Studying the properties of the genetic networks of eukaryotes, including the understanding of so-called 'functional modules' - a group of genes involved in the same biological process (e.g. transport, signaling, etc.), as well as revealing their new elements and understanding their impact on cellular processes and their regulation - is one of the key challenge of evolutionary biology. Much of the information on this subject was obtained from studies carried out in yeast *Saccharomyces cerevisiae*, which is the best genetically characterized model eukaryotic microorganism.

Broadening the knowledge about the genetic interaction network in yeast is of importance, because similar networks and dependencies are expected to exist also in human genome, in which the basic network properties are largely unknown. Thus, the characterization of genetic modules and examining their fate during evolution in yeast model is fundamental for studying genetic interactions in more complex systems.

The proposed project aims to test the stability of functional modules in the yeast genome and to verify the hypothesis that in *S. cerevisiae*, inactivation of one gene (in case of my studies *NUP133* and *COG7*) will lead in the population to evolutionary dominance of clones in which mutations that inactivate other genes associated with a given functional module (so called 'compensatory mutations') subsequently appeared. The project involves transcriptomic analyses of selected single mutant strains after experimental evolution in long-term continuous cultures. These analyses will enable more detailed characteristics of functional modules evolution.

To carry out the research, microarray technique - one of the most commonly used methods for characterizing changes in the gene expression profile will be used. In addition to large-scale identification of transcriptomic changes in yeast cells, selected genes will be subjected to in-depth studies using quantitative real-time PCR (qRT-PCR).

The project implementation will contribute to the enrichment of knowledge concerning functional modules and may reveal new, not yet known to science cellular processes and mechanisms as well as might indicate the existence of new, non-obvious metabolic pathways.

Study of mutation accumulation in *S. cerevisiae* will complement our knowledge about the evolution of entire genomes and may contribute to setting up a method for predicting the nature of genetic changes related to human diseases, which is extremely important from medical point of view.