Contact area-dependent cell communications and the morphological invariance of ascidian embryogenesis.

<u>Léo Guignard</u>^{1,2}, Ulla-Maj Fiuza³, Patrick Lemaire⁴, Christophe Godin⁵, Grégoire Malandain⁶ ¹Max Delbrück Center, Germany. ²Berlin Institute of Health, Germany. ³EMBL, Germany. ⁴CRBM, France. ⁵Inira - MOSAIC, France. ⁶Inria, France

Abstract Text

Ascidians show an extreme form of embryonic reproducibility: their early embryonic cell lineages are considered invariant and conserved between distantly-related species, despite rapid genomic divergence. Here, we addressed the drivers of this reproducibility. We used light-sheet imaging and automated cell segmentation and tracking procedures to systematically quantify the behavior of individual cells every 2 minutes during Phallusia mammillata embryogenesis. Inter-individual reproducibility was observed down to the area of individual cell contacts. We found a tight link between the reproducibility of embryonic geometries and asymmetric cell divisions, controlled by differential sister cell inductions. Combining modeling and experimental manipulations, we showed that the area of contact between signaling and responding cells is a key determinant of cell communication. Our work establishes the geometric control of embryonic inductions as an alternative to classical morphogen gradients and suggests that the balance between these two mechanisms sets the scale at which embryonic reproducibility is observed.



Reconstruction and modeling of Phallusia embryogenesis.

(Left) **Quantitative analysis of** *Phallusia* **embryogenesis.** We combined live light-sheet imaging of cell membranes (left images) with automated cell segmentation and tracking with color-coded cell fates (center images) to extract quantitative cell morphological properties (right images, color-coded by cell compactness). From top to bottom: embryo at the 64-cell, mid-gastrula, and late gastrula stages. (Right) Cell-cell signaling model. We first made simplifying assumptions concerning the distribution and diffusion of signaling pathway components (top), then integrated cell contact geometry with gene expression profiles to predict pathway activation levels in single cells (center) and binarized induction status (bottom).