



### Monday 9 March 2026

Main conference room - Station Biologique

8:40-9:00 Registration

9:00-9:10 Julia MORALES (SBR)

Welcome and Information

9:10-9:30 Lucas LECLÈRE (OOB), Jean-Michel GIBERT (DEV2A)

Presentation of the EDEN Network

9:30 - 10:30 Aissam IKMI (EMBL Heidelberg) - Invited Speaker-

Design principles of cnidarian shapes

10:30-11:00 Coffee break

*Session : Reproduction and Fertilization – Chair : Agnès Boutet*

11:00-11:20 Sébastien VACHÉ (IMEV)

Germline development in the Jellyfish *Clytia hemisphaerica*

11:20-11:40 Martina SANTONI (DEV2A)

Regulation of Prophase Arrest: a new PKA substrate controls Cdk1 activity

11:40 - 12:00 Fernando ROCH (SBR)

mTOR in the sea urchin embryo

12:00 -12:20 Angelina POTIN (SBR)

The mood for love: timing reproductive rhythms of brown alga

12:30-14:00 LUNCH Gulf Stream

14:10 -15:00 Raphaël AGUILLON (IBPC) - Invited Speaker -

Cellular logic of temporal regulation: sleep and circadian clocks from cnidarians to diatoms

*Session : Regulatory gene networks and gene regulation – Chair : Jean-Michel Gibert*

15:00-15:20 Clare HUDSON (IMEV)

A Quantitative Description of the Mechanisms Leading to a Switch-like Transcriptional Response during Ascidian Early Neural Induction

15:20-15:40 Christine VESQUE (DEV2A)

Uncovering signalling pathways regulated by primary cilia using human neural organoids

15:40-16:00 Marc MEYNADIER (IMEV)

Equivalence of cell type across species using single-cell RNAseq

16:00-16:30 Coffee Break

*Sessions: Regeneration / Mechanics of development I – Chair: Carine Barreau*

16:30-16:50 Silvia CABALLERO-MANCEBO (IMEV)

Cooperation between cortical and cytoplasmic forces shapes planar 4-cell stage embryos



- 16:50-17:10 Florian PONTHEAUX (OOB)  
Transcriptional and morphological insights on Clytia jellyfish manubrium regeneration
- 17:10 -17:30 Karen POTTIN (DEV2A)  
Role of Contactin 2 during the development of the zebrafish olfactory system

17:40 - 19:00 **Poster session** Gulf Stream

19.30 DINNER Gulf Stream

**Tuesday 10 March 2026**

Main conference room - Station Biologique

*Session: Mechanics of development II – Chair: Sébastien Darras*

- 8:50 - 9:30 Laurent FORMERY (OOB)  
Large-scale reprogramming of differentiated larval tissues establish adult body plan during sea cucumber metamorphosis
- 9:30-9:50 Camille CURANTZ (DEV2A)  
ECM-mediated inter-tissue mechanical coupling in olfactory placode morphogenesis in *Olfactores*
- 9:50-10:10 Josep MARTI SOLANS (OOB)  
Membrane potential mapping and genetic regulation in *Phallusia mammillata*
- 10:10-10:30 Clara DELEAU (OOB)  
How do medusozoans build striated muscles without MRFs? Insight from *Pelagia noctiluca* myogenesis

10:30 -11:00 Coffee Break

*Session : Evolution of development – Chair : Fernando Roch*

- 11:00-11:20 Cécile LEBLOND (OOB)  
Evolutionary variation of developmental mechanisms: the case of *Molgula appendiculata*
- 11:20-11:40 Luis Alberto BEZARES CALDERÓN (IMEV)  
Initial Morphological and Molecular characterisation of Sensory Systems in Ascidian Larvae
- 11:40-12:00 Sébastien DARRAS (OOB)  
Comparative Early Embryogenesis in Solitary and Colonial Ascidians
- 12:00 - 12:20 Guillaume LECOINTRE (MNHN)  
Hennigian hierarchy of ontogenetic time

12:30-14:00 LUNCH Gulf Stream

14:10 -15:10 Visit of the SBR Marine Resource facility (Sébastien Henry, Ronan Garnier, CRBM-EMBRC)

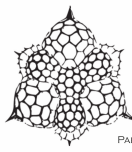
*Session : Environment and development – Chair : Lucas Leclère*

- 15:20-15:40 Clément CARRÉ (DEV2A)  
The RNA methyl-transferase enzyme FTSJ1: conserved role in neuron morphology & learning performance
- 15:40-16:00 Alexandre ALIÉ (IMEV)  
Linking environmental factors with cellular mechanisms of budding in the salp *Thalia democratica* (Tunicata)

16:00 -17:00 **General discussion - future of EDEN Picard Network**

19:00 Gulf Stream - Breton Cider and Beer tasting

19.30 DINNER Gulf Stream



## Talks - Abstracts

### Design principles of cnidarian shapes

Aissam IKMI

EMBL Heidelberg

How do animals build, modify, and restore their shape? Morphological form emerges at the organismal scale from distributed molecular, cellular, and biophysical processes acting across time and space. Because these processes operate at different levels of organization, morphogenetic causality is inherently cross-scale. In this talk, I will discuss how morphological identity is established, dynamically modified, and re-established through the integration of biomechanics, physiology, and environmental inputs. Using cnidarians, whose simple body architecture makes cross-scale causality experimentally tractable, we combine comparative analysis across species, genetic perturbation, quantitative live imaging, and theoretical modeling to uncover the organizing principles of shape control. We show that cnidarian morphogenesis is governed by a small set of conserved mesoscale mechanical modules that generate evolutionary shape diversity, are metabolically gated during life-cycle transitions, and are rescaled during regeneration to restore form from variable initial conditions. Together, this framework reveals how a limited biomechanical toolkit can produce robust yet evolvable organismal architecture.

### Germline development in the Jellyfish *Clytia hemisphaerica*

Sébastien Vaché, Carine Barreau, Evelyn Houlston, Catriona Munro

LBDV, Villefranche-sur-mer

When and where do germ cells and their precursor first arise during development? This is a key question in developmental biology that has been widely studied across metazoans. The traditional dogma is that germ cells and their precursors are set aside during embryogenesis as a distinct cell lineage, named the germline. This process, has been actively studied in animal model species (e.g Mouse, Xenopus, Zebrafish, Drosophila, C.elegans), all belonging to Bilateria. However, data from echinoderms and from newer model organisms (cnidarians, planarians) are challenging the dogma that the germline is a distinct cell lineage.

In cnidarians of the group Hydrozoa, germ cells derive from pluripotent adult stem cells, known as interstitial cells (or i-cells), which can give rise to somatic cells or germ cells. [2], [3].

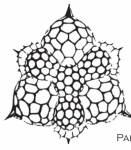
Until now, in *Clytia hemisphaerica*, cell lineages and cell derivatives from adult stem cell progenitors remains uncharacterised. Previously, *Clytia* i-cells were defined as cells expressing GMP (Germline Multipotency Program) genes such as *Vasa*, *Piwi*, *Nanos*, genes also known to be enriched in stem cells. By looking at their mRNA expression via in situ hybridization in *Clytia*, these genes have been described to be expressed during embryogenesis and in medusa (tentacle bulbs, manubrium (mouth), and within the gonads) [4]. It is not known whether these putative *Clytia* i-cells are one or several cell populations which differentiate into germ cells and/or somatic cells and if they are multipotent or pluripotent. Thus, the origin of germ cells and their precursors in *Clytia* remains to be fully explored.

