Ciência Rural, Santa Maria, v.50:10, e20190976, 2020
http://doi.org/10.1590/0103-8478cr20190976
ISSNe 1678-4596
CROP PRODUCTION

Estimates of genetic parameters, genetic variability, and selection in the S_1 generation of peach

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ABSTRACT: *The growing of peach in mild winter regions is made viable through the use of genotypes that have low need for cold conditions, and this is one of the main aims of breeding for these regions. Thus, the aims of this study were to estimate genetic parameters, evaluate genetic variability, and select families adapted to mild winter regions in the S_1 generation of peach through mixed model methodology (REML/BLUP). For that purpose, 22 populations, 84 families, and 2090 individuals were evaluated for the following traits: bud burst rate (BR), node density (ND), plant height (PH), and trunk diameter (TD). Genetic variability was found for all the traits. Individual heritability in the broad sense was of low and medium magnitudes. The PH trait had positive genotypic correlation of high magnitude with TD. The ND trait had moderate negative genotypic correlation with PH and TD. Clustering by the Tocher method resulted in the formation of six mutually exclusive groups. Considering selection intensity of 25%, simultaneous selection for BR, ND, and TD led to predicted gains of 11.3% for BR, 9.7% for ND, -14.2% for PH, and -14.3% for TD, showing the great potential of the germplasm evaluated.*

Key words: *Prunus persica, REML/BLUP, genotypic correlation, fruit tree breeding.*

Estimativas de parâmetros genéticos, variabilidade genética e seleção em geração S_1 de pessegueiros

RESUMO: *O cultivo do pessegueiro em regiões de inverno ameno é viabilizado pela utilização de genótipos que apresentam baixa necessidade de frio, sendo este um dos principais objetivos do melhoramento para essas regiões. Assim, os objetivos deste estudo foram estimar parâmetros genéticos, avaliar a variabilidade genética e selecionar famílias adaptadas a regiões de inverno ameno em geração S_1 de pessegueiros via metodologia de modelos mistos (REML/BLUP). Para isso, 22 populações, 84 famílias e 2090 indivíduos foram avaliados quanto as características: taxa de brotação (TB), densidade de nós (DN), altura da planta (AP) e diâmetro do tronco (DT). Verificou-se variabilidade genética para todas as características. As herdabilidades individuais no sentido amplo foram de baixa e média magnitudes. A característica AP apresentou correlação genética positiva de magnitude elevada com DT. A característica DN apresentou correlação genética negativa moderada com AP e DT. O agrupamento pelo método de Tocher resultou na formação de seis grupos mutuamente excludentes. Considerando intensidade de seleção de 25%, a seleção simultânea para TB, DN e DT propiciou ganhos preditos de 11.3% para TB, 9.7% para DN, -14.2% para AP e -14.3% para DT, evidenciando o grande potencial do germoplasma avaliado.*

Palavras-chave: *Prunus persica, REML/BLUP, correlação genética, melhoramento de fruteiras.*

INTRODUCTION

Peach (*Prunus persica* (L.) Batsch) is an autogamous species, originally adapted to temperate and subtropical zones, that needs a certain accumulation of winter cold after entering in dormancy to have normal flowering and budding. Growing in regions with mild winters, typical of subtropical regions or high altitude tropical regions, becomes possible with the use of genotypes that have low need for cold (RASEIRA& NAKASU, 2002; HAWERROTH et al., 2009).

Flowering time is generally used to evaluate the need for cold of the genotypes, and those least demanding in terms of cold are considered; i.e., those most adapted to regions of mild winter are those that achieve a determined flowering rate (generally 50% open flowers) at an earlier time (PEDRO JÚNIOR, 2007). However, as the vegetative buds also have the need for cold to break dormancy, determination of the budburst rate can likewise be used for the purpose of identifying more adapted genotypes (WAGNER JÚNIOR et al., 2010).

According to PÉREZ-GONZÁLEZ (2002), vigor, after the first and second cycles in the field, evaluated through trunk diameter, is recognized as an important indicator of adaptation of the genotypes

Received 12.10.19 Approved 05.07.20 Returned by the author 07.28.20
CR-2019-0976.R1

to subtropical conditions. That author observed that greater trunk diameter is associated with lower need for cold to break dormancy.

