

Mechanisms of the *Drosophila* Mid-blastula Transition

In *Drosophila*, the coordination of the mid-blastula transition and the maternal-to-zygotic transition is controlled by several factors, including (1) the ratio of chromatin to cytoplasm; (2) Smaug protein; and (3) the Zelda transcription factor. The ratio of chromatin to cytoplasm is a consequence of the increasing amount of DNA while the cytoplasm remains constant (Newport and Kirschner 1982; Edgar et al. 1986a). Edgar and his colleagues compared the early development of wild-type *Drosophila* embryos with that of haploid mutants. The haploid *Drosophila* embryos had half the wild-type quantity of chromatin at each nuclear division. Hence, a haploid embryo at nuclear division cycle 8 had the same amount of chromatin that a wild-type embryo had at cycle 7. The investigators found that, whereas wild-type embryos formed a cellular blastoderm immediately after the thirteenth DNA division, haploid embryos underwent an extra, fourteenth DNA division before cellularization. Moreover, the lengths of cycles 11–14 in wild-type embryos corresponded to those of cycles 12–15 in the haploid embryos. Thus, the haploid embryos followed a pattern similar to that of the wild-type embryos—but they lagged by one cell cycle.

Smaug is an RNA-binding protein with known roles in translational repression. During the mid-blastula transition, however, it targets the maternal mRNAs for destruction (Tadros et al. 2007; Benoit et al. 2009). Embryos produced by *Smaug* mutant females show disruption of the slowing down of DNA division, a block in cellularization, and a failure to increase zygotic (nuclear) genome transcription. Smaug is encoded by a maternal mRNA, and Smaug protein levels increase during the early cleavage divisions. These levels peak when the zygotic genome begins efficient transcription. Moreover, if Smaug is artificially added to the anterior of an early *Drosophila* embryo, there results a concomitant gradient in the timing of maternal transcript destruction, cleavage cell cycle delays, zygotic gene transcription, cellularization, and gastrulation. Thus, Smaug accumulation appears to regulate the progression from maternal to zygotic control of development and coordinates this progression with the mid-blastula transition.

In addition to its involvement in the decline of maternal mRNAs, the maternal-to-zygotic transition involves the activation of the zygotic genes. This activation appears to be regulated by the transcription factor Zelda (Liang et al. 2008), a name that stands for “zinc-finger early *Drosophila* activator.” Zelda is encoded by a maternal mRNA and binds to a CAGGTAG motif found in the promoters of the earliest transcribed zygotic genes. Many of the genes that initiate the pathways of sex determination, dorsal-ventral polarity, and anterior-posterior polarity are initiated by Zelda, and if this transcription factor is absent, these genes are not turned on at the correct times or places. It is possible that as concentrations of Zelda increase during the first few hours of *Drosophila* development, the genes with the highest affinity for Zelda get activated first, and those with lower affinities may be activated later (Harrison et al. 2011; Nien et al. 2011).

It should be noted, however, that even in organisms such as *Drosophila*, where there appears to be a large burst of zygotic gene activity during the mid-blastula stages, there are some genes that appear to be active earlier. Recent studies (Ali-Murthy et al 2013) show that the expression of some zygotic genes (including that encoding the Engrailed transcription factor) in *Drosophila* can be detected very early in cleavage (2-4 nuclei) and that embryos that fail to express these genes at these early stages fail to develop properly.

Literature Cited

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