By using *Vasa*/*Piwi* proteins as markers and antibody staining we identified potential i-cells/germ cells at different developmental stages, mainly larvae, polyp and medusa. We could distinguish 2 cell categories co-expressing *Vasa* and *Piwi*. We hypothesise that one is fated to the germline and the other to the somatic lineage. We are now using *Clytia* transcriptomic data (single cell, RNAseq), followed by HCR-RNA-FISH, to identify and study potential marker genes enabling the characterisation of their cellular fate.

So far, this study suggests that germ cells first arise, when putative germline cells approach the site of the future gonad during the medusa bud formation and provide the basis for future studies.

[1] Extavour et M. Akam, 2003, doi: 10.1242/dev.00804. [2] Siebert et al., 2019, doi: 10.1126/science.aav9314. [3] Varley et al., H. R, 2023, doi: 10.1016/j.cub.2023.03.039. [4] Leclère et al., 2012, doi: 10.1016/j.ydbio.2012.01.018.

*Picard Travel grant 2025*



## **Regulation of Prophase Arrest: a new PKA substrate controls Cdk1 activity**

Martina Santoni; Le Tran; Jessus Catherine; Daldello Enrico Maria.

Dev2A, IBPS, Sorbonne Université, CNRS UMR 8263 - Paris

Meiosis is characterized by two consecutive cell divisions without intervening DNA replication, leading to the formation of haploid gametes. Interestingly, the female germ cells (oocytes) remain arrested in prophase of the first division in the ovary for years. They resume meiosis and undergo the two meiotic divisions only at the time of ovulation. The oocytes then arrest again in metaphase of the second division, where they remain until fertilization.

As in mitosis, M-phase is orchestrated by the activity of the kinase Cdk1 (Cyclin-dependent kinase) associated with Cyclin B. Cdk1/Cyclin B activation occurs through a two-step mechanism. Initially, a “starter” pool of active Cdk1/Cyclin B is generated in a protein-translation-dependent manner. Once a threshold level of active Cdk1 is reached, it triggers multiple feedback loops that promote full Cdk1 activation (auto-amplification loop).

By contrast, maintenance of the prophase arrest requires inhibition of Cdk1/Cyclin B. In vertebrates, this depends on the activity of the cyclin AMP-dependent Protein Kinase A (PKA), which indirectly inhibits Cdk1/Cyclin B.

In our laboratory, we aim to elucidate the molecular pathways controlled by PKA that contribute to Cdk1 regulation, using *Xenopus* oocytes as a model system. We investigated the events induced by PKA inhibition that occur upstream of Cdk1/Cyclin B activation and identified a global increase in protein translation, including synthesis of the kinase Mos, as well as accumulation of Cyclin B1. In *Xenopus*, Arpp19 is the only known PKA substrate involved in both the maintenance and release of prophase arrest. However, our findings show that Arpp19 does not control any of the upstream events we described, highlighting the importance of additional, as yet unidentified, substrates of PKA.

Using *in vivo* proximity labelling followed by *in vivo* and *in vitro* functional assays, we identified a novel PKA substrate whose phosphorylation regulates the maintenance of the prophase arrest. Notably, the phosphorylation site is conserved across eukaryotes, supporting a widespread role in regulating Cdk1 activity in both meiosis and mitosis.

*Picard Travel grant 2025*

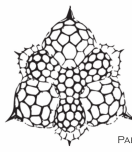
## **mTOR in the sea urchin embryo**

Dufour Sonia; Boulben Sandrine; Petit-Jamin Maiwenn; Cormier Patrick; Morales Julia;

Fernando Roch

Sorbonne Université, CNRS, Laboratoire de Biologie Intégrative des Modèles Marins, LBI2M, F-29680 Roscoff, France

The mTOR pathway controls the balance between anabolic and catabolic activities in animal cells, acting as a key coordinator of metabolic homeostasis. In fact, the activation of this conserved regulatory circuit promotes the biosynthesis of different macromolecules, including proteins, lipids and nucleic acids, and blocks simultaneously catabolic processes such as lysosome biogenesis. In this work we describe a biological system in which these two aspects of the mTOR function are uncoupled. Studying the sea urchin *Paracentrotus lividus*, we have found that the activation of the mTOR pathway in the fertilised egg, besides stimulating protein synthesis, contributes to the development of a dense array of acidic vesicles that behave as lysosomes. We present evidence indicating that mTOR could operate in this context enhancing the translation of the maternal transcripts that code for the multiple components of these organelles. We argue that the mTOR-mediated implementation of a typical catabolic process may in fact support the biosynthetic vocation of this pathway, providing energy and recycled blocks for construction.



### **The mood for love: timing reproductive rhythms of brown algae**

Anjelina Potin, Martina Lazioli, Kenny Bogaert, Rune Sommerkamp, Dan Potin, Inessa Chandra, Mark Cock and Andrés Ritter

Station Biologique de Roscoff, CNRS, Laboratory Integrative Biology of Marine Models (UMR 8227 CNRS SU), Sorbonne Université

Tidal and lunar clocks are widespread in marine organisms, with several species synchronizing reproduction with lunar cycles to increase external fertilization success. However, the environmental factors driving these rhythms remain largely unknown. *Dictyota dichotoma*, an oogamous brown alga with fortnightly reproduction controlled by an internal clock, has a broad distribution along the Atlantic European coast. We investigated whether *D. dichotoma* synchronizes under specific tidal or lunar conditions by monitoring reproductive rhythms across 10 populations with contrasting tidal timings along the English Channel. Using newly developed methods to assess gametophyte reproductive behavior, we found that populations spawn with precise semi-lunar synchronicity. Notably, spawning days varied among populations from different geographical zones, correlating with local tidal timing differences. Additionally, *D. dichotoma* consistently spawns at dawn, indicating a diurnal pattern. Our findings suggest that in these populations, reproduction correlates directly with tidal and diurnal cycles rather than moonlight. These insights represent a significant step toward understanding the environmental cues driving brown algae lunar clocks.

### **Cellular logic of temporal regulation: sleep and circadian clocks from cnidarians to diatoms**

Raphael Aguillon; Monteil Raphael; Cheminant-Navarro Soizic; Colina Moreno Irelka ; Maes Alexandre; Falciatore Angela

P3M UMR7141 Sorbonne Université

Evolutionary innovations can be high-gain yet costly, providing adaptive benefits while increasing physiological stress. One way to accommodate such innovations is to restrict their activity to specific times of day. Circadian clocks are conserved molecular timekeepers that schedule daily biological functions, yet how pre-existing clocks incorporate new, high-cost functions remains poorly understood. Here, this is examined by contrasting early-diverging metazoans and unicellular diatoms. In cnidarians, neuronal activity is metabolically demanding and requires coordinated regulation at the organism level. In diatoms, secondary endosymbiosis introduced a highly energetic chloroplast, imposing metabolic and oxidative constraints that must be managed within a single cell. In *Phaeodactylum tricorutum*, analyses identify plant-derived circadian regulatory components linked to chloroplast control that are integrated into the host circadian system. Overall, these results position circadian clocks not just as daily timers, but as a practical route for integrating physiologically demanding functions, either via organism-level control in animals or intracellular clock control in unicells.

