



EVALUATION OF THE MORPHOLOGIC, POLLEN VIABILITY AND GERMINATION IN PROGENY OF THE FIRST BACKCROSS GENERATION OF PASSIONFRUIT

*Onildo, NJ*¹, Soares, TL¹, Oliveira, EJ¹, Santos, TCP², Farias, DH², Bruckner, CH³, Novaes, QS⁴

onildo.nunes@embrapa.br

¹Embrapa Cassava & Tropical Fruits, Cruz das Almas (BA), Brazil

² Federal University of Recôncavo da Bahia, Cruz das Almas (BA), Brazil

³Federal University of Viçosa, Viçosa (MG), Brazil

⁴State University of Southwest Bahia, Vitória da Conquista (BA), Brazil

Brazil is considered the main center of the genetic diversity and greatest worldwide producer of passionfruit. This fruit is severely attacked by many phytosanitary problems, especially by the passionfruit woodiness virus which leads to severe losses in yield. Wild species of Passiflora are valuable sources of genetic resistance to this disease. Interspecific crosses is a promising method to incorporate characteristics of interest in commercial species (P.edulis f. flavicarpa Deg.), despite problems with male sterility of the developed hybrids. The objective of the present work was to characterize morphologically, and by viability and in vitro germination of pollen grains, progenitors as well as progenies of the first generation of backcross -BC1 [(P. edulis f. flavicarpa x P.cincinnata Mast.) x P. edulis f. flavicarpa]. For the virus analysis most genotypes were considered susceptible to highly susceptible. The resistant hybrids did not show symptoms of evident foliar deformation. Cluster analysis showed two major groups; one represented by P. cincinnata and the other by the hybrids and recurrent progenitor P. edulis. Morphological characterization of the hybrids showed phenotypic variation as to the color and shape of flowers; although these descriptors were not accurate to properly differentiate the progenies. As expected, the progenitors (*P. edulise P. cincinnata*) presented higher percentage of pollen viability, followed by the RC1-H45 progenies. The progenies of the BC1 will also be evaluated with molecular markers aiming to accelerate the selection of hybrids with higher percentage of the genome of the recurrent parent.