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Data Article

2-D DIGE proteomic profiles of three strains of *Fusarium graminearum* grown in agmatine or glutamic acid medium



Tommaso Serchi, Matias Pasquali*, Céline C. Leclercq, Sébastien Planchon, Lucien Hoffmann, Jenny Renaut

Department of Environmental Research and Innovation, Luxembourg Institute of Science and Technology, 41, rue du Brill, L-4422 Belvaux, Luxembourg

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ABSTRACT

2D DIGE proteomics data obtained from three strains belonging to *Fusarium graminearum* s.s. species growing in a glutamic acid or agmatine containing medium are provided.

A total of 381 protein species have been identified which do differ for abundance among the two treatments and among the strains (ANOVA < 0.05 and abundance ratio > ± 1.3).

Data on the diversity of protein species profiles between the two media for each strain are made available. Shared profiles among strains are discussed in Pasquali et al. [1].

Here proteins that with diverse profile can be used to differentiate strains are highlighted. The full dataset allow to obtaining single strain proteomic profiles.

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Specifications Table

Subject area	Biology Mycology
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* Corresponding author.

E-mail address: matias.pasquali@list.lu (M. Pasquali).

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More specific sub-
ject area

Type of data

How data was
acquired

Data format

Experimental
factors

Experimental
features

Data source
location

Data accessibility

Tables

2-D Fluorescence Difference Gel Electrophoresis (2-D DIGE) and mass spectrometry

Analyzed data and raw gels

Three different *Fusarium graminearum* strains belonging to three genetic che-
motypes, medium nitrogen source

Comparative strain proteomic of 3 strains using 2-D DIGE. Fungal strains were
grown in agmatine or glutamic acid containing medium for 8 days. Differentially
abundant protein species between the 2 media and the 3 strains were identified.

Luxembourg Institute of Science and Technology, Belvaux, Luxembourg Origin of
the three strains used in the study are Luxembourg, Ohio (USA), Michigan (USA).

The data are part of this article.

Value of the data

- Level of diversity of the proteome of 3 different strains of *F. graminearum* in two growing condi-
tions can be obtained from this dataset.
- Strain-dependent regulated protein species able to discriminate the three strains were identified.
- These data are useful to investigate strain specificity within *F. graminearum* species.

1. Data

Agmatine and glutamic acid have a different effect on the phenotype of *F. graminearum* [1] that is also reflected in shared proteomic profiles discussed in [1]. Here we detail the complete list of all identified proteins that change significantly among strains or between conditions for each strain. In the list of protein species that are significantly shifting their abundance in each of the three strains representing *F. graminearum* toxigenic variability (Supplementary material 38) proteomic profiles for each strain can be obtained. By selecting the protein species with opposite behaviour among the strains we identified a subset of proteins that can be used to discriminate the three strains used here (Fig. 1). This dataset is also useful for comparing how different strains behave at the proteomic level when grown in agmatine or glutamic acid as the sole nitrogen source.

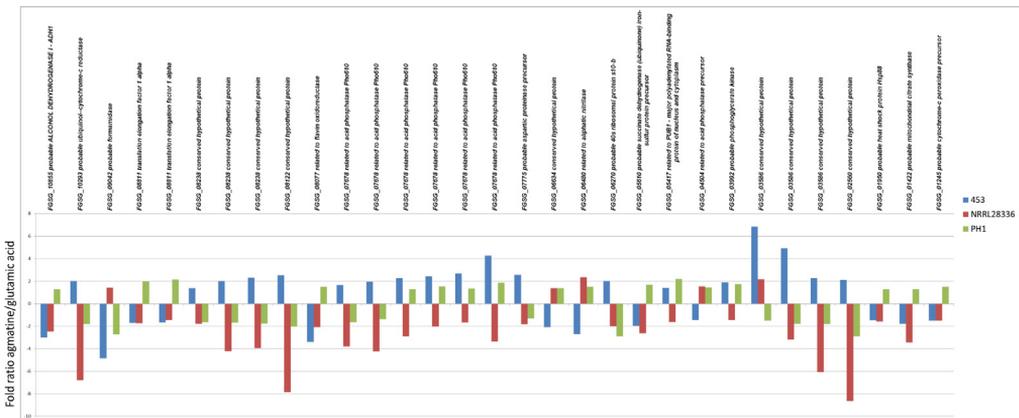


Fig. 1. Expression ratio of protein species abundance between agmatine and glutamic acid media. Each FGSG line corresponds to a protein species that shows significant opposite behaviour among the three strains.

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