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Individual selection of the first backcross generation of passion fruit potentially resistant to the fruit woodiness disease

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Abstract: The REML/BLUP procedure has been successfully used for genetic progress through individual selection of high-yielding passion fruit genotypes resistant to the *Cowpea aphid-borne mosaic virus*. This study was thus developed to estimate genetic parameters and predict the gain obtained from individual selection of genotypes in a population derived from backcrosses in passion fruit. The experiment was set up as a randomized block design with four replicates, involving five full-sib families (genotypes from the first backcross). Variance components and the genetic values were estimated for eight agronomic traits via the REML/BLUP procedure. For all traits, genotypic variance between the genotypes from the first backcross showed little contribution to the phenotypic variance. The low heritability estimates obtained for the traits are overcome via individual BLUP estimates. Therefore, it was possible to obtain considerable gains with individual selection for the variables fruit length, average fruit weight, and pulp weight (19.50 to 14.04%; 22.93 to 17.97%; and 10.08 to 7.95%, respectively). For the traits showing lower gains, it is possible to obtain gains indirectly by selecting genotypes for correlated traits. Because this population derives from the first backcross generation, agronomic traits still must be recovered.

Key words: Interspecific hybridization, *P. edulis*, REML/BLUP, virus.

INTRODUCTION

Brazil is the largest producer of passion fruits (*Passiflora edulis*), whose harvest in the year 2017 amounted to 703,489 t (IBGE 2018). However, its production and productivity have been undermined by several phytosanitary problems.

The fruit woodiness (hardening) disease caused by the *cowpea aphid-borne mosaic virus* (CABMV), transmitted non-persistently by several aphid species, is considered one of the most economically relevant diseases affecting this crop. Infected plants have a reduction in

their leaf area and fruit weight, which culminate in decreased number, quality, and commercial value of their fruits. Losses caused by CABMV infection are considered a very serious problem for the crop, as it can affect 100% of orchards, rendering passion fruit growing unfeasible (Nascimento et al. 2004, Cerqueira-Silva et al. 2008).

There are no efficient means of controlling this disease. Thus, the development of CABMV-resistant cultivars would be a viable alternative, since no resistant passion fruit cultivar has been registered to the present date despite

the endeavors put forward through different strategies. There are, however, reports of resistance to CABMV in various wild species (Maciel et al. 2009, Oliveira et al. 2013, Gonçalves et al. 2018) and interspecific hybrids (Freitas et al. 2015, Santos et al. 2015a).

Interspecific hybrids resistant to CABMV do not possess agronomic traits desirable to the consumer; for this reason, the genome of the commercial species (*P. edulis*) must be recovered. A possible method for genome recovery is backcrossing. For a trait whose expression is controlled by many genes, this method can also be efficient in the transfer, although the effective number of individuals in the population must be increased (Borém et al. 2017).

In addition to disease resistance, the breeding of passion fruit is also aimed at meeting the demands of the consumer market, especially in terms of fruit production and quality, requiring the use of more-accurate selection procedures (Freitas et al. 2016). In this context, the mixed models methodology emerges as an optimal procedure for plant selection. This methodology involves the estimation of variance components by the Restricted Maximum Likelihood (REML) method and prediction of genotypic values by the Best Linear Unbiased Prediction (BLUP), resulting in a selection process of greater accuracy. The use of BLUP in the selection of genotypes is highly advantageous in that it predicts genetic values free of environmental effects (Resende 2002, Viana & Resende 2014).

This method is very promising, especially for passion fruit breeding programs aimed at resistance to CABMV (Freitas et al. 2016). Problems inherent to the germination of progeny derived from interspecific crosses contribute to the existence of an uneven number of plants within each family, and thus imbalance becomes inevitable. Coupled with this fact, a high number of plants must be evaluated to elevate the

chances of selecting the desired plant. For this reason, mixed models have great applicability, since they allow for balancing, in addition to correcting the data for environmental effects and precisely and unbiasedly predicting genetic values, leading to maximized genetic gains from selection (Resende et al. 2001).

