

General information	
PPS-number	1406-056 / U-TKI-2014-03
Project title	An integrated genomics and effectoromics impulse for potato wart resistance management and breeding
Topsector and innovation theme	T&U, Meer met Minder
Project leader (research institute)	Jack Vossen
PPS-coordinator (on behalf of the private parties involved)	2015: Nick de Vetten; from 2016: Stan Oome
Government contact person	Jan van Vliet
Status (running or completed)	running
Type of research (F, S or A)	Fundamental and Strategic
True starting date	01-04-2015
True end date	01-10-2019
Brief description of project content	<p>Wart disease in potato is caused by the obligate biotrophic fungus <i>Synchytrium endobioticum</i> and is subject to quarantine containment. Unlike other diseases, the deployment of resistant varieties is the only disease management strategy. In this project we will acquire insights in the way polygenic disease resistance against obligate biotrophic pathogens is build up. This knowledge will be used to develop simplified, unambiguous functional and molecular tools for pathogen race typing, essential for resistance based quarantine management. Furthermore, the newly developed tools are essential to tag wart disease <i>R</i> genes in breeding programs, and to identify complementary wart resistance sources in breeding and germplasm material. This combined public private research effort will create a major breakthrough in potato wart disease resistance management and breeding.</p>

Highlights
<p>1. A draft genome sequence of <i>S. endobioticum</i> was available as background to this project. In 2015 the genome assembly was further polished and annotation was performed.</p> <ul style="list-style-type: none"> - A total of 804 contigs constituting a 21.6 Mb genome is predicted in <i>S. endobioticum</i> genome version 1.0. - 8408 genes were predicted which were functionally annotated using the InterProScan database. <p>2. Sequence data of additional <i>S. endobioticum</i> strains (including a pathotype 8 strain from a recent outbreak location) were generated to enable identification of pathotype specific effector candidates.</p> <p>3. SNP markers data in a panel of 170 varieties was available as background to this project. Public wart resistance data was used to perform a GWAS analyses to identify</p>

SNP markers associated with pathotypes 1, 2, 6 and 18 wart disease resistance. A new panel with an extended set of phenotypes has been created including data from various sources (public data, breeders) to perform a new GWAS. Different validation experiments (KASP and CAPS assays) have been planned to validate the promising associated markers in independent populations.

4. Potato populations segregating for resistance were available as background to this project. These populations have different donors of resistance. Preparations were made for QTL mapping and GWAS validation:

- Wart disease resistance tests with selected pathotypes have been performed and a new round of phenotyping tests has been planned for 2016.
- A panel of varieties has been selected to develop dedicated SNP markers for the genotyping of these mapping populations.

5. Two poster presentations were given during international conferences.

Delivered products

- Poster presentation Charlotte: An integrated genomics and effectoromics approach for potato wart disease resistance breeding. Prodhomme C.P.M., Vos P.G., Visser R.G.F., van Eck H.J., Vossen J. H. EUCARPIA Section Potatoes, 18th Joint Meeting. Vico Equense, Italy – November 15th – 18th, 2015.
- Poster presentations Bart: Unravelling potato wart disease; determination of the draft genome of the obligate biotrophic fungus *Synchytrium endobioticum*, B.T.L.H. van de Vossenbergh, M. van Gent-Pelzer, E.G.W.M. Schijlen, S. Warris, H.C. van de Geest, P. Bonants, C.A. Lévesque, J. Cullis, C.T. Lewis, J.T. Chapados, W. McCormick, K. Dadej, Z. Adam, G.J. Bilodeau, M. Gagnon, D.S. Smith, R.F.G. Visser, J.H. Vossen, T.A.J. van der Lee, COST action Sustain Workshop: Evolutionary Genomics of plant pathogens 26 - 28 August 2015, Christian-Albrechts University of Kiel, Kiel, Germany