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ANALYSIS OF GENE EXPRESSION ON *FRAGARIA VESCA–RHIZOCTONIA FRAGARIAE* INTERACTION

L. MILELLA. M. LAPELOSA, I. GRECO, G. MARTELLI

Dipartimento di Biologia, Difesa e Biotecnologie Agroforestali - Università degli Studi della Basilicata, Potenza

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Understanding of molecular mechanisms underlying host–pathogen interactions is of primary importance in devising strategies to control diseases. For this purpose, gene expression analysis is massively applied. Differential expressed DNA analysis was applied to characterize *Fragaria vesca –Rhizoctonia fragarie* interaction. Four *Fragaria vesca* genotypes obtained by a breeding programme were analyzed. The genotype analyzed could be classified two as resistant (PZ 99C 101; PZ 99 C102) and the other two as susceptible (PZ 99 SP 7.1; PZ 99 SP 8.1). For each genotype a total of 45 plants were utilized. In particular 25 of them were artificially inoculated with *Rhizoctonia* mycelium, the others were used as tester. Five sampling time were applied (15, 30, 45, 60, 75 days). For each sampling time 5 inoculate and 4 tester plants were collected. Root and leaf were separately stored in liquid nitrogen.

RNA was separately isolated from root and leaf. cDNA was obtained in order to isolate differentially expressed fractions. Specific and random primers were applied both in order to found differentially sequences among genotypes and among the sampling time in the same genotype.

All fragments differentially expressed isolated were sequenced. The sequences obtained were compared to databases to evaluate similarity with genes all ready isolated.

Sequences showed high homology with genes encoding protein with known activity as *β-galactosidase*, chitinase, glucanase etc. The *β-galactosidase* was expressed only in the resistant genotypes starting from the first sampling time. This results, considering the enzymatic activity of this gene, put in evidence a possible indirect control of the pathogen. All fragments isolated were used to produce specific cDNA library.