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MAPPING OF A POTATO WART DISEASE RESISTANCE GENE USING WHOLE GENOME SEQUENCING DATA

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Abstract: Long persistent spores and lack of chemical control make the potato wart disease, caused by the obligate fungus *Synchytrium endobioticum*, an important quarantine disease of cultivated potato (*Solanum tuberosum L.*). The cultivation of varieties resistant to a wider spectrum of pathotypes may be decisive to reduce the propagation of the disease. However, there is a lack of information about where various *R* genes are located and what pathotypes they recognise. The aim of this study was to identify a resistance locus segregating in a F1 tetraploid population. We performed a Bulk Segregant Analysis using Whole Genome Sequencing (WGS) data. A locus giving resistance to the pathotypes 2, 6 and 18 of the disease was identified on chromosome 11. Markers specific to the resistant haplotype were developed and can be used in Marker Assisted Selection (MAS).

Keywords: resistance breeding, potato wart disease, bulk segregant analysis (BSA), whole genome sequencing (WGS)

INTRODUCTION

Synchytrium endobioticum is a soil borne obligate biotrophic fungus responsible for the formation of warts on the tubers of potato (*Solanum tuberosum*). The potato wart disease causes important yield losses and has a worldwide quarantine status. In Europe, more than 30 different pathotypes have been recorded, among which pathotypes 1, 2, 6 and 18 are the most common.

Breeding for resistance to *S. endobioticum* is limited by the poor knowledge of the genomic regions involved in resistance and of the mode of inheritance of the resistance. No genes involved in resistance have been cloned so far. However, one locus (*Sen1*) involved in resistance to *S. endobioticum* has been mapped on the long arm of chromosome 11, in a region containing resistance genes clusters (Jupe *et al.*, 2012). Before 1942, only pathotype 1 was known and breeding programs were successful in creating resistant varieties to it. After 1942, new pathotypes emerged and most of the varieties among the breeding germplasm are susceptible since resistance to pathotype 1 is not effective against these new pathotypes. Genetic studies have been performed using diploid (Brugmans *et al.*, 2006) and tetraploid (Ballvora *et al.*, 2011; Groth *et al.*, 2013; Obidiegwu *et al.*, 2015) populations to identify resistance QTLs. *Sen1* is almost always identified besides several other QTLs either involved in resistance to several pathotypes or involved in pathotype specific resistance. Nevertheless, none of the markers linked to these QTLs have been validated in an independent panel. Identification of pathotype specific resistance genes and development of closely linked markers is essential for breeding resistant potato varieties.

METHODS

In this study, we used a tetraploid F1 population of 330 offspring from the cross between a parent (Pr) resistant to pathotypes 1, 2, 6 and 18 and a susceptible parent (Ps) resistant only to pathotype 1. The resistance to pathotypes 2, 6 and 18 segregates in a bimodal way, suggesting the segregation of one major gene giving resistance to the three pathotypes. In order to identify this gene, we built 2 bulks of 17 resistant (R-bulk) and 17 susceptible (S-bulk) progenies. Whole Genome Sequencing data were produced for the parents and the bulks with a high coverage (from 65 to 86x). A Bulk Segregant Analysis (BSA) was performed using the WGS data.

RESULTS AND DISCUSSION

The BSA highlighted a region on chromosome 11 as containing the resistance gene. To validate the results, we designed KASP markers targeting the resistant haplotype of chromosome 11 and screened a subset of the Pr x Ps population. All the markers designed were highly associated with pathotypes 2, 6 and 18 resistance. The identification of recombinants in the population allowed to fine-map the QTL to a 677 kb region containing several NBS-LRR genes (Jupe *et al.*, 2012).

CONCLUSIONS

Using Whole Genome Sequencing data proved to be a quick and efficient way to identify a locus giving resistance to three complex pathotypes of the potato wart disease. The KASP markers developed using the WGS data of the parents of the population as well as the bulks are haplotype specific and can be used by the potato breeders to screen their populations as well as the potato breeding germplasm for developing new resistant varieties.

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