

The Pannonian Plant Biotechnology Association (PPBA)

Integration of fundamental research into the practical agriculture

Progress and Perspectives

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Development of Multiplex PCR methods for simultaneous selection of some resistance genes in potato

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Potato (*Solanum tuberosum* L.) is the third most important food crop in the world. Significant damages in the potato production are caused by potato virus Y (PVY), potato virus X (PVX) and cyst nematodes (*Globodera* sp.). Nowadays there are number of economic and environmental protection arguments against traditional, chemical plant protection. The base of modern plant protection is the introduction of new resistant varieties to different abiotic stresses. For this the breeding of new varieties having complex resistance to major pathogens and pests is needed. However this process is difficult and very much time-consuming. For the success combination of conventional breeding methods with modern molecular genetic techniques is desired

Potato Research Centre at Keszthely has a unique resistance breeding program since more than fifty years. As a result of this work, several varieties with complex resistance have been developed for now. Different wild potato species as source of resistance genes were used in the program. Against PVY the extreme resistance gene, Ry_{sto} originating from wild potato species Solanum stoloniferum was applied. To introduce PVX resistance the extreme resistance gene Rx1 of Solanum tuberosum ssp. andigena was introduced into the varieties. This species carries the H1 gene offering resistance against the nematode Globodera rostochiensis as well. The resistance is often associated with undesirable characters. To eliminate them while keeping the advantageous resistance gene combinations during the breeding process is a complex and difficult task. Molecular markers linked to resistance genes of wild species can increase the effectiveness of this process. Markerassisted selection may also be useful where phenotypic selection of resistance genotypes is difficult or complicated (e.g. in case of quarantine nematodes).

During the first step of the present research project PVY, PVX, and nematode resistance genes of 21 potato cultivar with known resistance characters were investigated by molecular markers. For the detection of Rx1 and H1 genes, gene specific markers were used, while for Ry_{sto} gene a newly developed marker very closely linked to the gene was developed and applied.

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In the second step we developed multiplex PCR methods for the identification of resistance genes H1, Rx1 and Ry_{sto} in different combinations. Our results can decrease both the cost and time necessary for the detection of resistance genes during the breeding process.

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