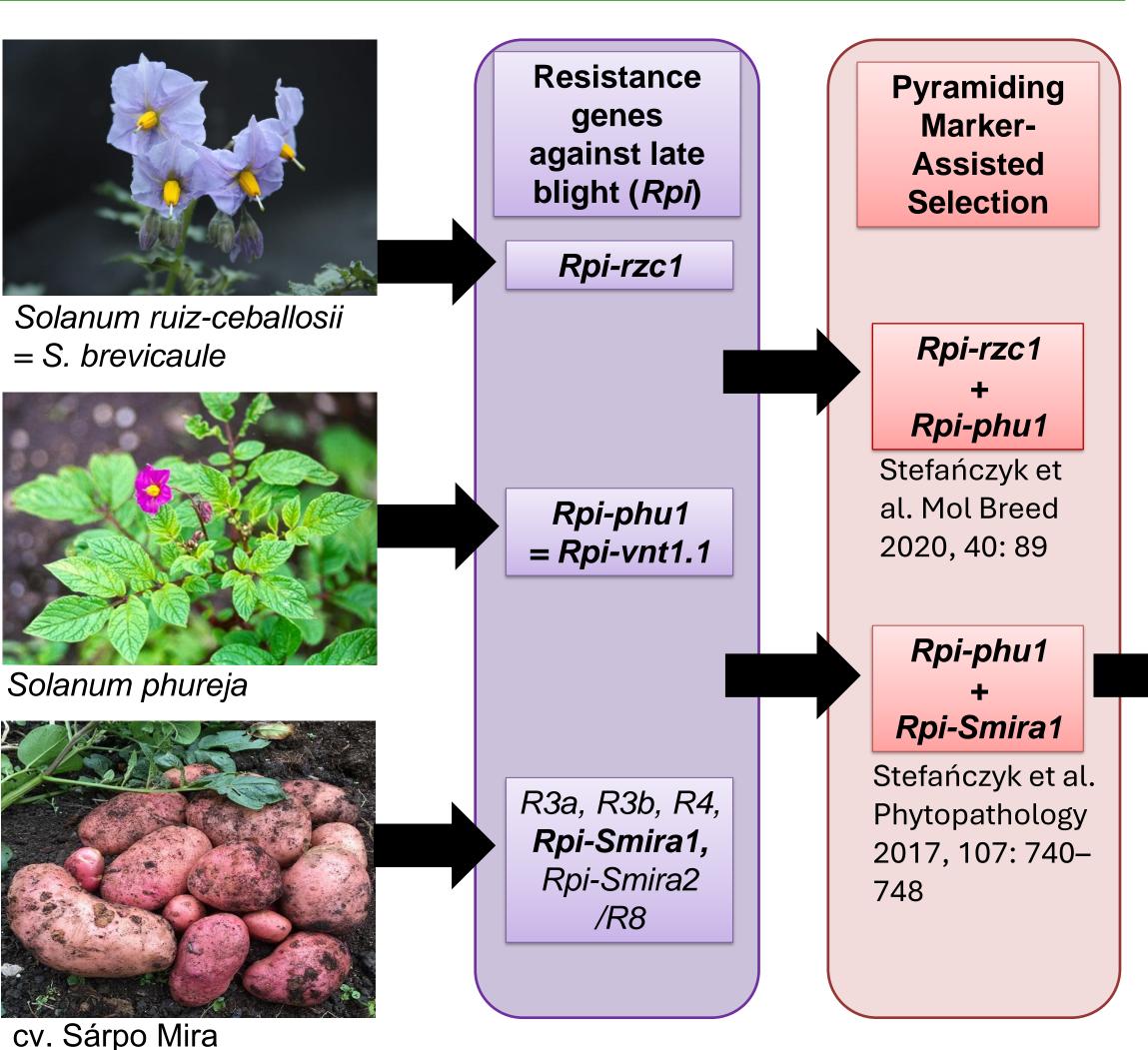
Late blight resistant potatoes – a sustainable solution for disease control



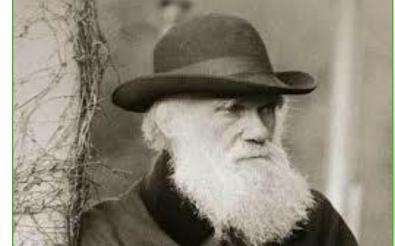
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Late blight, caused by *Phytophthora infestans*, is a highly destructive disease threatening potato and tomato cultivation worldwide. Annual global cost of crop losses and chemical control of late blight is estimated to exceed € 9 billion. A sustainable, alternative solution for disease control is growing late blight resistant cultivars.





Great Irish Famine 1840-1850, caused by potato late blight



Where can we find resistance to *P. infestans*?

