

XVI International Symposium on Flatworm Biology

Göttingen, 1st-4th September 2026

Confirmed Speakers

P. Reddien -Whitehead Institute for Biomedical Research

C. Bleidorn -Scientific Director Forum Wissen

J.J. Collins III -The University of Texas Southwestern Medical Center

P. A. Newmark -Morgridge Institute for Research

C. Laumer -The Natural History Museum

H. T.-K. Vu -European Molecular Biology Laboratory

N. Hall -The Graduate School of the Stowers Institute for Medical Research

B. Benham-Pyle -Baylor College of Medicine

S. Häberlein -Justus Liebig University Giessen

L. Gąsiorowski -University of Warsaw

L. Schärer -University of Basel

J. N. Brand -University of Basel

K. Brehm -University of Wuerzburg

T. Rozario -University of Georgia

E. Berezikov -European Research Institute for the Biology of Ageing

M. Riutort -Universitat de Barcelona

U. Koziol -Universidad de la República de Uruguay

Organisers

J. C. Rink -Max Planck Institute for Multidisciplinary Sciences

M. Vila-Farré -Max Planck Institute for Multidisciplinary Sciences

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Venue information

The conference will take place at the “Alte Mensa” (Old Mess Hall), located directly on the picturesque University Square/“Wilhelmsplatz” in the heart of Göttingen’s historic town center. The venue features beautifully restored historic rooms that will host the talks and poster sessions.

The closest pub (Thanners) lies just about 50 meters away, across the square, and many more pubs, restaurants, and shops are within easy walking distance — including several of our recommended hotels (Hotel Central: ~200 m; Hotel Freigeist-City: ~900 m). The “Barfüßer Straße” bus stop, located roughly 150 meters from the venue, provides convenient connections to the city’s public transport network.

Venue Address:

Alte Mensa am Wilhelmsplatz

Wilhelmsplatz 3

37073 Göttingen, Germany



Program

Tuesday, 1 September 2026

15:30 **Registration at the Alte Mensa**

Opening Session.

18:00 Welcome. Jochen C. Rink, Miquel Vila-Farré. MPI-NAT

18:10 Christoph Bleidorn, Univ. Göttingen. Keynote Speaker
Phylogenetic systematics and the animal tree of life

18:55 *Welcome dinner and scientific exchange*

Wednesday, 2 September 2026

Planarian Cell Biology I. Chair: Blair Benham-Pyle

- 09:00 Peter Reddien, Whitehead Institute. Invited Speaker
Stem cell choices in planarian regeneration
- 09:45 Han Vu, EMBL. Invited Speaker
Yin and Yang: what can planarian flatworms teach us about life history trade-offs
- 10:30 Jordi Solana, Univ. of Exeter. Short talk
Which cell types respond when a planarian is cut? A single-cell study
- 10:45 Leonard Drees, MPI-NAT. Short talk
Characterization of a novel invertebrate DNA sensor with ancient roots in bacterial immune defense
- 11:00 *Coffee break*

Planarian Cell Biology II. Chair: Han Vu

- 11:30 Phil Newmark, Morgridge Institute. Invited Speaker
Chromosome elimination in the male germline of Schmidtea polychroa
- 12:15 Blair Benham-Pyle, BCM. Invited Speaker
Signals and constraints shaping planarian plasticity across regeneration, damage, and aging
- 13:00 Uri Weill, Northeastern Univ. London. Short talk
Heterologous tissue transplants reveal competition amongst the somatic pluripotent stem cells of planarians
- 13:15 Shuchang Hu, EMBL. Short talk
To be or not to be a cyst: comparative analysis of two distinct regeneration modes in planarian Phagocata velata
- 13:30 *Conference picture and lunch break*

Parasite Cell Biology I. Chair: Uriel Koziol

- 15:30 James J. Collins III, UT Southwestern. Invited Speaker
You complete me: a uniquely schistosome love story
- 16:15 Tania Rozario, UGA. Invited Speaker
Conflicts and constraints on the regeneration potential of the tapeworm Hymenolepis diminuta
- 17:00 Inés Guarnaschelli, Udelar. Short talk
Comparative proteomics reveals a conserved core of tegumental proteins in cestodes
- 17:15 Christoph Gero Greveling, JLU Giessen. Short talk
Shedding new light on the male-female interaction of schistosomes: the first scRNA-seq analysis of a platyhelminth organ uncovered a RAR-family nuclear receptor in Schistosoma mansoni ovaries essential for meiosis progression

17:30 *Coffee break*

Parasite Cell Biology II. Chair: Simone Häberlein

18:00 Klaus Brehm, Univ. of Würzburg. Invited Speaker
Rewriting the body plan: host signals and body axis plasticity in the development of Echinococcus

18:45 Uriel Koziol, Udelar. Invited Speaker
Massive elimination of somatic nuclei and extreme metamorphosis of the oncosphere of Hymenolepis microstoma

19:30 *Poster session - finger food (odd-numbered posters)*

Thursday, 3 September 2026

Macrostomum Biology. Chair: Jordi Solana

- 09:00 Richard N. Hall, Stowers Institute. Invited Speaker
Multiplexed screening of genome editing techniques in Macrostomum
- 09:45 Eugene Berezikov, ERIBA, UMCG. Invited Speaker
Identifying somatic neoblast markers in the flatworm Macrostomum lignano
- 10:30 Peter Ladurner, Univ. of Innsbruck. Short talk
Temporary bioadhesion in flatworms
- 10:45 Matthew Voas, NCI. Short talk
Development of a Cre/loxP-based method of cell lineage analysis to assay neoblast potency in Macrostomum lignano
- 11:00 Coffee break

Flatworm Genomics I. Chair: Richard N. Hall

- 11:30 Jeremias Brand, Univ. of Basel & MPI-NAT. Invited Speaker
Stepwise loss of recombination preceded the origin of asexuality in Schmidtea mediterranea
- 12:15 Christopher Laumer, NHM. Invited Speaker
Microturbellarian genomics, one worm at a time
- 13:00 Ignacio Tenaguillo-Arriola, Univ. Of Barcelona. Short talk
No sex? No problem! High intraindividual genetic variability in ancient asexual freshwater planarians
- 13:15 Ulf Jondelius, NRM. Short talk
Hox genes in Xenacoelomorpha
- 13:30 Genome lunch

Flatworm Cell Biology. Chair: Tania Rozario

- 15:30 Ludwik Gąsiorowski, Univ. of Warsaw. Invited Speaker
Excessive feeding induces development of a colony-like body plan in paratomous flatworms
- 16:15 Simone Häberlein, JLU Giessen. Invited Speaker
Spatial omics of parasitic flatworms – from cell biology to drug discovery
- 17:00 Steffen Werner, WUR. Short talk
Generalized feedback control in stem cell systems – planarians as a case study
- 17:15 George Wendt, UT Southwestern & MPI-EvolBio. Short talk
Evidence of ancient horizontal gene transfer in the human parasite Schistosoma mansoni
- 17:30 Coffee break
- 18:00 Poster session – finger food (even-numbered posters)

20:00 *Conference social -Bullerjahn*

22:00 *After Party -Nautibar*

Friday, 4 September 2026

Taxonomy and Systematics I. Chair: Marta Álvarez-Presas

- 09:00 Lukas Schärer, Univ. of Basel. Invited Speaker
Exploring the taxonomical foundations of the genus Macrostomum- a current look at the past
- 09:45 Miquel Vila-Farré, MPI-NAT. Organiser talk
Surveying overlooked planarian diversity within the Mediterranean biodiversity hotspot: the Croatian karst and the Vjosa Basin
- 10:30 Ronald Sluys, Naturalis. Short talk
In memoriam: Masaharu Kawakatsu
- 10:45 Alejandro Catalá Jimenez, Univ. of Basel. Short talk
Measuring $\delta^{15}\text{N}$ in low-biomass flatworms: a denitrifier method approach
- 11:00 *Coffee break*

Taxonomy and Systematics II. Chair: Jeremias Brand

- 11:30 Marta Riutort, Univ. of Barcelona. Invited Speaker
Dugesia evolution and other stories: from single gene-based systematics to genomics
- 12:15 Aoi Tsuyuki, Univ. of Tsukuba. Short talk
Hide and seek on corals: unveiling hidden diversity of marine flatworms associated with a variety of corals from Japan
- 12:30 Srishti Arya, NHM & QMUL. Short talk
Phylogenomics for the masses: the utility of transcriptome skimming in limno-terrestrial Platyhelminth taxonomy
- 12:45 Vitor Milanese, USP. Short talk
Highly endemic and unknown: more than 50 undescribed species of land flatworms (Geoplanidae) found in a patch of the Brazilian Atlantic Forest
- 13:00 Marta Álvarez-Presas, Univ. of Barcelona. Short talk
Functional traits associated with invasiveness in terrestrial planarians: a comparative study of invasive and native species
- 13:15 **Concluding remarks**
- 13:30 *Lunch break*
- 15:30 *Collection tour and BBQ*

Saturday, 5 September 2026

Taxonomic Satellite Symposium

- 09:00 **Opening.** Lukas Schärer, Univ. of Basel.

Keynote Lecture

Phylogenetic systematics and the animal tree of life

Christoph Bleidorn

Georg-August-Universität Göttingen, Göttingen, Germany

Since Darwin, it has become clear that the diversity of life shares a common origin and that its evolutionary relationships can be visualized in the form of phylogenetic trees. Today, we are approaching a relatively robust backbone of metazoan phylogeny, with Xenacoelomorpha, Protostomia, and Deuterostomia emerging as major lineages. Flatworms find their place within the lophotrochozoan protostomes.

Here, I trace the changing views of animal evolution, from Haeckel's *Generelle Morphologie* to the era of genome-scale datasets, with a particular focus on flatworms and the methodological developments that have shaped our understanding of their evolutionary history, including an important chapter that unfolded in Göttingen.

Invited talks

Stem cell choices in planarian regeneration

Peter Reddien

Massachusetts Institute of Technology, Department of Biology and Whitehead Institute for Biomedical Research, Cambridge, MA, USA

We found that neoblast fate choices are made in a spatially highly intermingled manner, and are typically distributed broadly. From this disordered state, pattern must be maintained during tissue turnover and regenerated at wound sites. During tissue turnover, we find that post-mitotic progenitors migrate and assort to create pattern. Following injury, progenitor classes proximal to wounds are amplified by increased proliferation, and we suggest that the identity of amplified progenitors is predominantly determined by the positional information environment of the wound. After complete amputation, progenitors produce the blastema. Within the blastema some cellular processes must restore original anatomy pattern. However, a challenge to blastema pattern formation is the fact that differentiated cells appear in the blastema from an early stage of outgrowth. At this early stage, the pattern of positional information, which presumably has guiding influence on tissue organization is not fully restored. Therefore, formation of tissue pattern initiates in a positional information environment that is distinct from the homeostatic state. Indeed, we find that there are transient anatomy pattern errors present in blastemas, that ultimately become resolved. We suggest that cell death is one major route for resolving transient pattern abnormalities in regeneration.

Yin and Yang: what can planarian flatworms teach us about life history trade-offs?

Hanh Vu

European Molecular Biology Laboratory, Heidelberg, Germany

All organisms perform multiple tasks, such as growth, homeostasis, and reproduction. To survive and thrive in the face of competition for finite resources, all organisms evolve to invest energy in traits that maximize their fitness (i.e., reproductive success) within their environment, resulting in trade-offs. These trade-offs are expected to change throughout an organism's life cycle since young and old individuals have different functional demands. The mechanisms of such life history trade-offs are not well understood. Multicellular systems comprise many morphologically and functionally specialized cell types that uniquely influence an organism's ability to perform tasks. Thus, analyzing cellular composition at the organismal level could reveal key biological processes associated with life history traits and potential trade-offs. Here, I will discuss our efforts to use a concept from engineering and economics, Pareto optimality theory, to explore the possibility of inferring life history traits, their trade-offs, and potential regulatory mechanisms from high-dimensional organismal-scale single-cell transcriptomics of planarian flatworms, as well as the prospect of using the extensive functional genomics toolkit of planarians to directly test predicted cause-effect relationships.

Chromosome elimination in the male germline of *Schmidtea polychroa*

Yu-Hsuan Cheng^{1, 2}, Melanie Issigonis^{1, 3}, Phillip Newmark^{1, 2, 3}

¹*Morgridge Institute for Research, Madison, WI, USA*

²*Howard Hughes Medical Institute, Madison, WI, USA*

³*Department of Biology, University of Wisconsin–Madison, USA*

Classic experiments suggested that planarian germ cells could give rise to somatic cell types during regeneration. These experiments capitalized upon the ability of many planarian species to tolerate a wide range of ploidies, from diploid to pentaploid, with particularly intriguing examples of ploidy variation found in *Schmidtea polychroa*. In addition to standard diploids, parthenogenetic strains of *S. polychroa* are common. These animals possess triploid somatic tissues, but they generate haploid sperm: chromosome elimination occurs during male germ cell development to produce diploid, pre-meiotic germ cells. The haploid sperm they produce typically serve only to activate egg development but do not contribute to the zygotic genome. Over forty years ago, Gremigni and colleagues capitalized on these chromosomal differences to reveal that diploid male germ cells (i.e., which had undergone chromosome elimination) could contribute to the regeneration of somatic tissues, demonstrating transdetermination of germline-to-somatic fates. Here, we revisit these classic experiments, combining centromeric FISH probes and markers for progressive stages of germ cell development to define the cell type and developmental stage at which chromosome elimination is occurring. We will also discuss how our recent identification of beta-alanyl-tryptamine as a soma-to-germline signal regulating germ cell development and regeneration will enable studies of the mechanisms of chromosome elimination and germline-to-soma transdetermination.

Signals and Constraints Shaping Planarian Plasticity Across Regeneration, Damage, and Aging

Blair W. Benham-Pyle^{1, 2}

¹*Stem Cell and Regenerative Medicine Center, Baylor College of Medicine, Houston, TX*

²*Department of Molecular and Cellular Biology, Baylor College of Medicine, Houston, TX*

We hypothesize that planarians actively use physiological stress signals to regulate major organismal responses, including regeneration and asexual reproduction. To test this idea, we examined two contexts in *Schmidtea mediterranea* in which physiological state changes dramatically: genotoxic stress and size-dependent fission. Following sublethal irradiation, surviving stem cells remain capable of division and wound localization but fail to mount the proliferative response required for tissue replacement. This inhibition is transient and can also be induced by cisplatin, indicating that it reflects a broader response to genotoxic damage rather than a radiation-specific effect. Single-cell analyses identified changes in injury-responsive cell states and altered Activin/TGF- β signaling after irradiation. Surprisingly, RNAi of Activin pathway components increased injury-induced stem-cell proliferation and permitted regeneration despite substantial depletion of the stem-cell compartment.

We next asked whether physiological stress might similarly regulate the decision to reproduce by fission. Transcriptomic comparisons of large and small asexual animals revealed that increased fission propensity is accompanied by elevated immune, oxidative, proteotoxic, and other stress-associated programs, many involving genes expressed in the nervous system. Spatial transcriptomic analyses further identified size-dependent changes in microglia-like supporting cells, while a high-throughput RNAi screen of nearly 700 genes identified stress-response pathways and neuropeptide-processing enzymes as regulators of fission behavior. Together, these results support a model in which cellular and physiological stress are integrated into organism-level signaling programs that alter whether planarians are able to engage regenerative or reproductive responses. Rather than constitutively deploying their extensive plasticity, planarians appear to regulate and constrain these capacities according to internal physiological state.

