Session A

Validation of candidate genes as molecular markers for the apple replant disease

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Apple (*Malus × domestica* Borkh.) is the most important fruit produced in Germany, but apple orchards and tree nurseries increasingly face the problem of apple replant disease (ARD). ARD is a soil-borne disease that arises through replanting and leads to severe growth depression as well a decline in fruit quality and yield. Despite the economic relevance of this disease, its causes are poorly understood and so far no sustainable countermeasures are available.

The ORDIAmur project is a BMBF funded joint project for overcoming the apple replant disease by an integrated approach. Its aim is to investigate the causes of ARD and to develop sustainable, environmentally friendly and economically feasible measures against it. In previous studies of the project, it was shown that ARD is associated with deleterious shifts in soil biota community composition, and it is suspected that root exudates and decomposition products of dead apple plant material induce these changes of the soil biome. At the Institute for Breeding Research on Fruit Crops in Dresden-Pillnitz the focus of the project is on investigating the interactions between the plants and the soil and elucidating the genetic mechanisms that underlie tolerance to ARD.

Apple plants react with very high levels of stress defense to ARD, including the synthesis of phytoalexins, which are known to act in an induced defense mechanism against biotic stressors. This reaction varies in quality and quantity between different soils and genotypes.

Transcriptomic studies of apple plants grown in ARD soil revealed the induction of genes associated with the biotic stress response. Several genes, whose expression correlates closely with the phenotypic reactions of apple plants to ARD, as for example the biphenyl synthesis genes, have been identified.

The aim of this project is to identify further candidate genes that can be used as molecular markers for the reaction of apple plants to ARD. For this, 90 candidate genes were selected that have previously been shown to be differentially expressed in the susceptible rootstocks 'M9' and 'M26' as well as the ARD-tolerant wild apple accession *Malus × robusta* 5 under ARD conditions. These candidate genes will be validated by analyzing their expression by RT-qPCR with apple plants grown on 150 different sites in Germany.

Additionally, the effect of several ARD countermeasures on the expression of the candidate genes will be investigated in different apple genotypes. The experimental procedure of the candidate gene expression analysis will be optimized in order to develop a fast and cost-efficient molecular marker based method to measure the severity of ARD in soils.