species richness, polychaetes were the most diverse group with 49% of the diversity, followed by crustaceans with 26%. *Aricidea finitima* (Paraonidae) was the most abundant species (6.67%). Seasonally, the highest macrofaunal abundance and species richness were observed in the winter 2023 campaign, which also showed the highest concentration of organic matter and silt in the sediment. Polychaetes dominated in late summer (43.5%) and winter (59%), while crustaceans dominated in late winter (36%) and spring (49%). In relation to species richness, this index was dominated by polychaetes in all seasons. Statistical analyses (Kruskal-Wallis and PERMANOVA) revealed significant differences in abundance and richness across the four sampling campaigns, with the winter community being the most distinct. Ecological indices (Pielou's evenness, Shannon diversity, and Simpson dominance) indicated high diversity and homogeneity across the communities sampled throughout the study period. Finally, variance partitioning analysis suggested that organic matter content and sediment grain size were the most influential environmental variables affecting species abundance.

A.1.6 | New records of *Terebellides* species from the British Isles and nearby waters

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Within the Amgueddfa Cymru-Museum Wales collections, more than 1,600 specimens from British and nearby waters, bear the names *Terebellides stroemii* or *Terebellides* sp.. However, in the last 10-15 years, numerous publications have shown that the actual diversity of the *Terebellides* genus in this region is far higher than previously believed and that the type species, *Terebellides stroemii*, is most likely restricted to the area around its type locality in southern Norway. There is little recent data to indicate which species do actually reside in British waters and so the specimens were re-examined to determine their correct identification according to recent taxonomic revisions. Five nominal species were identified morphologically: *Terebellides bonifi*, *Terebellides europaea*, *Terebellides gracilis*, *Terebellides scotica* and *Terebellides shetlandica*, three of which were also confirmed through molecular methods. The records provide extended distributional knowledge for all species and two species were new records for British waters.

A.1.7 * | First record of boring spionid species on European flat oyster *Ostrea edulis* in Japan

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Some species belonging to the family Spionidae are known to bore into various calcareous substrates, including commercially important mollusk shells, causing a reduction of the host's growth and a decrease in commercial value. To address this, understanding the biological traits of these species is important. In this study, we investigated the shells of European flat oyster *Ostrea edulis* and examined the presence of boring worms with observations of their reproduction. *Ostrea edulis* was imported

* Denotes a student contribution eligible for a prize.

Presenting author shown in **bold**.

from Europe from 1952 to the 2000s in Japan as a new aquaculture species. However, cultivation halted due to poor farming efficiency and was thought to be extinct by the tsunami following the Great East Japan Earthquake in 2011. It was reported recently that *O. edulis* had established its population in the wild, and experimental farming is currently underway. From June 2025 to February 2026, shells of *O. edulis* that were reared in Iwate Prefecture, northeastern Japan, including farmed oysters cultured at Yamada Bay and tank-cultured oysters, were examined. Worms were identified morphologically to the species level under a stereomicroscope. Mud burrows were observed, and spionid worms were extracted from most of the oyster individuals. They were identified as *Polydora onagawaensis* and *P. hoplura*. Tank-cultured oysters tended to be more infested by *P. hoplura* with large and conspicuous mud burrows, while the species tendency differed in oysters farmed in the bay. Egg capsules and larvae of both species were observed. *Polydora onagawaensis* exhibited planktotrophic larvae, while *P. hoplura* exhibited adelphophagic larvae. As both species are well known to inhabit commercially important mollusk shells worldwide, it is necessary to clarify their life history and to discuss the origin of the two species.

A.1.8 | Biodiversity of polychaetes in oyster reefs of the northern South China Sea

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Abstract: Oyster reefs are biodiversity hotspots providing critical ecosystem services. Polychaetes are key faunal components in these systems. A biodiversity survey of oyster reefs along the Guangdong coast, northern South China Sea from August 2022–February 2023, recorded 84 polychaete species belonging to 56 genera and 23 families. Phyllodoidea (44 species), Sabellida (13), and Eunicida (8) were the most species-rich orders. Nereididae (16 species) and Syllidae (10) were the most diverse families; genera *Perinereis*, *Syllis*, and *Hydroides* each contained eight species. The highest species richness occurred in western Guangdong (54 species), and the lowest in the Pearl River Estuary (14–24 species). Polychaetes exhibited diverse lifestyles: sessile tube-dwellers, free-crawling predators, and parasitic forms, the latter potentially detrimental to oyster aquaculture. Dominant species based on dominance index (Y) included *Syllis* sp.1 ($Y = 0.068$), *Dipolydora giardi* (0.043), *Capitella* sp. (0.028), *Perinereis camiguinoides* (0.024), and *P. shikuei* (0.024). Mean biomass varied significantly among stations ($p < 0.001$), ranging from 1.287 to 31.186 g/m² (mean 10.798 ± 8.453 g/m²), with *P. shikuei* contributing the highest station-averaged biomass (2.920 ± 6.893 g/m²). Mean abundance was 1026.5 ± 679.7 ind/m² (range 105.5–3417.2 ind/m²), dominated by *Syllis* sp.1 (148.8 ± 269.8 ind/m²) and *P. shikuei* (92.8 ± 230.3 ind/m²). Multivariate analysis revealed nine SIMPROF-supported groups with distinct regional distributions, corresponding to estuarine, coastal, coastal-estuarine mixed, transitional, and anthropogenically impacted communities. Polychaete functional groups included such as predatory nereidids, rapidly reproducing syllids, shell-boring and parasitic spionids (e.g., *Polydora*), and tube-building terebellids and serpulids, etc., which are characteristic of intertidal hard-bottom habitats. K-dominance curves showed higher diversity in coastal and mixed zones than in impacted areas and estuaries. Spatial patterns were driven by runoff, hydrodynamics, reef-forming oyster species, and reef development, highlighting polychaetes as effective indicators of oyster reef ecosystem health. **Keywords:** Oyster reef; Polychaeta; Biodiversity; Community structure; South China Sea.

A.1.9 | Fauna D'Italia – Sabellida: a new comprehensive guide to the European Fan Worms species

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The “Fauna d'Italia” series is a collection of scientific monographs concerning different zoological groups occurring in the Italian national territory. Nonetheless, following the last volume dedicated to a marine group (Ascidacea), we extended the study area to the East Atlantic, ranging from the Arctic Ocean to the Canary archipelago, the Atlantic Ridge serving as western boundary, due to both historical and biogeographic reasons. The “Sabellida” volume concerns the diversity of families Sabellidae, Serpulidae and Fabriciidae, with more than 200 species reported supported by more than 250 figures, including line drawings, live photographs and S.E.M. scans. This is the first volume of the series treating annelids: for this reason, a general overview on this phylum was also included. This work wants to be a useful guide for both the sector specialists and the novices. Thus, comprehensive introductions for each family presenting and explaining their biology, ecology and morphology precede the respective taxonomic parts, which is supported by the presence of numerous dichotomous keys for genera and species identification. For each species synonymies

are reported, as well locus typicus, description, ecology and geographical distribution, with emphasis to distribution along the Italian coast. The volume will be available at the end of 2026.

A.1.10 * | Gateways of invasion: unveiling Polychaeta diversity in Tunisian ports

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The introduction and spread of non-indigenous species (NIS) are widely recognised as a major global threat to marine biodiversity, driven primarily by maritime transport and exacerbated by climate change. The Mediterranean Sea, a biodiversity hotspot hosting over 6% of known marine species, represents a key region for NIS introductions, particularly within port environments. Owing to its central geographic position and relatively warm waters, Tunisia plays a strategic role in shaping Mediterranean dispersal dynamics, acting as both a recipient of Lessepsian migrants and a gateway for Atlantic taxa entering through the Strait of Gibraltar. Despite this relevance, knowledge of NIS in Tunisian waters remains limited, especially for small benthic invertebrates such as marine annelids. This study provides the first integrative assessment of polychaete assemblages in eight Tunisian ports and marinas, surveyed between April and May 2025. Polychaetes were collected through standardised scraping of fouling on artificial substrates (i.e. pontoons, mooring lines and buoys) and identified using a combined morphological and molecular approach. A total of 35 taxa across 13 families were identified, including 17 species newly recorded for Tunisia. Among these, 11 species were classified as NIS and one as cryptogenic. These findings significantly enhance current knowledge of polychaete diversity and distribution in anthropogenic habitats, highlighting Tunisian ports as critical entry points and stepping stones for biological invasions. Filling such biogeographical gaps is essential for improving early detection frameworks and informing effective biodiversity management and conservation strategies in the Mediterranean.

A.1.11 * | Scaling up polychaete community assembly: scale-dependent environmental filtering, distance decay and upwelling effects

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Spatial beta diversity often increases as community similarity decays with distance. Yet, this pattern may be blurred under scale effects, given the high connectivity expected in marine systems, especially for small soft-bottom organisms with potentially dispersive propagules. Following a new scale-explicit mathematical decomposition, we partitioned polychaete Sørensen β -diversity across a hierarchical spatiotemporal design in Arraial do Cabo, southeastern Brazil. The study area comprises two contrasting coastal sectors: Inner Sea and Outer Sea, which are relatively separated by a cape and differ in hydrodynamics, sedimentary conditions, and the influence of South Atlantic Central Water (SACW) upwelling. In July 2017 (winter) and January 2018 (summer, under upwelling influence), we sampled three sites per sector and five sediment replicates at each site. β -diversity was partitioned into seven scale-specific components: five purely spatial components spanning 10 m to 5.37 km, one spatiotemporal, and one purely temporal. For each scale, we used GDM to model the influence and quantify the relative importance of sedimentary, seasonal upwelling-driven thermal, and geographic predictors, and tested distance decay of similarity by relating β -diversity to log spatial extent. Community dissimilarity increased with spatial extent, reaching the highest values between sectors, showing that the cape might also modulate polychaete distribution. This short seascape contains a clear distance-decay signal. Predictor importance was strongly scale-dependent. Fine-scale polychaete β -diversity was mainly associated with local sediment properties, especially organic matter, gravel, mud, and grain-size structure. Broader-scale β -diversity was more influenced by geographic distance, maximum temperature, and sediment skewness, whereas temporal-scale was linked chiefly to minimum temperature and skewness, consistent with the role of upwelling. Our results reveal marked hierarchical environmental filtering, as the cape acts as an eco-geographic barrier, and coastal connectivity does not erase hierarchical community assembly: local environmental filtering dominates at micro-scales, whereas broader spatial and upwelling-related processes increasingly shape polychaete β -diversity

A.1.12 * | When space gives way to time: global latitudinal patterns in polychaete β -diversity

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Latitudinal gradients in β -diversity are central to macroecology, yet their spatial and temporal components remain poorly integrated, particularly in marine benthic systems. Because spatial environmental heterogeneity, climatic stability, and niche breadth vary with latitude, species–environment sorting is expected to (1) generate stronger spatial β -diversity at low latitudes and (2) stronger temporal β -diversity toward temperate and polar regions. Here, we tested this prediction for marine annelid communities using 34 spatiotemporal datasets compiled from the literature and direct communication with authors, spanning from Antarctic to Arctic waters. For each dataset, we estimated total β -diversity (β_{total}) and partitioned it into independent spatial (β_{space}) and temporal (β_{time}) components. We then modeled the $\beta_{\text{space}}/\beta_{\text{time}}$ ratio along latitude using a quadratic generalized linear model. The ratio followed a hump-shaped latitudinal pattern ($\beta_{\text{space}}/\beta_{\text{time}} = 1.069 - 0.00016 - 0.000060 \cdot \text{lat}^2$), as only the quadratic term was significant (t -value = -2.389 , $p = 0.023$), with maximum values at low latitudes (ca. 0.95–1.50) and lower values toward both southern and northern high latitudes, ca. 0.70–0.85 towards Antarctic, and 0.50–1.18 towards Arctic and high-temperate datasets. Thus, polychaete β -diversity tends to be more spatially assembled in tropical and subtropical regions, whereas temporal variation becomes a relatively more important source of variation toward higher latitudes. This pattern is consistent with the hypothesis that stable climates and high environmental variation in space lead to high spatial niche specialization at low latitudes, which promotes spatial species sorting, while stronger climatic seasonality and temporal environmental non-stationarity toward higher latitudes increase temporal β -diversity. Our study extends recent freshwater evidence from subtropical–temperate regions to the marine realm and demonstrates that the balance between spatial and temporal drivers of polychaete β -diversity changes predictably across latitude. Next steps will incorporate environmental distances and niche-breadth metrics to test the mechanisms underlying this global pattern.

A.1.13 | Diversity and distributional patterns of soft-bottom polychaetes in Slovenian waters
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The Slovenian Sea, located in the Gulf of Trieste (northern Adriatic Sea, Mediterranean), is a shallow coastal system exposed to strong anthropogenic pressures. This study assessed the diversity and distributional patterns of soft-bottom polychaete assemblages in Slovenian marine sediments. Samples were collected twice annually, in spring and autumn, from 2022 to 2025 within the national monitoring programme supporting the implementation of European Directives (WFD and MSFD). Eighteen sites were sampled: eight coastal sites shallower than 20 m and ten offshore sites deeper than 20 m. At each site, three replicate samples were collected using a 0.1 m² van Veen grab and sieved through a 1 mm mesh. In total, 9,495 individuals belonging to 125 polychaete species were identified. These included two non-indigenous species, *Chaetozona corona* Berkeley & Berkeley, 1941 and *Notomastus aberans* Day, 1957, and one cryptogenic species, *Paraprionospio coora* Wilson, 1990. Assemblages showed no significant seasonal variation but were related to depth and sediment pelite content. Coastal sites had lower diversity than offshore sites, despite comparable species richness, reflecting higher dominance, greater abundances, and lower evenness. Differences between coastal and offshore zones were mainly driven by dominant taxa, including *Pseudoleiocardia fauveli* Harmelin, 1964, *Hilbigneris gracilis* (Ehlers, 1868), *Terebellides stroemii* Sars, 1835, and *Aonides oxycephala* Sars, 1862. Offshore assemblages were dominated by sensitive and indifferent species, which represented more than 60% of individuals, whereas in most of coastal assemblages their percentage was lower, and the proportions of tolerant and opportunistic taxa higher. These results confirm the usefulness of polychaetes as indicators of benthic environmental status and underline the importance of accurate taxonomic identification in long-term monitoring.

A.1.14 | Hidden bristles revealed; the potential for extension of Polychaeta knowledge in Aotearoa New Zealand via a citizen-naturalist social-network of observers.

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Collaboration between taxon experts and citizen observers on iNaturalist, a popular global biota photo-identification system, can lead to unexpected and often useful discoveries. We report examples of iNaturalist collaborations involving marine Polychaeta from Aotearoa New Zealand. An isolated country of three main islands in the South Pacific, spanning from S35° to S47°, New Zealand has a declining number of taxonomists but a population of about 5.3 million potential iNaturalist observers. Although Polychaeta are usually cryptic, thus under-represented compared to their abundance, and are difficult to identify without very close-up images, iNaturalist photos can provide unexpected and informative records for taxonomists and biologists to follow up on, hence greatly multiplying the effective geographic reach of a single worker. Unusual examples include photographic evidence of an immigrant eunicid arriving on a floating coconut shell, bioluminescent 'firefly' non swimming syllids, distinctive tube structures created by unknown terebellids, and the discovery of a rare large spionid far beyond its known range. More work-a-day uses include tracking the expanding distribution of the alien sabellid *Sabella spallanzanii* and noting new records of little-known surf-beach worms. Altogether biologists globally are discovering many uses for iNaturalist data.

A.2.15 | Unravelling the fatty acid profiles of different polychaete species influenced by river run-off

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River plumes export large quantities of terrigenous organic matter to coastal areas, providing important food sources for benthic communities. This study investigates how the input of freshly deposited organic material from the Isonzo River (northern Adriatic Sea) influences the diet of benthic primary consumers. We examined trophic responses to river run-off by analysing fatty acids (FAs), used as lipid biomarkers, in polychaete species. Sampling was conducted along a coast-to-offshore transect (IN1–IN4) in October 2024, during an autumn plume event. Potential primary food sources were collected from the water column, including marine particulate organic matter (POM), phyto- and zooplankton, as well as riverine POC and riparian vegetation. Polychaetes were sampled approximately one month later to allow suspended particles to settle into the sediment. Phytoplankton-derived lipid markers (EPA and DHA) showed higher values at offshore stations, reflecting a stronger marine influence. Deposit feeders such as *Dasybranchus* sp., *Nephtys hombergii*, and Orbiniidae sp. exhibited high percentages of EPA and DHA, whereas EPA was not detected in *Pectinaria auricoma*. Fatty acid profiles in *Nephtys hombergii* varied along the distance from the river mouth. In particular, higher percentages of eicosadienoic acid (20:2 n-6) were observed at the station closest to the river mouth (IN1: 2.1%), indicating a terrestrial autotrophic origin of food sources. These findings highlight the importance of allochthonous organic matter in the diet of benthic primary consumers. Furthermore, fatty acid profiles provide insights into dietary variability across spatial gradients and reveal the trophic plasticity of species inhabiting heterogeneous coastal environments influenced by riverine inputs.

A.2.16 * | Worm of thorns: aquarium and micro-CT observations on *Protodiopatra willemoesii* (Onuphidae: Annelida) and its intrafamilial phylogenetic position

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The family Onuphidae comprises approximately 360 described species, including both tube-dwelling and semi-infaunal forms that are genetically differentiated. However, the phylogenetic position of the monotypic genus *Protodiopatra* remains unresolved because no molecular data have previously been available. In addition, little is known about the biology of living *Protodiopatra willemoesii*, a deep-sea species that constructs characteristic spine-covered J-shaped tubes. Six tubes of *P. willemoesii*, including one live individual, were collected from southern Japan. Another live specimen was collected by ROV from around Okinawa Island and maintained at Okinawa Churaumi Aquarium for behavioral observations and exhibitions. Genomic DNA was extracted from the specimens collected from Kagoshima Bay, and four genetic markers (COI, 16S, 18S, and 28S) were used for phylogenetic analyses. Behavioral observations focused on feeding, tube maintenance, and responses to experimental manipulation of the tube and spines. We also performed the micro-CT scanning for 3-dimensional observation of the produced tube structures. Phylogenetic analyses recovered *Protodiopatra* as the sister group to *Americanuphis*, although deeper relationships within Onuphidae were poorly resolved. Captive observations showed that *P. willemoesii* are carnivorous or scavengers, capturing prey from the tube opening before retreating into the tube. Worms actively reoriented horizontally placed tubes into vertical positions within one night and manipulated external spines using their parapodia. A terebellid polychaete was frequently associated with the tubes, suggesting that the tube structures function as habitats for other benthic organisms. Micro-CT revealed internal features such as variation in tube diameter, wall thickness, curvature, and branching patterns.

A.2.17 | Scientific Collection of Polychaeta at the Rio de Janeiro State University

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The Scientific Collection of Polychaeta at the Rio de Janeiro State University (UERJ) is an important repository for the study of Brazilian marine biodiversity. Established in 2009 and housed at the Laboratory of Invertebrate Zoology, the collection currently comprises 9,456 lots totaling 49,168 specimens distributed across 302 species, 122 morphotypes, 212 genera, and 63 families. The material mainly originates from the Brazilian coast, including both shallow and deep environments, with emphasis on regions such as the Campos Basin, Ilha Grande Bay, and coastal areas of São Paulo and Bahia. This study aims to describe the history, composition, organization, and scientific relevance of the collection. The material was obtained through various research and environmental monitoring projects, using standardized methodologies for collection, sorting, identification, and curation. Specimens are preserved in wet collections and organized in both physical and digital cataloguing systems, ensuring traceability and accessibility of information. The collection plays a key role in reducing taxonomic, geographic, and ecological gaps in polychaete knowledge, supporting studies in taxonomy, benthic ecology, biogeography, and environmental monitoring. It also serves as a basis for integrative approaches, including morphological and molecular analyses, and contributes to the training of specialized human resources. Despite its importance, challenges remain, such as the need to expand digitization, improve geographic coverage, and strengthen infrastructure and curation. Therefore, the collection stands as a strategic scientific infrastructure, essential for advancing knowledge, conservation, and management of marine biodiversity in Brazil.