You complete me: a uniquely schistosome love story

James J. Collins III

University of Texas Southwestern Medical Center, Dallas, TX, USA

Abstract To Be Determined

Conflicts and constraints on the regeneration potential of the tapeworm *Hymenolepis diminuta*

Tania Rozario

University of Georgia, Athens, GA, USA

Regeneration is widespread in the animal kingdom but even within a limited clade like flatworms, the range of regenerative ability varies widely between species and contexts. Understanding the mechanisms that promote or restrict regeneration can inform us about natural constraints on regeneration and identify potential barriers that can be overcome. The rat tapeworm, *Hymenolepis diminuta*, provides a tractable experimental system that represents a parasitic flatworm with robust yet limited regenerative ability. We previously showed that regeneration competence is restricted to the neck/germinative region (GR), whereas all other tissues fail to regenerate following amputation. Regeneration requires cycling stem cells, but regeneration-competent tissues do not contain a unique stem cell population, and resident GR stem cells can be replaced by transplanted cells. More recent work reveals that the head/scolex exerts dual and apparently conflicting influences on regeneration: it is required for long-term maintenance of the GR, yet it also inhibits stem cell proliferation and proglottid formation. These opposing activities create a spatially defined threshold within the GR that determines regenerative success after injury. Multiple components of the Wnt signaling pathway are expressed in spatially distinct patterns throughout the GR and within developing proglottids. *H. diminuta* regeneration requires Wnt signaling for pleiotropic functions that introduces levels of conflict. Unlike excellent regenerating planarians like *Schmidtea mediterranea*, tapeworm stem cell maintenance requires an optimal level of Wnt signaling and both too little or too much signaling abrogates stem cells. In addition, Wnt signaling regulates the rate of proglottid regeneration in a dose-dependent manner. Together, these findings suggest that regenerative capacity in *H. diminuta* is constrained by competing requirements for stem cell maintenance and axial patterning, and this relationship may extend to other systems with more limited regeneration.

Rewriting the body plan: host signals and body axis plasticity in the development of *Echinococcus*

Klaus Brehm

Consultant Laboratory on Echinococcosis, Institute of Hygiene and Microbiology, University of Würzburg, Germany

The complex life cycle of the tapeworm *Echinococcus multilocularis* displays remarkable developmental plasticity. Following invasion of the mammalian intermediate host, the oncosphere larva undergoes a true metamorphosis into the metacestode, an indefinitely proliferating larval stage that lacks an anterior pole and consists entirely of posteriorized tissue. Conversely, transmission to the definitive host requires the de novo formation of protoscoleces and, consequently, the re-establishment of anterior identity.

Our work indicates that these developmental transitions are controlled by an interplay between conserved body-axis patterning mechanisms, parasite stem cells, and host-derived signals. Canonical WNT signalling plays a central role in maintaining the posteriorized state of the metacestode since interference with β -catenin signalling results in anteriorization, altered stem-cell proliferation, and impaired metacestode formation. During infection, host immune signals appear to be integrated into this developmental programme. Early inflammatory responses support parasite establishment and metacestode development, whereas the expanding parasite progressively generates an immunosuppressive environment. Parasite-derived factors such as the activin-like cytokine EmACT contribute to TGF- β -dependent regulatory immune responses. At later stages of infection, host TGF- β accumulating around parasite lesions can, in turn, activate parasite TGF- β signalling and promote the formation of brood capsules and protoscoleces, accompanied by the re-establishment of anterior identity.

These findings suggest that *Echinococcus* does not simply execute a fixed developmental programme. Instead, it dynamically rewrites its body plan in response to the immunological environment of its host. Recent single-cell transcriptomic analyses further reveal heterogeneity within the parasite stem-cell compartment and identify stem-cell populations associated with developmental competence. Finally, pharmacological manipulation of developmental signalling, including inhibition of WNT-associated pathways, indicates that the mechanisms underlying this extraordinary developmental plasticity may also expose vulnerabilities that can be exploited therapeutically.

Massive elimination of somatic nuclei and extreme metamorphosis of the oncosphere of *Hymenolepis microstoma*

Emilia Failache¹, Jimena Montagne¹, Uriel Koziol¹, Eija Jokitalo², Ilya Belevich²

¹*Universidad de la República, Montevideo, Uruguay*

²*University of Helsinki, Helsinki, Finland*

Cestodes have complex life cycles that include adult and larval forms. The first larva, known as the oncosphere, is highly reduced and specialized for infection of the first host. In this host, the oncosphere undergoes an extreme metamorphosis into the next larval stage (metacestode). Despite the importance of larval development in the life cycle of cestodes, very little is known about these processes.

We have characterized the development of the oncosphere and its metamorphosis in the model cestode *Hymenolepis microstoma*. By combining ultrastructural reconstructions of embryos and infective larvae together with molecular markers, we have characterized the development and cellular composition of the oncosphere. Surprisingly, most differentiated cells of the oncosphere eliminate their nuclei at the final stages of development, including all nerve cells and most muscle cells. These nuclei are eliminated progressively by autophagy, as nuclear herniations are pinched-off and incorporated into autophagosomes, and pharmacological inhibition of lysosomal function blocked the elimination of nuclei. In the infective oncosphere, fewer than 30 nucleated cells remain, including six quiescent undifferentiated germinative cells. After infection of the first host, the germinative cells resume proliferation, and new tegument, muscle and nerve cells differentiate from this pool of proliferating germinative cells. We have found no clear evidence of any differentiated cells from the oncosphere that are retained after metamorphosis. Altogether, our results show that larval metamorphosis corresponds to a form of maximal indirect development, in which tissues are generated de novo from stem cells that were set-aside during embryogenesis.

Multiplexed screening of genome editing techniques in *Macrostomum*

Richard N. Hall

Stowers Institute for Medical Research, Kansas City, MO, USA

Transgenesis is a powerful tool that enables the visualization and perturbation of the molecules and cells that make up an animal. *Macrostomum lignano* is emerging as a powerful system for studying regeneration, owing in part to its genetic tractability. However, developing efficient gene editing approaches has remained challenging, because adapting and testing an ever-growing set of possible techniques one at a time is prohibitively slow. Here, we present two multiplexed screening approaches that rapidly identify successful modes of gene editing in *M. lignano*. The first screen combines a pool of transposable elements with targeted sequencing of germline-transmitting animals, identifying Ac/Ds as an effective transposon for random integration (~20% germline transmission). The second screen measures rates of recombination mediated by phage-derived large serine recombinases and reveals Nm60 and eeBxb1 as efficient catalysts of recombination *in ovo*. Lastly, we combine the two techniques to randomly integrate landing pads throughout the genome, laying the foundation for well-characterized strains that enable the study of *cis*-regulatory logic in a constant genomic context. Together, these approaches accelerate the identification and use of efficient gene editing techniques in *M. lignano* and may be readily applied to other species within and beyond the genus *Macrostomum*.

Identifying somatic neoblast markers in the flatworm *Macrostomum lignano*

Eugene Berezikov

*European Research Institute for the Biology of Ageing, University Medical Center Groningen,
Groningen, The Netherlands*

We use the free-living marine flatworm *Macrostomum lignano* as a model organism to study how stem cells are regulated in the process of regeneration. Compared to the more widely used planarian flatworms, an important advantage of *M. lignano* is the availability of transgenesis methods. However, in contrast to asexual planarians, markers of somatic neoblasts in *M. lignano* were until recently lacking, in part because classic neoblast genes such as *piwi* cannot discriminate between somatic neoblasts and germline cells in sexual flatworms. To address this, we developed several tools in *M. lignano*: efficient knock-in methodology for endogenous tagging of proliferating cells, a single-cell RNA-seq atlas enriched in proliferating cells obtained by FACS-sorting of transgenic reporter lines, and SABER-based RNA in situ hybridization for spatial validation of candidate markers. Using the single-cell atlas we identified diverse germline cell types as well as the population of adult multipotent somatic stem cells driving regeneration. From this dataset, *hes-1* emerged as one of the first examples of genes specifically expressed in somatic neoblasts but not germline cells in *M. lignano*. RNAi of *hes-1* revealed an essential role in the self-renewal of the somatic neoblast, and since *hes* genes are broadly conserved and expressed in stem cells from Hydra to human, the *hes* family may be part of an ancestral program regulating stemness and self-renewal.

Stepwise loss of recombination preceded the origin of asexuality in *Schmidtea mediterranea*

Ajinkya Bharatraj Patil¹, Jeremias Brand², Jochen C. Rink¹

¹University of Basel, Basel, Switzerland

²Max Planck Institute for Multidisciplinary Sciences, Göttingen, Germany

The emergence of sex chromosomes is traditionally hypothesized to occur when a sex-determining locus acquires recombination suppression that subsequently expands. An alternative model suggests that recombination suppression occurs first, with the sex-determining locus emerging secondarily. Chromosome 1 of the hermaphroditic planarian *Schmidtea mediterranea* has been proposed as such a “sex-primed” autosome, characterized by a >300 Mb inversion with suppressed recombination. While *S. mediterranea* typically reproduces sexually, asexual strains also exist. This shift in sexual system is linked to a conspicuous heteromorphic chromosomal translocation also involving the same chromosome, but due to the lack of genomic resources the underlying genomic architecture could not be elucidated. Here we use a highly contiguous, haplotype-phased genome assembly to reconstruct the genomic rearrangements preceding the origin of asexuality. We identify the genomic breakpoint of the translocation to a large tandem repeat gene desert, suggesting no direct gene loss. But beyond this visible translocation, we uncover pervasive chromosomal restructuring across the entire genome. Genomic analyses of wild populations and laboratory strains reveal that these rearrangements are linked to elevated heterozygosity, confirming they acted as barriers to recombination. Our results suggest that successive rearrangements in a sexual ancestor, potentially driven by inbreeding pressure and local adaptation, rendered large portions of the genome functionally asexual prior to the transition to obligate asexuality. These findings support a model where the gradual loss of recombination facilitates shifts in reproductive systems and provides a framework for understanding the diverse sexual systems observed in flatworms.

Microturbellarian genomics, one worm at a time

Christopher Laumer¹, Witold Morek², Erna King², Mark Blaxter²

¹*The Natural History Museum, London, United Kingdom*

²*Wellcome Sanger Institute, Wellcome Genome Campus, Hinxton, Cambridge, United Kingdom*

The rapid improvement of long-read sequencing has precipitated a golden age of biodiversity genomics, with multiple initiatives aiming to assemble chromosome-level genomes from whole regional biotas. However, third-generation protocols still require hundreds of ng of input — around 1000 times the DNA extractable from many meiofaunal taxa, including most free-living flatworm biodiversity.

Here, we present the Picogram-input, Multi-modal Sequencing (PiMmS) protocol. Using open reagents, this enables efficient genomic DNA and mRNA extraction from a single specimen. High-molecular weight DNA is split for both long-range PCR library amplification and multiple displacement amplification (MDA), while the mRNA templates cDNA synthesis via a SMART-seq2-like approach. The protocol takes two days at the bench.

Using seven freshwater meiofauna phyla in laboratory culture, we demonstrate the efficacy of PiMmS with single specimen inputs. *C. elegans* experiments show that PCR and MDA libraries each yield contiguous assemblies but with distinct deficiencies: PCR reads show even coverage but drop out at secondarily-structured and microsatellite loci, MDA reads achieve near-complete base coverage but show wider coverage variation and artificial inversions, producing highly duplicated assemblies. Combining both amplification modes yields assemblies comparable in quality to native DNA, annotatable to a high standard using long-read cDNA from the same specimen. Optionally, PiMmS can also be adapted to amplify PoreC libraries from additional specimens to scaffold into pseudochromosomes.

We demonstrate a real-world application on an acoel collected in British Columbia, *Otocelis luteola*, recovering an assembly in 139 contigs (N50 3.57 Mbp) with 26,626 predicted genes and 74% BUSCO metazoa_odb10 completeness, comparable to other published acoel genomes.

Excessive feeding induces development of a colony-like body plan in paratomous flatworms

Ludwik Gąsiorowski, Katarzyna Tratkiewicz, Monika Sysiak, Denise Klinkenbuß

University of Warsaw, Warsaw, Poland

Microscopic catenulid flatworms reproduce primarily asexually through paratomy. In this process, new head structures are inserted in the trunk of the fully developed worm, followed by the transverse fission that separates the offspring. In some species, however, the regular paratomy might be altered –the new individuals (zooids) are produced, but do not separate. This leads to the development of so-called chains –linear conglomerates of multiple zooids that remain connected tail-to-head. While this phenomenon has been known for over a century, the cellular and molecular underpinnings of alternation between asexual reproduction and chain formation remain unknown. Here, we tested whether chain formation can be triggered by different feeding regimes in the common catenulid genus *Stenostomum*. By manipulating the concentration of the prey ciliate *Paramecium bursaria*, we were able to stimulate chain formation in four species of *Stenostomum*. Using in vivo measurements, staining of mitotically active cells, and transcriptomic analyses, we show that increased food availability accelerates cell division and longitudinal growth, but it does not affect head morphogenesis. Effectively, in the over-fed animals, the longitudinal growth rate exceeds the head morphogenesis rate, enabling the initiation of new head formation before the first round of paratomy concludes. Altogether, our results suggest that asexual reproduction and chain formation do not represent two independent developmental modalities, but rather two solutions of the same developmental program that depends on the environmental input.

Spatial omics of parasitic flatworms – from cell biology to drug discovery

Svenja Gramberg¹, Oliver Puckelwaldt¹, Carolin M. Morawietz², Carolyn E. Brewster³, Frederick Mann^{3,4}, Anoja Perera³, Kaitlyn Petentler³, Seth Malloy³, Erik Wotschel¹, Stefanie Gerbig², Alejandro Sánchez Alvarado^{3,4}, Bernhard Spengler^{2,5}, Simone Haeberlein¹

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⁵TransMIT GmbH, Giessen, Germany

The spatial gene expression and lipid landscape remains a black box for many multicellular parasites. To unlock the secrets of parasite development and organ function, we pioneered the application of spatial transcriptomics in the liver fluke *Fasciola hepatica*, a parasitic flatworm causing zoonotic disease that affects both human and animal health. We also generated the first spatial lipid atlas of *Fasciola*.

Using Curio Seeker, 10X Visium and high-resolution MALDI mass spectrometry imaging (MSI), we produced datasets covering numerous tissue and cell types in cryosections of both the migratory immature and the sexually reproducing adult stages of *F. hepatica*. We discovered distinct patterns of gene expression and lipid distribution along body axes, while other molecules localized specifically to organs such as the intestine or tegument. MSI further resolved several distinct lipid layers within the ovary and substructures within the fluke intestine. RNAi targeting an intestine-specific transcription factor demonstrated its essential role in gut function and intestinal cell proliferation.

In our applied work, we identified tissue-specific expression of drug target genes (β -tubulins, protein kinases) and drug resistance genes (GSTs, ABC transporters). Computational prioritization of targets in tissues critical for parasite survival identified a PKC β inhibitor capable of killing flukes (Gramberg et al., Nat Comm 2024). Similarly, the pan-flatworm target TRPMPZQ was expressed in the tegument, and agonist treatment disrupted this tissue (Sprague et al., Nat Struct Mol Bio. 2024).

The spatial age of parasitology has just begun. Our work demonstrates how spatial technologies can illuminate parasite cell biology and reveal new strategies to combat these pathogens.

Exploring the taxonomical foundations of the genus *Macrostomum*- a current look at the past

Lukas Schärer

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The genus *Macrostomum* (Macrostomorpha, Macrostomidae) currently contains about 200 valid species names, as well as >50 names that are considered doubtful or invalid. Additionally, recent comparative and phylogenomic work has revealed >100 additional species that have yet to be taxonomically named. This makes *Macrostomum* the largest genus of free-living flatworms, only approached by *Pseudoceros* (Polycladida), *Plagiostomum* (Prolecithophora), and *Dugesia* (Tricladida). Such a striking diversity was unforeseen by the founders of flatworm taxonomy, and hence the original species descriptions were often lacking in anatomical, ecological, and geographical detail, leading to open questions with respect to the applicability of these early species names. To make matters worse, recent studies have revealed remarkable convergent evolution in character traits commonly used in morphology-based species descriptions, leaving many of the foundational names on even shakier ground. These unstable foundations often hamper the efficient description of newly uncovered diversity in the genus. I report on my ongoing attempts to recast the taxonomical foundations of the genus *Macrostomum*—and eventually also the Macrostomidae and Macrostomorpha—including a thorough study and documentation of the type and reference materials available in museums and private collections. I conclude that many of the early species names in the genus *Macrostomum* cannot be clarified, and I propose solutions on how to deal with this taxonomically.

Organiser. Surveying overlooked planarian diversity within the Mediterranean biodiversity hotspot: the Croatian karst and the Vjosa Basin

Miquel Vila-Farré¹, Sajmir Beqiraj², Tobias Boothe¹, Maren Brockmeyer¹, Jochen C. Rink¹

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Freshwater ecosystems are among the most threatened habitats on Earth, with approximately one-quarter of freshwater species at risk of extinction. Effective conservation requires accurate biodiversity assessment, including that of overlooked invertebrate groups. Freshwater planarians are one such group. Despite a long history of research in several parts of the Mediterranean region, major geographic gaps remain, including the Croatian karst and the Vjosa River basin.

