



Structural Biology & Functional Genomics Lecture Series

## Seminar Announcement

*(Department of Biological Sciences & Office of Life Sciences, NUS)*

# Patterning the early mouse embryo: Traditional and genomic approaches

Our laboratory is interested in the mechanisms of early embryonic patterning and organogenesis. We have taken two separate approaches to address these questions in the early mouse embryo.

The first approach has involved focusing on a specific family of signaling factors and their role in a specific embryonic event. In particular, we are examining the formation and functions of the "node" in mouse gastrulation. The node is an organizing which coordinates the formation of the dorsal-ventral and left-right body axes. The node is also the primary source for the definitive mouse endoderm. However, how the node function to pattern the embryo and the cell-cell signalling involved remains poorly understood. One family of growth factors implicated in embryonic patterning and node functions is the transforming growth factor- $\beta$  (TGF $\beta$ ) family. This family can be subdivided into three classes, the TGF $\beta$ s, activins/nodals and bone morphogenetic proteins (BMPs). FoxH1 is a forkhead, DNA-binding protein that can mediate signals by nodal. Interestingly, mice containing mutations in FoxH1 fail to form embryonic endoderm or a node. Moreover, these mutants phenocopy many features of mice carrying mutations in the forkhead transcription factor, FoxA2. We are examining the mechanism through which FoxH1 and FoxA2 regulates specification of these cells.

The second approach has involved a genomic approach to expression profiling in the mouse embryo. Our project is designed to generate a comprehensive and quantitative profile of gene expression during mammalian development using the C57BL/6J mouse as a model organism. Various tissues representing key points in embryogenesis and organogenesis are being dissected from embryos and neonates and Serial Analysis of Gene Expression (SAGE) libraries are being prepared. Ultimately the Atlas project hopes to create and analyze 150 SAGE libraries. The resulting publicly accessible on-line expression database will provide insights into the progression and regulation of mammalian development.



### Dr Pamela Hoodless

Terry Fox Laboratory, BC Cancer Agency  
Vancouver, British Columbia  
Canada

**Date:** 26 Mar 2004, Fri

**Time:** 4 pm

**Venue:** LT 20

**Host:** Dr Ng Huck Hui

All are welcome