A.2.18 * | Morphological revision of *Pseudobranchiomma* and bioinvasion signals along the southeastern Brazilian Coast

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Pseudobranchiomma comprises species distributed in the tropical Atlantic, warm-temperate southern Africa, and the Indo-Pacific. Although the genus is delimited by shared morphological characters, no clear synapomorphy has been recognized. Here, we redescribe the species recorded from Brazil and update their morphology, ecology, and distribution. We examined 1,413 specimens from southeastern Brazil, including material from natural, biogenic, consolidated, unconsolidated, and anthropogenic substrates, as well as type material of these species. *Pseudobranchiomma minima* is known only from Alcatrazes Island and appears restricted to the infralittoral zone. However, its reassessment is hindered by the unavailability of most of its type series; only one paratype mounted in glycerine jelly appears accessible, limiting comparisons with newly collected material. *Pseudobranchiomma paraemersoni* occurs on natural and anthropogenic substrates and shows broader morphological variation than previously reported, including evidence of asexual fission, variation in the lateral collar, an anteroposterior reduction in interramal eyespots, paired cilia on the ventral shields, and a reinterpretation of the thoracic notochaetae. This variation partially overlaps with

* Denotes a student contribution eligible for a prize.

Presenting author shown in **bold**.

characters reported for *Pseudobranchiomma schizogenica*, a Californian species with invasive history, suggesting that the distinction between these taxa remains unresolved. These differences may represent stable species-level traits, but may also reflect ontogenetic, methodological, or population-level variation within a broader species complex. Multilocus studies are required to test whether these nominal species represent distinct evolutionary entities. *Pseudobranchiomma paulista* is widely recorded from southern and southeastern Brazil, including port areas and consolidated and unconsolidated substrates. Staining revealed undocumented characters, including a trapezoidal anterior ventral shield and paired cilia. The limbus of the thoracic notochaetae and abdominal neurochaetae are reinterpreted as shorter than the shaft. Overall, the distribution, morphological plasticity, reproductive traits, association with biofouling communities, and dense aggregations of Brazilian *Pseudobranchiomma* indicate uncertain species boundaries and reinforce the need for integrative taxonomy to assess their identity and invasive potential.

A.2.19 * | Shine bright like a diamond: UV-induced fluorescence in *Parasabella* and *Sabellomma* (Sabellidae) from Brazil

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Marine annelids exhibit a wide range of morphological, sensory, and optical traits, yet light-related responses remain poorly documented for most polychaete lineages. In Sabellidae, this gap is especially relevant because several taxa possess elaborate radiolar crowns, complex pigmentation patterns, and conspicuous radiolar eyes, all of which may carry taxonomic information. The distinction between *Sabellomma* and *Parasabella* is currently based on a narrow set of morphological characters, mainly the arrangement of radiolar eyes and the morphology of companion chaetae, making additional comparative observations potentially useful. Here we report for the first time localized UV-induced fluorescence in two morphotypes provisionally assigned to *Sabellomma* from the southwestern Brazilian coast and compare their response with two examined morphotypes of *Parasabella*. Under controlled UV illumination, all examined *Sabellomma* individuals showed fluorescence, whereas no comparable response was detected in *Parasabella*. In *Sabellomma*, radiolar eyes exhibited conspicuous orange fluorescence, while radiolar bands and white punctate markings showed green to white-green fluorescence; in one morphotype, the response was restricted to punctate markings at the distal tips of the radioles. All examined *Sabellomma* individuals also exhibited a pair of medially positioned fluorescent spots on the first dorsal segment and random fluorescent spots on the collar. Because the signal was detected only under UV excitation, the phenomenon is interpreted as UV-induced fluorescence rather than bioluminescence. These observations do not establish fluorescence as a diagnostic character for *Sabellomma*, nor do they demonstrate genus-level exclusivity. However, they suggest that controlled UV illumination may provide an auxiliary screening feature to be tested across broader taxonomic, ontogenetic, and geographic sampling. More broadly, this study adds an overlooked observational layer to sabellid taxonomy and shows how simple optical assays, when interpreted cautiously, can generate testable hypotheses for morphologically challenging annelid groups.

A.2.20 * | Insights into the function of soft-bottom polychaete communities in the Israeli Mediterranean Sea Marine Reserves

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Soft-bottom infaunal communities are central to benthic ecosystem functioning yet remain understudied in the oligotrophic eastern Mediterranean, particularly within Marine Reserves (MRs). Despite the ecological importance of polychaetes as sensitive indicators of environmental conditions and functionally important taxa, little is known about the effect of MRs on polychaete community composition, diversity, and function. This study addresses this knowledge gap through an integrative assessment of soft-bottom infaunal communities in Israeli MRs, focusing on polychaete assemblages and their ecological roles. We compare multiple sampling approaches including grab sampling, frame dredging, airlift sampling, and a novel "bucket burial" method, to evaluate methodological biases in soft-bottom biodiversity assessments. The bucket burial approach involves prolonged burial of collapsible buckets within the sediment prior to retrieval, aiming to better preserve intact infaunal assemblages while enabling direct coupling of community composition with metabolic chamber measurements. Fish exclusion experiments and spatial comparisons from rocky outcrops will help determine how predation and habitat connectivity influence infaunal assemblages.

* Denotes a student contribution eligible for a prize.
 Presenting author shown in **bold**.

Using these methods alongside high-resolution taxonomic identification, we aim to compare community composition and diversity across protected and unprotected sites. Preliminary results suggest grab and frame dredging methods may yield substantially different diversity estimates. Results also reveal high polychaete family richness along the Israeli coast including the potential presence of a novel Magelonidae and Spionidae species previously unrecorded in this region. These findings highlight the hidden diversity and taxonomic gaps of Levantine soft-bottom habitats. Integrating biodiversity patterns with ecosystem functioning, this work advances understanding of benthic-pelagic coupling and the ecological role of MRs in shaping soft-bottom systems, while informing future conservation and management strategies and emphasizing the importance of polychaetes.

A.2.21 * | Coral-associated polychaete assemblages in the Gulf of Aqaba: preliminary evidence of hidden diversity

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Coral-associated fauna plays key roles in reef ecosystems, contributing to vital processes such as organic matter decomposition, bioturbation, filtration, and water circulation. Despite their ecological importance, the diversity of coral-associated polychaetes remains poorly resolved across many coral-reef ecosystems worldwide. In the northern Red Sea, most knowledge of polychaete diversity is based on historical records from decades ago, with coral-associated taxa receiving little focus, and most attention targeting conspicuous polychaete-coral associations, particularly those involving serpulids and spionids. Here, we examine the diversity and abundance of coral-associated polychaete assemblages in hard and soft corals in the Gulf of Aqaba, combining field sampling with examination of historical records at the Steinhardt Museum of Natural History, Tel Aviv University, to detect previously overlooked polychaete symbionts. Preliminary results are shown for the soft coral *Dendronephthya hemprichi*. Nineteen coral fragments (3-5 cm) were examined, seventeen of which contained associated polychaetes, yielding 545 individuals. Most specimens belonged to a single dominant syllid taxon, while only two individuals belonged to the family Polynoidae. Abundance was high even within small fragments, with up to 160 individuals in a single fragment, suggesting that coral colonies harbor dense and previously overlooked annelid assemblages. Several individuals appear to be stolonizing, suggesting that reproduction may occur within or on the host. While atokous individuals are whitish, epitokes are brightly colored and visually resemble the coral. Initial morphological and molecular (16S rRNA) analyses indicate that the dominant syllid taxon may belong to a novel species closely related (97%) to *Alcyonosyllis aidae*. These initial findings indicate that coral-associated polychaete diversity in the Red Sea is underestimated and highlight the importance of targeted, host-specific surveys to uncover hidden reef biodiversity. By integrating taxonomy, host association, and museum-based biodiversity surveys, this study provides the basis for understanding coral-associated polychaete diversity in the Gulf of Aqaba.

A.2.22 | Metabolic and microbial integration within a sponge-annelid nested holobiont

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Holobionts are a functioning unit consisting of multiple living beings in close symbiosis with one another. Research into these systems is revolutionizing our understanding of marine ecosystem processes. A central question in such systems is how metabolic and microbial functions are partitioned between the partners, and how this organization reflects the ecological and evolutionary integration of the holobiont. The obligate partnership between the branching syllid annelid *Ramissyllis kingghidorahi* and sponges of the genus *Petrosia* offers a striking example, in which the sponge's filtration system and the worm's highly ramified body are physically interwoven, creating, together with their microbiomes, a single, metabolically coupled holobiont. The two partners share a single physical environment, with the worm's body distributed throughout the sponge's aquiferous system. Within this physically integrated unit, the metabolic and microbial organisation of each partner remains uncharacterised. However, how the metabolic and microbial functions are organised between the two partners. To what extent does each host harbour a distinct microbiome, and how do their predicted metabolic capabilities differ. To test this hypothesis, we will employ an integrative, holobiont focused multi omics strategy complemented by functional assays. (1) Spatially resolved omics, including genome, transcriptome, and proteome profiling of anterior, mid-body, and posterior segments, will be used to characterize and pinpoint functional and metabolic differentiation along the branching body, with particular emphasis on enzymes and transporters involved in external

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uptake and digestion. (2) Microbial community characterization through metagenomic sequencing will be conducted to identify symbiotic partners and assess their potential functional contributions to host metabolism. The project will deliver the first integrated characterization of the metabolic and microbial organization of a sponge-annelid nested holobiont, providing the molecular foundation for understanding how extreme body-plan diversification is reflected in the physiological architecture of the nested unit.

A.2.23 * | Hidden front, branching back: feeding ecology and spatial architecture of the sponge symbiotic syllid *Ramissyllis kingghidorahi*

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R. kingghidorahi, one of few laterally branching syllids, is an obligate endosymbiont of *Petrosia* sponges. In this project, the aim is to investigate the spatial distribution and feeding strategies of the polychaete within its host, through a series of interconnected hypotheses: (1) the worm's anterior end is hidden in the inner basal region of the sponge, while a dense network of posterior branches extends throughout the sponge's canal system; (2) the polychaete functions as a detritivore, exploiting particulate organic matter expelled by the sponge and/or dissolved organic matter; (3) nutrient uptake occurs primarily through the epidermis and posterior ends, not through the anterior end. Micro-computed tomography reconstructions reveal the anterior end lodged deep in the sponge interior and an extensive network of posterior branches that thread the canal system, confirming the worm's pervasive spatial occupation. Feeding experiments employed incubations with ferritin and fluorescent microspheres at four time points, followed by immunohistochemistry to trace particle localization. Preliminary data indicate ferritin accumulation in the digestive tract adjacent to the anus. Ferritin was also detected on the epidermal surface of posterior branches, suggesting epidermal absorption. Bulk stable isotope analysis and compound-specific isotope analysis of amino acids (CSIA-AA) of carbon (¹³C) and nitrogen (¹⁵N) show that branching worms occupy a narrower isotopic niche and a higher trophic position than their sponge hosts, supporting a direct trophic link in which *Ramissyllis* may act as a detritivore. The presence of the worm may not harm the sponge, but may help maintain canal patency by removing mucus and debris. Together, these results provide the first functional insight into how a branched annelid interacts with its sponge habitat, highlighting a potentially mutualistic relationship that may be pivotal for the persistence of both partners in marine benthic ecosystems.

A.2.24 | Environmental monitoring as a tool to inform polychaete diversity in Greece: new records, new species, and underestimated biodiversity

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Almost ten years after the last checklist of polychaete diversity in Greece was published, intense environmental monitoring, primarily at aquaculture farms, has significantly updated our knowledge of Greek polychaete diversity. Analysis of over 750 soft-substrate samples from depths of 0–140 m revealed 69 species recorded for the first time, 32 for the second time, and 8 for the third time. Three previously unknown species (*Iphitime* n. sp., *Flabelligeridae* n. sp., and *Axiokebuita* n. sp.) were found and at least another ten morphospecies are potentially new to science but require further research. After standardizing for sampling effort, most new records were from the south-eastern and north-eastern Aegean Sea and the Gulf of Corinth. Phytal habitats, including seagrasses (and dead matte), algae, and maerl, as well as sediments with shell detritus had the highest number of new records, due to their structural complexity but also their understudied nature. Most new records were from near aquaculture farms (< 150 m), although reference stations showed a higher frequency of new records when standardized for sampling effort. Syllidae accounted for most new records, followed by Paraonidae, Lumbrineridae, Cirratulidae, Eunicidae, and Nereididae. Recent taxonomic revisions of Paraonidae, Lumbrineridae, and Cirratulidae in the Eastern Mediterranean have contributed to this improved

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understanding of their diversity, while Eunicidae and Nereididae were mostly composed of non-native species. In total, eleven non-native species (mostly Lessepsian migrants) were recorded for the first time. This study confirms the importance of environmental monitoring in the absence of dedicated resources for taxonomic research, but also highlight the need for targeted studies in understudied habitats and regions of the Eastern Mediterranean. Despite the efforts presented here, the true extent of polychaete diversity in the region likely remains significantly underestimated. Further resolving this diversity will require dedicated taxonomic expertise, targeted funding, and sustained long-term effort.

A.2.25 | Spatial variability of polychaete assemblages in tropical soft-bottom habitats of the Western Gulf of Thailand

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Polychaetes are among the most important benthic invertebrates in tropical soft-bottom ecosystems and are widely recognized as effective indicators of environmental quality and ecosystem disturbance. This study investigated the diversity and distribution of polychaete assemblages around Ko Tao in the western Gulf of Thailand. Surveys were conducted across sandy beaches, coral reef-associated sediments, and offshore soft-bottom habitats located at varying distances from the shoreline. Sediment samples revealed the occurrence of several dominant polychaete families, including Capitellidae, Cirratulidae, Eunicidae, Lumbrineridae, Magelonidae, Maldanidae, Nephtyidae, Nereidae, Orbiniidae, Spionidae, and Glyceridae. Total polychaete abundance varied among stations, ranging from 93.4 to 160.0 individuals m^{-2} . Coral reef-associated soft-bottom habitats near Laem Ta To exhibit the highest abundance and family richness, whereas lower abundances were observed at several offshore and sandy beach stations. Spionidae, Cirratulidae, and Eunicidae were among the most frequently recorded taxa across the study sites, suggesting their ecological importance within disturbed and recovering sedimentary habitats. The observed polychaete assemblages indicate that soft-bottom ecosystems surrounding Ko Tao continue to support moderate benthic biodiversity. Spatial differences in community composition likely reflected habitat heterogeneity, sediment characteristics, and varying environmental conditions among coastal and offshore stations. The presence of several opportunistic and disturbance-tolerant taxa also highlights the potential utility of polychaetes as bioindicators for long-term environmental monitoring in coastal ecosystems. This study provides baseline ecological information for assessing benthic ecosystems and contributes to biodiversity conservation and sustainable management in tropical marine ecosystems.

A.2.26 | Richness, distribution and molecular barcode gaps of polychaetes from the Balearic Islands, Western Mediterranean

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Polychaetes are among the most diverse benthic groups in the Mediterranean Sea, yet their diversity and molecular characterization remain unevenly documented in many regions. This study provides an updated assessment of the richness, distribution, and barcode coverage of polychaetes from the Balearic Islands (Western Mediterranean). We compiled a georeferenced dataset integrating 134 records from the GBIF database, 2,631 literature records retrieved using custom AI-assisted tools, and 1,608 new records generated through targeted sampling of coastal and offshore habitats during oceanographic campaigns, revision of museum collections, and re-examination of material collected over the last decade. A total of 475 species belonging to 52 families were recorded, including 109 species newly reported for the archipelago and 23 non-indigenous species. Spatial analyses based on Simpson's dissimilarity index, using a regular $0.25^\circ \times 0.25^\circ$ grid, identified 11 polychaete assemblages across the region. Rarefaction and cumulative richness curves indicate that the regional diversity remains under-sampled, particularly in several offshore and deep-water sectors with high discovery potential. We additionally evaluated the availability of molecular barcodes in public repositories. Barcode coverage remains limited and uneven among markers, with available sequences for 44% of species for COI, 40% for 18S, 32% for 16S, 25% for 28S, and only 5% for 12S. Our results highlight the importance of

targeted sampling and the urgent need to expand molecular reference databases, particularly for taxonomically challenging polychaete families.

A.2.27 * | A global synthesis of annelid diversity across subterranean aquatic and terrestrial ecosystems

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Subterranean ecosystems span terrestrial and aquatic realms, from dry caves and fissure networks to springs, wells, anchialine systems, marine caves, coastal aquifers, and freshwater interstitial habitats. These systems provide key ecosystem services, all of which depend on ecosystem functioning and the biological communities that sustain it. Although subterranean biodiversity is dominated by endemic and morphologically specialized arthropods, annelids are increasingly recognized as important components of both aquatic and terrestrial subterranean communities. Yet global knowledge of subterranean annelids remains fragmented across taxa, regions, habitats, and literature sources. Using the Stygofauna Mundi database, we present the first global synthesis of annelids reported from subterranean habitats spanning terrestrial and aquatic subterranean systems. The dataset comprises 9,070 records assigned to 1,262 species and extracted from 1,136 sources, including scientific papers, grey literature, and public databases. These species span 92 families of polychaetes and clitellates. We quantify global patterns of taxonomic alpha and beta diversity, showing that reported annelid diversity is highest in Europe and North America, most likely reflecting greater sampling effort in these regions rather than a biologically meaningful diversity peak. By contrast, most other regions remain represented by sparse or isolated records. We also provide a qualitative discussion of functional and phylogenetic diversity. Our synthesis identifies major geographical, taxonomic, and habitat-related knowledge gaps and emphasizes that annelids must be integrated into broader assessments of subterranean biodiversity. Filling these gaps is essential for understanding the role of annelids in subterranean ecosystem functioning and for predicting the resilience of terrestrial and aquatic subterranean systems under global environmental change. We therefore invite annelid specialists working across different regions, habitats, and taxonomic groups to contribute to this collaborative global effort. Keywords: macroecology, taxonomic diversity, functional diversity, phylogenetic diversity, ecosystem services, global change.

A.2.28 | Are alien polychaetes a random subset of polychaete diversity? A global synthesis of invasion patterns

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Marine polychaetes are among the most frequently reported non-indigenous benthic invertebrates, yet global patterns underlying their invasions remain poorly understood. In particular, it remains unclear whether alien polychaete species represent a random subset of global annelid diversity or whether invasions are concentrated within specific lineages. Here, we combine a global synthesis of alien polychaete records with a focused analysis of Mediterranean introductions to evaluate taxonomic patterns of invasion and their potential association with major introduction pathways. A global dataset of approximately 340 alien polychaete species was compiled from published records and recent updates and compared to global family-level richness obtained from the World Register of Marine Species (WoRMS). Expected numbers of alien species per family were calculated under a null model assuming proportional representation according to global family richness. Chi-square goodness-of-fit tests and binomial generalized linear models were used to test whether invasion probability differs among families. Preliminary analyses reveal strong non-random taxonomic structure in alien polychaete assemblages. Alien species are significantly clustered within a limited number of families, with consistent patterns across alien, established, and established-plus-casual categories. Spionidae and Serpulidae are strongly over-represented relative to expectations based on global richness, whereas some highly diverse families, such as Polynoidae, are under-represented. More than half of all polychaete families contain no alien representatives, indicating substantial taxonomic restriction in both introduction and establishment processes. Ongoing analyses are examining whether these patterns are associated with ecological and functional traits, including feeding guilds, habitat affinity, and motility, as well as whether Mediterranean alien assemblages mirror global invasion trends. Together, these results suggest that marine polychaete invasions are strongly lineage-dependent and potentially shaped by shared ecological characteristics within particular families.

A.3.29 | Polychaetes associated with a red mangrove (*Rhizophora mangle*) ecosystem prior to its catastrophic destruction by two hurricanes in the Coral Reef National Monument, St. John, U.S. Virgin Islands.

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A formal database is being developed to document the polychaete species once associated with the mangrove-fringed bays comprising Hurricane Hole, a sector of the Coral Reef National Monument in St. John, U. S. Virgin Islands. Until September 2017, the fringing mangroves (*Rhizophora mangle*, L.) sheltered an assemblage of over 30 scleractinian corals, not seen in term of diversity and abundance in any other mangrove ecosystem within the Caribbean. Corals normally found at depth were growing on the mangrove prop roots, which also provided substrata for other epiphytes and natural fouling material. The diversity of sponges and fish was also high. Polychaetes collected from the mangrove fouling communities and from adjacent seagrass and sediments included species represented over 25 families, along with a new serpulid genus. The polychaete database includes new records for both the region and for the Caribbean Sea. In September 2017, two category-five hurricanes (Irma and Maria) caused catastrophic damage to the Hurricane Hole ecosystem, where entire mangrove trees were uprooted, and submerged roots were scoured bare. The unprecedented storms shattered large coral colonies and moved boulders. Nearly nine years later, the mangroves and associated fauna show minimal evidence of recovery. The development of a database for polychaetes collected over an 8-year period (2009–2017) offers a baseline for the historic (pre-hurricanes) polychaete species richness in the area, where polychaetes may serve as indicators for an ecosystem that may or may not recover.

