

Distribution of the *rolB/C*-like natural transgene in representatives of the genus *Vaccinium* L.



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Genetic colonization by agrobacteria is possible due to agrobacterial transformation, which implies interspecies transfer of genetic material (T-DNA). A transgenic tissue is formed on the whole non-transgenic plant during that process. However, it turned out that in nature there are plants containing T-DNA fragments in their genomes and they can inherit these T-DNAs sexually. Such T-DNA was called cellular, and such plants were called natural transgenic.

Examples of such organisms are plants of the genus *Vaccinium*. In the genomes of two species of this genus we found cT-DNA, represented by a *rolB/C*-like gene [1].

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 study, we performed analysis of the spreading of the *rolB/C*-like gene for its use as a molecular marker within *Vaccinium*.

We used molecular-genetic and bioinformatics methods for sequencing, assembly, and analysis of the *rolB/C*-like gene. We discovered 26 new *Vaccinium* species and *Agapetes serpens* (Wight) Sleumer as containing the *rolB/C*-like gene. Most of studied samples are characterized by the presence of full-size genes. This made it possible to develop approaches for alleles phasing of the *rolB/C*-like gene and reconstruct a *Vaccinium* phylogenetic relationship.

We subjected the studied species to phylogenetic analysis based on sequences of the *rolB/C*-like gene. The resulting phylogenetic tree of the genus *Vaccinium* divided the species into sections in accordance with the classical genus system based on morphological characters. At the same time, our tree did not confirm the taxa determined on the basis of ITS.

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

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