



Bio-chemical analysis in potato genotypes in response to *Alternaria alternata* causing early blight disease

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Abstract:

Solanum tuberosum L. (Solanaceae) known as potatoes is a globally important crop plant producing high yields of nutritionally valuable food in the form of tubers. It has been the focus of substantial study because of its use both as a staple food crop and as a potentially significant source of compounds of interest. One of the serious diseases of potato crops is leaf spot disease, *Alternaria alternata* (Fr.) Keissler (AA), causing brown spots with concentrated rings on the leaves, resulting in leaf death and sever yield losses. Identifying and using resistant sources can be an effective method of control for disease management planning programs. In this study, three resistant (10/33/R1, 3/33/R2 and 21/33/R2) and three susceptible (8707/106, 8703/804 and 8707/112) potato genotypes infected by AA were investigated using: evaluate changes in expression of PR-2, ChtA, PR-5, PR1-b, PIN2, ERF3, PAL and LOX genes by qPCR; and the antioxidant enzymes activity of catalase (CAT), superoxide dismutase (SOD), peroxidase (POD), polyphenol oxidase (PPOs) and phenylalanine ammonia-lyase (PAL) analysis. The results indicated that the expression of PR-2, ChtA, PR-5, PR1-b and PAL genes was significantly increased as high as 8.61 fold in inoculated resistant potato genotypes compared to those of susceptible and control genotypes, non-inoculated ones. Changes in the transcription levels of PIN2, ERF3 and LOX genes in inoculated resistant and susceptible potato genotypes showed a significant decreasing trend compared to controls, non-inoculated ones. Activities of the POD, SOD and PPOs enzymes were significantly increased as high as 7.40 fold in the three inoculated resistant potato genotypes, 10/33/R1, 3/33/R2 and 21/33/R2 compared to controls, non-inoculated ones. CAT enzyme in 21/33/R2 genotype, and PAL enzyme activity in resistant 21/33/R2 and 10/33/R1 genotypes, showed a significant increase as high as 3.3 fold compared to those of susceptible and controls, non-inoculated genotypes. The activity of all the related enzymes in susceptible genotypes did not change significantly after inoculation compared to controls, non-inoculated ones. Changes in biomass factors showed a decreasing trend in inoculated samples compared to the control, non-inoculated genotypes. The knowledge obtained from changes in gene expression levels, enzyme production and changes in biomass growth parameters in defense processes in infected potato plants can be determi-



native in future studies to identify the defense mechanism and generate resistant potato cultivars.

Biography:

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Publication of speakers:

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3. Hashemi, Lida & Nasr Esfahani, Mehdi & Golabadi, Maryam. (2020). Expression analysis of defense-related genes in cucumber (*Cucumis sativus* L.) against *Phytophthora melonis*. *Molecular Biology Reports*. 47. 10.1007/s11033-020-05520-5.
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