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СБОРНИК ТЕЗИСОВ

BOOK OF ABSTRACTS

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«VII СЪЕЗД ВАВИЛОВСКОГО ОБЩЕСТВА ГЕНЕТИКОВ И СЕЛЕКЦИОНЕРОВ, ПОСВЯЩЕННЫЙ 100-ЛЕТИЮ КАФЕДРЫ ГЕНЕТИКИ СПБГУ, И АССОЦИИРОВАННЫЕ СИМПОЗИУМЫ»
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AND ASSOCIATE SYMPOSIUMS OF VAVILOV SOCIETY OF GENETICISTS AND BREEDERS ON THE 100TH ANNIVERSARY OF THE DEPARTMENT OF GENETICS OF SAINT PETERSBURG STATE UNIVERSITY
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NEXT GENERATION WHOLE GENOME SEQUENCING OF *SACCHAROMYCES CEREVISIAE* STRAINS OF THE PETERHOF GENETIC COLLECTION

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Baker's yeast *Saccharomyces cerevisiae* is a well-known eukaryotic model organism. Most of the common laboratory yeast strains ascend to the so-called "Berkeley yeast", specifically, the reference strain S288C. Since half a century ago, the Peterhof genetic collection (PGC) of *S. cerevisia*e provides a unique example of a large genetic collection established independently. First PGC strains ascend to a distillery lineage ("race XII"), which is unrelated to the Berkeley yeast. For many years, studies of translation, prion biology, and other fields have benefited from PGC, and several laboratory strains are now widely used throughout the world.

A tremendous progress has been achieved in recent years in next-generation sequencing (NGS) with hundreds of yeast genomes already sequenced and analysed. These genomes show extensive diversity, especially within wild or industrial strains unrelated to S288C. To place the PGC into known interrelations of yeast lineages we attempted whole genome sequencing of several strains using Ion Torrent NGS technology. The closest strain to the PGC progenitor, 15V-P4, was shown to differ greatly from other laboratory stocks and is more similar to the two bakery strains, YS9 and RedStar. The genomes of several other PGC strains have also been analysed. Strain 25-25-2V-P3982, thought to be of pure PGC origin, was shown to descend partially from Berkeley yeast. Coverage estimation in two clones of this strain suggested chromosome II disomy to be responsible for the Isp^{-}/Isp^{+} phenotype. Known descendants of both PGC and S288C-derived strains, 74-D694, 6P-33G-D373, 1B-D1606, and 222-1B-D1606, were also analysed. This allowed the identification of genomic variations that caused several phenotypic traits in these strains, e.g., clumping phenotype, phenylalanine auxotrophy, nonsense suppression caused by defective *SUP35* transcription, etc.

Despite the progress achieved, the obtained assemblies of the PGC genomes were incomplete and required substantial improvement. So we attempted genome sequencing of one PGC strain, 1A-D1628, using Oxford Nanopore MinION sequencing. Using the obtained reads we made a draft assembly that indeed comprises all yeast chromosomes and mtDNA. Further improvement of this assembly would provide a high quality reference for comparative genomic studies.

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