

Unravelling animal regeneration success, insights from the annelid *Platynereis*

Regeneration, the ability to restore lost parts of the body, is a widespread phenomenon in animals. We use the annelid *Platynereis dumerilii*, an emerging developmental biology model (Ozpolat et al., 2021) to study regeneration in a comparative and evolutionary perspective. After amputation of the posterior part of their body, *Platynereis* worms are able to regenerate complex body structures in a cell proliferation dependent manner (Planques et al., 2019). *Platynereis* is also able to regenerate successfully its **appendages (parapodia)** (Velasquillo et al., in prep). After **head amputation**, while there is formation of a small blastema (a mass of undifferentiated proliferating cells that accumulate at the damaged surface underneath the wound epithelium, unpubl. data), there is no production of any differentiated head structures. One of the aims of the team is to understand **why some regeneration processes are successful**, i.e., allow the restoration of the amputated body parts (posterior and appendage regeneration) **while other are not** (anterior regeneration). The M2 student will participate to this major project of the team by investigating:

- **Morphological, molecular and cellular characterization of abortive anterior regeneration.** The M2 student will define stages of the process, characterize the mitotic behavior of the cells after amputation using EdU and cell cycle markers, study the occurrence of cell death with TUNEL, and establish the origin and fate of the cells during anterior regeneration using *in situ* hybridizations (ISH) for various cell and tissue markers and cell-lineage tracing experiments. Comparisons will be made with similar data from posterior and parapodial regeneration in order to define similarities and differences between the three regeneration processes occurring in *Platynereis*.
- **Single-cell transcriptomic analysis of regeneration types:** The M2 student will participate to an ongoing project (in collaboration with the team of N. Konstantinides, IJM) aiming to use single-cell transcriptomics (sc-RNA-seq) to identify and compare cell diversity and its dynamics during successful and abortive regenerations in *Platynereis*. sc-RNA-seq data have been already produced for posterior and parapodial regenerations (2 stages) using the ACME dissociation/fixation procedure, followed by 10X Chromium technology and Illumina sequencing (Velasquillo, unpubl data). Similar procedure will be applied on blastema cells of anterior aborted regeneration. Bioinformatic analysis (pipelines already available) and molecular validation of the potential cell populations will be performed (by ISH or Hybridization Chain reaction HCR, on whole mount or slices). This work is expected to provide key information about cellular states and populations during successful and abortive regeneration contexts, and through comparison providing crucial element about the success of regeneration in this species.

Mot clés:

Regeneration, success, scRNAseq, HCR, evolution, annelid