To address the Croatian knowledge gap, we applied an integrative framework that combined field sampling, COI barcoding, phylogenetics, karyology, and classical taxonomy. This approach doubled the number of freshwater planarian species recorded from Croatia, from eight to sixteen, and expanded taxonomically curated molecular resources for European planariids and dendrocoelids, including COI barcodes and transcriptomic data. The survey also led to the description of a new pigmented *Dendrocoelum* species, revealed highly differentiated haplotypic clades within widespread but poorly studied taxa, and resulted in the rediscovery of a species nearly a century after its last record in Croatia.

We are now applying a similar approach to the Vjosa River basin in Albania, one of Europe's best-preserved river systems, to characterise its planarian diversity and contribute baseline data to ongoing environmental assessment and long-term conservation. Together, these studies reveal substantial overlooked planarian diversity within the Mediterranean biodiversity hotspot and illustrate how integrative biodiversity surveys can fill knowledge gaps, generate robust taxonomic and molecular baselines, and support the conservation of freshwater ecosystems.

***Dugesia* evolution and other stories: from single gene-based systematics to genomics**

Marta Riutort

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The genus *Dugesia* Girard, 1850, is a species-rich group (~110 species) broadly distributed across freshwater environments in Africa, Eurasia and Australasia. In the western Mediterranean, it is the most species-rich freshwater planarian genus, with most species endemic to the region. This diversity, in a geologically and climatically active region, makes the group an interesting model for studying how biotic and abiotic factors drive the diversification and evolution of organisms.

However, there is something else that made them particularly appealing to me: the high proportion of *Dugesia* populations in the region that reproduce asexually by fission. Asexuality has long been considered an evolutionary dead-end because of the genetic load that the lack of recombination, among other effects, may result in. And yet planarians seem to be very successful fissioners, at least in the Mediterranean basin. In this talk, I'll review how 20 years of research in this group, in an original quest to understand the success of the fissiparous lineages, has driven my research into a diversity of fields (taxonomy, phylogeography, evolutionary biology, ...) and through changing technologies, to now reach the possibility of studying at the genomic level the mechanisms that drive their success.

Short Talks

Which cell types respond when a planarian is cut? A single-cell study

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Planarians regenerate entire body parts through the coordinated activation of stem cells and differentiated tissues following injury. The cellular mechanisms that initiate regeneration remain poorly understood.

To identify the earliest events following injury, we performed a highly replicated, high-temporal-resolution multiplex single-cell RNA sequencing time course of regenerating planarians. Our analyses reveal that phagocytic parenchymal cells are the earliest and most transcriptionally dynamic responders to injury, exhibiting two distinct phases of activation. Functional perturbation of phagocytic cell programs prevents neoblast activation, abolishes the early induction of the regeneration-associated transcription factor *runt*, and results in widespread defects in tissue regeneration. These experiments identify candidate signalling molecules required to activate neoblasts and begin to define the molecular mechanisms that initiate regeneration.

Phagocytic parenchymal cells are an enigmatic cell population with proposed immune functions and notable similarities to vertebrate macrophages, yet their role during regeneration has remained unclear. Our findings demonstrate that these cells play an instructive role in initiating regeneration. These results provide a framework for dissecting the molecular pathways that trigger regenerative programmes and offer new opportunities to investigate the evolutionary conservation of regeneration mechanisms across animals.

Characterization of a novel invertebrate DNA sensor with ancient roots in bacterial immune defense

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While regeneration is extensively studied in planaria, their innate immune system remains poorly understood. In an ongoing effort to identify components of the planarian innate immune system, we discovered a novel DNA-sensing protein.

This protein is highly conserved across Protostomia but absent in Deuterostomes. By RNAi-mediated knockdown in *S. mediterranea* we show that it is an essential regulator of cell death and the response to foreign DNA. CRISPR/Cas9 mediated knockout in *Drosophila*, together with *in vivo* infection experiments, corroborate a role as a central regulator of the innate immune response. Interestingly, a recent publication shows that this protein evolved from a bacterial immune effector Purine Nucleoside Phosphorylase (PNP), which halts phage infection by depleting cellular ATP in infected cells. While bacterial defense PNP is activated by upstream phage-sensing proteins, we show by biochemical assays and structural analyses that the planarian protein directly binds to DNA which likely regulates its activity. We therefore propose that this protein represents a novel DNA sensor with a conserved function in invertebrate innate immunity.

Heterologous tissue transplants reveal competition amongst the somatic pluripotent stem cells of planarians

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Cell competition is a fundamental process that influences tissue dynamics, homeostasis, and organismal evolution by regulating interactions between genetically distinct cell populations. While cell competition has been extensively studied in various systems, the mechanisms governing competition among adult pluripotent stem cells remain poorly understood. How genetically diverse stem cell populations coexist, compete, and contribute to tissue maintenance in continuously regenerating organisms remains an open question. Planarian flatworms provide a powerful model for addressing these gaps due to their unique reliance on neoblasts—pluripotent adult stem cells responsible for continuous tissue renewal. This study investigates how induced genetic heterogeneity affects neoblast competition by generating chimeric worms through reciprocal tissue transplantation between genetically distinct strains of the planarian *Schmidtea polychroa*. Using imaging and sequencing, we quantified donor-host cell dynamics, revealing a competitive hierarchy where strains with higher mitotic activity consistently outcompete others. Our findings support a neutral competition model, where proliferation rates, rather than direct antagonism, dictate competitive success. Computational simulations mirrored experimental outcomes and revealed how confirming mitotic fractions could determine the primary predictor of cell competition. Additional factors, such as differentiation rates and regeneration efficiency, further influenced competition outcomes, while genetic relatedness did not. These results suggest that planarians maintain genetic diversity through dynamic stem cell competition, with implications for regenerative biology and evolution. This study provides a novel framework for understanding stem cell competition in regenerating organisms, offering insights into the mechanisms maintaining tissue integrity and genetic heterogeneity.

To be or not to be a cyst: comparative analysis of two distinct regeneration modes in planarian *Phagocata velata*

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Regenerative capacity is a fundamental yet highly variable trait across Metazoa. Although many core mechanisms of regeneration are increasingly well characterized, how intrinsic and extrinsic factors such as age, anatomy, and temperature modulate regenerative outcomes remains poorly understood. Here, we capitalize on the unique regenerative plasticity of *Phagocata velata*, a non-model planarian species that regenerates through two distinct modes: blastema-mediated and cyst-mediated regeneration. Morphologically, the former resembles canonical blastema-mediated regeneration in other planarian species, whereas the latter involves the formation of a protective, jelly-like mucus envelope that encases the regenerating fragment. The regeneration mode adopted by a fragment depends on its size, anterior-posterior position, and culturing temperature, making *P. velata* a powerful system for studying how biological context shapes regeneration.

To establish a cellular and molecular foundation for this system, we generated an individual-resolved single-nucleus transcriptomic atlas from more than 100 animals covering a 1–10 mm size range. This atlas captures the growth trajectory of *P. velata* and identifies cellular and molecular changes associated with a characteristic physiological transition, marked by a yellow-to-gray color shift, that precedes spontaneous fission. In parallel, fluorescent *in situ* hybridization (FISH) of tissue-specific markers revealed extensive tissue remodeling during cyst-mediated regeneration, distinct from the tissue organization observed during blastema-mediated regeneration. Together, these results establish *P. velata* as a tractable comparative model for dissecting how context modulates regeneration.

Comparative proteomics reveals a conserved core of tegumental proteins in cestodes

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Parasitic flatworms are covered by a highly modified syncytial epidermis known as the tegument. In cestodes, the tegument is the main site of interaction between the parasite and the host, however the details of its organization and composition are essentially unknown. We characterized the composition of the tegument of *Hymenolepis microstoma*, *Mesocostoides corti* and the human pathogen *Echinococcus multilocularis* by proteomic analysis on tegument-enriched fractions, and found a conserved core of tegument-enriched proteins in cestodes, including members of the Tegument Allergen-Like (TAL) family, vesicular trafficking components and calcium-sensing proteins. We validated the tegument expression of a subset of such proteins by *in situ* hybridization in combination with tegument labeling. Among these proteins we found a putative active glucose transporter from the SLC5 family. By immunofluorescence we observed its localization on the surface of the tegument. Transcriptomic data suggest that SLC5 expression is activated in the transition between cysticercoid larvae and adult in *H. microstoma*, hence, we hypothesized that it could play a crucial role in the infection of the definitive host. In order to analyze its importance, we developed a tegument-specific knock-down method using morpholino oligos (oligonucleotides analogs) to target a splicing site in the SLC5 transcript. Knock-down in activated cysticercoids altered the splicing of SLC5 mRNA and preliminary results suggest that it slowed cysticercoid growth *in vitro*. Altogether, these results reveal an evolutionarily conserved composition of the tegument of cestodes, and provide a method for functional analysis of genes in this tissue.

Shedding new light on the male-female interaction of schistosomes: the first scRNA-seq analysis of a platyhelminth organ uncovered a RAR-family nuclear receptor in *Schistosoma mansoni* ovaries essential for meiosis progression

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Transcription regulation in platyhelminth development has not yet been adequately investigated, particularly for parasitic flatworms. Here, we made use of single-cell (sc) transcriptomics to detect genes involved in reproductive development of *Schistosoma mansoni* females. This parasitic trematode triggers schistosomiasis, a neglected infectious disease affecting > 240 million people and animals worldwide. The pathology of schistosomiasis is closely associated with schistosome eggs deposited in host organs, especially the liver. In contrast to other trematodes, schistosomes have evolved separate sexes. Remarkably, egg production depends on the pairing (male)-induced maturation of female reproductive organs. Despite this biological significance, molecular mechanisms underlying ovary development and oocyte differentiation remain largely unexplored. Based on an organ isolation procedure established for adult *S. mansoni*, we isolated ovaries of paired females for scRNA sequencing of disassociated oocytes. A total of 1,967 oocytes expressing 7,872 genes passed quality control filtering. Unsupervised clustering revealed four distinct cell clusters: somatic, germ cells and progeny, intermediate and late germ cells. Among distinct marker genes for each cluster, we identified a so far uncharacterized transcription factor of the retinoic acid receptor family, SmRAR. Functional analyses of SmRAR and associated genes demonstrated their sex- and pairing-dependent as well as ovary-preferential transcription patterns and their decisive roles in oocyte differentiation of *S. mansoni* (1).

These findings shed new light on the sexual maturation of the female schistosome which depends on the combination of constant pairing with a male partner plus a favourable host milieu.

(1) Moescheid et al. (2025) Nucleic Acids Res. 53(4):gkae1228. (PMID: 39676663)

Temporary bioadhesion in flatworms

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Macrostomid flatworms can attach and detach from all substrates in diverse aquatic environments several times in a second. This remarkable ability makes them ideal subjects for examining temporary bioadhesion. Using differential gene expression and in situ hybridisation screening, we have identified glue proteins in various species of flatworm from freshwater, brackish water and marine environments. The adhesive proteins are extremely large and not conserved within flatworm taxa. The nature of the releasing molecules remains elusive. To identify and characterise the releasing gland cell, we are employing genome sequencing, single-cell RNA sequencing and in situ hybridisation screening on a new macrostomid species. This species has several characteristics that make it ideal for this study, including a small genome, a very rapid generation time and selfing as a mode of reproduction. We expect the results to provide insight into the biology behind the release mechanism.

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Development of a Cre/loxP-based method of cell lineage analysis to assay neoblast potency in *Macrostomum lignano*

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Adult somatic stem cells (neoblasts) in flatworms are frequently endowed with broad potency and are required for cellular homeostasis and regeneration. Determining the potency of an individual neoblast requires knowledge of the cell lineage derived from a neoblast, and the fates adopted within that lineage. Currently lineage assays are performed either by transplanting a single neoblast into a lethally irradiated host, or by sub-lethally irradiating a flatworm and observing the behavior of the few remaining neoblasts, but an irradiated landscape may skew our understanding of how these cells behave in other contexts. A cell lineage assay should be flexible enough to perform in multiple contexts, and should also allow observation over many cell divisions. The flatworm *Macrostomum lignano* is a highly regenerative species with established transgenesis techniques, so we have undertaken the development of transgenic cell lineage assay in this organism. A “STOP-lox” reporter was designed in which Cre/loxP recombination activates expression of a fluorescent protein that is maintained in all progeny cells. A stable *STOP-lox* transgenic line was established, and when NLS-Cre enzyme is injected into one-cell-stage *STOP-lox* embryos, large regions of fluorescent tissue emerge throughout the course of development. To analyze clones derived from individual neoblasts in the context of homeostasis and regeneration, we are exploring methods for chemically inducing Cre activity in adults. Cell lineage analysis of individual neoblasts in adult *M. lignano* will allow more precise analysis of factors that may influence neoblast potency, such as anatomical position, developmental stage, tissue loss, and irradiation.

No sex? No problem! High intraindividual genetic variability in ancient asexual freshwater planarians

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Long-term asexuality has been considered an evolutionary dead-end, due to reduced genetic diversity and Muller's ratchet, as deleterious mutations cannot be purged through purifying selection. However, some asexual lineages have been proposed to be ancient asexuals, meaning they have maintained asexuality for long periods of evolutionary time, which are known as asexual scandals (i.e. oribatid mites). In a recent study of freshwater planarians of the genus *Dugesia*, asexual populations of the Iberian-Apennines-Alps clade (comprising *D. etrusca*, *D. liguriensis* and *D. ilvana*) showed an unusual phylogenetic pattern, hypothesized to be a consequence of long-term asexuality. This hypothesis was tested through an extensive workflow, showing that this pattern was not a methodological artifact, but the genetic footprint of ancient asexuality, pointing to these asexual populations as being a new asexual scandal.

However, little is known about the genomic consequences of long-term asexuality in agametic asexuality. To investigate this, we obtained SNP data from transcriptomic reads of sexual and asexual populations. At the intraindividual level, heterozygosity was higher in asexual than in sexual populations, meaning high levels of Meselson effect, which indicates the antiquity of asexuality. At the interindividual level, multidimensional scaling plots revealed higher divergence among asexual individuals than among sexuals. Moreover, the ratio of non-synonymous/synonymous mutations (dN/dS) was lower in asexuals, indicating that a mechanism purging deleterious mutations may exist to escape the Muller's ratchet. We will discuss how our results fit the expectations of an asexual scenario under agametic asexuality, and the adaptative potential of the increase in intraindividual diversity.

Hox genes in Xenacoelomorpha

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The explosion of body forms found in bilaterians is tied to the diversification of Hox transcription factors. Hox genes play a crucial role in body patterning along the anterior-posterior axis in most bilaterians. However, the evolutionary history of Hox genes in early bilaterians is unclear. Xenacoelomorpha, marine worms including *Xenoturbella* and the meiofauna groups Acoela and Nemertodermatida, have a simple Hox complement and are of particular interest as they are hypothesised to be the earliest extant bilateral branch. Past surveys of Hox in Xenacoelomorpha were taxonomically limited. Here we analyse the homeodomains and surrounding amino acid motifs coded by Hox, Para-Hox, and extended Hox genes across 40 xenacoelomorph transcriptomes and four genomes, along with representatives of other major bilaterian groups and the anthozoan *Nematostella vectensis*. We show that several previously proposed synapomorphies of Acoela are ubiquitous across both Xenacoelomorpha and the rest of Bilateria. We found new Hox content specific to Acoela and *Xenoturbella* and demonstrated homology between xenacoelomorph antHox and other bilaterian Hox1 genes, though the relationships of centHox and postHox genes remain unresolved either due to rapid sequence evolution or extensive birth-death processes. We propose an ancestral Hox complement for Xenacoelomorpha, and posit that diversification of bilaterian Hox involved both extensive retention and loss of ancestral content. Hox variability between xenacoelomorphs and other bilaterians reflects selective retention of ancestral Hox content rather than affinity to either deuterostomes or protostomes and does not remove support from a monophyletic Xenacoelomorpha sister group to all other Bilateria.

Generalized feedback control in stem cell systems - planarians as a case study

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Planarians, like the species *Schmidtea mediterranea*, are known for their high cellular turnover rate, reversible, allometric growth dynamics and remarkable regeneration abilities. Thus, the underlying stem cell system needs to continuously supply the body with new cells, to enable changes in cell number and composition while maintaining the body integrity, and to robustly respond to strong perturbations like the loss of entire body parts. Generally, this requires feedback loops to balance stem cell proliferation and differentiation as well as cell death, yet a unifying, conceptual understanding of how regulatory rules produce robust homeostasis and tunable growth is currently missing.

