



HAL
open science

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

Benoit Laurent, Nadia Ponts, Christian C. Barreau, Marie Foulongne-Oriol

► To cite this version:

Benoit Laurent, Nadia Ponts, Christian C. Barreau, Marie Foulongne-Oriol. Dynamic of the genome in *Fusarium graminearum*: insights on evolution of pathogenicity related traits. 14. European Fusarium Seminar, Apr 2018, Tulln, Austria. Austrian Association of Molecular Life Sciences and Biotechnology, 122 p., 2018, Proceedings of the 14th European Fusarium Seminar. hal-02736083

HAL Id: hal-02736083

<https://hal.inrae.fr/hal-02736083>

Submitted on 2 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License



April 8 – 11, 2018
Minoritenkloster
Tulln, AUSTRIA

ORGANIZING COMMITTEE

Gerhard Adam
(BOKU, AT)

Rainer Schuhmacher
(BOKU, AT)

Hermann Bürstmayr
(BOKU, AT)

Joseph Strauss
(BOKU, AT)

Rudolf Krska
(BOKU, AT)

Gerlinde Wiesenberger
(BOKU, AT)

Dieter Moll
(BIOMIN, AT)

Alexandra Khassidov
(ÖGMBT, AT)

INTERNATIONAL SCIENTIFIC COMMITTEE

Sarah M. De Saeger
(BE)

Ruth Dill-Macky
(US)

Doris Marko
(AT)

Thomas Miedaner
(DE)

Antonio Moretti
(IT)

Michele Suman
(IT)

B. Gillian Turgeon
(US)

Table of Contents

Table of Contents	2
General Information	3
Welcome Address	4
Invited Speakers	5
Detailed Program	13
SUNDAY - April 8	13
MONDAY - April 9	13
TUESDAY - April 10	16
WEDNESDAY - April 11	19
Posters Table	21
Lectures	22
Welcome Note & Plenary Session	23
Session 1: Fusarium genomics and virulence mechanisms, population genetics and diversity	25
Session 2: Host resistance: mechanisms, genetics, genomics and breeding	32
Session 3: Fusarium secondary metabolites and metabolomics of Fusarium-host plant interactions	39
Session 4: Fusarium mycotoxins - Toxicology, Metabolism and Remediation	46
Session 5: Integrated Fusarium management (pre/postharvest, epidemiology and forecasting, fungicide resistance, utilization of contaminated batches)	54
Poster Presentations	61
Author Index	110
Participant Index	115
Imprint	123

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

Tomke Musa¹, Eveline Jenny¹, Andreas Kägi¹, Hans-Rudolf Forrer¹, Felix E. Wettstein², Thomas D. Bucheli², Michael Sulyok³, Ulrich Buchmann⁴, Jürg Hiltbrunner⁴, Susanne Vogelgsang¹

¹ Agroscope, Switzerland

² Agroscope, Research Division Method Development and Analytics, RG Environmental Analytics

³ Center for Analytical Chemistry, University of Natural Resources and Life Sciences, Vienna

⁴ Agroscope, Research Division Plants and Plant Products, RG Varieties and Production Techniques, Zurich, Switzerland

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

Benoit Laurent, Nadia Ponts, Christian Barreau, Marie Foulongne-Oriol

UR1264-MycSA, INRA, France

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.