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## ГЕНЕТИЧЕСКОЕ РАЗНООБРАЗИЕ Y-ВИРУСА КАРТОФЕЛЯ В БЕЛАРУСИ

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*Изучен состав штаммов Y-вируса картофеля, обнаруженных на территории Беларуси, а также молекулярная вариабельность их геномов. Показано присутствие штаммов PVY<sup>NTN</sup> (генотип А) и PVY<sup>NW</sup> (генотипы А и В). Степень идентичности между отдельными регионами геномов исследованных изолятов колеблется в пределах от 100 до 97,33 %. В последовательностях выявлены нуклеотиды, находящиеся под действием очищающего отбора.*

**Ключевые слова:** Y-вирус картофеля, PVY<sup>NTN</sup>, PVY<sup>NW</sup>, генетическое разнообразие, очищающий отбор.

### GENETIC DIVERSITY OF POTATO VIRUS Y IN BELARUS

The strain composition of PVY from Belarus as well as the molecular variability of their genomes were studied. The presence of the strains PVY<sup>NTN</sup> (genotype A) and PVY<sup>NW</sup> (genotypes A and B) was shown using RT-PCR. The degree of identity between individual genome regions of isolates studied varies from 100 to 97.33 %. Nucleotides that are under purifying selection revealed in sequences. The study of the phylogenetic relationships of viral isolates from Belarus and other countries showed that there was no clear correlation between geographical origin or host plant species and the viral genomes fragments similarity degree. The high similarity of Y-virus genomes fragments obtained from different sources indicates that studied loci are highly conservative, which allows to use the molecular markers for accurate and quick viral infections detection and virus-free plants revealing. The studied fragments Y-virus genomes obtained from different sources were highly similar that indicates the conservatism of these loci. Therefore, molecular markers to these fragments can be

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used to accurately and quickly viral infections detection as well as virus-free plants revealing.

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