Estimation of genetic parameters and selection for rooting capacity in peach

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Abstract: *One of the most important criteria in the improvement of rootstocks is easiness of propagation. The objective of the present study was to verify the existence of genetic variability and the possibility of gains with selection in the rooting capacity among peach genotypes. Seventy-seven genotypes of peach belonging to five F_3 families were evaluated. Rooting percentage (RP), number of roots per cutting (NR) and mean root length (RL) were evaluated. Genetic values were estimated. The nineteen genotypes with the lowest rank summation index were selected to estimate the genetic gains. The variables RP, NR and RL had progeny mean heritabilities of 0.53, 0.60 and 0.83, respectively. Of the individuals selected, 89.5% belonged to the 713 (Talismã x Adafuel) family. The estimation of the genetic and phenotypic parameters show the possibility of success by selecting superior genotypes, with gains of 9.09, 17.47 and 24% for RP, NR and RL, respectively.*

Key words*: Prunus persica, Rootstock, REML/BLUP, Selection index, Cuttings.*

INTRODUCTION

The propagation of peach trees in Brazil is still based on grafting on rootstock seedlings derived from seeds obtained as by-products of fruit-processing industry, mainly in the South of the Country. This type of plant material results in rootstocks without guarantee of genetic identity, causing non-uniformity in clonal orchards and different reactions of plants to soil pathogens and abiotic stresses (Fachinello et al. 2005, Picolotto et al. 2010). For many years, the peach breeding programs in Brazil have aimed to improving scion cultivars and overlooked the improvement of rootstocks.

Different studies with *Prunus* spp. (Forcada et al. 2012, Mestre et al. 2015, Reig et al. 2016) revealed that the rootstock influences the agronomic performance (tree vigour, yield efficiency, water relations, leaf gas exchange, mineral nutrients uptake, plant size, bloom and harvest dates, and fruit bud survival). The rootstock choice represents one of the most important considerations for a productive peach orchard.

To help to address these research gaps, the Federal University of Viçosa has been conducting a genetic improvement program for peach rootstocks, hoping to obtain new high-performance rootstock cultivars adapted to the growing region and with good interaction with the scion cultivars.

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The use of genetically improved rootstocks demands changes in the propagation system. Vegetative propagation maintains a genetic identity of selected rootstocks, while seed propagation generates segregation and consequently non-uniformity. Research to improve the system of obtaining peach rootstocks have been carried out (Bruckner and Dejong 2014, Forcada et al. 2012), as well as using vegetative propagation by cutting as an alternative (Mayer et al. 2014).

Thus, the objective of the present study was to verify the existence of genetic variability and the possibility of gains with selection in the rooting capacity among peach genotypes.

MATERIAL AND METHODS

The experiment was conducted from November to December 2015, in an intermittent mist chamber at the Agricultural Department of the Federal University of Viçosa (lat 20° 45' 26'' S, long 42° 52' 08'' W and alt 638 m asl).

Softwood cuttings of 77 individuals from five peach families at the F_3 generation (S_2) belonging to the UFV Genetic Improvement Program were collected at the beginning of November (Table 1). The cuttings were standardized with a length of 15 cm, with a pair of leaves, cut straight at the base and the apex cut just above an auxiliary bud. Then, two opposite lesions (± 3 cm) were cut at the base of the cutting to expose the vascular cambium.

Table 1. Peach families, genealogy and number of individuals evaluated for selection of rootstock genotypes for rooting capacity.

Family	Number of individuals per family	Parent ♀	♂
613	20	Relíquia x Diamante	
713	23	Talismã x Adafuel	
913	12	Okinawa x GN9	
1013	20	Real x Premier	
1113	2	Okinawa x GN22	

The basal ends of cuttings were dipped into a hydro-alcoholic solution with a concentration of 3000 mg L^{-1} IBA for 5 seconds. The cuttings were then placed in (36.5 x 26.5 x 9.5 cm) perforated plastic trays containing sand, at 4 to 5 cm depth. The boxes were kept under intermittent mist spraying programmed for every 3.5 minutes for 5 seconds, only operating in daytime. The greenhouse is covered with polyethylene film and sides with anti-aphid screen.

The experiment was arranged in a completely randomized design, with five replications and each plot consisted of eight cuttings. After 46 days of the experiment installation, the following traits were evaluated: rooted cuttings (% of cuttings with at least one root) (RP); number of roots per cutting (only roots that originated directly from the cutting) (NR); mean length of five roots (cm) (RL).

