RÉSEAU
ANDRÉ PICARD
SORBONNE UNIVERSITE - MNHN
PARIS ROSCOFF BANYULS-SUR-MER VILLEFRANCHE-SUR-MER

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Journées André Picard 2019
21-22 March 2019
Roscoff

ABSTRACT BOOK

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The local organisers

Julia Morales et Bénédicte Charrier

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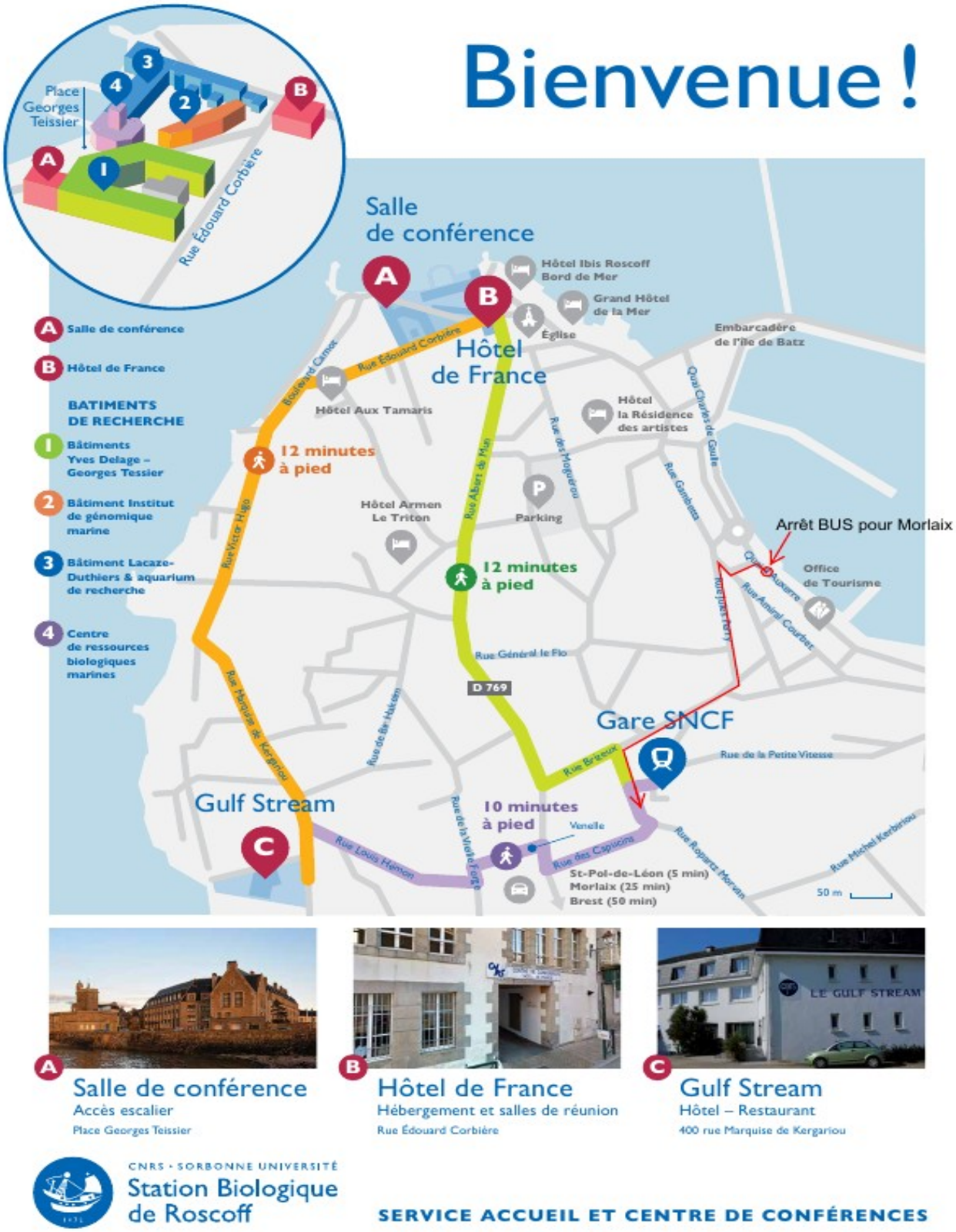

Code d'accès batiments : 31418

En cas de problème en dehors des jours et heures ouvrables, le gardien peut être contacté au ***02.98.29.23.90.***