The objectives of the present study were: i) to estimate genetic parameters for agronomic traits; ii) to obtain individual genetic values via the mixed models methodology (REML/BLUP); and iii) to select superior genotypes obtained from segregating populations derived from the first backcross generation between *P. edulis* and interspecific hybrids, aiming at generation advance in the passion fruit breeding program under development at the Universidade Estadual do Norte Fluminense Darcy Ribeiro.

MATERIALS AND METHODS

Passion fruit breeding program and origin of the backcross populations

Three hundred genotypes from the first backcross generation of the passion fruit breeding program developed at the Universidade Estadual do Norte Fluminense Darcy Ribeiro (UENF) were evaluated in this study. These genotypes originate from five full-sib families (Table I) and were characterized to resistance to CABMV (Preisigke 2017).

The backcrosses were made in the experimental area of the Escola Técnica Estadual Agrícola Antônio Sarlo, located in Campos dos Goytacazes - RJ, Brazil (21° 45' S, 41° 20' W, 11 m altitude), where the hybrids obtained by Santos et al. (2015a) were trained. Pollinations were carried out before flower opening, starting at 10h00. By that time, the *P. edulis* anthers were already open. *Passiflora edulis* genotypes were used as male parents and interspecific hybrids were used as female parents. Flower buds of

Table I. Study populations origin and identification of composed of full-sib families (FSF), interspecific hybrids (IH), *P. setacea* and *P. edulis*, and genotypes distribution on the experimental area. Campos dos Goytacazes, RJ, 2017.

| Description | Crossings | Genotypes total number | Evaluated genotypes number |
|-----------------------------|---------------------------|------------------------|----------------------------|
| FSF1* | HI5-14 x <i>P. edulis</i> | 160 | 85 |
| FSF2 | HI1-15 x <i>P. edulis</i> | 160 | 79 |
| FSF3 | HI5-16 x <i>P. edulis</i> | 160 | 87 |
| FSF4 | HI5-1 x <i>P. edulis</i> | 72 | 35 |
| FSF5 | HI2-10 x <i>P. edulis</i> | 48 | 14 |
| Parent HI5-14** | Ps 367 x Pe 139 (40) | 12 | - |
| Parent HI1-15 | Pe 139 (40) x Ps 367 | 12 | - |
| Parent HI5-16 | Ps 367 x Pe 139 (40) | 12 | - |
| Parent HI5-1 | Ps 367 x Pe 139 (40) | 12 | - |
| Parent HI2-10 | Pe 139 (38) x Ps 367 | 12 | - |
| Parent <i>P. edulis</i> | ***PMGMA-UENF | 12 | - |
| ProParent <i>P. setacea</i> | BAG from UENF | 12 | - |
| Total | | 704 | 300 |

* Full-sib families - backcrossing first generation.

** Selected interspecific hybrids (Santos et al. 2015a). Pe= *P. edulis*; Ps= *P. setacea*.

*** Passion fruit genetic breeding program by recurrent selection (PMGMA-UENF).

the hybrids were emasculated and pollinated with pollen from the *P. edulis* genotypes and subsequently protected. These crosses originated five full-sib families.

Experimental procedures

The seeds obtained from full-sib families were washed in running water and kept for 15 min in a solution containing 50% sodium hypochlorite and 50% water. After washing, they remained in water for 3 h. Seeds were sown in 128-cell Styrofoam trays containing organic substrate and kept in a fog chamber until the seedling stage. Subsequently, they were transplanted to black polyethylene bags with 1-L capacity containing vegetable soil, substrate, and sand (1:1:1 ratio) and transferred to a greenhouse. After 95 days, in October 2015, seedlings were transplanted to the experimental area of the Escola Técnica Estadual Agrícola Antônio Sarlo. The experiment was set up as a randomized

block design with four replicates unbalanced for plants within families.