We develop a minimal dynamical model, grounded in control theory and analyzed with both analytical and numerical methods, to identify the core principles that allow for robust stem-cell-driven tissue regulation. We examine different feedback paradigms from either stem cells or differentiated cells and quantify how each strategy copes with perturbations across short (homeostatic) and long (growth/degrowth) timescales. Finally, we apply our theoretical framework to the allometric growth dynamics in planarians, which allows us to predict experimentally observed features such as the scaling of stem cell number and activity with worm size.

Evidence of ancient horizontal gene transfer in the human parasite *Schistosoma mansoni*

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Parasitic flatworms include some of nature's most successful and devastating pathogens. Despite having remarkably different physiology and ecological niches, all parasitic flatworms derive from a common ancestor and consequently share several common features. Many of these features, such as the presence of a protective syncytial skin-like tegument, are clearly adaptive; in schistosomes, the tegument allows the blood fluke to hide from the host's immune system while the tapeworm's tegument is responsible for nutrient uptake in these gutless animals. Other common features are not obviously adaptive: parasitic flatworms lack many of the molecular pathways responsible for suppressing mobile genetic elements (MGEs). While the consequences of these absences are not known, it does suggest parasites may experience more MGE activity than other organisms. We recently identified a cki homolog that appears to have arrived in parasitic flatworms by horizontal gene transfer (HGT) from an ancient vertebrate host. MGEs are known to facilitate HGT, so we wondered if the lack of MGE suppression pathways may have created an environment conducive to unusual genetic inheritance in parasitic flatworms so we searched for any other schistosome genes that may have arisen from HGT. Using bioinformatic analysis, we were able to identify several genes that are absent from free-living flatworms but broadly present in parasitic flatworms and vertebrate animals, suggesting that they may have arisen from HGT. Ongoing work is centered on studying these genes to better understand what, if any, role HGT plays in the biology of parasitic flatworms.

In memoriam: Masaharu Kawakatsu

Ronald Sluys

Naturalis Biodiversity Center, Leiden, the Netherlands

The presentation provides a short sketch of the scientific career of Masaharu Kawakatsu and highlights his important contributions on the ecology, taxonomy, biogeography, and nomenclature of triclad flatworms.

Measuring $\delta^{15}\text{N}$ in low-biomass flatworms: a denitrifier method approach

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Despite the ubiquity, high abundance, and likely importance of microturbellarians in benthic food webs, their trophic ecology remains poorly characterized. Stable isotope analysis, an analytic technique that quantifies the ratios of heavy to light stable isotopes, is a commonly used tool for investigating food-web structure. Particularly, the proportion of the rare ^{15}N and the more common ^{14}N , denoted as $\delta^{15}\text{N}$, is widely used as an indicator of trophic position due to the characteristic enrichment of ^{15}N between trophic levels. However, conventional isotope ratio mass spectrometry typically requires milligrams of biomass, limiting the study of meiofaunal taxa. Here, we evaluate the nitrogen denitrifier method as an alternative approach for determining $\delta^{15}\text{N}$ values from few specimens of low-biomass flatworms. We estimated the amount of Nitrogen per worms constructing calibrations curves and evaluated the effect of different preservation techniques. Method performance was assessed using laboratory cultures of *Macrostomum* species as well as field-collected specimens. In addition, controlled trophic chains involving four *Stenostomum* species were established to test whether expected isotopic enrichment across trophic levels can be reliably detected using this approach. Our results show that the denitrifier method allows accurate $\delta^{15}\text{N}$ measurements from as little as six pooled *Macrostomum* specimens enabling trophic analyses of organisms that are typically difficult to access in conventional isotope techniques. This methodological approach provides a practical framework for incorporating microturbellarians into stable-isotope-based food-web studies and contributes to a better understanding of the ecological roles of meiofaunal flatworms in aquatic ecosystems.

Hide and seek on corals: unveiling hidden diversity of marine flatworms associated with a variety of corals from Japan

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Marine polyclad flatworms are mostly known as free-living, but some are specifically epibiotic on other invertebrates such as snails, crustaceans, and brittle stars. To date, polyclads associated with corals have been reported from scleractinian corals *Acropora* and *Montipora* (four species of Prosthiostomidae), the black coral *Antipathella subpinnata* (a single species of Notoplanidae), and *Melithaea* gorgonians (four species of Apidioplanidae). Most of these records are in older literature and their phylogenetic positions are unknown, to the exception of *Prosthiostomum* species associated with scleractinian corals. During our subtidal surveys along Japanese coastal regions, we found over 15 acotylean polyclad species from four families (Apidioplanidae, Notoplanidae, Planoceridae, and Stylochocestidae) attached to a variety of anthozoans. The hosts include not only previously reported taxa, but also other taxa such as toadstool leather coral *Sacrophyton* sp. Interestingly, most epibiotic flatworms are characterized by having similar color patterns with their host corals as reported in previous studies. We also inferred specimens' phylogenetic positions within Acotylea based on molecular phylogenetic analyses using 18S, 16S, 28S and COI sequences, which indicated multiple acquisitions of epibiotic life on corals in Acotylea. Our study contributes to understanding the biodiversity of flatworms as well as symbiotic evolutionary history of coral reefs.

Phylogenomics for the masses: the utility of transcriptome skimming in limno-terrestrial Platyhelminth taxonomy

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Accurate species tree reconstruction relies on integrating information from many genes and sequences. Popular techniques for gathering phylogenetic data suffer from low resolution due to limited sampled loci, priming-site divergence across diverse taxa, or high sample-preparation and sequencing costs.

Here, we explore the potential of transcriptome skimming, whereby we sequence highly expressed phylogenetic markers from the transcriptomes of individual meiofaunal specimens. We minimise library preparation costs by leveraging a bespoke protocol that uses off-the-shelf reagents, achievable in 2-3 days per 96-well plate. Keeping read depth intentionally shallow (50,000-100,000 Nanopore reads per sample), consumables and sequencing can be kept under €10/specimen.

We provide proof-of-concept data from 113 limno-terrestrial Platyhelminthes ('microturbellarians'), demonstrating the efficacy of this approach for molecular taxonomy. At the depths targeted, we recover full-length transcripts from 18S and 28S eukaryotic ribosomal genes, 13 mitochondrial protein-coding genes, and 483 nuclear marker genes, for the majority of sampled individuals. We assess the relative topological similarity and resolution of mitochondrial, nuclear ribosomal, and nuclear protein-coding genes. We also note sequences of non-flatworm origin, likely representing gut contents and/or symbionts, and posing both analytical challenges and opportunities to assess ecological interactions. We taxonomically bin these using a combination of phylogeny-based and sequence-similarity-based methods. We predict that this target PCR-free, transcriptome-wide skimming approach will have broad taxonomic applicability across microturbellarians and neodermatans, as well as other animal phyla. Techniques such as these will be transformative for biodiversity discovery and systematics in a time of rapid environmental change.

**Highly endemic and unknown: more than 50 undescribed species of land flatworms
(Geoplanidae)
found in a patch of the Brazilian Atlantic Forest**

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The Atlantic Forest (AF) is a global biodiversity hotspot and the most devastated Neotropical forest. The world's highest concentration of described species of land flatworms (Geoplanidae) is found in the AF of the Brazilian state of São Paulo (SPS). However, the diversity of these animals in most AF remnants, including large areas of SPS, is still unknown. Surveying new areas is especially important for discovering new species, as recent studies indicate that most of these flatworms have a very restricted range. We sampled two AF regions in SPS that were 100 km apart, one of them with four areas sampled within (5-20 km apart from each other). The animals were identified by morphology. We collected 542 specimens from 67 species. Of these, 58 were undescribed. Only 3 species were shared between the two regions, two of them belonging to species complexes not unveiled yet. In the region with 4 sampled areas, the distribution of the species was very heterogeneous, with only 4 (of the 36 species found) shared between the areas. The high number of undescribed species points to a still insufficient diversity knowledge of this group. The small number of species shared between the regions, even with others already prospected nearby, highlights a high endemism level of land flatworms in the AF. It indicates the need to preserve their remaining populations, since the destruction of small forest areas can lead to the extinction of a large number of species.

Functional traits associated with invasiveness in terrestrial planarians: a comparative study of invasive and native species

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Terrestrial planarians (Tricladida : Platyhelminthes) include some of the most successful invasive invertebrates worldwide, yet the functional traits underlying their invasion success remain poorly understood. In recent years, several alien land planarian species have established stable populations across Europe, raising concerns about their ecological impact on native soil fauna. Understanding the biological features that may facilitate their spread is therefore a big challenge.

Here, we present a comparative study of invasive and native terrestrial planarians combining laboratory observations and experimental approaches. We focus on three invasive species (*Obama nungara*, *Caenoplana coerulea*, and *Caenoplana variegata*) and two native European species of *Microplana*. Animals were collected from the field and maintained under standardised laboratory conditions, allowing controlled comparisons of functional traits.

We investigate regenerative ability, feeding behaviour, and reproductive traits, assessing the potential role of these features in invasion success. Preliminary results reveal interspecific differences in regeneration dynamics and dietary flexibility, with invasive species generally displaying higher tolerance to experimental manipulation and a broader range of acceptable prey. Reproductive observations are ongoing and provide initial insights into variability in reproductive strategies among invasive and native taxa.

Together, these results highlight the importance of functional traits in shaping the invasive potential of terrestrial planarians and establish a baseline for integrating experimental biology with ecological and genomic approaches in future studies.

Posters

Poster 1

Regulatory logic of size and allometry in planarian flatworms

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How animals coordinate the growth of tissues, organs, and the whole body to achieve appropriate size and proportion remains a fundamental unresolved question in biology. Planarian flatworms provide a unique opportunity to address this question due to their remarkable ability to reversibly adjust their body length over an order of magnitude in response to food availability. The overarching goal of my PhD project is to uncover the regulatory logic of size and allometry in planarians. To accomplish this, I will combine high-throughput single-cell transcriptomics and chromatin accessibility profiling to reconstruct cell-type-resolved gene regulatory networks associated with body size in the model species, *Schmidtea mediterranea*, and then assess the functional requirement of these networks through large-scale RNA interference screening. Here, I will first present our reconstruction of whole-animal growth dynamics across an order-of-magnitude variation in body length. We developed a multiplexed single-cell transcriptomic approach that preserves the cellular composition of individual animals, allowing us to systematically quantify how tissues and organs scale with body size. Second, I will describe our initial adaptation of a high-throughput multiplexed chromatin accessibility profiling workflow to planarians, enabling the identification of cell-type-specific cis-regulatory elements and transcription factors associated with body size across hundreds of individual animals. Together, these methods lay an important technical and conceptual foundation for studying the regulatory mechanisms that coordinate animal size, tissue scaling, and allometry.

Poster 2

***Camerata robusta* as new model for planarian embryonic development**

Philipp Weiss, Jochen C. Rink

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Planarian embryogenesis proceeds through blastomere anarchy, a highly derived developmental mode in which early blastomeres lose spatial attachment. They reassemble into a transient, yolk-feeding larva-like stage that subsequently remodels into the juvenile worm. The axial formation, tissue organization, and cell lineages remain poorly understood during this process.

Here, we introduce *Camerata robusta* as a tractable model producing large numbers of embryos, compatible with molecular approaches, including RNA interference, in situ hybridization, and hybridization chain reaction. Adding dense temporal sampling combined with transcriptomic profiling

and spatial validation, we are generating a developmental atlas spanning the complete 12-day embryogenesis, from cocoon deposition to hatching.

This analysis reveals two major, system-wide transcriptomic transitions occurring between days 2-3 and days 8-9, defining discrete phases of developmental reorganization. The early transition coincides with the emergence of piwi+ cells, suggesting the onset of neoblast lineage specification, and is accompanied by a global reduction in mitotic activity. The later transition aligns with axial elongation and consolidation of juvenile morphology.

Together, this work provides a high-resolution molecular framework for *Camerata robusta* embryogenesis and builds a foundation for comparative analyses of stem cell ontology, pattern formation, and developmental timing in planarians.

Poster 3

Hydroxyurea-mediated perturbation reveals quiescent neoblast populations during planarian regeneration

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Planarians are a powerful model for studying regeneration, driven by a population of adult stem cells known as neoblasts. While the proliferation peak after injury has been generally well characterized, the contribution of different cell-cycle states to the regeneration dynamics remains incompletely understood.

In contrast to the widely used irradiation approach to eliminate neoblast from the worm body, we apply a S-phase inhibitor as a chemical perturbation to reversibly suppress neoblast proliferation without inducing widespread tissue damage. Using this strategy, we investigated neoblast behavior during regeneration under defined perturbation conditions.

This treatment led to a rapid reduction in mitotic activity and impaired regenerative outcomes, consistent with effective depletion of actively cycling neoblasts. However, the recovery after drug removal suggests the persistence of a subpopulation of neoblasts that are not immediately affected by S-phase inhibition.

Our results support the existence of quiescent or slow-cycling neoblast populations, potentially residing outside the S-phase and capable of contributing to regeneration upon appropriate stimuli. These populations appear to be differentially recruited under conditions such as feeding or wounding, indicating dynamic regulation of stem-cell states.

Together, this work establishes pharmacological perturbations as a versatile approach to dissect neoblast cell-cycle heterogeneity and provides new insights into how distinct stem-cell states contribute to robust regeneration.

Poster 4

Comparative morphology and developmental mechanisms of planarian auricles

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Chemosensation plays a critical role in governing essential tasks such as foraging, predator avoidance, toxin evasion, and social interactions. In planarians, the chemosensory system is primarily localized within the auricles and pharynx; however, how auricle morphology and its underlying genetic mechanisms diversify across lineages to drive sensory adaptations requires further investigation. This project aims to investigate planarian chemosensory evolution by integrating morphometrics, behavioral assays, and transcriptomics across surface species and the cave dwelling *Girardia multidiverticulata*. Our previous results showed that a head shape PCA across four species with diverse auricle morphology (PC1 = 57.78%, PC2 = 23.06%) suggested that auricle variation may act as an important factor in shape diversification. To explore the molecular basis of these structures, ongoing comparative RNA-seq analyses aim to identify conserved genetic auricle markers across species. Regarding our current functional findings, we demonstrate that the cave planarian presents significantly longer auricles and larger pharynges than its surface congener. Behavioral assays using food stimuli revealed that while high concentrations elicit similar responses, cave planarians display higher sensitivity, velocity, and activity at low food concentrations (t-test or Kruskal-Wallis, $p < 0.05$). Conversely, they exhibit delayed missing-tissue response assessments and slower sensory recovery during regeneration. Transcriptomic analysis of head regenerating tissues identified 5,297 differentially expressed genes (DEGs), revealing a transcriptional shift at 14 days post-amputation that correlates with chemosensory functional recovery. Ultimately, by connecting these transcriptomic profiles to behavioral and structural adaptations, this study provides novel insights into the genetic and ecological mechanisms driving chemosensory auricle shape evolution.

Poster 5

Multiplexed gene expression detection in planarians using in situ hybridization chain reaction

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Planarians play an important role in uncovering the mechanisms behind whole-body regeneration. Due to the limited toolkit available for planarian research and the absence of stable transgenic lines, the standard approach to studying gene expression in intact animals is fluorescent in situ hybridization (FISH). However, the limited number of available haptens as well as the requirement for sequential probe development makes multiplexed experiments time-consuming and labor-intensive. A newer method, in situ hybridization chain reaction (HCR), addresses these challenges by offering parallel probe development using fluorescent labelled hairpins that allow for probe-specific binding. Although HCR is already been well-established method for many model organisms, the published protocols perform poorly on whole-mount planarian samples.

Using the model organism *Schmidtea mediterranea*, we present a systematic optimization of the HCR protocol for whole-mount staining in planarians. Our optimization results in robust staining that is faster and less labor-intensive than traditional FISH. We demonstrate that the protocol can be shortened by a day without compromising the quality of the signal, and show that HCR is compatible with several mounting media. Furthermore, we demonstrate that standard HCR protocol can be used to evaluate gene expression in cells dissociated by ACME. Overall, our optimizations establish HCR as a valuable addition to the planarian toolkit, particularly for multicolor gene expression studies in intact animals and enables highly sensitive, multiplexed gene expression visualization within three days, irrespective of the number of targets.