PROGRAMME

Thursday 21 March 2019			
8.45-9.00	Registration		Chair
9.00-9.15	Welcome	Julia Morales & Bénédicte Charrier, Hosts	Michel Gho
9.15-9.45	BEN AMAR Martine	*Biomechanical modelling from examples in developmental biology*	
9.45-10.00	WILLIAUME Géraldine	*Ephrin-mediated "damping" of FGF signalling underlies the spatial precision of ascidian neural induction*	
10.00-10.30	MEISTER BLANCO Lydvina*	*Evolution of somitogenesis in chordates and the appearence of the vertebrate head*	
10.30-11.00	Coffee Break		
11.00-11.30	CROCE Jenifer	*Characterization of the nervous system architecture of Paracentrotus lividus juveniles*	Elisabeth Christians
11.30-11.45	BONADE Morgane*	*Early functioning of the visual system of Sepia officinalis : Expression of photosensitive receptors*	
11.45-12.00	CASIER Karine*	*Environmentally-induced epigenetic conversion of a piRNA cluster*	
12.00-12.15	DONATI Antoine*	*Planar polarization of ciliated epithelia in jellyfish and zebrafish*	
12.15-12.30	DURANT-VESGA Jennifer*	*Role of Hox transcription factors and TALE cofactors during Xenopus pronephros development*	
13.00-14.30	LUNCH Gulf Stream		
14.30-15.00	POURADIER DUTEIL Nastassia	*Mathematical modelling of morphogen diffusion in developping organisms*	Benoit Sarels
15.00-15.30	DUMOLLARD Rémi	*Neurodevelopmental toxicity of Bisphenol A and other endocrine disrupting chemicals in the ascidian larva*	
15.30-16.00	GIBERT Jean-Michel	*Characterization of a gene regulatory network mediating the effect of temperature on pigmentation in Drosophila melanogaster*	
16.00-16.30	Coffee Break		
16.30-17.00	DARNAT Pénélope	*Cyclin A as a link between cell proliferation and cell polarity*	Agnès Boutet
17.00-17.30	LANOIZELET Maxence	*Habenula molecular organisation in the catshark Scyliorhinus canicula: implications for the evolution of epithalamic asymmetrie*	
19.00	Dinner (offered) at Gulf Stream		

Friday 22 March 2019			
8.45-9.15	GODFROY Olivier	*DISTAG/TBCCd1 Is Required for Basal Cell Fate Determination in Ectocarpus*	Alex McDougall
9.15-9.45	PONTHEAUX Florian	*Translation driven by the Cyclin B mRNA 5'UTR is controlled by mTOR and MAPK pathways following fertilization in sea urchi*	
9.45-10.00	CHOWDHURY Rafath	*Ventral peripheral nervous system formation in ascidians and amphioxus: insights into its origin and evolution in chordates*	
10.15-10.45	Coffee Break		
10.45-11.00	KHOURY Hanane*	*Molecular control of the Endothelial to Hematopoietic Transition*	Hitoyoshi Yasuo
11.00-11.15	PERON Sophie*	*Radial symmetry restoration in Clytia medusae*	
11.15-11.30	ROUX Natacha*	*The clownfish Amphiprion ocellaris: a model to study coral reef fish metamorphosis*	
12.00-13.30	LUNCH at Gulf Stream		
13.30-15.00	Assemblée générale Réseau Picard	Financial report, Future funding	Bénédicte Charrier, Michel Gho
15.00	Closure of meeting / Departure		

* Report « Aide au congrès »

Content

Biomechanical modelling from examples in developmental biology

Martine Ben Amar

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Abstract

Shapes in nature, from cauliflower to brain, emerge from growth of tissues. Growth intrinsically generates strains and stresses. Conversely, through mechanisms of mechanotransduction, stresses regulate growth. Understanding ultimately the emergence of shapes, in particular in biological tissues, requires to capture the mechanical properties of tissues that are inherent to living matter, and related to growth.
During the two last decades, biophysicists and bio-mechanicians have developed the formalism of elasticity of growing soft tissues. After showing why growth induces stresses at the origin of shape complexities, I will show 3 examples concerning morpho-genesis of algae and embryogenesis of *C elegans.*

Early functioning of the visual system of *Sepia officinalis* : Expression of photosensitive receptors

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Abstract

Cephalopods in general and cuttlesfish in particular, have been extensively studied for their visual-guided behaviour. Their visual system sets up during embryogenesis. Indeed, Sepia embryos are able to perceive light as early as stage 25 and to answer to a light stimulation during the last embryonic stage (stage 30). Until now, studies have focused on the behavioural aspect and, to our knowledge, no one has been investigated the molecular aspect of this response. In order to do so, we studied the expression of the photosensitive receptors enabling light perception. We focused our work on the opsin gene family which includes r-opsin1 a GPCR well-known for its role in vision in many metazoans. In addition, we investigated the cryptochrome gene family as it is involved in the control of circadian cycle in many Metazoans but still poorly studied in Cephalopods. We identified 5 opsin genes in Sepia including r-opsin1 and 2 cryptochrome gene. After a phylogenetical characterization of our receptors, we studied their expression in four late developmental stages (Stage 23/24, stage 25, stage 28 and stage 30) both through RT-qPCR (eyes) and regular PCR (skin, brain and opic lobes). We showed that except r-opsin2 and xenopsin, all these genes are expressed in the eyes of Sepia embryos and few of them seem to be specifically expressed in this tissue (CRY1 and retinochromes). We showed that r-opsin1 expression increases drastically in the eyes from stage 23 to stage 28 whereas cryptochroms and other opsins lack this drastic change. This shows that these genes might be important for the functioning of Sepia embryos' eyes.

