

Evolution of overlapping genes in *Drosophila* genomes

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Summary

Overlapping genes represent a pair of different genes which genomic regions cover to some extent. This phenomenon is often observed in viral, prokaryotic and also eukaryotic genomes. It is considered as a common strategy of genome organization and gene regulation in bacteria. Still increasing number of new evidences suggests that overlapping genes can regulate key processes of gene expression in Eukariota, including genomic imprinting, RNA interference, translational regulation and RNA editing.

One of the mechanisms explaining origination of gene overlap is the hypothesis by Keese and Gibbs. It says that overlapping genes are created in an overprinting process – new genes are generated from previously existing nucleotide sequences. That's why one of the genes from overlapping pair is representative of evolutionary and phylogenetically young protein coding genes.

In our studies we focused on closely related species - 12 species of *Drosophila* genus. Entirely studies were done with reference to a set from *D.melanogaster*. We examined conservation of overlapping genes pairs and single genes, being a member of particular pairs. Comparative analysis were done in three levels: for all representatives of *Drosophila* genus, other insects (mosquito and bee), and vertebrates (human, mouse, chicken, zebrafish).

From originally found 3504 unique genes overlapping in *D.melanogaster* the largest number of conserved genes (orthologs) was found within *D.yakuba* – 3022, and least in *D.persimili* – 2712. As compared to the group of model organisms, the highest number of orthologs were observed in mosquito – 2064 and least in mouse – 1147 genes. Out of the 2001 overlapping genes pairs found in *D.melanogaster* the highest number of conserved gene pairs in *Drosophila* genus were observed in *D.yakuba* – 1537, and least in *D.grimshawi* – 1270. In comparison with vertebrates and insect from the group of model organisms these numbers are much lower. The highest proportion of conserved gene pairs is observed in mosquito – 747, and lowest in chicken – 437 genes pairs.

All results show that within overlapping genes there are many formed relatively recently and even among the same genus like *Drosophila* these genes are not conserved. This confirms Keese and Gibbs hypothesis and demonstrates that overprinting is one of major mechanisms leading to gene overlaps.