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THE LUXEMBOURG DATABASE OF *FUSARIUM* STRAINS : POPULATION STRUCTURE AND RELATED VARIABLES

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RÉSUMÉ

La fusariose de l'épi est l'une des principales maladies sur blé entraînant des pertes de rendement et une réduction de la qualité. Le champignon responsable a la capacité de produire des mycotoxines telles que le déoxynivalénol et ses formes acétylées, et le nivalénol, impactant l'ensemble de la chaîne alimentaire. Dans le cadre d'un programme d'observation et de surveillance, le LIST isole des souches de *Fusarium* dans tout le pays depuis 10 ans dont plus de 650 d'entre elles sont accessibles sur le site Internet de la collection Luxembourg Microbial Culture collection (www.luxmcc.lu). En relation avec chaque souche, un ensemble de variables de base affectant les niveaux de mycotoxines est inclus, à savoir l'espèce de la plante hôte, la variété, le précédent cultural, le chimiotype. La connaissance de l'agent pathogène et des facteurs influençant sa distribution spatiale et temporelle est nécessaire pour envisager une stratégie de contrôle efficace et compatible avec le développement durable.

Mots-clés : *Fusarium*, base de données, chimiotype, plante hôte, précédent cultural.

ABSTRACT

Fusarium head blight is one of the major wheat diseases resulting in yield losses and reduction of the quality of wheat and its products. The causal fungi produce a variety of mycotoxins such as deoxynivalenol and acetylated forms, nivalenol, with impacts on the whole cereal food and feed chain. As part of a *Fusarium* observation and monitoring program, the Luxembourg Institute of Science and Technology has been collecting *Fusarium* strains from all over the country for about 10 years. A collection, that comprises over 650 different *Fusarium* strains is freely accessible on the Luxembourg Microbial Culture collection website (www.luxmcc.lu). Related to each strain, a core set of variables affecting mycotoxin levels are included, namely the host plant species, the host plant cultivar, chemotype of the fungal strains and preceeding crop. Knowledge of the pathogen and the factors influencing its spatial and temporal distribution is necessary to develop effective control strategies that support a sustainable development of agriculture.

Keywords: *Fusarium*, database, chemotype, host plant, preceeding crop.

INTRODUCTION

Fusarium head blight is a major fungal disease on small grains such as wheat or barley worldwide. This disease is responsible of considerable yield losses but it also impacts the quality of the grain. *Fusarium* species can deposit mycotoxins in the grain with negative consequences along the entire cereal food and feed chain. Disease management and infection control require an accurate and rapid detection of the pathogens involved in the disease complex.

The different species of *Fusarium* can coexist within the same field or even within the same ear (Logrieco et al., 2007). The composition of the *Fusarium* species complex is dynamic and depends on the ability of the strain to contaminate and colonize a field according to external parameters such as climatic conditions and agricultural practices (Logrieco et al., 2002, Köhl et al., 2007, Xu et al., 2008). Rain during anthesis, tillage, crop rotation, and cultivar are parameters known to influence outbreaks of FHB (Doohan et al., 2003 , Beyer et al., 2006 , Giraud et al., 2010). All these parameters contribute to the explanation of epidemics, the population development and its ability to adapt to climate change.

MATERIALS AND METHODS

PLANT MATERIALS

Plant materials were sampled during the last ten years according to the procedure outlined in Giraud et al (2010) and Beyer et al (2014) across Luxembourg with the aim to cover all geographic areas and therefore, all the contrasting topo-climatic conditions present in the Grand Duchy of Luxembourg.

FUNGAL STRAIN ISOLATION AND MOLECULAR CHARACTERIZATION

After isolation of the strains, species identification based on the sequencing of the elongation factor 1 alpha (EF1alpha) gene was performed according to the protocol described by Dubos et al (2011). In order to get more information on the ability of the strains to produce mycotoxins, the chemotype determination was done following the method described in Pasquali et al (2011).

