

P-030: Metabolite profiling of winter wheat grains from *Fusarium* head blight infected plants

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Fusarium head blight is one of the main fungal diseases of grain crops like wheat, barley or maize. The *Fusarium* species cause quality and yield reductions and it has been a great challenge for wheat producers to avoid consequent economic damage. Fungal pathogens not only result in a decrease in crop yield and quality, but also produce harmful mycotoxins which cause a health risk for humans and animals. *Fusarium* species accumulate a wide range of secondary metabolites contaminating cereal crops worldwide.

To investigate wheat grains from plants infected with *Fusarium* head blight UHPLC/ESI-QTOF-MS-based metabolite profiling studies were carried out. Wheat was grown in a field trial at Groß Lüsewitz (Germany) where *Fusarium* head blight occurred in 2017. Within the field trial eight different genotypes were grown without the use of any plant protection. To cover a wide range of metabolites with different polarity, two analytical methods were used to provide information about polar, semipolar and nonpolar compounds. In the chromatographic method specific UHPLC columns (C18 and C8), suited for metabolites of different polarity, were used.

The mycotoxin concentrations of deoxynivalenol, nivalenol, diacetoxyscirpenol, zearalenon, fumonisin B1 and B2, T-2-toxin and HT-2-toxin were quantified for the eight different genotypes. Based on the metabolite profiles features correlating with the deoxynivalenol concentration were analysed and with the help of accurate mass tandem mass spectrometry annotated. Around 20 metabolites could be annotated including peptides with the amino alcohol leucinol, stress markers and hydroxy fatty acid ester.