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FV-07 Role of the *Fusarium tricinctum* species complex in Fusarium Head Blight disease: virulence and mycotoxin production in durum wheat

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Fusarium head blight (FHB) is a worldwide-occurring cereal disease caused by several *Fusarium* species. They often cause indistinguishable symptoms and are responsible for yield losses, grain quality reduction and mycotoxin accumulation in the grains. The most frequent species causing FHB in Italy are: *F. graminearum* (Schwabe), *F. culmorum* (W. G. Sm.) Sacc., *F. poae* (Peck) Wollenw., *F. avenaceum* (Fr.) Sacc. The pathogenic role of the major FHB agents, *F. graminearum* and *F. culmorum*, is well known but little information is available about some of the less virulent species such as *F. acuminatum* and *F. tricinctum*, belonging to the *Fusarium tricinctum* Species Complex (FTSC), which are generally considered of secondary importance. The aim of the present study was to investigate the pathogenic role of the FTSC in greenhouse and field experiments and to evaluate their mycotoxin production. A population of ten FTSC strains isolated from Italian durum wheat grains was characterized both morphologically and molecularly, by partial sequencing of the *translation elongation factor 1-alpha* (*tef 1α*) gene. In addition, the strain capacity to produce secondary metabolites such as enniatins (A, A1, B, B1) and beauvericin both *in vitro* and *in vivo* was also investigated by HPLC-MS/MS. Artificially inoculated durum wheat heads, both in the greenhouse and in the field, allowed for the first time the detection of specific symptoms caused by *F. tricinctum sensu stricto* strains, which caused necrotic "peacock eye" shaped and necrotic spots at the glume level. *In vitro* beauvericin biosynthesis was absent, while enniatins were produced in significant amounts, independently of the phylogenetic group. In the greenhouse experiments, the enniatin amounts detected in durum wheat heads were higher than those of beauvericin. These results are useful to clarify the role of *F. tricinctum sensu stricto*, but further studies are necessary to better understand the role of each species of the FTSC in different climatic and environmental conditions, since their occurrence is increasing in different European areas.

FV-08 Intraspecific trait variations in *Fusarium langsethiae*

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Fusarium langsethiae, a strong producer of T-2 toxin, is distributed over the entire territory of Europe. In Russia, this species is found throughout the European part of the country. We have maintained a collection of 189 strains of *F. langsethiae* isolated from small grain cereals. Most of them (154 strains) were detected in the territory of Russia, and 35 strains originated from Germany, Greece, Finland, Italy, Latvia, Norway, Sweden, and the UK. Our studies considered the variation in diverse traits of *F. langsethiae*, including traditional phenotypes like size or morphology, sensitivity to abiotic factors (the temperature, fungicides application), and molecular-genetic differences.

langsethiae strains have various features, which indicated their high variability. These strains can be classified into prototrophs and auxotrophs (Gavrilova et al., 2017). Our investigations revealed that 24 strains of *F. langsethiae* were spontaneous auxotrophic mutants for biotin, and 4 strains required thiamine as a growth factor. In our collection of *F. langsethiae* strains, the auxotrophic mutants were detected only among strains originating from northern Europe. In addition, the genetic diversity of *F. langsethiae* has been established, which makes it possible to distinguish two subgroups (I and II) within the species (Konstantinova, Yli-Mattila, 2004). Interestingly, *F. langsethiae* strains belonging to subgroup II were detected only among those strains distributed in the northern part of Europe. Moreover, it was found that all strains of subgroup II stop growing at a temperature 30 °C. The development of different intraspecific responses to habitat is a remarkable property of fungi, conferring their broad adaptive capability and adaptation to the environment.

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References:

Gavrilova O., Skritnik A., Gagkaeva T. 2017. Identification and characterization of spontaneous auxotrophic mutants in *Fusarium langsethiae*. *Microorganisms*, 2017, 5 (2), doi: 10.3390/microorganisms5020014.

Konstantinova P., Yli-Mattila T. 2004. IGS-RFLP analysis and development of molecular markers for identification of *F. poae*, *F. langsethiae*, *F. sporotrichioides* and *F. kyushuense*. *Int. J. Food Microbiol.*, 95, 321–331, doi:10.1016/j.ijfoodmicro.2003.12.010