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MUSÉUM NATIONAL D'HISTOIRE NATURELLE

UNIVERSITÉ PARIS SORBONNE PARIS IV

INVESTISSEMENTS D'AVENIR

RÉSEAU ANDRÉ PICARD
UPMC - MNHN - PARIS 4 - SU
PARIS ROSCOFF BANYULS-SUR-MER VILLEFRANCHE-SUR-MER

7e

Journées du réseau André Picard

31 mars & 1er avril 2016

Paris

RDV : UPMC, Campus Jussieu
31 mars : Amphi 56B
1er Avril : Amphi Durand (Esclangon)

http://www.reseau-andre-picard.org/

Origine du Réseau André Picard

Le Réseau André Picard a été créé en 2010 autour du domaine de la « Biologie du développement » à l'UPMC. Il avait pour but initial de fédérer des équipes géographiquement éloignées, le site de Paris et les stations marines de Roscoff, Banyuls-sur-Mer et Villefranche-sur-Mer. En 2012, des équipes du MNHN rejoignent le Réseau, l'inscrivant naturellement dans une perspective Sorbonne Universités. Le Réseau André Picard a étendu ses objectifs à l'ensemble des chercheurs et enseignants-chercheurs de Sorbonne Universités s'intéressant à la biologie du développement et aux disciplines attenantes, Évolution-Développement (Évo-Devo), Écologie-Développement (Éco-Devo). En 2014, il implique des membres philosophes de Paris Sorbonne élargissant ainsi les approches.

Il évolue en 2015 en un programme de Soutien à des Actions Transversales et Structurantes (SATS) de Sorbonne Universités. La mise en place de projets ambitieux collaboratifs et multi-approches devient alors possible.

Les journées André Picard sont organisées tous les ans durant deux jours alternativement sur Paris et en station et sont un moment incontournable de rencontres et discussions autour de la Biologie du Développement.

Les hommes et femmes du Réseau André Picard

André Picard (1950-2004) était un biologiste cellulaire et du développement des ovocytes d'étoile de mer, il fut le créateur et directeur de l'UMR "Biologie Cellulaire et modèles évolutionnaires" à la Station Marine Arago de Banyuls -sur-Mer.

Patrick Cormier (UPMC- Roscoff) et Jean-Philippe Chambon (UPMC-Paris) ont créé le réseau et l'ont animé pendant 4 ans (avec de faibles moyens). Jean-Philippe Chambon (UPMC-Paris) et Alex McDougall (UPMC-Villefranche) ont porté le réseau vers le programme SATS qu'ils ont rédigé.

Laurinde Jaffe de l'Université de Connecticut Health Center, Etats-Unis, a effectué un don de 50.000 $ en 2014 qui a permis au réseau de se développer.

Sofie Vanmaele (UPMC Villefranche) a assuré remarquablement avec efficacité l'administration du Réseau Picard en 2015…et 2016.

Isabelle Mouas (MNHN) a contribué aux Journées 2016 par la création de l'affiche, la préparation du livret et le recensement des participant.e.s.

Financement : Le Réseau Picard est entièrement financé par Sorbonne Universités à hauteur de 207 252 euros

Organisateur/trice des JAP 2016 : Laure Bonnaud-Ponticelli (MNHN) et Michel Gho (UPMC).

7EME JOURNEES ANDRE PICARD 2016

Jeudi 31 Mars

(Amphi 56B)

09h-09h30 : **Bienvenue/Welcome**

Modérateur.trice/Chairman.women: Laure Bonnaud-Ponticelli/Michel Gho

9h30-9h45 **MC DOUGALL Alex** UMR 7009-UPMC-Villefranche
Le Réseau André Picard/SATS-SU : Bilan, éléments de réflexion, perspectives

9h45-10h **ATGER Véronique :** Directrice Recherche Sorbonne Universités
Echéances et perspectives de Sorbonne Universités

10h-10h20 **CHARRIER Bénédicte** UMR 8227-UPMC-Roscoff
Filamentous development of the brown alga *Ectocarpus*: from tip growth to cell differentiation.

10h20-10h35 **ESCRIVA Hector** UMR 7232-UPMC-Banyuls PEC+/Schubert
A single three-dimensional chromatin compartment in amphioxus indicates a stepwise evolution of vertebrate Hox bimodal regulation

10h35-10h50 **MC DOUGALL Alexander** UMR 7009-UPMC-Villefranche
Mechanisms controlling cell size, number and position during embryogenesis in the ascidian

10h50-11h20 ***Pause-café/Coffee break***

11h20-11h35 **COSSE-ETCHEPARE Camille** UMR 7622-UPMC-Paris PEC/Schubert-Lebouffant
Pou3f proteins and kidney development

11h35-12h20 **KLOAREG Bernard** Dir. Station Biologique de Roscoff-UPMC
EMBRC et EMBRC-France : que pouvez-vous en attendre ?

12h30-14h ***Déjeuner/Lunch at Cafetaria UPMC***

Modérateur/Chairman: Alex McDougall

14h-15h OPENING TALK: **PROCHIANTZ Alain, Collège de France**
Signaling with homeoprotein transcription factors from development to pathologies

15h00-15h15 **ALMEIDA Luis** UMR 7598-UPMC-Paris
Mathematical modeling of Epithelial Gap Closure

15h15-15h30 **MAZAN Sylvie** UMR 7232-UPMC-Banyuls PEC+/Schubert
Dual role of Nodal signaling in the control of asymmetric neurogenesis in the catshark developing habenulae

15h30-15h45 **SCHUBERT Michael** UMR 7009-UPMC-Villefranche PEC/Hirsinger
Evolution of retinoic acid signaling functions during nervous system development

15h45-16h15 ***Pause-café/Coffee break***

Modératrice/Chairwomen: Julia Morales

16h15-16h35 FLASH PRESENTATION/POSTER M2: **CYPRIA Julie, FAILLA Margaux, LEMONNIER Tom, RIO-CABELLO Antoine, SCAROS Alexia**

16h35-16h50 **QUIROGA ARTIGAS Gonzalo** UMR 7009-UPMC-Villefranche
Light-induced oocyte maturation in the hydrozoan *Clytia hemisphaerica*

16h50-17h05 **TOSTIVINT Hervé** UMR 7221-MNHN-Paris PEC/Escriva
Search for peptides related to urotensin II and somatostatin in amphioxus

17h05-17h20 **CHRISTIANS Elisabeth** UMR 7009-UPMC-Villefranche PEC/Geneviere
From Heat Shock to Stress Response in marine organisms

17h20-17h35 **DONATI Antoine** UMR 7622-UPMC-Paris PEC/Momose-Vesque
How to position cilia along the Antero/Posterior axis?

17h35-17h50 **FERREIRA-GONÇALVES João** UMR 7138-UPMC-Paris
Anthozoan polarity axis: insights from the study of two antipatharian species

19h00 ***Buffet Réunionnais, posters, et vue sur Paris - Tour ZAMANSKY-UPMC/ Buffet of Reunion Island, posters, and Paris view – Zamansky Tower-UPMC***

Vendredi 1er avril

(Amphi Durand-Bâtiment Esclangon)

Modératrice/Chairwomen : Frédérique Peronnet

09h30-9h45 **BONNAUD PONTICELLI Laure** UMR 7208-MNHN-Paris PEC+/Escriva
Extraocular photoreception in aquatic species and its developmental control: a comparison between amphioxus and cuttlefish.