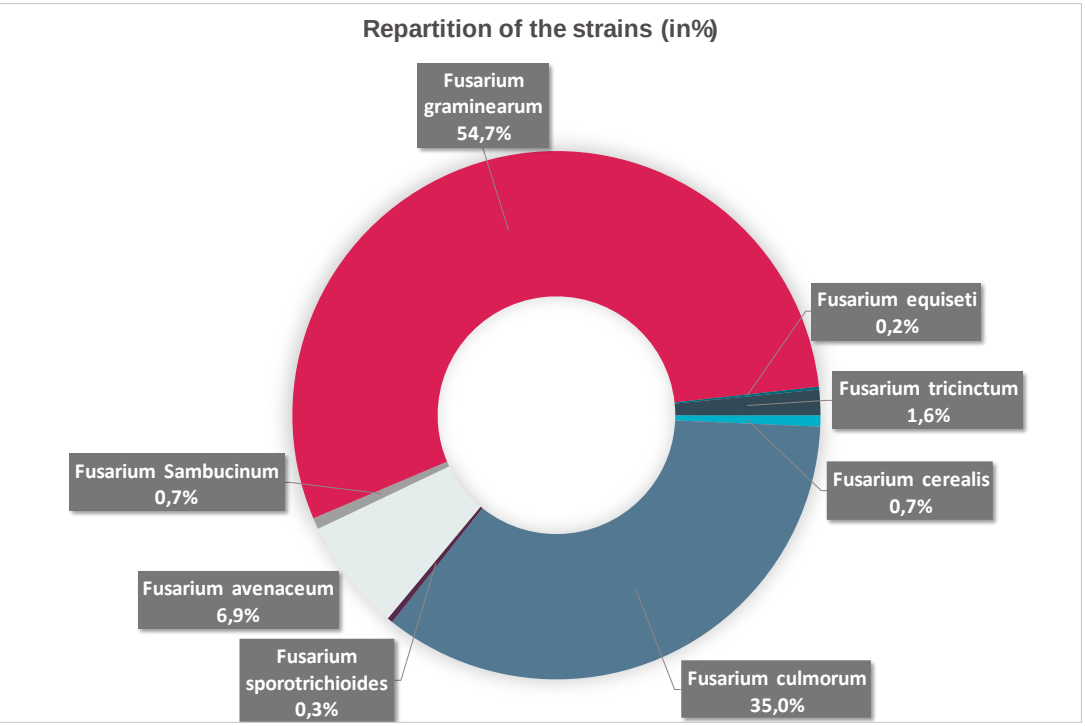
DATA COLLECTION

The information on each strain was collected during ten years of a campaign of *Fusarium* monitoring in Luxembourgish fields from 2007 to 2017. For each field at the origin of the samples taken, a set of information was collected including GPS coordinates, the crop from which the strain was isolated, the cultivar, the previous crop, the method of isolation, the fungal species, the genetic chemotype and the corresponding publications (Piec et al., 2016).

