## Poster Abstract – D.37

## THE GENE ENCODING CERATO-ULMIN, AN *OPHIOSTOMA*-PRODUCED PROTEIN INVOLVED IN THE DUTCH ELM DISEASE, HAS BEEN INTROGRESSED OR HORIZONTALLY TRANSFERRED IN AN UNRELATED SPECIES OF THE GENUS *GEOSMITHIA*

## A. SCALA, C. COMPARINI, S. TEGLI

Department of Agricultural Biotechnology, Laboratory of Molecular Plant Pathology, University of Florence, Via della Lastruccia 10, 50019 Sesto Fiorentino, Italy – aniello.scala@unifi.it

## Ophiostoma, DED, Geosmithia, hydrophobin, cerato-ulmin

Cerato-ulmin (CU) is a class II hydrophobin protein of about 8000 Da, produced by the Ascomycota Ophiostoma novo-ulmi, O. ulmi and O. himal-ulmi (Whiteford and Spanu 2002, Mol Plant Pathology 3: 391–400). They are responsible of the Dutch elm disease (DED), well known to have destroyed in the 20<sup>th</sup> century the most part of native European and North-American elms (Ulmus spp.). CU is a component of the mycelial surface and is released in the medium when the fungus is grown in liquid shake culture (scarcely by O. ulmi). Many evidences suggested a key role of CU in the virulence of DED pathogens (Takai 1974, Nature 252: 124-126), but the involvement of CU in DED pathogenesis is still debated (Del Sorbo et al 2002, In "Advances in microbial toxin research and its biotechnological exploitation", Upadhyay R. (ed.), Kluwer Academic/Plenum Publishers, NY, U.S.A: 93-104). Another ophiostomatacea species, O. quercus, non pathogenic towards elm trees, has been shown to possess the CU protein in the fungal cell walls (Scala et al. 1997, Mycol Research 101: 829-834); recently, the gene encoding CU in O. quercus (cu gene) was isolated and characterized (Scala et al 2005, manuscript). Comparison of the cu gene sequences and of the rDNA regions of various Ophiostomas are consistent with the view that the DED pathogens evolved from O. quercus or from an O. quercus-like fungus (Pipe et al 2000, Mycol Research 148: 533-539). Until now, attempts to find the *cu* gene and/or CU-like protein in other fungal species were unsuccessful.

In this paper we demonstrate that a strain of *Geosmithia* sp., an unrelated species to the genus *Ophiostoma*, possesses the *cu* gene, and a CU-like protein is abundantly excreted in the liquid Takai medium. The strain, named IVV7, was isolated near the Vibo Valentia town (Italy) from elms showing the typical DED symptoms. IVV7 was determined to belong to the genus *Geosmithia* on the basis of the sequences of the internal transcribed spacers 1 and 2 and the 5.8S ribosomal RNA genes. The IVV7 *cu* gene has been isolated using primers based on the published *cu* gene sequence from *O. novo-ulmi* (Bowden et al 1994, Curr Genetics 25: 323-329); the analysis of the sequence showed that the *cu* gene of IVV7 is identical to that of *O. novo-ulmi* (score > 1000; E value = 0.0). The strain IVV7 has been defined on the basis of various morfological, physiological and pathological characters: (i) the morfology of the colony onto Malt Extract Agar (MEA) and of the conidia grown in liquid shake culture in Takai medium; (ii) the radial growth rate on MEA and the temperature growth optimum; (iii) the cerato-ulmin production index, assayed by the turbidimetric method and by ELISA; (iiii) the pathogenicity on elm trees (*Ulmus glabra* Huds.).

The significance of the cu gene presence in a fungal species so distant from the Ophiostomas will be discussed also in order to try to understand if the cu gene has been introgressed in IVV7 by sexual contact and hybridization, or if it has horizontally been transferred via hyphal anastomosis.