

Insect comparative genome analysis.

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Several insect genomes have been recently sequenced, including the genetic workhorse fruit fly and a major malaria vector mosquito [1]. Over a dozen additional *Drosophila* species, the honey bee, another mosquito *Aedes aegypti* and the crustacean *Daphnia* are expected to be completed soon, and many more genomes are anticipated in the future. Knowledge of the genome sequences gives us unprecedented wealth of molecular details, posing however many new questions and challenges. The first step toward understanding insect biology in molecular details is to characterize their functional genes encoding proteins and non-coding RNAs. Comparative analysis, establishing correspondences among elements in different organisms, is not only crucial for transferring our knowledge from the well studied model organisms to the newly sequenced ones, but also have a predictive power. I will present current approaches in computational comparative analysis of gene repertoires and their chromosomal arrangements, as well as preview of multiple comparisons among currently sequenced 11 insect genomes, focusing on what kind of questions could be approached and what kind of surprises we might expect.

1. Zdobnov EM ... Bork P, et al. (2002) Comparative genome and proteome analysis of *Anopheles gambiae* and *Drosophila melanogaster*. *Science*. **298(5591)**:149-59.