

Title Comparative analysis of proteome changes induced by the two spotted spider mite *Tetranychus urticae* and methyl jasmonate in citrus leaves

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Abstract

Citrus plants are currently facing biotic and abiotic stresses. Therefore, the characterization of molecular traits involved in the response mechanisms to stress could facilitate selection of resistant varieties. Although large cDNA microarray profiling has been generated in citrus tissues, the available protein expression data are scarce. In this study, to identify differentially expressed proteins in *Citrus clementina* leaves after infestation by the two-spotted spider mite *Tetranychus urticae*, a proteome comparison was undertaken using two-dimensional gel electrophoresis. The citrus leaf proteome profile was also compared with that of leaves treated over 0–72 h with methyl jasmonate, a compound playing a key role in the defense mechanisms of plants to insect/arthropod attack. Significant variations were observed for 110 protein spots after spider mite infestation and 67 protein spots after MeJA treatments. Of these, 50 proteins were successfully identified by liquid chromatography–mass spectrometry–tandem mass spectrometry. The majority constituted photosynthesis- and metabolism-related proteins. Five were oxidative stress associated enzymes, including phospholipid glutathione peroxidase, a salt stressed associated protein, ascorbate peroxidase and Mn-superoxide dismutase. Seven were defense-related proteins, such as the pathogenesis-related acidic chitinase, the protease inhibitor miraculin-like protein, and a lectin-like protein. This is the first report of differentially regulated proteins after *T. urticae* attack and exogenous MeJA application in citrus leaves.