09h45-10h00 **CHAMBON Jean-Philippe** UMR 7138-UPMC-Paris PEC/Tiozzo
Constructive function of apoptosis during morphogenetic process: a comparative approach

10h-10h15 **SCHNEIDER-MAUNOURY Sylvie** UMR 7622-UPMC-Paris
Avec **Marie POSTEL** UMR7598-UPMC-Paris
Designing a mathematical model of the dynamics of progenitor cell populations in the mouse cerebral cortex

10h15-10h30 **LECLERE Lucas** UMR 7009-UPMC-Villefranche PEC/Copley
Genome and life stage-specific transcriptomic data from the hydrozoan medusae *Clytia hemisphaerica*

10h30-11h00 ***Pause-café/Coffee break***

11h-11h30 **DUMOLLARD Rémi** UMR 7009-UPMC-Villefranche
Phallusia mammillata: an emerging model for molecular toxicology and image-based screens

11h30-11h45 **TIOZZO Stefano** UMR 7009-UPMC-Villefranche PEC/Chambon
Co-option of germ layers related TFs shows regionalized expression during two non-embryonic developments

11h45-12h00 **CASTELLANE Ariane** Paris Sorbonne-Paris IV
La métaphore cognitive en biologie

12h-12h15 **CROCE Jennifer** UMR 7009-UPMC-Villefranche PEC/DeLishi
Towards the identification of an ancestral *Wnt* function

12h15-12h30 **DARRAS Sébastien** UMR 7232-UPMC-Banyuls PEC/Chenevert
Comparative development of the neurogenic tail epidermis midlines in ascidians

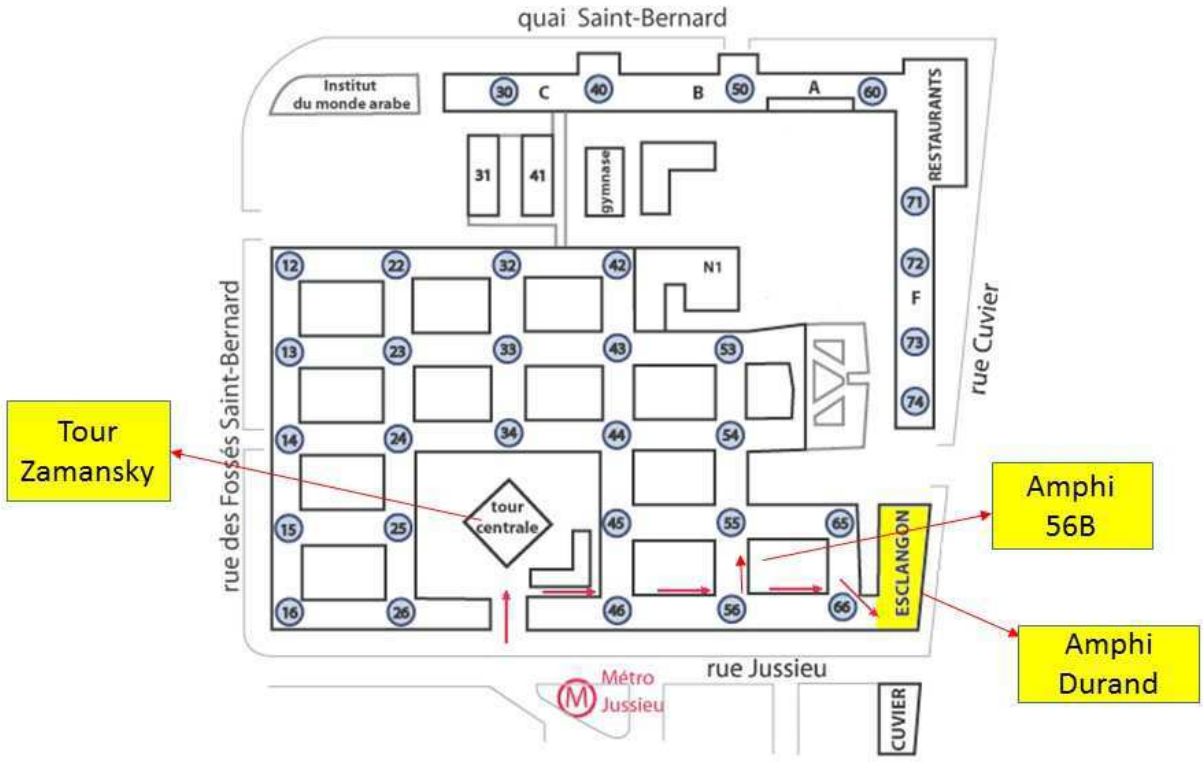
12h30-14h00 **Déjeuner/*Lunch at Cafetaria UPMC***

14h-14h15 **CORMIER Patrick** UMR 8227-UPMC-Roscoff
Towards a model of the spatio-temporal dynamics of the translation repressor 4E-BP regulation network

14h15-14h30 **MOMOSE Tsuyoshi** UMR 7009-UPMC-Villefranche PEC/Giovannangeli
Gene KO technique in *Clytia hemisphaerica*: taking advantages of asexual reproduction and stem cell specific DNA repair

14h30-14h45 **VANMAELE Sofie** UMR 7009-UPMC-Villefranche
CORBEL: A new H2020 project for biomedical research

15h00-15h30 **Discussion générale-Bilan-Perspectives**
General discussion-Synthesis-Prospects.



Communication

Filamentous development of the brown alga *Ectocarpus*: from tip growth to cell differentiation

CHARRIER Bénédicte

UMR 8227-UPMC-Roscoff

Ectocarpus body organisation looks simple: it is formed by branched filaments all made of a single row of cells. While growth (cell division) takes place at the apex of each filament, newly produced cells progressively differentiate and supply the center of the filaments. Morphologically, this differentiation corresponds to a change of cell shape, from polarised cylindrical cells to spherical cells. For both the apical tip growth and the cell differentiation processes, we aim to decipher the role played by several physical and cellular factors at the cell and sub-cellular levels: 1- the internal cell pressure, 2- the “deformability”of the envelop, 3- the production of energy, 4- the role of the cytoskeleton and 5- the cell-specific gene expression pattern. Comparison of the WT landscape with mutants impaired in these processes will also help elaborating a mechanistic scenario accounting for *Ectocarpus* morphogenesis.

Communication

A single three-dimensional chromatin compartment in amphioxus indicates a stepwise evolution of vertebrate Hox bimodal regulation

ESCRIVA Hector

UMR 7232-UPMC-Banyuls

The HoxA and HoxD gene clusters of jawed vertebrates are organized into bipartite three-dimensional chromatin structures that separate long-range regulatory inputs coming from the anterior and posterior Hox-neighboring regions1. This architecture is instrumental in allowing vertebrate Hox genes to pattern disparate parts of the body, including limbs2. Almost nothing is known about how these three-dimensional topologies originated. Here we perform extensive 4C-seq profiling of the Hox cluster in embryos of amphioxus, an invertebrate chordate. We find that, in contrast to the architecture in vertebrates, the amphioxus Hox cluster is organized into a single chromatin interaction domain that includes long-range contacts mostly from the anterior side, bringing distant cis-regulatory elements into contact with Hox genes. We infer that the vertebrate Hox bipartite regulatory system is an evolutionary novelty generated by combining ancient long-range regulatory contacts from DNA in the anterior Hox neighborhood with new regulatory inputs from the posterior side.

