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Bio-chemical analysis for resistance to Alternaria alternata early blight disease in potato Solanum tuberosum

Neda Peymani¹, Mehdi Nasr Esfahani^{*2}, Ahmad Reza Golparvar¹, Esmaeil Mahmmodi¹, Majid Shams¹ ¹Department of Agronomy and Plant Breeding, College of Agriculture, Isfahan (Khorasgan) Branch, Islamic Azad University, Isfahan, Iran; ²Plant Protection Research Department, Isfahan Agriculture and Natural Resource Research and Education Center (AREEO), Isfahan, Iran

Early blight disease of potato, caused by the potato pathotype Alternaria alternata (Fr.) Keissler (AA), is one of the most serious fungal diseases to affect potatoes globally. To develop an understanding of how potatoes respond to AA potato pathotype infection, we examined the host transcript accumulation over the period of a week post AA inoculation on three resistant and three susceptible potato genotypes, using marker genes, PR-2, ChtA, PR-5, PR1-b, PIN2, ERF3, PAL and LOX and enzymes activity, catalase (CAT), superoxide dismutase (SOD), peroxidase (POX), polyphenol oxidase (PPOs) and phenylalanine ammonialyase (PAL) analysis. The results indicated expression of PR-2, ChtA, PR-5, PR1-b and PAL genes by qPCR was significantly increased up to 8.61 fold in inoculated resistant genotypes to susceptible and controls, not inoculated potato genotypes. Transcription levels of PIN2, ERF3 and LOX genes were significantly decreased in resistant inoculated potato plants. Activities of POX, SOD and PPOs enzymes were also significantly increased up to 7.40 fold in inoculated resistant potato genotypes, 10/33/R1, 3/33/R2 and 21/33/R2 compared to susceptible and controls. CAT enzyme in 21/33/R2 genotype, and PAL enzyme activity in resistant 21/33/ R2 and 10/33/R1genotypes, showed a significant increase by 3.3 fold in susceptible and control plants. Biomass growth factors (BGPs) showed a decreasing trend in inoculated samples compared to control genotypes. The knowledge obtained from changes in gene expression levels and enzyme production in defense processes in infected potato plants can inform future studies to identify the 🛛 defense mechanism and generate resistant potato cultivars.

Keywords: Alternaria alternata, Antioxidant enzymes, biomass, defense mechanism, qPCR, Solanum tuberosum.

mne2011@gmail.com

