Characterisation of F. musae strains obtained from plants and humans

V. TAVA (1), E. Calastri (2), A. Kunova (3), M. Saracchi (3), A. M. Tortorano (2), M. C. Esposto (2), P. Cortesi (3), M. Brock (4), G. Vande Velde (5), M. Pasquali (3), (1) Università degli studi di Milano, Milano, ITALY; (2) Università degli studi di Milano, Milano, ITALY; (3) DeFENS, Università degli Studi di Milano, Milano, ITALY; (4) University of Nottingham, Nottingham, ENGLAND; (5) KU Leuven, Leuven, BELGIUM S2.21

Fusarium musae was described for the first time as a species in 2011. It appears to have its evolutionary origin within the African clade of the F. fujikuroi species complex. Recent reports have identified F. musae strains in human patients causing various diseases such as nail and skin lesions as well as systemic infections in immunocompromised patients. A worldwide collection of Fusarium strains attributed to F. musae obtained from banana and human patients was characterised phylogenetically using four informative genes β tubulin, Translation Elongation Factor 1 α , DNA-directed RNA polymerase II subunit and calmodulin; appropriate classification of the different strains was then established. The draft genomes of two representative strains colonizing banana and humans were obtained (genome size: 45Mb). Furthermore, the pathogenic behaviour of each strain on detached bananas was investigated, showing the ability of the strains of human origin to cause significant crown rot infection on banana fruit. To identify the virulence and the pathogenicity mechanisms differences of representative strains, Galleria mellonella model is currently being employed. Bioluminescent and fluorescent strains are currently being produced to study the interactions with the different hosts