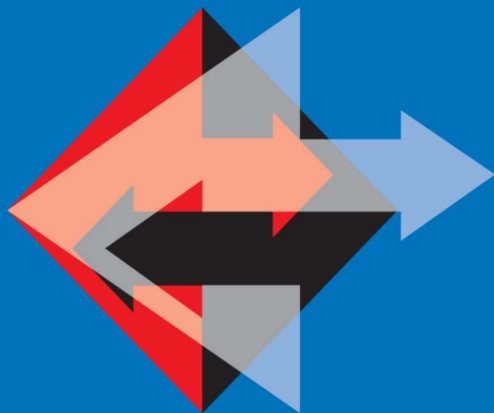


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**Second International Conference
“Genetically modified organisms:
The History, Achievements, Social
and Environmental Risks”**

Saint Petersburg, Russia. December 6–8, 2022



**Saint Petersburg
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Second International Conference “Genetically modified organisms. The history, achievements, social and environmental risks”

Second international conference “GMO: history, achievements, social and environmental risks” was held on December 6–8, 2022 in Saint Petersburg State University, Saint Petersburg, Russia in mixed format (full-time and remote participation).

The conference was attended by scientists from Russia (from Saint Petersburg to Vladivostok), China, USA, Germany. They discussed the history of the development and application of genetic engineering methods, promotion of their results in society. Of great interest was the section devoted to the application of genetic engineering methods in fundamental science aimed to study the plant growth and development. A number of reports aimed to study the fundamental problems of biology and medicine using genetically modified microorganisms and animals. Many reports reflected practical results that are of interest for agriculture and medicine. The whole section was devoted to environmental research related to genetic engineering, in particular biodiversity of “agrobacteria” and natural GMOs that arose without human intervention. Discussion of society’s attitude towards GMOs concluded the conference, where the importance of training specialists in interdisciplinary areas, as well as closer interaction between biologists and lawyers for improving legislation in the field of GMOs was noted.

The conference was held with support of the Ministry of Science and Higher Education of the Russian Federation in accordance with agreement No. 075-15-2022-322 date 22.04.2022 on providing a grant in the form of subsidies from the Federal budget of Russian Federation. The grant was provided for state support for the creation and development of a World-class Scientific Center “Agrotechnologies for the Future”.

Prof. Tatiana V. Matveeva

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Genetically modified yeasts in studies of human amyloidosis

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Amyloid protein aggregation is a key factor in the development of a variety of serious diseases in humans, commonly named as amyloidoses (Alzheimer's and Parkinson's diseases, type II diabetes, etc.), and a determinant of protein-based inheritance in lower eukaryotes. In yeast, translation termination factor Sup35 is one of the most extensively studied amyloidogenic proteins. Aggregation of Sup35 (induction of $[PSI^+]$ prion) decreases its functional activity and leads to the suppression of nonsense-mutation as stop-codons become recognized as meaningful more frequently. This phenomenon is the basis of phenotypic detection of Sup35 aggregation in yeast strains possessing nonsense mutation *ade1-14* in *ADE1* gene.

Yeast is convenient model for genetic, biochemical and molecular biology studies. Yeast genome can be easily edited and plasmids can be used for induction of gene expression. Yeast is suitable for analysis of mammalian genes and proteins and thus can be applied for the analysis of amyloidogenic properties of proteins associated with human diseases. Phenotyping detection of $[PSI^+]$ prion can be modified for the analysis of amyloid aggregation of mammalian proteins in yeast.

We use genetically modified yeasts *Saccharomyces cerevisiae* adopted for amyloid biology research. The mutations leading to auxotrophy toward certain amino acids (leucine, lysine, tryptophane, histidine) and nucleobases (adenine, uracil) were implemented into yeast genome allowing phenotyping detection of $[PSI^+]$ and the usage of plasmids for the investigation of mammalian protein in yeast.

Application of yeast-based experimental system for studies of different aspects of human amyloidoses is discussed.

This study was supported by Saint Petersburg State University (project 93025998).

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