

ADAPTABILITY AND STABILITY FOR FRUIT QUALITY OF HALF-SIBS PROGENIES OF *ANNONA SQUAMOSA* L. USING METHODOLOGY OF MIXED MODELS

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RESUMO

The pine (*Annona squamosa* L.) is plant of medicinal potential, with the bioactive principles in mosting parts (fruits, seeds and leaves). The objective this work was to estimate the genetic parameters, predict the genotypic gains for fruit quality and select progenies of half-sibs of *A. squamosa* based on stability and adaptability. Parental genotypes were selected from the *A. squamosa* germplasm collection by Unimontes. To obtain the four progenies, fruits from natural pollination were selected, identified: UNI-1 (1), UNI-2 (2), UNI-3 (3) and UNI-4 (4), distributed in the experimental area in DBC, with three replications and a plot containing five plants. Were evaluated the length (LFr) and diameter (DFr) the fruits (mm); mass fresh the fruit (MFr), pulp (MP) (grams); and contente of soluble solids (SS) (°Brix), of four harvests. The analyzes were made via mixed models, using the REML/BLUP procedure, the model was the 62, using Selegen®. It was observed for individual heritability among progenies values of 39% (LFr), 35% (DFr), 36% (MFr), 35% (MP), and 0.03% (SS). The genotypes were highlighted: 47 (UNI-2), 11 (UNI-3) for CFr, DFr, MFr, MP and 12 (UNI-3) for SS. There was agreement between the methods of MHVG (which refers to stability), PRVG (adaptability) and MHPRVG (stability and adaptability interaction), for CFr, DFr and MFr highlighted the progenies 1, 2, 3 and 4. The three parameters nor did differ for SS, highlighting progenies 3, 4, 2 and 1, indicating a high stability and adaptability in the face of harvests variations. The results of the estimates of stability and adaptability for the MP character did not differ (1,2,4 and 3), indicating that the progenies of better adaptability are the same for stability. Considering the results of the present work, genotypes 47 (UNI-2) and 11; 12 (UNI-3) are very promising to continue the breeding program.

PALAVRAS-CHAVE: *Annona squamosa* L, REML/BLUP method, Genotype selection

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