Due to the high cost of labor in fruit growing, studies have been performed aiming to obtain smaller size plants through exploitation of new types of growth habit, adoption of new ways of training the plant, and selection of dwarf rootstock to ease management and allow greater mechanization in the orchards (BYRNE, 2005).

Most traits of economic importance in peach crop are of quantitative inheritance. Thus, estimation of genetic parameters and prediction of genetic values are essential activities in peach breeding programs. The standard procedure of estimation/prediction is that of Restricted Maximum Likelihood/Best Linear Unbiased Prediction (REML/BLUP) (RESENDE, 2016). However, estimates of genetic parameters are rare in peach trees (MILATOVIĆ et al., 2010; SILVA et al., 2020; SOUZA et al., 1998a; SOUZA et al., 1998b).

Based on the above considerations, the aims of this study were to estimate genetic parameters, evaluate genetic variability, and select families adapted to regions of mild winter in the S_1 generation of peach through mixed model methodology (REML/BLUP).

MATERIALS AND METHODS

Experimental data

The 22 populations of peach (including nectarines) evaluated in this study originated from natural self-pollination of S_0 plants obtained from single crosses involving nineteen peach and nectarine genotypes. The populations contained from six to 693 individuals each, totaling 2090 individuals, distributed in 84 families. Among the parent plants are cultivars with low and medium need for cold released by the Instituto Agronômico de Campinas (IAC) and the Centro de Pesquisa Agropecuária de Clima Temperado (CPACT/EMBRAPA) and selections obtained by the Peach Breeding Program of the Universidade Federal de Viçosa (UFV).

The experiment was set up in field, in the municipality of Araponga, MG, Brazil (20°40’S and 42°31’W; 885 m ASL), in a completely randomized design at a spacing of 3.5 m between rows and 0.5 m between plants. Climate in the region according to the Köppen classification is Cwb (ANTUNES, 1986). Plants were trained in the “central leader” system. Traits evaluated at two years after planting were bud break rate of lateral buds in mixed branches (BR), node density in mixed branches (ND), plant height (PH), and trunk diameter (TD).

The BR and ND traits were obtained after determination of the number of nodes, vegetative buds, and sprouts on mixed branches (productive branches of one year of age containing vegetative and flowering buds) during the spring, after natural release from the period of dormancy. Two branches per individual, one from each side of the plant, turned toward the between-row area, were evaluated. Lengths of the branches were measured with a metric measuring tape. BR was expressed as the percentage value of buds that sprouted in relation to the total number of vegetative buds. The ND was expressed as the number of nodes per linear meter of branch. The TD was obtained at 10 centimeters (cm) from ground level using a digital caliper, with results expressed in cm. The PH was obtained using a ruler, with results expressed in meters (m). Evaluations were made in September 2006 after flowering and sprouting.

Statistical analyses

The REML method (PATTERSON & THOMPSON, 1971) was used to estimate the variance components, and the BLUP method (HENDERSON, 1975) was used to predict the genetic values. The statistical model was given by the following equation: $y=Xu+Za+Wp+e$, in which y is the vector of phenotypic data, u is the scalar in reference to the effect of the overall mean (fixed effect), a is the vector of the individual additive genetic effects (assumed as random) [$a{\sim}N(0,\sigma_a^2)$, in which σ_a^2 is the additive genetic variance among families], p is the vector of the effects of populations (assumed as random) [$p{\sim}N(0,\sigma_p^2)$, in which σ_p^2 is the genetic variance among populations], and e is the residual vector (random) [$e{\sim}N(0,\sigma_e^2)$, in which σ_e^2 is the residual variance]. X, Z, and W represent the incidence matrices for the u, a, and p effects, respectively.

