

Protein identification before and after glyphosate exposure in Italian ryegrass genotypes

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Weeds can reduce crop yields, and among the methods used to control these plants, chemical use is preferred. However, the repeated application of herbicides with the same mechanism of action selects for resistant populations. The aim of this study was to evaluate glyphosate resistance in *Lolium multiflorum* (Lam.) and relate the resistance to protein expression in the absence and presence of the herbicide using a metabolic-proteomic approach. For this, an initial study was done evaluating the resistance factor between genotypes using a dose-response curve with crescent glyphosate concentrations. Later, shikimic pathway metabolites alterations before and after glyphosate spray were calculated (glyphosate, shikimic acid, quinic acid, amino acids and AMPA). In a sequential study, protein expression was determined in each genotype before and after glyphosate spray. Glyphosate resistance was confirmed in one genotype, with a sevenfold difference in resistance between susceptible. Among the possible mechanisms affecting resistance, mutations in the enzyme 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS), herbicide differential translocation and overexpression of EPSPS are suggested. Susceptible plants had higher growth than did resistant plants in the absence of the herbicide, in addition to greater expression of protein groups related to photosynthesis and to tolerance to biotic and abiotic stresses. With application of glyphosate, resistant plants maintained their metabolism and began to express EPSPS and other candidate proteins related to herbicide resistance. In the absence of glyphosate, the susceptible plants should replace the resistant plants over time, and abiotic or biotic stresses could accelerate this.

Palavras-chave: aromatic amino acids, stress tolerance, heat shock protein, shikimic acid

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