

# Molecular evolution and variations in Fruit Flies

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## ABSTRACT

The fruit fly belongs to the diptera family- 'Tephritidac'. It has been solidified as a key model organism for elucidating many aspects of human diseases also. For experiments the fruit fly Biology is reviewed and the most relevant genetic tools available to fruit fly researchers are covered.

After that we outline the use of fruit fly as a model organism to study a wide array of pathologies in which it has been used along with key advances made in the specific field using the fly. The fruit fly genome has been sequenced making it very simple to study and manipulate a particular gene. Amongst the fruit fly genome, the genome of *Drosophila* is 60% homologous to ours. About seventy five percent of the gene responsible for human disease have a homology in the flies. In addition, their small size (2-3 mm), short generation time, the easy and inexpensive way to culture them in the laboratory and their powerful genetic tools have established fruit fly (mainly *Drosophila*) as one of the leading animal models for education and biomedical research. Indeed it can be used anywhere for teaching basic genetics for understanding the more complicated metabolic pathways controlling fundamental physiological and pathological conditions. Thomas Hunt Morgan clarified the theory of inheritance and the identification of the gene previously defined by 'Mendel White' got Noble prize for physiology and medicine for the role of chromosomes in heredity since then fruit fly evolution and mutation are studied so extensively. Fruit flies have a short simple reproductive cycle. It is normally about 8-14 days depending on the environmental temperature. This means that several generations can be observed in a matter of month. It measures approximately 3 mm in length. Larvae are small, white and glossy with a similar appearance of worms. They increase several times of their weight within 5-6 days. They are so susceptible to temperature variations. Female live for about one month at room temperature. But this can be increased to over two months at lower temperature. At room temperature female lay 30-50 eggs per day but the daily production of eggs reduces to lower temperature. It is ideal for the study of genetic researches evolutions and mutations. Biological research began in the 20<sup>th</sup> century. There is close relationship between human genes and fruit fly. The sequence of human genes in the fly including disease genes. For experiments in the laboratory they require a simple diet of cornmeal and yeast extract. They are oversized and have barcode like banding patterns of light and dark having polytene chromosomes. Because of chromosomal re-arrangements and deletions it can be identified under the microscope. Fruit fly genes can be easily disrupted and altered. There are several research devoted to the study of the fruit fly biology. It provides a simple means of creating transgenic animals to express certain protein such as the green fluorescent protein of jellyfish. Nucleotide composition in *Drosophila melanogaster* varies regionally and base composition is correlated between introns and exons. This species also show striking patterns of non random codon usage. Pattern of synonymous codon usage and the biochemistry of translation suggest that natural selection may act at silent sites. Mutational biases, biased gene conversion and the natural selection have been proposed as cause of variations. A relationship between recombination rates and codon usage and comparisons of the evolutionary dynamics of silent mutations within and between species support natural selection discriminating amongst synonymous codons. The further developments in functional studies of non coding DNA, further investigations of genome patterns and statistical tests based on evolutionary theory will lead to a greater understanding of the contributions of mutational processes and natural selection in patterning genome-wide nucleotide composition. A study of correlation between introns and coding region base composition shows that variation in mutation pattern also contributes to codon bias variations. The strength of base composition correlations between introns and codons third positions is greater for gene with low codon bias. In particular this correlation is absent when examining fourfold degenerate sites of highly biased genes. Generally it appears that selection acts more strongly in choosing among fourfold degenerate codons than among two fold degenerate codons. Although the result indicate regional variation in mutational bias, no evidence is found for large scale regions of compositional homogeneity. Genome sequencing in a number of taxa has revealed variation in nucleotide composition both among regions of the genome and functional classes of sites in DNA. Genetic recombination affects levels of variability and the efficacy of selection because natural selection acting at one site affects evolutionary processes at linked sites across the *Drosophila* genome provide excellent material for testing hypothesis concerning the evolutionary consequences of recombination.