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Evolution of the pattern of *Fusarium* species infecting French wheat over 15 years: first results.

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Fusarium Head Blight (FHB) is one of the most devastating diseases affecting wheat, caused by fungal species belonging to the genus *Fusarium*. Beyond the significant impact on yields, FHB alters also grain quality with contamination by mycotoxins leading to significant economic losses and food safety issues. It is clearly acknowledged that the patterns of *Fusarium* spp. infecting wheat and associated mycotoxins are dependent on global changes. Understanding the drivers, either climatic or agronomic, that determine the balance of *Fusarium* species representativeness is crucial to ensure the tomorrow's safety of cereal products. The purpose of this study was to draw the spatio-temporal dynamic of the *Fusarium* species occurrence in French wheat fields over the last 15 years, in the light of climatic conditions and/or agricultural practices evolution. Near 1350 samples of wheat kernels harvested between 2007 and 2022 were analyzed. Together with mycotoxins profiling, a metabarcoding approach targeting the *EF1α* gene was used to assess the diversity of *Fusarium* spp. infecting French wheat and its evolution.

The obtained data will be analyzed in the light of collected metadata (temperature, rainfall, soil conditions and agricultural practices) to dissect the relative contribution of key environmental factors that could drive the occurrence of one species vs. another. This study will provide key results that will be used to feed mycotoxin-risk-prediction models, and by this way, will help designing the most efficient management for future mycotoxin issues in wheat crops.

Keywords: *Fusarium* spp., metabarcoding, *EF1α* gene, global changes, representativeness