A.3.30 * | High-density association of a putative new *Haplosyllis* species with *Ircinia* sponges in the Gulf of Aqaba

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Symbiotic polychaetes are important contributors to coral reef biodiversity, yet sponge-associated polychaete assemblages in the Gulf of Aqaba (northern Red Sea) remain poorly characterized, with most available records being historical (1950s–1970s) or anecdotal. Other than a few spionid records, little is currently known regarding the diversity and ecology of sponge-associated polychaetes in the region. This project aims to investigate the diversity, community composition, and host associations of sponge-inhabiting polychaetes through field sampling and examination of collections at the Steinhardt Museum of Natural History, Tel Aviv University. Ongoing surveys include multiple sponge taxa with differing morphologies, particularly larger species with extensive canal systems and oscula that may facilitate diverse endobiont assemblages. Preliminary results reveal a dense and consistent association between a sponge of the genus *Ircinia* (likely *I. echinata*, representing the first formal record from Israel) and a possibly undescribed species of *Haplosyllis*. This species is notably small compared to most congeners and possesses a short proventriculus spanning only 1.5–2 chaetigers. Phylogenetic analysis based on 16S rRNA places the species within Clade II of *Haplosyllis*, alongside *H. tenhovei*. The species was found in all examined *Ircinia* specimens, with densities reaching hundreds of individuals per sponge fragment, suggesting a persistent and potentially host-dependent association rather than an incidental occurrence. Members of *Haplosyllis* are commonly associated with sponges, yet the abundance observed here is unusual and may indicate strong host dependence. These findings highlight the potential for overlooked host-associated polychaete diversity within Red Sea sponges. Ongoing work will expand this survey across additional sponge taxa to establish a modern baseline for sponge-associated biodiversity in the region.

A.3.31 | Seasonal variation in microplastic ingestion by a cirratulid polychaete

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Microplastic (MP) contamination in benthic ecosystems is an increasing concern, particularly for deposit-feeding organisms that interact directly with contaminated sediments. This study evaluated temporal variation in MP ingestion by the cirratulid polychaete *Timarete ceciliae* on an intertidal sandy flat in northeastern Brazil over a 20-month period. A total of 200 individuals were collected, measured, and analyzed for the presence, type and size of MP's. Ninety-seven percent of the individuals contained MPs, totaling 1,054 particles. Fibers were the predominant type (77%), followed by fragments, with mean values of 3.6 ± 2.49 fibers and 1.07 ± 1.25 fragments per individual. Particles smaller than 1 mm were dominant. MP ingestion showed significant temporal variation, with higher values during the dry season ($p = 0.0023$); this difference was significant for fibers ($p < 0.05$), but not for fragments. Blue fibers were the most frequent, representing more than 50% of the items. Generalized linear models indicated no significant relationship between MP ingestion and environmental variables (temperature, salinity, rainfall, and tide height; $p > 0.05$). Similarly, no relationships were found between MP ingestion and biological traits such as body size, number of segments, or presence of regeneration. These results indicate that temporal variability, particularly seasonality, is the main factor regulating MP availability in the studied site, whereas specific environmental variables and organismal traits exert limited influence. The results, together with the high frequency of ingestion and sensitivity to temporal variation, indicate that *T. ceciliae* has strong potential as a sentinel species for microplastic biomonitoring in tropical coastal ecosystems.

A.3.32 | Unraveling the diversity of *Phyllodoce* Lamarck, 1818, from a Brazilian oceanic archipelago

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Phyllodocidae Örsted, 1843 is a highly diverse family of annelids with a worldwide distribution across depths. Most species are free-living and benthic, with few occurring in estuarine and rare freshwater habitats. They are carnivorous or scavengers, using an eversible pharynx to capture prey. *Phyllodoce* Lamarck, 1818, the most speciose genus, is characterized by a nuchal papilla on the prostomium and a proboscis divided into a proximal papilla-bearing region and a distal region with rows of tubercles. Although the taxonomy of the group has been extensively studied in several regions – such as southeastern Brazil – significant gaps in knowledge remain, particularly along the northern and southern coasts of Brazil and in its oceanic islands. In this study, two new species of *Phyllodoce* from the Trindade and Martin Vaz Archipelago, South Atlantic Ocean are described. Samples were obtained between 2012 and 2019 under the scope of the project PROTRINDADE, from the intertidal zone and by scuba diving and snorkelling, between the depths of 5 m to 30 m. The collected specimens were examined under stereomicroscope, compound light microscope and scanning electron microscope (SEM). *Phyllodoce* sp. A is most similar to *Phyllodoce brasiliensis* Oliveira, Magalhães & Lana, 2021, whereas *Phyllodoce* sp. B is most similar to *Phyllodoce madeirensis* Langerhans, 1880; however, the two species differ in cirri morphology as well as in the number and distribution of papillae on the proboscis. *Phyllodoce* sp. A is unique in having oblong dorsal and ventral cirri throughout, as well as a rounded to oval prostomium with distinct nuchal organs. Additionally, *Phyllodoce* sp. B differs from its congeners in having dorsal cirri that are oval to foliaceous, ventral cirri that are anteriorly subrectangular with rounded edges and posteriorly lanceolate, and six longitudinal rows of papillae on the proboscis (14–16 rounded papillae), along with a cordiform to pentagonal prostomium.

A.3.33 | A new species of *Polyophthalmus* Quatrefages, 1850, from Trindade Island, South Atlantic Ocean

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The Opheliidae Malmgren, 1867 is a family of annelid worms comprising about 160 living species distributed in seven genera. Members of this family are considered burrowing subsurface deposit feeders that may use an unarmed pharynx to actively collect organic particles deposited in the sediment. They are found in soft sediments at all ocean depths, although different genera seem to inhabit different environments. *Polyophthalmus* Quatrefages, 1850 is a small opheliid genus whose members are readily recognizable at the generic level, but species-level identification remains challenging due to its long and complex history of taxonomic synonymization. Currently, the genus consists of only 10 valid species, but recent revisions suggest that several previously synonymized taxa probably correspond to separate species, and additional valid species are still being identified. In this study, a new species of *Polyophthalmus* from the Trindade and Martin Vaz Archipelago, South Atlantic Ocean is proposed. Samples were obtained between 2012 and 2019 under the scope of the project PROTRINDADE, from the intertidal zone and by scuba diving and snorkelling, between the depths of 5 m to 30 m. The collected specimens were examined under stereomicroscope, compound light microscope and scanning electron microscope (SEM). The new species is most similar to an undescribed species of *Polyophthalmus* from Bahia, currently being described, by the presence of minute dorsal and ventral cirri, interparapodial papillae throughout and six pairs of marginal papillae in the anal tube. Nevertheless, it can be distinguished from its congeners by the presence of 14-15 pairs of lateral eyes starting from chaetiger 6 (with the first and the last five ones comparatively smaller in size), the unique pigmentation on dorsum, distinctively unequal lengths of noto- and neuropodial capillaries and presence of 2-5 short companion capillaries.

A.3.34 * | Biological Traits Analysis uncovers spatiotemporal functional dynamics of soft bottom polychaetes in Terra Nova Bay (Ross Sea, Antarctica)

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Polychaetes are a dominant component of Antarctic macrobenthic communities and play a key role in ecosystem functioning through sediment reworking, bioturbation and organic matter remineralization. Despite their ecological importance, integrated studies linking taxonomic composition and functional traits across Antarctic soft-bottom environments are still developing.

This study contributes to advancing this field by examining the spatiotemporal functional dynamics of polychaete assemblages in shallow soft bottoms of Terra Nova Bay (Ross Sea) by comparing four distinct sites (TB, RB, Fr, AC) over two consecutive austral summers (PNRA 2021/22 and 2022/23). To provide a detailed functional characterization, we applied Biological Trait Analysis (BTA) using a fuzzy coding approach (0-3 scores) to account for species plasticity across three ecological trait categories: feeding strategies, motility and habitat preference. The functional trait information was integrated into a Community Weighted Mean (CWM) matrix to describe the functional structure of the assemblages. Multivariate analyses on the CWM matrix, based on Euclidean distance, using PERMANOVA analysis, revealed significant temporal ($p=0.0093$) and spatial ($p=0.0001$) variations, even though pairwise comparisons performed separately for each year did not reveal significant differences. The nMDS ordination revealed two distinct clusters of sites, with two sites grouping closely together in each cluster. SIMPER analysis identified the functional components contributing to these differences, suggesting the presence of two main functional configurations across the study area. TB and Fr were associated with highly motile predator/scavenger and epifaunal traits, mainly linked to the dominance of *Aglaophamus trissophyllus* (Grube, 1877) and *Barrukia cristata* (Wiley, 1902). Conversely, RB and AC were characterized by infaunal sub-surface deposit feeders, largely associated with the dominance of *Leitoscoloplos kerguelensis* (McIntosh, 1885). These findings demonstrate the effectiveness of BTA in detecting spatiotemporal functional variability in Antarctic benthic assemblages and highlight the key role of environmental heterogeneity in shaping benthic assemblage structure over time.

A.3.35 * | Population structure and genetic divergence of *Escarpia* spp. (Siboglinidae) collected from the eastern Pacific and Gulf of Mexico methane seeps

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Methane seep ecosystems are isolated and chemically extreme habitats on the ocean floor that support dense chemosynthetic communities. Among the dominant macrobenthic fauna inhabiting these environments are vestimentiferan tubeworms (Siboglinidae), some of which are notable for their abundant tube aggregations and exceptional longevity of over 150 years. One representative of this group, *Escarpia spicata* Jones, 1985, is distributed throughout the eastern Pacific Ocean, from southern California to Chile. Specimens collected from the Gulf of Mexico on the Atlantic side are regarded as a separate species, *E. laminata* Jones, 1985. However, the absence of mitochondrial haplotype differentiation between the Pacific and Atlantic populations has left species boundaries and patterns of population connectivity unresolved. Using whole genome sequencing data from over 75 *Escarpia* individuals collected across four Pacific and one Atlantic location, we investigated population structure and connectivity among *Escarpia* individuals. Comparative analyses of full mitochondrial genomes and millions of nuclear genomic SNPs revealed the absence of ongoing gene flow between Pacific and Atlantic populations, as indicated by the lack of admixture and high levels of genetic differentiation. This suggests that *E. laminata* is a valid species, though investigating the presence of *Escarpia* from the South American margin would be very valuable to further assess its status. We further find low levels of heterozygosity and high inbreeding in the individuals from the Gulf of Mexico population, which we discuss with regard to the biogeographic history of the Atlantic group.

A.3.36 | Filling the gaps: new records and diversity of polychaete in tide pools of Fernando de Noronha Archipelago, Brazil

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Fernando de Noronha is a Brazilian oceanic archipelago characterized by high endemism and diverse marine habitats, such as tide pools. These rocky shore depressions retain seawater during low tide, forming unique environments. Despite the archipelago's ecological relevance, polychaete knowledge remains scarce, with only 16 species previously recorded, mostly from subtidal zones. This study aims to characterize and compare polychaete diversity in tide pools from six sites: Boldró, Caieiras, Sapata, Caracas, Leão and Sueste. Hard substrate was qualitatively scraped at each site; specimens were fixed in formalin 10%, conserved in 80% ethanol, sorted and identified to the lowest taxonomic level. Up to now, material from 5 sites was analysed and a total of 581 specimens representing 69 taxa within 19 families were identified. Taxonomic richness was highest in Caieiras (S=38), followed by Caracas (S=26), Sueste (S=24), Boldró (S=21), and Sapata (S=11). Syllidae was the most representative family (54.6%), followed by Eunicidae (27.0%), dominating most sites (47.4%–71.7%) except Caracas, where Eunicidae was dominant (50.0%). Diversity indices followed a similar pattern; the highest values were recorded in Caieiras ($H'=3.14$; $1-D=0.94$), while Sapata showed the highest evenness ($J'=0.96$). The UPGMA cluster analysis revealed high faunal heterogeneity, with dissimilarities between all sites exceeding 61%. Sapata was the most distinct assemblage, showing up to 93% dissimilarity compared to other sites. SIMPER analysis indicated that *Eunice imogena* (8.3%), *Brania armini* (6.0%), and *Haplosyllis* sp. (5.5%) were the main responsables for the high dissimilarity among the studied locations. Our findings expand the archipelago's biodiversity records, adding 65 new records and increasing the total richness from 16 to 81 taxa. The identified fauna exhibits both Caribbean and Brazilian influences, highlighting Noronha's strategic biogeographical role. The high faunal heterogeneity reinforces the unique ecological value of each tide pool, emphasizing the need for broad spatial conservation strategies across the archipelago.

A.3.37 | Revisiting *Sabella braziliensis* (Treadwell, 1932): a morphological comparison with *Sabella spallanzanii*

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The genus *Sabella* Linnaeus, 1767 currently comprises 72 valid species. Eight species have been recorded along the Brazilian coast, six of which were originally described from the region but were later synonymized with *Sabella spallanzanii* (Gmelin, 1791), a species first described from the Iberian Peninsula (Mediterranean). Among them was *Sabella braziliensis* (Treadwell, 1932), formally described from material collected at São Sebastião Island (São Paulo, Brazil) and recently revalidated. Consequently, three species are currently recognized as valid in Brazilian waters: *S. braziliensis*, *S. fusca* (Grube, 1870), and *S. spallanzanii*. In order to describe morphological differences between *S. braziliensis* and *S. spallanzanii*, specimens of the latter and the holotype of former, deposited in the Zoological Collection of the National Museum of Natural History, Smithsonian Institution, were examined. Morphological analysis revealed significant differences between the specimens, including coloration and shape of the radiolar crown; number of whorls on the spiral side; morphology of the collar, particularly in the dorsal and ventral regions; and the number of abdominal neurochaetal whorls arranged in a spiral, among other characteristics. Thus, we consider both species distinct and support the revalidation of *S. braziliensis*. The presence of *S. spallanzanii* in Brazil was confirmed from the analyses of specimens recently sampled in Cagarras Islands Natural Monument (Rio de Janeiro), a no-take Marine Protected Area, by the Coastal Islands Monitoring Project (PMIC); a requirement of the federal environmental licensing process, conducted by IBAMA, for Oil & Gas exploration by Petrobras in Santos Basin Pre-Salt. This material is deposited in the Annelida Collection of Museu Nacional/UFRJ. However, given the historically confused taxonomic framework of the genus and the confirmed occurrence of the three *Sabella* species in Brazil, specimens previously identified as *Sabella* should be reexamined to verify their specific identity and refine the distributional limits of each species in Southwestern Atlantic.

A.3.38 | Century-long changes in the White Sea ecosystem: a case study of polychaete diversity (Annelida, Polychaeta)

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Polychaetes are a key component of benthic communities, often dominating in both species richness and abundance. The White Sea, a subarctic inland sea, has experienced climatic and possible anthropogenic changes over the past century. This study aimed to assess changes in the diversity and distribution of White Sea polychaetes between 1922 (the expedition of Konstantin Mikhailovich Deryugin) and 2023–2024. Polychaete species lists from historical and recent surveys were compared, taking into account taxonomic revisions and methodological differences, including sampling gear and mesh size. Species accumulation curves and Chao estimators were used to evaluate sampling completeness, while community similarity was assessed using the Sørensen index, Mantel test, and Forbes coefficient. A total of 97 operational taxonomic units (OTUs) were recorded across both periods. Trawl data revealed 71 OTUs in 2023–2024 and 60 OTUs in 1922, with 44 shared species. Most apparent species “gains” and “losses” were attributable to rarity, taxonomic inconsistencies, or methodological differences, particularly the use of finer mesh sizes in modern surveys. Multivariate analyses demonstrated substantial overlap in community structure between the two periods: stations similar in 1922 remained similar in 2023–2024 (Mantel test, $p = 0.002$). Centres of polychaete diversity have largely persisted through time. A positive correlation was found between the persistence of dominant taxa and overall assemblage stability, while deeper stations exhibited greater conservatism. Overall, the polychaete fauna of the White Sea has remained relatively stable over the past century. Most observed differences reflect improved sampling methods and taxonomic resolution rather than genuine faunal change. These results provide an important baseline for detecting future climate-driven changes in Arctic benthic ecosystems. The work was performed as part of Rosneft’s innovation activities.

A.3.39 | Carrier-like structures in Dorvilleidae family (Eunicida)

Anna Koroleva & **Alexander Tzetlin**

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Jaw morphology plays an important role in the systematics and evolutionary interpretation of Eunicida, including the family Dorvilleidae. Based on morphology, several types of eunicidan jaw apparatus are recognized, including ctenognath, prionognath, symmetragnath, eulabidognath, and the extinct placognath type. In several eunicidan lineages possessing prionognath, eulabidognath, or symmetragnath jaw apparatuses, paired sclerotized plates termed carriers are typically present and form the most basal (posterior) part of the maxillary apparatus. In contrast, “true carriers” are generally considered absent in dorvilleids, whose jaw apparatus belongs to the ctenognath type, often interpreted as a comparatively less specialized and potentially basal condition within Eunicida. At the same time, the literature reveals considerable terminological inconsistency regarding structures in dorvilleids that have been interpreted as carrier-like structures. Different authors have referred to these elements as “carrier-like structures”, “pseudocarriers”, or “dorsal carriers”, while in palaeontological studies comparable structures have also been interpreted as basal plates. Additionally, these terms have often been applied to different jaw elements, further complicating comparisons between taxa and studies. Notably, ventral pseudocarriers have not been described in fossil representatives, obscuring attempts to establish homologies between extant and extinct forms. We provide an overview of carrier-like structures reported in dorvilleids and summarize the terminology applied to these jaw plates across the literature. In addition, histological images of dorvilleid jaws at the level of pseudocarriers are presented as supplementary anatomical material relevant to the discussion of these structures.

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A.3.40 * | Assessing the biodiversity of intertidal annelids across the European North Atlantic coastline through morphological and molecular approaches

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The global distribution of marine biodiversity has long been discussed among researchers, and over the past two centuries, two major biodiversity trends were established: a decrease in marine biodiversity from west to east and an increase in biodiversity towards the equator. For annelids, however, large-scale assessments of biodiversity patterns along latitudinal gradients remain scarce. Within the BIOcean5D/TREC framework, standardized sampling was conducted across a coordinated network of European coastal sites, where multiple habitats have been surveyed using harmonized protocols to collect biological and environmental data along latitudinal and ecological gradients. Based on this sampling design, we show how the species richness and evenness change along a gradient of 20° latitudinal degrees with 830 total samples taken from 18 collection sites along the Northeast Atlantic coastlines, while also determining whether a difference in biodiversity is found between the two habitat types of sandy beaches and rocky shores. Samples were identified using both morphological and molecular approaches, with 18S1 and *cox1* as target genes for sequencing. We found that both species diversity and evenness increased with proximity to the equator, with this trend being more pronounced on sandy beaches than on rocky shores. Northern sandy beaches were oftentimes heavily dominated by a single species, whereas this dominance diminished progressively toward southern regions. Overall, species diversity was higher in rocky shore habitats than sandy beaches, likely due to greater habitat heterogeneity. Our results improve the understanding of large-scale biodiversity patterns along European coastlines and provide new insights into the composition of annelid communities in intertidal zones across Western Europe.

B.1.41 * | Re-evaluation of Polynoidae diversity based on available sequences from vouchered specimens
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The Polynoidae are a very diverse family of marine polychaete worms, with more than 900 described species across all oceans, habitats, and depths. Their ubiquitous distribution makes them a relevant model for studying evolution in the oceans and adaptations to different benthic environments, from intertidal zones to deep-sea trenches, including anchialine caves and hydrothermal vents. However, the taxonomy of Polynoidae is unstable and undergoes frequent taxonomic rearrangements. It seems lack of reliable diagnostic morphological characters to define genera results in nearly half of the genera being monotypic and in the presence of a few “wastebasket” genera containing hundreds of species. We aimed to investigate the species diversity of Polynoidae from a molecular perspective, as well as the concordance with taxonomic assignments. As taxonomic identifications are hypotheses, which can be particularly unstable in Polynoidae, we built a dataset in which specimens are the primary unit rather than sequences or taxonomic assignments. We compiled all publicly available genetic data for Polynoidae. The majority of sequences correspond to four markers: COX1, 16S, 18S, and 28S. Each sequence was linked to its original specimen, for which we retrieved metadata used to assess taxonomic identifications. More than 200 specimens from the collections of Muséum National d'Histoire Naturelle, Paris, collected during oceanographic campaigns over the past 20 years, are also included in the dataset and expand its species, geographic, and environmental coverage. Our dataset includes more than 4,000 specimens, each associated with metadata allowing evaluation of taxonomic identification (GPS coordinates, depth, photographs, etc.) and for which at least one genetic sequence is available. We performed molecular species delimitation based on mitochondrial markers COX1 and 16S using ASAP and mPTP approaches, recovering more than 600 molecular species from the currently sequenced Polynoidae specimens. A broad-scale phylogeny for the family was subsequently reconstructed using the delineated MOTUs as species-level units. Our dataset allows us to re-evaluate and test taxonomic hypotheses. Taxonomic species assignments can be compared with the molecular operational taxonomic units (MOTUs) inferred from our delimitation analyses. The associated metadata, particularly GPS coordinates and sampling depth, allow assessment of sampling biases within the family and comparison of genetic sampling with occurrence data from GBIF and OBIS. We observe a strong sampling bias toward the Northern Hemisphere, hydrothermal vents, and Antarctica. This study highlights under-sampled lineages and environments for genetic data and provides a new framework for revising the systematics and evolutionary history of Polynoidae.

