CDB SEMINAR

Parker B. Antin

Department of Cell Biology and Anatomy,
Molecular Cardiovascular Research Program, University of Arizona

Thursday, June 24, 2010
16:00~17:00 C1F CDB Auditorium

FGF signaling during avian gastrulation and mesoderm lineage diversification

Summary

Fibroblast growth factors and their receptors are expressed in complex and overlapping patterns in the amniote embryo, indicative of their diverse roles in regulating key developmental processes. We have investigated the function of FGF signaling during gastrulation and development of the cardiovascular mesoderm lineages in avian embryos. Inhibition of FGF signaling blocks migration of epiblast cells through the primitive streak by mechanisms that are independent of overt changes in E-Cadherin expression or localization. Candidate gene and whole genome expression analyses show that FGF signaling is required for expression of a large number of genes in the primitive streak that include members of multiple signaling pathway and transcription factor families. Most FGF-dependent genes in the primitive streak are regulated via a RAS/MAPK downstream pathway, while some are regulated through PI3K/AKT signaling. Of pathways regulated by FGF signaling, non canonical WNT and Eph-Ephrin pathways regulate migration of cells through the primitive streak. Following gastrulation, reactivation of FGF signaling is required for development of the endothelial and cardiac myocyte cell lineages. Using a microarray based strategy we have defined the contribution of FGF and BMP signaling to gene expression during early stages of heart muscle cell development. When integrated with in situ hybridization expression information, this dataset provides a molecular basis for understanding the spatial distribution of differential gene expression across the medial to lateral domains of the heart field.

Host:
Guojun Sheng
Early Embryogenesis, CDB
sheng@cdb.riken.jp
Tel:078-306-3132
(ext:4201)