Communication

Mechanisms controlling cell size, number and position during embryogenesis in the ascidian

MC DOUGALL Alexander

UMR 7009-UPMC-Villefranche

Authors: Alex McDougall, Janet Chenevert, Vlad Costache, Céline Hebras and Rémi Dumollard Sorbonne Universités, UPMC Université Paris 06, CNRS, Laboratoire de Biologie du Développement de Villefranche-sur-mer (LBDV), Observatoire Océanologique, 06230 Villefranche sur-mer, France

Ascidians are marine invertebrate chordates that belong to the tunicate subphylum and are a sister group to the vertebrates (Delsuc et al., 2006). Ascidians are split into three orders (the aplousobranchs, the phlebobranchs and the stolidobranchs). Based on non-coding DNA sequence, it has been estimated that two disparate ascidian species may be as different from each other as fish are from humans (Stolfi et al., 2014). Despite this difference at the level of their genomes, the morphology of gastrula-stage ascidian embryos from different orders is almost identical. For example, the system for naming the different blastomeres up to the gastrula stage developed by Conklin in 1905 for a stolidobranch ascidian (*Styela partita*) is currently used for phlebobranch embryos (*Ciona*, *Phallusia*). This indicates that the precise position of every cell is the same between different embryos (i.e. conserved invariant cleavage pattern). In addition, ascidians from different orders also display the same three rounds of unequal cleavage in germ cell precursors from the 8 to 64-cell stage. Finally, ascidian embryos have the same relative asynchrony in cell cycle duration in vegetal versus animal blastomeres which begins at the 16-cell stage. One of our aims has therefore been to identify the cell biological mechanisms that control cell size, number and position in early ascidian embryos. Moreover, since neither apoptosis nor cell migration occur prior to the gastrula stage we can ignore these two mechanisms making the analysis simpler.

I will present our past and recent work describing the mechanisms controlling unequal cleavage in the germ cell precursors (Kif2, Pins and NuMA proteins), cell number control mechanisms up to the gastrula stage (□-catenin controlled gene-regulatory network affecting Wee1 and Cdc25 proteins), and finally how the conserved spatial pattern of cell division underlying the invariant cleavage pattern described by Conklin is controlled by cell shape at metaphase.

Communication

Pou3f proteins and kidney development

COSSE-ETCHEPARE Camille

UMR 7622-UPMC-Paris

Authors: Camille COSSE-ETCHEPARE, Isabelle GERVI, Isabelle BUISSON, Jean-François RIOU, Muriel UMBHAUER and Ronan LE BOUFFANT
Laboratory: UMR 7622, Team Signalisation et Morphogenèse

The kidney is composed of a filtrative unit and a tubule that allow the excretion of the urine. We showed that among the four members of Pou3f transcription factor family, *pou3f3* and *pou3f4* are regionally and differentially expressed in the developing kidney. Pou3f4 loss of function prevents intermediate tubule marker gene expression and leads to a decrease of differentiation marker gene expression in the distal tubule. Pou3f4 gain of function induces an expansion of intermediate tubule marker gene expression and a decrease of differentiation marker gene expression in the distal tubule. Pou3f3 loss of function also prevents intermediate tubule marker gene expression and leads to a decrease of differentiation marker gene expression in the distal tubule. Pou3f3 and Pou3f4 play crucial roles in tubule regionalization and differentiation.

EMBRC et EMBRC-France, que pouvez-vous en attendre ?

KLOAREG Bernard

Directeur de la station biologique de Roscoff-UPMC

Les Stations marines de Roscoff, Banyuls et Villefranche-sur-Mer fournissent des modèles microbiens, végétaux ou animaux qui représentent des lignées évolutives majeures et dont certaines ne sont pas présentes dans les écosystèmes terrestres. Elles se sont organisées en une Infrastructure Nationale en Biologie Santé, EMBRC-France, le nœud pour la France de l'Infrastructure Européenne « European Marine Biological Resource Center ».

EMBRC et EMBRC-France sont construits autour des services suivants : accès aux écosystèmes marins ; accès à des dispositifs d'expérimentation *ex situ* ; accès aux modèles biologiques marins ; accès à des ressources génétiques pour certains organismes modèles ; accès aux moyens logistiques pour le génotypage et le phénotypage de ces modèles. Dans cet exposé, je décrirai les dispositifs permettant d'accéder à l'infrastructure.

Communication

Signaling with homeoprotein transcription factors from development to pathologies

PROCHIANTZ Alain

Collège de France

Several homeoprotein transcription factors present non-cell autonomous signaling functions. These functions have now been explored in different animal species from fly to mouse. In this presentation I shall discuss our latest data on *Engrailed* and *Otx2* homeoproteins. It will be shown that *Otx2* transfer from the choroid plexus to parvalbumin inhibitory interneurons regulates cerebral cortex plasticity during post-natal development and in the adult. The role of Engrailed as an axon guiding morphogen and as a survival factor/therapeutic protein for adult mesencephalic dopaminergic neurons in animal models of Parkinson disease will be presented.

Communication

Mathematical modeling of Epithelial Gap Closure

ALMEIDA Luis

UMR 7598-UPMC-Paris

We will present work on epithelial wound healing in drosophila pupae and on gap closure in monolayers of MDCK cells or keratinocytes. These works concern mathematical modeling of the dynamics of epithelial tissues pulled by lamellipodal crawling or the contraction of actomyosin cables at the gap boundary. We are particularly interested in the influence of the wound geometry and the adhesion to the substrate on the closure mechanism.

Communication

Dual role of Nodal signalling in the control of asymmetric neurogenesis in the catshark developing habenulae

MAZAN Sylvie

UMR 7232-UPMC-Banyuls

Authors: R. Lagadec[1] , H. Mayeur[2] , B. Billoud[3] and S. Mazan[1]
[1] CNRS, Sorbonne Universités, UPMC Univ Paris 06, UMR7232, Observatoire Océanologique, Banyuls, France.[2] CNRS, Sorbonne Universités, UPMC Univ Paris 06, FR2424, Station Biologique, Roscoff, France .[3] CNRS, Sorbonne Universités, UPMC Univ Paris 06, UMR8227, Station Biologique, Roscoff, France

Epithalamic asymmetries are frequently observed across vertebrates, albeit with substantial variations in degree and laterality. Comparisons of a cartilaginous fish, the catshatk *Scyliorhinus canicula*, and an agnathan, the lamprey *Petromyzon marinus* with the zebrafish have shown that these species employ different strategies for their elaboration, a conserved, left restricted Nodal activity being required in the former two but dispensable in the zebrafish. These data support an ancient role of Nodal signalling in epithalamic asymmetry formation but the ancestral cellular mechanisms controlled by the pathway remain unknown. We show that in the catshark, developing habenulae display marked, Nodal dependent neurogenetic asymmetries. These asymmetries include an accelerated regression of the major population of proliferative neuroepithelial cells but a delayed neuronal differentiation of more lateral ventricular neural progenitors in the left habenula compared to the right one. These data reveal context dependent functions of Nodal in habenular asymmetry formation, suggesting opposite effects of the pathway on the maintenance of neural progenitors. This functional duality provides new clues on the origin of the mechanisms controlling epithalamic asymmetry formation and their diversifications across vertebrates.