B.1.42 | Microbiome variation and symbioses in the *Platynereis* species complex across Europe
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Host-microbe interactions are critical sources of phenotypic variation, playing key roles in the development, evolution, and physiology of many organisms. However, marine annelids are often underrepresented in these studies. Further, we lack a detailed understanding of how host-associated microbiomes vary across cryptic species complexes and wide geographic distances. To address both points, we profiled the microbiome of wild *Platynereis dumerilii*, a model marine annelid, and other members of the cryptic species complex across its European range. We found that *P. dumerilii* microbiomes differ greatly between sites, often being dominated by bacterial taxa such as *Endozoicomonas* and *Arcobacter* that are known symbionts in other marine hosts. We also find evidence of a core microbiome, with *Aliivibrio* being lowly abundant but highly prevalent in *P. dumerilii* across sites. By contrast, worms from a different molecular taxonomic unit classified as a *Nereis* sp. show microbiomes consistently dominated by *Arcobacter* across sites. Finally, *Nereis* sp. and *P. dumerilii* worms collected from the same site show distinct microbiomes, despite ostensibly sharing the same morphology, diet, and environment. These findings suggest that geography and host identity are both associated with microbiome composition. To characterize the function of these dominant microbial taxa, we cultured *Endozoicomonas* and generated a draft genome. We found several genes encoding nutrient transporters and secretion systems that suggest *Endozoicomonas* adopts a facultative symbiosis with wild *P. dumerilii*, and are currently pursuing this for further investigation. To date, this is the first documented symbiosis of this clade of symbiotic bacteria in a polychaete. Altogether, our findings reveal environmental and host genotypic associations with microbiome composition in the *Platynereis* species complex, as well as potentially novel symbioses in a tractable model for developmental, host-microbe, and evolutionary studies.

* Denotes a student contribution eligible for a prize.

Presenting author shown in **bold**.

B.1.43* | Multi-loci high-throughput genotyping of the *Platynereis dumerilii* species complex along European Coastlines

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A scalable multi-locus barcoding workflow for adaptive field sampling and integrative microbiome studies. Marine invertebrate biodiversity is often underestimated due to reliance on morphology-based taxonomy, which can fail to resolve cryptic diversity, as exemplified by the *Platynereis dumerilii* species complex, where multiple molecular operational taxonomic units (MOTUs) cannot be distinguished morphologically. Preliminary analyses indicate that these MOTUs are associated with distinct whole-body microbiome profiles, highlighting the need for accurate and scalable genotyping in ecological and functional studies. We present a high-throughput multi-locus barcoding workflow for rapid genotyping of field collected specimens. The protocol simultaneously targets four loci (16S, 18S, 28S and COI) using a two-step PCR strategy, in which multiplexed amplification is performed in a single reaction, followed by indexing for downstream sample demultiplexing. The resulting libraries are compatible with both Illumina and Oxford Nanopore sequencing platforms, enabling flexible deployment either in-field or in the laboratory. Using this approach, we generated multi-locus Illumina libraries for over 200 field-collected specimens, revealing extensive cryptic diversity within co-occurring populations. These results, together with parallel microbiome analyses, demonstrate that unresolved host identity can confound downstream ecological interpretation. Our workflow provides a scalable and cost-efficient alternative to traditional Sanger sequencing and supports rapid, high-resolution genotyping that can be easily adopted by non-specialist laboratories and field-based researchers. The approach is broadly applicable across diverse invertebrate taxa and can be extended to include metabarcoding, enabling integration of host genotyping with microbiome profiling. By enabling near real-time assessment of genetic diversity, this framework supports adaptive field sampling and integrative studies linking host genotype, microbiome composition and ecological context in polychaetes.

B.1.44 | A multiomic perspective on the invasive polychaete – *Hypania invalida* (Grube, 1860)

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Hypania invalida (Grube, 1860) represents a remarkable evolutionary case study, a member of the Ampharetidae family that has successfully transitioned from marine to brackish and freshwater habitats. This environmental plasticity is underpinned by a unique tolerance to diverse salinities, temperatures and depths. In this study, we generated an extensive suite of genomic resources, including a fragmented, albeit functionally complete, draft nuclear assembly, a comprehensive de novo transcriptome assembly, as well as the first fully annotated mitogenome for the Ampharetidae family. We performed repeat annotation of the nuclear genome and the transcriptome which revealed a sophisticated and expansive repetitive landscape for this species. The genomic resources generated here provide a foundation for future studies on adaptation, invasion biology, osmoregulation and annelid genome evolution. Furthermore, they offer new opportunities to investigate the molecular mechanisms underlying successful habitat transitions and biological invasions in aquatic ecosystems.

B.1.45 | Stuck for Life, Flexible Before That: Settlement, Sex, and Sessility in Marine Invertebrates

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¹Ocean Wolf, Nelson, New Zealand

Sessile marine invertebrates face a fundamental life-history challenge: once the adult is fixed to the substrate, the most important habitat decisions must be made earlier in their development. This poster explores the hypothesis that the evolution towards sessility shifts flexibility into the larval, settlement, juvenile, and reproductive stages. Using serpulid polychaetes as the central

* Denotes a student contribution eligible for a prize.

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example, I argue that settlement is not a single event but a staged process. In *Spirobranchus cariniferus*, observations suggest a sequence involving metamorphic competence, prolonged exploration, settlement competence, attachment, primary tube formation, and later physiological metamorphosis. This distinction between habitat transition and physiological metamorphosis reframes settlement as a decision-making process. Comparative examples from molluscs help position serpulids within a broader evolutionary context. Abalone represent a semi-sessile intermediate: larvae have a limited time to settle, but juveniles may still gain a “second chance” through secondary passive migration. Mussels show another intermediate condition, where post-settlement juveniles can relocate before final attachment. In oysters, barnacles, and serpulids, however, adult attachment becomes much more permanent, leading to increased selection for flexibility prior to irreversible settlement. The same constraint may also influence reproductive biology. Variable sex ratios, rare hermaphrodites, and potential alternating sexuality in serpulids and oysters suggest that reproductive flexibility may accompany permanent attachment. By linking abalone, mussels, oysters, barnacles, and serpulid polychaetes, this poster presents sessility not as the end of movement, but as an evolutionary shift in the timing and location of flexibility.

B.1.46 | Cellular senescence during the regeneration of *Syllis malaquini* (Annelida, Syllidae)

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Cellular senescence is a stable cell-cycle arrest triggered by diverse stressors and is widely recognized for its role in aging when senescent cells accumulate in tissues. However, transient senescence also serves important physiological functions in development, wound repair, and regeneration, partly through senescence-associated secretory signaling. Whether senescence contributes to regeneration in highly regenerative bilaterian invertebrates, however, remains poorly understood. We examined this question in the syllid annelid *Syllis malaquini*, which can regrow both its anterior end (including the nervous system) and posterior body. We found that senescent cells appear briefly during the early stages of blastema formation and are located in specific regions of the regenerating tissue. Removing these cells with the senolytic drugs dasatinib and quercetin reduced the senescence marker signal, shrank the blastema, and slowed the rebuilding of body structures and neural networks. Even when senolytics were applied after the blastema had formed, later tissue differentiation was disrupted. Together, these findings suggest that transient cellular senescence contributes to regenerative processes in annelids and supports regeneration of complex tissues, including the nervous system.

B.1.47 * | Towards the connectome of the 6-day-old *Platynereis dumerilii* larva

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Connectomics is a rapidly expanding field, driven in part by recent advances in volume electron microscopy (vEM). However, current efforts are primarily focused on well-established model organisms, particularly murine and human tissue connectomes. Thus, existing protocols are often difficult to adapt to less established organisms. In marine worms, factors such as a thick cuticle and the osmolarity of seawater can present major challenges during sample preparation. To address these limitations, we tested multiple preparation protocols using 6-day-old *Platynereis dumerilii* larvae and developed a workflow that can be further optimized for a broader diversity of marine worm species. We compared different fixation, contrasting, and embedding protocols with the aim of preserving the larvae as close to their native state as possible while maintaining intact ultrastructure and achieving high sample contrast and preservation quality. Critical steps required for obtaining high-quality samples were identified, as well as workflow stages that should be adapted depending on the intended downstream application. In addition, we incorporated X-ray tomography after embedding to assess sample quality, specifically structural damage and the amount of contrast. This substantially accelerated workflow evaluation and increased throughput, allowing us to screen large numbers of embedded samples and identify optimal candidates for sectioning and volume reconstruction. This work resulted in a vEM sample preparation

workflow optimized for *Platynereis dumerilii* larvae that can be adapted to other similar organisms. The connectome generated from this work will provide an important resource that can be integrated with existing datasets for this organism, further supporting its development as a well-established model system. In addition, this atlas will provide insights into the evolution and development of the nervous system in marine annelids. We additionally show the value of integrating X-ray tomography into the sample preparation pipeline as a complementary technique that supports and enhances EM-based workflows.

B.1.48 * | Genomic Underpinnings of Miniaturised Annelids

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Secondary evolution of extremely small body size has occurred multiple times across the annelid tree, with many extant meiofaunal (< 1 mm in size) lineages descending from macroscopic ancestors, making Annelida an ideal phylum to study the process of miniaturisation. These transitions involve dramatic morphological changes, which can include reduction and/or loss of parapodia, chaetae and segmentation, changes in circulatory, excretory and sensory systems, and loss of adult-associated morphology. Through comparative genomic analyses, we explore the underpinnings of miniaturisation; one of the most widespread evolutionary drivers across the animal tree of life, and one of the most common routes to drastic changes in body plan organisation. Meiofaunal annelids are difficult to study, owing to their small size, fragility, varied distribution, and challenging taxonomy. Genomic analyses face the additional hurdle of extracting high quality data from ultra-low DNA input specimens. However, by leveraging advances in genomic techniques and through optimisation of protocols for meiofaunal species, we are now finally able to generate chromosome-scale genomes for meiofauna. This allows for unprecedented comparisons of their genomic profiles. One well-studied miniaturised species, *Dimorphilus gyrocolatus* (Dinophilidae), displays a simplified segmental body plan of six segments, reduced body cavity, and no appendages. On a genomic level, *D. gyrocolatus* has a greatly reduced genome, fewer repeat elements, evidence of intron loss, but retention of a gene complement comparable to larger annelids. To compare, we generated a chromosome-level genome for two additional independently miniaturised annelids, *Diurodrilus subterraneus* (Diurodrilidae) and *Trochonerilla cf. mobilis* (Nerillidae). We are investigating their genomic landscapes, assessing genome size, Hox gene repertoire, differential gene expression, and structural elements. With their diverse morphology and independent miniaturisations, we aim to utilise these annelid genomes to answer fundamental questions about the genomic mechanisms of one of life's most ubiquitous evolutionary transitions.

B.1.49 | Biomechanical Modelling of *Arenicola marina* locomotion in silico

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Many modern annelids burrow through sediment. Worms, such as *Arenicola marina*, are thought to use their bodies as muscular hydrostats, allowing them to generate peristaltic waves that enable burrowing, a method widespread amongst soft-bodied taxa. While there is much interest in the burrowing process, especially in model organisms, practical considerations restrict the amount and type of data that can be collected directly from burrowing experiments. Consequently, there are limited experimental biomechanical analyses of the shape changes needed for muscular hydrostat burrowing. This is important because understanding the biomechanics of burrowing is key to elucidating how burrowing evolved. The origin of burrowing fundamentally reshaped the world at the end of the Ediacaran (~541 million years ago), creating the extensive environmental changes core to many suggested drivers of the 'Cambrian Explosion', a dramatic, rapid radiation of animal life that established most modern phyla. Most fossil evidence points to muscular hydrostat-driven locomotion as the best candidate for the first burrower's movement. Without a robust model of this locomotion system in modern animals, we cannot begin to test hypotheses about extinct organisms or the basic anatomical requirements needed for transitioning to sediment movement during the critical time period. To address this, we are using an integrated approach to create the first experimentally-supported simulations of hydrostatic burrowing. Here we present our initial findings: by combining experimental data with AI image processing, we characterise *A. marina* locomotion, and provide

* Denotes a student contribution eligible for a prize.

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direct evidence for the muscular hydrostatic system underpinning movement. We also demonstrate the classic and novel anatomical descriptive approaches that will enable the generation of a digital model organism. Finally, we outline a new software pipeline currently in development to produce burrowing simulations, which will allow us to test hypotheses about organism-sediment interactions and answer our key question: “How did the first burrowers move through sediments?”

B.1.50 * | Two hunters with different minds: Comparative brain anatomy of two species of predatory polychaetes

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Active hunting lifestyles are commonly associated with increased neural complexity; however, this relationship is not always as straightforward among polychaete annelids. This study compares the brain anatomy of two actively hunting species, *Nephtys hombergii* and *Alentia gelatinosa*, which occupy distinct habitats despite exhibiting comparable predatory behavior. *N. hombergii* inhabits sandy beaches, whereas *A. gelatinosa* is primarily associated with rocky shore environments. Both hunt with a jaw-equipped protrudable proboscis. The comparative analysis using Azan-stained histological serial sections and μ CT reveals differences in nervous system organization and complexity between the two species. The brain of *A. gelatinosa* exhibits a remarkably elaborate architecture characterized by the presence of mushroom bodies, highly developed visual organs, numerous distinct tracts within the neuropil, and well-developed glial cells. In contrast, the brain of *N. hombergii* lacks recognizable higher brain centers, neural tracts are only weakly developed, and visual organs are present in the form of small cup-shaped eyes. Despite these differences, both species possess three major neuronal cell types as well as giant neurons. These findings raise important questions regarding the evolutionary drivers of neural complexity in polychaetes. The highly elaborate brain organization observed in *A. gelatinosa* and other members of Polynoidae is remarkable when compared with other actively hunting annelids that possess less complex nervous systems. The results therefore suggest that factors beyond predatory behavior alone, such as habitat complexity, reproduction, sensory integration, or phylogenetic constraints, may have contributed to the evolution of advanced neural architectures in Polynoidae. This study highlights the need for broader comparative investigations into the relationship between ecology, reproduction, hunting strategies, and nervous system evolution within Polychaeta.

B.1.51 | Occurrence of unusual fauveliopsids in coralline environments from the Southern Gulf of Mexico

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The fauveliopsids are widely distributed in bathyal or abyssal zones, usually in low abundance, but their presence in shallow waters is very unusual. So, it was amazing to discover two specimens of this family, each one from a different species of the genus *Fauveliopsis* at 0.5–1 m depth in a coralline island in the Southern Gulf of Mexico. In addition, their morphology exhibits some differences with those characterizing the family. As all members of the genus *Fauveliopsis*, the examined specimens only have capillaries and thicker and thinner acicular chaetae in both rami along their body, but unusually, these new species lack interramal papillae, and one of them has a noticeable mid-dorsal groove. We compare their affinities with other polychaete families having thick acicular spines in all parapodia, as some cirratulids (genus *Chaetocirratulus*), but we did not find evidences of any dorsal tentacles or branchiae, confirming that they do not belong to Cirratulidae. On the other hand, *Mucibregma spinosa*, with spines in all parapodia, showed greater affinity to fauveliopsids, but because the absence of interramal papillae, it is now considered as a scalibregmatid, even if they remarkably lack the furcate chaetae, diagnostic for this family. No molecular studies can help elucidate further their recognition as fauveliopsids (because fixation in the field was made with formalin) but it is clear that the examined specimens do belong to this family also because they are clearly distinct from the cirratulids, scalibregmatids or other close families.

B.2.52 | Revision of *Euphionella* Monro, 1936 and *Dilepidonotus* Hartman, 1967 (Polychaeta, Polynoidae, Lepidonotinae)

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The subantarctic genera *Euphionella* Monro, 1936 and *Dilepidonotus* Hartman, 1967 are characterized by the presence of pseudelytra and smooth neurochaetae. These genera are separated by the presence of parapodial branchial filaments in *Euphionella*, which are missing in *Dilepidonotus*. Parapodial branchial filaments are rare among lepidonotin polynoid polychaetes. After the study of most type specimens and additional material, we conclude that *Euphionella* and *Dilepidonotus* are synonyms, and only two species are regarded as valid: *E. lobulata* (Seidler, 1921) which includes *E. robusta* Wesenberg-Lund, 1962, and *E. patagonica* Monro, 1936 which includes *Dilepidonotus falklandicus* Hartman, 1967, *Lepidonotus brasiliensis laevis* Rullier & Amoureux, 1970, and *E. besnardi* Amaral & Nonato, 1982. Redescriptions and illustrations for all included species are provided, and a key to identifying *Euphionella* species is also included.

B.2.53 * | Life on the back end: a new genus of epibiotic serpulids from deep-sea wood-fall chitons

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Recently collected specimens of the chiton *Fereirarella populi* Sigwart, 2026 from a wood-fall habitat in the Izu-Ogasawara Trench (5506 m) hosted multiple tubes of an unidentified epibiotic serpulid on their posterior (tail) valves. Comparable associations have been reported from other polyplacophorans but have not been investigated using an integrative approach. Micro-computed tomography (microCT) enabled non-destructive visualization of tube occupancy, allowing assessment of whether tubes on a given host were inhabited. Morphological analyses, including scanning electron microscopy, revealed a distinct combination of diagnostic characters distinguishing this taxon. To resolve its phylogenetic position, we generated a complete mitochondrial genome and compared it with other available serpulid mitogenomes, revealing a novel gene arrangement and expanding the known diversity of mitochondrial architectures in the family. In addition, a concatenated dataset of four markers (cytB, H3, 18S, 28S) with expanded taxon sampling was used to refine its placement within Serpulidae. Both approaches consistently recover this lineage within Filigraninae as a distinct and previously unrecognized genus. Notably, it clusters with species associated with chemosynthetic or otherwise reducing environments, suggesting a potential ecological signal within this clade. These results support the establishment of a new genus of serpulid worms associated with deep-sea reducing habitats.

B.2.54 * | Long hidden in tubes: First Steps Towards Resolving the *Filigrana/Salmacina* Complex

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The genus *Salmacina* Claparède, 1870 has long been associated with taxonomic uncertainty and is frequently discussed as part of the *Filigrana-Salmacina* complex. Although the presence or absence of an operculum has traditionally been used to distinguish *Salmacina* from *Filigrana*, reports of both operculate and non-operculate individuals within single populations challenge the reliability of this character. Despite these uncertainties, the taxonomy of this group has remained largely unresolved, and comprehensive molecular investigations are still lacking. Here we present an integrative taxonomic framework for the study of *Salmacina*, combining detailed morphological analyses with genomic approaches. Recently, we described *Salmacina stellaebayensis* Cremer et al., 2026 based on extensive morphological characterization using scanning electron microscopy (SEM), complemented by high-throughput genome skimming. This approach yielded the first mitochondrial genome for the *Filigrana-Salmacina* complex, providing an important genomic resource for future phylogenetic investigations. Building upon

* Denotes a student contribution eligible for a prize.

Presenting author shown in **bold**.

this foundation, ongoing analyses of additional populations and historical material are revealing unexpected diversity within the genus and suggest that multiple undescribed or misidentified lineages may occur across its reported distribution range. Our results demonstrate that integrative taxonomy is essential for resolving species boundaries in this morphologically challenging group and provide a framework for reassessing the diversity and evolutionary history of *Salmacina*.