Poster 6

The curious case of tryptophan: how an amino acid shapes sex in planarian flatworms

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Reproductive strategy is a central determinant of fitness, shaping how successfully an organism propagates in a changing environment. Although obligate sexual reproduction is prevalent in the animal kingdom, asexual and facultative reproduction have evolved repeatedly across many lineages. This raises two compelling questions: What fitness advantages do these reproductive strategies confer? And how do novel reproductive phenotypes and behaviors arise mechanistically? Planarians are excellent model systems to answering these questions, as many species can switch between reproductive modes in response to environmental cues. Beyond temperature, essential nutrients also play a role. Kobayashi and his colleagues demonstrated that dietary tryptophan promotes post-embryonic ovarian development in *Dugesia ryukyuensis*. However, it is unknown whether tryptophan exerts the same effect to facilitate sexual reproduction in other planarian species. Here, we present our ongoing efforts to systematically investigate the role of tryptophan in sexual reproduction across several non-model planarian species, including *Phagocata morgani*, *Girardia tigrina*, and *Phagocata velata*, as well as the model species *Schmidtea mediterranea*. Our work aims to lay the groundwork for testing the hypothesis that the differential regulation of tryptophan metabolism is a central mechanism underlying the evolution of asexual reproduction across planarian lineages.

Poster 7

Riboflavin (Vitamin B2) supports neuronal regeneration and sensory function in the freshwater planarian *Schmidtea mediterranea*

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Regeneration requires the coordinated restoration of complex tissues and is influenced by cellular redox metabolism, which regulates cell survival and differentiation. While riboflavin (vitamin B2) is an essential precursor of the metabolic cofactors flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD), the role of these redox-sensitive flavins during whole-body regeneration remains poorly understood. Here, we investigate the spatial distribution and functional significance of riboflavin and its associated metabolic machinery during regeneration in the highly regenerative planarian *Schmidtea mediterranea*.

Using live *in vivo* imaging, we identified neural-like strands enriched in flavin-derived fluorescence that exhibit dynamic responses to external stimuli. Spectral analyses confirmed emission characteristics consistent with flavins. Spatial mapping at both the transcript and protein levels demonstrated that riboflavin transport and metabolism are associated with neural tissues, including the cephalic ganglia, ventral nerve cords, and the subepidermal nerve net. Functional disruption of riboflavin metabolism impaired locomotion, reduced neuronal marker expression, and impaired eye formation as well as cephalic ganglia development, indicating that flavin metabolism is required for proper nervous system function and reconstruction. As riboflavin and its cofactors are known to influence the redox balance, we further explored their potential role as redox-sensitive components during regeneration.

Together, our work identifies a critical role for riboflavin during neuroregeneration and expands our understanding of the metabolic requirements underlying regeneration in *Schmidtea mediterranea*.

Poster 8

Decoding selective autophagy in planarian regeneration

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Planarians have a remarkable capacity to regenerate entire organisms from small tissue fragments and continuously remodel their body proportions in response to intrinsic and extrinsic factors, making them exceptional model systems for studying tissue homeostasis and regeneration. While autophagy has emerged as a critical regulator of regeneration, the molecular components of these pathways remain largely uncharacterized in flatworms.

Selective autophagy stands out among the autophagy pathways as a precise degradation mechanism, ensuring the removal of damaged components to preserve cellular integrity, particularly in response to stress. This specificity is conferred by selective autophagy receptors (SARs), which recognize cargo and shuttle it to the degradation machinery via conserved ATG8-interacting motifs that bind directly to ATG8, a ubiquitin-like protein at the core of the autophagic machinery. Despite their functional importance, the full repertoire of SARs across species is still poorly understood.

The overarching goal of my master's project is to use cross-species ATG8 interactome analyses to identify candidate ATG proteins and SARs in planarians. Then, we will use RNAi-mediated knock-down to functionally assess their roles during regeneration. This combined approach enables us to transition from molecular identification to functional characterization, offering new insight into the evolutionary conservation of selective autophagy and its role in driving stem cell-mediated tissue plasticity in planarians.

Poster 9

Transcriptional dynamics of position-dependent regeneration failure in *Planaria torva*

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Regeneration varies widely across animals, yet the regulatory basis for this variation remains poorly understood. Planarians are ideal for studying this: *Schmidtea mediterranea* can regenerate an entire animal from a single stem cell, whereas others, including *Planaria torva*, cannot even regenerate heads from tail pieces.

Using FISH, we found that *P. torva* exhibits highly conserved position-dependent patterning gene expression comparable to *S. mediterranea*, including head marker *sFzd1*, tail markers *Wnt11-1* and *Wnt11-2*, neural marker *Hh*, and midline marker *Slit1*. Despite similar expression patterns, *P. torva* has markedly different regenerative capacity, making it an ideal model for investigating regeneration defects.

We generated a time-course RNA-seq dataset (0-336 hpa) by sampling matched regions along the anterior-posterior axis during *P. torva* regeneration. We identified known wound-response genes (e.g., *Egr* and *Evi*) and previously undescribed candidates. Anterior marker orthologs were not detected in posterior head-regenerating fragments. Instead, these fragments expressed posterior pole markers. Two key regulators, *Notum* and *Wnt1*, showed divergent expression patterns compared to *S. mediterranea*. *Notum* expression was initially restricted to a small number of cells at head-regenerating wounds before later appearing at other wound sites, while injury-induced expression remained restricted to anterior wounds.

Combined with previous findings that β -catenin knockdown partially rescues *P. torva* head regeneration defects, our results suggest that the upstream regulatory network of Wnt/ β -catenin signaling may represent an evolutionary hotspot underlying variation in regenerative capacity. These findings provide new insight into the transcriptional logic underlying position-dependent regeneration failure in planarians.

Poster 10

Bacterial Infection-Associated Mortality in *Dugesia gonocephala* Cultures Using Metagenomic Sequencing and Histology

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The freshwater planarian *Dugesia gonocephala* is a species commonly found in clean, well-oxygenated freshwater habitats and it is considered an indicator of good water quality. However, long-term maintenance of laboratory cultures was often complicated by unexplained mortality events frequently associated with the appearance of tissue lesions. Bacterial infections were suspected to play a major role in these processes, yet their progression and causative agents remained poorly characterized.

In this study, the course of bacterial infection-associated mortality in *D. gonocephala* cultures was monitored and compared between untreated populations and cultures treated with the antibiotic gentamicin. The presence and distribution of bacteria within planarian tissues were examined using Gram staining techniques. In parallel, metagenomic sequencing was exploited to characterize the microbial communities associated with affected individuals and to identify potential pathogenic taxa involved in lesion formation and mortality. Based on the metagenomic results, a targeted qPCR panel was developed for the detection and quantification of selected bacterial taxa associated with infection.

This combined histology, metagenomic, and molecular approach aimed to provide insight into the dynamics of bacterial infections in planarian cultures and to improve culture management strategies through better understanding of infection sources and progression.

Poster 11

Probing the existence of genetic mosaicism in the freshwater planarian *Dugesia subtentaculata*

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Genetic mosaicism, defined as the co-existence of genetically distinct cell lineages within a single individual, arises from the accumulation of somatic mutations throughout life. Nevertheless, how different reproductive strategies influence the transmission and extent of this intra-individual variability remains unclear. We address this in the freshwater planarian *Dugesia subtentaculata*, which exhibits egg-laying, fissiparous, and facultative populations. By combining field sampling across the Iberian Peninsula with ploidy assessment and population phylogenomics, we characterized five populations with diverse reproductive modes. We identified a predominance of triploid individuals ($3n=24$) alongside diploids ($2n=16$), which occasionally originate from the same egg capsule in a facultative population, suggesting irregular meiosis in which uneven chromosome pairing generates oocytes with different chromosome numbers. Phylotranscriptomic analyses recovered a geographic structure rather than clustering by reproductive strategy. Using this population-level framework as a baseline, we found that while adults can be mosaics regardless of reproductive mode, divergent haplotypes are more predominant in fissiparous individuals. Interestingly, recently hatched individuals were not mosaics, demonstrating how the zygotic bottleneck prevents the inheritance of mosaicism. Nevertheless, highly divergent haplotypes were detected in triploid, non-mosaic hatchlings from a facultative population, suggesting that mutations accumulated during asexual periods could be retained in unreduced oocytes, and then transmitted to the offspring upon fertilization by haploid sperm. Together, our findings suggest that asexual reproduction could act as a catalyst for somatic evolution rather than being an evolutionary dead end, allowing somatic mutations to be transmitted across generations and transforming individuals into dynamic mosaics of actively evolving cell populations.

Poster 12

Middle juice: designing a book to share the secrets of planarian cells

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Middle Juice is an illustrated book exploring high resolution cellular anatomy of the planarian flatworm *Schmidtea mediterranea* using SBF-SEM data. The title “middle juice” is a translation of the word “mesenchyme”—a reference to the messy, seemingly-unordered appearance of the internal structure of these animals. The primary goal of this work is to communicate to a general audience how animals are composed of cells. Secondary goals include: (1) teaching how to interpret EM images, especially as a section of a 3D structure, paused at a particular moment in time, and (2) to serve as a reference of different cell types, including 3D morphology, for planarian and other flatworm researchers.

Poster 13

Toward automated morphological stereotype acquisition of flatworm for neuroactivity assessment of compounds

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Planarians are aquatic flatworms with a centralized nervous system harbouring neurotransmitter systems including serotonergic, dopaminergic, GABAergic and cholinergic pathways. This neurochemical complexity makes planarians powerful invertebrate models for the pharmacological and ecotoxicological assessment of active compounds. Upon exposure to such compounds, planarians adopt characteristic and reproducible body postures, termed morphological stereotypes, that reflect perturbations in specific neurotransmitter circuits. However, the manual scoring of these stereotypes across large experimental cohorts remains a time-consuming bottleneck, introducing inter-observer variability and severely limiting experimental throughput.

We present FlatMorphAI, an end-to-end automated pipeline combining semantic segmentation and prototype-based classification to enable objective, high-throughput morphological stereotype classification from brightfield images. Individual worm body regions are first delineated using a Mask2Former model. Each segmented individual is then classified into one of six known stereotypes (C-shape, Screw-like, Snake-like, Walnut, Wildtype, Bridge-like) using a FasterViT-2 encoder operating in a learned embedding space. Classification relies on Mahalanobis distance scoring against class prototypes anchored in this embedding space, conferring inherent few-shot adaptability to novel stereotypes without full model retraining. Segmentation-aware classification ensures predictions are conditioned on anatomically coherent body regions, reducing the influence of environmental confounders.

The pipeline is a standalone desktop application to facilitate community adoption. FlatMorphAI achieves high segmentation fidelity on challenging images of planarians within well-plates, alongside high classification accuracy, providing a standardised, reproducible and scalable framework for neuroactivity profiling of compounds in planarian models, with direct applicability to neuropharmacological and ecotoxicological research.

Poster 14

From histology to 3D micro-volumetry

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Reconstruction of sexual apparatus in planarians for taxonomic purposes is tedious microscopy process which require a bit of drawing skills from the researcher. In this work, we have prepared set of high-density histology slides from a single animal (*Schmidtea polychroa*) and after digitalisation, we processed them into a high resolution 3D model, enabling micro-precise volumetric imagery and analysis of internal organs.

Counting of planarian endobionts, epibionts and parasites, their distribution and orientation is also possible using this method. Scans of individual slides - layers - can be used in WSI imagery tools as well.

Poster 15

Uncovering the molecular mechanisms underlying genomic plasticity in planarians

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Planarians have the exceptional capacity to perform full body regeneration, which is made possible by neoblasts: adult pluripotent stem cells that allow the dynamic renewal of all cell types through the life of the worms, hence also depriving them from a developmental single-cell bottleneck. The Rink laboratory recently discovered the general loss of Metazoan ancestral linkage groups (MALG) in Platyhelminths, including a drastic randomization of gene order in multiple planarians with no apparent synteny emergence (Ivanković et al. 2024). Interestingly, flatworms are also known for their remarkable resilience to irradiations. We hypothesize that the highly efficient DNA repair machineries at work in neoblasts for this exceptional coping capacity to genotoxic stress are the same error-prone pathways responsible for the rapid synteny degradation within and between species. However, planarians' intriguing evolution goes along with a loss of many otherwise highly conserved genes, and neither the mechanisms nor the genomic consequences of planarian DNA repair have been clearly elucidated. This project aims at filling this gap and systematically investigating DNA repair pathways in planarians. After identifying DNA repair orthologs, we assess their involvement in *Smed*'s response to irradiative stress and study the associated genomic structure variations. These observations will be confirmed by deciphering DNA scar patterns at translocation loci in structurally divergent *Schmidtea* species and functionally testing the discovered mechanisms in evolutionary distant planarians. This multidisciplinary approach will shed light on planarians extreme resilience to genotoxic stress and associated rapid, non-conservative genome evolution.

Poster 16

To die or not to die: cell-type-specific turnover dynamics during homeostasis and regeneration of the planarian flatworms.

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Cellular turnover, the continuous replacement of cells through proliferation, differentiation, and death, underlies tissue homeostasis and regeneration. Yet, we lack a mechanistic understanding of how turnover is regulated in a cell-type-specific manner across the organism and how it is linked to regenerative capacity. Planarian flatworms offer an ideal system to address these questions, as they not only maintain high lifelong turnover but can also regenerate a complete organism from any cut fragment within weeks.

We are currently developing TrackerSci2, a sequencing-based method that converts metabolic DNA labeling into a quantitative, single-cell-resolved signal integrated with whole transcriptome profiling, enabling organism-wide, longitudinal measurement of cell-type-specific turnover dynamics. We aim to apply this technique to the model planarian *Schmidtea mediterranea* to generate a turnover atlas resolved by cell type across the entire organism. By comparing homeostatic and regeneration-induced dynamics, we will investigate how turnover programs are rewired to support tissue rebuilding while maintaining organismal size and proportionality. Finally, functional perturbation of candidate regulators identified through this analysis will be used to find pathways that causally control turnover modulation during regeneration.

Together, this work aims to establish a single-cell framework to measure cellular turnover dynamics across all tissues in an entire organism and to investigate its regulation and its link to regenerative capacity.

Poster 17

No guts, no glory: morphometric analysis of the planarian gut in 2D and 3D

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The planarian *Schmidtea mediterranea* possesses a highly branched intestinal network composed of three primary gut branches and multiple secondary and tertiary branches. In asexual strains, these animals undergo dramatic and reversible changes in body size in response to feeding and starvation, enabling the study of organ scaling independently of chronological aging. During growth, the gut develops increasingly complex branching patterns, whereas during degrowth this complexity is reduced, raising fundamental questions about the mechanisms regulating gut architecture and remodeling.

Despite the importance of the planarian gastro-vasculature in physiology, a comprehensive quantitative characterisation of gut morphology has not yet been performed. Here, we establish imaging and analysis pipelines to quantify planarian gut architecture in both 2D and 3D. Using newly identified gut markers in combination with confocal and light-sheet microscopy, we generated high-resolution datasets of the intestinal network across different body sizes.

In 2D, we quantified key branching parameters including while in 3D, volumetric reconstructions enabled measurements of intestinal volume and global architectural organization. Together, these approaches provide the first systematic morphometric framework for the planarian gut and establish quantitative tools to investigate how intestinal architecture scales during growth and degrowth. Our work lays the foundation for future studies addressing the molecular and cellular mechanisms underlying gut remodeling and organ-scale plasticity in planarians.

Poster 18

Comparative functional genomics approach in cestodes: regeneration as a drug target

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Cestodes exhibit a remarkable regenerative capacity that is essential for their growth, persistence, and pathogenicity within the host. However, the molecular mechanisms underlying this process remain poorly understood, particularly in medically relevant parasitic species such as *Echinococcus granulosus* and *Echinococcus multilocularis*.

This project aims to decipher the molecular basis of regeneration in cestodes and evaluate its potential as a therapeutic target. Using *Mesocostoides corti* as a tractable experimental model, we have defined early, intermediate, and late stages of regeneration following tissue amputation and *in vitro* culture. We combined morphological and cellular analyses with markers of proliferation and the nervous system. After longitudinal cutting of the worms, there is a large increase in proliferation in the first 48 h after amputation. The nervous system was followed by immunofluorescence; a partial recovery was observed at 72 h after amputation and normal morphology was reached after one week.

We are currently generating biological samples for stage-specific transcriptomic profiling (RNA-seq) to identify key genes and regulatory pathways driving regeneration. These pathways will be functionally evaluated using pharmacological inhibitors to assess their role in regenerative processes. Preliminary results will be presented at the conference.