Communication

Evolution of retinoic acid signaling functions during nervous system development

SCHUBERT Michael

UMR 7009-UPMC-Villefranche

Retinoic acid (RA), a small diffusible signaling molecule derived from vitamin A, controls both regional patterning and neuronal differentiation in the developing nervous system. Moreover, RA signaling has also been shown to affect the neurotransmitter phenotypes of specific neuronal subsets in both the central and peripheral nervous system. This study aims at characterizing the roles played by RA in the formation of different neural populations in the developing nervous system of the invertebrate chordate amphioxus. To this end, immunohistochemical approaches and gene expression analyses were used to identify distinct subsets of neural progenitors and neural cell types. Furthermore, RA levels were manipulated pharmacologically at different stages of development to assess the involvement of RA signaling in patterning and differentiation of the identified neural cell populations. Several context-dependent functions of RA were hence revealed, including the generation of discrete boundaries in the amphioxus central and peripheral nervous system and the cell type-specific regulation of neural progenitors in the peripheral nervous system.

Poster

Anteroposterior ectodermal patterning by canonical Wnt signaling in ascidian embryos

CYPRIA Julie

UMR 7232-UPMC-Banyuls

The Wnt signaling pathway is involved in many aspects of metazoan embryonic development, such as the formation of the anteroposterior axis and the posterior growth. Preliminary results indicate that the canonical Wnt pathway is sufficient to posteriorize ascidians embryonic epidermis. In this study, we want to determine whether this pathway patterns the ectoderm along its anteroposterior axis during ascidian embryogenesis. Three axes will be developed: determination of the posteriorization phenotype using molecular markers of both epidermis and nervous system, mapping of Wnt signaling activation using reporters and block the transcriptional response using tissue-specific Wnt pathway inhibition using electroporation mediated loss-of-function.

Poster

Unequal Cleavages in Ascidian Embryo

FAILLA Margaux

UMR 7009-UPMC Villefranche

During the series of three successive unequal cleavages which specify the germ line in the ascidian embryo, one pole of the mitotic spindle migrates towards a cortical structure called CAB (for « Centrosome Attracting Body »). The CAB is both necessary and sufficient for unequal cleavage in the ascidian but whether it generates force to pull the spindle towards the cortex is not known. Using timelapse microscopy and fluorescent labelling, we observe that membrane invaginations form around the CAB after destabilization of the acto-myosin cortex (by the addition of cytochalasin D or latrunculin A). These invaginations could indicate cortical sites where force generators, i.e. motor proteins, are enriched. The aims of this project are (1) to establish a correlation between invaginations and spindle migration in time and space, by 3D reconstruction of embryos labelled for centrosomes and DNA prior to cytochalasin treatment and (2) to determine if these invaginations/forces depend on microtubules and molecular motors (dynein, kinesin, myosin) by the use of specific inhibitors. These studies will advance our understanding of spindle positioning mechanisms.

Poster

Etude de la conservation des gènes cibles de la voie de signalisation à l'acide rétinoïque au cours de l'embryogenèse entre un vertébré (Xénope) et un invertébré chordé (Amphioxus)

LEMONNIER Tom

UMR 7622/7009-Paris/Villefranche

L'acide rétinoïque, dérivé biologiquement actif de la vitamine A, régule l'expression de gènes durant le développement des vertébrés, la différenciation cellulaire ou encore impliqués dans l'homéostasie. Afin de mieux comprendre la régulation des gènes développementaux ciblés par l'acide rétinoïque dans le mésendoderme et de définir leur conservation au sein des chordés, deux analyses transcriptomiques comparatives ont été réalisées chez le vertébré Xenopus laevis et chez l'invertébré chordé Branchiostoma lanceolatum. Une liste de gènes candidats conservés a été retenue et est en cours de validation par hybridation in situ et par la PCR quantitative chez les deux espèces. L'objectif étant, au final, de caractériser les fonctions de ces gènes cibles dans le réseau de gènes contrôlés par l'acide rétinoïque et d'établir la conservation de ce réseau au cours du développement de chordés.

Poster

Contrôle de la mise en place des structures photoréceptrices chez deux organismes aquatiques : l'amphioxus (*Branchiostoma lanceolatum*) et la seiche (*Sepia officinalis*)

RIO-CABELLO Antoine

UMR 7208-MNHN-Paris

Auteurs : Antoine RIO-CABELLO[1], Laure BONNAUD-PONTICELLI[1], Yann BASSAGLIA[1,2], Hector ESCRIVA[3]
[1]UMR 7208, Sorbonne Universités, [2]MNHN, IRD, UPMC, UCN, UA, UPEC, [3] UMR 7232, Sorbonne Universités, UPMC

La perception de la lumière dépend de molécules photosensibles présentes dans des cellules différenciées : les photorécepteurs. Ces photorécepteurs peuvent être condensés en un œil antérieur mais de nombreuses espèces présentent aussi des structures photoréceptrices périphériques. Nous étudions la mise en place de ces structures au cours du développement dans deux espèces marines benthiques, la seiche (mollusque céphalopode à photoreception oculaire et cutanée) et l'amphioxus (céphalochordé présentant un œil frontal et des structures périphériques). Les gènes candidats potentiellement intéressants sont ceux du réseau PSED (Pax6, Six, Eya, Dashung) pour la détermination, les opsines et PNR (Photoreceptor-specific nuclear receptor = NR2E3), un récepteur nucléaire orphelin, pour la fonction. Notre travail concerne actuellement ces deux derniers gènes.

Chez la seiche, nous avons caractérisé l'expression de PNR lors des stades tardifs de développement par hybridation *in situ* (ISH) in toto. Nous avons observé une expression dans la zone supra œsophagienne du cerveau mais pas d'expression cutanée. Nous testons en parallèle l'expression de la protéine par immunohistochimie. L'opsine a été détectée dans la rétine par ISH sur coupe et la dynamique de son apparition est en cours d'étude. Nous complèterons ce travail en étudiant l'expression de PNR chez l'amphioxus dès la disposition du matériel biologique.

Ces travaux comparatifs visent à émettre des hypothèses sur les relations évolutives entre œil et structures périphériques.

Poster

Development of Olfaction in *Sepia officinalis*: Are Glomeruli shared across Metazoa?

SCAROS Alexia

UMR 7208-MNHN-Paris

Authors: Alexia SCAROS[1], Roger CROLL[1], Sébastien BARATTE[2].

[1] Department of Physiology and Biophysics, Dalhousie University, Halifax, Nova Scotia, Canada.[2] Biologie des Organismes et Ecosystèmes Aquatiques (BOREA), Sorbonne Universités, MNHN, CNRS 7208, IRD 207, UPMC,UCN, UA

Olfaction is an important but little understood sense in nearly all Metazoa. Arthropods and vertebrates have units of organized synapsis, called glomeruli, which connect the olfactory receptor cells to the brain. This glomerular organization is a prominent and comparable feature between vertebrates and arthropods, and is the basis for multiple evolution theories. However few comparisons have been made outside these two groups. As a predatory mollusk, *Sepia officinalis* has a complex brain with a highly developed olfactory system, which could provide a novel perspective. Using immunohistochemistry and *in situ* hybridization, we are describing the development of the olfactory system, searching for glomeruli in the CNS of *S. officinalis*. Our results could help elucidate whether the observed olfactory similarities across metazoans originate from convergent or divergent evolution.

Communication

Light-induced oocyte maturation in the hydrozoan *Clytia hemisphaerica*

QUIROGA ARTIGAS Gonzalo

UMR 7009-UPMC-Villefranche

Authors: Gonzalo QUIROGA ARTIGAS, Pascal LAPÉBIE and Evelyn HOULISTON
Sorbonne Universités, UPMC Université Paris 6 and CNRS, Laboratoire de Biologie du Développement de Villefranche-sur-mer (LBDV), 06230 Villefranche-sur-mer, France.