B.2.55 | Splitting more: cryptic diversity within *Scolecopsis squamata* species complex (Annelida: Spionidae) reveals a new species of *Scolecopsis* from the Black Sea

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The genus *Scolecopsis* is one of the most diverse and problematic genera within the family Spionidae. Its members are common and usually abundant component of sandy littoral communities worldwide, playing an essential role in the food web dynamics and sediment ecology. *Scolecopsis squamata* (O.F. Müller, 1806) is the first species described (nominotypical) in the genus. The poor original description and the absence of type material led to its erroneous application to populations from different parts of the world, with several distinct local species inadvertently incorporated into this taxon. Recent accumulation of morphological and molecular data has enabled removal of most of these species from synonymy with *S. squamata*. In a previous study we have shown that in the Black Sea under the name '*Scolecopsis squamata*' there are two genetically distinct species, but none of them is identical to the North Atlantic *Scolecopsis squamata*. While one of them was identified as *S. mesnili* (Bellan & Lagardère, 1971), for the second it was plausible to assume that it belongs to *S. cirratulus* (Delle Chiaje, 1829), a species originally described from the Mediterranean Sea and later synonymized with *S. squamata*. To ascertain the identity of *Scolecopsis* from the Black Sea we have sampled close to the type locality of *S. cirratulus* (littoral sandy sediments from Licola, north of Naples). Molecular analysis of the mitochondrial COI marker revealed that the Black Sea species is sufficiently divergent from the Mediterranean *S. cirratulus* to warrant description as a new species, a result further supported by species delimitation analyses. Therefore, the aim of the study is to provide a comprehensive morphological and molecular characterization of both species, with the designation of a neotype for *S. cirratulus* and formal description of the new species from the Black Sea.

B.2.56 | What's in a name? Gender representation in polychaete eponyms

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Scientific names that refer to people are called eponyms and are chosen by authors to honour a person, real or fictional. Recently, there has been a growing interest in eponyms; historical and current gender representation in scientific naming has been considered in social and cultural contexts for diverse taxonomic groups. Among invertebrates, Vendetti (2022) examined gender patterns in eponyms for molluscan fauna, Poulin et al. (2022) analyzed recent naming trends for parasitic helminths, and De Grave et al. (2025) and Montana et al. (2025) studied eponyms in decapods and spiders, respectively. These and other studies show that the vast majority of eponyms for species across diverse taxonomic groups honour men. In our study of polychaete eponyms we expected that while gender bias was very likely it would not be as strong as observed in other taxonomic groups, because women have historically held a relatively high proportion of leadership roles in polychaete taxonomy. In our analysis of polychaete eponyms, we began by focusing on two large groups, Terebellidae (~ 750 species) and Polynoidae (~ 900 species). As expected, there is a significant gender bias in eponyms for both the Terebellidae and Polynoidae; however, with 27.2% female eponyms in the Terebellidae and 23.6% female eponyms in the Polynoidae, the overall gender bias for these polychaete groups since the mid-1800s is significantly lower than that observed for other invertebrate taxonomic groups. Over the past ~ 40 years, an increase in multi-author species descriptions, including increasing numbers of female co-authors, is evident for both Terebellidae and Polynoidae; there is also a narrowing of the gap between male and female eponyms over the past ~20 years in both groups. The patterns of naming polychaete species in honour of people likely reflects historical and strengthening female representation in the field of polychaete taxonomy.

B.2.57 | Deep-sea polynoid scale worms from the western Pacific: hidden diversity, phylogenetic instability, and morphological character evolution

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Deep-sea ecosystems of the western Pacific, including hydrothermal vents, cold seeps, seamounts, trenches and back-arc basins, harbour a remarkable diversity of polynoid scale worms, yet their taxonomy, phylogenetic relationships and evolutionary history remain insufficiently understood. Over the past several years, we have investigated deep-sea polynoids collected mainly by the ROV FaXian from the Manus Back-Arc Basin, the South China Sea and tropical western Pacific seamounts. By integrating detailed morphological observations, scanning electron microscopy, DNA barcoding and genome-skimming data, our studies have revealed multiple undescribed species and clarified the systematic positions of several poorly known lineages. In chemosynthesis-based ecosystems, newly described species of *Levensteiniella* and *Branchinotogluma* from hydrothermal vents and cold seeps have improved our understanding of sexual dimorphism, branchial evolution and the biogeographic connections of vent and seep polynoids. Further analyses showed that the traditional concept of *Branchinotogluma* is not monophyletic, indicating that several diagnostic characters used in vent polynoid taxonomy require re-evaluation. In non-chemosynthetic deep-sea habitats, our studies of seamount-associated taxa, including *Admetella* and *Alentiana*, revealed unexpectedly high species diversity and demonstrated that some classical subfamilial characters, such as the insertion of lateral antennae and deeply incised neuropodia, may represent plesiomorphic or convergently evolved conditions rather than reliable indicators of close relationship. Recent work on *Macellicephaloides* from the South China Sea also suggests that the evolutionary history of Macellicephalinae is more complex than previously recognized, with possible links among deep-sea, chemosynthetic and anchialine cave lineages. Together, these findings highlight the western Pacific as a key region for understanding deep-sea polynoid diversification. They also emphasize the necessity of integrative taxonomy combining morphology, molecular phylogenetics and biogeographic evidence for revising the classification of Polynoidae and reconstructing character evolution in deep-sea annelids.

B.2.58 | Molecular analyses detect depth-structured diversity in *Phylo norvegica* (Annelida, Orbiniidae) in Norwegian waters

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Phylo Kinberg, 1866 is a genus of polychaetes of the family Orbiniidae Hartman, 1942 characterized by the presence of modified chaetae associated with glands in posterior thoracic neuropodia, a unique character in the family. Most species also bear a ventral fringe of subpodal and stomach papillae. Three species have been reported from Norway: *Phylo norvegica* (M. Sars in G. O. Sars, 1872), *Phylo grubei* (McIntosh, 1910) and *Phylo kupfferi* (Ehlers, 1874), all occurring across a wide depth range. This study investigates morphological and genetic divergence among populations of *P. norvegica* along the Norwegian coast. *Phylo norvegica* was originally described from 20–220 m in Oslofjord and Lofoten archipelago and later reported across the North Atlantic and Arctic Ocean, at depths reaching 2,900 m. Our molecular analyses based on mitochondrial COI and nuclear ITS2 showed that *P. norvegica* is a species complex comprising at least two genetic lineages in the Norwegian waters. One lineage occurs at depths above 700 m (shallow clade), whilst the other below 600 m (deep clade). Based on the depth of the type locality, the shallow clade likely corresponds to *P. norvegica* sensu stricto, while the deep clade may represent an undescribed species. Ongoing work integrating morphological data, including both type and newly collected non-type material of the species, will further assess these hypotheses.

B.2.59 | First integrative approach to *Theodisca laevigata* (Grube, 1855) complex with the reinstatement of *Theodisca anserina*

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Since the 20th century, several European annelid species have been treated as cosmopolitan, often recorded from geographically distant localities, including members of the family Orbiniidae (Annelida, Sedentaria). *Theodisca* (*Theodisca*) *laevigata* (Grube, 1855) is one of the most problematic species within *Theodisca* Müller, 1858, and probably within Orbiniidae as a whole. The species was originally described from Naples, Mediterranean Sea and assigned to *Aricia* Quatrefages, 1866. Later, Eisig (1914) transferred *T. (T.) laevigata* to *Naineris* and synonymized several species from different localities outside the Mediterranean under this name. Since then, *T. (T.) laevigata* has been regarded as cosmopolitan in the literature. Recently, Álvarez et al. (2025), using an integrative taxonomic approach, revised *Naineris*, transferred most of its species to a reinstated *Theodisca*, and demonstrated that *T. (T.) laevigata* represents a species complex. Here, based on COI, 16S, and 28S sequences from specimens collected in different Mediterranean localities, we recovered three well-supported clades within this complex, delimited as three species in ASAP and mPTP: one from the Black Sea, and two from the Mediterranean Sea. We examined the syntypes of *T. (T.) laevigata* and found that they comprise a mixture of two species, which matches both Mediterranean clades. Based on these results, we decided to redescribe *T. (T.) laevigata*, designate a lectotype, and reinstate *Theodisca* (*Theodisca*) *anserina* (Claparède, 1864). *Theodisca* (*T. (T.) laevigata* sensu stricto is distinguished by the presence of subuluncini and large uncini in the transverse rows of thoracic neuropodia, whereas *T. (T.) anserina* possesses only subuluncini in these rows. Our results reinforce the importance of integrative taxonomy as a powerful tool for resolving the identity of marine taxa. Additionally, we emphasize that records of *T. (T.) laevigata* from other regions worldwide should be re-evaluated to reassess its presumed cosmopolitan distribution.

B.2.60 | Demystifying the *Leitoscoloplos robustus* and *Leitoscoloplos fragilis* complexes (Annelida: Orbiniidae) in the Southwestern Atlantic: an integrative taxonomic approach

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Leitoscoloplos Day, 1977 is a genus of Orbiniidae, characterized by a pointed prostomium, only crenulated capillary chaetae on the thoracic neuropodia, and abdominal neuropodia supported by one or few embedded aciculae. In Brazil, only three species have been reported from shallow waters: *Leitoscoloplos robustus* (Verrill, 1873) and *Leitoscoloplos fragilis* (Verrill, 1873), both originally described from the western North Atlantic, and *Leitoscoloplos kerguelensis* (McIntosh, 1885) from the Indian Ocean. This study reviews records of *Leitoscoloplos* in the Southwestern Atlantic using an integrative taxonomic approach to assess the presence of previously reported species in the region. Fragments of mitochondrial COI and 16S, and nuclear 28S were amplified from 15 specimens from south and southwestern Brazil and compared with publicly available sequences. Our specimens collected along the Brazilian coast from Rio de Janeiro to Santa Catarina previously identified as *L. robustus* or *L. fragilis* formed a separate well supported clade, here named *Leitoscoloplos* sp. 1. Analysis of COI barcodes from BOLD showed that the new species is closely affiliated with *L. fragilis* (Maryland–Virginia, USA), *L. robustus* (Maine–Florida, USA), and three other unidentified species. *Leitoscoloplos* sp. 1 belongs to the group of three species described by Blake (2017), characterized by branchiae arising from transitional segments between the thorax and the abdomen. However, it differs from the other species of the group by having between 16 and 19 thoracic chaetigers, with branchiae starting between chaetigers 14 and 19. Our results provide no evidence for the presence of *L. robustus* and *L. fragilis* in the southeastern Atlantic. All previous records of these two species belong to *Leitoscoloplos* sp. 1. This study corroborates the view that integrative taxonomy is a fundamental tool for species identification and the study of widely distributed taxa and improves our understanding on the Brazilian orbiniid fauna.

B.2.61 | New species of *Prionospio* (Annelida: Spionidae) from Guanabara Bay, Brazil (Southeast Atlantic Ocean)

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Prionospio includes about 125 valid species, predominantly inhabiting sandy and muddy sediments in coastal and estuarine environments. Although previously thought to include widely distributed cosmopolitan species, recent integrative analyses combining morphology and molecular data reveal that many species of *Prionospio* represent complexes of regionally restricted taxa. Currently, 24 species have been registered along the Brazilian coast and five from Guanabara Bay (Rio de Janeiro), which were originally described from the North Atlantic or Pacific Oceans: *Prionospio cirrifer* Wirén, 1883, *P. heterobranchia* Moore, 1907, *P. malmgreni* Claparède, 1868, *P. multibranchiata* Berkeley, 1927 and *P. steenstrupi* Malmgren, 1867. In this study, we did not recover any of these species and describe a new species of *Prionospio*. A total of 51 individuals were collected from unconsolidated substrates between 3.8 and 32.2 meters across four stations. Thirty specimens were examined morphologically, while additional material was used for molecular analyses. The new species is distinguished by a unique combination of branchial morphology, chaetal characters and pigmentation patterns. Molecular data support its separation from congeners and reinforce the need for reassessment of historical records of *Prionospio* in the southwestern Atlantic.

B.2.62 | An undescribed genus and two undescribed species of Acrocirridae from the western Pacific

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Marine biodiversity remains vastly understudied, and deep-sea habitats are likely to harbor many undescribed annelid lineages. During an JAMSTEC–Ocean Census expedition in the western Pacific, acrocirrid worms were collected off Japan using the manned vehicle Shinkai 6500 from a methane seep site in Ryuyo Canyon, Nankai Trough and a seamount habitat on Nichiyo Seamount. From these samples, we discovered two undescribed acrocirrid species, including one belonging to an undescribed genus from the seep environment and one in the genus *Flabelligena* from the seamount. The species requiring a new genus is characterized by a rounded, bulbous prostomium, four pairs of branchiae, reduced parapodia, spinous capillary notochaetae, and compound neurochaetae. Its golden-yellow head in life makes it morphologically distinctive among all known acrocirrid genera. Molecular phylogenetic analyses based on five genes indicate that the undescribed genus is distinct from the *Acrocirrus*–*Macrochaeta* clade, whereas the undescribed seamount *Flabelligena* species is closely related to another western Pacific congener. These findings expand the known diversity and ecological range of Acrocirridae and suggest that under-explored chemosynthetic and seamount environments contain hidden lineages that are important for understanding the evolutionary ecology of this small but morphologically diverse annelid family.

B.3.63 | Magelonidae Cunningham & Ramage, 1888 – an update on key morphological characters

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The Magelonidae are a relatively small family of polychaete annelids commonly referred to as shovel head worms, a name derived from their characteristically dorsoventrally flattened prostomia. The family currently comprises 83 described species assigned to two genera, *Magelona* F. Müller, 1858 and *Maea* Johnston, 1865. A comprehensive global identification key for the Magelonidae—the first produced in more than five decades—was recently published (Mortimer et al., 2026). The work included a dichotomous key structured by marine realms and a complementary pictorial key organised into nine putative morphological groupings. An updated assessment of diagnostic morphological characters for the family, alongside an overview of the current state of knowledge regarding magelonid taxonomy, morphology, and natural history is provided.

B.3.64 * | Revision of the family Phascolosomatidae Stephen & Edmonds, 1972 (Sipuncula)
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The family Phascolosomatidae (Sipuncula) presents significant taxonomic challenges due to its apparent morphological simplicity, which historically led to the mass synonymization of species and the postulation of cosmopolitan taxa. However, recent studies suggest that many of these records actually correspond to pseudo-cryptic species complexes. This research aims to conduct a comprehensive systematic revision of the genera *Apionsoma* and *Phascolosoma*, evaluating the taxonomic status of 64 nominal species. The methodology integrates the analysis of type and non-type material from major global biological collections (e.g., NMNH, MCZ, MNHN, NHMUK). Stereoscopic and compound microscopes are used to standardize external diagnostic characters, such as the ultrastructure of hooks and papillae, along with detailed dissections of internal anatomy. These data are complemented by phylogenetic analyses using the COI molecular marker to delimit lineages and assess the monophyly of genera and subgenera. To date, the list of valid species has been consolidated, and the examination of specimens on loan and through research stays at international museums has begun. Preliminary results will allow for the re-evaluation of synonymies, the recovery of valid names, and the generation of updated identification keys worldwide. A preliminary revision of the genus *Apionsoma* Sluiter, 1902 has shown that the subgenera could change their status and be considered separate genera. In case of the genus *Phascolosoma* Leuckart, 1828 special attention has been taken with the characterization of the hooks. This work not only clarifies the systematics of the group but also contributes to a realistic estimate of the biodiversity of these unsegmented coelomate worms, which are fundamental in bioturbation and bioerosion processes in marine ecosystems.

B.3.65 * | A first assessment of polychaete diversity in the North Adriatic Sea using DNA barcoding
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Annelids are a key component of marine benthic ecosystems, although gaps remain in their taxonomic resolution, particularly in combining morphological and genetic approaches. Polychaetes are highly diverse and abundant in marine ecosystems, yet they have historically received less attention than other ecologically relevant taxa. Traditional morphology-based taxonomy can be challenging and may lead to inconsistencies among taxonomists, especially in groups that are difficult to identify, often limiting reliable identification to higher taxonomic levels. This study presents a first assessment of DNA barcoding applied to selected polychaete species from the North Adriatic Sea, focusing on a sublittoral Long Term Ecological Research (LTER) monitoring station within the Marine Protected Area of Miramare in the Gulf of Trieste (Italy). The main objectives were to evaluate the effectiveness of DNA barcoding for species identification and to contribute to the enrichment of reference databases with barcode sequences from Northern Adriatic polychaetes. Macrofaunal invertebrates were sampled in July 2019 and identified to the lowest possible taxonomic level based on morphological traits. Molecular analyses were conducted using the mitochondrial cytochrome c oxidase subunit I (COI) marker, obtaining barcode sequences for 11 species. Preliminary results showed matches with sequences available in public databases, such as the NCBI nucleotide database and the Barcode of Life Data System (BOLD), including similarities with specimens from other geographic regions (e.g., southern Italy). These findings highlight the DNA barcoding potential in polychaete identification, while also indicating some limitations, including partial reference coverage and technical challenges in laboratory procedures. Further analyses are planned to refine and improve protocols and to increase the number of reference sequences focusing on species not yet genetically characterised, aiming for an updated, comprehensive and integrated taxonomy framework.

B.3.66 | Molecular phylogenetic hypothesis of *Leodice* Lamarck, 1818 (Annelida: Eunicidae)

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Leodice Lamarck, 1818, was revalidated by Zanol et al. (2014) to represent a clade that includes the type species, *Leodice antennata* Savigny in Lamarck, 1818. Members of this genus are diverse and widely distributed, occurring in all oceans, predominantly in warm waters, often associated with hard substrates such as coral reefs and calcareous algae. Currently, *Leodice* includes 40 valid species, characterized by at least one of the following exclusive characters: regularly articulated prostomial appendages, tridentate compound falcigers, light bidentate or tridentate subacicular hooks, and black dots in median and posterior parapodia. However, several species that exhibit these features are still classified within the genus *Eunice* Cuvier, 1817. To understand the evolutionary relationships among species with *Leodice* exclusive features, we present a molecular phylogenetic hypothesis of *Leodice* using a combined dataset of three markers (COI, 16S, and 18S rDNA) and 52 ingroup terminals representing 42 species. Topologies were reconstructed using maximum likelihood and Bayesian Inference. Additionally, 23 morphological characters were optimized into the tree to understand the evolution along the history of this group. Our analyses recovered *Leodice* as a monophyletic group containing all species that exhibit the exclusive features of the genus, with maximum support. This clade contains two main clades. Clade 1 comprises all species with light bidentate and tridentate subacicular hooks, and Clade 2 includes all species with regularly articulated prostomial appendages and dark bidentate subacicular hooks. Based on molecular results and literature review, we propose 94 new combinations within *Leodice* for species previously classified as *Eunice*. Among these, 47 species are identified as *Leodice* by possessing light tridentate subacicular hooks, 37 by possessing light bidentate hooks, and 10 species by regularly articulated prostomial appendages and dark bidentate subacicular hooks. Our results reinforce the importance of integrating data types for taxonomic revisions.

B.3.67 | Digital collections of annelids: defining priorities for the digitalization of different taxa

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The online availability of biodiversity data has become a global priority for natural history institutions and was formalized as Target 21 of the Convention on Biological Diversity (COP 15), to be achieved by 2030. Although widely recognized as essential for preserving and democratizing access to information associated with biological collections, digitization still faces significant challenges. It is a slow and costly process, requiring standardization and optimization aligned with institutional goals and the needs of the scientific community. For taxonomic studies, analyses of different taxa may require the observation of a diverse set of features present in different regions, thus requiring the production of different digital objects and the need for digitization protocols adapted to each taxon. This approach avoids both insufficiently documented digital objects and excessive data production, which can waste time and resources. This study examines the user profile of annelid collections and proposes strategies for the efficient digitization of polychaetes — three-dimensional organisms preserved in liquid media and characterized by wide variation in size and collection typologies. A case study at the Annelida Collection of the National Museum (MN/UFRJ), using a sample of five families: Chaetopteridae, Eunicidae, Nereididae, Sabellidae, and Spionidae. The approach combined bibliographic research with analysis of curation workflows, institutional goals, and available resources. Results indicate that the set of digital objects differs for each taxonomic level and taxon, demonstrating the need for taxon-specific mapping according to the desired resolution. At the family level, stereomicroscopy is sufficient, whereas genus-level identification requires microscopy and dissections. For example, identification of some Eunicidae genera depends on mandible morphology, while Nereididae emphasizes paragnaths. For teams lacking taxonomic expertise, prior standardization enables efficient data capture, reducing time and resource expenditure while meeting collection user needs.

