In sexually reproducing organisms, including humans, genetic recombination during meiosis leads to reshuffling of the already existing gene combinations so that new combinations can be passed on from the parents to the offspring. This is why every human being is genetically unique. Can we imagine a sexually reproducing human population consisting exclusively of genetically identical individuals ? The fact of the matter is that nature sometime plays such tricks. There is an unusual group of plants which form sexual reproductive cells, but as a result of fertilization, the whole progeny are clones. These plants have suffered complex chromosomal rearrangements in the past, as a result of which nowadays they lack recombination and form rings during meiotic division. They are called „permanent translocation heterozygotes". Evening primrose (Oenothera) and a spiderwort named Tradescantia spathacea are the most known examples of this plant group.

Complex chromosomal rearrangements and the chromosomal framework conditioning the lack of recombination are of prime interest for biology. Resolving them in such plants like Oenothera could learn us how to create sexually reproducing clones ! Such a possibility is especially important for agriculture. When breeders cross two varieties to obtain a hybrid with the desired combination of genes from both parents, they want this combination to be permanent and transmitted into next generations. But this is merely possible if recombination is at work.

This is why we are going to start our research on such plants. To find out how to become a permanent translocation heterozygote, we are going to reveal chromosomal structural properties in Oenohera and our T. spathacea. To achieve that, the chromosomal arrangement and structure of repetitive DNA sequences, including mobile elements, will be studied. The fluorescence in situ hybridization, molecular and bioinformatic techniques will be applied as basic tools. To elucidate the epigenetic status of chromatin chromatin modifications will be mapped using immunodetection with anybodies against histone and DNA modifications (methylation, acetylation).