Plants were trained in the field using vertical stakes with 2.5-m-high fence posts spaced 4 m apart, with 12-gauge wire at 1.80 m from the soil. The distance between planting rows and furrows was 3.5 m and 2 m, respectively. Upon planting, 10 L cattle manure, 200 g limestone, 400 g single superphosphate, and 250 g potassium chloride were applied in the furrows. The drip irrigation system was adopted.

Evaluated traits and estimates of genetic parameters

The fruit harvest and evaluation period began in March 2016 and ended in January 2017. Three hundred genotypes were evaluated, all of which produced at least one fruit per plant. All plants bearing fruit were evaluated. Plant that produced up to 15 fruits were sampled 15 times. The following traits were evaluated:

- Number of fruits per plant (NF): fruits were harvested twice weekly for nine months, and at the end of the evaluation period, the total number of fruits per genotype was counted;
- Fruit length (FL): determined in the longitudinal region of the fruits using a caliper ruler, expressed in mm;
- Total fruit weight (TFW): all ripe fruits collected throughout the evaluation period were weighed on a semi-analytical digital scale and their weight was expressed in grams;
- Average fruit weight (AFW): determined as the arithmetic mean of one sampling of at least one and at most 15 fruits from each genotype. Fruits were weighed individually on a semi-analytical digital scale and their weight was expressed in grams;
- Pulp weight (PW): calculated as the arithmetic mean of one sampling of at least one and at most 15 fruits from each genotype, obtained by weighing the pulp (seeds with aril) on a semi-analytical scale, expressed in grams;
- Peel thickness (PT): determined as the arithmetic means of the measurements of four points of the outer peel, using a digital caliper, expressed in millimeters;
- Soluble solids content (SSC): obtained by refractometry, using a portable digital refractometer with reading performed in the range of 0 to 32 °Brix;
- Number of seeds (NS): determined as the arithmetic mean one sampling of at least one and at most 15 fruits from each genotype, counted individually per fruit.

Variance components (REML) and additive genetic effects predicted by BLUP were estimated for each trait. Analyses were carried out using Selegen-Reml/Blup software (Resende 2016),

which followed the statistical model, where y is the vector of observations; r is the vector of replicate effects (assumed fixed) added to the overall mean; g is the vector of individual genotypic effects (assumed random); p is the vector of plot effects (random); and e is the vector of errors or residuals (random). Uppercase letters represent the incidence matrices for the said effects.

The following variance components (REML) were estimated:

$\hat{\sigma}_g^2$: genotypic variance between full-sib progeny, corresponding to $\frac{1}{2}$ of the additive genetic variance plus $\frac{1}{4}$ of the dominance genetic variance, ignoring epistasis;

σ^2_{within} : residual variance within the plot;

$\hat{\sigma}_f^2$: individual phenotypic variance;

\hat{h}^2_a : individual narrow-sense heritability, obtained by ignoring the fraction ($\frac{1}{4}$) of dominance genetic variance;

\hat{h}^2_{mp} : heritability of the progeny mean, assuming complete survival;

Acprog : progeny selection accuracy, assuming complete survival.

This model allows for the evaluation of individuals in full-sib progenies with various observations per plot. The evaluation took place in one location, in a randomized block design with several plants per plot.

The significance of model effects was estimated by deviance analysis, as recommended by Resende (2007). Deviances were obtained by analyses with and without the g effects. Subsequently, the deviance without the said effect was subtracted from each deviance of the full model and it was confronted with the chi-squared value with one degree of freedom, at the 1% and 5% probability levels.

Additionally, the simple correlation for each pair of traits was calculated using GENES software (Cruz 2013).

RESULTS AND DISCUSSION

Nature of the variances: genetic or environmental

For all traits, genotypic variance contributed little to phenotypic variance, ranging from 1035.41 to 0.0014 for total fruit weight (TFW) and soluble solids content (SSC), respectively (Table II). Fruit length, AFW, and PT were the only the traits that showed significance by the chi-square test for the estimates of genetic variance. Consequently, these traits had higher heritability and selection-accuracy values.

