A Combinatorial Repression Mechanism Involving Tailless in the Segmentation Cascade of *Drosophila*

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Introduction. The antero-posterior patterning in *Drosophila* is set by the segmentation cascade. At the level of pair rule genes, each gene shows the seven striped pattern, which is the first molecular sign of the division of the body in segments. However, in the presumptive anterior head region, no pair rule stripes are formed. Each stripe is controlled by a cis regulatory region (CRM), and we are working with the hypothesis that pair-rule stripe CRMs are able to be activated but impeded to be expressed in more anterior regions because the additive activity of several repressors. **Objectives**. Our goal is to identify repressors and investigate transcription regulation underlying this network. Here we investigated tailless (tll) activity on the pair-rule genes even-skipped (eve) and hairy (h). Methods. To accomplish that, we integrate different approaches: genetic and misexpression assays, bioinformatics and biochemistry. Results. We used a computational tool to investigate pair-rule striped patterns and gap domains in different genetic backgrounds. With that we were able to detect small pattern deviations of h 1 and eve 1 in tll- and in slp-;tll- embryos, consistent with repression roles of Tll. Reporter constructs under h 1 and eve 1 CRMs in the genetic assays further confirmed that. Indeed, using a misexpression system we confirmed *tll* repression on these CRMs. We also investigated anterior gap genes in different genetic backgrounds and with the misexpression system. We did detect TII effects on empty-spiracles and buttonhead in these assays, but not consistent with TII indirect roles on h 1 and eve 1. We are presently testing tll and target CRMs interactions in vitro. Conclusions. These results point to TII as being part of an anterior repression mechanism in the anterior blastoderm controlling pair-rule CRMs.

Keywords: *Drosophila*, segmentation, transcriptional regulation.

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