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## *Fusarium verticillioides* Italian isolates are characterized by unique regions

Grottoli A.<sup>1</sup>, Faino L.<sup>1</sup>, Beccaccioli M.<sup>1</sup>, Brown D.W.<sup>2</sup>, Blandino M.<sup>3</sup>, Scala V.<sup>4</sup>, Reverberi M.<sup>1</sup>

<sup>1</sup>Department of Environmental Biology, University of Rome "Sapienza", 00185 Rome, Italy;

<sup>2</sup>US Department of Agriculture, Agriculture Research Service, Peoria, Illinois, USA;

<sup>3</sup>Department of Agricultural, Forest and Food Sciences, Università degli Studi di Torino, Italy;

<sup>4</sup>CREA-DC, 00156 Rome, Italy;

E-mail: alessandro.grottoli@uniroma1.it

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 core chromosomes. These SCs may differ among isolates in presence/absence, length and gene-abundance. SCs are important in the biology of pathogenic fungi. In this study, thought bioinformatics and molecular biology analysis revealed the presence of additional “extra” genomic regions (EGRs) in the genome of Italian *F. verticillioides* strain ITEM10027 which are not present in the *F. verticillioides* strain 7600 reference genome assembly. To assess the distribution of these EGRs within the Italian strains, over 180 *F. verticillioides* were isolated from maize kernels collected between 2013 to 2016 in the whole North Italy Po valley. Twenty-four strains were chosen after an endpoint PCR approach (presence/absence of the EGRs) for genome sequencing by Illumina MiSeq. Over 500 putative genes were found in the EGRs with high identity to different *Fusarium* species, prevalently *F. fujikuroi*, and other Ascomycota fungal species. Interestingly, patterns of presence/absence genes were found among the 24 *F. verticillioides* strains showing a high genetic heterogeneity among the Italian isolates. Moreover, a *Zea mays* kernel infection assay displayed three group of disease severity among the analyzed *F. verticillioides* samples. In order to unravel the genomic organization of the ~500 genes identified in the Italian isolates, two *F. verticillioides* strains were sequenced using Oxford Nanopore Technology allowing us to point out the location of these genes. The analysis revealed that about 80 (20 % of the total identified genes) gene were located in a genomic region of ~700kbp specific to the Italian isolates. These findings open new avenue on the understanding of genome biology and evolution in *F. verticillioides*.