



Supporting Online Material for

Gene Regulatory Networks and the Evolution of Animal Body Plans

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This PDF file includes:

SOM Text
Fig. S1
Reference and Notes

SUPPORTING ONLINE INFORMATION

SOURCES OF LINKAGES SHOWN IN FIG. S1:

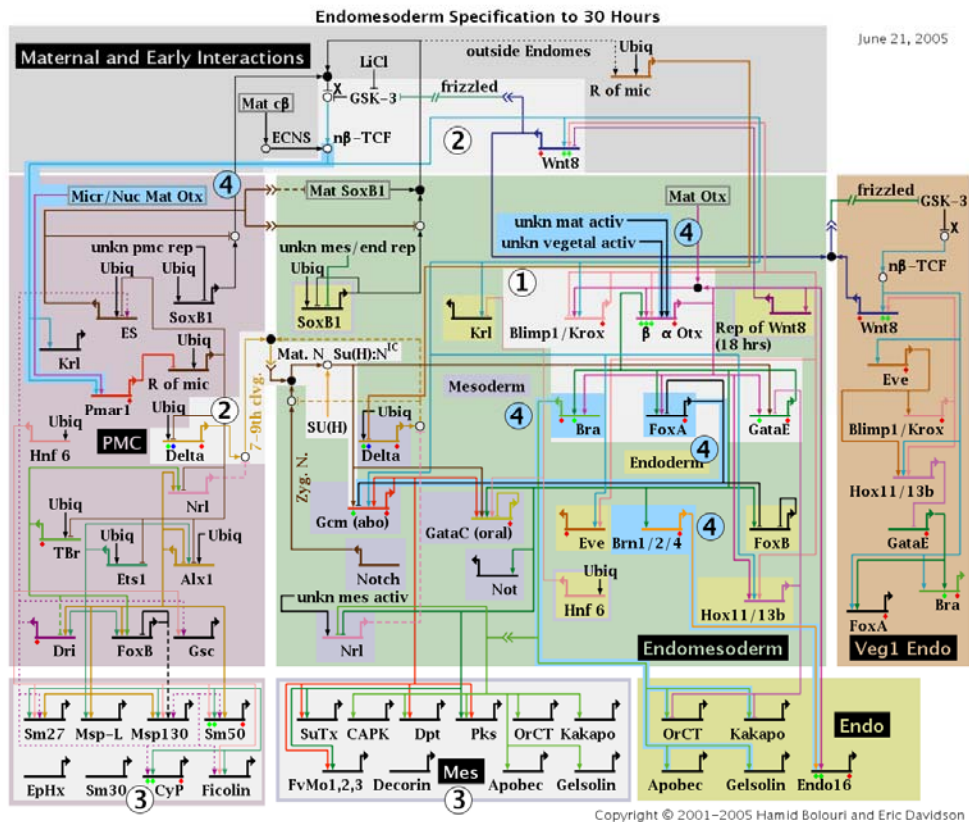
For *Drosophila* network specification subcircuit, sources are as follows (for earlier references see (1,2) Linkages of *pnr* to *hand* and *tin* to *hand*, (3); *mid* (and *h15*) to *tin*, (4); *pnr* to *mid* (and *h15*) and *tin* to *mid* (and *h15*), (4,5,6); *tin* repression of *doc* (4); *tin* to *sur*, (1,4,7); *doc* to *pnr*: inferred from early coexpression of *pnr* and *doc* and dependence of downstream *pnr* target genes including *mid* on *doc* expression (4) in certain later cells of the heart that do not then express *tin*; *tin* to *toll* and *doc* to *toll*, (8); *dpp* to *pnr*, (9). *doc* is considered equivalent to *tbx4/5/6* of vertebrates since there may have been a common ancestor of these vertebrate Tbox genes (10). For the vertebrate heart specification network subcircuit, note that amniotes have primary and secondary heart fields, but this is a derived condition since fish have only the equivalent of the primary field, so linkages of both primary and secondary fields are here included. Sources are as follows (see ref 1 for earlier references): For *tbx5* autoregulation, (11,12); for linkages from *gata4* and *isl1* to *mef2c* (in anterior heart field, not primary heart field), (13); *foxh1* and *nkx2.5* to *mef2c* (primary heart field), (14); for possible *gata6* to *gata4* linkage, (15,16); *tbx5* to *gata4*, (11,17); *mef2c* to *bop*, (18); *gata4*, *nkx2.5*, and *tbx5* to *connexin40*, (19); *dhand* to *atrial natriuretic peptide* (Anp), (20); *smad* to *nkx2.5*, (1,21); for possible repression of *tbx5* by *tbx20* (in zebrafish), (22; however this does not occur in *Xenopus*; 23), and repression of *tbx2* by *tbx20* (in mouse, 24); for possible linkage *nkx2.5* to *gata4*, presence of putative *nkx2.5* sites in *gata4* heart *cis*-regulatory expression module (19).

Note added in proof: Further evidence for many of the linkages in the *Drosophila* diagram is to be found in I. Reims, M. Frasch, *Development* **132**, 4911 (2005).

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Fig. S1. Illustrations of different classes of parts in a gene regulatory network. The sea urchin endomesoderm network is reproduced from ref (26), but grayed out so as to illustrate by colored highlight various types of subcircuit or linkage: (3), differentiation gene batteries, here skeletogenic gene batteries and pigment cell gene battery; (2), plug-ins, here the *wnt8*-Tcf1/ β -catenin subcircuit and the *delta*-Su(H)-Notch signaling systems; (4), examples of I/O linkages, here the maternal inputs into the *pmar1* gene and into the *otx α* transcription unit, the repressive output from the *foxa* gene to the *gcm* gene, the output from the *bra* gene to cell motility genes of the gastrulating endoderm, and the outputs of the kernel shown in (4); (1), kernel.



Corrected 22 February 2006

In the legend to fig. S1, the numbers 1 to 4 have been corrected to match those in the figure.