Functional Genomics

Program/Abstract # 359
GXD: A gene expression resource for developmental biologists
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The Gene Expression Database (GXD) is an extensive and easily searchable database of gene expression information about the mouse that is freely available online. GXD collects different types of expression data from wild-type and mutant mice, including RNA in situ hybridization and immunohistochemistry results. A strong emphasis is on gene expression during development. The GXD staff reads the scientific literature and enters the expression data from those papers into the database on a daily basis. GXD also acquires expression data directly from researchers, including laboratories doing large-scale expression studies. GXD currently contains over 420,000 expression results for more than 9200 genes. In addition, it has over 70,000 images of expression data, allowing users to search for these data and to interpret the experiments themselves. By being an integral part of the larger Mouse Genome Informatics (MGI) resource, GXD combines its expression data with other genetic and disease-oriented information. GXD is unique because it collects complex data from disparate sources, integrates it, and then provides tools that make it possible for researchers to search these data in ways unavailable elsewhere. GXD is available through the MGI web site at http://www.informatics.jax.org. GXD is funded by NIH grant HD033745.

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Program/Abstract # 360
Quantitative analysis of cis-regulatory genes and networks
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cis-Regulatory components of the genome are crucial players of gene regulatory networks. Efficient discovery and functional characterization of cis-regulatory modules (CRMs), and their integration into gene regulatory networks have remained a major challenge in genomic regulatory biology. To accelerate these processes, we recently developed a set of “barcoded” reporters that enable us to track in vivo activities of ≥100 CRMs simultaneously. These reporters are powerful tools for high-throughput and quantitative discovery and characterization of CRMs. We will present methods for efficiently studying interactions between cis and trans-regulatory networks using this system.

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Program/Abstract # 361
Gene regulatory network model of sea urchin ectoderm formation
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Gene regulatory networks (GRNs) consist of interacting regulatory genes and provide a mechanistic understanding of developmental processes. Here we conducted a systematic approach to construct the sea urchin ectodermal GRN during early embryogenesis. We first identified genes involved in ectodermal formation by whole mount in situ hybridization. To see the interaction among those regulatory genes, we carried out large-scale perturbation assays in which translation of each gene was interrupted by introduction of morpholino antisense oligonucleotides (MASO). Resultant expression changes were quantified by QPCR and nCounter Analysis System. Perturbation data and spatiotemporal expression patterns were combined to infer network linkages, and construct a provisional GRN model. We also carried out cis regulatory analysis to characterize modules that define specific expression patterns of regulatory genes. Our current ectodermal GRN includes 22 transcription factor genes, 4 genes encoding known signaling ligands, and 3 signal genes with unknown function. Key GRN features relevant to the ectoderm formation include: 1) a nodal pathway that initiates the oral ectoderm formation; 2) a double negative gate of gsc and sip1 that specifies the lineage of the oral ectodermal cells; and 3) a number of aboral genes of the homeobox family that lock the fate of aboral ectoderm through mutual feedback activation.

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Program/Abstract # 362
Transcriptomics during maternal-to-zygotic transition in the zebrafish: An mRNA-seq approach
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Maternally deposited mRNAs direct early development before zygotic transcription initiation during the mid-blastula transition (MBT). In order to gain insights into the mechanisms involved in maternal-to-zygotic transition in the zebrafish (Danio rerio), we performed high throughput mRNA sequencing of oocytes, cleavage-, blastula-, and early