To establish translational relevance, selected targets will be validated in *Echinococcus* spp. using established *in vitro* culture and drug screening systems, linking regeneration mechanisms to parasite survival and viability.

Overall, this study aims to identify conserved regeneration pathways as essential drivers of parasite biology and novel druggable targets, providing new insights into cestode regeneration and opening avenues for improved therapeutic strategies.

Poster 19

From a complex parasite to single cells: the road towards a single-cell atlas of *Fasciola hepatica*

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The parasitic trematode *Fasciola hepatica* causes the globally prevalent zoonotic disease fascioliasis. The widespread rise of resistance against the gold standard drug triclabendazole generates a need for novel treatment options. To date, basic knowledge of the cell-specific gene expression repertoire is missing. Advances in transcriptomic technologies enable transcriptome analysis of a whole organism at single-cell resolution. These kinds of data could be an invaluable resource for research on drug target genes.

Here, we report the journey towards the first whole-organism cell atlas of the adult stage of *F. hepatica*, which will serve as a basis for single-cell expression analysis.

Using a novel workflow featuring a dissociation protocol that produced high-quality single-cell preparations, we successfully annotated 15 distinct cell clusters. The clusters were mapped to multiple tissues of the parasite, including gut, vitellaria, ovary, and testes. Given the essential roles of protein kinases (PKs) in cellular processes, we furthermore curated the full kinome of *F. hepatica* using a genomic-phylogenetic approach, which identified 245 PKs. Transcriptome-wide expression analysis of PKs revealed cluster-preferential expression of several kinases. We prioritized one of the described clusters based on its expression of already known drug targets. The p21-activated kinase PAK4 was targeted using an commercially available inhibitor, which showed in vitro activity against all intra-mammalian stages of the parasite.

With the *Fasciola* cell atlas, we can gain valuable insights into the biology of this parasite, predict gene function, and cell differentiation. Furthermore, the dataset proved its value as a resource for future drug target discovery.

Poster 20

Head regeneration in *Microstomum lineare*

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We investigated de novo brain regeneration in *Microstomum lineare*, a limnic flatworm of the order Macrostomorpha. This species reproduces asexually through paratomy, a process in which new zooids develop their organs before separating from the parent.

Worms were decapitated anterior to the pharynx of the anterior-most zooid to remove the mature brain. However, the exact position of the amputation varied slightly among individuals. To determine whether the amputation had completely removed the brain or had only partially injured it, we immediately fixed the excised head fragment from each worm and stained its serotonergic nervous system. The corresponding headless amputees were allowed to regenerate for seven days before fixation and staining. This approach enabled a direct comparison between each regenerated individual and its corresponding excised head fragment at day 0.

Our findings revealed that amputees from which the brain had been entirely removed failed to regenerate at all. In contrast, individuals that retained some partial brain tissue were able to regenerate anterior structures. These regenerates not only restored their injured brains but also developed a new rostrum.

These results reveal a striking contrast between pregeneration and regeneration in *Microstomum lineare*. During paratomy, these flatworms can pregenerate, forming new brains and anterior structures before fission. However, after decapitation, individuals were unable to regenerate brains de novo. Successful regeneration occurred only when some residual brain tissue was present.

Poster 21

Efficient genomic sample preparation via barcoded multiple displacement amplification, with applications to marine meiofauna

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Communities of microscopic organisms, such as the interstitial meiofauna or zooplankton, represent a major reservoir of Earth's biodiversity but remain understudied and poorly represented in databases. The unparalleled phylogenetic diversity of such communities presents a key technical challenge: "universal" COI primers often show variable amplification success across taxa, while more conserved markers (e.g. 18/28S rRNA) fail to capture species-level divergences. Skim-sequencing is a compelling alternative, promising target-PCR-free retrieval of high copy number loci.

Here, I present a novel wet-lab approach to genomic library preparation suited to such aims, essentially a modification of the well-known "multiple displacement amplification" technology. In barcoded MDA (bMDA), sample-specific indexes are incorporated at the 5' of the random primers. An additional 5' tag allows indexed molecules to be immobilized on streptavidin beads and released as needed, enabling bead-based sample normalization and further simplifying workflows.

Given an initial investment in consumables, bMDA allows operators to spread the cost of library preparation across dozens of samples. The marginal cost for a single sample in a 96 well plate may be as low as €3-5. With contemporary sequencing costs now well under €5 (in some cases, under €1) per Gbp, this positions genome skimming on economic parity with conventional Sanger DNA barcoding.

I will show pilot data proving the principle with nanopore sequencing of model freshwater invertebrates, plus preliminary results demonstrating a real-world application of bMDA to genome skimming of digitally photo-vouchered marine microturbellarians, annelids, and other meiofauna, collected subtidally in British Columbia in 2023.

Poster 22

Chromosome-scale genomes of *Dugesia* reveal contrasting modes of genome size evolution and structural stability in flatworms

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High-quality, chromosome-scale genomes are crucial for understanding biological processes, yet many metazoan lineages, including most Lophotrochozoa, remain underrepresented in genome databases. Among these, planarians (Platyhelminthes, Tricladida), particularly *Dugesia*, are a globally distributed and phenotypically diverse group that has become an important model in evolutionary biology, notably for investigating the genetic effects of agametic asexuality. However, the lack of chromosome-scale assemblies has limited progress. Here, we present the first chromosome-scale genomes of four Western Mediterranean *Dugesia* species, displaying the first intra- and intergeneric comparative analyses. Comparison with the regeneration model organism *Schmidtea mediterranea*, rejects a whole-genome duplication event as the cause of differences in chromosomal number and genome size between genera. Instead, *Dugesia* shows extensive lineage-specific and differential expansions of DNA transposable elements, likely contributing to genome size variation during diversification. Despite differences in the dynamics of structural genome rearrangements observed between genera, both groups lack the conservation of ancestral metazoan linkage groups, supporting the idea that genome structural instability is a key feature of flatworm genome evolution. Our newly generated genomic resources and findings offer vital insights into the genetic basis of diversification and establish *Dugesia* as a valuable model for studying metazoan genome dynamics, and pave the path for future endeavours in the group, including the study of the evolution of alternative reproductive systems.

Poster 23

Genome-wide histone modification maps reveal stage-specific chromatin remodeling in *Echinococcus multilocularis*

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Echinococcus multilocularis, the causative agent of alveolar echinococcosis, undergoes major developmental transitions requiring extensive regulation of gene expression, yet its epigenetic landscape remains uncharacterized. Here, we established an integrated genomic, transcriptomic, and epigenomic resource for *E. multilocularis*. RNA-seq-guided genome reannotation identified 11,108 gene models, including 1,977 candidate novel loci, and substantially improved gene structures and untranslated-region annotation. We further identified 1,596 long non-coding RNA transcripts representing 810 loci, many of which displayed developmental- or condition-specific expression. We generated the first high-resolution genome-wide ChIP-seq maps of eight histone modifications (H3K4me3, H3K9ac, H3K9me3, H3K36me3, H3K27me3, H4K20me1, H4K12ac, and H3K23ac) across non-activated and activated protoscoleces, metacestodes, and stem cell-enriched primary cell cultures. Chromatin-state analysis revealed extensive remodeling during development. Differences between stem cell-enriched primary cells derived from metacestodes and metacestodes consisted predominantly in H4K20me1 gain and H3K27me3 loss. Protoscolex activation, an essential infection step, was dominated by widespread H3K27me3 loss, affecting 42.5% of genome-wide domains. Integration with transcriptomic data showed that histone modification profiles predicted gene expression with moderate-to-strong accuracy and revealed developmental differences in chromatin–transcription coupling. Together, these results establish a comprehensive epigenomic framework for *E. multilocularis* and identify extensive, stage-specific chromatin remodeling as a prominent feature of parasite development.

Poster 24

Applicability of a formalin-fixed paraffin-embedded DNA extraction kit for acoel specimens and the effects of fixatives on DNA sequencing

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In acoel systematics, morphological descriptions based on serial histological sections have been the norm since the early 20th century. Acoel classification has been established primarily on the basis of features of the copulatory organs. Since nucleotide sequencing technology became widely available in the 21st century, DNA barcode sequences (e.g., COI) have increasingly been provided alongside descriptions of new species. However, the simultaneous preparation of serial sections and extraction of DNA from a single specimen has not been commonly practised because acoels are generally small and fragile.

In this study, we applied a DNA extraction kit designed for formalin-fixed paraffin-embedded (FFPE) samples to acoels and evaluated its usefulness for preparing serial sections of the body region containing the copulatory organs, extracting DNA from the remaining body parts, and determining partial COI sequences. With regard to fixatives, formalin has been suggested in previous studies to be insufficient for histological observation of acoels, whereas Bouin's fluid, a traditional fixative, is expected to promote DNA fragmentation because of its strong acidity. We therefore also explored fixatives suitable for both histological preservation and DNA retention.

We present a novel specimen-preparation method using a DNA extraction kit for FFPE samples and report the effects of several fixatives on the recovery of partial DNA sequences.

Poster 25

Evolutionary restructuring of the flatworm Hox system through duplication, gene loss and cluster disintegration

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Many flatworms repeatedly re-establish axis polarity during regeneration or asexual reproduction. Hox genes are key regulators of anterior-posterior patterning in bilaterians and are typically organized in conserved genomic clusters exhibiting spatiotemporal collinearity. However, studies in the planarian *Schmidtea mediterranea* have revealed a reduced and genomically dispersed Hox complement, raising questions about the evolutionary history of Hox genes in flatworms and the extent to which this organization is shared across the phylum.

Therefore, we performed comparative genomic and transcriptomic analyses across early-branching and nested lineages, including catenulids, macrostomorphans, parasitic flatworms and the planarian *S. mediterranea*. The results suggest a shared reduction of ancestral Hox genes predating the diversification of flatworms, followed by substantial divergence in complement composition and genomic organization. Early-branching taxa display increased lineage-specific duplications and residual Hox clusters, whereas planarians and neodermatans exhibit reduced repertoires and increasingly fragmented or dispersed genomic organization. We furthermore examined Hox gene expression in the regenerating and asexually reproducing catenulid *Stenostomum brevipharyngium*. Regeneration time-course transcriptomics revealed temporally dynamic repression and activation during anterior and posterior axis remodeling. Notably, Hox genes display predominantly staggered anterior-posterior expression patterns during asexual reproduction despite extensive genomic reorganization. Together, these findings suggest that canonical anterior-posterior Hox expression may be maintained in flatworms despite extensive Hox complement restructuring and genomic disintegration, further challenging assumptions about the strict relationship between cluster organization and spatial expression.

Poster 26

Connectome reconstruction and functional study of the visual circuit in flatworms

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Light is a universal physical factor that most animals use as a cue to navigate their environment. A large variety of eyes and other light sensing structures, as well as light-guided behaviours, evolved across animals. Their origins and diversification represent a key question in biology. My aim is to reveal the whole-body neuronal circuits –from sensors to effectors –using array tomography, and the molecular pathways mediating visual behaviour in two species of flatworms. While the visual systems of the established model organisms (e.g. mouse, *Drosophila*, zebrafish) have been extensively studied, there is a large knowledge gap concerning vision in marine invertebrates even though they represent a vast fraction of animal diversity. Thus, studying these organisms is crucial to better understand the evolution of complex eyes across the tree of life.

Poster 27

The evolution of asymmetric cell division in Spiral cleavage

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Spiral cleavage is unique among animals in specifying the first embryonic fates through three distinct cell division patterns. In “equal” spiral cleavage, the first two zygotic divisions are symmetric, producing four equipotent blastomeres of equal size, with cell fates specified later through inductive interactions. This equal development is ancestral, occurring in all phyla with spiral cleavage, including flatworms, and showing high molecular conservation. In contrast, many molluscan (e.g., snails and clams) and annelid (e.g., lugworms) embryos undergo “unequal” spiral cleavage, where post-fertilisation divisions are asymmetric, segregating maternal cytoplasmic mRNAs into a larger cell. These asymmetric divisions involve the mitotic spindle’s asymmetric positioning, or a unique cortical protrusion called the polar lobe.

The transition to unequal development, including polar lobe evolution, has occurred independently multiple times, making it a remarkable case of parallel evolution. In clams and snails, the actin cytoskeleton is involved in the early stages of polar lobe formation, and myosin and microtubules contribute to its resorption into the larger cell. However, whether similar mechanisms act in other molluscs and annelids, and the exact molecular and mechanical mechanisms that trigger polar lobe formation, are largely unknown. To fill this knowledge gap, we are investigating a range of molluscs and annelids, exploring the cytoskeleton organisation during early spiral cleavage. Together, our work can identify cytoskeletal mechanisms involved in the parallel evolution of asymmetric divisions in Spiralia.

Poster 28

Expanding the diversity and distribution of a cryptic species complex: *Gyratrix* Ehrenberg, 1831 (Platyhelminthes) from the (sub)tropics

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The microturbellarian flatworm *Gyratrix* (Kalyptorhynchia: Polycystididae) has long been hypothesised to constitute a vast species complex, a view recently confirmed by molecular and morphological evidence. Following a recent integrative taxonomic revision of the complex, we here expand the available framework using newly collected material from previously underrepresented (sub)tropical regions. By combining DNA sequence data, morphometric analyses, and high-resolution Scanning Electron Microscopy (SEM), we investigate the diversity of *Gyratrix* across previously underrepresented (sub)tropical regions. We reveal substantial morphological and molecular diversity within the genus and extend its known geographical distribution. Species delimitation is primarily based on variation in the morphology of the sclerotised copulatory organ, with SEM images providing additional resolution of diagnostic features. The morphological patterns are supported by preliminary molecular and morphometric evidence, enabling the assignment of specimens to recently described.

Poster 29

Population dynamics of *Temnocephala* (Platyhelminthes) on fresh-water decapods: host-driven patterns in a multispecies assemblage

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Ectosymbiotic assemblages on freshwater decapods provide an excellent framework for investigating flatworm ecology and population dynamics, while also allowing evaluation of the roles of host traits and interspecific interactions in structuring multi-species infracommunities. We examined the co-occurrence and population structure of two common ectosymbionts, *Temnocephala axenos* (Platyhelminthes) and *Stratioidrilus platensis* (Annelida), associated with the anomuran crab *Aegla platensis*. Using a year-round sampling design, we quantified prevalence, intensity, and life-stage composition, and evaluated whether patterns of co-distribution reflect biological interactions or responses to host morphometry and temporal variation. Both taxa exhibited high prevalence and aggregated distributions across hosts, with frequent co-infection. Despite reports that *Stratioidrilus* may be ingested by temnocephalans, co-occurrence patterns and population-level analyses provided no evidence of antagonistic structuring within infracommunities. Instead, variation in abundance was largely explained by host morphometry, with both taxa increasing in intensity with host size, albeit following distinct scaling patterns. Temporal variation influenced overall infrapopulation dynamics but was not associated with divergent responses between taxa. Consistently, full models incorporating host morphometry, temporal factors, and symbiont intensity failed to detect meaningful interdependence between the two taxa. Residual associations between their infrapopulations were negligible, indicating that apparent co-occurrence arises primarily from shared host-related gradients rather than from competitive or facilitative interactions. These results demonstrate that even highly co-occurring ectosymbionts may exhibit effectively independent population dynamics and highlight host morphometry as a central structuring axis in symbiotic communities.

Poster 30

When barcodes fail: an introduced population of *Dugesia semiglobosa* reveals considerable variation in 28S and COI markers

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During a survey of the tropical greenhouse of the Botanical Garden of Innsbruck (Austria), we detected an asexually reproducing population of *Dugesia*. Species identification was initially attempted using PCR amplification and Sanger sequencing of the nuclear 28S rDNA marker. However, direct sequencing consistently produced ambiguous chromatograms, preventing reliable consensus sequences. To investigate the origin of this signal, PCR products from multiple individuals were cloned using the pGEM-T Easy system and several clones per specimen were sequenced. The resulting data revealed multiple divergent 28S variants within individual worms, confirming previous suggestions that asexual planarians may carry several distinct copies of this marker. Similar patterns were also observed for the mitochondrial COI gene, where cloning likewise uncovered considerable sequence variation within individuals. Despite these challenges, analyses of cloned sequences enabled identification of the population as *Dugesia semiglobosa*, a species originally described from Hainan Island, China. Its occurrence in a tropical greenhouse highlights the role of anthropogenic environments in the dispersal of freshwater flatworms. Our findings demonstrate that intragenomic variation can complicate species identification based on direct Sanger sequencing of commonly used markers in asexual planarians. We therefore recommend caution when interpreting 28S and COI sequence data and emphasize the value of cloning approaches for accurate taxonomic identification.

