

A trade off between constraints in embryo geometry and on regulatory genome evolution.



Léo GUIGNARD

INRIA project-team Virtual Plants, joint with CIRAD and INRA, UMR AGAP, Université Montpellier 2, FRANCE

Ascidian embryos develop with stereotyped and evolutionarily conserved invariant cell lineages to produce in a few hours or days tadpole larvae with a small number of cells. They thus provide an attractive framework to describe with cellular resolution the developmental program of a whole organism. We developed a quantitative approach to describe the evolution of embryonic morphologies during the development of the ascidian *Phallusia mammillata*. We then used this approach to systematically characterize in detail the logic of cell fate induction events.

To quantitatively characterize cell behaviors during embryogenesis, we used multi-angle light-sheet microscopy to image with high spatio-temporal resolution entire live embryos with fluorescently labeled plasma membranes. To extract biological information from this imaging dataset, we then developed a conceptually novel automated method for 4D cell segmentation, ASTEC. Applied to a *Phallusia mammillata* embryo imaged for 6 hours between the 64-cell and the initial tailbud stages, this method allows the accurate tracking and shape analysis of 1304 cells across 671 cell divisions.

Based on this quantitative digital representation, we systematically identified cell fate specification events up to the late gastrula stage. Computational simulations revealed that remarkably simple rules integrating measured cell-cell contact areas with boolean spatio-temporal expression data for extracellular signalling molecules are sufficient to explain most early cell inductions. This work suggests that in embryos establishing precise stereotyped contacts between neighboring cells, the genomic constraints for precise gene expression levels are relaxed, thereby allowing rapid genome evolution.