Individual narrow-sense heritability for all traits was of low magnitude, ranging from 0.37 to 0.00087 (Table II). For the traits NF, TFW, PW, SSC, and NS, the additive narrow-sense heritabilities were practically zero. Santos et al. (2015b) evaluated a population of interspecific hybrids and observed values of 0.50, 0.25, 0.61, and 0.62 for the traits NF, AFW, PT, PW, and SSC, which are higher than those obtained in the current study. A possible cause for such discrepancies is the genetic structure of the population, considering that in this experiment the progeny derived from backcrosses with the commercial species. By contrast, in the study of Santos et al. (2015b), the progeny derived from contrasting interspecific crosses which greater genetic variability, with contributed to the high magnitudes of that parameter.

The low heritability estimates found in this study, both in the individual narrow sense and on the basis of the family means, may be related to several factors, e.g., the polygenic nature of those traits, which are highly influenced by the environment; the low genetic variability between the studied genotypes; and, mainly, the size of the experimental plot. In this study, the effective number of genotypes was very large requiring large growing areas, and this might have contributed to the greater within-plot

heterogeneity. The higher variance observed within the plot (Table II) might have affected the evaluation of the genotypes performance, as might the estimates of variance components. This can be prevented by reducing the number of genotypes within the plot and increasing the number of replicates.

Fruit length, PT, and AFW showed the highest h^2_a values: 0.37, 0.18, and 0.11, respectively (Table II), considered low according to the classification of Resende (2002). Similar values were found by Santos et al. (2015b) for the traits FL (0.26) and AFW (0.25). As regards the trait PT, Assunção et al. (2015) studied a passion fruit population and obtained a higher h^2_a (0.41) than that observed here. The individual narrow-sense heritability values obtained for those traits in our study indicate that it is possible to obtain greater gains from individual selection of genotypes for those traits.

The low heritability estimates obtained for the traits NF, TFW, PW, SSC, and NS are overcome via individual BLUP estimates, since, despite this low-heritability character, genetic gains are predicted and the genotypes have the potential to be selected for future generations (Santos et al. 2015b). On the other hand, the estimates obtained for FL, AFW, and PT allow for considerable gains with individual selection of genotypes.

Just as for h^2_a : individual heritability in the narrow sense the traits FL, PT, and AFW had higher h^2_{mp} estimates: 0.95, 0.89, and 0.86, respectively (Table II). In this situation, selection can be effective by using information of the families or of individual genotypes, given the fact that individual narrow-sense heritability estimates and those based on the family mean were significant. However, individual heritability is more important for the passion fruit breeding program aimed at resistance to CABMV, since this is a segregating population from which

the best genotypes are selected for generation advance.

In terms of selection accuracy, breeders should aim for values higher than 70% (Resende 2007). In the present study, estimates higher than 70% were observed for the traits FL, AFW, PW, and PT (Table II). As described by Resende (2007), these accuracy estimates are highly precise, facilitating the identification and selection of genotypes with desirable traits. Number of fruits, TFW, SSC, and NS, on the other hand, showed low selection accuracy, which is due to the low heritability and genetic variability between the genotypes evaluated for those traits, making selection of superior genotypes for those traits a difficult task. However, it is known that heritability is not immutable and that it is not conditioned only to the trait but also to the population, to environmental conditions, and to the experimental designs to which the population was subjected. In this way, those estimates can be improved in future assessments (Falconer 1987, Ferreira et al. 2016).

Correlation analysis suggests that in addition to the gain obtained with direct selection by estimating individual BLUPs for traits with low heritability estimates, it is possible to obtain gains indirectly by selecting correlated traits. In this way, by selecting genotypes for FL, one can obtain gains with selection for the traits TFW (0.129), AFW (0.731), PW (0.628), and NS (0.568) (Table III), since they are positively correlated. Selecting genotypes for AFW may result in gains for TFW (0.262), FL (0.731), PW (0.896), PT (0.259), and NS (0.842). When genotypes are selected for the trait PT, gains can be achieved for AFW (0.259), SSC (0.178), and NS (0.159) (Table III).

