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Poster Abstract – C.14

PROTEINS AND GENES INVOLVED IN THE *FUSARIUM OXYSPORUM* F.S. *MELONGENAE* RESISTANCE MECHANISM IN NEW EGGPLANT INTROGRESSED BREEDING LINES

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Interspecific somatic hybridization is considered a valid option to transfer useful agronomic traits, such as disease resistance, from the allied species into *Solanum melongena* L. genome, overcoming the barriers of sexual incompatibility existing between eggplant and its wild relatives.

Dihaploids derived from anther-culture of somatic hybrids between *S. melongena* L. and its wild relative *S. aethiopicum* gr. *aculeatum* (= *S. integrifolium*) were employed in several cycles of backcrosses with eggplant to obtain advanced progenies resistant to the soil borne disease caused by *F. oxysporum* f.s. *melongenae*.

In order to characterize genes involved in the early plant-pathogen interaction occurring in eggplant (or in its wild relatives) when infected with *F. oxysporum*, we analysed the radical extracts from young plants of the susceptible parent *S. melongena* $1F_5(9)$, of the resistant parent *S. integrifolium* and of the resistant backcrossed progeny All 96-6 x $1F_5(9)$.

Plant samples were taken at different times after artificial inoculation by a conidia suspension of *F. oxysporum*. Preliminary chromatographic studies indicated that the most interesting stages for the plant defence response seemed to be included between 8 (T0+8h) and 24 hours (T1) from the inoculation.

First aim of this work was to create a library of genes involved in the host-pathogen interaction: mRNAs were extracted from roots of the resistant genotype All 96-6 x 1F5(9) 8 hours after drenching with the conidia suspension. PCR-select comparison between mRNAs from infected and un-infected tissues led to the subtractive enrichment of the mRNA sample with differentially expressed sequences, 1000 of which were cloned. Confirmation of truly differentially expressed sequences was subsequently obtained through reverse-Northern analysis. Up to now, we chose from the library the most promising 200 cDNAs and their characterization through sequencing analysis is currently underway.

Protein analyses evidenced marked differences between the susceptible and the resistant genotypes. The extracts were fractionated by anionic exchange-high performance liquid chromatography (AE-HPLC) and the eluates of three successive separations were collected every minute for sixteen minutes and pooled. The pools were concentrated about 50 times, analysed through SDS-PAGE and stained by silver staining method. The results indicated the presence, in several fractions, of proteins putatively belonging to the fungus or newly and differently synthesized by the plant in response to the *Fusarium*. Such proteins, of which the molecular weight is known, will be analysed by mass spectrometry and/or MALDI-TOF in order to clarify their chemical identity.