



HAL
open science

Several mutations of *Zymoseptoria tritici* field strains lead to MFS1 overexpression and multi-drug-resistance (MDR)

Sabine Fillinger, Selim Omrane, Colette C. Audeon, Amandine Ignace, Clémentine Duplaix, Lamia Aouini, Gert Kema, Anne-Sophie Walker

► To cite this version:

Sabine Fillinger, Selim Omrane, Colette C. Audeon, Amandine Ignace, Clémentine Duplaix, et al.. Several mutations of *Zymoseptoria tritici* field strains lead to MFS1 overexpression and multi-drug-resistance (MDR). ECFG13. European conference on fungal genetics, Apr 2016, PARIS LA VILLETTE, France. p.94. hal-02796869

HAL Id: hal-02796869

<https://hal.inrae.fr/hal-02796869>

Submitted on 5 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.

CONCURRENT SESSION ABSTRACTS
CS8: Adaptation to xenobiotics

Wednesday 6th April

17:20 - 17:40

Louis Armand Est

FILLINGER Sabine (1)

OMRANE Selim (1), AUDEON Colette (1), IGNACE Amandine (1), DUPLAIX Clémentine (1), AOUINI Lamia (2), KEMA Gert (2), WALKER Anne-Sophie (1)

(1) BIOGER, INRA, AgroParisTech, Thiverval-Grignon, France

(2) PRI, Wageningen University, Wageningen, The Netherlands

Several mutations of *Zymoseptoria tritici* field strains lead to *MFS1* overexpression and multi-drug-resistance (MDR)

Multidrug resistance (MDR) is a common trait developed by many organisms to counteract chemicals and/or drugs used against them. The basic MDR mechanism is relying on an overexpressed efflux transport system that actively expulses the toxic agent outside the cell. In fungi, MDR (or PDR) has been extensively studied in *Saccharomyces cerevisiae* and *Candida albicans*. Plant pathogenic fungi are also concerned by this phenomenon. MDR strains were detected in septoria leaf blotch (*Zymoseptoria tritici*) field populations since 2008. These strains are cross-resistant to fungicides with different modes of action due to active fungicide efflux. In a previous study, we identified the *MFS1* gene overexpressed in all tested MDR field strains (1). This gene encodes a major facilitator membrane transporter whose inactivation abolished the MDR phenotype in two resistant isolates (MDR6 and MDR7). To identify the mutation(s) responsible for MDR phenotype we applied bulk-progeny sequencing to crosses involving MDR6 and MDR7 strains. This analysis enabled us to identify a 519 bp insert in the *MFS1* promoter in both strains. The insert, a reminiscence of a recent retrotransposition event, is responsible for *MFS1* overexpression and the MDR phenotype. Genotyping of various field strains revealed that at least one additional mutation is responsible for the MDR phenotype.

1- Omrane et al., (2015), Env. Microbiol., 17: 2805-2823.