Selection of genotypes and estimates of gains via BLUP

The 15 best genotypes were ranked for each analyzed variable, corresponding to 5% of the evaluated genotypes. Genetic gains were predicted and the new means were estimated (Table IV).

Despite the low heritability of the evaluated agronomic traits in the selection of genotypes,

Table II. Estimates of genetic parameters in passion fruit segregating populations by REML procedure for characteristics number of fruits per plant (NF), fruit length (FL), total fruit weight (TFW), average fruit weight (AFW), pulp weight (PW), peel thickness (PT), soluble solids content (SSC) and number of seeds (NS).

| Genetic Parameters | NF | FL | TFW | AFW | PW | PT | SSC | NS |
|--------------------|-----------------------|-----------------------|------------------------|-----------------------|------------------------|----------------------|------------------------|-----------------------|
| σ_g^2 | 0.274 | 17.060 | 1035.410 | 35.168 | 3.010 | 0.248 | 0.0014 | 2.149 |
| σ_f^2 | 462.847 | 90.591 | 2370367.075 | 586.836 | 164.787 | 2.648 | 2.399 | 1909.300 |
| h_a^2 | 0.0011 ± 0.0080 | 0.3766 ± 0.1417 | 0.00087 ± 0.0068 | 0.1198 ± 0.0800 | 0.03654 ± 0.0441 | 0.18748 ± 0.10 | 0.00124 ± 0.0082 | 0.0022 ± 0.0110 |
| h^2_{mp} | 0.058 | 0.957 | 0.043 | 0.866 | 0.603 | 0.894 | 0.059 | 0.089 |
| Ac_{prog} | 0.241 | 0.978 | 0.208 | 0.930 | 0.777 | 0.945 | 0.244 | 0.299 |
| LRT(χ^2) | 0.01 ^{ns} | 12.62 ^{**} | 0.0 ^{ns} | 5.72 [*] | 0.89 ^{ns} | 5.97 [*] | 0.0 ^{ns} | 0.03 ^{ns} |
| Average | 16.126 | 65.760 | 1027.202 | 62.602 | 23.661 | 7.809 | 13.341 | 82.845 |

σ_g^2 : Genotypic variance between passion fruit families; σ_f^2 : individual phenotypic variance; h_a^2 : individual heritability in the narrow sense; h^2_{mp} : heritability at family-based mean level; Ac_{prog} : accuracy of family selection. LRT(χ^2): likelihood ratio test.

* and **: Significant by the chi-squared test at 5% (3.84) and 1% (6.63) respectively. ns: not significant.

Table III. Estimates of phenotypic correlations for number of fruits per plant (NF), fruit length (FL), total fruit weight (TFW), average fruit weight (AFW), pulp weight (PW), peel thickness (PT), soluble solids content (SSC) and number of seeds (NS) in full-sib families from the backcross first generation in passion fruit for resistance to CABMV, Campos dos Goytacazes-RJ, in the agricultural year 2016/2017.

| Traits | FL | TFW | AFW | PW | PT | SSC | NS |
|--------|----------------------|---------|---------------------|---------------------|---------------------|----------------------|---------------------|
| NF | -0.030 ^{ns} | 0.886** | 0.029 ^{ns} | 0.013 ^{ns} | 0.015 ^{ns} | 0.074 ^{ns} | 0.027 ^{ns} |
| FL | | 0.129* | 0.731** | 0.628** | 0.087 ^{ns} | -0.021 ^{ns} | 0.568** |
| TFW | | | 0.262** | 0.229** | 0.062 ^{ns} | 0.103 ^{ns} | 0.237** |
| AFW | | | | 0.896** | 0.259** | -0.019 ^{ns} | 0.842** |
| PW | | | | | 0.101 ^{ns} | 0.075 ^{ns} | 0.929** |
| PT | | | | | | 0.178** | 0.159** |
| SSC | | | | | | | 0.096 ^{ns} |

**** and*** Significant at 1% and 5% probability by the t test, respectively.

ns: not significant.

relevant gains could be obtained in selection for some traits via individual BLUP estimates. For the traits SSC (0.07 to 0.06%) and NS (0.75 to 0.63%) (Table IV), gains were practically inexistent. The increase in mean values for these traits varied little between the first- and last-ranked genotypes.