We are studying the regulation of oocyte meiotic maturation and spawning in the hydrozoan jellyfish *Clytia hemisphaerica,* an emerging model species. Meiotic maturation in hydrozoans is triggered daily by dark-light transitions. Fully grown, prophase I arrested, oocytes in the gonad resume meiosis when they are stimulated by a diffusible Maturation Inducing Hormone (MIH), released from the gonad somatic tissues immediately following a light signal. In collaboration with N. Takeda (Asamushi Research Center for Marine Biology) and R. Deguchi (Miyagi University of Education, Sendai), we have identified *Clytia* endogenous MIH as several structurally-similar amidated neuropeptides, synthesized by cleavage of two distinct peptide precursors. From generated gonad tissue transcriptomes, I was also able to identify an opsin protein (i.e. light-sensitive GPCR) highly expressed in the gonad epithelia as a strong candidate to initiate the oocyte maturation process.

Communication

Search for peptides related to somatostatin (SST) and urotensin II (UII) in amphioxus

TOSTIVINT Hervé

UMR 7221-MNHN-Paris

Neuropeptides are important players in neuronal communication but also in development. Most of them belong to gene families. Many of the neuropeptide families known in vertebrates have also members in "invertebrates", suggesting that they have a very ancient origin and already existed in the common ancestor of all bilaterians. Our current research is centered on the study of the family of SST and UII. The occurrence of peptides of this family is well attested in all vertebrates but is still controversial in other metazoan groups. Our project aims to search for the counterparts of SS and UII in amphioxus, a species belonging to the group of cephalochordates considered evolutionarily very close to that of vertebrates. A preliminary study has led us to identify in the genome of amphioxus two SS- and UII-like sequences. Our goal is now to characterize the corresponding genes and investigate their functions during development of the amphioxus.

Communication

From Heat Shock to Stress Response in marine organisms

CHRISTIANS Elisabeth

UMR 70009-UPMC-Villefranche

PEC : GENEVIERE Anne Marie

First discovered in Drosophila, Heat Shock Response was quickly found to be one of the most conserved system of cellular gene regulation. Exposure to deleterious environmental conditions induces the over-activation of the transcription factor named Heat Shock Factor (HSF). This leads to the induction of heat shock genes and the increased synthesis of Heat Shock Proteins. While this gene regulatory network is frequently implicated in papers studying marine organisms, those investigations are also often partial or even incorrect. Taking advantage of our respective background (HSR, toxicology, sea urchin), we have exploited this PEC to pave the way for a more in-deep analysis of HSR, which should provide new knowledge and tools to assess environmental impact on marine organisms.

Communication

How to position motile cilia along the Antero/Posterior axis?

DONATI Antoine

UMR 7622-UPMC-Paris

Authors: DONATI Antoine (PHD)[1], MOMOSE Tsuyoshi[2], VESQUE Christine[1]
[1] Morphogénèse du cerveau des vertébrés, UMR7622 CNRS, UPMC, Paris, [2] Mécanismes développementaux chez Clytia, UMR7009, Villefranche.

Motile cilia polarization is crucial for oriented fluid flow production and for left-right asymmetry determination in most bilaterians. It is really striking that the position of motile cilia along the apical surface of the laterality organ or within floor-plate cells is at the posterior pole relative to the antero-posterior axis of the vertebrate embryo (Borovina et al, 2010), whereas the position of motile cilia on the ectoderm of swimming larvae is also at the posterior pole of each cell, as in an embryo of a hydrozoan jellyfish *Clytia hemisphaerica* (Momose et al, 2012). In both cases, this stereotyped position depends on an active Wnt-PCP pathway. It is proposed that cilia which breaks L/R asymmetry in vertebrates have evolved by internalizing the ectodermal motile cilia by gastrulation (Blum et al., 2014). If cilia of the Clytia ectoderm and zebrafish floor plate have a common origin, they could use common molecular players to position their cilia at the posterior pole.
We have previously shown that, a ciliary protein Rpgrip1L is involved in posterior cilia positioning in zebrafish floor-plate cells (Mahuzier et al, 2012). It is interesting to test whether it plays an « evolutionary conserved » function and how Wnt-PCP molecules and Rpgrip1L modulate centrosome/cilia positioning in *Clytia* planula larvae. We propose to perform a loss of function of cherpgrip, the unique *Clytia* orthologue of rpgrip1/1L by CRISPR/Cas9 technology developed in the Villefranche laboratory and analyze cilia formation and positioning as described in Momose, 2012.

Communication

Anthozoan polarity axis: insights from the study of antipatharian species

FERREIRA-GONCALVES João

UMR 7138-UPMC-Paris

Authors: João FERREIRA-GONCALVES[1], Muriel JAGER[1], Michael MANUEL[1], Eric QUEINNEC,[1]
1 Institut de Biologie Paris Seine - Université Pierre et Marie Curie, Paris 6
UMR 7138: Evolution Paris-Seine, Team: Phylogeny, Anatomy, Evolution

The origin of body axis is one of the central themes on animal evolution. Usually regarded as an innovation of Bilateria, the bilateral symmetry is broadly distributed in the Anthozoan class of Cnidarians. The molecular basis of this Anthozoan bilaterality have only been studied in *Nematostella vectensis* (Actiniaria order), and the discovery that the *BMP*-pathway was differentially expressed along the secondary axis lead some authors to presume that bilaterality was ancestral to the Cnidaria/Bilateria divergence (Finnerty *et al*. 2004, Matus *et al*. 2006), while Manuel (2009) preferred a convergence hypothesis based on comparative anatomy and phylogeny.
In opposition to Bilateria (where *Hox* genes are expressed along the primary axis) *Hox* genes have recently been shown to be differentially expressed along the secondary axis of *Nematostella vectensis* (Leclère & Rentzsch 2014). In order to do evolutive inferences from this result it is necessary to study the *HOX* genes expression patterns in other Anthozoan species.
Our study with the colonial antipatharian species *Antipathes caribbeana* focuses on the detailed anatomy of the polyp, confirming the previously doubtful bilateral organization of its polyps. Furthermore, the study of the expression of HOX genes shows that they are, as in *Nematostella*, differentially expressed along the secondary axis, having their expression associated with the position of specific mesenteries. The same type of bilateral patterning of *Nematostella* has now been found in another order of Anthozoans, reinforcing the idea that bilaterality is ancestral to the Cnidaria/Bilateria divergence and that HOX genes have a patterning role on the secondary axis of Anthozoans.

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Communication

Extraocular photoreception in aquatic species and its developmental control: a comparison between amphioxus and cuttlefish

BONNAUD-PONTICELLI Laure

UMR 7208-MNHN-Paris

Authors: Antoine RIO-CABELLO[1], Laure BONNAUD-PONTICELLI[1], Yann BASSAGLIA[1,2], Hector ESCRIVA[3]
[1]UMR 7208, Sorbonne Universités, [2]MNHN, IRD, UPMC, UCN, UA, UPEC, [3] UMR 7232, Sorbonne Universités, UPMC

Development of animals' eyes has been extensively studied but recent works on unconventional animal models have revealed that molecular control of eye development is more complex than expected. Besides the “eyes”, we are interested in “extraocular photosensitive cells” (EOPCs) in the general context of “visual perception” evolution. Our aim is to study photoreceptor cells (*sensu lato*, including EOPCs) development using two emblematic aquatic species in distant phylogenetic groups, a lophotrochozoan, the cuttlefish *Sepia officinalis*, and a chordate, amphioxus *Branchiostoma lanceolatum*. They are both benthic, living in coastal areas (with similar environment) and both have different ways of photosensitivity. We study genes involved in photoreceptor development and/or in photoreception, the Pax6-Six-Eya-Dachshund network (PSEDN), functional molecules, the opsins and PNR, a nuclear receptor. Putative roles of these genes in eyes and EOPCs development as well as how and when the photoreception function appears in the two species could help to understand the evolutionary relationships between eye and EOPCs and the selective advantage of EOPCs in aquatic environment.

