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Dynamic of the genome in *Fusarium graminearum*: insights on evolution of pathogenicity related traits

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April 8 – 11, 2018
Minoritenkloster
Tulln, AUSTRIA

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PP-13 Cropping factors which increase the risk of *Fusarium* infection and mycotoxin contamination in Swiss silage and grain maize

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Maize is frequently infected by a complex of *Fusarium* species, leading to mycotoxins, which represent a severe threat to animal health. To assess the risk of infection and mycotoxin contamination in silage (SM) and grain maize (GM), multi-year surveys were conducted (SM: 2010-14; GM: 2008-10). Harvest samples from commercial SM fields (n=169) of two cantons and GM fields (n=288) of 16 cantons, together with information on the cropping history, were collected. Despite a high *Fusarium* species variability in SM and GM as well as a strong year effect on their occurrence, deoxynivalenol (DON) was the most prevalent mycotoxin. An alarmingly high proportion of SM (68%) and GM (51%) samples exceeded the European guidance value for DON in swine feed (0.9 mg kg⁻¹). The mean content of DON was equal for SM (2.2 mg kg⁻¹) and GM (2.5 mg kg⁻¹), however, the mean zearalenone level was higher in SM (0.5 mg kg⁻¹) than in GM (0.3 mg kg⁻¹). In both surveys, the average concentrations of fumonisins were substantially lower (SM: 0.6; GM: 0.3 mg kg⁻¹) and mainly found in samples from the South. As DON was the dominant mycotoxin in SM and GM samples and *F. graminearum* (FG) the predominant species in GM, we focussed on identifying cropping factors influencing these two parameters. In SM and GM, samples from fields with reduced tillage showed a significantly higher mean DON content (SM: 2.9; GM: 3.2 mg kg⁻¹) compared with samples from ploughed fields (SM: 1.5; GM: 2.1 mg kg⁻¹), irrespective of the previous crop. In addition, late harvest dates resulted in higher levels of FG and DON compared with those from earlier harvest dates. In the GM survey, maize grains from mid-late maturing hybrids had higher mean DON contents (3.8 mg kg⁻¹) than grains from early (2.3 mg kg⁻¹) or mid-early (1.8 mg kg⁻¹) maturing hybrids. Cereals or maize as pre-previous crops significantly increased the DON content in samples from ploughed fields, compared with samples from fields with other pre-previous crops. Since effects of hybrids and pre-crops might have been masked by the highly variable cropping conditions in our first dataset, we examined GM samples from Agroscope variety trials with eight different hybrids (2011-2013). The analyses demonstrated that samples from fields with previous crop maize resulted in increased FG infection and DON contents. In addition, we revealed substantial differences in hybrids irrespective of the maturity class, with DON mean values ranging from 0.6 to 1.9 mg kg⁻¹.

PP-14 Dynamic of the genome in *Fusarium graminearum*: insights on evolution of pathogenicity related traits

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The ascomycete *Fusarium graminearum* is a devastating pathogen of cereal crops, and can contaminate food and feed with harmful mycotoxins. Previous studies suggest a high-adaptive potential of this pathogen, illustrated by an increase of pathogenicity and resistance to fungicides in some populations. The foundation of this ability to evolve remains largely unknown. The pathosystem *F. graminearum*/wheat does not fit to the gene-for-gene relationship and is a model to study the quantitative host-pathogen interaction. Deciphering the genetic architecture of the pathogenicity in *F. graminearum*, in terms of number of loci/genes, heredity, and evolvability, is a key prerequisite to understand how the fungus adapts to its environment. Through a combination of classical quantitative genetic and genomic approaches, we provide new insights on the evolutive potential of this pathogen. The construction of a high-density genetic linkage map gave a detailed picture of the recombination landscape. The recombination rate had a strong positive correlation with nucleotide diversity, and recombinant active regions were enriched for genes with a putative role in host-pathogen interaction. The quantitative trait locus (QTLs) involved in pathogenicity related traits, such as disease severity or toxin production, obtained in our studies or described in literature, were mainly found in the most dynamic part of the genome. Consequences for the evolutive potential of this major pathogen will be discussed.