The low gain for the trait SSC is linked to the little genetic variability among the genotypes. This finding confirms the low gains (between -0.42 and 0.95%) reported by other authors for SSC (Krause et al. 2012, Silva & Viana 2012, Assunção et al. 2015). On the other hand, Santos et al. (2015b) and Freitas et al. (2016) described higher gains for SSC in segregating populations of passion fruit: 13.43% and 7.88%, respectively. Because these are interspecific hybrids derived from parents that contrast for this trait, genetic variability is higher, resulting in the possibility of gains from selection. In the population of the present study, though, genetic variability is lower, since it derives from the first backcross generation. However, gains can be obtained indirectly for SSC via selection for PT, since these two are correlated.

The trait NS was highly influenced by environmental factors, since only 2.14 of the total

190.30 phenotypic variance are due to genotypic variance (Table II), which complicates the selection of superior genotypes. Nevertheless, by selecting genotypes for the traits FL, AFW, and PW, which obtained expressive gains, one can obtain gains for NS, since they are strongly correlated.

The highest gains were obtained for the variables FL, AFW, and PW (19.50 to 14.04%; 22.93 to 17.97%; and 10.08 to 7.95%, respectively) (Table IV), indicating success in selection for those traits. These findings corroborate Silva et al. (2017), who evaluated a population of passion fruit in the third cycle of recurrent selection and observed gains similar to the above-mentioned ones for those traits.

Gains predicted for PT were substantial, despite the low genetic heritability value observed. For this trait, it is desired to reduce its mean. These results suggest the possibility of improving this trait. Many authors have reported lower estimates for gains from selection for PT (Krause et al. 2012, Assunção et al. 2015, Santos et al. 2015b, Silva et al. 2017). Peel thickness is an important trait for both the concentrated-juice industry and for the fresh-fruit market, as

it is inversely proportional to juice yield (Vianna-Silva et al. 2010).

For TFW and NF, low gains were obtained with selection: 1.17 and 1.33%, respectively (Table IV). These production-related traits showed elevated phenotypic variance values as compared with genotypic variance, indicating greater environmental influence on their expression. Santos et al. (2015b) evaluated a population of interspecific hybrids (*P. edulis* × *P. setacea*) and obtained a gain of 319.15% for NF. Freitas et al. (2016) also evaluated the same population of interspecific hybrids, in two harvests, and reported high gains for the traits NF (305.97%) and TFW (167.18%). These estimates were much higher than those obtained in this study. The backcross population (BC₁) might have contributed to these lower gains, since the genotypes are more homogeneous and thus have lower genetic variability. However, gains can be obtained for TFW by selecting genotypes for CP, AFW, and PW, which are correlated traits (Table III).

Regarding selection among the 15 best genotypes for fruit quality, genotype 223 ranked best for FL, AFW, PW, and NS (Table IV); i.e., this genotype has good fruit quality, but low production. Gains predicted with the selection of this genotype were 19.50, 22.93, 10.08, and

0.74% for FL, AFW, PW, and NS, respectively (Table IV). For the production traits NF and TFW, the best-ranking genotypes were 553, 391, 387, and 81, whose gains ranged from 1.33 to 1.24% for NF and 1.17 to 0.83% for TFW (Table IV). In addition to displaying good agronomic performance, genotypes 223 and 553 were resistant and genotypes 391, 387 and 81 were moderately resistant to the fruit woodiness disease (Table IV), in a study led by Preisigke (2017).

Because this population is derived from the first backcross generation, agronomic traits must still be recovered, although some genotypes closer to recurrent parent *P. edulis* were identified.