B.3.68 | Species delimitation of *Oenone fulgida* (Lamarck, 1818) (Oeononidae: Eunicida)

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Oenone Lamarck, 1818 is the type genus of the family Oeononidae. These polychaetes are characterized by three antennae and two pairs of ocelli on prostomium, prionognath maxillary apparatus, foliaceous parapodial dorsal cirri, geniculate chaetae and subacicular hook. Over the years, ten species from different localities were synonymized with *Oenone fulgida* Lamarck, 1818, type species of the genus. Although researchers have argued that the wide distribution and morphological variation could indicate the existence of a species complex, *Oenone fulgida* was the only valid species of the genus until the revalidation of *Oenone diphyllidia* Schmarida, 1861 in 2009 and the description of *Oenone ventrioculata* Zanol & Ruta, 2015. We used an integrative approach to assess the species diversity within *Oenone fulgida* complex. The morphology of specimens of *Oenone* from the Lizard Islands (Australia), Hawaii (USA), Pacific Islands and Brazil were analyzed. Cytochrome oxidase 1 (COI) sequences generated here and available in GenBank were aligned using ClustalW implemented in MEGA. Species molecular delimitation were evaluated using: Automatic Barcode Gap Discovery (ABGD), Assemble Species by Automatic Partitioning (ASAP) and General Mixed Yule Coalescent Model (GMYC) based on an ultrametric phylogenetic tree generated in BEAST using default settings. The consensus of morphology and molecular data indicated the existence of at least three species in *Oenone*. The morphospecies differ mainly in the maxillary apparatus and hook morphology. Among the analyzed material, *O. ventrioculata* is restricted to the Lizard Islands, Australia. *Oenone telura* Chamberlin, 1919 is a valid species, and is distributed along the Pacific islands (Lizard Islands, Hawaii, Mariana Islands, Marshall Islands and Fiji). There is also a possible new *Oenone* species to science from Brazil's rocky shores. GenBank sequences also suggest the presence of other species in Lebanon, India, Hawaii (USA) and the Pacific coast of Mexico.

B.3.69 | New species of *Acoetes* and *Euarche* (Aphroditiformia: Acoetidae) from Brazilian coast

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The genus *Acoetes* was established based on a specimen from Martinique (West Indies) in *Classification des Annélides et description de celles qui habitent les côtes de la France*. Similarities with *Polyodontes* were noted early on, although both differ in subtle morphological traits, particularly in neurochaetae. Kinberg later proposed the genera *Eupompe* and *Panthalis*, and subsequent species formerly attributed to *Acoetes* were reassigned to these genera or to *Polyodontes*. Pettibone revised the group, recognizing *Eupompe* as a junior synonym of *Acoetes* and synonymizing several species of *Polyodontes* and *Panthalis* under *Acoetes*, including *Acoetes bicolor* and *Acoetes mortenseni*. Since this revision, no new species of *Acoetes* have been described, and the genus currently includes 12 valid species. The genus *Euarche*, established from material in the Caribbean and Gulf of Mexico, has *Euarche tubifex* as its type species. It is characterized by a prostomium with pigmented eyes lacking lenses and ommatophores. Pettibone examined the Gulf of Mexico holotype but treated specimens from different regions as a single species, resulting in taxonomic uncertainties. *Euarche* remains poorly studied, with only five recognized species to date, from 1887 to the most recent, *Euarche cristata*. This study identified six new species through a review of Brazilian Annelida collections. Specimens were fixed in 4% formalin and preserved in 70% or 100% ethanol. Analyses were conducted using stereomicroscopy and optical microscopy, with photographic and illustrative documentation. Material is deposited in collections in Rio de Janeiro and São Paulo. All species exhibited ventral papillae, a feature not reported for other Acoetidae. Two new records were documented for Espírito Santo and Pernambuco, and the bathymetric range was expanded to 0–2,013 m, extending the previous limit of 1,500 m.

B.3.70 | Systematics of gastropod shell-dwelling maldanids from offshore seamounts
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Offshore seamounts are typically exposed to strong currents, particularly at their summits, where fine sediments are rarely retained and substrates are dominated by exposed rocks or coarse mineral grains. These conditions present a challenging environment for many infaunal and epifaunal benthic invertebrates. Annelids in the family Maldanidae are distributed across a broad bathymetric range and typically dwell in tubes that they construct in soft sediments. Here, we discovered unusual maldanids that inhabited empty shells of small, coiled gastropods belonging to four families (Newtoniellidae, Triphoridae, Raphitomidae, Mangeliidae), from coarse sediments on rocky substrates between 500–600 m deep on offshore seamounts around Japan. We carried out detailed morphological observations using light microscopy and scanning electron microscopy, focusing particularly on chaetal structures, in combination with molecular phylogenetic analyses. Our results revealed clear distinctness among specimens from different seamounts in terms of segment number and chaetal morphology. Genetic analyses supported the presence of at least three distinct, undescribed species of the genus *Boguella*, with their placement in Maldanidae supported by our phylogenetic reconstruction. Until now, *Boguella* was considered a monotypic genus known only from the Bermuda Rise in the North Atlantic. Our findings therefore provide the first evidence for a previously unrecognized diversity of this genus in Pacific seamount ecosystems. These results provide important insights into the diversity and adaptive evolution of benthic invertebrates in offshore seamount ecosystems.

B.3.71 | Genetic differentiation between *Spirobranchus akitsushima* and *Spirobranchus* sp. 6 based on genome-wide SNPs
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Spirobranchus kraussii is a species of Serpulidae inhabiting the intertidal zone. It attaches to rocks and constructs calcareous tubes characterized by flap-like projections at their openings. Although this species was once considered cosmopolitan, the South African lineage from the type locality was shown to be genetically highly distinct from congeners in other regions. Only the South African lineage should be recognized as *S. kraussii*. The lineage found at Manazuru on Honshu Island, central Japan, was regarded as *Spirobranchus* sp. 1. Later, in addition to *Spirobranchus* sp. 1, *Spirobranchus* sp. 5 and sp. 6 were recorded from Japan, specifically from Okinawa Island. While *Spirobranchus* sp. 5 was clearly distinct from the other sequenced lineages, the divergence between *Spirobranchus* sp. 1 and sp. 6 was small compared with that observed among other lineages within this species complex. It was approximately 2% in p-distance of mitochondrial cytb gene sequences, and the two were not clearly distinguishable in the nuclear ITS2 region. Subsequently, *Spirobranchus* sp. 1 was described as a new species, *Spirobranchus akitsushima*. In the present study, we further examined the genetic differentiation between *S. akitsushima* and *Spirobranchus* sp. 6 using genome-wide single-nucleotide polymorphisms (SNPs) obtained through MIG-seq. MIG-seq is an effective PCR-based method for generating SNP data using multiplexed inter-simple sequence repeat (ISSR) primers. In the presentation, we will present the results of the MIG-seq analysis, including new records of *Spirobranchus* sp. 6.

B.3.72 * | Bathymetric distribution and genetic boundaries of Nephtyidae off northeastern Japan
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In the deep sea, the habitat depth of species primarily depends on bathymetrical changes of physicochemical conditions, such as water temperature and pressure. Investigating the boundaries of bathymetric distribution of species and the barrier causing intraspecific genetic differentiation is therefore crucial for understanding how deep-sea species diversity is generated and maintained. Recent genetic studies have revealed the presence of morphologically indistinguishable species in annelids. The family Nephtyidae Grube, 1850 currently includes about 140 species described within four or five genera. Nephtyids burrow into sandy substrates and are highly active, inhabiting a wide range of environments from the intertidal to hadal zones. In this study, we investigate the bathymetric distribution of Nephtyidae off the Pacific coast of Tohoku, northeastern Japan. This region was chosen as the study site because the water depth increases sharply toward the Japan Trench, allowing us to test the influence of depth gradients on both bathymetric distribution and intraspecific genetic differentiation while minimizing the effects of geographic distance on genetic differentiation. We conducted a phylogenetic analysis of Nephtyidae based on mitochondrial COIII gene sequences using specimens collected at depths of approximately 30–3,000 m. Preliminary analysis revealed 12 genetically distinct lineages. While most lineages were found in limited depth ranges, our results also suggested that some lineages inhabit broader depth ranges spanning both the upper and lower bathyal zones. We will also present results on the bathymetric distribution of each species and intraspecific genetic differentiation across water depths.

B.3.73 | *Lagis depende* a new member of the Pectinariidae
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The family Pectinariidae Quatrefages, 1866 comprises more than 70 nominal species distributed across five genera. Six species have been reported in the Northeast Atlantic Ocean: *Amphictene auricoma* (O.F. Müller, 1776), *Cistenides granulata* (Linnaeus, 1767), *Cistenides hyperborea* Malmgren, 1866, *Lagis koreni* Malmgren, 1866, *Pectinaria belgica* (Pallas, 1766) and *Petta pusilla* Malmgren, 1866. Molecular evidence has suggested that the specimens identified as *L. koreni* represent a complex of at least two pseudo-cryptic species. Although these lineages have been genetically delimited before, it remains unclear which corresponds to the nominal species, and the additional lineage has not yet been formally described. In this study, specimens from Norway, Sweden, Spain, and Portugal, previously identified as *Lagis koreni* and *Amphictene auricoma*, were genetically and morphologically studied. Maximum likelihood phylogenetic analyses of mitochondrial markers, cytochrome c oxidase subunit I (COI) and 16S rRNA, were carried out using maximum likelihood methods. Furthermore, specimens were morphologically examined using light microscopy and scanning electron microscopy. Species delimitation analyses confirmed the presence of two distinct and well-supported evolutionary lineages within material identified as *Lagis koreni*. One lineage has been described as *Lagis depende* Barroso et al. 2026, which can be distinguished from *L. koreni* by the shape and number of the marginal crenulations of the anal flap. Additionally, the variation in the morphology of scaphal hooks has been studied in these and other pectinariid species, defining three types of hooks according to their curvature. These results highlight the importance of integrative taxonomy in resolving cryptic diversity and refining species boundaries within Pectinariidae.

C.1.74 | New bathyal Terebelliformia (Annelida) from the Brazilian continental slope: hidden diversity and wide-distribution signals in the South Atlantic

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Terebelliform annelids are common benthic taxa, but their diversity in deep-sea environments remains poorly resolved, especially in the South Atlantic. In Brazil, species-level knowledge of deep-water Terebelliformia is based on few taxonomic contributions, leaving bathyal habitats of the continental margin underdocumented. Here, we report taxonomic data on terebelliform annelids collected from the continental slope of two basins off southeastern Brazil. Specimens came from two projects at 600 to 2,000 m depth and were examined using comparative morphology. Three taxa are documented. A new species of *Pista* is described from the upper continental slope and is distinguished by the unusual combination of a single pair of plumose branchiae on segment 2, reduced anterior lobes, giving it a superficially *Pistella*-like appearance, but with long-handled thoracic uncini extending to the last notopodial segments. A new species of *Terebellides* is recognized, characterized by branchiae from segment 2, four branchial lobes completely free from the stalk, no fifth branchial lobe, notopodia from segment 3, neuropodia from segment 8, and a conspicuous pale transverse collar on segment 6. Brazilian specimens identified as *Streblosoma* cf. *atlanticus* are recorded from the southwestern Atlantic, matching northwestern Atlantic material in major diagnostic traits but differing mainly in branchial filament length. This conservative identification expands the known occurrence of the taxon while keeping open the possibility that similar Atlantic populations represent a complex of sibling species. Together, these records add two bathyal species and one relevant occurrence to the Brazilian deep-sea terebelliform fauna. They also reinforce that apparent wide distributions in deep-sea annelids should be treated cautiously until broader comparative and molecular data are available. The study highlights the Brazilian continental slope as an undersampled component of South Atlantic annelid diversity and provides a taxonomic baseline for future biogeographic and integrative studies.

C.1.75 * | A Caribbean Anamobaea in taxonomic limbo: reassessment of a long-recognized undescribed species
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Anamobaea comprises large and conspicuous split-crown feather duster worms from Caribbean reef environments. Although members of the genus are frequently observed in the field and citizen-science records, only two species are currently described: *Anamobaea phyllisae* and *A. orstedii*, both as sclerozoans in dead coral masses. Here, we describe a new species of *Anamobaea* from Curaçao corresponding to *Anamobaea* sp. 1 sensu Tovar-Hernández & Salazar-Vallejo (2006), a morphotype previously recognized but left unnamed because of limited material. Newly collected ethanol-preserved specimens during December 2025 allowed a detailed morphological comparison with congeners and molecular sequencing based on mitochondrial DNA (COI and 16S) sequence data. The new species differs from *A. phyllisae* based on the absence of dorsal kidney-shaped shields on the basal flanges, among other differences. It also differs from *A. orstedii* by a combination of features related to basal flange morphology, distribution of radiolar eyes, and tube characteristics. Molecular analyses support its distinction from other available sabellid lineages. This study resolves a long-standing taxonomic uncertainty and highlights the importance of combining historical taxonomic knowledge with modern integrative approaches to delimit species boundaries in conspicuous but poorly studied reef-associated annelids.

C.1.76 | Phylogeography and biogeography of Phyllodocida Dales, 1962 (Annelida): a systematic review

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The order Phyllodocida comprises one of the most diverse and ecologically significant clades of polychaete annelids, including around 4,800 recognized species and 20 families distributed across a wide range of marine habitats. Despite their ecological importance and evolutionary diversity, phylogeographic and biogeographic knowledge remains highly uneven across families. This study presents a systematic review of phylogeographic and biogeographic research on Phyllodocida, following the PRISMA 2020 guidelines. Searches were performed in the Scopus, Web of Science and ScienceDirect databases in mid-March, 2026, using combinations of family names with the terms "phylogeography" and "biogeography". From an initial set of 167 references, 51 studies met the inclusion criteria, representing only nine of the twenty recognized families within the order; the earliest study was published in 1984. The literature review revealed strong taxonomic and geographic biases, with most studies concentrated on Nereididae, Polynoidae, and Syllidae, as well as in Mediterranean and adjacent European seas, Indo-Pacific and North Atlantic regions, whereas several families, particularly deep-sea taxa and poorly sampled groups, remain virtually unexplored. Biogeographic studies were more frequent than explicit phylogeographic analyses, and molecular approaches were predominantly based on mitochondrial COI sequences. Across taxa, molecular data revealed cryptic diversity, restricted connectivity, and significant regional genetic structuring, challenging the traditional concept of cosmopolitan polychaete species. Phylogeographic patterns were strongly influenced by oceanographic barriers, habitat discontinuity, dispersal potential, and reproductive strategies, especially larval development modes. In contrast, some taxa exhibited genuine broad or pan-oceanic distributions, in some cases associated with anthropogenic dispersal and marine invasions. Overall, this review highlights major knowledge gaps in the evolutionary biogeography of Phyllodocida and emphasizes the need for broader taxonomic and geographic sampling, multilocus and phylogenomic approaches, and integrative studies that combine morphology, molecular, ecological and historical data to improve understanding of diversification and connectivity patterns in marine annelids.

C.1.77 | Uncovering intraspecific morphological variation in *Poecilochaetus australis* Nonato, 1963 (Spionidae, Annelida)

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Description of intraspecific variation in polychaete species, including morphological, genetic, and biological aspects, have improved understanding of biodiversity of Spionidae, such as *Polydora* and *Prionospio*. In the case of *Poecilochaetus*, species are usually described on few specimens, mostly incomplete, thus intraspecific variation of its 33 valid species is poorly understood. Species differentiation relies on characteristics including length and shape of nuchal organs, presence or absence of branchiae, presence and number of interramal cirri, chaetae shape and distribution, and prostomium shape. *Poecilochaetus australis*, whose type locality is Brazil, represents the most abundant species of the group on this coast. The aim of this study is to describe intraspecific morphological diversity revealed in *P. australis* through integrative taxonomy. The morphology of 220 specimens was analyzed using stereomicroscope, compound microscope, and scanning electron microscopy. Two mitochondrial markers (16S rDNA and COI) of six specimens were analyzed under maximum likelihood and Bayesian inference. Pairwise K2P genetic distances were calculated for these two markers and for the nuclear ITS2. Morphological observations revealed three morphotypes with variation in taxonomic characters, such as the shape (unilobated, bilobated and trilobated) and length of the median nuchal organ, shape of the parapodia lobes, and distribution of chaetae throughout the body. Molecular analyses indicate that all morphotypes, despite variation, correspond to *P. australis*. The nuchal organ shape varied in around 10% of all examined specimens and may indicate anomalies associated with pollution typical of port areas. Despite variations in other characters, variation of nuchal organ shape and size can more easily lead to species delimitation errors because it is a prominent feature and considered an important diagnostic feature. Thus, in *Poecilochaetus* species delimitation this character must be carefully evaluated alongside other diagnostic characters previously used, such as types of chaetae, distribution of ampullaceous cirri, among others.

C.1.78 | Resolving species complexes among early described polychaetes – tracing the footprints of O.F. Müller (1776)
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Otto Friderich Müller (1730-1784) was one of the most influential early naturalists in the Nordic countries with particular interest in aquatic invertebrates. With regard to polychaetes, Müller collected and described about ten species, among them *Scoloplos armiger* (original name *Lumbricus armiger*) and *Pista cristata* (original name *Amphitrite cristata*). The species were listed with short Latin diagnoses in a catalogue 'Zoologia Danica prodromus' (1776) and later described in a large and ambitious work 'Zoologia Danica' (1777-1806). The 'prodromus' has been the source of numerous scientific names of marine species. In recent years modern integrative taxonomy including DNA barcoding has demonstrated that many early described and widely reported species essentially are complexes of confused similar-looking species. In DNA barcoding, both *S. armiger* and *P. cristata* split into several clades or BINs (= putative species), for *P. cristata* more than five BINs. *Pista cristata*, in particular, has further had a taxonomic history including several redescrptions (M. Sars 1861, Malmgren 1866, Saphronova 1988) based on various morphological characters that has led to a presently uncertain species status. In a recently established Norwegian project, 'Polytype' (2026-2028), aimed at resolving species complexes, a main activity is to locate and revisit original sampling localities (type localities) to collect topotypic specimens for DNA barcoding and morphological studies. This is, in line with provisions in ICZN (1999), attempting to anchor original species name to 'correct' genetic clade. The type localities of *S. armiger* and *P. cristata*, being in the vicinity of Kristiansand, southern Norway, are exactly known from Müller's original descriptions and a travel report (1778; in Danish). In 2025 several topotypic specimens of both 'species' were sampled. We here present some provisional results, and for *P. cristata* also give an account of the taxonomic history through the 19th and 20th centuries.

C.1.79 | An unusual behavior of epibenthic tube-dwelling *Hyalinoecia* (Hyalinoeciinae, Onuphidae) in Amami-Oshima, Japan
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Species of the family Onuphidae are tube-dwelling polychaetes that include the semi-infaunal or infaunal subfamily Onuphinae and the mobile Hyalinoeciinae, which possess portable tubes. Within Hyalinoeciinae, *Nothria* and *Anchinothria* construct tubes using sediment particles, whereas *Hyalinoecia* and *Leptoecia* possess transparent tubes composed of a sugar phosphate polymer known as onuphic acid. Although *Hyalinoecia* comprises approximately 22 described species worldwide, its taxonomy has long been considered problematic because the arrangement of chaetae and the chaetigers bearing branchiae may vary during growth. In this study, specimens of *Hyalinoecia* were collected from various localities in Japan using dredge surveys and SCUBA diving. Molecular phylogenetic analyses based on three markers (COI, 16SrRNA and 28SrRNA) revealed the presence of seven distinct clades among Japanese specimens assigned to *Hyalinoecia tubicola*. These findings suggest greater diversity within the genus than previously assumed. One of the most noteworthy lineages found in this study was *Hyalinoecia* sp. collected from Kakeroma Island, Amami-Oshima, southern Japan. Previously known species of *Hyalinoecia* have mainly been recorded from depths of approximately 30 m to several hundred meters; however, this species inhabits sandy bottoms at depths as shallow as approximately 6 m. Furthermore, the species exhibited a remarkable burrowing behavior. When individuals collected by SCUBA diving were placed on the sediment surface, they immediately extended the anterior body from the tube and burrowed into the sand, gradually pulling the tube beneath the sediment until the entire body became completely buried. These observations suggest that this species may possess a lifestyle distinct from the epibenthic habits previously reported for *Hyalinoecia*. Alternatively, members of the genus may generally adopt an infaunal lifestyle except during active surface foraging.

