

Phenotypic and molecular characterisation of new clubroot resistance genes derived from the primary gene pool of *Brassica napus*

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Clubroot is a serious soil-borne disease of cruciferous crops caused by the obligate biotrophic protist *Plasmodiophora brassicae* which causes galls on roots leading to premature death of the plant. Most problematic is the longevity of the resting spores in the soil up to 20 years and the fact that there are no economically reasonable control measures once a field has been infested. Currently, due to the raising density of oilseed rape cultivation within the last decades the number of contaminated fields detected in many European regions is constantly increasing. Therefore, as up to now only one race specific resistance is incorporated in adapted winter

oilseed rape cultivars, it is essential to broaden the genetic base of resistance.

Potential resistance donors out of forage rape (*Brassica napus*) and rutabaga (*B. napus* var. *napobrassica*) cultivars have been selected by phenotypic resistance against several clubroot isolates in order to generate segregating RIL and DH populations. By phenotyping with clearly differentiating *P. brassicae* isolates under greenhouse conditions, genotyping with a SNP marker set and subsequent QTL mapping several genomic regions which presumably are involved in clubroot resistance have been detected in 2 RIL populations.