Data were analyzed using the methodology of mixed linear models. The estimation of the genetic parameters was performed by REML (Restricted Maximum Likelihood) and genotypic values were estimated by the BLUP method (best non-biased linear predictor) using the Selegen REML/BLUP software (Resende 2016). The statistical model adopted was: $y = Xr + Zg + Wp + e$, where y is the data vector, r is the vector of the repetition effects (assumed as fixed) added to the general mean, g is the vector of the additive genetic effects (assumed as random), p is the vector of the plot effects and e is the vector of errors (random); The capital letters (X, Z and W) represent the incidence matrices for the said effects.

The REML/BLUP method ranked the individuals according to the predicted genotypic values found for each trait. From these values, the selection was applied based on the Mulamba and Mock (1978) index. This index consists of classifying the individuals, in relation to each trait, in an order that favors improvement. The orders referring to the traits are summed for each genotype, obtaining the sum of ranks. Thus, the lower the value obtained in the sum of ranks, the better the performance of the genotype, in relation to the different traits evaluated (Cruz et al. 2012). The 19 genotypes (25%) with the lowest value of the sum of ranks were selected, and the selection gain was estimated by the equation $G_s = (\overline{X}_s - \overline{X}_0)h^2$ where: GS is the selection gain; $\overline{X}_s$ is the mean of the 19 selected genotypes; $\overline{X}_0$ is the mean of the 77 genotypes evaluated and h^2 is the individual broad-sense heritability.

RESULTS AND DISCUSSIONS

Rooting percentage had the highest genotypic variance (σ^2_g), which was 127.5 (Table 2), indicating a favorable condition to the genetic improvement program of peach rootstock, enabling the identification of superior genotypes. Falconer & Mackay (1996) points out that the existence of genetic variation in the population is a basic condition for obtaining gains from selection.

Estimates of individual broad-sense heritability (h^2) were considered moderate, ranging from 0.15 (RP) to 0.42 (RL) (Table 2), according to Resende (2007), who considered heritability of low magnitude when $h^2 <$0.15, medium magnitude when 0.15 $<h^2>$ 0.50, and high magnitude when $h^2 >$ 0.50. The magnitude of the heritability obtained shows that a moderate genetic control can be obtained, which ensures that the selection, at individual and progeny levels, would provide significant gains for the trait. Varago et al. (2017) discuss that the individual heritability of 51.4% found in the selection of peach genotypes for resistance to bacterial leaf spot (*Xanthomonas arboricola* pv. *pruni*) implies the existence of genetic variability in the studied progeny, enabling us to infer that selection may be effective for obtaining genetic gains for the evaluated characteristic.

The estimates of progeny-mean heritability (h^2_{mp}) for RP, NR, and RL were of high magnitude: 0.53, 0.60, and 0.83, respectively (Table 2), and were superior to those obtained by the individual heritability, showing that, in this case, the selection may be more effective and indicating a greater prospect of genetic gain. Falconer & Mackay (1996) describes heritability as a property not only of a trait but also of the population and the environmental conditions to which individuals are subjected. Therefore, its value may be affected if there is a change in any of the components of the genetic and phenotypic variances.

The coefficient of determination of plot effects (C^2_{plot}) was considered low for the traits evaluated, 0.09, 0.09, and 0.06 for RP, NR and RL, respectively, indicating the presence of a small environmental variation within the plots, that is, the effect of plots was small.

The estimate of the individual genotypic variation coefficient (CV_{gi}), expresses the amount of genetic variation that exists. Expressive values were observed for the traits studied, ranging from 25.86 (RP) to 41.56 (NR). This result indicates that populations are susceptible to genetic progress by continuing selection cycles. Maia et al. (2009) argues that with values of this magnitude, it is possible to obtain success with the selection of genotypes and considerable gains.

In general, the coefficient of residual variation (CV_e) values obtained were from low to medium, ranging from 17.09 (RL) to 33.64 (NR), remaining at acceptable levels for the experimentation. However, the CV_e is little informative, thus the analysis and interpretation of the accuracy estimate is more important (Resende and Duarte 2007).

The relative coefficient of variation (CV_r), equivalent to the variation index, refers to the magnitude of the CV_g/CV_e ratio, and according to Resende and Duarte (2007), CVr values equal to 1.0 are adequate for providing high-accuracy and high-precision inferences. The present study found CV_r values between 1.06 (RP) and 2.21 (RL) (Table 2), showing that there is a possibility of success with progeny selection, since this parameter indicates that the genetic variation between the

Table 2. Estimates of genetic parameters for the traits percentage of rooting cuttings (RP), number of roots per cutting (NR), and mean length of roots in cm (RL)

