

In Silico Evolution of Even-skipped Stripe 2

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One of the challenges in the post-genome era is to understanding how the spatial and temporal patterns of gene expression encoded by *cis*-regulatory elements evolve. An understanding of the rules and principles governing enhancer evolution can give us insights into speciation, and gene regulation. In our lab we have developed a mechanistic model of gene regulation based on our understanding of the biochemical interactions thought to drive gene expression of the *Drosophila even-skipped* gene. The model takes as input, the expression pattern of maternal factors (bcd, cad) and zygotic gap genes (hb, kr, kni, gt, tll) that make part of the segmentation pathway. The model accurately predicts the pattern of gene expression of the eve-skipped stripe 2 element to a high degree of precision. Using our transcriptional model, we have done computational simulations of the evolution of the enhancer and generated novel *cis*-regulatory elements predicted to generate the same stripe pattern as the native element. We plan on testing a few of these solutions by synthesizing the artificial construct and injecting them into *Drosophila* embryos. By validating the artificial constructs we will be in a position to develop novel tools for creating designer *cis*-regulatory elements.