

PROJECT TITLE

GC-MS based metabolic profiling identifies changes in the winter wheat seed following Fusarium treatment

CONSORTIUM

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SUMMARY OF THE REPORT

Wheat is the most important cereal worldwide and is widely consumed by humans and there is no doubt that this cereal is the substantial part of the diet of several billions of people. Wheat end-use depends on the variety, environment and their interaction. The wheat flour quality and grain yield are strongly controlled by genetic factors but the environmental conditions during grain filling considerably affect their expression. Furthermore, environmental conditions can provoke wheat diseases which can occur during this period. One of occurring disease is Fusarium head blight (FHB) or scab of wheat which develops on plants in the flowering to early grain fill stages of growth.

FHB, mainly caused by *Fusarium graminearum*, is a serious disease of wheat. It causes a significant reduction in wheat grain yield, quality and produces the mycotoxins that affect food safety and may cause serious health problems in human and domestic animals. FHB continues to threaten susceptible wheat varieties where environmental conditions such as high humidity and temperature persist during the flowering period.

Consequently, FHB can affect the production and accumulation of important grain components such as polar metabolites in wheat, including carbohydrates, organic acids, amino acids, choline, glycine betaine etc, thus influencing the antioxidant activity and nutritional quality of the grain. Besides that, polar metabolites are not only valuable nutrients but they also have a role in the accumulation of other nutritionally important compounds like proteins, starch and dietary fibre. Despite of importance of polar metabolites for human nutrition, wheat remains understudied from a metabolomics point of view, especially during FHB infestation, which occurs globally each year in more or less percentage at different locations.

Recent advances in metabolomics offer new opportunities as metabolomics is increasingly being applied in various fields offering a highly informative tool. This could allow for the definition of a large set of compounds potentially involved in FHB modulation. Previously it was concluded that various combinations of resistance-related (RR) metabolites can be accumulated through breeding in a variety to achieve higher levels of quantitative resistance. So far, a little work seems to have been done on FHB in wheat caused by *Fusarium spp.* by examining different polar metabolites. The study therefore provides information how *Fusarium spp.* influence those components in wheat grain. Furthermore, the goal of this study was to explore potential resistance-related (RR) metabolites in wheat seed. The application of this could be a valuable tool for the rapid detection of new traits and differentiation among varieties.