RESULTS

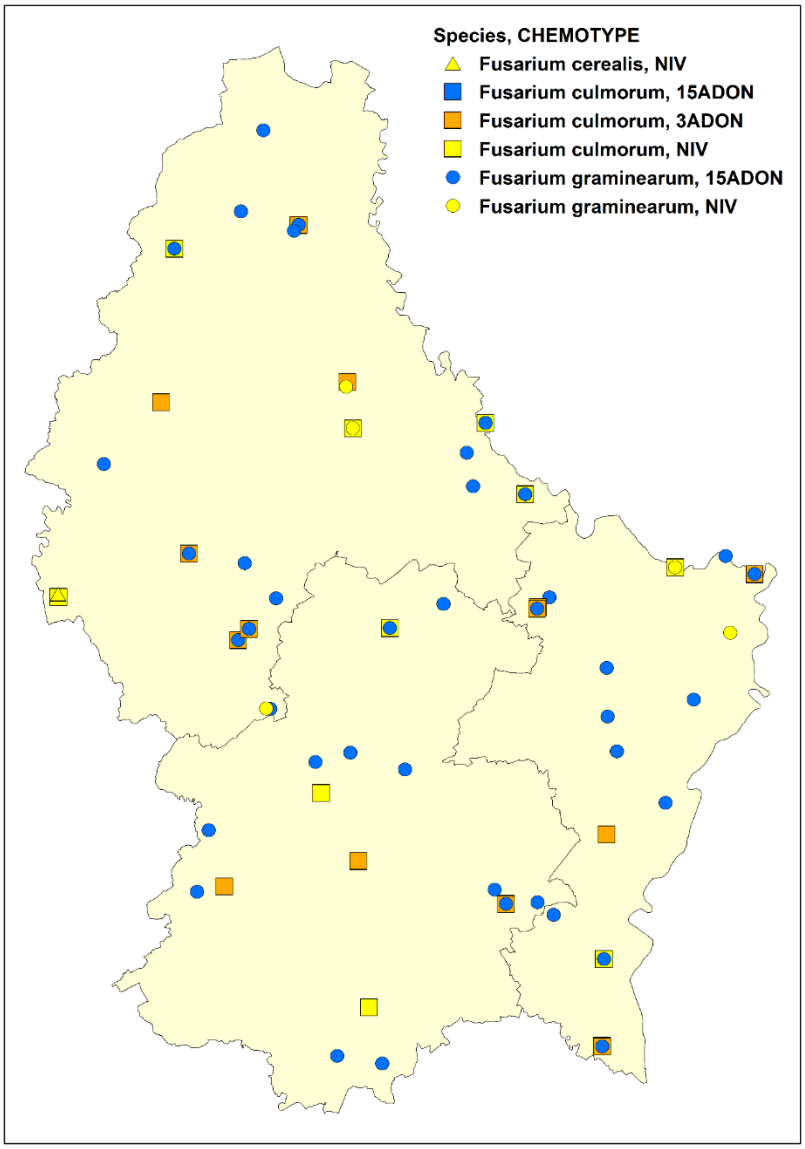
At the summer period 2018, properties of a total of 678 strains are fully described. Originally focussing on *F. graminearum* and *F. culmorum* strains isolated by LIST, the collection was extended to others species such as *F. poae, F. avenaceum* and rarer species like *F. cerealis, F. equisiti, F. triticintum, F. sporotrichioides, F. sambucinum (Fig. 1).*

Figure 1 : Repartition of the strains in the database (in %) – Répartition des souches dans la base de données (en %).



For each strain, a set of data is provided after collecting information from network farmers or laboratory analysis. A webpage dedicated to each strain includes the reference of the strain, chemotype, the year of isolation, the place of isolation as well as the geographical coordinates, the species from which the strain was isolated as well as the cultivar, the previous crop, the method of isolation and determination of the species. For those that have been used in previous publications, the corresponding reference is cited to allow referencing, whenever needed.
The entire database can be exported to Microsoft excel format, which leaves the field free for many applications such as prediction models or population map construction for example (Fig. 2).

Figure 2: Mapping of the strain distribution in Luxembourg. Cartographie de la distribution des espèces au Luxembourg.



DISCUSSION

The knowledge of all the parameters gathered in this database, allows deriving predictive models as well as better understanding the evolution of the populations of *Fusarium* within the same territory. The prediction of the evolution of the population will make it possible to define potential risks as well as at the level of the diseases as at the level of the mycotoxins production. Due to their global importance in terms of economic losses or the health quality of harvested products, the prediction of mycotoxin risk is a major issue in the context of food security and growth of the world population. Researchers or companies are invited to include strains from the collection in their activites.

CONCLUSION

The collected data on the *Fusarium* strains from Luxembourg are stored in a web database. This work aims to characterise the *Fusarium* population in one country as well as the thricothecene genotype of strains over time to follow the population evolution but also to provide information for potential global epidemiological studies. Disease management, infection control and toxin prediction are crucial axes in the framework of new regulations related to the current issue of agriculture.

The LuxMCC site has also been enriched with the European Database Fusarium, which has been created within the framework of FP7 European project MycoRed (Novel Integrated Strategies for Worldwide MYCOtoxin Reduction in Food and Feed Chains).

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