Poster 31

Population genetics of *Crenobia alpina* across Tyrol

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The Alps have been repeatedly influenced by numerous geological and climatic events, which have impacted the geographical structure of these mountains, with strong effects on the diversity and distribution of Alpine life. To analyse this diversity and distribution of Alpine life, I want to analyse the molecular sequence divergence of the freshwater flatworm *Crenobia alpina* across Tyrol. *C. alpina* occurs in most parts of Europe, including Germany, eastern Austria, Italy and Switzerland. However, a molecular dataset covering Tyrol is still lacking.

In the Alps, *C. alpina* inhabits streams and the bottom of Alpine lakes, occurring at elevations up to 3000 m a.s.l. Springs and streams at high altitudes represent extreme environments, characterised by consistently low water temperatures and limited nutrient availability. These harsh conditions provide ideal natural settings for investigating how environmental conditions and geographic isolation shape genetic divergence. To address the existing molecular gap for Tyrol and to capture the influence of these extreme, isolated habitats, I collected specimens from various streams across the region and aim to characterise the genetic divergence among *C. alpina* populations in Tyrol between streams and at different altitudes within the same stream. We will test if there is evidence of geographic isolation within Tyrol, specifically whether populations within the same river are genetically more similar to each other than to populations from different rivers, and whether geographic distance contributes to genetic differentiation. Comparisons with populations from Germany, eastern Austria, Italy, and Switzerland will further place the Tyrolean populations into a broader Alpine context.

Poster 32

Combined effect of organic matter and temperature on the structure of a turbellarian assemblage in experimental microcosms

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A multifactorial microcosm experiment was conducted to analyse the response of interstitial turbellarian assemblages to organic enrichment, increased temperature, and their combined effects. Microcosms were exposed to four temperature scenarios: the average estuarine water temperature (control), and temperatures one, two, and three degrees above the baseline. This design was combined with four levels of organic matter enrichment: no addition (control), low (0.5 g), medium (0.8 g), and high (1.10 g) organic matter additions. The experiment was maintained for 20 days under controlled laboratory conditions.

Diversity remained unaffected by temperature and organic matter enrichment. In contrast, temperature alone had a positive effect on species richness, whereas the combination of increasing temperature and high organic matter enrichment resulted in a negative effect on richness.

Within the meiofauna community, the turbellaria assemblage provides valuable information of the meiofaunal community dynamics, in this study case, regarding the combined effects of high organic matter enrichment and elevated temperature; two major anthropogenic drivers affecting coastal biodiversity, highlighting the importance of considering their interactions when predicting ecological responses to environmental change.

Poster 33

Integrative taxonomy reveals three new *Novibipalium* species (Tricladida: Geoplanidae) from South Korea, including a morphologically variable taxon and a comment on parasitism

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Although the Korean Peninsula experienced extensive habitat degradation throughout the 20th century, recent molecular evidence has revealed a substantial, yet still poorly documented, diversity of land planarians. In this study, we apply an integrative taxonomic framework to describe three new species of the genus *Novibipalium*, based on material collected across South Korea.

Morphological characterization was conducted through histological examination of serial sections and complemented by molecular phylogenetic analyses using concatenated nuclear (18S and 28S rDNA) and mitochondrial (COI) markers (5,022 bp). Species boundaries were further assessed using species delimitation analyses (ASAP).

The results support the recognition of three distinct species, all presenting a female atrium inclined about 45° toward the gonopore, as in two previously known species. *Novibipalium* sp. 1 and sp. 2 characteristically lack a sphincter in the pseudophallus and are morphologically similar, differing mainly in the dorsal expansion of the sperm ducts in *Novibipalium* sp. 1; however, they are not recovered as sister species. Interestingly, *Novibipalium* sp. 1 exhibits variation in external coloration and internal anatomy, including the distribution of cilia within the pseudophallus epithelium. *Novibipalium* sp. 3 is readily distinguished by a flattened penis papilla.

Phylogenetic reconstruction and ASAP consistently corroborate the distinctiveness of these taxa.

Additionally, secondary, non-functional female copulatory structures in one specimen of *Novibipalium* sp. 3 are tentatively interpreted as a consequence of nematode parasitism.

These findings expand the known diversity of Korean land planarians and highlight the importance of integrative taxonomy in resolving species boundaries in morphologically variable groups.

Poster 34

Species diversity, phylogenetic relationships and biogeography of *Rogneda* (Eukalyptorhynchia, Polycystididae) Uljanin, 1870

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With approximately 1,800 described species, Rhabdozoa is a highly diverse clade of free-living flatworms. Representatives occur worldwide in marine, brackish, freshwater, and limno-terrestrial habitats, while some species have evolved endo- or ectosymbiotic lifestyles. Roughly half of all known rhabdozoan species are marine or brackish. Together with the North Sea, the Mediterranean is among the best-studied regions for rhabdozoan diversity. Nevertheless, extensive sampling during the last two decades, particularly in the western Mediterranean around Banyuls-sur-Mer, Cerbère, and Sardinia, continues to reveal substantial undescribed diversity.

Polycystididae, the largest traditional “family” of eukalyptorhynchids, currently comprises 271 formally described species, of which 221 marine. About 50 marine species have been reported from the Mediterranean region. The most species-rich genus is *Rogneda* Uljanin, 1870, with 23 described species. Seventeen of these occur in the Mediterranean, and fourteen have been recorded from its western basin, indicating that this region represents a centre of diversity for the genus.

Recent sampling efforts in the western Mediterranean yielded four previously undescribed species of *Rogneda*. Together with three additional new species from Lanzarote, these discoveries increase the number of known species in the genus to 30. We present these seven new species and discuss phylogenetic relationships within *Rogneda*, including a reassessment of the morphology-based species groups proposed by Artois (2008). The biogeographical distribution and diversification of the genus are also evaluated.

Artois T. (2008). Revision of *Rogneda* Uljanin, 1870 (Rhabditophora, Eukalyptorhynchia, Polycystididae) with the description of seven new species. *Zoological Journal of the Linnean Society* 153(1): 1-28.

Poster 35

Paws and planarians: training Swedish sniffer dogs to detect invasive flatworms in potted plants

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Non-native land flatworms pose significant threats to European ecosystems due to their voracious predation on earthworms and snails. To design effective control policies, accurate distributional data is vital. Currently, 28 non-native species are recorded across Europe, with four listed as invasive alien species of Union concern. Among these, the New Zealand flatworm (*Arthurdendyus triangulatus*) has generated over 5,000 citizen science records since 1962, primarily in the British Isles. More recently, the Argentine flatworm *Obama nungara* entered Europe in 2008, rapidly accumulating nearly 2,000 records across 19 countries.

Due to its invasive status, EU member states must implement containment measures. Sweden enforces the most stringent protocols: if *O. nungara* is detected on a pallet of potted plants, the entire batch must be sanitised (via heating or freezing), destroyed, or returned. Following sanitization, manual inspections must yield zero findings for three consecutive days. These procedures are financially devastating, costing major horticultural companies up to 4 million Euros annually to maintain pest-free status.

Consequently, the industry demands cost-effective, rapid screening methods. A novel approach currently under investigation involves training conservation canines to detect the specific scent of *O. nungara* within commercial nurseries. Although the exact efficacy of this method remains to be determined, this innovative bio-security approach offers a potentially non-destructive tool for early detection, with the ultimate goal of preventing further anthropogenic spread of invasive flatworms via the plant trade.

Which *Otoplana* species (Proseriata: Otoplanidae) lives in the ‘*Otoplana*-zone’? Taxonomic deflation and hidden diversity in the genus *Otoplana* (Proseriata: Otoplanidae)

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Species descriptions of microturbellarians are often based on few specimens coming from a single locality, and reports on their intra- and inter-populational variability are generally lacking. This raises questions about the validity of species distinguished solely by minute morphological differences, particularly within geographically restricted areas. Species of the genus *Otoplana* Du Plessis, 1889, the namesake taxon for the swash-zone (“*Otoplana*-zone”) worldwide, may represent a striking case of taxonomic inflation. Six species have in fact been described from the coasts of the Ligurian Sea (from Nice to Livorno), often based on few specimens and without consideration of population-level and ontogenetic variability. The morphological characters diagnosing these taxa are subtle and of questionable reliability. To assess the species boundaries within the genus, we undertook an integrative molecular, morphological, karyological study across its entire distribution range, including the type populations of all nine species currently reliably assigned to *Otoplana*. Preliminary analyses revealed a clear distinction of the Macaronesian species for all markers examined. In contrast, most Mediterranean populations were only weakly separated into two clusters based on molecular and morphological data, but these clusters were strongly supported by karyotype and sediment preference. Our results therefore suggest a complex evolutionary history involving both allopatric speciation, and, in sympatry, the action of both pre-mating (habitat-related), and post-mating (karyological) reproductive barriers. Not without irony, although this study was initially motivated by the suspicion of taxonomic inflation, our findings reveal both taxonomic deflation and hidden diversity. All the recently described Mediterranean taxa appear to be junior synonyms of the two earliest described species, *O. intermedia* Du Plessis, 1889 and *O. bosporana* Ax, 1959. At the same time, three previously unrecognized lineages from Macaronesia and northern Aegean Sea likely represent new species and will require formal description. Overall, our results indicate that the swash-zone is an evolutionary arena whose diversification potential has been underestimated. Far from being a

homogeneous and barren habitat, it appears to be the home of a highly specialized and unexpectedly diverse microturbellarian fauna.

Poster 37

First record of the introduced land planarian *Obama nungara* (Platyhelminthes: Geoplanidae) in Austria

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Obama nungara is a land planarian species native to South America that has become a cause for concern as an introduced species in Europe. Because it preys on earthworms, detrimental effects on native biodiversity and soil productivity are expected. It is up to 70 mm long and 5 mm wide, with a brown dorsal side with longitudinal black stripes and numerous eyes arranged in lateral bands. Here, we present the first record of *O. nungara* in Austria confirmed by DNA sequence data. An exotic land planarian was first seen in November 2022 in a perennial nursery in Lower Austria, and by August 2024, three additional specimens had been recorded. The specimens showed close similarity to *O. nungara* in external appearance, however, to confirm the species identification, a partial sequence of the cytochrome c oxidase subunit I gene (COI) was sequenced in two specimens. The sequences were incorporated in a maximum likelihood phylogenetic analysis alongside published sequences of *Obama* species. The Austrian sequences clustered with sequences of *O. nungara* of the “Argentina 1” lineage, a lineage originating from Argentina that has spread widely over Europe. Thus, the results indicate beyond doubt that *O. nungara* is present in Austria at least since November 2022. It remains to be seen whether *O. nungara* will spread as extensively in Austria as it has in Western European countries characterized by a more oceanic climate.

Poster 38

Cave Planariidae of the Dinaric karst: phylogenetic diversity, multiple colonisation events, and convergent trait evolution

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The Dinaric karst, with more than 10,000 caves, represents one of the most important hotspots of subterranean biodiversity, where cave planarians have long been recorded. However, there was no integrative research on this group, and the evolutionary relationships of cave Planariidae have not yet been resolved.

We combined field sampling, phenotypic characterisation, and *COI*- and *18S*-based phylogenetic analysis, to address these gaps.

Our results showed that cave Planariidae are widespread across Croatia and neighbouring countries, and belong to at least three genera. The number of cave records was increased from 26 to 37, documenting the genera cf. *Atrioplanaria* and *Phagocata* in the caves of Croatia for the first time. The phylogenetic analyses, supported by variability in body pigmentation and eye reduction, indicated multiple independent cave colonisations and heterogeneous evolutionary trajectories within the genera cf. *Atrioplanaria* and *Crenobia*.

This study provides the first genetic information on cave Planariidae from the Dinaric karst, revealing a group with a complex evolutionary history of subterranean colonisations in the region. The genetic and trait diversity position the family Planariidae as a valuable model for investigating the convergent evolution of cave-related pigment loss and eye reduction, while biogeographical patterns open a broader question about the dispersal of subterranean fauna in this geologically unique landscape.

Poster 39

Species diversity and taxonomy of Dakuidae (Acoela)

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Acoela are a group of microscopic worms that remains poorly known despite their high abundance and world-wide distribution. Within Acoela, the family Dakuidae has undergone several taxonomic changes in recent decades, yet its internal phylogeny remains unclear. Herein, we describe seven new species of Dakuidae from Croatia, Germany, Italy, Panama, and Sweden: *Philactinoposthia brunopunctata* sp. nov., *Philactinoposthia centrofusca* sp. nov., *Philactinoposthia raikovae* sp. nov., *Philactinoposthia gracilia* sp. nov., *Philactinoposthia parvipenis* sp. nov., *Philocelis leasae* sp. nov. and *Philocelis dunensis* sp. nov. Mitochondrial (COI) and nuclear (18S, 28S) sequences were used to assess the phylogenetic relationships within the family, supporting the presence of two sister groups: the first comprising species of the genus *Philocelis* along with *Philactinoposthia saliens*, *Philactino-posthia rhammifera* and *Daku woorimensis*, and the second consisting of other species of the genus *Philactinoposthia*. *P. saliens* and *P. rhammifera* are transferred from *Philactinoposthia* to *Philocelis*. The genus *Daku* is synonymised with *Philocelis*. Finally, we assessed the diagnostic relevance of the morphological characters traditionally used in the taxonomy of Dakuidae, proposing emended diagnoses for the genera *Philocelis* and *Philactinoposthia*.

Poster 40

Interactions with dangerous prey may influence the selection of the regeneration capacity in land flatworms (Platyhelminthes: Geoplanidae)

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Regeneration is likely a homologous mechanism to all metazoans that has been lost multiple times in different lineages. Species of freshwater planarians have great regenerative capacity, and regeneration in this group is evolutionarily preserved by pleiotropy, since it is strictly genetically related to reproduction and there is no evidence of injured bodies in the wild. If tissue loss is not frequent in the wild, regeneration tends to be lost, if not retained by pleiotropy. In contrast, the Neotropical land planarians of the subfamily Geoplaninae reproduce sexually and also regenerate. We evaluated if tissue loss is frequent in Geoplaninae, and thus, whether regeneration could be maintained by direct selection in this group. We documented injuries (including amputations) for the first time in wild populations of planarians. Almost 25% of the individuals of *Cephaloflexa* genus were found injured, mainly in the head region, which is used for capturing prey. The injuries of *Cephaloflexa* seem to be caused by predator-prey interactions. Other species with similar sizes but preying on inoffensive prey had no injuries recorded. Moreover, our data are in agreement with laboratory experiments that documented *Cephaloflexa* specimens being injured by prey such as spiny harvesters (Arachnida, Opiliones). This scenario suggests that regeneration may be directly selected in species of Neotropical land flatworms, unlike other Tricladida groups. It also supports a scenario in which prey may influence the maintenance of a predator's regenerative capacity throughout evolution, unlike most cases where sublethal interactions with predators cause prey tissue loss in the wild.

Poster 41

Revisiting species diversity in *Promesostoma*: morphology, taxonomy, and species groups

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With over 40 described species, the microturbellarian genus *Promesostoma* Graff, 1882 (Promesostomidae) is one of the largest genera within Rhabdocoela (Platyhelminthes). Its members occur worldwide in marine and brackish habitats. *Promesostoma* is characterised by a high degree of morphological similarity among species, and species delineation has traditionally relied on subtle differences in the sclerotised stylet of the copulatory organ. Recent molecular studies suggest that the genus comprises several distinct evolutionary lineages, some of which correspond to traditionally recognised morphological groups. Nevertheless, intrageneric relationships remain incompletely re-solved.

This contribution presents our proceedings for a taxonomic re-evaluation of *Promesostoma* based on newly collected material from marine and brackish habitats in the Mediterranean, the subtropical Atlantic, and the Indo-Pacific, as well as a reassessment of historical material. Current material indicates substantial undescribed diversity within the genus, and additional distribution records are provided for several previously described species. Newly obtained morphological data are discussed in the context of recent advances in rhabdocoel systematics, and discussed within a molecular phylogenetic framework. This study contributes to a refined taxonomic framework for Promesostomidae, and provides new insights into the diversification and biogeography of these intriguing flatworms.