Genetic variance among families (σ_g^2), individual phenotypic variance (σ^2_{phen}), individual broad sense heritability (h_g^2), coefficient of determination of the genetic effects of populations (c_p^2), total heritability (among and within populations) (h_r^2), individual genetic coefficient of variation (CV_g), residual coefficient of variation (CV_e), and relative coefficient of variation (CV_r) were obtained, respectively, by the following expressions (RESENDE, 2002; 2007a):

$$\sigma_g^2 = \sigma_a^2 + (1/4)\sigma_d^2,\ \sigma_{phen}^2 = \sigma_g^2 + \sigma_p^2 + \sigma_e^2,$$

$$h_g^2 = \sigma_g^2/\sigma_{phen}^2,\ c_p^2 = \sigma_p^2/\sigma_{phen}^2,\ h_t^2 = (\sigma_g^2 + \sigma_p^2)/\sigma_{phen}^2,$$

$CV_g = \left(\sqrt{\sigma_g^2}/\mu\right)100$, $CV_e = \left(\sqrt{\sigma_e^2}/\mu\right)100$, and $CV_r = CV_g/CV_e$, in which σ_d^2 is the dominance genetic variance, and μ is the overall mean.

The genotypic correlations (Pearson correlation) were obtained using the predict genetic values. The significance of the genotypic correlation coefficients was tested by the t-test, using following expression: $t_c = r\sqrt{(n-2)/(1-r^2)}$, in which r is the genotypic correlation coefficient, and n is the number of individuals (2090). Genetic variability among families was evaluated based on mean genetic Euclidean distances, and clustering was made by the Tocher method. Ranking of the genotypes was obtained by the mean rank index adapted from MULAMBA & MOCK (1978), based on the BR, ND, and TD traits, seeking to maximize BR and ND and minimize TD; and the intensity of selection was 25%. All statistical analyses were performed through the Selegen-REML/BLUP software (RESENDE, 2007b; RESENDE, 2016).

RESULTS AND DISCUSSION

According to the standard deviations of the estimates of broad-sense individual heritability and of coefficient of determination of the genetic effects of populations, there are genetic variability among families and populations for all the traits evaluated (Table 1). Genetic variances among families were greater than the variances among populations for all the traits, especially for ND, PH, and TD. Values of residual variance near the values of phenotypic variance were obtained for the BR and ND traits, resulting in high residual coefficients of variation (Table 1).

The lowest coefficient of genetic variation was obtained for the ND trait (10.9%) and the highest for the TD trait (19.8%). This coefficient allows inferences to be made regarding the magnitude of the variability present in the populations and serves to compare the levels of variability between different populations and traits. This is possible because the coefficient of genetic variation is expressed in relation to the mean value of the traits in the populations. Coefficients of genetic variation of around 10% or more are sufficient for practicing effective selection (RESENDE, 2002).

Coefficients of relative variation were lower than one for all the traits evaluated, since most of the variation was due to non-controlled environmental effects (Table 1). According to RESENDE (1997), the estimated individual heritability in the broad sense are of low ($0.01 \leq h^2 \leq 0.15$) and medium ($0.15 < h^2 < 0.50$) magnitudes. The lowest estimate was obtained

Table 1 - Estimates of variance components and genetic and non-genetic parameters for the following traits: budburst rate (BR), node density (ND), plant height (PH), and trunk diameter (TD), evaluated in 2090 S_1 individuals of peach.

Estimate	BR (%)	ND	PH (m)	TD (cm)
σ_g^2	44.4909*	15.9370*	0.1798*	0.4673*
σ_p^2	36.5594*	3.5789*	0.0414*	0.0889*
σ_e^2	338.7026	110.4571	0.2861	1.3575
σ_{phen}^2	419.7529	129.9730	0.5073	1.9138
h_g^2	0.11±0.02	0.12±0.02	0.35±0.04	0.24±0.03
c_p^2	0.09±0.019	0.03±0.011	0.08±0.017	0.05±0.014
h_t^2	0.19	0.15	0.44	0.29
$CV_g(\%)$	14.8	10.9	19.2	19.8
$CV_e(\%)$	40.9	28.6	24.2	33.7
CV_r	0.36	0.38	0.79	0.59
μ	44.99	36.79	2.21	3.46

σ_g^2: genetic variance among families, σ_p^2: genetic variance among populations, σ_e^2: residual variance, σ_{phen}^2: individual phenotypic variance, h_g^2: individual broad sense heritability, c_p^2: coefficient of determination of the genetic effects of populations, h_t^2: total heritability (among and within populations), CV_g: individual genetic coefficient of variation, CV_e: residual coefficient of variation, CV_r: relative coefficient of variation, and μ: overall mean. *:significant by the t Student test.

for the BR trait (0.11) and the highest for the PH trait (0.35) (Table 1).

