



Prediction of genetic gains in fruit production of six full sib families of *Passiflora edulis*

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Sour passion fruit (*Passiflora edulis*) occupies important place in the Brazilian agriculture, being Brazil the largest world producer. However, its production has declined in the last decade caused by several factors. Among them, the viral disease known as fruit woodiness caused by *Cowpea aphid-borne mosaic virus* (CABMV). This disease causes a distortion in the development of plants affecting fruit production and reducing the lifespan of the crop. Due to the lack of cultivars resistant to CABMV to reduce production losses, the goal of the current study was to establish the genetic parameters and predict the genetic gain of fruit production in six full sib families from the second backcross generation (RC_2) of CABMV resistant passion fruit. The experimental design was a randomized block with six blocks containing six full sib families (17, 153, 293, 355, 501 and 516). The characteristics of total fruit production (TFP), number of fruits per plant (NF), average fruit weight (AFW) and productivity (P) were used to evaluate the genotypes. The analyzes were performed via the REML/BLUP using Selegen genetic analysis software, model 147. The genotypic variation in relation to the phenotypic variation was 23.88% for TFP, 30.95% for NF, 17.63% for AFW, and 23.63% for P. This genetic parameter showed that the inheritable portion of the evaluated characteristics and the predicted genotypic values are low. This indicates to which extent the environment influences these characteristics. The average inheritability of the progenies (h^2_{mp}) for the four characteristics predicted values above 95%. This indicates that in order to select genotypes more precisely, the selection must be based on the family. Nevertheless, the inheritability in the narrow-sense (h^2_a) varied from 35% to 62%, thus selection among individuals can also be considered to maintain genetic variability within the passion fruit breeding program. The accuracy was classified as very high ($\geq 95\%$) showing high precision in the predicted values and making the selection of individuals more reliable and concise. The families 293 and 355 showed the best genetic gains and performances for the characteristics linked to fruit production. Genotypes of these families are the most suitable to continue the passion fruit breeding program, aiming to find resistance to CABMV.

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