Feldversuche wurden mit verschiedenen Kartoffelsorten und künstlichen Infektionen mit verschiedenen *A. solani* und *A. alternata* Isolaten durchgeführt. Vergleichbar mit den Ergebnissen der Gewächshausversuche waren in allen mit *A. solani* infizierten Parzellen Krankheitssymptome schon nach 4 Tagen zu sehen, während *A. alternata* Isolate nicht infizierten.

Aufgrund der obigen Befunde (Isolation beider Arten aus typischen Läsionen und fehlende oder geringe Virulenz von *A. alternata*) sollte untersucht werden, ob *A. alternata* eine Infektion von *A. solani* benötigt und sich auf den Läsionen saprophytisch weiterentwickelt. Hierzu wurden Mischungen von Sporensuspensionen von Isolaten beider Arten in unterschiedlichen Verhältnissen hergestellt und anschließend Tomaten- und Kartoffelpflanzen in Gewächshaus und Feldversuchen damit inokuliert. Der Verlauf der Krankheit wurde bonitiert und im befallenen Pflanzenmaterial der relative Anteil von *A. solani* und *A. alternata* mit molekulargenetischen Verfahren bestimmt.

Literatur

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Genetic variability among *Plasmodiophora brassicae* collections from different regions in Germany

Genetische Variabiltität von Plasmodiophora brassicae-Feldisolaten aus unterschiedlichen Regionen Deutschlands

Clubroot disease, caused by the soil-borne, obligate plant pathogen *Plasmodiophora brassicae,* is an economically important disease of cruciferous crops including oilseed rape. Chemical control of the pathogen is not possible at present and cultural practices can only limit the infestation with *P. brassicae.* Therefore the development of resistant cultivars is considered the most economical and efficient method for clubroot control.

Different field isolates of *P. brassicae* could not be distinguished by phenotype except for virulence patterns. Therefore pathogenicity-based classifications are used to differentiate field isolates. These bioassays are time and space consuming and subject to varying environmental conditions. Molecular markers specific to isolates or pathotypes would be an efficient tool to identify *P. brassicae* field isolates.

The objectives of the current research were to develop a molecular approach to characterize *P. brassicae* populations concerning the genetic variability and genomic polymorphism directly related to pathotype classification. Amplified fragment length polymorphisms (AFLP) were detected within and between field isolates from regions in Germany with different oilseed rape cropping intensity.

AFLP profiles of 12 field isolates from Southern Germany and 35 field isolates from Northern Germany were compared. Five selective AFLP Primer combinations were used to genotype these isolates, resulting in 137 amplicons with 73 (53 %) informative polymorphic bands. These polymorphic bands were used for genetic diversity analysis. Compared to the *P. brassicae* population from Northern Germany the southern isolates were more homogeneous, only 70 % instead of 95 % of the informative bands were polymorphic. Each field isolate had a specific AFLP pattern; within one field and one club the AFLP patterns showed no difference. Cluster analysis (Neighbour-joining method, NJ) divided the field isolates into three clusters primarily based on their geographical origin: All of the southern isolates belong to one cluster and most of the northern isolates assort to another cluster. Principal coordinate analysis (PCO) approved these results, but separated three *P. brassicae* isolates from fields close to Greifswald. In this region field isolates were detected with virulence towards the resistant cultivar 'Mendel'.

Breeding of clubroot-resistant plants requires an understanding of pathogen diversity and the variation of pathogenicity in *P. brassicae* populations. Molecular markers specific to *P. brassicae* isolates may be an important tool in breeding strategies to develop durable clubroot resistance in oilseed rape.