

The low level of variability is depicted in plastomes of early soybean varieties

Aleksandrovich V.*, Siniauskaya M., Liaudanski A., Mishuk Y., Shatarnova T., Danilenko N., Davydenko O.

Institute of Genetics and Cytology, National Academy of Sciences of Belarus, Minsk, Belarus

* *valeria.alexandrovich@gmail.com*

Key words: soybean, genetic diversity, plastid genomes, next-generation sequencing

Motivation and Aim: The chloroplast genome of land plants is usually conservative in structure, but variable in sequence. Today the information about the complete plastidial sequences is growing fast. Phylogenetical comparative studies between taxons based on organellar DNA became deeper and more complicated. Intraspecies diversity of organellar DNA became apparent and possibly play an important role in successful breeding and creation of the new varieties in plants. Here we report about the sequencing of complete plastomes of 24 early-maturing soybean (*Glycine max* (L.) Merr.) cultivars. The aim of our study was to evaluate the level of chloroplast genomes diversity in specific group of *Glycine max* varieties.

Methods and Algorithms: DNA was obtained from the 7-day-old seedlings by phenol-chlorophorm extraction from the chloroplast fraction, isolated by differential centrifugation. The chloroplast DNA was then sequenced on Illumina MiSeq using Illumina DNA Prep library preparation kit and MiSeq Reagent Kit v3 (600-cycle). The NGS data processing algorithm included reads alignment on reference *G. max* plastid sequence (NC007942.1) using Burrows-Wheeler Alignment Tool followed by converting to .bam format and sorting with Samtools. Variant calling was performed with GATK HaplotypeCaller followed by filtering with Bcftools.

Results: Analysis of 24 complete soybean chloroplast genome sequences demonstrated the drastically low level of genetic diversity in studied varieties of *Glycine max*. Only 3 INDELs and 6 SNP were revealed between samples under investigation. 4 SNPs were located in coding sequences of *atpB*, *rps4*, *accD* and *rps3* genes. All of them were synonymic. The studied chloroplast genomes can be subdivided into at least 3 subtypes based on found polymorphisms, possibly linked with origin of maternal form. There can be revealed more distinct subtypes of chloroplast DNA, as we are planning to investigate other cultivars from our collection. Mitochondrial genomes of the same 24 soybean cultivars now are also under investigation.

Conclusion: Here we report about low level of variability in chloroplast DNA of *Glycine max*. Possibly it is the result of the founder effect – evidently a narrow range of ancestors was used when this group of varieties was created. Mitochondrial genomes of the same 24 soybean cultivars now are under investigation.

Acknowledgements: The study was carried out as a part of the State Scientific Research Program «Biotechnologies» 2021–2023, Subprogram 2 «Structural and functional genomics», assignment 2.1.3.