Streszczenie rozprawy doktorskiej w języku angielskim

Summary

Evaluation of genetic resources of the genus *Nicotiana* for the resistance to major viral diseases of tobacco

Key words: *Nicotiana*, tobacco, *Tobacco mosaic virus*, *Tomato spotted wild virus*, *Potato virus Y*, resistance to viral diseases

The genus *Nicotiana* is one of the more numerous in the Solanaceae family. It contains more than 80 species highly diverse in morphological characteristics, chromosome number and geographic distribution, as well as differing in alkaloid composition and disease and pest resistance. The natural place of origin of wild tobacco species is North and South America, Australia and Pacific Islands, and Africa. The most well-known and widespread species of the genus *Nicotiana* is tobacco (*Nicotiana tabacum*). It was created by spontaneous crossbreeding between *Nicotiana sylvestris* and *Nicotiana tomentosiformis*. It includes many cultivars today and is one of important industrial plants in Poland and worldwide.

The collection of the genus *Nicotiana* gathered at the Institute of Soil Science and Plant Cultivation - State Research Institute currently includes 1008 objects, within which there are both wild *Nicotiana* species, as well as *Nicotiana tabacum and Nicotiana rustica* cultivars. The enormous diversity within the *Nicotiana* genus makes it an excellent source of variation in a narrowing gene pool and can be used in breeding programs, especially for resistance breeding. This is why detailed knowledge of the resistance of collection materials to the most economically important pathogens is so essential.

Among the diseases causing losses in tobacco cultivation, viral ones are of particular importance due to the very low effectiveness of chemical protection which only reduces the incidence of the vector. The greatest threat to tobacco cultivation in Poland and in many countries of the world are *Potato virus Y* (PVY), *Tomato spotted wilt virus* (TSWV) and *Tobacco mosaic virus* (TMV) which appears more and more frequently in recent years.

The aim of the dissertation was to evaluate the gene pool of the genus *Nicotiana* for resistance to major viral diseases. Resistance studies included observation of disease symptoms resulting from inoculation, determination of the presence of the virus in infected

plants based on serology and the evaluation of genotypes in terms of resistance to specific pathogens using specific molecular markers.

A study of the genetic resources of the genus *Nicotiana* in terms of resistance to the most important viral pathogens of tobacco showed its great diversity in biological, serological as well as molecular evaluation.

Tests for resistance to *Potato virus Y* showed that within the genus *Nicotiana*, four species: N. africana, N. raimondii, N. knightiana and N. glauca, were characterized by complete resistance, and 26 species showed symptoms of tolerance to all PVY isolates tested. The others were characterized by varying resistance depending on the isolate used. Molecular studies showed that within 25 tobacco cultivars, the Va susceptibility gene was found in 9, while the remaining 16 did not amplify these markers. The lack of amplification products indicated that these cultivars had a deletion within the susceptibility gene (va-type resistance). Cultivars with va-type resistance showed varying level of response to PVY infection, which may indicate different length of deletion in the susceptibility gene. The highest resistance was in cv. VAM. Five cultivars showed tolerance to all tested PVY isolates. They did not develop necrosis, only vein clearing and chlorotic spots. Molecular studies showed that they had the Va susceptibility gene which may indicate a different genetic basis for their tolerance. Cultivar Wegierski Ogrodowy, despite the presence of the Va gene, was not affected by the isolate considered as weak. Moreover, this cultivar reacted only with tolerance symptoms after inoculation with the medium isolate while strong ones caused vein necrosis. This allows us to conclude that cv. Wegierski Ogrodowy has a different type of resistance than the other tested cultivars.

Tests for resistance to *Tomato spotted wilt virus* indicated that in the species *N. alata* and *N. forgetiana*, the hybrid *Nicotiana* x *sanderae* and two tobacco cultivars (Polalta and Wiktoria) the resistance of the hypersensitive type is present. The resistance of *N. alata* accessions was varied, as within the several tested populations, some plants became systemically infected. The response to TSWV inoculation of the remaining collection accessions was also varied. Tolerant symptoms were observed in case of 9 wild species while 71 species showed much stronger disease symptoms. The resistance tests of a relatively recently discovered species *Nicotiana mutabilis* indicated that it was tolerant to PVY and showed a hypersensitive response to TSWV. It is worth noting that the results concerning the resistance of this species has been presented for the first time.

The resistance tests against *Tobacco mosaic virus* were conducted under varying temperature conditions and as a result four types of plant reactions were reported. The most common reaction was susceptibility which consisted mainly of the appearance of mosaic

discoloration on the leaves. The second type of reaction was tolerance characterized by the absence of visible symptoms at 22/20°C (day/night) while the virus was present in a plant whereas mosaic symptoms were visible at 30/28°C. The third group of tested *Nicotiana tabacum* cultivars had resistance conditioned by the *N* gene originated from *N. glutinosa*. They developed hypersensitivity symptoms regardless of what the temperature was. It has been shown that in the genus *Nicotiana*, an alternative source of TMV resistance is the species *N. gossei* which exhibits a hypersensitive response and does not amplify the *N* gene. The resistance of this species is independent of temperature.

The presented studies have shown great variation within the genus *Nicotiana* for resistance to viral pathogens. Collection accessions resistant to individual viruses are a valuable sources of genes for resistance breeding and may be the objects of further research.

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