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MÖLLER Mareike *(1), SOYER Jessica (2), SCHOTANUS Klaas (1), FREITAG Michael (3), STUKENBROCK Eva (1)*
(1) Environmental Genomics, Christian-Albrechts University, Kiel; Max Planck Institute for Evolutionary Biology, Kiel/Plön, Germany
(2) INRA-AgroParisTech BIOGER, Thiverval-Grignon, France
(3) Department of Biochemistry and Biophysics, Center for Genome Research and Biocomputing, Oregon State University, Corvallis, USA

The role of histone-methyltransferases KMT1 and KMT6 in chromatin organization and gene regulation in *Zymoseptoria tritici*

Zymoseptoria tritici is a plant pathogenic fungus specialized to infect wheat (*Triticum aestivum*). The genome of the sequenced reference *Z. tritici* isolate consists of 21 chromosomes of which eight are accessory chromosomes. These chromosomes are highly instable during meiosis, transcriptionally repressed and show enrichment in repetitive elements and heterochromatic histone marks. The methylation of specific histone tails and the resulting changes in chromatin structure has been shown to play a crucial role in the regulation of secondary metabolism and pathogenicity-associated gene expression in filamentous fungi. To elucidate the role of histone modifications on transcriptional regulation and pathogenicity in *Z. tritici*, we created deletion mutants of the methyltransferases KMT6 and KMT1 that are responsible for the methylation of histone 3 at H3K27me3 and H3K9me3, respectively. We combined genetic and phenotypic analyses to follow the impact of these deletions *in vitro* and during the infection of the host plant. We used ChIPseq and RNAseq to compare changes in chromatin structure and the resulting differences in gene expression between mutants and wild type strains. We observed dramatic chromatin and genome rearrangements reflected in severe phenotypical changes in the *Δkmt1* mutants. The *Δkmt6* mutants however showed little differences to wild type under normal growth conditions *in vitro* and *in planta*, but significant alterations in secondary metabolite production under stress conditions. Based on these results we conclude a strong impact of H3K9me3 in chromatin organization and normal growth, and an important role of H3K27me3in gene regulation and the production of secondary metabolites in *Z. tritici*.