CONCLUSIONS

Despite the low heritabilities for all traits, gains could be obtained with selection via estimation of individual BLUPs. The traits fruit length, peel thickness, and average fruit weight showed the highest heritability values. Selecting genotypes based on those traits provides greater gains. Genotypes 223, 553, 391, 387, and 81 ranked best for fruit quality, number of fruits, and total fruit weight; therefore, they can be used for the continuity of the passion fruit breeding program developed at UENF.

Table IV. Ranking of the 30 genotypes with the highest estimates for additive genetic value (a), genetic gains and new predicted averages, estimated by REML / BLUP, in passion fruit genotypes from the first backcrosses generation.

| Order | Progeny (AUDPC) | Fruit number (plant) | | Progeny (AUDPC) | Fruit length (mm) | | Progeny (AUDPC) | Total fruit weight (g) | | Average fruit weight (g) | |
|-------|--------------------|----------------------|-------------|---------------------|-------------------|-------------|--------------------|------------------------|-------------|--------------------------|-------------|
| | | Gain (%) | New average | | Gain (%) | New average | | Gain (%) | New average | Gain (%) | New average |
| 1 | 553 (472.5) | 1.33 | 16.34 | 223 (487.5) | 19.50 | 78.59 | 391 (667.5) | 1.17 | 1039.22 | 22.93 | 76.96 |
| 2 | 387 (693.7) | 1.30 | 16.34 | 384 (615) | 17.64 | 77.36 | 81 (765) | 0.99 | 1037.37 | 21.16 | 75.85 |
| 3 | 81 (765) | 1.26 | 16.33 | 377 (667.5) | 16.76 | 76.78 | 387 (693.7) | 0.92 | 1036.70 | 20.50 | 75.43 |
| 4 | 391 (667.5) | 1.24 | 16.33 | 520 (412.5) | 16.24 | 76.44 | 259 (566.2) | 0.88 | 1036.29 | 20.14 | 75.21 |
| 5 | 83 (851) | 1.23 | 16.32 | 518 (491.25) | 15.86 | 76.19 | 87 (562.5) | 0.86 | 1036.04 | 19.75 | 74.97 |
| 6 | 246 (483.7) | 1.21 | 16.32 | 206 (480) | 15.53 | 75.97 | 83 (851.25) | 0.84 | 1035.85 | 19.40 | 74.75 |
| 7 | 87 (562.5) | 1.19 | 16.32 | 50 (828.75) | 15.28 | 75.81 | 553 (472.5) | 0.83 | 1035.72 | 19.12 | 74.57 |
| 8 | 259 (566.2) | 1.18 | 16.32 | 363 (540) | 15.08 | 75.67 | 261 (1162) | 0.81 | 1035.56 | 18.91 | 74.44 |
| 9 | 545 (615) | 1.16 | 16.31 | 521 (487.5) | 14.90 | 75.56 | 99 (645) | 0.80 | 1035.42 | 18.73 | 74.33 |
| 10 | 94 (521.2) | 1.15 | 16.31 | 354 (622.5) | 14.75 | 75.46 | 246 (483.7) | 0.79 | 1035.30 | 18.58 | 74.23 |
| 11 | 261 (1162) | 1.13 | 16.31 | 80 (528.7) | 14.60 | 75.36 | 94 (521.2) | 0.78 | 1035.19 | 18.45 | 74.15 |
| 12 | 251 (480) | 1.12 | 16.31 | 213 (423.7) | 14.47 | 75.27 | 545 (615) | 0.77 | 1035.10 | 18.33 | 74.08 |
| 13 | 113 (693.7) | 1.11 | 16.31 | 372 (1012.5) | 14.35 | 75.20 | 251 (480) | 0.76 | 1035.01 | 18.21 | 74.00 |
| 14 | 268 (907.5) | 1.11 | 16.30 | 367 (866.25) | 14.18 | 75.09 | 268 (907.5) | 0.75 | 1034.93 | 18.08 | 73.92 |
| 15 | 551 (645) | 1.10 | 16.30 | 529 (821.2) | 14.04 | 74.99 | 85 (682.5) | 0.75 | 1034.86 | 17.97 | 73.85 |