The estimated total heritability for ND was of low magnitude (0.15). SOUZA et al. (1998b) obtained narrow-sense heritability for ND of 0.48 in peach trees of 3 years of age. As heritability is a specific parameter of each population, differences among estimates in the different studies are expected. The fact that the population studied by the authors cited above was S_0 and the data were collected over two years may explain the higher value of heritability reported. According to BORÉM et al. (2017), the heritability estimates vary according to the method of estimation, the diversity of the population, the level of inbreeding of the population, the number of environments considered, and the accuracy in carrying out the experiment and collecting data, among others.

The TD and PH traits, which indicated vigor, are important for definition of the spacing to be adopted in the orchard and for decision making regarding management practices. The trunk basal area is a reference, for example, for calculating the amount of fruit that should remain on the plant after thinning (SCARPARE FILHO et al., 2000).

The ND is a trait that affects the number of vegetative and flowering buds on the mixed branch of peach and; consequently, the amount of fruit per plant. In each node of the productive branch (mixed branch), on average, from one to two flower buds are observed (SOUZA et al., 1998b; BASSI, 2008).

Not every flowering bud is converted into harvested fruit, and abortion of buds, flowers, and fruit compromises potential production. The two risk factors that lead to the need for selection of genotypes with a moderate to high number of flowering buds on the plant are frosts and abortion of flowers due to pollen infertility problems. In most of the genotypes grown, flower bud density is high, and thinning of fruit is recommended for the purpose of obtaining fruit of greater size and quality (SCARPARE FILHO et al., 2000).

The PH and TD traits showed high genotypic correlation (0.94) (Table 2). According to ALVES et al. (2018), pleiotropy and genetic linkage are the two main causes to genotypic correlations. Thus, the same genes must be involved in control of growth and diameter. That way, in future evaluations, one of these characteristics alone can be chosen for purposes of selection. The most recommended is TD, since it is more easily measured and less subject to phenotyping errors.

The ND trait showed moderate negative genotypic correlation with PH (-0.56) and TD (-0.54) (Table 2), indicating that direct selection aiming at an increase in ND will result in a decrease in PH and TD. Greater ND along with lower PH is favorable to modern production systems that aim greater crop density. The greater concentration of flower buds that is expected because of greater node density tends to result in higher production. Thus, these negative correlations observed are favorable to the aims of breeding because they make it easier to select high yielding genotypes with smaller size. Genotypes that have greater ND consequently have shorter internodes. That way, lower vigor genotypes (lower PH and TD) have shorter internodes.

The clustering promoted by the Tocher method based on mean Euclidean distances of the predicted genetic values resulted in the formation of six mutually exclusive groups. Groups I, II, III, IV, V, and VI were formed by 68, 5, 5, 3, 2, and 1 families, respectively (Table 3). In plant breeding, Tocher´s clustering is very useful in the orientation of selection of parents, which, when crossed, increase the chances of obtaining superior genotypes.

Clustering did not place all the families that originally belonged to the same population within the same group. This result can be explained by the fact that some parents are common to different crosses that generated the populations. The cross between genotypes belonging to different groups is recommended with the aim of maximizing genetic variability and heterosis (for characteristics that exhibit dominance) in the segregating populations (RESENDE, 2002).

The genetic variability in the germplasm evaluated can be exploited on the level of populations, families, and individuals. Selection indices which aim to gain in a genotypic aggregate formed by various traits normally lead to more balanced gains

Table 2 - Genotypic correlation coefficients among the following traits: budburst rate (BR), node density (ND), plant height (PH), and trunk diameter (TD), evaluated in 2090 S_1individuals of peach.

	ND	PH	TD
BR	0.02^{ns}	0.06^{*}	0.05^{*}
ND		-0.56^{*}	-0.54^{*}
PH			0.94^{*}

^{ns} and *: not significant and significant at 5% probability by the t-test. The null hypothesis tested was that the genotypic correlation coefficient did not differ from zero.

