

PATHOGEN GENOMICS TO DESIGN DISEASE RESISTANCE MANAGEMENT STRATEGIES

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Genomics and novel breeding techniques have sparked renewed international efforts to design environmentally sustainable crop protection strategies. Host encoded disease resistance is a key component of such strategies, but is prone to be overcome by high adaptation rates from pathogens. It is therefore mandatory to monitor virulence development in pathogen populations. Here we show how pathogen genomics can be deployed to design resistance management strategies for air and soilborne diseases in potato.

Phytophthora infestans and *Synchytrium endobioticum*, the causal agents of late blight and wart disease, respectively, are renowned for their adaptability resulting in complex pathotypes that overcome host resistance. Resistance (R) gene stacking and monitoring virulence in pathogen populations are two key elements for durable R gene management and disease control.

European *P. infestans* populations were monitored during the growing seasons 2006 – 2017. *P. infestans* samples were collected from bait fields in which R gene containing potato clones were grown without fungicide protection. Late blight development during the growth season was recorded and *P. infestans* samples were collected. All samples were genotyped using SSR markers and a selection of the samples were used to isolate *P. infestans* in vitro culture. Subsequently, isolates were characterized for virulence to a range of late blight R genes using a detached leaf bio-assay. Fungicide spraying schedules, adapted towards local pathogen virulence, were applied to varieties with late blight R genes.

This resulted in >70% reduction of fungicide application, but still prevented novel virulence to evolve. *S. endobioticum* is a soil borne pathogen and has quarantine status in Europe. Pathotype specific host resistance is an essential component of quarantine regulations, but pathogen virulence is often hard to determine due to time consuming bio-assays that can have ambiguous outcomes. For more reliable pathotype analyses, we sequenced the genome of this obligate biotrophic fungus. A worldwide collection of *S. endobioticum* isolates identified single nucleotide polymorphisms in the mitochondrial genomes that are highly predictive for pathotype and virulence of the isolate.

It is concluded that pathogen genomics is an increasingly important tool to design disease resistance management strategies, to improve resistance durability, to reduce fungicide input, and to support quarantine regulation.