Mycotoxin biosynthesis and central metabolism are two interlinked pathways in Fusarium graminearum, as demonstrated by the extensive metabolic changes induced by caffeic acid exposure

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MB-03 Metabolomics of Fusarium head blight: Examining the attack of Fusarium graminearum during infection of two near isogenic wheat lines differing in the resistance QTLs Fhb1 and Qfhs.ifa-5A

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The fungus Fusarium graminearum (*Fg*) is able to infect wheat and other small grain cereals. Major problems arising from this so called Fusarium head blight (FHB) disease comprise yield and quality losses as well as mycotoxin contamination of the affected crop. In the present study a greenhouse experiment has been carried out with the aim to investigate fungal attack of two near isogenic wheat lines differing in the FHB resistance QTLs Fhb1 and Qfhs.ifa-5A. To this end, we have developed an isotope-assisted, untargeted metabolomics approach to distinguish fungal metabolites from those produced by the affected plants.

Within a time course experiment encompassing 3, 6, 12, 24, 36, 48, 72 and 96 hours after infection (hai), about 100 metabolites were determined to be explicitly deriving from *Fg*. For another approximately 250 metabolites, all of which were found to be induced by fungal infection, we were able to classify as being either produced by *Fg* to support infection, the plant in defence or by both interaction partners. Ca. 50% of the fungal metabolites could be annotated including those belonging to the type B trichothecene pathway. Many of the *Fg* assigned metabolites were found to be produced in both genotypes. Towards the end of the time course, most of the detected fungal metabolites were more abundant in the susceptible wheat genotype, lacking the two resistance QTLs. Interestingly, at an earlier stage during infection (about 48 hai) some of these fungal compounds were found to be more abundant in the resistant compared to the susceptible genotype. Our data suggest that in the resistant cultivar, the fungus is either “forced” to produce more and higher amounts of secondary metabolites at an early infection stage or alternatively, higher toxin formation by *Fg* in the resistant wheat genotype may help the plant to induce a quicker/stronger response against the pathogen including the detoxification of mycotoxins via glycosylation. Towards the end of the monitored time window (96 hai) we observed that *Fg* is not only able to produce higher amounts of well-known toxins, but also to produce a much higher number of metabolites in the infected plants, as was particularly observed for the susceptible wheat line.

MB-04 Mycotoxin biosynthesis and central metabolism are two interlinked pathways in *Fusarium graminearum*, as demonstrated by the extensive metabolic changes induced by caffeic acid exposure

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Fusarium graminearum is a major plant pathogen that causes Fusarium Head Blight in wheat and Gibberella Ear Rot in maize and produces type B trichothecene mycotoxins (TCTB) in infected grains. A comprehensive understanding of the molecular and biochemical mechanisms underlying the regulation of TCTB biosynthesis is required for improving or developing novel strategies to efficiently manage the risks posed by F. graminearum. Elucidation of the association of TCTB biosynthesis with other metabolic processes, central and specialized ones was the focus of this study. Combined ^{1}H-NMR and LC-QTOF-MS analyses were used to investigate and compare the exo- and endo- metabolomes of *F. graminearum* grown in toxin-inducing and repressing caffeic acid-conditions. Ninety-five metabolites were putatively or unambiguously identified including 26 primary and 69 specialized metabolites. Our data demonstrated that the inhibition of TCTB production induced by caffeic acid exposure was associated with significant changes in secondary and primary metabolism of F. graminearum although the fungal growth was not affected. The main metabolic changes were an increase in the accumulation of several polyketides including toxic ones, alterations in the tricarboxylic organic acid cycle and modifications in the metabolisms of some amino-acids and sugars. While these findings allow improving the knowledge on the mechanisms that govern the inhibition of TCTB production by caffeic acid, they also demonstrate the interdependence between the biosynthetic pathway of TCTB and several additional metabolic pathways including primary and specialized ones. These outcomes provide further evidence of the multifaceted role of TCTB in the life cycle of *F. graminearum*.