### **A Quantitative Description of the Mechanisms Leading to a Switch-like Transcriptional Response during Ascidian Early Neural Induction**

Clare Hudson

CNRS, Sorbonne Universities, IMEV, LBDV

Understanding how graded signalling inputs are converted into switch-like transcriptional responses is a fundamental question in developmental biology. During development, cells are often exposed to gradients of signalling molecules that convey positional information within the embryo. In some contexts, cells must interpret these graded signals to make binary decisions about whether or not to activate specific genes. The molecular mechanisms underlying such threshold responses - by which analogue signals are transformed into digital outputs - remain poorly understood, in part due to the intrinsic heterogeneity of cellular responses.



This study focuses on the conversion of a graded FGF-ERK signal into a bimodal ON/OFF transcriptional response of an immediate-early gene (IEG), using early neural induction in ascidian embryos as a model system. The invariant cell arrangement and lineage of ascidian embryos allow precise identification of individual cells based on their position. During early neural induction, all eight anterior ectoderm cells contact FGF-expressing mesendoderm, yet only two adopt neural fate by activating the IEG *Otx*. ERK activation levels in ectoderm cells mirrors their contact areas with FGF-expressing mesendoderm, and this graded input is converted into a sharp, bimodal *Otx* transcriptional response.

Our working hypothesis is that this transition arises from opposing ERK-regulated ETS-family transcription factors - *Ets1/2* acting as an activator and *ERF2* as a repressor - competing for shared regulatory DNA sites. We are investigating how this regulatory architecture integrates binding-site competition, cooperative DNA binding and synergistic transcriptional activation, multisite phosphorylation, nuclear import-export, and protein stability to drive a robust transcriptional switch. I will present our recent results addressing these mechanisms, and discuss how ongoing collaboration with mathematical modellers will help determine whether this configuration is sufficient to account for the observed switch-like behaviour.

### **Uncovering signalling pathways regulated by primary cilia using human neural organoids**

Brunetti, Wiegner, Anselme, ..., Stedman, Schneider-Maunoury S, [Christine Vesque](#)

Sorbonne Université, CNRS, Inserm, Development, Adaptation and Aging, Dev2A, F-75005 Paris, France

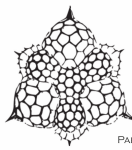
Cerebellar hypoplasia and dysplasia are features of neurodevelopmental ciliopathies such as Joubert syndrome. These disorders are caused by dysfunction of the primary cilium, involved in signal reception and transduction. Pathogenetic mechanisms linking ciliary gene dysfunction to Joubert syndrome defects are poorly understood. In this study, we generate cerebellar organoids from human induced pluripotent stem cells carrying either null mutations or patient-derived variants in *RPGRIP1L*, a Joubert syndrome causal gene encoding a scaffold protein crucial for ciliary function. While control organoids express markers of cerebellar glutamatergic and GABAergic lineages including Purkinje cells, *RPGRIP1L*-deficient organoids display a severe reduction in Purkinje cell markers, along with impaired neurogenesis and increased progenitor proliferation. These defects coincide with overactivation of the FGF signaling pathway. Remarkably, pharmacological inhibition of FGF signaling rescues both the neurogenesis and Purkinje lineage formation. Thus, our findings provide new insights into the developmental origin of cerebellar impairment in a neurodevelopmental ciliopathy.

### **Equivalence of cell type across species using single-cell RNAseq**

[Marc Meynadier](#), Richard R. Copley

LBDV Villefranche-sur-mer

Traditional cell type classification is based on phenotypic and developmental criteria. With the evolution of bioinformatics, new tools for studying cell characteristics have emerged. Single-cell transcriptomics allows for cataloging expressed genes at the cellular level, clustering cells with similar expression patterns. This method can address various issues related to cell type identity. While several tools integrate different datasets, few specialize in cross-species comparison, often requiring manual annotation or reprocessing user data. We present *equivalentcell*, a dual aspect tool which can automatically assess equivalent cell types across species and extract the transcriptional signature of a target cell type by leveraging orthologous genes through statistical tests. It is flexible, accepting input data from various tools like Seurat, Scanpy, and SAMap without altering them. Focusing on Cnidaria, we leverage available single-cell transcriptomic data from Hydrozoa and Anthozoa species. Our results show clear mapping of equivalent cell types across cnidarian species, consistent with manual annotations. A focus has been made on cnidocytes, the characteristic stinging cells, which have been suspected to share a common evolutionary ground with neurons since decades. Transcriptional signature captures reveal overlap between orthologous genes of cnidocytes and neurons, providing insights into their common ancestral state and



cell type evolution. Those results also tend to validate in a cross-species context transcription factors previously found in individual species while uncovering new transcription factors never tested in this phylum yet. Beyond Cnidaria, neuronal transcriptional signature applied to two Spiralia larvae also revealed a corpus of genes consistent with the neuronal identity literature.

### **Cooperation between cortical and cytoplasmic forces shapes planar 4-cell stage embryos**

Silvia Caballero-Mancebo; Gonzalez Suarez Daniel; Chenevert Janet; Ben-Aicha Sameh; Besnardeau Lydia; McDougall Alex; Dumollard Rémi

Laboratoire de Biologie du Développement de Villefranche-sur-Mer

Early embryonic cleavages often follow conserved geometric rules, resulting in species-specific cleavage patterns. How these rules are mechanistically implemented, however, varies widely across species and remains poorly understood. Here, using quantitative 3D live imaging and mechanical and biochemical manipulations, we dissect the mechanisms governing centrosomal complex (CC) migration and spindle orientation in ascidian 2-cell stage embryos to generate the characteristic planar, square 4-cell stage. We show that following the first mitotic division, CCs in the two blastomeres form at variable orientations relative to the mother spindle and progressively achieve parallel and coplanar alignment during interphase of the 2-cell stage. Final spindle orientation is established prior to nuclear envelope breakdown, contrasting with dynamic spindle reorientation reported in other systems.

Our analyses reveal that CC rotation is driven by forces acting on long astral microtubules and guided by an anisotropic, ER-rich cytoplasmic domain that surrounds the CCs. This ER domain correlates with a dense astral microtubule network, enabling length-dependent microtubule pulling that orients the CCs independently of cell shape. In parallel, dynein-mediated cortical pulling refines spindle tilt and maintains coplanarity. Together, these findings uncover a cell-cycle-regulated, finely tuned balance between ER-mediated cytoplasmic forces and anisotropic cortical forces that ensures robust planar cleavage in ascidian early embryos.

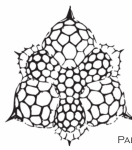
### **Transcriptional and morphological insights on Clytia jellyfish manubrium regeneration**

Florian Pontheaux, Guillaume Florian, Leclère Lucas, Sinigaglia Chiara

Sorbonne Université, CNRS, Biologie Intégrative des Organismes Marins (BIOM), Banyuls-sur-Mer, France  
Regeneration is the capacity of an organism to restore integrity and functionality of tissues, organs or even body parts after damage. The dynamics of progenitor cells, their recruitment, proliferation and differentiation - and the morphogenesis of new structures are tightly controlled processes. The regenerative capacity is widely found among cnidarians, the sister group to bilaterian animals.

