Molecular genetic and bioinformatic approaches for the allele reconstruction of the *rolB/C*-like gene in representatives of the genus *Vaccinium* L.

Roman R. Zhidkin [1], Peter M. Zhurbenko [1, 2],
Elizabeth Yu. Gorodilova [1], Tatiana V. Matveeva [1]

[1] Saint Petersburg State University, Saint Petersburg, Russia;
[2] Komarov Botanical Institute of the Russian Academy of Sciences, Saint Petersburg, Russia

Agrobacterium mediated transformation is one of the most studied examples of horizontal gene transfer between pro- and eukaryotes. During this process a part of the Ti-plasmid — T-DNA — is transferred into the plant cell genome. These sequences could be preserved in the genomes during evolution and inherited in a series of sexual generations. Such plants are described within the genus *Vaccinium* L. [1]. Our research team is currently analyzing natural transgenes in *V. oxycoccos* L., *V. japonicum* Miq., *V. conchophyllum* Rehder, *V. emarginatum* Hayata, *V. myrtilloides* Michx., *V. virgatum* Ait., *V. corymbosum* L., *V. darrowii* Camp, *V. smallii* A. Gray, *V. praestans* Lamb., *V. ovalifolium* Sm., *V. myrtillus* L., *V. uliginosum* L., *V. vitis-idaea* L.

Previously, analyzing the natural transgenes in another genus (*Camellia* L.) [2], we showed the importance of reconstructing the allelic states of transgenes for phylogenetic studies.

In this paper, we present a comprehensive approach for studying the allelic state of the *rolB/C*-like gene in plants of the genus *Vaccinium*. It combines molecular genetic and bioinformatic research methods.

Molecular genetic methods involve Sanger sequencing of a gene sequence in a large number of samples, while for each sample the sequence is presented as a set of polymorphic positions in binary form. Allele resolution occurs based on the description of alleles in homozygotes and a series of "subtractions" of known alleles in heterozygous samples. The second method involves the analysis of SRA (Sequence Read Archive) sequences available in the databases. SRA is a repository of high-throughput sequencing raw data.

Based on our work, we can conclude that both of these approaches make it possible to describe the allelic state of the *rolB/C*-like gene in representatives of the genus *Vaccinium*.

Keywords: naturally transgenic plants; *Vaccinium*; *rolB/C*-like gene.

Second International Conference
Genetically modified organism. The History, Achievements, Social and Environmental Risks

37

REFERENCES

1. Matveeva TV. New naturally transgenic plants: 2020 update. *Biol Commun*. 2021;66(1): 36–46. DOI: 10.21638/spbu03.2021.105

2. Zhurbenko P, Klimenko F. Phase All: a simple tool for read-based allele phasing. *Ecological Genetics*. 2022;(In Press). (In Russ.)

AUTHORS' INFO

Roman R. Zhidkin, Graduate Student. Saint Petersburg State University, Saint Petersburg, Russia. E-mail: st085586@student.spbu.ru

Peter M. Zhurbenko, Researcher, Laboratory of Biosystematics and Cytology, Komarov Botanical Institute of the Russian Academy of Sciences, Saint Petersburg, Russia; Junior Researcher, Department of Genetics and Biotechnology. Saint Petersburg State University, Saint Petersburg, Russia. E-mail: pj_28@mail.ru

Elizabeth Yu. Gorodilova, Sequencing Specialist, Resource Center of Saint Petersburg State University "Development of Molecular and Cellular Technologies". Saint Petersburg State University, Saint Petersburg, Russia. E-mail: elizaveta.gorodilova@spbu.ru

Tatiana V. Matveeva, Dr. Sci. (Biol.), Professor. Saint Petersburg State University, Saint Petersburg, Russia. SPIN: 3877-6598; e-mail: radishlet@gmail.com