Alternative Transcription Start Sites: Core Promoters and Spatiotemporal Regulatory Signatures

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Transcription initiation is a key component in creating RNA isoforms associated with spatiotemporal expression profiles. During initiation, unique combinations of transcription factors bind to the DNA in distal enhancers, and to the sequence immediately surrounding the transcription start site (TSS) in the core promoter. They assist in opening up the chromatin, recruiting RNA polymerase II to the DNA, and initiating transcription.

In this work, the widespread existence of alternative TSS and their relationship to expression patterns in *Drosophila melanogaster* is investigated. 5'capped ESTs from libraries of different body parts (head, testis, ovary) and developmental stages (embryo, larvae pupae, schneider cell) are non-parametrically clustered. Embryonic data is supplemented with Affymetrix tiling arrays for the more precise determination of the timing of transcription initiation during development. In this way, the most highly utilized TSSs are identified and the condition specificity of each is measured by Shannon entropy.

Using these TSS associations, the condition specific significance of core promoter motif combinations is evaluated and new motifs are searched for using Expectation Maximization and Gibbs sampling. Recent studies have shown the existence of testis specific TBP associated binding factors (TAFs) that bind upstream of the RNA polymerase II in the core promoter. However, the exact binding motif remains unknown. Therefore, through this research, we hope to gain a clearer understanding of the way in which motifs in the core promoter of alternative TSS function as signatures of eukaryotic spatiotemporal gene transcription.