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The current theory of eukaryotic gene expression suggests that each individual gene is under the control of its own promoter sequence. In the launch issue of *Journal of Biology*, Paul Spellman and Gerald Rubin at Howard Hughes Medical Institute and Department of Molecular and Cell Biology, University of California, Berkeley, show that the *Drosophila* genome contains groups of adjacent genes that have similar gene expression profiles, despite being functionally distinct (*Journal of Biology* 2002, 1:5).

Spellman and Rubin collected gene expression profiles under 88 different experimental conditions from a total of 267 GeneChip *Drosophila* Genome Arrays, which had been used to examine a number of experimental conditions in adult and embryonic fruit flies. After mapping the profile for each gene to the gene's chromosomal position they observed that about 20% of the genes occurred in physically adjacent groups that shared strikingly similar expression patterns.

Along the entire genome they identified about 200 of these groups, each containing between 10 and 30 genes. The average group size was 125 kbp (± 90 kbp), with a range of 22 to 450 kbp. In addition they found that the groups are not related to chromosomal structures such as polytene bands or nuclear scaffolding sites. At present the mechanism underlying this phenomenon remains unclear, but they postulate that it may be related to 'open' domains of chromatin around a key gene, such that neighboring genes are 'carried along for the ride'.

"As further experiments are carried out it may be that our observation of similarly regulated groups will grow to include all genes - that is, the entire euchromatic genome may be structured in such domains," conclude the authors.

References

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