The hydrozoan jellyfish *Clytia hemisphaerica* possesses excellent repair capacities, reshaping efficiently its circular umbrella in less than 12 hours and regenerating missing organs within a week. The regeneration of the feeding organ, called manubrium, is a stereotypical and tractable process, which allows dissecting the post-embryonic morphogenesis of an organ. We investigate here this regeneration case study, presenting both transcriptional and morphological data.

Previous work provided a description of the repair process, showing that the primordium of the new manubrium emerges from a blastema, an accumulation of diverse cell types that derive, at least in part, from other intact organs of the jellyfish, travelling through the system of endodermal canals. This heterogeneous population of progenitors includes stem cells (called i-cells in hydrozoans), differentiated digestive cells and maturing gametes. Cells within the blastema proliferate and the structure thickens, while the new gastric cavity develops and an opening appears. From the rim of the opening a tubular outgrowth emerges, within which the endodermal and ectodermal layers differentiate (separated by a thin extracellular matrix, called mesoglea). Within four days from dissection, the new structure recovers the original shape, forming the characteristic tetradial folding of the lips.



We are now dissecting the spatial and temporal dynamics of precursor cells differentiation, combining our time-course data of scRNA-seq targeting the regenerating manubrium, in situ hybridization and immunostaining. Morphological data from live-imaging and scanning electron microscopy further provide a more in depth understanding of the recovering shape.

Overall, our data provide a finer description of the cellular dynamics and tissue morphogenesis during manubrium regeneration.

### **Role of Contactin 2 during the development of the zebrafish olfactory system.**

Karen Pottin; Cabrera Mélody; Trembleau Alain; Breau Marie

CNRS, Sorbonne Université, IBPS, Développement Adaptation et Vieillessement

During the development of the zebrafish olfactory system, neurons generated in the olfactory placodes grow axons which enter the brain grouped as a dense fascicle on each side of the embryo. These axons then migrate dorsally towards the developing olfactory bulb, where they defasciculate and coalesce into several protoglomeruli (immature glomeruli), neuropile structures in which the sensory axons make synapses with target cells. The mechanisms driving the formation of the protoglomeruli are still poorly understood. We are particularly interested in the implication of the Contactins (Cntn), adhesion proteins known for their role in cell/cell interactions and axonal development. We showed that Cntn2 is expressed in the olfactory neurons and their axons, and in the presumptive olfactory bulbs during the formation of the protoglomeruli. To assess its function, we generated a loss of function mutant. While heterozygous mutants show no apparent defect, homozygous mutants display a localised axonal phenotype: the axons that specifically innervate one of the protoglomeruli, the dIG (dorso-lateral glomerulus), are misplaced, leading to a delay in the proper formation and innervation of this protoglomerulus. Using live imaging of axonal behaviours, we discovered several scenarios for the development of the dIG. One of these scenarios, observed mainly in Cntn2 heterozygous mutants, reveals an unexpected mechanism involving dynamic axon/axon interactions, which fail to occur in homozygous mutants. Taken together, these results show the importance of Cntn2 for the proper innervation of the dIG, and reveal the plasticity and robustness of olfactory system development in zebrafish.

### **Large-scale reprogramming of differentiated larval tissues establish adult body plan during sea cucumber metamorphosis**

Laurent Formery; Tate Heidi; Ferreira-Candido Ivan; Rokhsar Daniel; Lowe Christopher

Observatoire Océanologique de Banyuls-sur-Mer; Hopkins Marine station of Stanford University; University of California Berkeley

Most of our understanding of animal body plan formation come from the study of a handful of selected model organisms. These model species are predominantly direct developers, in which the adult body plan arises directly from embryogenesis. However, this developmental strategy is not broadly representative of animal diversity. In many taxa the formation of the adult body plan is postponed by one or several larval stages, a strategy known as indirect development. How an adult body plan arises through the transformation of a pre-existing larva, rather than as a direct outcome of embryogenesis, remains poorly understood, biasing our view of animal body plan evolution. To address this gap, we have started investigating the molecular and cellular mechanisms underlying adult body plan formation in the indirect-developing sea cucumber *Apostichopus parvimensis*. Larval and juvenile stages in this species are completely transparent, making it amenable for live imaging through metamorphosis. Using cell tracking, fluorescent in situ hybridization and single-cell RNA sequencing, we show that metamorphosis in *A. parvimensis* involves extensive reprogramming of differentiated larval tissues into adult structures. In particular, portions of the larval ciliary band give rise to the adult central nervous system. These findings challenge the existing dogma of metamorphosis, in which most larval tissues are presumably simply



discarded. Instead, it suggests that cellular reprogramming might be an important but underappreciated mechanism when building an adult body plan from a larval stage.

### **ECM-mediated inter-tissue mechanical coupling in olfactory placode morphogenesis in *Olfactores***

Camille Curantz, Ronan Lagadec, Sylvie Rétaux, Sylvie Mazan, Marie Breau

Développement, Adaptation et Vieillesse UMR8263 Paris / Biologie Intégrative des Organismes Marins UMR7232 Banyuls-sur-Mer

Understanding how organ shapes emerge and diversify in animal is a fundamental question in developmental biology. While molecular signalling has been extensively studied, the contribution of mechanical forces to morphogenesis, particularly at the interfaces where neighbouring tissues interact, remains less understood. The extracellular matrix (ECM) often mediates the mechanical coupling between tissues and can transmit forces across tissue boundaries, potentially influencing organ morphogenesis and its diversification across evolution. Yet, the role of ECM-mediated inter-tissue coupling in development and evolution remains largely unexplored. Here, we propose to address this question using the olfactory placode and its interaction with the neighbouring eye as a model system across different species. By integrating live imaging, force mapping, cross-species comparisons and mechanical perturbations, we aim to determine how ECM-mediated inter-tissue coupling contribute to organ morphogenesis and its diversification across evolution.

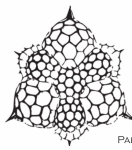
*EDEN André Picard Network 2025 grant*

### **Membrane potential mapping and genetic regulation in *Phallusia mammillata***

Josep Martí-Solans, Martin, Anouck; Darras, Sébastien

Sorbonne Université, CNRS, Biologie Intégrative des Organismes Marins (BIOM), F-66650 Banyuls-sur-Mer, France