Table 3 - Groups of genetic similarity obtained by the Tocher method considering the following traits: budburst rate (BR), node density (ND), plant height (PH), and trunk diameter (TD) evaluated in 2090 S_1individuals of peach.

Group	Families
I	2003 2803 6103 8103 8403 9303 2303 4703 5603 9503 9903 4103 6203 4503 5303 6603 3003 3403 4003 4403 7803 7903 8503 8903 9403 2103 7403 2503 9103 3803 4603 5003 6003 1903 3703 6903 7703 9203 403 603 3503 3603 3903 4203 7103 8003 1303 2603 803 1603 2703 5403 5803 6403 1203 1803 8203 2403 3103 8703 203 1103 2903 6303 7003 1003 4903 5703
II	4803 2203 6503 6703 5503
III	3303 9003 7203 5103 303
IV	503 1503 9703
V	1403 4303
VI	703

(RESENDE, 2002). Using the mean rank index adapted from MULAMBA & MOCK (1978), seeking to increase the BR and ND traits and decrease the TD trait, and considering selection intensity of 25% (21 families), the predicted gains from selection were 11.3% for BR, 9.7% for ND, -14.2% for PH, and -14.3% for TD. In addition, it was reported that 15 of the 22 populations were represented in the selection. The total number of individuals selected was 539.

Genotypes with higher BR are not only more adapted to the edaphic and climatic conditions of the place of evaluation, but also result in a greater number of leaves and accumulation of photoassimilates for fruit development and for accumulation of plant reserves. In addition, as peach bears fruit on one-year-old branches, a higher BR ensures continuity of plant production in the next crop year. In contrast, an exaggerated increase in BR can result in greater self-shading and greater need for pruning. Therefore, evaluation of the optimal range of BR may be the aim of new studies.

An increase in ND is desirable to obtain genotypes with a larger number of flowering buds and thus ensure higher production in the face of possible risks of abortion of buds, flowers, and fruit as a result of biotic and abiotic factors. Nothing impedes selection of genotypes with greater internode lengths and that have fruit set compatible with the size and vigor of the branches so as to obtain larger fruit.

For the PH and TD traits, the two directions of selection (increase or decrease) can be taken, especially depending on the spacing to be adopted. More vigorous genotypes may be recommended for greater spacing, while those of small size should be recommended preferentially for smaller spacing. It is noteworthy that commercial orchards are formed through vegetative propagation.

In Brazil, the seedling is predominantly formed with the use of grafting of fragments containing vegetative buds from the canopy cultivar on rootstocks obtained from seeds. The TD, PH, and canopy volume traits, which express vigor, are affected by the specific rootstock *x* canopy cultivar combination (MARRA et al., 2013). The main line of investigation seeking to understand that interaction is related to changes in the level of endogenous hormones among the different plant organs (JACKSON, 1993). Anatomical differences of xylem vessels in the rootstock regarding diameter and number are also studied. According to TOMBESI et al. (2011), less vigorous rootstocks have more slender xylem vessels and lower hydraulic conductivity. It is expected that canopy genotypes that grow at greater rates end up producing trees with larger canopies, combined to normal (non-dwarf) rootstocks. In this case, selecting genotypes with lower vigor is advantageous when selection is directed to denser plantings.

Although, adaptation is the basis for success in growing peach in regions of mild winter, a genotype will only be released as a cultivar if it has fruit characteristics compatible with the demands of the consumer market. Most of the genotypes used as parents in crosses to obtain the populations evaluated in this study are cultivars. Therefore, it is expected that the descendants have attributes that make them attractive to producers and consumers.

CONCLUSION

The genetic materials are promising for resistance to mild winter regions. For the next step in this breeding program, the cross between genotypes with high genetic values and belonging to different groups is recommended with the aim of maximizing genetic variability and heterosis in the segregating populations. Results obtained in this study can add important information to the literature and practice of peach breeding.

ACKNOWLEDGMENTS

We appreciate the financial support from the Brazilian government offered through the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) and the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES) - Finance Code 001.

