Drosophila GRN Quality

Diagram

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Figure S17: Gene regulatory network of early Drosophila development. Not all regulations are

represented, nor pair-rule genes odd & prd. Frequently selected genes are represented in bold.

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***Little trust in details of this scheme. Not referenced meaningfully in paper.***

![Diagram

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High trust, although the model is simplified, even the connectionist model. We don’t have pair-rule genes in this model.

![A picture containing diagram

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No pair rule genes. Paper hasn’t been published (BioRivX only). The paper references Jaeger as the source of the gap gene interactions.

Figure 4. Gap Gene Network. A) Interaction network of the gap genes and maternal-effect genes. It is still unclear the strength of all these interactions. B) Comparison between in vivo and in silico gap-gene expression regions. Hb presents a full expression from the anterior end to the center and a smaller band near the posterior border. In the simulations, we reproduced these behaviors. Kr is expressed in a central band, although this band is wider in the in vivo results. Also, in both cases, Gt is expressed in two bands bordering the central region. In our model we have expression of giant in the anterior end region. This could be due our model does not simulate most of the terminal genes, a group of genes which is only expressed in the terminal regions and with a great influence there. Finally, Kni is correctly expressed in our model in the central region but it lacks the small anterior band. This also could be caused by the lack of many terminal genes in our model.

Chart, diagram

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Fig 1A from Clark, Dynamic patterning by the Drosophila pair rule network reconciles long-germ and short germ segmentation PloS Biology 2017.

This is a worthwhile paper and figure. We only need to consider the “Early network”

Timeline

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Fig. 3 Early versus late gap gene regulation. Gap gene regulation can

be divided into two distinct phases: early regulation of gap mRNA

domains is based on maternal gradients only, while late regulation of

protein domains involves gap–gap cross-regulatory interactions. The

position of gap domains along the major, or antero-posterior (A–P)

axis of the embryo is shown schematically as colored boxes. Only the

trunk region of the embryo (approx. 35–95% A–P position) is

included in the diagram. Anterior is to the left, posterior to the right.

Background color represents activating inputs by Bcd and Cad. Top

panel: arrowheads represent activating; T-bars represent repressive

inputs responsible for setting specific domain boundaries. Bottom

panel: arrows and T-bars represent activating and repressive gap–gap

cross-regulation, respectively. Circular arrows represent auto-activation.

The thickness of the T-bars corresponds to repressive strength.

Question marks indicate missing or ambiguous evidence, or other

open questions regarding gap gene regulation (see text for details)

From Jager paper (2011; The Gap Gene Network). This can be believed.

Diagram

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This figure is from “Mathematical Models of Morphogenesis” and a journal titled “ITM Web of Conferences” Figure originally appeared in F. Alves and R. Dilão, Modeling segmental patterning in Drosophila: Maternal and gap genes, J. Theor. Biol. 241 (2006) 342-359. This looks solidly referenced in the J. Theor. Biol. paper. The references are old (largely from the 1990’s) but **are believable**.

“in Fig. 3, we show, the biological information of some of the known interaction between the

proteins of maternal origin, the mRNAs and the gap-genes, in Drosophila early development.

In the double graph of Fig. 3, the green-solid arrows represent activation interactions and the red

arrows inhibitory mechanisms.”