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UNIVERSITÀ POLITECNICA DELLE MARCHE

XXIV National Congress Italian Phytopathological Society (SIPaV)

BOOK OF ABSTRACTS

Ancona, 5-7 September, 2018

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Edited by
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Aula Azzurra

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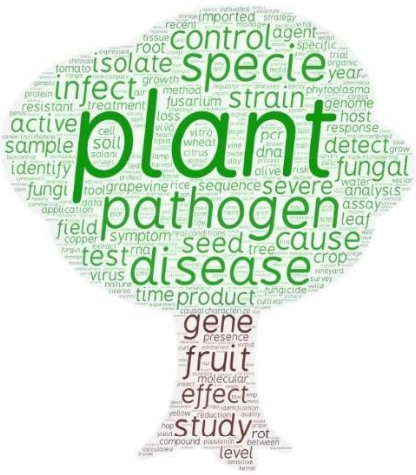

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Assessing the variability of pathogenicity within a group of Italian isolates of *Fusarium verticillioides*, pathogen of *Zea mays*, differing in unique genes of virulence

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The *Fusarium fujikuroi* species complex (FFSC) is one of the largest *Fusarium* complexes. Phylogenetic and molecular analyses show a close relationship within the FFSC species; they may have distinct phenotypic traits, like mycotoxin production, host-specificity and supernumerary chromosomes (SCs) in addition to species-specific core chromosomes that may even differ among isolates in presence/absence, length and gene-abundance. SCs are important in the biology of pathogenic fungi. In a previous study, adopting a bioinformatic approach, we ascertained the presence of "extra" genomic regions (EGRs), a putative SC, in the genome of an Italian *F. verticillioides* isolate ITEM10027, which lacked in the *Fv*. reference genome *Fv*7600. For assessing the putative peculiarity of this EGRs within the Italian fungal strains, we collected *Fv* samples from maize kernels sampled in the whole Po valley, Northern Italy. To select a subset of strains, we analyzed the EGRs presence by a PCR approach (presence/absence). The genomes of 24 strains were sequenced by Illumina MiSeq. A bioinformatic pipeline able of highlighting *inter* and *intra* specific differences within the EGRs among the 24 samples was designed. An interesting set of genes with a Gene Ontology differing among the 24 *Fv* strains were found. *In vivo* pathogenicity assays on *Zea mays* kernels indicated significant difference among the 24 samples. We can argue that some of the unique and specific genes found in the 24 strains may provide a sort of "gain of function" in the pathogenicity toolkit that can possibly explain the difference emerged in the pathogenicity assays *in planta.*