Bioelectricity represents a fundamental regulatory layer in morphogenesis, yet the functional dialogue between membrane potential ( $V_{mem}$ ) and gene regulatory networks remains largely unexplored. Far from being exclusive to excitable tissues, bioelectric signaling arises from ion flux across all cellular membranes, creating subtle voltage gradients that orchestrate large-scale tissue patterning. In the developing embryo, these signals coordinate complex events and guide the precise cellular movements essential for tissue remodeling. However, because electrophysiology and developmental biology are traditionally investigated separately, the precise mechanisms by which bioelectric states interface with genomic control remain poorly understood. The ascidian *Phallusia mammillata* offers a powerful system to bridge this disciplinary gap. As a basal chordate with a transparent embryo and a highly stereotyped developmental program, it provides an ideal model for the real-time observation of physiological changes alongside genetic analysis. Through the use of synthetic voltage-sensitive dyes, we have captured high-resolution, live imaging of voltage dynamics throughout the ascidian development. Preliminary results from this high-resolution mapping reveal dynamic bioelectric signatures that characterize specific embryonic domains. These patterns demonstrate that distinct voltage gradients precede major morphological shifts, suggesting that electrical states provide a vital spatial scaffold for downstream developmental events. To test the functional necessity of these gradients, pharmacological perturbations targeting specific ion channels were employed. Initial data indicate that disrupting the endogenous bioelectric state leads to significant deviations from normal morphogenesis and alterations in the expression of key developmental genes. Integrating these voltage maps with 3D spatial gene expression analysis provides a comprehensive view of the relationship between ion channel activity and gene regulatory states. Furthermore, exploring the feedback between bioelectric signaling and morphogen pathways clarifies how electrical cues modulate transcriptional programs and vice-versa. By utilizing combined perturbations to restore normal voltage in signaling-defective embryos, this work aims to test whether bioelectric states function as necessary intermediates in developmental cascades. Ultimately, this research will uncover fundamental mechanisms



by which cells encode positional information, offering new insights into the orchestration of complex morphogenesis.

### **How do medusozoans build striated muscles without MRFs? Insight from *Pelagia noctiluca* myogenesis**

Clara Deleau, Lucas Leclère

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Striated muscle cell contraction relies on a highly organised actomyosin network. In contrast to smooth muscle, striated muscle cells contain repeated contractile protein subunits called sarcomeres. Within sarcomeres, thick myosin filaments are surrounded by thin actin filaments anchored between cross-linking structures known as z-disks. While smooth muscles are found in bilaterians, anthozoans and medusozoans, striated muscles are restricted to bilaterian and medusozoan lineages. A widely shared hypothesis proposes that striated muscle cells evolved independently in these two groups. The absence of homologs of bilaterian myogenic regulatory factors (MRFs; MyoD, Mrf4, MyoG, and Myf5) in cnidarian genomes supports this hypothesis. However, recent studies have shown striking similarities between bilaterian and medusozoan sarcomeres in their protein organisation. How medusozoans assemble sarcomeric structures that are so similar to those of bilaterians in the absence of MRFs remains an open question. A comparative analysis of cnidarian and bilaterian myogenesis is an essential step toward constructing an evolutionary scenario. Here we use the emerging jellyfish model *Pelagia noctiluca* to study the mechanism underlying the development of medusozoan striated muscles. Whereas most medusozoan models develop striated muscle late in their life cycle, *Pelagia noctiluca* has evolved a direct life cycle in which functional smooth and striated muscles develop within the first five days post-fertilization. We identified homologs of bilaterian myogenic transcription factors in the *P. noctiluca* genome and analysed their expression during early striated muscle development. We also performed an unbiased screen of transcription factors expressed in muscle cell precursors using transcriptomic data. These results bring new insights into the evolution of striated muscle across metazoans.

*Picard Travel grant 2025*

### **Evolutionary variation of developmental mechanisms: the case of *Molgula appendiculata***

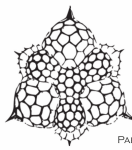
Cécile LEBLOND, Sébastien DARRAS

Biologie Intégrative des Organismes Marins, Observatoire Océanologique de Banyuls sur mer, CNRS, SU

The development of organisms relies on finely coordinated mechanisms, such as gene regulatory networks and inductive signals. While these mechanisms are globally conserved, their modification can lead to the emergence of new structures, morphological losses, or disease. To understand how these programs evolve, this project focuses on the larval peripheral nervous system (PNS) of ascidians, marine invertebrates belonging to the sister group of vertebrates.

In ascidian larvae, the PNS consists of epidermal sensory neurons derived, as in vertebrates, from the neural plate borders. The anterior palp neurons are comparable to the vertebrate olfactory placodes, while posterior tail neurons share similarities with neural crest cells. Through a comparative study of four species (*A. mentula*, *P. mammillata*, *C. lepadiformis*, and *M. appendiculata*), I show that while the morpho-molecular organization of sensory neurons is largely conserved, *Molgula appendiculata* exhibits significant differences. This species is characterized by a drastic reduction in neuron number, associated with altered gene expression patterns and atypical BMP signaling dynamics. These results demonstrate how comparative approaches can link the evolution of biological structures to specific modifications in the underlying developmental mechanisms.

*Picard Travel grant 2025*



## **Initial Morphological and Molecular characterisation of Sensory Systems in Ascidian Larvae**

Luis Alberto BEZARES-CALDERÓN; Sébastien DARRAS

Author 1: LBDV (UMR7009) ; Author 2: BIOM (UMR 7232)

Ascidian larvae display the characteristic chordate body plan: a swimming tadpole with a peripheral nervous system (PNS), a brain, notochord and muscle cells. These planktonic larvae can sense and respond to multiple stimuli including light, gravity, flow and pressure. The underlying sensory-motor systems driving some of these behaviours have been functionally dissected with unprecedented detail in the model ascidian *Ciona*. It is so far unknown to what extent these sensory systems are conserved in other Ascidian larvae. We aim to characterize the pattern of evolutionary conservation and divergence of sensory systems across development and levels of organisation, from molecules to behaviour. We will leverage the overall conservation in cellular composition, as well as the experimental tractability and availability of species across the entire Ascidian phylogeny.

We will begin this EDEN collaboration by characterizing the molecular, cellular, and developmental makeup of sensory systems in a variety of ascidian larvae with key phylogenetic positions. We will use the knowledge gained in *Ciona* spp. as reference. We will use a combination of in situ hybridization, immunochemistry and transient transgenesis to assign cell and neuromodulator identity and thus characterise the overall conservation of sensory cells and downstream networks in each species. We will also test emergent techniques such as expansion microscopy that can reveal a more detailed view of the sensory-motor architecture of each species (e.g. major ganglia, muscles). This knowledge will synergise with that gained from previous and ongoing work on the development of the PNS in the species to be used in this study. We will focus on sensory systems with expected variation, such as the photolith in the Botrylloides group or the semi-degenerated ocellus of Molgulids. We will also explore the suitability of additional species that extend our coverage of the Ascidian phylogeny. In parallel, we will mine the single cell RNA sequencing atlas in *Ciona* for expression in sensory cells of conserved molecules with light- and mechano-transduction function that we can search in homologous cells in other species. This initial morphological and molecular mapping will form the basis for further inquiries at the behavioural and neurophysiological levels.

*EDEN André Picard Network 2025 grant*

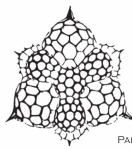
## **Comparative Early Embryogenesis in Solitary and Colonial Ascidians**

Stefano TIOZZO; Sébastien DARRAS

UMR7009 - Villefranche-sur-Mer; UMR7232 - Banyuls-sur-Mer

Ascidians belong to the sub-phylum of Tunicata, the sister group of vertebrates, and their embryogenesis has long stood as a classical example of highly conserved, mosaic development. Across species that diverged hundreds of millions of years ago, ascidian embryos display a remarkably stereotyped cleavage pattern, characterized by invariant blastomere lineages. Since the pioneering work of Edwin G. Conklin, these early cell divisions have been described with exquisite precision, allowing the naming and tracing of blastomeres through the first 10-12 cleavage stages. This robust and evolutionarily stable developmental program is so reliable that solitary ascidians became a textbook model for cell-fate specification and mosaic development.

