

Flies are one of four super radiations of insects that account for the majority of life on Earth. Although recent studies employing phylogenetic tools have provided insights into the timing and pattern of the evolution of flies, there are still many caveats and problems. One of problems is that the standard molecular Sanger multilocus data are still the most popular for reconstructing phylogenetic relationships in flies. This approach lacks power to resolve shallow and deep nodes in phylogenetic trees. Moreover, fly phylogenies often demonstrate an over-reliance on mitochondrial markers, which does not guarantee that the resultant tree represents the true species tree. The emergence of genome-scale data was thought to solve many of these issues. However, empirical and simulated datasets have shown that phylogenomics deals with an array of its own problems. In this project, we intend to generate phylogenomic data using different next-generation methods and use various approaches to reconstruct dated phylogenies of a highly diversified branch of 'higher flies' – superfamily Oestroidea. Oestroidea include some of the best known and most regularly encountered insects, such as blowflies (Calliphoridae), flesh flies (Sarcophagidae) or bot flies (Oestridae) characterized by a wide variety of life history strategies utilized by adults and/or larvae. Many of these species are of applied importance to humans. Despite high morphological and biological diversity, oestroid flies are not particularly old (≈ 50 Myr) according to the fossil record. Recent molecular studies are in agreement that the superfamily Oestroidea is monophyletic, although relationships within the taxon, especially among higher taxonomic groups, are complicated and still unresolved. Two processes, non-biological and biological, are responsible for this problem. First, the analyses have been carried out exclusively using Sanger-generated data. Second, the evolution of this group is characterized by episodic ancient rapid radiations indicated by short internal branches which affect phylogenetic methods by the generation of artefacts. Solving this issue requires a large amount of data and various methods. In this project, we plan to approach the problem of the phylogeny of Oestroidea by three steps: (1) generation of four types of phylogenomic data, (2) using two alternative methods to analyse these data (concatenation and coalescence) and (3) dating of highly supported and congruent trees using fossil data. As a final result we expect to obtain the best possible reconstruction of the tree of life of the higher flies representing the superfamily Oestroidea.