C.1.80 | Old synonyms getting a second wind: integrative taxonomy to the rescue of Alciopini (Annelida, Phyllodocidae)

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Alciopini are notorious for the lack of reliable diagnostic features which has led to the erection and subsequent synonymization of redundant genera and species; some species were successively referred to almost every genus within the tribe. After the system has eventually stabilized, most synonymies were never questioned. Still, complementing traditional morphology with molecular methods reveals “over-synonymization” which demands resurrecting some old names with new, more precise, diagnoses; we present two such examples. *Vanadis* specimens morphologically pertaining to *V. minuta* form two well supported clades arising within a single polytomy with *V. studeri* in the phylogenetic tree. No strict morphological differences could be found; one clade included the Red Sea material with colored segmental glands in the anterior of the body and Atlantic individuals lacking coloration anteriorly but faintly pigmented posteriorly. Another clade featured uncolored individuals from both basins. Based on original descriptions of *V. minuta*'s synonyms, we restrict the original name to the lineage with pigment present at least in posterior segmental glands. The uncolored morphospecies is attributed to *Vanadis longirhyncha* Greeff, 1885. The other case is the type species of *Rhynchonereella*, *R. gracilis*. The long-persisting disambiguation regarding the presence or the reduction of parapodia in segment 4 was checked with molecular analyses and the existence of two species was confirmed. The original name should be retained by the species with reduced first parapodia which agrees with most descriptions. The oldest remaining synonym *Rhynchonereella (Callizona) nasuta* Greeff, 1876 characterized by the absence of reduced parapodia is resurrected to harbor the corresponding clade.

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C.1.81 | Aphroditiformia (Annelida) of the Aleutian Trench & Bering Sea (NE Pacific)

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Aphroditiformia comprises six families of scale-worms which together represent 1,344 accepted species occurring around the world from shallow water to the deep sea with the Polynoidae as the most diverse, followed by Sigalionidae and Aphroditidae. Of the six families, only three appeared in the samples collected from the eastern Aleutian Trench & the southern Bering Sea during the AleutBio expedition (Aleutian Trench Biodiversity Studies) in 2022 onboard RV Sonne (SO293), which covered a distance of 1,200 km. More than 10,000 annelids were collected using box corer, epibenthic sledge and Agassiz trawl. The present study aims to characterize the Aphroditiformia species sampled belonging to Polynoidae, Sigalionidae (except Pholoinae) and Aphroditidae using morphology together with molecular data (COI, 16S and 18S) where available. A total of 224 specimens were collected using the box corer and epibenthic sledge. With 110 specimens representing 14 species, Polynoidae was the most diverse family; notably, nine of these species are new to science. Sigalionidae was the most common family with 101 specimens belonging to two species, one of them representing a new genus and species. With 13 specimens of a single species, Aphroditidae emerged in the samples as rare, but widely distributed; surprisingly the specimens found appear to belong to a species originally described from Australian waters.

C.1.82 | Biogeography of polychaetes (Annelida) in the Bay of Biscay (NE Atlantic): new records and distribution patterns

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The Bay of Biscay is a vast and still poorly studied area, characterized by a wide continental shelf (150 km at its widest point). It acts as a biogeographical transition zone capable of hosting various Atlanto-Mediterranean faunal assemblages with different temperature affinities: warm, moderate, and cold temperate. According to local temperature variabilities, various benthic species are differentially distributed across the area. This study aims to list the new species' occurrences and to trace their origin by temperature affinity. A two-year (2023–2025) survey mapping of soft bottom benthic habitats was performed to assess the environmental baseline for the offshore wind farm project off Oléron Island (430 km²), France. This survey took place during two distinct periods of the year: late summer/early autumn and the end of winter. In total, 444 stations (with five replicates each) were collected using a Day grab (0.1 m²) that provides a sampled surface of 222 m². A total of 49,483 polychaetes individuals were sampled and 166 species formally identified; other 24 species (cf.) remained to be fully checked. Among the 166 identified species, 150 (90%) were already recorded to the bay whereas 16 (10%) have not been recorded in the area (based on public data WoRMS and GBIF). Two of these species have already been recorded along the southern Spanish coast; for which our study confirms a northward expansion of their distribution range. Six of these species are present in both the Mediterranean and the English Channel which may represent a continuous distribution between these two regions. Three species exhibit cosmopolitan distribution which requires further genetic investigation to be confirmed. While the immediate impact of climate-driven water temperature changes in the distribution of species is hard to assess, it underscores the necessity of long-term monitoring.

C.1.83 | *Flabelligera* (Annelida) in Norwegian waters reveals hidden diversity

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The type genus of Flabelligeridae, *Flabelligera* Sars, 1829, has historically been represented by only two species in Norwegian waters: *Flabelligera vaginifera* (Rathke, 1843) and the type species *Flabelligera affinis* M. Sars, 1829. Originally described from shallow waters along the Norwegian coast, *F. affinis* has since been regarded as a cosmopolitan species. However, recent revisions have restricted its distribution. In addition, available DNA barcoding data indicate hidden diversity within *Flabelligera*. Using an integrative taxonomic approach, combining molecular and morphological analyses, we assessed the diversity and the geographic and bathymetric distribution of putative species in Norwegian and adjacent waters. Two DNA markers, the universal mitochondrial barcoding region CO1 and the 16S rDNA region, were sequenced from 57 specimens. These sequences, together with available sequences from the Barcode of Life Data System (BOLD), were analysed using phylogenetic inference and the species delimitation methods ASAP and bPTP. The results reveal a significantly higher diversity within *Flabelligera* than previously recognised, with 12 well-supported clades recovered in the concatenated analysis. Several species are delimited within the putative species suggested by the molecular analyses, using morphology, geographic and bathymetric distribution. A new deep-water species of *Flabelligera* is confirmed, and a sympatric species complex of possibly three new species is uncovered. *F. affinis* is confirmed as a well-supported clade and is redescribed with a neotype and genetically characterised. *F. vaginifera* appears to be a more complex group, separated into three clades that need further examination. French specimens included fell into a highly supported separate clade. Additionally, several small but well-supported clades suggest an even higher species diversity and warrant further investigation.

C.1.84 | Uncovering hidden diversity in *Amphicteis gunneri* (Ampharetidae)

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The genus *Amphicteis* is among the most widely distributed and species-rich genera within the family Ampharetidae, with several species described from the North Atlantic. The type species of the genus, *Amphicteis gunneri*, was originally described by Michael Sars (1835) based on material collected from Glesvær and Florø in western Norway. Although the species has historically been reported as cosmopolitan, this view has been challenged by several authors, who instead restrict its distribution to Arctic and European waters, with the English Channel proposed as its southern limit. Preliminary DNA barcoding of specimens identified as *A. gunneri* has revealed substantial hidden diversity, with four well-supported genetic clades exhibiting overlapping geographic distributions. Notably, one clade appears to range from Norway to the Mediterranean Sea and northwestern Africa. Here, we present ongoing work revising the *A. gunneri* species complex using an integrative taxonomic approach that combines morphological and molecular data (mitochondrial COI and 16S, and nuclear 28S markers). The study is based on extensive material collected from a wide range of localities across the North Atlantic and Arctic regions. *Amphicteis gunneri* is redescribed, and one genetic clade is linked to the species based on newly sequenced specimens from the type locality. In addition, three species are described as new to science.

C.2.85 | Comparative analyses of mitogenomes in Eunicidae Berthold, 1827 (Annelida)

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Mitochondrial genomes are powerful tools for comparative genomics, allowing the identification of rearrangements and genomic patterns. Mitochondrial arrangement in Annelida is typically conserved; however, within Eunicidae, exceptions occur relative to the Pleistoannelida pattern. Characterization of one *Eunice* and three *Marphysa* mitogenomes reveals transpositions in at least two different species. Given the limited knowledge of rearrangements within Eunicidae, this study aims to identify patterns and structural variations within the family. We obtained three mitogenomes of *Eunice* and one of *Nicidion* through high-throughput sequencing (Illumina) and low-coverage genome skimming. The reads were assembled using SPAdes 3.15, and contigs were identified via BLAST searches against closely related species. Gene annotation was performed using MITOS2; molecular analyses and manual adjustment were conducted in Geneious. Comparative analyses include the data generated here and seven published mitogenomes (one from *Eunice*, one from *Leodice*, four from *Marphysa*, and one from *Paucibranchia*). Preliminary results revealed that all analyzed species retain the canonical bilaterian gene complement (13 protein-coding genes and two ribosomal RNAs). Gene order varies slightly from the Pleistoannelida pattern, mainly the tRNAs order. The presence of tRNAs also varies from Bilateria pattern. *Eunice* sp. (East Timor), *E. sebastiani*, and *Marphysa aegypti* have 21 tRNAs due to the absence of trnC, trnI, and trnD, respectively. *Paucibranchia bellii* presents 20 tRNAs, lacking trnF and trnK. All other species retained the bilaterian condition of 22 tRNAs, except for *Nicidion* sp., for which the complete mitogenome was not recovered and therefore could not be considered in assessing tRNA composition. A Group II intron was identified in COI of *Eunice* sp. (East Timor), *Eunice* sp. (Brazil), and *E. sebastiani*. With the addition of previous records, Group II introns have been found in six Eunicidae species and 11 other species across Annelida. Thus, it may be more common in Metazoa than previously considered.

C.2.86 | Species delimitation of epitokous *Eunice* sp. (Eunicidae, Annelida) from East Timor

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Epitoky involves modifications of the entire body (epigamy) or posterior end (schizogamy) during the reproductive period. In *Eunice* Cuvier, 1817, schizogamy is known for *Eunice fucata* Ehlers, 1887 (Dry Tortugas, USA), which shares with *Eunice coccinea* Grube, 1878 and *Eunice reducta* Fauchald, 1970 ventral cirri without tips and compound falcigers with short blades. Recently, schizogamous epitokes of *Eunice* aff. *fucata* were identified in East Timor and Indonesia. This study aims to identify the East Timor epitokes using morphological and molecular data. Samples include 29 *Eunice* sp. (atokes and epitokes) from East Timor, one from Papua New Guinea, and 13 *E. fucata* from three Atlantic regions (Guadalupe, Curaçao, and USA). DNA was extracted using Zymo Quick-DNA kit; 16S rDNA and ITS2 sequences were obtained by Sanger sequencing. Outgroups included sequences of *Eunice norvegica* (Linnaeus, 1767), *Eunice roussaei* Quatrefages, 1866, *Leodice torquata* (Quatrefages, 1866), and *Diopatra* cf. *sugokai* Izuka, 1907. After alignment (MAFFT), phylogenetic analyses included maximum-likelihood (IQ-TREE) and Bayesian inference (MrBayes). Species delimitation was performed with ABGD, ASAP, bPTP, and GMYC (ultrametric tree generated in BEAST). Bayesian inference recovered a monophyletic group with all the samples and *E. fucata* from Belize (GenBank: GQ478143.1), with posterior probability (PP=1). Atlantic specimens formed a monophyletic group (PP=1), while East Timor specimens formed a polytomy. Delimitation methods identified three species: *Eunice* sp. (East Timor), *Eunice* sp. (Papua New Guinea), and *E. fucata* (Atlantic). Pairwise genetic distance (K2P) for 16S between lineages was 0.09-0.11 (*Eunice* sp. East Timor × *Eunice* sp. Papua New Guinea), 0.13-0.18 (*Eunice* sp. East Timor × *E. fucata*), and 0.16-0.20 (*Eunice* sp. Papua New Guinea × *E. fucata*). Our findings indicate a schizogamous *Eunice* species, distinct from *E. fucata*. Further morphological analyses will be carried to understand whether the species is *E. coccinea*, *E. reducta* or a new species to science.

C.2.87 * | Polychaete diversity from La Caleta (Cádiz, southern Iberian Peninsula) reveals putatively undescribed lineages of Nereididae
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Polychaete diversity in the Gulf of Cádiz (southern Spain) has been widely studied. Nevertheless, some rocky intertidal habitats remain poorly characterized, such as those in and around the Bay of Cádiz. La Caleta, an urban beach of major cultural and historical importance in the city of Cádiz, is located adjacent to the Bay of Cádiz Natural Park, an area recognized for its high benthic diversity. To improve current knowledge of its benthic fauna, polychaete assemblages from the rocky intertidal zone were surveyed through morphological and molecular analyses. A total of 355 specimens belonging to 14 families were examined, with 15 taxa identified to species level. Nereidids were the dominant group with 219 individuals. Given the occurrence of cryptic diversity and species complexes within nereidids, a molecular phylogeny based on cytochrome oxidase I (COI) and 16S rRNA markers was constructed to assess the taxonomic status of the collected material. The analyses recovered a new lineage within the *Perinereis cultrifera* (Grube, 1840) species complex, together with two additional lineages assigned to the genera *Nereis* Linnaeus, 1758 and *Composetia* Hartmann-Schröder, 1985, which may represent undescribed taxa or taxa requiring taxonomic reassessment. Our work highlights the importance of local-scale biodiversity surveys in apparently well-known regions and underscore the importance of integrative approaches for revealing hidden diversity in marine annelids.

C.2.88 | A new 518-million-year-old stem annelid illuminates the ancestral body plan of Annelida
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Burgess Shale-type deposits provide excellent insights into the Cambrian explosion of animal body plans and the origins of major modern phyla. Fossil evidence from Cambrian Lagerstätten reveals that early annelids have rapidly radiated into marine benthos and developed remarkable ecological and morphological diversity. However, their enormous morphological disparity and flexibility in body plan organisation pose a severe challenge to the reconstruction of ancestral anatomy and, hence, the early evolutionary history, of the group. Here, I present new annelid-like fossils from the ca. 518-million-year-old Qingjiang biota of China. Exceptional preservation and extensive sampling between 2014 and 2025 (>500 collected specimens) enable a detailed reconstruction of the organism's morphology, ecology, and ontogeny, with key juvenile specimens occurring alongside abundant large adults. This new taxon is characterized by flattened protective sclerites, numerous trunk segments, and a sediment-filled gut indicative of deposit feeding. Morphologically, it resembles the 508-million-year-old stem-group annelid *Canadia* from the Burgess Shale, and its character combination is broadly consistent with molecular predictions for ancestral annelids. However, the new fossil also shares some similarities with *Wiwaxia*, a Cambrian scleritome-bearing stem-group mollusc, particular in sclerite/chaetal pattern, likely reflecting traits inherited from their common ancestor. Notably, it lacks a differentiated head or palps, prominent parapodia, and other lateral outgrowths that define the ground pattern for annelid crowns. Its overall simplicity suggests that this fossil species represents an early stage in annelid evolution, sitting at the base of the annelid tree. This discovery suggests that segmented annelid worms evolved from an epibenthic, homonomous, metameric and apodal ancestor that lacked a differentiated head and associated appendages.

C.2.89 * | One species, many faces: integrative taxonomy uncovers the Mediterranean expansion of the Lessepsian polychaete *Syllis crassicirrata*
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The Mediterranean Sea is one of the regions most affected by biological invasions, particularly after the opening of the Suez Canal, which facilitated the arrival of Indo-Pacific species from the Red Sea. Ports and marinas serve as major gateways for alien species, enhancing the secondary spread of Lessepsian migrants and raising concerns about their impacts on native ecosystems. Although polychaetes are key components of marine benthic assemblages, limited genetic data and insufficient taxonomic revisions hinder accurate identification of non-indigenous species (NIS). With the aim of tracing the distribution and invasion pathways of polychaete NIS in the Mediterranean, this study focuses on *Syllis crassicirrata* (Treadwell, 1925), originally described from the Hawaiian Islands and widespread in the Pacific and Indian Oceans. In the Red Sea, this taxon has been reported as two divergent lineages, differing from Pacific populations and exhibiting partially overlapping colour polymorphism. The species was recently recorded in the eastern Mediterranean Sea, with individuals showing the most common colour pattern observed in Red Sea specimens. An integrative taxonomic approach, combining morphological and molecular analyses, was applied to specimens collected from Tunisia, Sicily, Apulia, Crete, and Rhodes, and compared with material from Lebanon. Preliminary molecular results indicate genetic homogeneity across all populations, closely matching Red Sea sequences and supporting the Lessepsian origin of this species in the Mediterranean Basin. These data demonstrate that, despite its recent discovery, *S. crassicirrata* is already widespread in the Mediterranean Sea, reaching as far west as Tunisia and the northern coast of Sicily. Morphological analyses reveal colour polymorphism, with some morphotypes differing from the typical one and overlapping with native *Syllis* species, possibly leading to issues in detecting this expanding NIS. These findings highlight the importance of integrative morphological and molecular approaches to accurately estimate biodiversity and understand ongoing invasions.

C.2.90 | Mitochondrial genome of *Chitinopoma serrula* (Filigraninae, Serpulidae, Annelida)

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We report the first mitochondrial genomes from the annelid genus *Chitinopoma* (Serpulidae). The mitogenome was assembled into a circular contig (33,949 bp in length). All standard mitochondrial genes have been annotated in the genome, with the exception of ATP8 (the ATP8 gene is known to be difficult to annotate). Phylogeny based on mt genomes aligns with estimated based on nuclear 28S, 28S, H3 and mitochondrial (cytb) gene fragments. Gene order supports the pattern for this family: every so far species has its own order. We observed two long non-coding regions in the genome, in one of which the MITOS programme proposed the annotation of two additional copies of the 12S rRNA gene. We also sequenced the transcript, which confirmed the annotation of the protein-coding genes of the main rRNA gene copies. The expression of the second copy of 12S rRNA was also demonstrated – lower than that of the first, but significantly higher than that of the protein-coding genes. The expression of the third copy of 12S rRNA was found to be comparable (slightly higher) to that of the most highly expressed protein-coding genes. We also observed two highly expressed regions in which no sense sequences could be annotated. The polychaete mitochondrial genome length typically falls within the range of 15,000 to 17,000 bp. In Serpulidae mt genome length ranges from 15,853 bp in *Ficopomatus enigmaticus* to 25,087 bp in *Hydroides minax*. Thus, *Chitinopoma serrula* has the longest reported mt genome for all polychaetes.

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C.2.91 | A new species of *Levinsonia* Mesnil, 1897 (Paraonidae) from the White Sea

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The polychaete fauna of the White Sea has been studied for more than a century, yet new findings remain possible due to modern taxonomic approaches and the use of finer mesh sizes. One such finding is a new species of *Levinsonia* (Paraonidae), collected from muddy sediments at depths of 30–60 m. The new species shares key characters with other members of the genus, including a prostomium lacking antennae, transverse dorsal ciliary bands connecting the branchiae, capillary notochaetae, and modified neurochaetal spines with a distinct fringe. However, it also possesses several unique features. A small ciliated bulge is located anterior to the nuchal organs, in the position occupied by a median antenna in other genera. The most distinctive character is the presence of only one pair of branchiae, on segment 7. The species also lacks parapodial postchaetal lobes in both notopodia and neuropodia. The pygidium is short and rounded, with three anal cirri. SEM examination revealed several types of segmental sensory organs, including reduced lateral organs and dorsal and ventrolateral sense organs. The species is very small, measuring 3.3–4.34 mm in length and consisting of 30–39 segments, although many specimens contained gametes. The only species previously recorded from the region, *Levinsonia gracilis* (Tauber, 1879), is much larger, possesses 7–16 pairs of branchiae, and has developed postbranchial notopodial lobes. Recent surveys failed to confirm its presence in the White Sea, and all examined records proved to be misidentifications. These results demonstrate that the polychaete fauna of the White Sea remains insufficiently investigated.

C.2.92 | A novel *Phyllochaetopterus* Grube, 1863 (Annelida: Chaetopteridae) from Northeastern Brazilian waters

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Phyllochaetopterus Grube, 1863 has approximately 22 valid species and is characterized by the presence of a second pair of palps. In Brazil, only two broadly distributed taxa have been reported, *P. socialis* Claparède, 1869 and *P. gracilis* Grube, 1863, with the latter being the only species recorded in the Northeastern region. This study aimed to identify and describe a *Phyllochaetopterus* species from shallow waters of the state of Bahia. The specimens belong to the *Phyllochaetopterus* species Group C by the presence of nine chaetigers in tagma A, two in B and 3-4 cutting chaetae. They are distinct from other species in this group by the presence of a triangular prostomium, ventral shield with distinct color sections (yellow in A1-A3/A5-A6, white in A4 and brown in A7-A9), lanceolate (A1-A9) and paddle-shaped chaetae (A8-A9) and single row of uncini with 6-7 teeth in tagma B and C. Based on the morphological observations, the specimens differ from other species of the same group and the two species reported to the Brazilian coast. The most similar species is *P. verrilli* Treadwell, 1943, which differs by the presence of eyes, peristomium that covers the prostomium, shape of the prostomium, ventral shield, length of tagma A notopodia and types of chaetae, rows and the number of teeth of uncini and number of chaetigers of tagma C. These specimens may belong to an undescribed species but additional analyses are necessary to confirm the identification.

