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Quantification of the metabolic response of wheat to Fusarium Head Blight in changing climate

Diseases of agricultural crops caused by fungi have devastating economic and health effects. Fusarium head blight (FHB) is one of the most damaging diseases of wheat and other small grain cereals. FHB contamination of wheat has been steadily increasing over the last decade leading to an increase in the associated risk of mycotoxin contamination in food and feed. Climate change and associated rise in CO2 levels are hypothetical causes of this rise but their effects on Fusarium graminearum and the spread of FHB are still unknown. In this study the defense response of wheat plants grown at ambient (400 ppm) and elevated (800 ppm) CO2 was evaluated and compared. Plant and fungal metabolites play a major role in defense and virulence with significant differences in metabolic response in resistant and susceptible plants. 1D and 2D 1H NMR spectroscopy performed in this work have provided detailed metabolite information leading to possible metabolic markers discriminating metabolic changes in wheat subtypes with different resistance and at changing CO2 levels. Computational methodology for metabolite quantification from NMR data that automatically aligns spectra of standards and samples prior to quantification utilizing multivariate linear regression optimization of spectra of assigned metabolites to samples' 1D spectra is described and used. Fusarium infection-induced metabolic changes in different conditions will be discussed in the context of metabolic network and resistance.