
Quantitative mechanisms explain system drift in the dipteran gap gene network

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Résumé

Dipterans (flies, midges, and mosquitoes) determine segmentation along their main body axis during the blastoderm stage of embryogenesis. In the initial phase of segmentation, maternal gradients are interpreted by the gap genes, the first set of zygotic genes that divide the embryo in antero-posterior regions. Analysis of spatio-temporal expression and systematic knock-down of these gap genes in the scuttle fly *Megaselia abdita* reveals quantitative differences in gap gene cross-regulation between this species and *Drosophila melanogaster*. We have used mathematical modelling and reverse engineering of this gene network to gain insight into the regulatory mechanisms that underlie the observed differences in expression dynamics between the two species. Our models confirm that the qualitative structure of the gap gene network is conserved. Differences in expression dynamics are fully explained by distinct initial placement of the gap gene expression domains, and quantitative modifications of specific interactions. Our models agree with the available evidence from RNAi, and go further as they provide a precise understanding of the causal effects of each change in interaction strength. To our knowledge, this is the first time that anybody has been able to study the mechanistic effects of such subtle changes at the level of an entire evolving developmental gene regulatory network. In addition, it provides a new perspective on regulatory evolution by system drift, where instead of changing the nature of regulatory interactions, the system is constrained to changes in the ratios of interaction strengths.

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