Communication

Constructive function of apoptosis during morphogenetic process: a comparative approach

CHAMBON Jean-Philippe

UMR 7138-UPMC-Paris

Despite considerable advances in our understanding of programmed cell death by apoptosis in different contexts, such as homeostasis or cancer, the mechanisms controlling its integration into morphogenetic processes is only partially understood. Based on extensive studies on embryogenesis and metamorphosis in Bilateria, apoptosis has long been mainly described as required for the removal of obsolete structures, i.e., as having a *Destructive Function*. However, it is possible to identify a *Constructive Function* of apoptosis which involves an instructive role of the dying cells: (i) by exerting mechanical forces inside the tissues (ii) by secreting molecular cues that affect their environment in a caspase-dependent manner. The study of constructive function just emerged and researches in this sense are still sporadic. In fact, the constructive role has been described essentially in non-bilaterians, in Drosophila, as well as a few examples in chordates. In this collaborative project we aim to compare apoptotic-dependent morphogenetic events, during metamorphosis, asexual development and regeneration, focusing on two phylogenetically distant phyla: cnidarians and urochordate. By combining the experience of the two partners in cnidarians, solitary and colonial ascidians and apoptosis studies, we aim to integrate existing and new analyses of patterns of apoptosis and proliferation during morphogenetic processes and to characterize apoptotic signaling pathways involved in these processes. The outcome of in this collaboration will hopefully provide solid preliminary data to develop a wider proposal for application to ANR funding.

Communication

Designing a mathematical model of the dynamics of progenitor cell populations in the mouse cerebral cortex

SCHNEIDER-MAUNOURY Sylvie

UMR 7622-UPMC-Paris

Authors: Marie Postel[1,2], Alice Karam[3], Mérina Latbi[1], Guillaume Pezeron[3], Long Tran[1], Frédérique Clément[2], Sylvie Schneider-Maunoury[3]*. *Co-senior authors*

[1]Sorbonne Universités, UPMC Université Paris 6, Laboratoire Jacques-Louis Lions, CNRS UMR7598, France. [2]Mycenae Team, Inria Paris Rocquencourt, France. [3]Sorbonne Universités UPMC Université Paris 6, IBPS-Developmental Biology Laboratory, CNRS UMR7622, Inserm U1156, France.

The objective of our project, based on synergistic interactions between mathematicians and biologists, is to develop a multi-scale mathematical model of neurogenesis in the cerebral cortex, and to use it to help understand the perturbations occurring in mouse models of neurodevelopmental diseases. As a proof of concept, we use a mouse model of ciliopathies, a mutant for the *Rpgrip1l* gene, in which cortical neurogenesis is abnormal. Ciliopathies are caused by defects in the formation or function of a cellular sensory organelle called the primary cilium. They are characterized by a wide range of brain developmental defects, from anencephaly to intellectual disabilities. Our experimental data show that several, temporally distinct, aspects of the production and proliferation of cortical progenitors are perturbed in the Rpgrip1l mouse mutant. We are currently developing the model and calibrating it with data from the literature and from our own experiments. We hope that this model will help us decipher the cellular bases of progenitor expansion and differentiation in the developing mouse cerebral cortex, in normal conditions as well as in models of neurodevelopmental disorders such as the *Rpgrip1l* ciliopathy gene mutant.

Communication

Genome and life stage-specific transcriptomic data from the hydrozoan medusae *Clytia hemisphaerica*

LECLERE Lucas

UMR 70009-UPMC-Villefranche

Cnidarians are the closest relative to bilaterians and hold a key position for understanding metazoan evolution. We have produced a draft genome assembly and a comprehensive transcriptome of the medusozoan cnidarian, *Clytia hemisphaerica*, using multiple RNA-seq libraries covering the major stages of the life-cycle, partially funded by the Picard Network. This represents the first comprehensive data for a cnidarian exhibiting polyp and medusoid stages. I will show the current state of analysis of our comprehensive RNA-Seq libraries and identification of transcripts that are specific to particular life stages – for instance, the medusa, the polyp or the planula. I will also present the results from our *in situ* hybridization screen of key developmental genes present in the *Clytia* genome, conserved between cnidarians and bilaterians, to gain insight into the likely functional role of bilaterian gene orthologs in cnidarians.

Communication

Phallusia mammillata: an emerging model for molecular toxicology and image-based screens

DUMOLLARD Rémi

UMR 70009-UPMC-Villefranche

The use of invertebrate embryos for toxicological screening tests or analysis offers the possibility to image a large number of samples which is a requisite for image-based screens. Ascidians are members of a sister clade to the vertebrates and make a tadpole larva with vertebrate body plan composed of only 2600 cells. The neural complex of the ascidian larva is made of only 350 cells (of which 100 are neurons) and functional genomic studies have now uncovered numerous GRNs underpinning ascidian brain formation. Efficient transgenesis coupled to the unique optical properties of *Phallusia mammillata* embryos now afford to follow brain development at the single cell level. We recently observed that *Phallusia* neural development is impaired by endocrine disrupting chemicals (EDCs) and now want to use this embryological model to study neurodevelopmental toxicity of EDCs. Beyond characterizing the GRNs affected by EDCs we want to devise GFP molecular indicators of endocrine disruption that can be applied to high content screening of marine water samples or man-made molecules.

Communication

Co-option of germ layers related TFs shows regionalized expression during two non-embryonic developments

TIOZZO Stefano

UMR 7009-UPMC-Villefranche

Developmental processes, such as budding or whole body regeneration, lack the familiar temporal and spatial cues classically associated with embryogenesis, like maternal determinants, or gastrulation. We have addressed this question in the colonial ascidian *Botryllus schlosseri*, which undergoes an asexual reproductive process (blastogenesis), as well as a whole body regeneration one (vascular budding). We followed the fate of differentiating tissues during non-embryonic developments by monitoring the expression of genes known to play key functions in germ layer specification with well conserved expression patterns in ascidian embryogenesis. Our results indicate that during both normal and injury induced regeneration a similar alternative developmental program operates via early commitment of epithelial regions.

Communication

La métaphore cognitive en biologie

CASTELLANE Ariane

Paris Sorbonne-Paris IV

L'usage des métaphores en biologie n'est pas un phénomène exceptionnel : l'évolution figurée par un arbre, ou bien la fécondation imagée avec le conte de la belle au bois dormant (métaphore cependant abandonnée aujourd'hui) en sont deux exemples bien connus. Ce type de métaphore a été introduit pour expliciter un phénomène complexe et le rendre plus intelligible intuitivement. Le langage de la biologie est cependant truffé de métaphores d'un autre type, non-explicites. En biologie cellulaire, entre autres, les cellules sont décrites comme reconnaissant (d'autres cellules), mémorisant (les lymphocytes B "se souviennent" d'un antigène en particulier) ayant telle préférence (pour tel environnement), etc. Ce vocabulaire constitue une métaphore dite cognitive, en ce qu'elle attribue des états psychologiques (croyance, mémoire, désir, etc.) à des entités auxquelles on n'accorde pas de psychologie.
Mon travail consiste à montrer que l'emploi de ce vocabulaire est bien métaphorique, de comprendre le rôle qu'il joue dans la description de phénomènes biologiques en explorant notamment la notion d'agentivité et de montrer l'intérêt qu'il peut présenter pour penser la notion de mental et d'intentionnalité (le fait d'avoir des états mentaux, tels que des désirs ou des croyances, à propos d'un ou plusieurs objet-s du monde) en philosophie.