Table IV (continuation)

| Order | Progeny (AUDPC) | Pulp weight (g) | | Progeny (AUDPC) | Peel thickness (mm) | | Progeny (AUDPC) | Soluble solids content (° brix) | | Progeny (AUDPC) | | Number of seeds | |
|-------|--------------------|-----------------|-------------|---------------------|---------------------|-------------|---------------------|---------------------------------|-------------|---------------------|-------------|-----------------|--|
| | | Gain (%) | New average | | Gain (%) | New average | | Gain (%) | New average | Gain (%) | New average | | |
| 1 | 223 (487.5) | 10.08 | 26.05 | 435 (660) | 1.26 | 7.91 | 149 (690) | 0.07 | 13.35 | 384 (615) | 0.75 | 83.47 | |
| 2 | 384 (615) | 9.68 | 25.95 | 276 (738.75) | 1.30 | 7.91 | 293 (427) | 0.07 | 13.35 | 223 (487.5) | 0.74 | 83.46 | |
| 3 | 200 (495) | 9.27 | 25.86 | 430 (562.5) | 1.34 | 7.91 | 142 (615) | 0.07 | 13.35 | 206 (480) | 0.72 | 83.44 | |
| 4 | 51 (858.7) | 8.99 | 25.79 | 437 (660) | 1.38 | 7.92 | 294 (690) | 0.07 | 13.35 | 52 (855) | 0.70 | 83.43 | |
| 5 | 52 (855) | 8.79 | 25.74 | 584 (416.25) | 1.42 | 7.92 | 448 (446) | 0.07 | 13.35 | 532 (637.5) | 0.69 | 83.41 | |
| 6 | 530 (821.2) | 8.62 | 25.70 | 125 (1001.2) | 1.46 | 7.92 | 600 (457) | 0.07 | 13.35 | 377 (667.5) | 0.68 | 83.41 | |
| 7 | 206 (480) | 8.50 | 25.67 | 440 (633.7) | 1.50 | 7.93 | 145 (738.7) | 0.07 | 13.35 | 354 (622.5) | 0.67 | 83.40 | |
| 8 | 377 (667.5) | 8.41 | 25.65 | 283 (618.75) | 1.54 | 7.93 | 143 (735) | 0.07 | 13.35 | 218 (600) | 0.66 | 83.39 | |
| 9 | 506 (401.2) | 8.33 | 25.63 | 427 (461.25) | 1.58 | 7.93 | 291 (468.75) | 0.06 | 13.35 | 529 (821.2) | 0.66 | 83.39 | |
| 10 | 359 (663.7) | 8.25 | 25.61 | 289 (468.75) | 1.61 | 7.94 | 292 (795) | 0.06 | 13.35 | 65 (675) | 0.65 | 83.39 | |
| 11 | 529 (821.2) | 8.17 | 25.60 | 126 (806.25) | 1.65 | 7.94 | 597 (431.25) | 0.06 | 13.35 | 200 (495) | 0.65 | 83.38 | |
| 12 | 194 (615) | 8.11 | 25.58 | 589 (735) | 1.69 | 7.94 | 147 (870) | 0.06 | 13.35 | 531 (637.5) | 0.64 | 83.38 | |
| 13 | 218 (600) | 8.05 | 25.57 | 135 (813.75) | 1.72 | 7.94 | 141 (735) | 0.06 | 13.35 | 530 (821.2) | 0.64 | 83.38 | |
| 14 | 520 (412.5) | 8.00 | 25.55 | 432 (573.7) | 1.76 | 7.95 | 594 (573.75) | 0.06 | 13.35 | 372 (1012.5) | 0.64 | 83.37 | |
| 15 | 372 (1012) | 7.95 | 25.54 | 134 (652.5) | 1.80 | 7.95 | 587 (468.75) | 0.06 | 13.35 | 506 (401.25) | 0.63 | 83.37 | |

AUDPC- Area under the disease progress curve. The AUDPC was estimated for young leaves and total plant area using a scale of scores. After the estimates, an average was obtained from the AUDPCs.

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