In wild potato relatives from South America! (C. Darwin)



Cultivar Gardena 2018, PL, HZ Zamarte IHAR Group Short vegetation period:

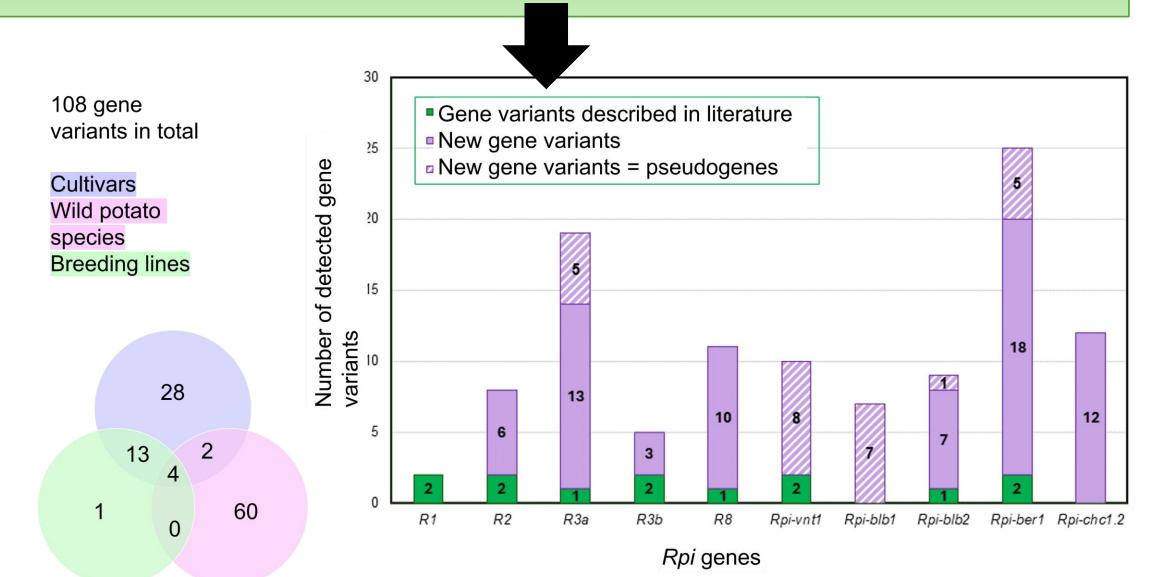
99 days
PCN: Ro1 – resistant
Synchytrium endobioticum:
D1 – resistant

Foliage blight: 8.0 – high Tuber blight: 8.0 – high Potato virus Y (PVY): 7.0 – high

What resistance genes against late blight are there in the existing potato cultivars?

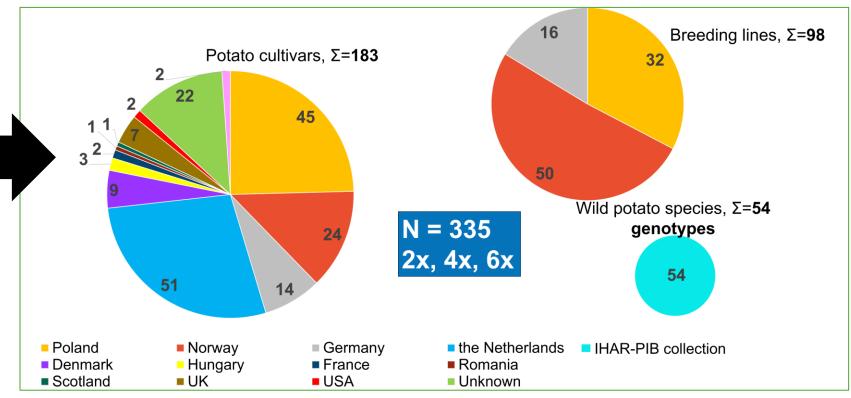
We investigated the presence and diversity of twelve *Rpi* genes in 183 potato cultivars, 98 breeding lines and 54 genotypes of wild potato species using an Amplicon Sequencing (AmpSeq) approach based on PacBio single molecule real time sequencing method.

In 247 potato genotypes, 108 variants of 10 *Rpi* genes were detected (from two to 25 amplicon sequence variants per gene).



Amplicon sequencing of the *Rpi* genes - results

The research leading to these results has received funding from the Norwegian Financial Mechanism 2014-2021, project DivGene: UMO-2019/34/H/NZ9/00559
Research supported by Polish Ministry of Agriculture and Rural Development



Plant material

Summary

- R1, R2-like, Rpi-ABPT, R3a and R3b widespread in cultivars
- Rpi-vnt1 and Rpi-ber1 are in breeding lines
- Wild potatoes a source of new genes and gene variants
- Old:

Klepa: R1, R2-like, R3a-v9, R3a-v13, R3b^{G3111}
Rudawa: Rpi-abpt^{T86}, R3a, R3a-v3, R3b, R3b^{G3111}
And new:

Gardena: R3a, R3b-v1, Rpi-vnt1.1, Rpi-chc1.2-v1 late blight resistant potato cultivars are foundation of sustainable disease control.

• Data on the distribution and sequence diversity of the *Rpi* genes can facilitate new breeding strategies and lead to the discovery of new *Rpi* variants.