SUMMARY

Determination of *Plasmodiophora brassicae* pathotypes in Poland and characterization of Brassicaceae resistance to clubroot

Clubroot caused by *Plasmodiophra brassicae* Wor. is one of the most devastating soilborne diseases of Brassicaceae vegetables and agricultural crops worldwide. The aim of the study was to determine the pathotypes of *P. brassicae* obtained from winter oilseed rape grown in different regions of Poland and to find the sources of resistance to clubroot in the *Brassica* and *Raphanus* genera, available from worldwide genebank collections. Moreover, healthy and *P. brassicae* contaminated soil samples were compared in respect to soil enzymes, resulting from the activity of their specific soil microbiomes.

The pathotyping study was done for 10 isolates originating from different regions of Poland and collected in 2016-2020. Four systems used worldwide, including Somé, Williams, Buczacki (European Clubroot Differentials, ECD) and Strelkov (Canadian Clubroot Differentials, CCD) were applied. The CCD differential set was used for the first time outside Canada. The study used 25% and 50% thresholds of the index of disease (ID) to distinguish susceptible vs. resistant reactions. For ID 25%, there were **3** pathotypes identified using the system elaborated by Somé, **6** based on the system of Williams, **10** when using the ECD set, and **2** with the existing CCD designations. However, based on a threshold of ID 50%, there were **5** distinct pathotypes identified based on the differentials of Somé, **7** based on the system of Williams, **10** with the ECD set, and **8** different pathotypes classified with the CCD designations (found for the first time worldwide). It has been concluded that the threshold greatly modifies the result of the pathotyping study.

The screening for resistance against P1A and P3A, the most common pathotypes of *P. brassicae* in Poland, concerned 222 *Brassica* accessions (mainly *B. oleracea*) and 307 accessions of *Raphanus sativus* from the Centre for Genetic Resources (CGN), the Netherlands. The average ratio between the resistance categories (Resistant: Intermediately Resistant: Intermediately Susceptible: Susceptible) greatly differed between the studied genera and it was **0.7 : 3.7 : 6.4 : <u>89.2</u>** for *Brassica* compared to <u>**91.6**</u> **: 6.4 : 1.2 : 0.8** for *R. sativus*. The resistance to *P. brassicae* was pathotype specific. Sources of resistance to clubroot were rare in the genus of *Brassica* but common in *Raphanus*. CGN11053 (*B. oleracea* Savoy cabbage cv. Vertus-Verius) was the only accession resistant to P1A among *Brassica* studied. Three accessions of *B. oleracea* were intermediately resistant to P3A, including CGN15207 (kohlrabi), CGN11025 (Brussels sprouts, cv. Roem van Barendrecht-sel.Groeneboom Group 1) and CGN15229 (white cabbage, cv. Bindsachsener).

The study of soil enzymes revealed high activity of dehydrogenase and alkaline phosphatase in healthy soils and high activity of urease and acid phosphatase in samples contaminated by *P. brassicae*, with no activity of proteases in any of these soils. The differences between the activity of soil enzymes were statistically significant and evident based on Principal Component Analysis.

The complex pathotype composition of *P. brassicae* populations in Poland and infrequent sources of resistance to the common pathotypes suggest that clubroot disease needs a lot of attention to be controlled properly.