Environmentally-induced epigenetic conversion of a piRNA cluster

Karine Casier[1], Valérie Delmarre[1], Nathalie Gueguen[2], Catherine Hermant[1,3], Elise Viodé[1], Chantal Vaury[2], Stéphane Ronsseray[1], Emilie Brasset[2,] Laure Teysset[1] And Antoine Boivin[1]

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Abstract

Transposable element (TE) activity is repressed in animal gonads by PIWI-interacting RNAs (piRNAs) produced by piRNA clusters. Current models in flies propose that piRNA clusters are functionally defined by the maternal inheritance of piRNAs produced during the previous generation. Taking advantage of an inactive, but ready to go, cluster of P-element derived transgene insertions in Drosophila melanogaster, we show here that raising flies at high temperature (29°C) instead of 25°C triggers the stable conversion of this locus from inactive into actively producing piRNAs. The amount of antisense transcripts from the cluster specifically increases at 29°C. Furthermore, the activation depends on Dicer-2 and on the transcription of euchromatic homologous sequences, strongly suggesting a role of double stranded RNA in the production of de novo piRNAs. This report describes the first case of the establishment of an active piRNA cluster by environmental changes in the absence of maternal inheritance of homologous piRNAs.

Ventral peripheral nervous system formation in ascidians and *Amphioxus*: insights into its origin and evolution in chordates

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Abstract

It is well known that the peripheral nervous system (PNS) arise, in vertebrates, from dorsal structures, the neurogenic placodes and the neural crest. However, these structures are specific to vertebrates; and in invertebrate chordates (amphioxus and ascidians) the PNS also originates from the ventral ectoderm.
To better understand PNS evolution in chordates, my PhD project aims at performing a side-by-side functional comparative analysis of the ventral PNS (vPNS) formation in invertebrate chordates, using the cephalochordate Branchiostoma lanceolatum and the ascidian Phallusia mammillata. In both species, BMP and Delta/Notch signaling pathways control the formation of the vPNS. And I will make use of these shared mechanisms to tackle the following major steps: 1) identify vPNS gene markers in amphioxus and ascidian, 2) characterise their expression patterns, 3) determine whether they are regulated by BMP and Delta/Notch pathways and 4) establish vPNS gene regulatory networks for each organism.

Characterization of the nervous system architecture of *Paracentrotus lividus* juveniles

Laurent Formery, Michael Schubert, Jenifer Croce

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Abstract

The development of a nervous system represents a key innovation in the evolution of metazoans. Nervous systems are found in most animals, although ranging from nerve nets observed in cnidarians to complex centralized organs found in higher bilaterians. Due to these disparities, the evolutionary history of nervous systems in metazoans remains unclear. Among metazoans, sea urchin represent an interesting model to study nervous system evolution both from a structural and functional point of view. As echinoderms, sea urchins belong to the most basal phyla of deuterostomes, hence providing key inputs to establish the anatomical and molecular neural features of the last deuterostome common ancestor as well as to allow distinguishing between protostome and deuterostome features. Sea urchins are animals mainly subjected to indirect development, with the formation of bilateral swimming larvae displaying a neural ciliary band and an apical concentration of neurons. The larvae then undergo a drastic metamorphosis to become a benthic pentaradial adult with five radial nerve cords and a basiepidermal neural plexus. Survey on the establishment of the sea urchin nervous system have so far been focused chiefly on elucidating the molecular mechanisms involved in the establishment of the main neurogenic areas of the larvae, i.e. the apical ganglion and the ciliary band, while comparatively virtually nothing is known about the development and the molecular patterning of the adult nervous system. Nevertheless, the study of the adult nervous system of echinoderm models appears to be unavoidable to address a comprehensive comparison of nervous systems across metazoans. In this study, I will describe a first thorough molecular characterization of the architecture of the nervous systems of the early juvenile of the sea urchin species Paracentrotus lividus.

Cyclin A as a link between cell proliferation and cell polarity

Pénélope Darnat[1], Jérémy Sallé[2], Agnès Audibert[1] and Michel Gho[1]

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Abstract

Cell proliferation and planar cell polarity (PCP) are two processes required for morphogenesis. It is known that defects in one induce defects in the other. However, how the two processes crosstalk remains poorly understood. I aim to study how proteins involved in the cell cycle interact with those regulating the PCP. These links are studied in the asymmetric cell divisions occurring during the formation of the Drosophila melanogaster bristle, which generate cell fate diversity through the polarization of precursor cells. We have shown that Cyclin A, essential for mitosis entry, acts as a bridge between cell proliferation and PCP. Indeed, we have observed that a pool of Cyclin A was asymmetrically localized at the apical posterior cortex of the precursor cells during mitosis. This particular Cyclin A asymmetric localization is abolished when the PCP was disrupted in fz and dsh mutants. Also, using STED microscopy and PLA, we have shown that Cyclin A was part of the complex formed by Frizzled and Dishevelled. More importantly cell divisions are disoriented in a cycA loss of function and when Cyclin A was ectopically localized at the cell cortex. Together, these data unravel the role of this asymmetric Cyclin A localization in cell division orientation and, highlight a new function never observed in other systems for this cell cycle factor.

