A European Database of Fusarium graminearum and F-culmorum Trichothecene Genotypes

Matias Pasquali, Marco Beyer, Antonio Logrieco, Kris Audenaert, Virgilio Balmas, Ryan Basler, Anne-Laure Boutigny, Jana Chrpova, Elzbieta Czembor, Tatiana Gagkaeva, et al.

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PT J
AU Pasquali, M
Beyer, M
Logrieco, A
Audenaert, K
Balmas, V
Basler, R
Boutigny, AL
Chrpova, J
Czembor, E
Gagkaeva, T
Gonzalez-Jaen, M
Hofgaard, IS
Koycu, ND
Hoffmann, L
Levic, J
Marin, P
Miedaner, T
Migheli, Q
Moretti, A
Muller, MEH
Munaut, F
Parikka, P
Pallez-Barthel, M
Piec, J
Scauflaire, J
Scherm, B
Stankovic, S
Thrane, U
Uhlig, S
Vanheule, A
Yli-Mattila, T
Vogelgsang, S
AF Pasquali, Matias
Beyer, Marco
Logrieco, Antonio
Audenaert, Kris
Balmas, Virgilio
Basler, Ryan
Boutigny, Anne-Laure
Chrpova, Jana
Czembor, Elzbieta
Gagkaeva, Tatiana
Gonzalez-Jaen, Maria
Hofgaard, Ingerd S.
Koycu, Nagehan D.
Hoffmann, Lucien
Levic, Jelena
Marin, Patricia
Miedaner, Thomas
Migheli, Quirico
Moretti, Antonio
Mueller, Marina E. H.
Munaut, Francoise
Parikka, Paivi
Pallez-Barthel, Marine
Piec, Jonathan
Scauflaire, Jonathan
Scherm, Barbara
Stankovic, Slavica
Thrane, Ulf
Uhlig, Silvio

