Transcriptional dynamics in the early *Drosophila* embryo

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Multicellular organisms use morphogen gradients to determine cell identities in a concentration-dependent manner. Although the dynamics of these gradients is now well described, precision and noise in the gene activation processes acting downstream of morphogens remain unclear. Recently, the simple Bicoid/*hunchback* gene network in the *Drosophila* embryo has been quantitatively investigated with the aim to uncover the transcriptional dynamics of Bicoid target genes. A steady Bicoid gradient is established in one hour providing stable positional information along the antero-posterior axis. The main Bicoid target gene *hunchback* is efficiently expressed 30 min later, in an anterior domain of expression with a sharp posterior boundary. Based on Bicoid physical parameters, theoretical models predict a realistic timing from the Bicoid concentration measurement to the establishment of this step-like expression pattern. However, given the interruption of transcription during mitosis, it remains difficult to understand how such precision is achieved so rapidly despite the challenge imposed by the three nuclear divisions occurring during this short period of development. To access the temporal dynamics of the transcription process in this system, we recently used the MS2/MCP approach, which allowed the fluorescent tagging of RNA expressed from the *hunchback* promoter in living embryos. This approach revealed that the early expression of *hunchback* does not exclusively rely on Bicoid and likely involves other maternal regulators. Analysis of bursts features revealed that Bicoid is not required for burst initiation but it significantly increases their duration, suggesting a potential function for Bicoid in maintaining the flux of polymerases initiating transcription.