Planar polarization of ciliated epithelia in jellyfish and zebrafish

Antoine Donati[1], Isabelle Anselme[1], Marie Breau[1], Alexis Eschstruth[2], Sylvie Schneider-Maunoury[1], Tsuyoshi Momose[3], Christine Vesque[1]

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Abstract

Planar cell polarization (PCP) of motile cilia allows them to generate directional fluid flow within body cavities and is required for the directional swimming of larvae in various metazoan species. However the molecular mechanisms underlying PCP of ciliated epithelia are still poorly understood. We use the zebrafish floor plate (FP) as a model system to investigate the mechanisms leading to a coordinated asymmetric positioning of cilia and their associated basal bodies (modified centrioles) in epithelial cells.
Using both fixed samples and live-imaging on anterior spinal cord, we show that asymmetric cilia positioning at the posterior side of FP cells is a progressive and asynchronous process between neighbouring cells. As development proceeds, basal bodies spend more and more time in contact with the posterior membrane and stop making contacts with the anterior membranes. The time-frame corresponds to the establishment of apical junctions within floor-plate cells.
Following these observations, we made the hypothesis that the protein Par3, involved in many polarization processes across metazoans and present on apical junctions, could be asymmetrically localized in FP cells. Indeed, Par3 is enriched at the posterior membrane, before the asymmetric positioning of cilia. Strikingly, at early stages, Par3 accumulates as patches at the level of apical junctions and basal bodies only contact anterior or posterior membranes at the level of these patches. In addition, Par3 over-expression along apical junctions disrupts floor-plate PCP. These results strongly suggest that Par3 is a critical

player in floor-plate basal bodies posterior positioning.
Finally we show that in zebrafish mutated for the PCP gene vangl2 (Vangm209 mutants), both Par3 patches intensity and polarisation are disrupted, which could explain floor-plate polarization defects in these PCP mutants. Since Vangl2 is anteriorly enriched in FP cells, this suggests an antagonistic relationship between both polarisation players.

We also investigate a potentially conserved role of the ciliary protein Rpgrip1l in PCP establishment of the ciliated ectoderm of Clytia hemisphaerica larvae. We previously showed that rpgrip1l is required for floor-plate PCP in zebrafish embryos. Here we found that in Clytia embryos, Rpgrip1l assumes a conserved localization at the base of ectodermal motile cilia. Trying to generate Rpgrip1l defective polyps with CRISPR/Cas9 technology, we could only recover mutants that had repaired the gene in frame, suggesting that rpgrip1l loss of function is deleterious. Preliminary results with MO knockdown suggest that rpgrip1l could have a conserved role in ciliated epithelia PCP.

Neurodevelopmental toxicity of Bisphenol A and other endocrine disrupting chemicals in the ascidian larva

Isa Gomes, Ievgeniia Gazo, Lydia Besnardeau, Alex Mcdougall And Rémi Dumollard

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Abstract

The Marine-EmbryoTox project is aimed at establishing the ascidian larva as a model system to assess the toxicity of chemicals and of the marine environment. A pipeline of analysis has been developed to analyse the teratogenicity and genotoxicity induced by the tested compounds. Using this workflow we were able to establish different toxicities of chemicals according to their dose. We have also screened several suspected endocrine disrupting chemicals (EDCs) and compared their phenotypes with non-specific toxics to find that EDCs impair specifically brain formation whereas non-specific toxics affect broadly larval morphogenesis. The example of Bisphenol A will be described in more details in relation to its potential targets in the ascidian larva. Some nuclear receptors (NRs) are known targets of bisphenol A (and other EDCs) and are found to be expressed in the forming brain in the ascidian larva suggesting that NR-targeting EDCs may specifically affect ascidian larval brain development. Together this work illustrates how the ascidian larva may prove to be an advantageous model for marine toxicology and more specifically to study the impact of EDCs on neural development of marine invertebrate organisms.

Role of Hox transcription factors and TALE cofactors during *Xenopus pronephros* development

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Abstract

The Xenopus' tadpole kidney (pronephros) shares key characteristic features with the mature mammalian nephron, thus providing a highly useful model to study kidney development and disease. In *Xenopus*, specification of mesodermal cells into a pronephric fate is achieved at late gastrula/early neurula stages. At this stage, the renal precursors localize in a region of the anterior dorso-lateral mesoderm named pronephric/kidney field. The kidney field is characterized by the co-expression of the transcription factor encoding genes *lhx1*, *pax8* and *osr1* and *2*. Depletion of these transcription factors all lead to an impaired development of the pronephros. Retinoic Acid (RA) signaling is required for kidney field induction during gastrulation. Disruption of RA signaling at late gastrula stage results in a loss of *pax8* and *lhx1* expression in the kidney field. Evidence show that RA might control *lhx1* expression, however, control of *pax8* expression in pronephric precursors remains largely elusive. Results from the lab have shown that Hox genes and TALE co-factors are major RA signaling targets in pronephric precursors. With this project we intend to evaluate the role of hox transcription factors and TALE co-factors in the control of *pax8* expression during early pronephros development. Gain and loss of function ex vivo experiments support the idea that pronephric kidney gene expression, particularly that of *pax8*, involves hox and TALE cofactors. Culturing animal caps in activin and retinoic acid is known to induce pronephric tubules at tadpole stages. We performed this *ex vivo* assay during a hox loss of function. We observed that at neurula stage, *pax8* induction is down regulated upon Morpholino (MO) injection targeting hox paralog group 1 (PG1) whereas *lhx1* expression does not seem to be perturbed. This

