Using Robotics to Assay for Gene Expression in Morphogenesis of Drosophila Melanogaster Embryos

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Research on Drosophila melanogaster has provided much valuable insight into biological processes such as gene expression and morphogenesis. Dorsal closure in the Drosophila embryo is a morphogenetic process that refers to the dorsalward migration of the lateral and ventral epidermis to enclose the embryo. Dorsal closure is analogous to several vertebrate closure processes, including neurulation, eyelid fusion, and wound healing; thus, it has become an ideal model system for studying coordinated cell migration and fusion processes during development. Genetic studies show that a network of interacting signaling molecules, including the Jan N-terminal kinase (JNK) cascade, act at the leading edge of the migrating epidermis of Drosophila embryos to regulate cingal closure. In order to identify targets of the JNK signaling cascade, especially those functioning downstream of dpp, we have undertaken a high-throughput molecular screen to identify dpp-target genes that exhibit shared patterns of gene expression.

More than 15,000 genes have been identified in the Drosophila genome and we have obtained 16384 well plates containing cDNA bacterial stocks that represent over 5,000 genes in the Drosophila unigene collection (Research Genetics). With the cDNAs in hand, we are now using robotic automation to rapidly perform a large-scale hybridization screen on whole mount embryos in situ to determine the expression pattern of each gene. Our lab has previously shown that an automated approach provides a straightforward and powerful method to extensively assess gene expression in early embryos (Simin et al., 2002).

We will document the genetic expression patterns of the embryos in an online database which we have named Embryonic Drosophila Gene Expression (EDGE). We will subsequently use reverse genetic methods to reveal target gene functions. We expect that genes with shared patterns of expression will function together in spatially-restricted differentiation programs, and thus that this strategy will enable us to identify novel genes that are transcriptionally regulated targets of known signaling cascades, particularly those of the JNK cascade.