Poster 42

Hidden biology of hammerhead flatworms in Japan revealed by mitochondrial genomics and behavioral observations

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Hammerhead flatworms (Geoplanidae: Bipaliinae) are terrestrial predators of soil organisms. Several species have spread globally as non-native taxa, raising concerns about their ecological impacts. In Japan, although some non-native species are established, their distribution, genetic diversity, and ecology remain poorly understood, and the diversity of native species has yet to be fully characterized. In this study, we report the mitochondrial genome sequences of 14 individuals of hammerhead flatworms collected in Japan, along with the genetic diversity and reproductive behavior of *Bipalium nobile*, which is known to be a non-native species in Japan.

The mitochondrial genomes of these 14 individuals were sequenced and assembled using shortread sequencing, and complete or nearly complete genome sequences were obtained. Phylogenetic analysis based on COX1 sequences showed that none of the individuals examined clustered with any previously described species. Among them, 11 individuals with black body coloration were divided into at least six distinct lineages, while the remaining three were each placed in distinct phylogenetic positions. Although their relationships with known species remain to be determined in future studies, these results suggest that at least nine genetically uncharacterized hammerhead flatworm species inhabit Japan and highlight the unexpected cryptic diversity of hammerhead flatworms in Japan.

We also examined the COX1 and 28S rRNA sequences of *B. nobile* collected from various localities across Japan and found that they exhibit limited genetic diversity. Furthermore, behavioral observations of *B. nobile* revealed that they display a unique reproductive behavior not previously reported.

Poster 43

Made in China: first occurrence of *Girardia sinensis* in Czechia

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Freshwater planarians of the genus *Girardia* are well-known invasive species with a widespread non-native distribution globally. The European region is known to host several invasive *Girardia* species, namely two species from Nearctic origin —*Girardia tigrina*, which has a widespread distribution, and *Girardia dorocephala* in the Mediterranean region —as well as the Chinese species *Girardia sinensis*, described in 2015. Since its description, this Chinese species has been adding newly conquered localities across the world to the map. With the nearest known occurrence of *Girardia sinensis* being close to Dresden, Germany, new records in the Czechia were likely a matter of time and systematic sampling. Prior to this work, the only invasive *Girardia* species known in the Czechia was *Girardia tigrina*, often noted in identification keys as an easily determinable species due to its distinct shape and unique coloration. During fieldwork in the Central Bohemian Region between 2022 and 2025, several localities containing sexual planarians of the genus *Girardia* were found and some turned out to be *Girardia sinensis*. In this work, we focus on new occurrences of *Girardia sinensis* in Czechia and present preliminary morphological and genetic results regarding this species.

Poster 44

Sun, sand, and flatworms: unveiling Florida's hidden proseriate treasure

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Florida's sandy beaches are renowned worldwide for their recreational value, yet the microscopic flatworm communities dwelling within their interstices remain conspicuously absent from the literature. A survey of shallow subtidal and intertidal sediments along Florida's eastern coast has now revealed a taxonomically diverse fauna. Among the discoveries, we report two new species of *Yorknia* (Yorkniidae), a new species of *Duplominona* (Monocelididae) characterised by a strongly sclerotised, tubular stylet, a morphology known from only a few species within the genus, and a new species of *Cirrifera* (Coelogynoporidae). Most notably, we present a new species of *Prosogynopora*. Until now, the genus has been considered monospecific, known only from its type species, *P. riseri* Laumer & Curini-Galletti, 2014, from the New England coast. The discovery of a second species from Florida substantially expands the genus's known distribution and suggests that *Prosogynopora* may represent a diverse and previously overlooked lineage within North American coastal waters. In addition to these new taxa, we provide records of *Promonotus wilsoni* (Monocelididae) and *Polystyliphora karlingi* (Polystyliphoridae) from Florida, extending their known distributions across the southeastern United States. These findings establish Florida as a promising frontier for flatworm taxonomy, with implications for understanding patterns of cryptic diversity, biogeographic connectivity, and the conservation of coastal meiofaunal communities.

Poster 45

Reassessing land planarian diversity and species delimitation in South Korea through extensive sampling and integrative analyses

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Land planarians (Geoplanidae) in South Korea have historically been poorly studied, with only two species reported in 1923 and none formally recognized in the National Species List of Korea (NSLK). In a previous nationwide survey (2020–2022), we identified 21 putative species based on phylogenetic and COI-based delimitation analyses, indicating that terrestrial flatworm diversity had been substantially underestimated. Here, we reassess species diversity using expanded sampling and integrative molecular approaches.

Sampling effort increased nearly fourfold from 69 to 271 sites between 2020 and 2025. A novel collection method (water spraying technique) was applied to improve detection of hidden individuals under conditions of low detectability. In total, 51 morphospecies were identified based on external morphology. Phylogenetic relationships were reconstructed using concatenated 18S, 28S, and COI data, and species delimitation was evaluated using ASAP based on COI.

We detected higher diversity than previously recognized, with 50–61 putative species depending on delimitation thresholds. While morphological and molecular results were largely congruent, three patterns of species delimitation were identified: congruent cases, species complexes, and under- and over-splitting. These results indicate that species boundaries are more complex than previously assumed and largely reflect intrinsic biological complexity, although incongruence may arise from methodological limitations. Distance-based approaches such as ASAP may lead to over- or under-splitting, whereas morphology based on external characters may fail to resolve species boundaries or detect cryptic diversity.

Overall, this study demonstrates that land planarian diversity in South Korea is substantially underestimated and highlights integrative taxonomy for accurate species delimitation.

Poster 46

Diversity and distribution of estuarine microturbellarians along a salinity gradient

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Microturbellarians are diverse meiofaunal flatworms found worldwide in freshwater, marine, and brackish habitats. Despite their ecological importance and value for taxonomic research, they remain understudied because of their small size and difficult identification. Brackish habitats, including estuaries and lagoons, are biodiversity hotspots often protected at the (inter)national level. They are highly dynamic, shaped by tides, wind, river discharge, anthropogenic pressures, and climate change. Salinity gradient is among the most important factors shaping the distribution of aquatic organisms in these habitats. Estuarine environments often support high meiofaunal abundances, but salinity strongly affects species diversity. Although they occur in a wide variety of aquatic habitats, most of the described microturbellarian species are found in marine littoral environments. This project explores the diversity of microturbellarians along salinity gradients in brackish habitats and investigates whether some species occur across multiple salinity zones. At the start of this project, a pilot study was conducted in the estuary of the river Scheldt in Belgium and the Netherlands. Samples of sediment, algae, and aquatic vegetation were collected across five localities in oligo-, meso-, and polyhaline salinity zones. Microturbellarian diversity in this area proved to be low and was dominated by a few species, mainly belonging to the genera *Baicalellia* and *Placorhynchus*. Proseriate flatworms were also found, although their distribution was not continuous across the salinity gradient. Although the influence of salinity could not be separated from other environmental factors affecting flatworm diversity, this study provides a baseline for future salinity-related research in the Scheldt estuary.

Poster 47

How to find exotic worms in a temperate climate?

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Catenulida is an order of free-living, microscopic flatworms, occupying a sister position to all of the other platyhelminths. They remain poorly studied because of challenges in their species identification, such as a lack of reproductive structures and prevalent phenotypic plasticity.

Although the majority of the species have been described from tropical and subtropical waters in South and North America, most of the molecular studies have been done in the temperate regions in Europe. We tried to overcome this gap through sampling for catenulid species in the unique exotic localities available in temperate climate, namely aquatic habitats in the greenhouses of the botanical garden (in Warsaw, Poland). We investigated different artificial tropical habitats (e.g., aquariums, tanks in cabinets with tropical flora, waterbodies in bromeliads) for the presence of catenulids. Specimens were photographed and barcoded for 18S, 28S, and COI markers. Among others, we found species recorded previously from tropical areas (*Stenostomum corderoi*, *Stenostomum paraguayense*, *Catenula evelinae*), and provided for the first time the reference molecular sequences for them. We then placed these species on the catenulid phylogeny, enhancing our understanding of their taxonomy.

Our data suggest that in temperate climates, sampling in greenhouses is a simple and cost-effective alternative to field studies, especially in the case of barcoding of microscopic invertebrates. Green-house's environments are regarded as tropical islands in a moderate zone and can be a source of non-native animal species, characteristic of warmer habitats.

Poster 48

Unveiling a hotspot of microturbellarian diversity: The Indian River Lagoon and the Floridian coast of the United States

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The marine microturbellarian fauna of the United States is currently represented by 165 species, with research historically concentrated in California and the Carolinas. In contrast, the Floridian coast and the Indian River Lagoon (IRL) have remained largely overlooked, with only six and three species recorded, respectively. Despite their ecological importance as key predators and biomass contributors in meiofaunal communities, the diversity of these organisms in Florida's unique transition zone—between the tropical Caribbean and temperate Carolinas—has remained unknown. To address this gap, intensive sampling was conducted between 2025–2026, focusing on the IRL, oceanic beaches, and offshore areas. This effort has revealed an extraordinary diversity of 370 species, shattering previous records for the region. The most diverse taxa include Rhabdocoela (246 spp.), Proseriata (52 spp.), and Macrostomorpha (31 spp.). Preliminary morphological assessment suggests that 70% of the total fauna is new to science, potentially exceeding 90% within Proseriata. Other identified taxa include Catenulida, Gnosonesimida, Polycladida, Prolecithophora, Tricladida, and Bothrioplanida. Biogeographically, the Floridian fauna shows stronger affinities with the Caribbean (20 shared species) and the Eastern Atlantic/Mediterranean (12 shared species), though these patterns are likely influenced by global sampling biases. To put these findings into perspective, the island of Sylt (Germany)—historically considered the best-documented area in the world—has yielded 320 species over a century of research. In just over a year, this study has documented 370 species in Florida, suggesting that hundreds more remain undiscovered. These results position Florida as a global hotspot for microturbellarian diversity.

Poster 49

Diversity of turbellarian flatworms from Peru: an updated checklist with new species records of Proseriata

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Non-neodermatan Platyhelminthes, or “Turbellaria,” are primarily free-living flatworms classified into two main clades: Catenulida and Rhabditophora. Catenulida includes families like Catenulidae and Stenostomidae, while Rhabditophora encompasses Rhabdocoela, Proseriata, and Tricladida (e.g. Geoplanidae). These organisms display a range of ciliated body shapes and inhabit marine, brackish, freshwater, and humid terrestrial environments globally, with Geoplanidae requiring specific ecological conditions. In the Neotropics, turbellarian species remain underexplored, particularly in Peru. Our study aimed to assess species diversity in Peru by reviewing specialised literature and conducting marine sampling near Lima in December 2025. We identified 91 species of turbellarians from the literature, of which 46 are either endemic or have only been recorded in Peru. The most diverse taxa included Geoplanidae (36 species), Stenostomidae (15 species), and Dalielliidae (8 species). Additionally, four new records of Proseriata species—*Kata evelinae*, *Itaspiella* cf. *helgolandica*, *Archi-monocelis* cf. *bathycola*, and *Pseudoinvenusta paracnida*—were identified. Notably, 46.3% of species inhabit limnic and brackish environments, with *Stenostomum* (14 species) and *Gieysztorina* (7 species) being the most diverse genera. Approximately 37.9% occupy terrestrial environments, mainly represented by *Geoplanea* (21 species). Although the species known from Peru were identified by specialists, they were not local or did not train students who could continue this research line today. This is unfortunate, as it leaves an important research potential untapped. The overall diversity of turbellarians in Peru is likely much higher than currently documented, highlighting the potential for future research to explore their role as environmental indicators, especially in a country with rich biodiversity.

Poster 50

New records of marine Rhabdocoela (Platyhelminthes: Kalyptorhynchia: 'Schizorhynchidae') from Turkey, and description of a new species of *Carcharodorhynchus* Meixner, 1938

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Rhabdocoel flatworms (Platyhelminthes) are an important component of the interstitial fauna of sandy beaches, contributing to benthic ecosystem processes through sediment reworking and interactions with organic matter and microorganisms. Despite their ecological importance, the diversity and distribution of marine rhabdocoels remain poorly documented worldwide. Along the Turkish coast, knowledge is limited to a few localities, with approximately 40 species previously reported only from the Black Sea and the Sea of Marmara. This study provides an overview of rhabdocoel species collected during a four-week survey along the Turkish Black Sea coast and includes the description of a new species of *Carcharodorhynchus*. Samples were collected from fine and coarse sandy beaches near Sinop in the lower intertidal and shallow subtidal zones using manual tube corers. Flatworms were extracted using the MgCl₂ decantation method. Specimens were studied alive, photographed, drawn, and whole-mounted in lactophenol or fixed in Bouin's fixative for histological analysis. *Carcharodorhynchus* n. sp. is characterised by a male copulatory bulb with a short cylindrical cirrus bearing longitudinal and circular sclerotised ridges, creating a mesh-like pattern. The sclerotised tissue extends outward within the duct, forming a cap with irregular distal ends. In addition, six rhabdocoel species are recorded for the first time from the Turkish Black Sea coast, increasing the total number of known Turkish species to 45. These findings highlight the rich but understudied diversity of benthic rhabdocoels along the Turkish coast and emphasise the need for further research in the region.

Poster 51

Marine Schizorhynchia (Platyhelminthes: Rhabdocoela) from South Korea, with the description of eight new species

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The diversity of interstitial rhabdocoel flatworms in Asia remains severely understudied, with South Korea representing a major geographic gap. Schizorhynchia form a distinct group of rhabdocoels that features a bifurcated muscular proboscis and includes five families: Cheliplanidae, Diascorhynchidae, Karkinorhynchidae, Nematorhynchidae, and 'Schizorhynchidae'. Schizorhynchia also shows considerable taxonomic instability in recent phylogenetic studies. This study aims to document the diversity of Schizorhynchia along the southern coast of South Korea using an integrative taxonomic approach. Samples were collected during a sampling campaign along the southern coast of Korea, incorporating both morphological observations and molecular phylogenetic methods using 18S and 28S rDNA. Samples were collected from different localities along sandy beaches in the West Sea, the Yellow Sea, and the South Sea, in areas ranging from the lower intertidal to the shallow subtidal. The flatworms were extracted from sand samples using the MgCl₂ decantation method, then observed alive, photographed, and prepared for further analysis. We identified a previously unrecorded species, *Paraschizorhynchoides glandulis*, and several new species primarily distinguished by the morphology of their male copulatory organs: the new species described here belong to three different families: *Freddius* n.sp., *Cheliplana* n.sp., *Diascorhynchus* n.sp. 1, *Diascorhynchus* n.sp. 2, *Schizochilus* n.sp.1; *Schizochilus* n.sp. 2., *Schizochilus* n.sp.3, and *Pseudoshizochilus* n.sp. These findings raise the total number of recorded Rhabdocoela species in Korea from one to ten and highlight the remarkably diverse but underexplored schizorhynchs along the South Korean coast.

Poster 52

Neuropeptide co-expression and ultrastructural reconstruction in the oncospherical nervous system of *Hymenolepis microstoma*

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Cestodes have experienced an evolutionary loss of genes required for several classical neurotransmitter systems, accompanied by a remarkable expansion of genes involved in neuropeptidergic signaling. Moreover, in the oncosphere—the first larval stage of cestodes—only glutamatergic and peptidergic markers are detected. This suggests a central role for neuropeptides in larval neural function.

We have analyzed the composition of the oncospherical nervous system in the model cestode *Hymenolepis microstoma* using serial block-face scanning electron microscopy (SBF-SEM) combined with immunofluorescence analyses based on newly generated antibodies against highly expressed neuropeptides. Our results demonstrate that the larval nervous system consists of five molecularly heterogeneous and bilaterally organized neurons that establish synaptic contacts with each other and with the larval hook musculature. Differential neuropeptide expression defines three neuronal subpopulations: two external lateral neurons co-express NPP36, NPP46, NPP33, and NPP20.3.1; two internal lateral neurons express exclusively NPP36; and a central neuron co-expresses NPP36, NPP28, and NPP20.3.1.

In a comparative approach, we examined the expression of these neuropeptides in adult worms and revealed marked changes in co-expression patterns relative to the larval stage. Overall, our findings show that the oncospherical nervous system of *H. microstoma* exhibits greater complexity than previously reported, both in neuronal number and molecular heterogeneity, and uncover life stage-specific shifts in neurotransmitter co-expression patterns throughout the parasite life cycle. Furthermore, we confirmed that the antibodies developed here are effective in *Echinococcus*, *Mesocostoides*, and *Rhinebothrium*, establishing them as powerful tools for comparative studies of the nervous system in different cestodes.