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A new clubroot resistance for a broadened race-specific resistance in rapeseed

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Background:

The soil-borne plant pathogen *Plasmodiophora brassicae* causes clubroot disease in major rapeseed cropping areas worldwide. Once a field is infested clubroot resistant varieties are the most effective if not the only option to continue rapeseed production. *P. brassicae* exists with diverse pathotypes and plant resistance is generally race-specific. Thus, effective and versatile resistance traits are needed in rapeseed breeding to cope with diversity and dynamics of *P. brassicae* in the field.

Objective:

The aim of the presented work was to generate a *Brassica napus* line with resistance to *P. brassicae* pathotypes that are virulent on plants carrying known resistance QTLs inherited from chromosomes A03 and A08 of *Brassica rapa*. These pathotypes also infect the MENDEL-resistance which has been widely used in rapeseed breeding and production of a resistant *B. napus* line would broaden race-specific resistance.

Methods:

A recipient *B. napus* line BN-1750 harbouring race-specific resistance from *B. rapa* chromosomes A03 and A08 has been crossed to a *B. rapa* line Br-14 resistant to two *P. brassicae* isolates (Pb-0, Pb-1) able to infect the *B. napus* line BN-1750. Introgression of *B. rapa* resistance into the *B. napus* genome and its dominance was inferred from segregation ratio of resistant and susceptible F2-plants using a greenhouse biotest. Mapping and identification of the introgressed new resistance in the *B. napus* genome was carried out using DNA-array and phenotypes of an F2-population and sequencing of bulk segregant pools of resistant and susceptible BC2F3 individuals, respectively.

Results:

Crosses between oilseed rape Bn-1750 carrying partial clubroot resistance and the resistance donor line Br-14 produced F1 seeds. These seeds and further back-cross generations were either infected with Pb-0 or Pb-1 both virulent on Bn-1750. We identified resistant F1-Plants and screened respective F2-populations for resistance. Two populations showed a segregation ratio of 3:1 between resistant and susceptible individuals matching the expectation of an introgressed single dominant resistance locus. Genotypic data from Illumina DNA-array analysis were combined with biotest scores and allowed the localisation of one yet unknown major QTL on chromosome A06 (CR-A06). Sequencing of resistant and susceptible plant bulks of an advanced back-cross population revealed one major region in the *B. napus* genome derived from Br-14 which co-localized with the above mapped region in the F2-population. Infection tests in the greenhouse with various isolates demonstrated that this new QTL on chromosome A06 confers race-specific resistance mainly against pathotypes virulent on resistance traits derived from chromosomes A03 and A08 of *B. rapa*.

Conclusions:

Genetically, the resistance of *B. rapa* constitutes of various loci that are mainly located on chromosomes A03 and A08. Here, we have identified a new dominant resistance locus on chromosome A06 and transferred this resistance into *B. napus* genome. The new resistance CR-A06 confers high resistance against various isolates virulent on major QTLs on A03 and A08. Thus, addition of CR-A06 in breeding of clubroot resistant varieties will provide resistance to more pathotypes of *P. brassicae* in the field.

References:

WO2022136239A1 (patent)