Despite this, our understanding rests almost entirely on solitary, non-colonial species such as *Ciona intestinalis* or *Phallusia mammillata* or *Halocynthia roretzi*. It is widely assumed that colonial ascidians follow the same early embryonic program. Yet this assumption lacks evidence: the literature on cleavage patterns in colonial species is nearly non-existent, and no modern high-resolution reconstruction of colonial ascidian embryogenesis is currently available. This represents a striking gap, especially given the deep biological differences between solitary organisms and colonial lineages capable of agametic reproduction, whole-body regeneration, and formation of modular chimeric systems.



In Tiozzo's lab, the colonial species *Botryllus schlosseri* is a central model. As we develop zygotic microinjection and transgenesis protocols, we simultaneously aim exploiting these early embryos to generate a comprehensive description of the first 9-10 cleavages, using confocal and SPIM microscopy coupled with nuclear (propidium iodide) and cell-membrane (phalloidin, CellMask) labelling we aim to segment and generate 3D reconstructions from which we aim to extract detailed morphometric parameters and produce a digital atlas of early *Botryllus* development. In parallel, the Darras lab is establishing embryological and molecular tools in *Clavelina lepadiformis*, a colonial ascidian belonging to a distinct order from *Botryllus*. Together, these species offer a powerful comparative framework: two independently evolved colonial lineages contrasted with the classical solitary ascidian cleavage program. The joint aim of this EDEN project is to combine expertise and resources to generate two complete, openly accessible 3D atlases of early embryogenesis in *B. schlosseri* and *C. lepadiformis*, and to compare them with the well-characterized solitary ascidian models.

*EDEN André Picard Network 2025 grant*

### **Hennigian hierarchy of ontogenetic time**

#### Guillaume Lecointre

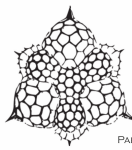
Institut de Systématique, Évolution et Biodiversité (UMR 7205 CNRS-MNHN-SU-EPHE-UA), Muséum national d'Histoire naturelle, Paris Systematics used to compare adult semaphoronts of different species, while developmental Biology used to compare semaphoronts of different stages within a same species. Empirical ontophylogenetics compare in a single tree semaphoronts of different stages for different species [Lecointre et al., 2020]. This provides a hierarchy of ontogenetic time, allowing a better study of developmental heterochronies and a possibility for a hennigian nomenclature of ontogenetic stages. This scientific program is embedded within a view of ontology where ontogeny is an evolutionary phenomenon. It is not really new, but it is not considered as such when we teach Biology. For example, EvoDevo called homeotic genes "architect genes" because they "control" "body plans". The first metaphor involves purposefulness and brings finalism, the second one is cybernetic, the third one is idealistic/platonic, three ways of thinking that are incompatible with today's evolutionary theory. Using such ordering causal factors, EvoDevo partly stayed outside biology -and evolution as well- because in biology order is not causal, it is a consequence that we need to explain. Natural selection is the concept explaining the rise of apparent short-term biological order, or regularities. Genes do not "control" anything [Nijhout, 2022], they just impulse or contribute. Natural selection and Descent with modification, the two pillars of the Darwinian approach of life [Gayon, 2009], are entering the soma (not restricted to the functioning of the adult soma, but also to the entire developing soma, avoiding "adultocentrism" [Minelli 2014: 233]). The first pillar, natural selection within the body, anticipated by Roux [1881, 2013], but occulted during the past century [Heams, 2013b], is now allowing to understand cancer dynamics, ageing, neurogenesis, etc. With the second pillar, it is now possible to construct the phylogeny of cells of a single developing organism, or to perform a phylogenetic analysis of metastases from a single patient. Ontogenesis and phylogenesis are no more two distinct processes: natural selection and descent with modification both contribute to explain both the developing individual and its stability, as well as the regularity of individuals of a same population from which we name species. The resulting phenomenon is ontophylogenesis [Kupiec 2012], which is actually studied by EvoDevo.

*EDEN André Picard Network 2025 grant*

### **The RNA methyl-transferase enzyme FTSJ1: conserved role in neuron morphology & learning performance**

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Transfer RNAs (tRNAs) are crucial for translation, with their function heavily influenced by modified ribonucleotides. One such modification, 2'-O-methylation (Nm), affects the ribose moiety and is particularly present on the anticodon loop of some tRNAs. In humans, Nm is catalyzed by the SAM-dependent methyltransferase FTSJ1. Loss of FTSJ1 leads to intellectual disability (ID), though the mechanisms are not fully understood. Our studies in human neural progenitor cells showed that inhibiting FTSJ1 increases dendritic spines, a feature common in neurodevelopmental disorders. This phenotype is also observed in *Drosophila* larvae with mutated FTSJ1 orthologs and mice. Transcriptome analysis revealed deregulation of mRNA and miRNA involved in brain morphogenesis in human cells, suggesting defective gene expression regulation contributes to the observed morphological defects. Additionally, long-term memory is affected in *Drosophila* mutants of FTSJ1. Given tRNAs' role in translation, transcriptome-wide profiling of ribosome footprints was conducted on human and *Drosophila* cells affected by FTSJ1 activity. These analyses are ongoing and recent results will be presented. Those results indicate significant regulation of brain-specific genes, morphological defects in neuronal cells lacking FTSJ1 and codon bias, interestingly highly conserved through evolution. The goal is to identify genes involved in the defective morphology of neuronal tissues without tRNA Nm, determine if the regulation occurs at the translational level, and understand the mechanisms behind FTSJ1-related intellectual disability using 3 models' systems, *Drosophila*, human patient cells and mice.

### **Linking environmental factors with cellular mechanisms of budding in the salp *Thalia democratica* (Tunicata)**

Léa Bastid-Solinas 1; Manon Boosten 1; Dany El Gharbi 1; Svenja Müller 2,3; Bettina Meyer 2,3; Stefano Tiozzo 1; [Alexandre Alié](#) 1

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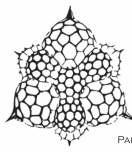
Agametic reproduction is a developmental process by which species can reproduce clonally from strictly somatic cells, bypassing fertilization and embryogenesis. The central role of agametic reproduction in the demography of many animal species is widely recognized. Yet, a deeper understanding on the cellular and molecular mechanisms of agametic reproduction is crucial to measure the impact of environmental factors on the dynamic of clonally reproducing populations.

Salps are holoplanktonic tunicates that play a major ecological role in the world's oceans, where they form vast seasonal swarms. These seasonal demographic explosions are driven by an agametic reproduction phase, during which an individual produces hundreds of clones in just a few days through a process called budding.

To better understand the link between salp demography and budding dynamics in the Mediterranean species *Thalia democratica*, we first described the anatomy of the stolon, the organ in which agametic reproduction takes place. We identified populations of stem cells residing at the base of the stolon, which supplies the tissues required for the continuous clonal production. We established a single-cell transcriptomic atlas of the stolon, to further characterize the differentiation potential of these stem cells, revealing multiple lineage-restricted populations that coordinately give rise to fully functional adults.

