

Structural analysis of genes affecting the tuber starch content and properties in Russian potato varieties

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The potato *Solanum tuberosum* is the fourth agronomically important crop and starch producer in the world. The large number of genes involved in carbohydrate turnover and starch metabolism described to date. However, the data for allelic combinations of genes associated with increased starch content remain unknown. In this work, we analyzed the nucleotide sequences of 21 genes coding for starch synthases, starch phosphorylases, AGPase, beta-amylase, sucrose synthases, in 7 Russian potato varieties with different starch content (Fritella, Grand, Krasa Meschery, Krasavchik, Krepysh, Kolobok, Severnoe Siyanie). Gene sequences were obtained with *Illumina* platform and MUSCLE multiple alignments performed. The SNP density in the coding regions ranged from 1/22 bp to 1/89 bp, average was 1/43. From them the proportion of nonsynonymous substitution sites ranged from 3 to 58%. The sequence comparison by phylogenetic analysis showed that for 10 genes the candidate variants characteristic to high and low starch content could be identified.

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