

QUALITATIVE AND QUANTITATIVE CHARACTERIZATION OF A PINEAPPLE BC1 FAMILY DURING SEXUAL AND CLONAL CYCLES

Junghans, DT¹, Curado, M², Santos Filho, SA²

davi.junghans@embrapa.br

¹Embrapa Cassava & Fruits, Cruz das Almas, Brazil

²Universidade Federal do Recôncavo da Bahia, Cruz das Almas, Brazil

A pineapple backcrossed progeny, consisting of 92 genotypes from the cross between hybrid 60 (Perolera x Smooth Cayenne) and the Smooth Cayenne cultivar was evaluated in the sexual cycle (plants from seeds) and clonal cycle (plants from shoots) using 12 and 16 qualitative and quantitative, plant and fruit variables, respectively. During the sexual cycle one plant was evaluated per genotype. During the clonal cycle the number of plants varied from one to 12 plants/genotype. The variables showed, on average, higher values in the clonal cycle than in the sexual cycle due to the environment. Considering the main selection criteria in pineapple breeding, six genotypes (6.52% of the population) would be selected in the sexual cycle for the clonal cycle. Using the same criteria, eight genotypes (8.69% of the population) would be selected during the clonal cycle. Some genotypes that would be discarded in the sexual cycle (# 43, 90, 129 and 172) were selected in the clonal cycle. Other genotypes selected in the sexual cycle did not show the same performance in the clonal cycle (# 13 and 16). Furthermore, a third group of genotypes (# 1, 3, 5 and 6), selected during the sexual cycle, maintained their good performance and are possible candidates to be released as a new cultivar. This strategy showed that it is very important to optimize the environmental conditions during the sexual cycle in order to reduce errors caused by the elimination of promising genotypes.