

Brief history of the group

The Genomics Group, Bioinformatics and Evolution (GGBE) Department of Genetics and Microbiology at the UAB as an independent group born in late 1993 when it requested and received his first research project. During the time since then has been stable under the coordination of Dr. Alfredo Ruiz and the natural renewal of some of its members and the incorporation of new researchers. The Governing Board of the Autonomous University of Barcelona approved the authorization of specific name (ENA) in February 2000. In 2005, the Catalan group recognized him as Research Group 2005SGR00892 file.

The GGBE right now has 17 members, where officials highlight two professors, A. Ruiz (coordinator) and A. Barbadilla (sub-coordinator or coordinator in training) and an investigator "Ramón y Cajal" (Isaac Salazar-Ciudad). During its history, GGBE has demonstrated a capacity for innovation and progression in the quality of their research quite remarkable. The achievements are the result of effort and a determined pursuit of excellence. The line of investigation on the chromosomal polymorphism of *Drosophila* clearly framed within what we call the classical population genetics. From this starting position, the group has evolved in several directions of interest today, and great-looking, such as genomics and bioinformatics, has also incorporated new investigators with their own lines of research.

So now, the group has three lines of research and BioinfoUAB platform.

The line of comparative and functional genomics of *Drosophila*, seeks to understand the causes and consequences of natural chromosomal rearrangements. Previous work GBE group, have shown that transposable elements are responsible for the generation of chromosomal inversions of *Drosophila*. However, it is not known how general the results are. Is needed to analyze the investment breakpoints of different ages to better understand the nature and future development of these regions. Also lacking is an adequate explanation of the coincidence between breakpoints of different investments. The presence at the point of breakage hotspots for insertions of transposable elements seems a reasonable hypothesis. It is necessary therefore to determine whether the coincidence of the cytological breakpoints overlap also implies a molecular level, and if these sites are hotspots for transposable elements. It also seeks to determine the frequency with which natural investments have an effect on the expression of genes adjacent to breakpoints. This hypothesis, known as "position effect" has not been systematically investigated at the molecular level by any research group. Since the GBE group has discovered that one of the genes adjacent to a breaking point of an investment is muted. However, there is a direct effect on investment, but a transposon inserted in the break point. Given that transposons are often at the point of rupture, this type of situation could be much more common than previously thought. It requires, in particular, investigate the effects of fixed investment position as interspecific differences. These investments could owe its adaptive advantage to position effects, and may also have contributed to the process of speciation. The role of chromosomal rearrangements in the generation of biodiversity will be studied from the phylogenetic analysis of groups of Lepidoptera with unusually variable chromosome number.

On the other hand, is the line of Bioinformatics research of genetic diversity . The representation, analysis and interpretation of nucleotide variation and its relationship with genomic variants, phenotypic and environmental are the subject of this investigation. He wants to carry out large-scale meta-analysis of nucleotide diversity in metazoans for a description of the patterns of nucleotide variation in a wide range of species and genes. We will use the powerful tools of bioinformatics to make a statistical study of large-scale association with various factors that include features taxonomic, ecological and gene in order to discover factors that play a role in varying levels. At this time of flood of genomics data, transcriptomics, protein, this integrative approach is very relevant and valuable. In particular, studying the patterns of variation in *Drosophila*, we discovered that the protein variation of a gene is influenced by the structural complexity of it, regardless of the specific sequence of the protein, so that structural complexity is a candidate variable study. We will use the powerful approach that involves the use of combined data of polymorphism and divergence. This way you can detect many functional elements throughout the genome. In a recent paper, we have demonstrated the action of purifying selection in different regions of the X chromosome of *Drosophila melanogaster*. To carry out this meta-analysis of data requires the development of bioinformatics tools that automate the collection of sequences, make the love of diversity and stored.

Finally, the group also has a line of research of Evolutionary developmental biology that studies the morphological evolution of developing theories about the dynamics of interdependence between development and evolution.

Our group has also created the UAB Bioinformatics Platform three areas of activity in the area of Bioinformatics: resources, training and research, bioinformatics, playing a major role as a resource for research by research institutes hospitals associated with the UAB and the research groups of the University.

Historically, the Group has received GBE line research Study led by butterflies Dr. Roger Vila and supplemented by the researchers: Vlad Dinca, Gerard Talavera, and Claudia Margarita Marin Sanudo, the description of patterns of diversity genetic and morphological phylogenetic level using butterflies as a model. Currently this research group is working at the CSIC.