further supports the idea that control of *pax8* and *lhx1* expression in pronephric precursors involves distinct mechanisms, and suggests that hox may play a role in the regulation of *pax8* expression. Furthermore, we are considering that such regulation might be direct and involve hox and cofactors. Ochi et al. in 2012 identified four conserved non-coding sequences, (CNS1-4) as candidates for pax8 enhancers. One of them (CNS1) is responsible for *pax8* expression in the pronephric primordium and contains three conserved hox/pbx binding motifs encompassing a conserved Meis/TGIF motif. We have shown by transactivation assays in HEK293 cells that CNS1 is responsive to co-transfection of vectors expressing *Xenopus* hox and TALE cofactors. Mutations of the three putative hox/pbx binding motives present in pax8-CNS1, result in a significant diminution of the luciferase activity. These sites seem to be important for pax8-CNS1 responsiveness. Moreover, our first gel shifts results indicate that they interact with in vitro translated *Xenopus* hoxb4 and pbx1. Finally, we have some hints showing that the regulation of *pax8* by Hox-TALE cofactors during pronephros development might involve binding to consensus sites present in the *pax8* enhancer CNS1.

Characterization of a gene regulatory network mediating the effect of temperature on pigmentation in *Drosophila melanogaster*

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Abstract

Phenotypic plasticity describes the ability of a given genotype to produce distinct phenotypes in different environments. It is widely observed in the wild and is thought to facilitate evolution. As a model of phenotypic plasticity, we study the temperature sensitivity of female abdominal pigmentation in Drosophila melanogaster. We found that temperature modulates the expression of the pigmentation enzyme coding genes tan and to a lesser extent DDC and yellow. This is, at least partly, a consequence of the temperature sensitivity of the expression of bab1 and bab2 genes, encoding transcription factors repressing tan, DDC and yellow. In order to enrich the gene regulatory network involved in the regulation of pigmentation genes and their thermal plasticity, we have performed a genetic screen to identify regulatory genes affecting abdominal pigmentation. We have identified 56 genes involved in abdominal pigmentation. Among them, 27 regulate tan expression. Two of them, foxo and lid, are currently studied more precisely to analyse their position in the network and whether they are involved in thermal plasticity of pigmentation using mutants.

DISTAG/TBCCd1 is required for basal cell fate determination in *Ectocarpus*

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Abstract

Brown algae are one of the most developmentally complex groups within the eukaryotes. As in many land plants and animals, their main body axis is established early in development, when the initial cell gives rise to two daughter cells that have apical and basal identities, equivalent to shoot and root identities in land plants, respectively. We show here that mutations in the *Ectocarpus* DISTAG (DIS) gene lead to loss of basal structures during both the gametophyte and the sporophyte generations.
Several abnormalities were observed in the germinating initial cell in dis mutants, including increased cell size, disorganization of the Golgi apparatus, disruption of the microtubule network, and aberrant positioning of the nucleus. DIS encodes a TBCCd1 protein, which has a role in internal cell organization in animals, *Chlamydomonas reinhardtii*, and trypanosomes. Our study highlights the key role of subcellular events within the germinating initial cell in the determination of apical/basal cell identities in a brown alga and emphasizes the remarkable functional conservation of TBCCd1 in

regulating internal cell organization across extremely distant eukaryotic groups.

Molecular control of the endothelial to hematopoietic transition

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Abstract

Hematopoietic Stem and Progenitor Cells (HSPCs) are at the basis of the regulated functioning of the hematopoietic system throughout the life of the individual. In adult amniotes, HSPCs reside in the bone marrow but are produced early during development, transiently and in small numbers at the level the dorsal aorta from specialized endothelial cells (EC), termed hemogenic. These hemogenic ECs are themselves derived from non-hemogenic ECs. Hemogenic ECs, under the influence of signals yet to be defined, lose their endothelial fate and acquire a hematopoietic identity through a mechanism designated as endothelial-to-hematopoietic transition (EHT). How hemogenic ECs are specified and how EHT is fine-tuned remain unanswered questions but has major implications in regenerative medicine.

