BIOL 4061 Midterm Test 1
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1. The hunchback (hb) gene is present in the early Drosophila embryo, and Hunchback mRNA can be found originating from two sources; maternal mRNA, inherited from the zygote's mother and present in the egg at fertilization, and zygotic mRNA which is transcribed from the zygote's own genome. In the early embryo, the maternal hb mRNA is distributed equally across the embryo from anterior to posterior.

When the gene bicoid is transcriptionally activated in the zygote, this activates the transcription of zygotic Hunchback mRNA. The bicoid mRNA is located at the anterior end of the fertilized egg, and forms a gradient with the level of bicoid protein decreasing toward the posterior pole of the cell. Due to the gradient of bicoid concentration, there is a corresponding gradient of protein made from zygotic Hunchback mRNA, with Hunchback protein concentration being highest at the anterior of the cell and decreasing towards the posterior.

The mRNA for another gene, nanos, is highest at the posterior of the cell. Nanos protein forms a gradient across the cell similar to that of bicoid, but running in the opposite direction; nanos concentration is highest at the posterior of the cell, and decreases toward the anterior end. Nanos acts as a translational repressor of the Hunchback mRNA. The presence of Nanos establishes a gradient of maternal Hunchback mRNA across the embryo, with the highest concentration being found at the anterior end, and decreasing toward the posterior. This gradient of Hunchback protein is further enhanced by the action of bicoid activating zygotic Hunchback mRNA transcription, as described above.

In the staufen mutant, the normal gradient of bicoid is disrupted; there is some bicoid mRNA at the posterior of the oocyte, where it should not be, and there is some drift of bicoid mRNA into the middle of the cell. In this mutant, we might expect the gradient of Hunchback mRNA to be disrupted by these changes. Since bicoid activates zygotic Hunchback mRNA, we could expect to see more Hunchback mRNA being produced at the posterior end of the oocyte, where it is not normally found. Instead of a smooth gradient from anterior to posterior, we might see high levels of Hunchback mRNA and protein at both the anterior and posterior poles, and slightly less in the middle of the oocyte.

3. The gene "even skipped" (eve) is an important segmentation gene and illustrates some important concepts of enhancers, their regulatory proteins, and how they function in the embryo. Eve forms a pattern of expression that forms a segmentation pattern of seven stripes in the anterior-posterior axis of the embryo. In addition, eve is expressed in the central nervous system, the mesoderm, and the anal pad, each at different times during development. This is an example of how gene expression can have a spatial and temporal pattern of control.

The eve gene locus contains multiple enhancers which control its expression in different locations at different times during development. In order to identify when and where a particular enhancer activated gene expression in the embryo, an experiment was devised where each enhancer was paired with the reporter gene lac Z. To clarify, only one enhancer at a time would be paired with the reporter gene, in order to isolate its action. When this hybrid gene was introduced into a Drosophila embryo, the lac Z reporter gene would cause beta galactosidase to be made in the region controlled by the enhancer it was linked to. By using X-gal to stain sections of the embryo, researchers could determine where in the embryo the enhancer was driving expression of the reporter gene.