

Comparative and Functional Genomics of Drosophila

The line of research on Comparative and Functional Genomics of Drosophila, is encompassed within the GBE group (Genetics Bioinformatics and Evolution).

The main objective of this line is to understand the molecular causes and consequences of chromosomal rearrangements. It tries to explain the observed non-random patterns in the distribution of investments among lineages in Drosophila chromosomes and regions within chromosomes (coincidence of the break points). The working hypothesis is that the highly variable activity of transposable elements (TEs) can help explain the high rate of evolution of some lineages of some chromosomes and the coincidence of breakpoints between independent investment. So far the Galileo element (TE) is the only one that has unequivocally demonstrated a causal role in generating investment in natural Drosophila. Their presence in the six other Drosophila species other than *D. buzzatii* (species discovered by our group), suggests that the contribution of Galileo to the chromosomal evolution in Drosophila could be much larger than previously thought.

- Search for Galileo in other species of Drosophila: detection of horizontal transfer.
- Galileo support development of Drosophila and molecular analysis of breakpoints overlap between different investments.
- Effect of natural Drosophila investments on the expression of genes adjacent to breakpoints.