We recently designed an ex vivo culture system, starting from the quail pre-somitic mesoderm, that mimics the steps occurring in the aorta to produce the first HSPCs (Yvernogeau et al., 2016; Development, 143: 1302). We have exploited this system to capture transcriptomic signatures specific for the mesoderm, ECs, hemogenic ECs and HSPCs. Using an ensemble of systems biology approaches, we have isolated gene networks specific for the different cell categories and have identified strong candidate genes, highly connected to the network, likely acting on the passage from one state to another with a particular emphasis for the specification of the hemogenic endothelium and the control of EHT. We have selected four genes that are currently under functional validation with siRNA approaches i.e., POFUT2, TESTIN, EMILIN 1&2. In addition the NOTCH and WNT pathways were also explored using small molecules.

Taken together our results should help to better define key steps in the commitment towards HSPC to further produce safe and robust cells for therapeutic purposes.

Habenula molecular organisation in the catshark *Scyliorhinus canicula*: implications for the evolution of epithalamic asymmetries

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Abstract

Left-right asymmetries at the level of habenulae, a bilateral epithalamic structure, are widespread across vertebrates but their conservation and mode of evolution across the taxon are unknown. In order to provide a molecular reference for comparisons, we have analysed the development of habenular asymmetries in a cartilaginous fish, the catshark Scyliorhinus canicula. A transcriptomic comparison between the left and right habenulae at an advanced stage of organ differentiation provides a list of about 400 genes differentially expressed between the left and right habenulae. Analysis by in situ hybridisation of a selection of these genes highlights a lateral to medial subdomain organisation of the catshark habenulae, suggestive of a temporal regulation of neuronal cell fate choices. It also allows the identification of novel molecular asymmetries in the catshark habenulae, observed both at lateral and medial levels of the organ. Some asymmetrically expressed genes exhibit territories restricted either to the left or the right habenula, while others are bilaterally expressed, with territories occupying different proportions between the left and the right. Comparisons with data available in the zebrafish provide no evidence for a conservation of right or left specific neuronal identities between the two species. In particular, orthologues of several genes, whose expression is restricted to a right restricted territory in the catshark, are co-expressed in a

ventral, symmetric domain of the habenulae in the zebrafish. These data provide the first description of the subdomain organisation of habenulae in chondrichthyans. They suggest that habenular asymmetries may extensively diverge across vertebrates and provide a basis to unravel underlying mechanistic diversifications.

Evolution of somitogenesis in chordates and the appearence of the vertebrate head

Stéphanie Bertrand, Hector Escriva, Lydvina Meister

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Abstract

One central question in the history of vertebrate evolution is to understand the origin of the vertebrate head. The appearance of new head structures derived from the central nervous system, neural crest cells and placodes has been thoroughly studied. However, how the anterior unsegmented paraxial mesoderm of the vertebrate head emerged from a segmented mesoderm is still an unresolved issue. Cephalochordates (i.e. amphioxus) represents the most basally divergent group among chordates and probably the best extant proxy to the ancestor of all chordates including vertebrates. Additionally, in a similar way to the hypothetical ancestor of chordates, amphioxus possesses a paraxial mesoderm segmented in somites extending from the most anterior to the most posterior part of its body. Therefore, comparing somitogenesis between amphioxus and vertebrates might shed light on how the unsegmented head mesoderm of vertebrates evolved. Previous work in our laboratory has shown the central role of the FGF signal, through the MAPK pathway, in the formation of the anteriormost somites in amphioxus. Indeed, inhibition of this signalling pathway during gastrulation induces a specific loss of these structures in amphioxus. My first aim is to understand the fate of the cells of the presumptive anterior paraxial mesoderm in embryos after FGF signalling inhibition. To tackle this question I used new approaches such as Kaede photoconversion or double fluorescent *in situ* hybridization in order to define a possible conversion of fate of the paraxial mesoderm into axial mesoderm or endoderm in treated embryos. In amphioxus we also recently showed that the formation of both anterior and posterior somites relies on the function of transcription factors (Six1/2 and Pax3/7) that are orthologues of major actors of vertebrate trunk, and not head, muscle formation. Moreover, the master gene of the formation of head mesoderm in vertebrates, *Tbx1*, is expressed in the ventral part of amphioxus somites. From these data, we hypothesize that vertebrate pharyngeal head mesoderm is of lateral/ventral and not paraxial origin and we propose a multistep evolutionary scenario explaining the appearance of this structure. My second aim is to further test this scenario

by (i) analyzing in amphioxus the expression of genes known as playing a role in the formation of head mesoderm and lateral plate mesoderm in vertebrates and by (ii) isolating putative enhancers of amphioxus genes expressed in ventral somites to see if they are able to drive expression of a reporter gene in head and/or lateral/ventral mesoderm in a vertebrate model, the zebrafish.

Radial symmetry restoration in *Clytia medusae*

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Abstract

Cnidarians are well known for their huge regeneration capabilities. Given their phylogenetic position as sister group to the bilaterians, they can offer an informative perspective on animal developmental mechanisms including regeneration. Cnidarians have two adult stages, the polyp and the medusa, with regeneration research having so far focused mostly on the polyp-only models Hydra, Hydractinia and Nematostella. The medusa stage also displays efficient healing and repatterning in response to injury, and can restore its radial symmetry after loss of large portions of the body, but little is yet known about the mechanisms involved.

