DANIELA CHRIST[1], ANDREAS BENKE[2], SEBASTIAN LIEBE[1], ANDREAS E. MÜLLER[2], SANDRA FISCHER[2], MARK VARRELMANN[1]

[1] Institute of Sugar Beet Research, Holtenser Landstr. 77, D – 37079 Göttingen

[2] Strube Research GmbH & Co. KG, Hauptstraße 1, D – 38387 Söllingen

OF SYMPTOMS AND TRANSCRIPTOMES – *APHANOMYCES COCHLIOIDES* IN SUGAR BEET

ABSTRACT

Aphanomyces cochlioides belongs to the economically most important pathogens in worldwide sugar beet production. The soil-borne oomycete causes damping-off in seedlings as well as Aphanomyces root rot (ARR) in mature beets. As fungicidal control is restricted to seedling infection, cultivar resistance is the only strategy available to avoid severe losses due to ARR. However, little is known about the genetic basis of ARR resistance. A bioassay with genotypes differing in their reaction to *A. cochlioides* was developed in the greenhouse. At 10 days post inoculation (dpi), beets of the susceptible genotype uniformly displayed severe ARR symptoms; thus allowing for a clear visual distinction. In order to identify key events in the early infection process and to determine sampling dates for transcriptome analysis, confocal laser scanning microscopy was applied. Subsequently, pathogen-induced differentially expressed genes in a susceptible and a resistant genotype at 4 and 7 dpi were identified by RNA-sequencing. On average, 95.8% of the reads were mapped to the sugar beet genome. In order to validate potential resistance-associated genes, a subset of the 37 (4 dpi) and 62 (7 dpi) differentially expressed genes was further analyzed by quantitative RT-PCR. The results of this study will increase the understanding of host-/pathogen-interaction in this important plant-oomycete pathosystem.