

The Sea Urchin Endomesoderm Gene Regulatory Network, an Encoded Logic Map for Early Development

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Abstract

The regulatory program for animal development is "wired" into the *cis*-regulatory networks of the genome. At the DNA level these networks consist of the clusters of *cis*-regulatory transcription factor target sites (modules) that direct the spatial and temporal expression of each phase of activity of those genes; and the linkages amongst them. Here "linkage" refers to the relation between genes encoding transcription factors and the target sites of genes which they control, and between the genes encoding elements of signal systems and their ultimate target genes. We are engaged in an effort to define at the genomic sequence level the gene regulatory network

(GRN) controlling endomesoderm specification in sea urchin embryos. The proposed GRN is based on the following information: spatial and temporal expression patterns of all genes included; constraints from experimental embryology; and a massive perturbation analysis in which expression of every relevant gene is perturbed and the effects on all other genes measured. The GRN consists of predicted inputs into the *cis*-regulatory modules controlling the endomesoderm expression of the genes involved. These predictions can be tested at the *cis*-regulatory level: here several such tests are presented. They show that the perturbation analysis is a surprisingly informative predictor of DNA sequence-level regulatory transactions.