DECLARATION OF CONFLICTS OF INTERESTS

The authors declare no conflict of interest. The founding sponsors had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, and in the decision to publish the results.

AUTHORS' CONTRIBUTIONS

All authors contributed equally for the conception and writing of the manuscript. All authors critically revised the manuscript and approved of the final version.

REFERENCES

ALVES, R.S. et al. Multiple-trait BLUP: a suitable strategy for genetic selection of *Eucalyptus*. **Tree Genetics & Genomes**, v.14, n.77, 2018. Available from: <https://doi.org/10.1007/s11295-018-1292-7>. Accessed: Jul. 04, 2020. doi: 10.1007/s11295-018-1292-7.

ANTUNES, F.Z. Caracterização climática do Estado de Minas Gerais. **Informe Agropecuário**, v.12, n.138, p.9-13, 1986. Not available.

BASSI, D.; MONET, R. Botany and taxonomy. In: LAYNE, D.R. **The peach: botany, production and uses**. Wallingford: CABI, 2008. 615p.

BORÉM, A. et al. **Melhoramento de plantas**. Viçosa: Editora UFV, 2017. 543p.7ed.

BYRNE, D.H. Trends in stone fruit cultivar development. **HortTechnology**, v.15, n.3, p.494-500, 2005. Available from: <https://doi.org/10.21273/HORTTECH.15.3.0494>. Accessed: Jul. 04, 2020. doi: 10.21273/HORTTECH.15.3.0494.

HAWERROTH, F.J. et al. Efeito do frio e do desponte na brotação de gemas em pessegueiro. **Revista Brasileira de Fruticultura**, v.31, n.2, p.440-446, 2009. Available from: <http://dx.doi.org/10.1590/S0100-29452009000200018>. Accessed: Jul. 04, 2020. doi: 10.1590/S0100-29452009000200018.

HENDERSON, C.R. Best linear unbiased estimation and prediction under a selection model. **Biometrics**, v.31, p.423-447, 1975. Available from: <https://www.jstor.org/stable/2529430>. Accessed: Jul. 04, 2020. doi: 10.2307/2529430.

JACKSON, M. B. Are plant hormones involved in root to shoot communication? **Advanced Botanical Research**, v.19, p.104-181, 1993. Available from: <https://doi.org/10.1016/S0065-2296(08)60204-9>. Accessed: Jul. 04, 2020. doi: 10.1016/S0065-2296(08)60204-9.

MARRA, F.P. et al. Growth, yield and fruit quality of 'Tropic Snow' peach on size-controlling rootstocks under dry Mediterranean climates. **Scientia Horticulturae**, v.160, n.27, p.274-282, 2013. Available from: <https://doi.org/10.1016/j.scienta.2013.06.004>. Accessed: Jul. 04, 2020. doi: 10.1016/j.scienta.2013.06.004.

MILATOVIĆ, D. et al. Variability, heritability and correlations of some factors affecting productivity in peach. **HortScience**, v.37, p.79-87, 2010. Available from: <https://doi.org/10.17221/63/2009-HORTSCI>. Accessed: Jul. 04, 2020. doi: 10.17221/63/2009-HORTSCI.

MULAMBA, N.N.; MOCK, J.J. Improvement of yield potential of the Eto Blanco maize (*Zea mays* L.) population by breeding for plant traits. **Egyptian Journal of Genetics and Cytology**, v.7, n.1, p.40-51, 1978. Not available.

PATTERSON, H.D.; THOMPSON, R. Recovery of inter-block information when block sizes are unequal. **Biometrika**, v.58, n.3, p.545-554, 1971. Available from: <https://www.jstor.org/stable/2334389>. Accessed: Jul. 04, 2020. doi: 10.2307/2334389.

PEDRO JÚNIOR, M.J. et al. Época de florescimento e horas de frio para pessegueiros e nectarineiras. **Revista Brasileira de Fruticultura**, v.29, n.3, p.425-430, 2007. Available from: <http://dx.doi.org/10.1590/S0100-29452007000300005>. Accessed: Jul. 04, 2020. doi: 10.1590/S0100-29452007000300005.