Finally, by combining multi-year monitoring of *Thalia democratica* populations with aquarium experiments, we found a positive correlation between budding rate and salp abundance under environmental conditions (temperature and food availability) favorable to swarms formation. We are now working to link population growth rate to cell proliferation rate in the stolon. Together, these results begin to reveal how environmental fluctuations may influence stem cell activity, thereby impacting the demography of these planktonic organisms.

*EDEN André Picard Network 2025 grant*



## Posters – Abstracts

### **Circatidal and circadian rhythms in brown algae**

Mikaela Chandra; Potin Anjelina; Nuzhdin Sergey; Gracey Andrew; Ritter Andrés

Station Biologique de Roscoff; Ghent University; Max Planck Institute for Biology; University of Southern California

Biological rhythms pervade throughout the tree of life, as a response to selective pressures for organisms subject to intense environmental cycles (e.g. intertidal creatures) and an opportunity for those dependent on temporally dynamic resources (e.g. photoautotrophs) or periodic events for demographic synchronization (e.g. broadcast spawners). Members of the brown algal clade often fall into multiple of these categories at once, explaining the prevalence of biological rhythms in this lineage. All are photosynthetic, but habitat niches span from tidal and subtidal zonations to pelagic floating states, and reproduction spans from asexual to broadcast spawning and functional brooding. Accordingly, evidence supports widespread circadian rhythms and patchier circatidal and circa(semi)lunar rhythms; however, there is a dearth of information regarding the underlying mechanisms controlling these rhythms. Here, we present a meta-analysis of circatidal and circadian rhythms in mRNA abundance across 2 brown algal species: *Macrocystis pyrifera*, a perennial canopy-forming subtidal kelp, and *Dictyota dichotoma*, an annual turf-like/epiphytic brown alga spanning the subtidal to mid-intertidal zones. In addition to having a habitat distribution shifted up the shore, *D. dichotoma* displays circasemilunar rhythmicity of gamete release, thought to be dependent on interacting circatidal and circadian clocks. While we find general similarity in the functional themes in our rhythmic datasets, gene expression of predicted homologs of transcription factors and photoreceptors containing common clock protein domains behaved differently across species.

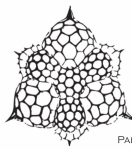
### **The spatio temporal development of amphioxus muscles**

Lucille Cornand, Bertrand Stéphanie, Escriva Hector

Sorbonne Université, CNRS, Biologie Intégrative des Organismes Marins, BIOM, F-66650, Banyuls-sur-Mer, France

An important question in evolutionary biology is the emergence of the head in vertebrates. Among the tissues that form the head, the musculature remains particularly poorly understood. Unlike trunk muscles, which arise from the segmentation of the paraxial mesoderm into somites, head muscles develop from non-segmented mesodermal territories : the prechordal plate and the pharyngeal mesoderm, which are considered vertebrate-specific innovations.

In cephalochordates (i.e. amphioxus), which occupy a basal position within the chordate group, the paraxial mesoderm is fully segmented along the anteroposterior axis. It has been proposed that the organization of mesodermal territories in amphioxus corresponds to that of the last common ancestor of chordates. Thus, although trunk muscles also derive from somites, the origin of head muscles remains unknown. Studying this model allows the exploration of the spatio-temporal development of larval muscles, particularly those of the mouth and pharynx. Given to its basal phylogenetic position and the organization of its mesodermal territories, which is supposed to be similar to that hypothesized for the chordate ancestor, amphioxus represents a highly relevant model for this study. First a single cell RNA sequencing (scRNA-seq) analysis was performed. These data enabled the characterization of distinct muscle cell types and the identification of multiple putative populations displaying distinct expression profiles of muscle-related genes, such as myosins. Based on these results, the expression of selected genes was detected during larval development using single in situ hybridization (ISH) and multiplex hybridization chain reaction (HCR). These experiments will allow validation of scRNA-seq, defined subpopulation profiles, examination of gene co-expression within specific muscle populations, and characterization of their spatial distribution within the larva.



This work will bring to light muscles cell types in amphioxus and allow comparison with their emergence in vertebrates.

### **Reawakening the Ribosome: Mechanisms of ribosome de-hibernation during oocyte meiotic divisions**

Mariam Gachechiladze; Riou Jean-Francois; Daldello Enrico Maria

IBPS; Sorbonne University

The molecular mechanisms that control translation during oocyte maturation remain one of the major open questions in developmental biology. Understanding how protein synthesis is regulated in time and space is essential, as disruptions in these processes are closely linked to infertility, reduced oocyte quality, and early embryonic arrest. Oocytes arrest in prophase I during oogenesis, and they undergo extensive growth while accumulating maternal mRNAs, proteins, and ribosomes that later support meiotic divisions and embryonic development. Once growth is complete, transcription ceases, and the oocyte remains in a quiescent state until hormonal stimulation induces meiotic maturation. In all vertebrates, meiotic maturation is triggered by PKA inactivation that starts as a signalling pathway leading to Cdk1 activation, which drives the transition from prophase arrest to meiosis. Because transcription is shut down at this stage, changes in protein levels depend entirely on translational control. This regulation operates through both the selective activation of stored mRNAs, mediated by mechanisms such as cytoplasmic polyadenylation, and by modulation of the translation machinery itself. Recent evidence indicates that a substantial fraction of ribosomes in oocytes are inactive. In *Xenopus* and zebrafish, about 40% of ribosomes exist in a “hibernating” state, where large and small ribosome subunits are assembled together. This project aims to uncover the mechanisms governing ribosome hibernation and de-hibernation during oocyte maturation and to define their functional significance in translation and meiosis. Ribosome-associated proteins and their post-translational modifications will be identified using biochemical and mass spectrometry approaches, while the roles of candidate regulators will be assessed through functional assays of translational activity and meiotic progression. Ribosome dynamics and activity will be monitored using polysome profiling. By combining molecular, biochemical, and imaging approaches, this work seeks to elucidate how the translational machinery is reactivated during oocyte maturation, providing broader insights into how cells regulate translation, quiescence, and reactivation across biological systems.

### **Nutrition-dependent dynamics of progenitor cells during the regeneration of *Clytia hemisphaerica***

Gaspar Thomas, Sinigaglia Chiara

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Regenerative processes are increasingly viewed as coordinated organismal-level responses involving complex communication between injured and uninjured body parts. This could be modulated by physiological parameters such as metabolism and aging. Investigating these processes in traditional models remains challenging due to their biological complexity and slower repair processes. My thesis project focuses on the hydrozoan jellyfish *Clytia hemisphaerica*, an emerging model for regenerative studies, thanks to its rapid and tractable repair (the feeding organ- manubrium, regenerates in just four days, and the animal is amenable to organismal-level experimental manipulations, such as live-imaging). *Clytia* possesses a system of gastrovascular canals connected to the manubrium that distribute nutrients; previous work has shown that they also serve as pathways for migratory progenitor cells, originating from niches within the intact organs. Two key cell populations contributing to regeneration were identified: stem cells (called i-cells in hydrozoans) and a novel type of digestive cell called Mobilizing Gastro-Digestive (MGD) cells.

