

PROTEOMIC ANALYSIS OF *CUCUMIS MELO* L. PHLOEM AS AN APPROACH TO STUDY RESISTANCE TO *BEMISIA TABACI* GENN

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Bemisia tabaci Genn, a phloem-feeding insect, constitutes one of the most harmful pests affecting melon (*Cucumis melo* L.). It causes important crop losses due to direct feeding damage being also an efficient vector of important viruses. Recent reports indicate that *Cucumis sativus* phloem sap contains several defense proteins against biotic and abiotic stresses (Walz et al., 2004). If these proteins are present in whitefly resistant melon genotypes they could be associated to melon resistance to whitefly and could be used as markers in plant breeding programmes. In order to test this hypothesis, a preliminary proteomic analysis of the melon phloem is being carried out. Three melon genotypes were evaluated: 'Bola de Oro', a Spanish cultivar highly susceptible to *Bemisia tabaci*, 'TGR-1551', a Zimbabwean genotype and 'PI 414723', an Indian genotype, the last two ones being partially resistant to *B. tabaci*. Phloem exudate was collected from melon leaves 8 days after whitefly release on plants. Proteins were precipitated by acetone-0.1 M HCl, dissolved in Laemmli buffer and subjected to SDS-PAGE, being the gels Coomassie stained. Qualitative and quantitative differences in the protein banding between genotypes and treatments (infected and non-infected) were observed. Differential protein bands were subjected to MS analysis after trypsin digestion, with some of them being identified as peroxidases, lipoxygenases and lectins. A 17 kDa phloem protein, corresponding to a RNA-binding protein (Gómez et al., 2005), was detected in 'Bola de Oro' and 'PI 414723' but not in 'TGR-1551'. So far, any of the defense proteins found in *C. sativus* was found in melon genotypes.

Work is now in progress by using a more powerful and resolutive technique as it is two-dimensional gel electrophoresis. 2-DE Coomassie stained gels of phloem proteins from the three genotypes, including infected and non-infected plants, have been analyzed, and differences among genotypes and treatments were observed. The responses to whitefly was genotype-dependent, with 'Bola de Oro' and 'PI 414723' showing more quantitative and qualitative differences than 'TGR-1551'. Differential spots are now being subjected to MS analysis for identification.

Gómez G, Torres H and Pallàs V. Identification of translocatable RNA-binding phloem proteins from melon, potential components of the long-distance RNA transport system. *The Plant Journal* 2005, 41: 107-116.

Walz C, Giavalisco P, Schad M, Juenger M, Klose J and Kehr J. Proteomics of cucurbit phloem exudate reveals a network of defense proteins. *Phytochemistry* 2004, 65: 1795-1804.