

Variability and robustness of the functioning of gene regulatory networks: role in the evolution of early embryogenesis

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The early *Drosophila* development is one of the best studied evo-devo processes. In the first few hours of a fruit fly development, processes of biochemical blueprint take start, predefining the segment organization of the embryo body. Broad spatial gradients of maternally-derived factors sequentially activate cascades of embryonic segmentation genes. These patterns determine the segmented insect body plan in more and more detail. This process should be extremely robust as it determines the correct further development and survival of an individual.

Researchers have long noted that segmentation genes are expressed with greater spatial precision than the maternal patterns. Computational modelling of the gene-gene regulatory interactions provides a mechanistic understanding for this robustness to maternal variability in wild-type (WT) patterning. Functioning of the segmentation gene network is also robust to many of experimental perturbations and a number of mutations. These observations once again raise a long-standing question in evolutionary developmental biology: how such, highly robust to mutations, gene ensembles nevertheless are still evolvable?

What levels of variability and what types of variability are still capable of “pushing out” such a system beyond the WT limits? The more fundamental question is: Are there any pathways in gene regulations which are more vulnerable to losing the WT form? We analyze these problems using our specific models of three segmentation gene ensembles. These are gap, pair-rule, and segment polarity genes. We investigate the question of what alternative (or pathological) dynamic forms are close to WT? Accordingly, if robustness is overcome by a specific perturbation (primarily by a specific mutation), what alternative forms of segmentation patterns are most likely to be realized? Numerically manipulating with maternal patterns in several ways, we have revealed common scenarios in the loss of WT. They consist, typically, in the loss of one or more anterior or posterior segments. So far, we have not been able to find simple scenarios for the emergence of new segments. We discuss these results in terms of the evolvability of insect segmentation, and in terms of experimental perturbations and mutations which could test the model predictions.

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