The hydrozoan medusae Clytia hemisphaerica has recently emerged as a model for developmental biology. Its triphasic life cycle is completed in the lab, and genomic and transcriptomic data are publicly available. The body plan of the medusa is organized with tetraradial symmetry around the digestive organ (manubrium), centrally positioned on the subumbrellar surface. Each of the four identical quadrants contains a quarter of the manubrium, linked to one radial canal bearing a gonad, and a balanced number of tentacle bulbs which increases with medusa growth.

We show that Clytia medusae are able both to reform their circular shape and to regenerate their main organs (manubrium, gonads and tentacle bulbs) after loss of large parts of the body through injury. We have characterized two successive phases of this symmetry restoration process: 1) a remodeling step, independent of cell proliferation, allowing the bell to quickly restore its shape; 2) cell proliferation-dependent regeneration of missing organs in appropriate positions. Remodeling is driven by actomyosin cables constricting around the wound area, and is accompanied by reorganization of the subumbrellar radial muscle fibers. The manubrium, if missing, then reforms at a central site. We show that

structural cues likely direct the positioning and symmetry of the regenerating manubrium. Specifically, we could demonstrate that 1) manubrium regeneration is always initiated on a radial canal; 2) manubrium regeneration always occurs at a site where radial smooth muscle fibers gather to form a hub; 3) the symmetry of the newly formed manubrium is not necessarily tetraradial, but is instead dictated by the number of remaining radial canals. These results highlight the importance of structural elements in Clytia medusae patterning, allowing for a rapid restoration of the radial symmetry after loss of body parts.

Analysis of the role of 5'UTR mRNA sequences in translational activity following fertilization in sea urchins

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Abstract

Translation of proteins in sea urchin is stimulated upon fertilization, and is necessary for cell cycle progression and development (1). Among the endogenous mRNAs specifically recruited onto polysomes triggered by fertilization are found Cyclin B, Death Associated Protein 5 (DAP5) and Ribonucleotide reductase small subunit (R2) (2). The increase of translation activation upon fertilization depends on the mechanistic Target of Rapamycin (mTOR) signalling pathway. Strikingly, mTOR pathway inhibition differentially affects polysomal recruitment of these mRNAs. While DAP5 mRNA recruitment appears mTOR independent, R2 and Cyclin B recruitment onto polysomes are mTOR dependent. How the translation of these mRNAs is differentially regulated remains unknown.

Here, we tested whether the 5'UTR (untranslated region) sequences of Cyclin B, DAP5 and R2 mRNAs can affect translational efficiency and whether they can drive different mTOR sensitivities. We compared their translation abilities to the *Xenopus β*-globin 5'UTR mRNA, used commonly as a control in translational assays. Translational efficiency and mTOR pathway sensitivity were measured using luciferase reporter mRNAs, flanked with the 5' UTR of the different mRNAs, introduced by microinjection into sea urchin eggs. We show that mRNA translation activity is detectable following fertilization from only 5 microinjected eggs. While *Xenopus β*-globin 5'UTR presents the strongest ability to drive the *in vivo* translation, R2 shows the weakest one and DAP5 and cyclin B 5'UTR have intermediate activity. Using PP242, a specific inhibitor of mTOR, our results suggest that the different sensitivities of DAP5, Cyclin B and R2 mRNAs to mTOR signalling pathways are independent of their respective isolated 5'UTR sequence.

Taken together, these results demonstrate that the respective 5'UTR sequences of Cyclin B, DAP5, R2 and *Xenopus* *β*-globin mRNAs differentially affect the translational efficiency of the mRNA. However, the 5'UTR of these mRNA should be analysed in combination with their respective 3'UTR sequences and/or by structural study for understanding their different sensitivities to mTOR signalling pathway following fertilization.

References

1. Cormier P, Chassé H, Cosson B, Mulner-Lorillon O, morales J. Translational Control in Echinoderms: The calm before the storm. Evolution of the protein synthesis machinery and its regulation: Springer International Publishing Switzerland, 2016:413-34.
2. Chasse H, Aubert J, Boulben S, Le Corguille G, Corre E, Cormier P, et al. Translatome analysis at the egg-to-embryo transition in sea urchin. Nucleic acids research. 2018 Apr 6.

Mathematical modelling of morphogen diffusion in developping organisms

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Abstract

Among the main actors of development are morphogens, signaling molecules that diffuse in the developing organism and act on cells to produce local responses. One specific example of morphogens is Gurken, whose distribution during Drosophila oogenesis (i.e. egg formation) is related to the morphology of the fully grown egg.
In collaboration with the developmental biology laboratory of CCIB (Rutgers-Camden), we developed a model in the aim of explaining the spatiotemporal distribution of Gurken, taking into account mechanisms such as diffusion of Gurken on the surface of the oocyte, growth of the oocyte, and multiple reactions (binding to receptors, negative feedbacks etc.). Via numerical simulations, we are able to compare experimental and simulated perturbations of the system. This provides a useful tool for biologists to predict numerically the outcome of perturbations and to guide future experiments. The model will be used to explore the mechanisms responsible for the diversity of Gurken distributions observed in other Drosophila species.