The cellular nature of MGD and its potential role in the distribution of nutrients between organs remain unexplored. Interestingly, the behaviour of these progenitors appears linked to the animal's nutritional



status. While manubrium shape recovery is independent of food availability, appropriate feeding is essential for size recovery.

In parallel, both regeneration and starvation trigger the systemic migration of MGD cells through the canals. At the molecular level, the mTOR signalling pathway, which is sensitive to nutritional status, plays a key role in regeneration. Coherently, available transcriptomic data show an early upregulation of mTOR signaling-related genes following injury.

This project aims to characterize the diversity and transcriptional signatures of MGD cells in various physiological states, map the morphological behaviors of i-cells and MGD cells under conditions of nutritional fluctuations, and dissect the role of the mTOR pathway as a putative molecular mediator of nutritional signals. By manipulating both molecular regulators and gastrovascular flow, this research seeks to establish how systemic nutritional status and progenitor dynamics are integrated to achieve efficient tissue repair. By investigating the mTOR pathway, this project will contribute to the development of *Clytia* as a model suited for a systemic and integrative understanding of regeneration

### **Role of the extracellular matrix in force transmission at the olfactory placode/eye interface in teleosts.**

Johann Jamet, Camille Curantz, Sylvie Rétaux, Alexis Eschstruth, Marie Breau  
Dev2A, IBPS, Sorbonne Université, CNRS UMR 8263

Understanding how organs acquire their shape during development remains a major challenge in developmental biology. While morphogenesis has been largely studied through genetic and biochemical signalling, mechanical forces are now recognised as key regulators of tissue shaping. Recent studies have shown that the extracellular matrix (ECM) can transmit mechanical forces between neighbouring tissues, thereby contributing to shaping organs and tissues. However, the mechanisms by which ECM-mediated inter-tissue coupling influences organ morphogenesis and its evolution remain poorly understood. To tackle this question, we propose to use a comparative approach and study the development of the olfactory placode and its interaction with the neighbouring eye in two teleosts species: *Danio rerio* and *Astyanax mexicanus* (species known to exhibit different eye/placode configurations). In *D. rerio*, the morphogenesis of the olfactory placode partially relies on extrinsic mechanical forces generated by the developing eye and transmitted through a shared interstitial ECM. Here, we aim to characterise both the composition of this ECM and the nature of the forces it transmits. We combined immunostaining and live imaging of embryonic development to map the spatial organisation of major ECM components, preliminary data showed the presence of fibrous network of Collagen IV at the eye/olfactory placode interface, known to be involved in long-range force transmission in other contexts. Using targeted laser ablations of the ECM to probe mechanical forces at the eye/olfactory placode interface by analysing tissue recoil, preliminary results showed tension and shear stresses at the interface between the two tissue that vary across time. By correlating variation in these stresses with changes in the olfactory placode geometry, we should highlight the role of these inter-tissue forces in the acquisition of the olfactory placode's early shape.

### **Dynamics of translational control at fertilization**

Maiwenn Petit-Jamin, Sandrine Boulben, Olivier Godfroy, Lucie Caradec\*, Gwenn Tanguy\*, Julia Morales  
Sorbonne Université, CNRS, Laboratoire de Biologie Intégrative des Modèles Marins, LBI2M, Roscoff;  
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Early embryo development relies on precise temporal control of the translation of maternal mRNAs stored in the oocyte prior to fertilization. The sea urchin embryo provides an ideal system to study translational control independently of transcription, as meiotic maturation is completed before fertilization and zygotic transcription remains silent during the first cleavages. mRNA translation is stimulated upon fertilization, and is required for progression through the first cell cycles of the sea urchin embryo. By a polysome

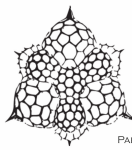


profiling approach, we have identified a pool of mRNAs specifically recruited into polysomes in response to fertilization. The set of translated mRNAs encodes for proteins implicated in different regulatory circuits, such as those controlling the cell cycle. Cis-regulatory elements of mRNAs, among which poly(A) tail length and epitranscriptomic modifications are dynamic features allowing the cell to adapt according to its needs, by regulating selective recruitment of mRNA into polysomes. To better understand the mechanisms regulating selective mRNA translation during early embryonic development, we investigated the dynamics of poly(A) tail length and methylation at single-transcript resolution in response to fertilization in the sea urchin, by combining polysome profiling with Nanopore RNA direct sequencing.

### **Ontogeny of the caudal neurosecretory system in zebrafish**

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The caudal neurosecretory system (CNSS) is a neuroendocrine complex whose existence is unique to fishes. In teleosts, the neuroendocrine neurons of the CNSS, called Dahlgren cells, are located in the terminal segments of the spinal cord and project to a neurohaemal organ, the urophysis. The urophysis is known to release several neuropeptides, including urotensins. Very little is currently known about the development of the CNSS. This study aimed to investigate the ontogeny of the caudal neurosecretory system in zebrafish (*Danio rerio*). For this purpose, a new Tg(uts2a:gfp) fluorescent reporter line was constructed, in which green fluorescent protein (GFP) expression is driven by a 1 kb fragment of the urotensin 2a (uts2a) gene promoter. The Tg(uts2a:gfp) line recapitulates faithfully the endogenous expression profile of the uts2a gene and hence allows us to visualize Dahlgren cells that express this gene. With this line, the first GFP<sup>+</sup> cells could be detected as early as 3 dpf. Their cell bodies were distributed in two rows along the anteroposterior axis, on both side of the spinal cord. Their initial number was about twenty, then gradually rose to around 150 per animal in adulthood. GFP<sup>+</sup> cells were seen to project both caudally, towards the urophyseal anlage, and rostrally, towards the hindbrain. Their rostral projections formed two parallel bundles running along the spinal cord. Accumulations of GFP<sup>+</sup> material distributed repeatedly along these bundles were observed at the level of the intervertebral discs. The development of the urophysis was also monitored and revealed progressive morphogenesis until adulthood. In conclusion, the present work provides the basis for further studies regarding the mechanisms of development of the CNSS in zebrafish.



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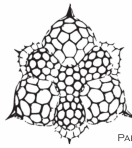
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## Practical information

# Bienvenue !



**A** Salle de conférence  
Accès escalier  
Place Georges Teissier



**B** Hôtel de France  
Hébergement et salles de réunion  
Rue Édouard Corbière

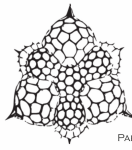


**C** Gulf Stream  
Hôtel – Restaurant  
400 rue Marquise de Kergariou



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**SERVICE ACCUEIL ET CENTRE DE CONFÉRENCES**



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Entrances to the Biological Station are secure. The code **21417** will allow access to the Gulf Stream hotel-restaurant (400 rue Marquise de Kergariou, **C**), to the Hotel de France (**B**) and to the conference room located on the 1st floor of the Yves Delage building (granite staircase, **A**). The room allocation list will be displayed in the entrance to the Gulf Stream.

The rooms will be open, with keys available inside the rooms. They must be vacated on the day of departure after breakfast.

Breakfast is served from 7:30 a.m. to 8:30 a.m. in the dedicated room on the ground floor of the building.

If you have any problems outside of service hours, you can contact the caretaker at +33 (0)6 26 32 42 13.

Wi-Fi is available in all buildings via Eduroam or Wifi guest (code in the rooms).