Communication

Towards the identification of an ancestral *Wnt* function

CROCE Jenifer

UMR 70009-UPMC-Villefranche

Wnt genes encode secreted glycoprotein ligands that, from an evolutionary point of view, are considered to be a metazoan innovation. Wnt genes have been reported to date from sponges to vertebrates, although in non-planulozoan metazoans (i.e. sponges, placozoans and ctenophores) their overall number, within a given animal, is usually smaller than that observed in planulozoans (which encompass both bilaterians and cnidarians). This observation has led to the suggestion that, while Wnt genes have appeared at the base of the metazoans, a major diversification of their complement must have occurred prior to the cnidarian-bilaterian split. The goal of our study is to investigate the underlying gearing of this diversification and to determine through functional analyses, conducted in parallel in sea urchin and Xenopus (i.e. an invertebrate and a vertebrate deuterostome), the likely ancestral function(s) of these developmentally important signaling molecules.

Communication

Comparative development of the neurogenic tail epidermis midlines in ascidians

DARRAS Sébastien

UMR 7232-UPMC-Banyuls

The larval tail epidermis midlines of the ascidian *Ciona intestinalis* are specialized epidermal domains from which peripheral sensory neurons arise. These domains are specified by inductive mechanisms (Fgf, Nodal, Bmp and Wnt signals) early during embryogenesis. Their specific molecular identity is characterized by the dynamic expression of 7 transcription factors. By combining gene function studies and *cis*-regulatory DNA analysis, we show that *Msx* is at the top of an unexpectedly complex network of regulations among these genes. Ascidian larvae appear very similar between different species despite high genomic divergence. I will present our current efforts at determining whether the network that we have unveiled in *C. intestinalis* is deployed similarly in other ascidian species.

Communication

Towards a model of the spatio-temporal dynamics of the translation repressor 4E-BP regulation network

CORMIER Patrick

UMR 8227-UPMC-Roscoff

Authors: CORMIER Patrick, DEMOUY Josselin, MOUNDOYI-MBOUNGOU Harold Amen, GLIPPA Virginie, LE PANSE Sophie, MORALES Julia, MULNER-LORILLON Odile, PERTHAME Benoit and SARELS Benoit.

The protein synthesis rate of sea urchin eggs before fertilization remains remarkably low. Fertilization is the starting signal, which triggers off eggs awakening and induces a dramatic increase of mRNA translation. Fertilization induces an increase in cap-dependent protein synthesis associated with a decrease in the amount of the translation initiation repressor 4E-BP [1]. A Biocham model for the m^7GTPcap-dependent translation [2] and a minimal model involving the main molecular actors that control the increase of mRNA translation in the sea urchin eggs following fertilization [3] were initially produced. We provided evidence that the mTOR (mechanistic Target Of Rapamycin) pathway controls the degradation of 4E-BP and consequently the cap-dependent initiation of cyclin B mRNA translation [4]. We now aim to study different levels of the dynamics of the translation repressor 4E-BP.
I will introduce the project that we are currently developing with the Jacques-Louis Lions Laboratory. The project aims to analyze the spatio-temporal dynamics of the TORC1 (Target Of rapamycin Complex 1) and its impact on 4E-BP degradation and the protein synthesis in sea urchin eggs.

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Communication

Gene KO technique in *Clytia hemisphaerica*: taking advantages of asexual reproduction and stem cell specific DNA repair

MOMOSE Tsuyoshi

UMR 7009-UPMC-Villefranche

Gene editing by CRISPR/Cas9 is a powerful tool and will provide true genetics framework into marine model animals. We have developed a full protocol for gene knockout (KO) in a cnidarian *Clytia hemisphaerica*, with successful creation of mutants for cilia regulator *rfx1* and two GFP genes *gfp1* and *gpf2*. Mutants for RPGRP1/1L gene are also in production. The protocol takes full advantages of an unknown mechanisms/phenomenon in polyp-forming stem cell, which favor deletion caused between two short identical sequences. It suggests microhomology mediated end-joining (MMEJ/alt-NHEJ) is dominant for double strand break repair in the stem cells.

Communication

CORBEL: A new H2020 project for biomedical research

VANMAELE Sophie

UMR 7009-UPMC-Villefranche

CORBEL is a Horizon 2020 initiative linking eleven biological and medical research infrastructures (BMS RIs). The goal is to allow harmonized user access for biological and medical technologies, biological samples and data services to boost the efficiency, productivity and impact of European biomedical research. The CORBEL project is structured into 9 work packages, of which WP4 drives the development of interactions between European Research infrastructures in selected areas of biological research. The EMBRC members are coordinating Use Case 4.4, within WP4: “Marine metazoan developmental models for biomedical research from predictive integrated databases to functional testing”. One central part of this action is to develop user-friendly genomic databases for three animals, the small hydrozoan jellyfish *Clytia hemisphaerica*, the European sea urchin *Paracentrotus lividus* and the cephalochordate amphioxus (*Branchiostoma lanceolatum)*. The aim is to promote more widely these alternative models to the larger bioscience community, as they have the potential to unlock questions intractable to conventional models. This activity will be undertaken by researchers at five EMBRC marine station sites in Scotland, Italy and France (the three UPMC/CNRS marine stations), interacting closely with other members of the European Research Infrastructures, notably ELIXIR and Euro-BioImaging.

