

Potato is the fourth, after wheat, maize and rice, most important human food crop. The significance of potato cultivation in preventing hunger and malnutrition has led the United Nations to award it a special rank. The potato virus Y (PVY) together with *Phytophthora infestans*, a microorganism that causes late blight, are the two main pathogens responsible for great losses in potato yield (that reach as much as 10 to 80% depending on the year and cultivar) both in Poland and other countries around the world. Since PVY is transmitted through tubers, obtaining tuber seeds free from PVY is one of the most important challenges of modern agriculture.

In this project, we will attempt to isolate genes conferring extreme resistance (ER) from the genomes of various potato cultivars. The ER phenomenon occurs within the cells adjacent to the infection site and manifests itself in the complete inhibition of PVY multiplication. In order to find the genes responsible for ER, we will use the most advanced plant gene isolation techniques such as: RenSeq (Resistance gene enrichment sequencing) or the third-generation long read PacBio SMRT (Pacific Biosciences Single-Molecule Real Time sequencing) sequencing. Comparison of the sequences obtained will allow to pinpoint conserved amino acids that can possibly play an important role during the resistance response. To confirm participation of the isolated genes in ER response, we will generate mutants, using the CRISPR-Cas9 technique, that are unable to synthesize a functional protein or encoding its variants. To investigate the proteins' subcellular localization we will use confocal microscopy imaging techniques.

The results obtained will contribute to a more comprehensive understanding of molecular bases underlying potato resistance to PVY