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in toto live imaging and cell lineage analysis of the spiralian development

Metazoans specify germ layers during early development in a process called gastrulation. Gastrulation involves massive cell movements during which the specified germ layers are divided into molecularly distinct domains, which later gives rise to diverse differentiated cell types. Gastrulation movements have been described at both the cellular and molecular levels in vertebrates and insects in considerable detail. Similar in-depth analysis in other animals is hampered by technical difficulties, both concerning imaging techniques and available molecular tools. This generates a noticeable gap of biological knowledge for larger branches of the metazoan phylogenetic tree, e.g. the spiralians, which constitute 1/3rd of the metazoan phyla (Zhang, Z (2013), Laumer et al., 2015). To address this issue, we have first recorded the embryological development of the spiralian ragworm *Platynereis dumerilii* at cellular resolution for more than one day. We have used SiMView microscopy for high-speed *in vivo* and *in toto* imaging (Tomer et al., 2012). Second, through a combination of semi-automated cell segmentation and tracking (TGMM, Amat et al., 2014) and manual correction by using CATMAID (Saalfeld et al., 2009, Schneider-Mizell et al., 2016), we have generated the entire cell lineages of a one-day old *Platynereis* embryo. Third, we have produced gene expression data for key developmental genes in the one-day old *Platynereis* embryo. Overall, this allows us to present an analysis of the cellular movements and behavior during gastrulation and the mapping of genes important for gastrulation and axis formation onto the cell lineages. This work presents the first whole-embryo analysis at cellular resolution of the gastrulation process in a spiralian. It offers a resource for analyzing molecular underpinning of cell behavior in wild-type and functionally perturbed spiralian embryos.

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Terms and Conditions

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