Liste des participant.e.s

ALMEIDA Luis UMR 7598-UPMC-Paris luis.almeida@upmc.fr	**CARRON Clémence** UMR 7622-UPMC-Paris Clemence.Carron_Homo@upmc.fr	**CROCE Jenifer** UMR 7009-UPMC-Villefranche Jenifer.Croce@obs-vlfr.fr
ATGER Véronique Sorbonne Universités veronique.atger@sorbonne-universites.fr	**CASTELLANE Ariane** Paris Sorbonne-Paris IV ariane7.castellane@gmail.com	**CYPRIA Julie** UMR 7232-UPMC-Banyuls julie.cypria@hotmail.com
ANDOUCHE Aude UMR 7208-MNHN-Paris andouche@mnhn.fr	**CHAMBON Jean-Philippe** UMR 7138-UPMC-Paris jean-philippe.chambon@upmc.fr	**DARNAT Pénélope** UMR 7622-UPMC-Paris 1.darnat.penelope@gmail.com
BARATTE Sébastien UMR 7208-MNHN-Paris baratte@mnhn.fr	**CHARRIER Bénédicte** UMR 8227-UPMC-Roscoff benedicte.charrier@sb-roscoff.fr	**DARRAS Sébastien** UMR 7232-UPMC-Banyuls sebastien.darras@obs-banyuls.fr
BARREAU Carine UMR 7009-UPMC-Villefranche carine.barreau@obs-vlfr.fr	**CHEVALIER Sandra** UMR 7009-UPMC-Villefranche chevalier@obs-vlfr.fr	**DENIS Guillaume** UMR 7622-UPMC-Paris denis.guillaume86@gmail.com
BASSAGLIA Yann UMR 7208-MNHN-Paris bassaglia@mnhn.fr	**CHRISTIANS Elisabeth** UMR 7009-UPMC-Villefranche christians@obs-vlfr.fr	**DEUTSCH Jean** UMR 7622-UPMC-Paris jean.deutsch@upmc.fr
BELIERES Alice Ecole de Biotechnologies Sup'biotech alice.belieres@gmail.com	**CONCORDET Jean-Paul** UMR 7196-MNHN-Paris jean-paul.concordet@mnhn.fr	**DONATI Antoine** UMR 7622-UPMC-Paris antoine.donati@upmc.fr
BELLO Valérie UMR 7622-UPMC-Paris valerie.bello@upmc.fr	**CONDAMINE Thomas** UMR 7138-UPMC-Paris thomas.condamine@upmc.fr	**DUFOUR Sylvie** UMR 7208-MNHN-Paris dufour@mnhn.fr
BONNAUD PONTICELLI Laure UMR 7208-MNHN-Paris bonnaud@mnhn.fr	**COPLEY Richard** UMR 7009-UPMC-Villefranche copley@obs-vlfr.fr	**DUMOLLARD Rémi** UMR 7009-UPMC-Villefranche remi.dumollard@obs-vlfr.fr
BULLIER-MARCHANDIN Erika UMR 7622-UPMC-Paris erika.bullier@upmc.fr	**CORMIER Patrick** UMR 8227-UPMC-Roscoff cormier@sb-roscoff.fr	**DUPRE Aude** UMR 7622-UPMC-Paris aude-isabelle.dupre@upmc.fr
BURG Angélique UMR 7622-UPMC-Paris angelique.burg@upmc.fr	**COSSE-ETCHEPARE Camille** UMR 7622-UPMC-Paris camille.cosse-etchepare@upmc.fr	**DURANT Jennifer** UMR 7622-UPMC-Paris jdurant90@gmail.com

Liste des participant.e.s (suite)

ESCRIVA Hector UMR 7232-UPMC-Banyuls hescriva@obs-banyuls.fr	**HOULISTON Evelyn** UMR 7009-UPMC-Villefranche houliston@obs-vlfr.fr	**MAZAN Sylvie** UMR 7232-UPMC-Banyuls mazan@obs-banyuls.fr
FAILLA Margaux UMR 7009-UPMC-Villefranche margauxx_06@hotmail.fr	**IMARAZENE Boudjema** UMR 7208-MNHN-Paris boudjema.imarazene@gmail.com	**MC DOUGALL Alexander** UMR 7009-UPMC-Villefranche dougall@obs-vlfr.fr
FERREIRA-GONÇALVES João UMR 7138-UPMC-Paris fgoncalves.joao@gmail.com	**KLOAREG Bernard** UMR 8227-UPMC-Roscoff bernard.kloareg@sb-roscoff.fr	**MIOT Marika** UMR 7622-UPMC-Paris marika.miot-marinho@upmc.fr
FRANCOISE Jean-Pierre UMR 7598-UPMC-Paris jean-pierre.francoise@upmc.fr	**LAPEBIE Pascal** UMR 7009-UPMC-Villefranche lapebie@obs-vlfr.fr	**MOMOSE Tsuyoshi** UMR 7009-UPMC-Villefranche tsuyoshi.momose@obs-vlfr.fr
GENEVIERE Anne-Marie UMR 7232-UPMC-Banyuls anne-marie.geneviere@obs-banyuls.fr	**LE BOUFFANT Ronan** UMR 7622-UPMC-Paris ronan.le_bouffant@upmc.fr	**MORALES Julia** UMR 8227-UPMC-Roscoff morales@sb-roscoff.fr
GHO Michel UMR 7622-UPMC-Paris Michel.Gho@snv.jussieu.fr	**LECLERE Lucas** UMR 7009-UPMC-Villefranche leclere@obs-vlfr.fr	**MOUAS Isabelle** UMR 7208-MNHN-Paris mouas@mnhn.fr
GIOVANNANGELI Carine UMR 7196-MNHN-Paris carine.giovannangeli@mnhn.fr	**LEMONNIER Tom** UMR 7622/7009-Paris/Villefranche tomlmnn@gmail.com	**MOUCHEL-VIELH Emmanuèle** UMR 7622-UPMC-Paris emmanuele.mouchel@upmc.fr
GOEA Laura Elena UMR 7622-UPMC-Paris laura.goea@upmc.fr	**LEPABIC Charles** UMR 7208-MNHN-Paris clepabic@mnhn.fr	**PATERNOTTE Cédric** Paris Sorbonne-Paris IV cedric.paternotte@gmail.com
HONG Elim UMR 7622-UPMC-Paris elim.hong@inserm.fr	**MANGIN Jean-Marie** UMR 7622-UPMC-Paris jean-marie.mangin@inserm.fr	**PERON Sophie** UMR 7009-UPMC-Villefranche speron@obs-vlfr.fr

Liste des participant.es (suite)

PERONNET Frédérique UMR 7622-UPMC-Paris Frederique.Peronnet@upmc.fr	**RIOU Jean-François** UMR 7622-UPMC-Paris jean-francois.riou@upmc.fr	**TIAN Lei** UMR 8256- UPMC-Paris tianlei2012@sjtu.edu.cn
PERTHAME Benoît UMR 7598-UPMC-Paris benoit.perthame@upmc.fr	**RONSSERAY Stéphane** UMR 7622-UPMC-Paris stephane.ronsseray@upmc.fr	**TIOZZO Stefano** UMR 7009-UPMC-Villefranche tiozzo@obs-vlfr.fr
POSTEL Marie UMR 7598-UPMC-Paris marie.postel@upmc.fr	**ROUAN Alice** UMR 7009-UPMC-Villefranche alicerouan@gmail.com	**TOSTIVINT Hervé** UMR 7221-MNHN-Paris herve.tostivint@mnhn.fr
POTTIN Karen UMR 7138-UPMC-Paris karen.pottin@upmc.fr	**SARELS Benoît** UMR 7598/UMR 8227-UPMC-Paris/Roscoff benoit.sarels@sb-roscoff.fr	**VANMAELE Sofie** UMR 7009-UPMC - Villefranche Sofie.Vanmaele@obs-vlfr.fr
PROCHIANTZ Alain Collège de France Alain.Prochiantz@college-de-france.fr	**SCAROS Alexia** UMR 7208-MNHN-Paris alexia.scaros@gmail.com	**VESQUE Christine** UMR 7622-UPMC-Paris christine.vesque@upmc.fr
QUEINNEC Eric UMR 7138-UPMC-Paris eric.queinnec@upmc.fr	**SCHNEIDER-MAUNOURY Sylvie** UMR 7622-UPMC-Paris sylvie.schneider-maunoury@upmc.fr	**WEIL Dominique** UMR 7622-UPMC-Paris dominique.weil@upmc.fr
QUIROGA ARTIGAS Gonzalo UMR 7009-UPMC-Villefranche gonzalo@obs-vlfr.fr	**SCHUBERT Michael** UMR 7009-UPMC-Villefranche michael.schubert@obs-vlfr.fr	
RIO-CABELLO Antoine UMR 7208-MNHN-Paris antoine.riocabello@gmail.com	**STEGER Julia** UMR 7009-UPMC-Villefranche steger@oceane.obs-vlfr.fr