Correct genomes of diploid organisms are formed by pairs of chromosomes. One chromosome of every pair comes from a mother and the other from a father and the whole set is expected to persist in every cell of a multicellular organism. Cells, and whole organisms, function correctly when genomes contain full sets of chromosome pairs but they usually malfunction when some chromosomes are single or more than double, which is called aneuploidy. Not only the change in number of entire chromosomes but also deletions, amplifications or translocations of fragments of chromosomes can be deleterious to fitness (health) of organisms. However, when environment is new to an organism (such as the body of an AIDS patient for the budding yeast) then some of genome rearrangements may turn out to be actually advantageous. Most importantly, destabilized genomes are typical for cancer cells

Destabilization of a genome can be caused by external factors, especially those damaging DNA and thus provoking its repair which not always restores original content and archtecture of a genome. There causes of genome destabilization can be also intrinsic if genes coding for proteins taking care of replication and segregation are mutated and thus malfunctioning. There are several hundred of such genes. It is not easy to identify them. Most of cell divisions are successful in producing two correctly replicated genomes and therefore any search for new aberrant genomes must involve large numbers of organisms. The most useful models are eukaryotic microorganisms, such as yeast. Researchers look for such phenotypic changes that specifically signal chromosomal mutations. Former studies were limited in this way that only single phenotypic changes, and thus single chromosomal changes, were scored. It is well possible, however, that destabilizations involve more than one chromosome at a single event. Multiple changes are potentially most dangerous. The proposed research will identify which genes, when mutated, tend to increase the rate of such complex chromosomal rearrangements. We will simultaneously test for at least two phenotypic markers residing on two different chromosomes. We will then verifyt whether the visible two phenotypic rearrangements are indeed a good signal of alterations on the level of chromosomes.

Identification of genes which are required to suppress the danger of complex chromosomal rearrangements could be important from practical reasons. It has been recently established that some cancers are not only associated with chromosomal rearrangements but that a single but complex rearrangement have helped them to cross critical barriers in their development. In this way, cancer cells get adapted to proliferate more effectively and/or to avoid killing by the immune system. Research applying a model organism will help to understand the origin and course of this dangerous phenomenon.