C.2.93 | Two new species of Phyllodocidae Örsted, 1843 from Northeastern Brazil

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There are few records of Phyllodocidae in Brazil, and existing taxonomic studies are limited to the southern regions. The present study describes two new species of Phyllodocidae collected from the intertidal zone of rocky reefs in Salvador, Bahia, Brazil. The organisms were collected associated with macroalgae, including *Amphiroa* sp. and *Caulerpa* sp., and were observed and photographed alive in the laboratory. *Nereiphylla* sp. nov. presents a slender body, bright green coloration with dorsal brown pigmentation, an oval prostomium longer than wide, lanceolate dorsal cirri along the entire body, and small size, reaching up to 4 mm in length. The species differs mainly from *N. fragilis* and *N. castanea* in the shape of the prostomium, the form of the dorsal cirri, and body size, indicating that previous records attributed to these taxa in southern Brazil may correspond to the new species. *Pterocirrus* sp. nov. differs from its congeners by the position of the median antenna inserted in the central region of the prostomium, by the configuration of the ventral cirri of the second segment, and by parapodial morphology, being especially distinguishable from *P. burtoni*, *P. parvoseta*, and *P. remus* based on these characteristics. The results expand the knowledge of Phyllodocidae diversity along the Brazilian coast and reinforce the relevance of taxonomic studies in intertidal environments of the Northeastern region, which remain poorly sampled.

C.2.94 | A new species of *Syllidia* Quatrefages, 1866 (Annelida: Hesionidae) from Brazil

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Brazil has a considerably diverse polychaete fauna with records distributed along the entire coastline, although the northern coast is poorly studied. The most recent survey of the Hesionidae in Brazil recorded 17 valid species distributed across eight genera, including one species of *Syllidia*. This genus currently comprises only three valid species: the type-species *Syllidia armata* Quatrefages, 1866, described from the French coast but also recorded from the North Atlantic and the Mediterranean Sea; *Syllidia hongkongensis* Ruta & Pleijel, 2006, described from Hong Kong; and *Syllidia amaralae* Rizzo & Salazar-Vallejo, 2014, described from southeastern Brazil. Abundant material of a new species of *Syllidia* was collected from several artificial substrates (piers and marinas) in Todos-os-Santos Bay, Bahia, northeastern Brazil. *Syllidia* sp. nov. is characterized by the presence of four pairs of tentacular cirri; palps and lateral antennae of similar lengths; palps' palpophores about one-third the length of the palpostyles; distinct jaws with two basal rods, one straight and one rounded; the straight rod separated by a small space forming a 60° angle

* Denotes a student contribution eligible for a prize.

Presenting author shown in **bold**.

from the denticulated margin with 5–10 denticles (size-related); and anterior neurochaetae with 6–12 falcigers, median chaetigers with 20–30 falcigers, and the last chaetiger bearing 6–10 falcigers. This new species is most similar to *S. hongkongensis* in the presence of four pairs of tentacular cirri (instead of six pairs as in *S. armata* and *S. amaralae*), but differs in the structure of the jaws, the comparative lengths of palpopores and palpostyles, and by the presence of bidentate neuropodial falcigers in *Syllidia* sp. nov., whereas *S. hongkongensis* bears unidentate falcigers. *Syllidia* sp. nov. was collected in abundance in estuarine environments and in association with biological substrates such as the invasive sun-coral *Tubastraea* spp. and diverse assemblages of sponges.

C.3.95 | Deep-sea and coastal Cirratulidae (Annelida) from the Southwestern Atlantic: advances in systematics and diversity

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Cirratulidae is a family of polychaete annelids comprising about 380 valid species in 16 genera, occurring from intertidal zones to abyssal depths worldwide. Despite their broad distribution, the taxonomy and diversity of the family remain poorly known worldwide, with most systematic knowledge historically concentrated in the North Atlantic. This study is based on material obtained during extensive oceanographic expeditions along the Brazilian continental margin, between Espírito Santo and Paraná states, and at Atol das Rocas, between 2008 and 2020, covering shallow-water and deep-sea environments from 13 to 3,000 m depth. Taxonomic studies were conducted on formalin-fixed specimens using standard taxonomic methods. In this study, we present recent systematic contributions to the genera *Aphelocheata*, *Caulleriella*, *Chaetozone*, *Dodecaceria*, and *Kirkegaardia*. These contributions include new species and records for Brazilian waters. These contributions considerably expand the known diversity of Cirratulidae along the Brazilian coast, where the number of recorded species has increased from approximately 28 to more than 40. These results advance the taxonomy, diversity, and distribution of Cirratulidae in the Southwestern Atlantic and reinforce the still underestimated diversity of benthic annelids in the region.

C.3.96 | Taxonomic contributions to Hesionidae (Annelida) along the Brazilian coast

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Hesionidae is a diverse family of errant polychaetes widely distributed across marine environments worldwide. Species of the family range from a few millimeters to several centimeters in length and are characterized by extremely fragile bodies. As a result, complete and well-preserved specimens suitable for taxonomic identification are rarely obtained unless collected and preserved under conditions that maintain diagnostic morphological characters. Consequently, the diversity and systematics of hesionids remain poorly understood worldwide, particularly in the Southwestern Atlantic and along the Brazilian coast. This study is based on material collected during oceanographic expeditions conducted along the Brazilian continental margin, between Espírito Santo and Paraná states, between 2008 and 2020, covering shallow-water and deep-sea environments from 13 to 3,000 m depth. Taxonomic studies were conducted on formalin-fixed specimens using standard morphological approaches. Here, we present recent systematic contributions to the genera *Hesiospina*, *Heteropodarke*, *Micropodarke*, and *Nereimyra*, including new species and new records for Brazilian waters. The analyzed material revealed a still underestimated diversity of Hesionidae associated with coastal and deep-sea environments along the Brazilian coast. These results expand the current knowledge of Hesionidae diversity and distribution in the Southwestern Atlantic and reinforce the importance of taxonomic studies and deep-sea expeditions for understanding marine annelid biodiversity in the region.

C.3.97 * | Climate change responses across the life cycle of *Platynereis dumerilii*: insights from the first Southern Hemisphere culture

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Coastal ecosystems are increasingly affected by climate-driven stressors, including ocean warming, acidification, and salinity fluctuations. While most studies have focused on calcifying organisms, the effects of climate change on non-calcifying marine invertebrates remain poorly understood. The annelid *Platynereis dumerilii* is an emerging model organism due to its well-characterized life cycle, regenerative capacity, and suitability for laboratory cultivation. This study is based on the first established culture of *P. dumerilii* in the southern hemisphere, maintained at the Federal University of Rio de Janeiro (UFRJ), Brazil. We investigate the isolated and combined effects of temperature, reduced pH, and salinity variation across multiple life stages, integrating larval development, regeneration, metabolism, and reproductive performance. Controlled laboratory experiments simulating projected climate scenarios exposed different developmental stages to environmental stress gradients. Moderate warming accelerated larval development to the nectochaeta stage, whereas reduced salinity delayed development and increased morphological anomalies. Independent regeneration experiments demonstrated that salinity reduction had little effect on posterior regeneration, while moderate warming accelerated segment regeneration but induced post-regenerative abnormalities, including impaired parapodial development. Ongoing reproductive assays indicate that elevated temperatures accelerate epitokous metamorphosis, potentially at a high physiological cost due to reduced post-epitoky survival. In contrast, extreme stressor combinations, particularly severe warming, resulted in high mortality across developmental stages. By integrating developmental, regenerative, and reproductive responses, this study highlights the vulnerability of marine annelids to cumulative climate stressors and emphasizes the importance of multi-stressor approaches for understanding population persistence under future climate scenarios.

C.3.98 * | Reassessing Central Pacific Eunicidae: diversity and discovery from the remote Palmyra Atoll

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Taxonomy underpins our understanding of marine biodiversity, yet many invertebrate groups remain poorly resolved, particularly in understudied regions such as the Central Pacific. The polychaete family Eunicidae exemplifies this problem, as regional species records frequently rely on names established from distant type localities, often without direct comparison to type material. As a result, reported distributions may reflect historical taxonomic practice and sampling bias rather than true species ranges. This study reviews previously reported Central Pacific Eunicidae based on published literature and museum records to establish the current taxonomic context and assess the reliability of existing species assignments. New material collected from Palmyra Atoll, a remote, minimally disturbed reef system, was examined using an integrative approach, combining detailed morphological analysis, advanced imaging techniques, and mitochondrial DNA barcoding. Comparative morphological assessments included type and non-type material housed in museum collections, and micro-computed tomography (micro-CT) was used to visualise and compare jaw apparatus morphology across Palmyra specimens and relevant reference material. Three new Eunicidae morphotypes were recognised from Palmyra Atoll. Two morphotypes differ from all previously reported Central Pacific species, indicating previously unrecognised regional diversity, while the third closely resembles *Lysidice unicornis* (Grube, 1840), a species currently recorded from a wide range of locations. Molecular data were generated where possible to complement morphological conclusions, although broader geographic sampling remains necessary. These findings highlight persistent taxonomic uncertainty within Central Pacific Eunicidae and question the validity of assumed wide distributions for nominal species such as *L. unicornis*. Resolving these issues will require redescription of key type material and expanded comparative morphological and molecular analyses across reported species ranges. By refining species boundaries and improving identification accuracy, this work contributes to a more realistic understanding of Central Pacific biodiversity and demonstrates the necessity of integrative taxonomy in poorly studied marine systems.

C.3.99* | Re-building the Syllid Tree: phylogenomics, mitochondrial gene-order shifts, and genome-size dynamics

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The family Syllidae is one of the most diverse groups within Annelida and occupies virtually every marine habitat and depth. Its extraordinary diversity of reproductive strategies has made the group a model for studying trait evolution, yet the phylogenetic framework supporting these studies rests on a limited set of markers (16S, 18S, COI, with occasional 28S or ITS2). Although these analyses consistently recover the traditional subfamilies Autolytinae, Exogoninae and Syllidae as monophyletic, relationships among subfamilies remain poorly resolved and several genera fall outside the established classification. Here we present a genome-scale phylogenomic reconstruction of Syllidae using universal single-copy orthologs (USCOs) mined from genome-skimming data through a hit-stitching approach. Subsequent data curation and phylogenetic inference were carried out with an analysis pipeline. The resulting dataset (1,139 USCOs) provides unprecedented resolution of deep and shallow nodes, allowing us to test the monophyly of existing subfamilies, clarify the placement of some independent genera, and evaluate the impact of hyper-variable regions that have confounded earlier ribosomal-DNA-based trees. In parallel, we estimate nuclear genome sizes and genomic complexities for all sampled taxa. By analyzing k-mer spectra, we generate the first comparative genome-size database for syllids. By integrating these estimates with published life-history information, we test the hypothesis that genome size and complexity may correlate with reproductive modes and other ecological traits. Complete mitochondrial genomes are also assembled, enabling a detailed survey of gene-order rearrangements. Preliminary analyses reveal two highly divergent mitochondrial architectures that correspond to the Anoplosyllinae and Syllinae clades, suggesting independent episodes of genome reorganization. Our results deliver a robust, genome-scale phylogeny of Syllidae, provide the first broad assessment of genome-size evolution in annelids, and explore mitochondrial architecture. This integrative framework sets the stage for future investigations of genome evolution, genome dynamics, and the genomic underpinnings of life-history diversity in marine annelids.

C.3.100* | Several new species of the deep-sea genus *Anguillosyllis* Day, 1963 (Annelida, Syllidae) from the Aleutian Trench

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The Aleutian Trench is located between the North American continent and Asia, stretching across the North Pacific. It is over 7,800 meters deep and harbours a unique deep-sea benthic ecosystem. This ecosystem has been the subject of a recent expedition striving to investigate its taxonomic diversity. Therein the polychaete fauna in general and, based on its high diversity, the genus *Anguillosyllis* Day, 1963 (Syllidae) has been of particular interest. During the past six years, more than 20 new species of *Anguillosyllis* have been described and our findings suggest that there are still more to discover. Using a combination of both morphological and molecular methods, we are able to describe several new species of *Anguillosyllis* from the Aleutian Trench. Detailed SEM observations of both chaetae and prostomial morphology are reported and based on 16S, 18S and COI markers an updated phylogeny for the genus is provided.

C.3.101 | Taxonomical and ecological features of Glyceridae and Goniadidae (Polychaeta) species distributed along the coasts of Türkiye

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This study, which includes data from a doctoral dissertation conducted between 2016 and 2021, contains a detailed taxonomic examination of Glyceridae and Goniadidae (Annelida/Polychaeta) species distributed along all coasts of Türkiye (Levant Sea, Aegean Sea, Marmara Sea, Black Sea). This study is the first to analyze Glyceridae and Goniadidae species from both taxonomic and ecological perspectives. Previous research on members of this family in Turkish waters has generally been faunistic studies that also include other polychaetes and macrozoobenthic invertebrates. Samples collected from 299 stations within the scope of 8 different projects conducted between 1999 and 2018 were examined. As a result of the detailed examination of 3237 individuals belonging to Glyceridae and Goniadidae species, 1 genus and 7 species belonging to the Glyceridae and 3 genera and 7 species belonging to the Goniadidae were identified. Of these species, *Glycera lapidum* for the Sea of Marmara and the Levant Sea coasts of Türkiye; *Glycera oxycephala* for the Sea of Marmara and the Aegean Sea; *Goniada hexadentes* for the Marmara, Aegean Sea and Levant Sea; *Goniada vorax* for the Aegean Sea; and *Glycinde nordmanni* for the Marmara Sea; *Goniadella bobrezkii* for the Turkish coast of the Aegean Sea and the Turkish coast of the Levant Sea are new records. All species are described and taxonomic key for the species are provided.

C.3.102 | Small adult body size and intratubular brooding in a new cryptogenic species of *Protula* from southern California

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While searching for the non-native serpulid *Protula balboensis* in floating dock fouling communities in San Diego Bay (California, USA) for studies of its larvae, we collected many specimens of another previously unreported and undescribed species of *Protula*. Adults of the new species are small in maximum length (12–19 mm); bear a yellow branchial crown with 8–13 radioles, each with 3–4 paired red compound radiolar eyes; have a trilobed collar and thoracic membrane starting wide then short; bear *Apomatus* chaetae between the 5th–7th thoracic chaetigers, 1–3 sickle chaetae in abdominal segments, and capillary chaetae present in the last 8–10 abdominal chaetigers; and have a posterior glandular pad. Cytochrome B sequences (244 bp) obtained from multiple individuals of the new species and four *Protula* spp. (including two species known from the eastern Pacific, *P. balboensis* and *P. superba*) show that the new species is genetically distinct from other sampled species. Adults collected in their tubes and isolated in small containers often released free-swimming trochophore larvae into the water. Of >200 adults observed alive in the field, none were brooding embryos or larvae in the branchial crown, and embryos or larvae were also never found brooded in the coelom. Thus the new species is likely an intratubular brooder, a reproductive mode suspected in only one other member of the genus, *P. apomatoides* from Japan. We suspect that the new species is not native to southern California because we have only observed it in fouling communities, and because we have not seen references to it or photographs of it in guides to the fauna of southern California and Baja California. A formal description of this new species is currently in progress.

C.3.103 | Polychaete (Annelida) diversity in the impacted Berg River Estuary, South Africa

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Although Ramsar-listed, the Berg River estuary (South Africa) is anthropogenically impacted and severely understudied. Four studies conducted between the 1950s and 2000s found that polychaetous annelids in the estuary are represented predominantly by capitellid, spionid and nereidid species. This study provides an updated taxonomic inventory of polychaetous annelids in this estuary, with COI, cytb and 16S DNA sequence data to facilitate future molecular-based biodiversity studies. 3840 specimens (16 species from seven families) were collected from 9 sites from the mouth of the estuary to 15 km upriver; Spionidae was the most species-rich, followed by Nereididae, with remaining families represented by one or two species each. Richness decreased further from the estuary mouth with only *Capitella* sp. and *Prionospio sexoculata* present throughout. *Capitella* sp. contributed 70% to 100% of individuals collected at sites near urban and industrial areas, suggesting widespread pollution. Nereididae were abundant in less saline waters, while *Boccardia* spp were abundant at the mouth only. Bayesian analyses of sequences generated for abundant and widespread taxa in the Berg River Estuary retrieved eight monophyletic groupings supporting morphological identifications, although multiple lineages exist for *Boccardia pseudonatrix*, *Simplisetia* cf. *erythraeensis* and *P. sexoculata* from multiple locations globally. Multiple Barcoding Identification Numbers for *Capitella* sp. and *Orbinia angrapequenes* contradict Bayesian analyses, suggesting species-complexes for these taxa too. All taxa therefore require revision locally and or globally.

C.3.104 | Occurrence and establishment of the alien polychaete *Alitta succinea* (Annelida: Nereididae) along the southern French Mediterranean coast

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Alitta succinea (Leuckart, 1847) belongs to Nereididae, one of the most representative families of marine polychaetes. Its members are generally large, errant organisms that inhabit a wide variety of marine environments, ranging from the intertidal zone to the deep sea. *Alitta succinea* is typically found in intertidal habitats and exhibits a remarkable tolerance to broad salinity fluctuations. Nereidids also constitute an important food resource for numerous fish and seabird species, making them a crucial component of coastal and marine ecosystems.

The biogeographical history of *A. succinea* is complex and characterized by a remarkably broad distribution. Originally described from the North Sea (Helgoland, Germany), the species has since been reported from numerous regions worldwide, including South and North America, Hawaii, or China. This extensive and discontinuous distribution has led several authors to regard *A. succinea* a species complex, while in many areas, it has been reported as introduced, with a high invasive potential. During the first half of the 20th century, several nereidid species, including *A. succinea*, were intentionally introduced into aquatic systems such as the Aral and Caspian seas as a food source to support commercial fisheries, contributing to their subsequent dispersal.

Field surveys carried out during the last three decades have revealed the presence of numerous individuals of *A. succinea* in many marine lagoons and coastal marshes along the Mediterranean coast of Southern France. These reports, confirm the presence of this species so we can publish that this species in the Northwestern Mediterranean, likely introduced through mollusc aquaculture or ship fouling, and, together with previously documented populations from Sardinia (Italy) and the Saronikos Gulf (Greece), provide evidence that *A. succinea* is now established in the Mediterranean Sea and should be considered part of its alien marine fauna.

C.3.105 | Diversity of symbionts within Chaetopteridae (Polychaeta), with description of a Vietnamese *Chaetopterus*-associated member of the *Hololepidella nigropunctata* species-complex (Polynoidae)

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Chaetopterids are globally distributed tube-dwelling polychaetes whose distinctive body organisation, powerful ventilation mechanisms, and structurally complex parchment- or chitin-like tubes make them prominent habitat-forming benthic organisms (Britayev & Martin 2019). These same traits favour the establishment of diverse symbiotic assemblages, enhanced by the architecture and hydrodynamics of their tubes, particularly within *Chaetopterus*, where continuous water flow, abundant suspended organic particles, and accessible anterior and posterior openings facilitate colonisation and coexistence of multiple associated taxa (Britayev & Martin 2019). As ecosystem engineers, chaetopterids substantially modify soft-bottom habitats while providing stable, resource-rich microhabitats for a diverse array of symbiotic multi-individual communities, whose components are comprehensively reviewed in this study.

From the 96 recorded host-symbiont associations analysed, species of *Chaetopterus* dominate as hosts (15% of the species, 76% of the relationships), followed by *Phyllochaetopterus* (22.2%, 10.4%), *Mesochaetopterus* (18.5%, 8.3%), and *Spiochaetopterus* (2.8%, 2.1%). The associated fauna spans Decapoda, Polychaeta, Amphipoda, Copepoda, Nudibranchia, and Teleostei. Decapod crustaceans comprise about half the species and relationships (and pinnotherid and porcellanid crabs account together for over 90% of all them), followed by polychaetes (33.8%, 40.2%). Among polychaetes, polynoid scaleworms are particularly dominant (79.2%, 87.2%), with many of which displaying evident host specificity.

Two of these host-specific scaleworms occur in Natharng Bay (Vietnam) as members of the symbiotic communities associated to two undescribed, sympatric species of *Chaetopterus*; one is the well-known *Ophthalmonoe pettiboneae* whereas the other is an undescribed member of the *Hololepidella nigropunctata* complex (Britayev *et al.* 2017, Britayev & Martin 2019, Britayev & Martin 2021). This species is larger than other members of the complex and has a wide, flattened body apparently adapted for life inside tubes and in close contact with the host. Accordingly, it is here morphologically described and molecularly characterised.

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