In this applied model, we took into account the effect of growth on the morphogen diffusion via the time-evolving Laplace-Beltrami operator, but the growth itself was prescribed a priori by a known vector field. However, morphogens are susceptible to act on the organism to influence growth. In other words, there is a complete coupling between the diffusion of the signal and the evolution of the surface on which it diffuses. We introduce a general mathematical model to investigate such coupling.

The clownfish *Amphiprion ocellaris:* a model to study coral reef fish metamorphosis

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Abstract

As most marine fishes, coral reef fishes have a biphasic life cycle with two phases. An oceanic larval dispersive phase and a reef phase at juvenile and adult stages. The transition between the oceanic and the reef phase, called larval recruitment, is crucial. Indeed, during this transition, larvae have to choose the most suitable habitat conditioning their survival and thus ensuring the renewal of adult populations. Interestingly, the oceanic transparent larvae are facing major ecological, morphological and physiological changes at the end of the larval phase suggesting it corresponds to a real metamorphosis. We recently showed that, as in amphibians, metamorphosis in the coral reef fish *Acanthurus triostegus* is triggered by thyroid hormones (TH). However, even if *A. triostegus* is an excellent ecological model, we don't have access to open ocean larvae. We therefore decided to develop an experimental model the clownfish *Amphiprion ocellaris* as it is one of the rare coral reef fishes which can be reared in laboratory. Using *A. ocellaris* as model, we are tackling three questions: Which are the morphological changes happening during clownfish metamorphosis? Are these transformations under TH control? What are the molecular players of metamorphosis? We established a developmental table based on qualitative criteria and we characterized seven developmental stages. Theses stages have been used for TH dosage and

transcriptomic analysis whose first results are suggesting that metamorphosis is triggered at stage 4. In an Eco/Evo/Devo perspective, our study paved the way for molecular analysis of key developmental processes in coral reef fishes.

Key words: Metamorphosis – Coral reef fishes – Thyroid hormones – *Amphiprion ocellaris* – Developmental transcriptomic

Ephrin-mediated “damping” of FGF signalling underlies the spatial precision of ascidian neural induction

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Abstract

We study the initial step of ascidian neural induction to address how a cell interprets a graded signal to generate a threshold response. During this process, four ectoderm cells among a total of sixteen are selected as neural precursors. FGF9/16/20, derived from mesendoderm cells, acts as a neural inducer and directly activates Otx expression though the canonical RTK-Ets pathway (Bertrand et al, 2003, Cell). Quantitative measurement of cell surface contacts between ectoderm cells and FGF-expressing mesendoderm cells has revealed that each ectoderm cell is in direct contact with mesendoderm cells and is thus exposed to FGF, with neural precursors having the largest area of cell surface contact and thus, presumably, the highest FGF exposure (Tassy et al, 2006, Curr. Biol).

Using quantitative measurements of endogenous ERK activation, we have revealed that each ectoderm cell exhibits a level of ERK activation largely corresponding to its area of cell surface contact with FGF-expressing mesendoderm cells. In contrast, smFISH analysis of Otx expression showed that this transcriptional response is restricted to only the four neural precursors. Consistently, when explanted ectoderm cells are treated with increasing doses of exogenous FGF, while ERK activation levels increase gradually, the Otx gene is activated in a bimodal manner (ON or OFF). These results suggest that a threshold response is in operation and acts at the level of Otx transcriptional regulation.

In addition to FGF, ephrin signals also play a critical role during ascidian neural induction. An ephrin ligand, Efna.d, is expressed in the ectoderm cells and forward ephrin/Eph signals, mediated intracellularly via p120RasGAP, act antagonistically to FGF signals at the level of Ras regulation (Picco et al, 2007, Development; Haupaix et al, 2013, Development). In embryos inhibited for ephrin/Eph signals, ERK activation levels are increased in all ectoderm cells, in a manner proportional to their cell surface contact with the FGF-expressing mesendoderm cells. Under these conditions, the spatial precision of

Otx expression is lost with additional ectoderm cells exhibiting the ‘ON’ status of Otx expression. This suggests that ephrin/Eph signals act to reduce the overall levels of ERK activation, such that the non-neural ectoderm cells remain below the threshold required for Otx gene activation. In other words, ephrin/Eph signals are required simply to “damp-down” FGF signalling. To test whether a damping-down mechanism was sufficient to explain the spatial precision of the Otx response, we treated embryos, in which ephrin signals were blocked, with low doses of the MEK inhibitor U0126. This treatment was sufficient to re-establish the normal Otx expression profile specifically in the four neural precursors. Our study has thus uncovered a mechanism whereby signal damping underlies the spatial precision of threshold response to graded signal inputs.

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