

Analysis of the genome structure and its variations in potato cultivars grown in Russia

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Solanum tuberosum L. is one of the most important agricultural crops grown almost all over the world. Potato genomic sequences pave the way for the study of molecular variation associated with diversification. We have assembled the genomic sequences of 15 tetraploid *S. tuberosum* potato varieties growing in Russia. We have identified protein-coding genes, identified orthologous groups, and characterized conserved and variable parts of the pangenome and the repertoire of NBS-LRR genes. We have identified copy number variations in the genomes of Russian varieties and South American varieties, conducted a comparative analysis, and identified genes associated with CNV. We have reconstructed complete assemblies of potato plastomes. Based on these assemblies, single nucleotide polymorphisms, insertions and deletions, microsatellites were identified, and the types of potato chloroplast DNA were determined.

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