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Investigating the Metabolism of Clubroot-Infected Plants by Integrating Metabolomic and Transcriptomic Approaches

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Clubroot (*Plasmodiophora brassicae*) is a serious agricultural problem affecting Brassica crop production worldwide. It also infects the model plant *Arabidopsis thaliana*. During infection, this biotrophic pathogen manipulates the development and metabolism of its host leading to the development of galls in the root and hypocotyl. In turn, its own development is strongly influenced by the host. The aim of this study is to investigate the metabolism of clubroot-infected plants using a combination of transcriptomic and metabolomic approaches. We have used direct injection mass spectrometry to obtain a metabolic fingerprint of when changes in the metabolome occur and linked this with changes in host and pathogen gene expression. We have identified alterations in carbohydrate metabolism that occur during *P. brassicae* infection of *A. thaliana* plants. Transcriptomic analysis showed that host genes associated with sugar transport and metabolism were induced during gall formation and that the pathogen also expresses genes associated with these processes. We have examined the impact of inactivating host sucrose synthase, cytosolic invertase and sugar permeases on gall formation, identifying host genes that are required for gall formation. We have also explored how sugar status is changed in root tissue, developing and mature leaf during infection of wild type and mutant plants.