Vanheule, Adriaan
Yli-Mattila, Tapani
Vogelgsang, Susanne
TI A European Database of Fusarium graminearum and F-culmorum Trichothecene Genotypes
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DE acetyldeoxynivalenol; chemotype; database; Fusarium; genotype; mycotoxin; nivalenol; trichothecene
ID SMALL-GRAIN CEREALS; HEAD BLIGHT PATHOGEN; ALPHA-GENE SEQUENCES; SPECIES COMPLEX; MICRODOCHIUM-NIVALE; FUNGAL PATHOGENS; SOFT WHEAT; PCR ASSAY; CHEMOTYPES; MYCOTOXIN
AB Fusarium species, particularly Fusarium graminearum and F culmorum, are the main cause of trichothecene type B contamination in cereals. Data on the distribution of Fusarium trichothecene genotypes in cereals in Europe are scattered in time and space. Furthermore, a common core set of related variables (sampling method, host cultivar, previous crop, etc.) that would allow more effective analysis of factors influencing the spatial and temporal population distribution, is lacking. Consequently, based on the available data, it is difficult to identify factors influencing chemotype distribution and spread at the European level. Here we describe the results of a collaborative integrated work which aims (1) to characterize the trichothecene genotypes of strains from three Fusarium species, collected over the period 2000-2013 and (2) to enhance the standardization of epidemiological data collection. Information on host plant, country of origin, sampling location, year of sampling and previous crop of 1147 F graminearurn, 479 F culmorum, and 3 F cortaderiae strains obtained from 17 European countries was compiled and a map of trichothecene type B genotype distribution was plotted for each species. All information on the strains was collected in a freely accessible and updatable database (www.catalogueeu.luxmcc.lu), which will serve as a starting point for epidemiological analysis of potential spatial and temporal trichothecene genotype shifts in Europe. The analysis of the currently available European dataset showed that in F. grarninearum, the predominant genotype was 15-acetyldeoxynivalenol (15-ADON) (82.9%), followed by 3-acetyldeoxynivalenol (3-ADON) (13.6%), and nivalenol (NIV) (3.5%). In F culmorum, the prevalent genotype was 3-ADON (59.9%), while the NIV genotype accounted for the remaining 40.1%. Both, geographical and temporal patterns of trichothecene genotypes distribution were identified.
C1 [Pasquali, Matias; Beyer, Marco; Hoffmann, Lucien; Pallez-Barthel, Marine; Piec, Jonathan] Luxembourg Inst Sci & Technol, Dept Environm Res & Innovat, Belvaux, Luxembourg.
[Logrieco, Antonio; Moretti, Antonio] CNR, Inst Sci Food Prod, I-70126 Bari, Italy.
[Audenaert, Kris; Vanheule, Adriaan] Univ Ghent, Fac Biosci Engn, Dept Appl Biosci, B-9000 Ghent, Belgium.
[Balmas, Virgilio; Migheli, Quirico; Scherm, Barbara] Univ Sassari, Dept Agr, I-07100 Sassari, Italy.
[Basler, Ryan] INRA, BIOGER UMR, F-78850 Thiverval Grignon, France.
[Boutigny, Anne-Laure] ANSES, Plant Hlth Lab, Angers, France.
[Chrpova, Jana] Crop Res Inst, Div Crop Genet & Breeding, Prague, Czech Republic.
[Czembor, Elzbieta] Nat Res Inst, Plant Breeding & Acclimatizat Inst, Dept Grasses Legumes & Energy Plants, Radzikow, Poland.
[Gagkaeva, Tatiana] All Russian Inst Plant Protect, Lab Mycol & Phytopathol, St Petersburg, Russia.
[Gonzalez-Jaen, Maria; Marin, Patricia] Univ Complutense Madrid, Fac Biol, Dept Genet, E-28040 Madrid, Spain.
[Hofgaard, Ingerd S.] Norwegian Inst Bioecon Res, As, Norway.
[Koycu, Nagehan D.] Namik Kemal Univ, Fac Agr, Dept Plant Protect, Tekirdag, Turkey.
[Levic, Jelena; Stankovic, Slavica] Maize Res Inst, Lab Phytopathol & Entomol, Belgrade, Serbia.
[Miedaner, Thomas] Univ Hohenheim, Plant Breeding Inst, Stuttgart, Germany.

[Mueller, Marina E. H.] Inst Landscape Biogeochem, Leibniz Ctr Agr Landscape Res, Muncheberg, Germany.
[Munaut, Francoise; Scauflaire, Jonathan] Catholic Univ Louvain, Appl Microbiol Earth & Life Inst, Louvain La Neuve, Belgium.
[Parikka, Paivi] Nat Resources Inst Finland Luke, Dept Nat Resources & Bioprod, Jokioinen, Finland.
[Thrane, Ulf] Tech Univ Denmark, DTU Syst Biol, Sect Eukaryot Biotechnol, DK-2800 Lyngby, Denmark.
[Uhlig, Silvio] Norwegian Vet Inst, Sect Chem & Toxicol, Oslo, Norway.
[Yli-Mattila, Tapani] Univ Turku, Dept Biochem, Mol Plant Biol, SF-20500 Turku, Finland.
[Vogelgsang, Susanne] Agroscope, Res Div Grassland Sci & Agroecosyst, Inst Sustainabil Sci, Zurich, Switzerland.
RP Pasquali, M (reprint author), Luxembourg Inst Sci & Technol, Dept Environm Res & Innovat, Belvaux, Luxembourg.; Vogelgsang, S (reprint author), Agroscope, Res Div Grassland Sci & Agroecosyst, Inst Sustainabil Sci, Zurich, Switzerland.
EM matias.pasquali@list.lu; susanne.vogelgsang@agroscope.admin.ch
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PU FRONTIERS MEDIA SA
PI LAUSANNE
PA PO BOX 110, EPFL INNOVATION PARK, BUILDING I, LAUSANNE, 1015, SWITZERLAND
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