morphogenesis. We study the conserved L-sided signaling from Nodal (Xnr1 in *Xenopus*) in the left lateral plate mesoderm (L LPM), which is transient and dynamic, and induces asymmetric expression of its antagonist Xlefty and transcriptional regulator Pitx2. Interference with the L-sided Nodal pathway is associated with improper situs and congenital abnormalities. We, and others, have determined that a system of self-enhancement and lateral inhibition (SELI) exists within the LPM. Autoregulatory Nodal expression induces the feedback inhibitor Lefty, and long-range contralateral communication from the L LPM acts to suppress R-sided expression of Nodal/Lefty. There are significant gaps in our understanding of how the Nodal/Lefty/Pitx2 cascade connects to downstream asymmetric morphogenesis at a cell biological level. For example, there is a poor understanding of the organization and structure of the LPM during the period of Xnr1 signaling. We are characterizing LPM architecture at high-resolution before, during and after Xnr1 signaling, and testing if specific tissue properties (e.g., planar polarity, epithelial state) contribute to the rapid directional propagation of asymmetric Nodal expression, or to the contralateral communication process. We are also using tagged Lefty and Xnr1 to determine the routes, speed and mechanisms of transport within and from the L LPM, to understand the biochemical and cellular basis for a pan-embryonic integrated L-R morphogenetic program.

doi:10.1016/j.ydbio.2007.03.629

Program/Abstract # 330
FACS-assisted microdissection of early zebrafish embryos for transcriptional profiling and cell behavioral studies
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In zebrafish, the mesoderm and endoderm precursors are intermingled near the blastula margin. Using our in-house technique for dissecting embryonic cells from regions of interest, FACS-assisted Microdissection of Photolabeled cells (FAM-P), we separated mesoderm and endoderm precursors from ectoderm precursors. To compare the transcriptomes of ectoderm and mesendoderm precursors, RNA was extracted from sorted margin and non-margin cells, amplified, labeled and hybridized to a custom microarray representing over 20,000 different zebrafish genes. In validation of our method, a number of genes known to have elevated expression in the late blastula margin were re-identified by this approach, including *no tail*, *fgf8*, *chordin*, *wnt11*, and *squint*. We found dozens of additional genes with a greater than 3-fold enrichment in the mesendoderm precursor population (*p* < 0.0015) whose late blastula expression has not been previously described. Validation studies on a selected sample of 21 genes indicated that about 50% show margin-specific staining by whole mount *in situ* hybridization. We also found that FAM-P cells remain viable and are suitable for primary cell culture and transplantation experiments. Differentiation spectra of margin-derived cells transplanted to host animal poles and animal pole-derived cells transplanted to host margins indicate that each cellular population is in a relatively committed state.

doi:10.1016/j.ydbio.2007.03.631

Program/Abstract # 329
Withdrawn.

doi:10.1016/j.ydbio.2007.03.630