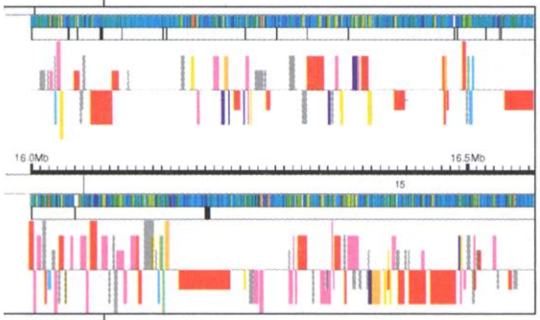
The Universe of *Drosophila* Genes

This special section looks at the generation of the *Drosophila* genome sequence from a variety of perspectives—from the historical to the technical to forecasts of the future. For a more global discussion of our perception of the scientific and political significance of the findings, please see the Editorial on p. 2157; here we present an introductory map to guide you.

"How close is the genome sequence to being really complete? How was the assembly done?" Adams *et al.* (p. 2185) present an overview of the status of the project, including an attempt to define completion. Information about the multiple stages of the assembly process and the methods used to validate the sequence can be found in Myers *et al.* (p. 2196). See also the Report on the bacterial artificial chromosome–based physical map and clones for chromosomes *2* and *3* of *Drosophila* that were used in the assembly and validation process (Hoskins *et al.*, p. 2271).

The initial attempts to annotate the sequence in order to identify genes and begin to predict their function were made in a unique meeting that is described as "a Woodstock for science nerds" in the News story by Elizabeth Pennisi. The fruits of this labor can be found in a foldout summarizing the coding content of *Drosophila* and in discussions of the gene complement needed for fundamental operations, including DNA replication, transcription, and translation. Comparisons of protein families in *Drosophila*, *Caenorhabditis elegans*, and yeast can be found in Rubin *et al.* (p. 2204) as well as a look at developmental and cellular processes and similarities to human disease genes. The *Drosophila* genome provides further evidence that evolution to more complex forms of life does not principally depend on the generation of new genes, but on new combinations of protein domains or novel interactions. However, as you will see in these pages, even this initial examination of the genome revealed surprises that could not have been predicted from other organisms and that will open doors to new research.



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To help in digesting this mass of information, the three Reviews are accompanied by other short pieces. A historical Viewpoint is presented by Rubin and Lewis (p. 2216), two descendants of the traditions of the Fly Room at Columbia University, where so much of the early history was made. In the Perspectives section, Brenner (p. 2173) uses the sequencing of *Drosophila* as a starting point to discuss the issues facing pre- and postgenomic genetics. Three Viewpoint pieces focus on directions for the future. The cDNA resource described by Rubin *et al.* (p. 2222) will be crucial for studies of gene expression and protein function. Benos *et al.* (p. 2220) give us an advance look at the insights that are being gained by the European *Drosophila* Genome Project from their analysis of the tip of the *X* chromosome, including an explanation for a puzzling structural feature. Kornberg and Krasnow (p. 2218) describe how the universal language of DNA will have profound implications for the use of *Drosophila* as a model system in understanding biological processes and human disease.

–BARBARA R. JASNY

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See also Editorial on p. 2157, Perspective on p. 2173, and Report on p. 2271.

Science