# Investigation of the mechanism of adaptation to mutations in the translation termination factor genes in yeast

P-01.1-37

**E. Maksiutenko**[I,II], S. Moskalenko[I,II], M. Lenyashina[II], Y. Barbitoff[II], A. Matveenko[II], G. Zhouravleva[II]

[I]St. Petersburg Branch, Vavilov Institute of General Genetics of the Russian Academy of Sciences, St. Petersburg, Russia, Saint-Petersburg, Russia, [II]Dpt. of Genetics and Biotechnology, St. Petersburg State University, St. Petersburg, Russia, Saint-Petersburg, Russia

In the yeast *Saccharomyces cerevisiae*, there are two translation termination factors eRF1 and eRF3. These factors are encoded by the *SUP35* and *SUP45* genes and deletion of any of them leads to the death of yeast cells. However, viable strains with nonsense mutations in both the *SUP35* (Chabelskaya et al., (2004) Mol. Genet. Genomics 272, 297-307) and *SUP45* genes (Moskalenko et al., (2003) BMC molecular biology, 4, 2) were previously obtained in our laboratory. To invesigate the genetic factors supporting the viability of these *SUP35* and *SUP45* nonsense mutants, we performed whole genome sequencing of strains carrying mutant alleles *sup45-n* and *sup35-n* using Illumina technology. While no common SNPs or indels were found in these genomes, we discovered a systematic increase in the copy number of the plasmids carrying mutant *sup35-n* and *sup45-n* alleles. To validate these findings, we used qPCR method which confirmed the differences in the relative number of *SUP35* and *SUP45* gene copies between strains carrying wild-type or mutant alleles of *SUP35* and *SUP45* genes. Moreover, we used qPCR to compare the number of copies of the *SUP45* and *SUP35* genes in strains carrying different nonsense mutant variants of these genes in chromosomal location. qPCR results indicate that the number of mutant gene copies (in particular, *sup35-218*, *sup35-222*, *sup45-104*, *sup45-105*, *sup45-107*) is increased compared to the wild-type control, possibly due to tandem duplications or other chromosomal abnormalities. The results obtained support the hypothesis that an increase in the copy number of a mutant gene may be a universal mechanism of yeast adaptation to mutations of essential genes encoding translation termination factors. This work was supported by the RSF grant “Genetic and Epigenetic Control of Translation Termination” 18-14-00050. Equipment of the Resource Centers “Development of Molecular and Cellular Technologies” and “Biobank” of SPBU was used in this study.