

Impact of transposable elements dynamics on inter and intraspecific evolution of structural genomic variation in amphibians.

The evolutionary success of any species is strictly related to its genome composition and functionality. Transposable elements (TEs) represent a considerable fraction of the nuclear DNA content and, given their ability to spread throughout the genome, they are responsible for structural variations at gene, chromosomal and genomic level. Vertebrates represent a highly successful taxon and its lineages are characterized by a variable TEs content suggesting different impacts on their genome. Amphibians represent a transition step in tetrapods' evolution and, because of their largest genome sizes among terrestrial vertebrates, offer unique opportunities to explore vertebrate genome evolution and function. Novel bioinformatics tools and affordable next-generation sequencing techniques now allow whole genome and transcriptome sequencing for multiple specimens of the same species.

The PhD project, in collaboration with the University of Ferrara and the Tuscia University, is based on a *de novo* reference genome assembly for *Bombina pachypus* and on genomic data from two different populations. The main aims of the project are: *i*) the characterization of TEs in the genome of *B. pachypus*, *ii*) the identification of active TEs using transcriptomic data from different tissues, *iii*) the comparison between data obtained from *B. pachypus* and data available for different amphibians' species, *iv*) the investigation of TEs dynamics in populations of different effective size, *v*) the analysis of the relationship between the dynamics of TEs, as due to different effective population size, and of the structural genomic polymorphism.