

## SUMMARY

### RESPONSE OF THREE VARIETAL GROUPS OF *Sechium edule* (Jacq.) Swartz INOCULATED WITH *Phytophthora capsici*

*Phytophthora capsici* causes destructive diseases in Solanaceae and Cucurbitaceae crops throughout the world. *P. capsici* has been identified as the causal agent of chayote wilt (*Sechium edule*) and is present in the productive soils of this crop. On the other hand, Veracruz is a state that harbors a great wealth within the species, with different phenotypic characteristics among fruits, forming different varietal groups, which have been little studied regarding their resistance, tolerance or susceptibility to pathogens. Therefore, the objective of this work was to characterize the responses of three varietal groups of chayote (*S. edule* var. *virens levis*, *S. edule* var. *nigrum xalapensis* and *S. edule* var. *albus dulcis*) inoculated with *P. capsici*. Symptomatology of plants and the expression of defense-related genes in plants during wilting of the plant were evaluated, in order to understand the mechanisms that regulate plant defense responses and identify the varietal group with greater resistance or tolerance to inoculation with the oomycete. Fifteen plants of three weeks of age of each varietal group were evaluated. They were inoculated with *P. capsici*, measuring the length of the necrosis in the transition zone between the stem and the root, and the percentage of leaves withered throughout 11 days, to later design a scale of severity and build a curve of the progress of the disease (AUDPC). On the other hand, six pairs of defense-related gene primers were designed: a glutathione-S-transferase (GST), an ethylene response factor (ERF), two proteins with leucine-rich repeats and a binding site nucleotides (NBS-LRR), and two mitogen-activated protein kinases (MAPK), were used to evaluate their expression in foliar tissue of plants inoculated with *P. capsici* at different post-inoculation times (0, 0.25, 1.5 and 24 h). The results showed that *S. edule* var. *nigrum xalapensis* was the most tolerant, followed by *S. edule* var. *virens levis* and the most susceptible was *S. edule* var. *albus dulcis*, with average AUDPC values of 4.5, 6.7 and 8.5, respectively. Regarding to gene expression, it was observed that GST1 was expressed only in the varietal group *S. edule* var. *virens levis* in different times, that is why it is difficult to relate the expression of GST1 with tolerance. In MAPK1 the gene expression was homogeneous except for *S. edule* var. *albus dulcis* where it was expressed with less intensity and at times 1.5 and 24 h is observed more reduced, coinciding with the greater susceptibility to oomycete in the AUDPC. In NBS-LRR1 there is a silencing in the gene expression in *S. edule* var. *albus dulcis* in the post-inoculation times 1.5 and 24 h. in MAPK3 and NBS-LRR2 no expression was registered.

Key words: Varietal groups, GST, MAPK, NBS-LRR, AUDPC, Necrosis in the transition zone of stem and roots