Nucleosome dynamics in the toxin-producing plant pathogen Fusarium graminearum

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MB-09 Annotation of *Fusarium graminearum*'s dark matter: Clustering of unknown, structurally similar fungal metabolites during wheat infection by molecular networking

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The fungus *Fusarium graminearum* is a potent pathogen for wheat and other important agricultural crop plants. It causes the devastating *Fusarium* head blight disease thereby contaminating crop yield with mycotoxins and rendering the yield unsafe for animal and human consumption. While there are great efforts in investigating the roles of the currently known major *Fusarium* compounds involved in the disease (e.g. the mycotoxin deoxynivalenol), both structure, function and involvement of many other fungal metabolites during the infection process are currently unknown.

To shed light on these unknown compounds, which are referred to as dark matter in untargeted metabolomics applications, we have carried out a greenhouse experiment involving susceptible and resistant wheat plants (QTLs Fhb1 and Qfhs.ifa-5A) and infected them with *Fusarium graminearum*. All samples have been measured with liquid chromatography-high resolution mass spectrometry and the generated data have been processed with an untargeted data processing approach in order to detect all wheat- and *F. graminearum*-derived metabolites. A sophisticated statistical and biological analysis of these mostly unknown compounds has been carried out to separate fungal and wheat compounds thereby reporting a total of 107 fungal metabolites of which the majority remained unknown without any information about their structure.

Subsequently to the statistical analysis, fragmentation spectra of the fungal metabolites have been acquired.

These fragment spectra of the fungal unknowns have then been organized in a graph with the aim to group compounds with similar MS/MS fragment spectra as compounds with common fragments and/or neutral losses can be assumed to have structural similarities (molecular networking [1]). Clusters of similar MS/MS spectra and therefore tentatively related chemical structures have been correlated with their abundance patterns obtained from the statistical analysis. Results of applied molecular networking approach will be presented for *F. graminearum*'s so far unknown chemical constituents.

[1] Watrous et al. Mass spectral molecular networking of living microbial colonies, PNAS 2012 109 (26) E1743–E1752, doi:10.1073/pnas.1203689109

MB-10 Nucleosome dynamics in the toxin-producing plant pathogen *Fusarium graminearum*

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Nucleosome dynamics are the first level of regulation of all eukaryotic molecular processes that use genomic DNA as a template, including gene expression. Abundant literature on various organism, notably in yeasts, reports that the position of nucleosomes and their relative stabilities are major parameters influencing gene expression. Changes in nucleosome positioning during cell differentiation and growth are commonly observed in eukaryotes in general. In the yeast, *Candida albicans*, such mechanisms were shown to be involved in morphological plasticity that plays a role in virulence. Here, we report the investigation of nucleosome dynamics during the development *in vitro* of the mycotoxin-producing phytopathogen *Fusarium graminearum*. Nucleosome landscapes were investigated using MNase-Assisted Isolation of Nucleosomal Elements coupled to deep sequencing, or MAINE-seq. The general nucleosomal organization extensively described in various organisms appears conserved in *F. graminearum*, with most nucleosomes arrayed and well-positioned relative to start and stop codons of genes. In the details, nucleosome positioning at promoters and gene expression are well correlated. Strong nucleosome rearrangements are observed in culture conditions when significant metabolomics changes are observed, including regarding toxin production. The observed events regard mostly differences in nucleosome stability, sometimes referred to as occupancy. Additional transcriptomics data provide leading information regarding the significance of these observations.