PÉREZ-GONZÁLEZ, S. Variables associated with evolution and adaptation of peach seedlings to subtropical environments. **Acta Horticulturae**, v.592, p.143-148, 2002. Not available.

RASEIRA, M.C.B.; NAKASU, B.H. Pessegueiro. In: BRUCKNER, C. H. **Melhoramento de Fruteiras de Clima Temperado**. Viçosa: Editora UFV, 2002. p.89-126.

RESENDE, M.D.V. Avanços da genética biométrica Florestal. In: Encontro sobre temas de genética e melhoramento, 14, 1997, Piracicaba. **Anais**. Piracicaba: ESALQ-USP, 1997. p.150-158.

RESENDE, M.D.V. **Genética biométrica e estatística no melhoramento de plantas perenes**. Brasília: Embrapa Informação Tecnológica, 2002. 975p.

RESENDE, M.D.V. **Genética Quantitativa e de Populações.** Visconde do Rio Branco: Suprema, 2015. 463p.

RESENDE, M.D.V. **Matemática e estatística na análise de experimentos e no melhoramento genético**. Colombo: Embrapa Florestas, 2007a. 561p.

RESENDE, M.D.V. **Software SELEGEN-REML/BLUP: sistema estatístico e seleção genética computadorizada via modelos lineares mistos**. Colombo: Embrapa Florestas, 2007b. 359p.

RESENDE, M.D.V. Software Selegen-REML/BLUP: a useful tool for plant breeding. **Crop Breeding and Applied Biotechnology**, v.16, n.4, p.330-339, 2016. Available from: <http://dx.doi.org/10.1590/1984-70332016v16n4a49>. Accessed: Jul. 04, 2020. doi: 10.1590/1984-70332016v16n4a49.

SCARPARE FILHO, J.A. et al. Intensidade de raleio de frutos em pessegueiros Flordaprince conduzidos em pomar com alta densidade de plantio. **Pesquisa Agropecuária Brasileira**, v.35, n.6, p.1109-1113, 2000. Available from: <http://dx.doi.org/10.1590/S0100-204X2000000600006>. Accessed: Jul. 04, 2020. doi: 10.1590/S0100-204X2000000600006.

SILVA, J.O.C. et al. Estimates of genetic parameters and repeatability coefficients in S_2 peach genotypes grown in a subtropical environment. **Functional Plant Breeding Journal**, v.2, n.1, p.25-33, 2020. Available from: <http://dx.doi.org/10.35418/2526-4117/v2n1a3>. Accessed: Jul. 04, 2020. doi: 10.35418/2526-4117/v2n1a3.

SOUZA, V.A.B. et al. Heritability, genetic and phenotypic correlations, and predicted selection response of quantitative traits in peach. I. An analysis of several reproductive traits. **Journal of the American Society for Horticultural Science**, v.123, n.4, p. 598–603, 1998a. Available from: <https://doi.org/10.21273/JASHS.123.4.598>. Accessed: Jul. 04, 2020. doi: 10.21273/JASHS.123.4.598.

SOUZA, V.A.B. et al. Heritability, genetic and phenotypic correlations, and predicted selection response quantitative traits in peach. II. An analysis of several fruit traits. **Journal of the American Society for Horticultural Science**, v.123, n. 4, p.604–611, 1998b. Available from: <https://doi.org/10.21273/JASHS.123.4.604>. Accessed: Jul. 04, 2020. doi: 10.21273/JASHS.123.4.604.

TOMBESI, S. et al. Phenotyping vigour control capacity of new peach rootstocks by xylem vessel analysis. **Scientia Horticulturae**, v.127, p.353-357, 2011. Available from: <https://doi.org/10.1016/j.scienta.2010.11.007>. Accessed: Jul. 04, 2020. doi: 10.1016/j.scienta.2010.11.007.

WAGNER JÚNIOR, A. et al. Adaptação de genótipos de pessegueiro F_2 para condições de baixo acúmulo de frio hibernal. **Bragantia**, v.69, n.4, p.815-822, 2010. Available from: <https://doi.org/10.1590/S0006-87052010000400006>. Accessed: Jul. 04, 2020. doi: 10.1590/S0006-87052010000400006.