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CO-TRANSFORMATION OF PECTINASE AND XYLANASE INHIBITORS (PGIP, PMEI AND XI) TO ENHANCE WHEAT RESISTANCE TO FUNGAL DISEASE

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The reinforcement of plant cell wall compartment can efficiently protect plants against those pathogens that need to overcome this barrier to colonize the host tissue. Plant cell wall contains Polygalacturonase inhibitor protein (PGIP) that inhibits the endopolygalacturonase (PG) secreted by pathogens during the initial phase of infection. Moreover, plants cell walls with higher level of methyl esterified pectin are less susceptible to the hydrolysis by pectin enzymes such as fungal PG. The degree of cell wall pectin methyl esterification can be controlled by increasing the level of the protein inhibitor PMEI that inhibit the activity of pectin methyl esterase (PME), that is the enzyme responsible for removing the methyl ester group from the newly synthesized pectin. Cereals contain also xylanase inhibitors (XIs) which inhibit microbial xylanases from glycoside hydrolase families 10 and 11. Endo-β-1,4-xylanases are key enzymes in the degradation of arabinoxylans (AXs), the main non-starch polysaccharides from cereal cell walls.

Transgenic plants overexpressing the bean PvPGIP2 or the kiwi AcPMEI showed increased resistance to fungal pathogens *Bipolaris sorokiniana* and *Fusarium graminearum*, whereas the effect of XI in the defence response has not been yet reported. Transformation experiments using single components makes possible to define the contribution of the specific component. However, the feasibility to test several components at the same time offer the possibility to verify their combined contribution and to reduce the necessary to analyze more components. Moreover, depending on linkage relationships between the transgenes used, transgenic plants with single components can be also obtained. The aim of this study was the determination of the co-transformation frequency of four trangenes, *Pvpgip2, Acpmei, TaxiIII* and *Bar* genes, and their mode of inheritance. The four constructs were co-bombarded into immature embryos of durum wheat cv Svevo. Sixteen transgenic lines were obtained in two separate bombardment experiments. PCR analysis of T0 plants revealed a co-trasformation frequency of all four transgene of about 50%. The segregation frequency in those lines containing the four transgenes were analyzed in the T1 and T2 progenies. Three of these lines showing the three transgenes of interest linked were subjected to infection experiments with *B. sorokiniana*. The analysis of the data showed a significant reduction in symptom severity of about 60% compared with non transgenic plants. Further characterization of the transgenic lines will be also presented.