Parameter	Trait		
	RP	NR	RL
σ^2_g *	127.47	4.44	2.48
h^2	0.15	0.19	0.42
C^2_{plot}	0.09	0.09	0.06
h^2_{mp}	0.53	0.60	0.83
Acs	0.73	0.78	0.91
CV_{gi}(%)	25.86	41.56	37.81
CV_e(%)	24.26	33.64	17.09
CV_r	1.06	1.23	2.21
Overall mean	43.66	5.07	4.17

*σ^2_g: genetic variance among progenies; h^2: individual broad-sense heritability among families, equivalent to narrow-sense heritability, since ignoring the fraction (1/4) of the dominance genetic variance; C^2plot: coefficient of determination of plot effects; h²mp: progeny mean heritability; Acs: accuracy of progeny selection; CVgi%: coefficient of individual additive genetic variation; CVe%: coefficient of residual variation; CVr: relative coefficient of variation (CVgi/CVe).

Table 3. Peach individuals selected (at 25% intensity) by the Mulamba and Mock (1978) index and their respective genetic values for the variables rooting percentage (RP), number of roots per cutting (NR) and mean root length in cm (RL)

Individual	RP	NR	RL	Index
	Genetic value (u + a)			
613-2	48.99	5.81	6.51	60
613-17	49.23	6.43	6.77	60
713-2	55.10	7.16	5.70	44
713-3	52.95	7.29	5.67	49
713-4	55.58	7.70	6.12	23
713-5	58.45	8.75	5.60	28
713-7	58.45	8.27	6.10	16
713-8	54.86	7.44	5.75	38
713-9	53.58	7.19	5.09	62
713-10	54.46	7.08	5.61	52
713-14	51.51	6.65	6.00	52
713-15	55.34	7.42	5.37	51
713-17	54.14	6.81	5.65	57
713-18	56.53	7.67	5.71	34
713-19	57.97	7.81	6.78	12
713-20	57.25	7.73	5.77	25
713-21	58.45	8.62	5.64	29
713-22	58.69	8.41	6.84	5
713-23	57.25	7.66	5.76	31

progenies is much higher than the environmental variation.

In the genotypic evaluation, accuracy (Acs) is also an important statistical parameter because it refers to the correlation between the predicted genetic values and the true genetic values of the individuals and is linked to trait heritability (Resende and Duarte 2007). The accuracy ranged from 0.73 (RP) to 0.91 (RL), which were considered values of high precision. Thus, the high experimental rigor of the present study and the reliability in the selection of genotypes for the traits related to rooting capacity stand out in this experiment.

Table 4. Estimates of selection gains for traits related to peach rooting capacity

Trait[1]	Original mean	Mean of selected individuals	Selection gain	% of selection gain
RP (%)	43.66	70.13	3.97	9.09
NR	5.07	9.73	0.88	17.47
RL (cm)	4.17	6.53	1.0	24.0

[1] RP: percentage of rooting cuttings; NR: number of roots per cutting and RL: mean root length.

Among the top 25% individuals (19 genotypes) based on the Mulamba and Mock (1978) index, aiming to increase rooting percentage, root numbers and root mean length (Table 3), only families 613 (2 genotypes) and 713 (17 genotypes) had individuals selected. One possible explanation for the best result obtained by the family 713 is its genealogy (Table 1). One of its parents was the rootstock 'Adafuel', a hybrid between almond and peach selected by ESAD-CSIC (Zaragoza, Spain), and according to Reighard and Loreti (2008), it is easily propagated by cuttings and extremely vigorous and compatible with most peach cultivars.

The index based on genotypic values was consistent in ranking individuals based on all traits evaluated; it is therefore suitable to be used as a strategy in the selection of superior genetic material. Resende (2007) states that the REML/BLUP methodology puts the potential genotypes into an order for selection, exploring all the genotype variation among and within progenies, however, considering each trait analyzed separately. This procedure has been shown to be efficient, for passion fruit (Freitas et al. 2016, Santos et al. 2015), guava (Paiva et al. 2016), and papaya (Oliveira et al. 2012, Vivas et al. 2014).

The selection of the 19 genotypes provided direct predicted gains of 9.09% for rooting percentage, 17.47% for number of roots per cutting, and 24.0% for mean root length (Table 4). The selection of these genotypes in this selection cycle promoted high genetic gains; however, the recombination of the selected genotypes could lead to a reduction of the gains, in the next selection cycles, due to the probable process of inbreeding. One of the most important criteria in the improvement of rootstocks is easiness of propagation since farmers will require rapid availability of the new rootstock cultivar. Thus, the use of genetically improved rootstocks requires modification of the propagation system, with the vegetative propagation by cuttings being the most recommended, as it preserves the genetic identity of the selected rootstocks (Bruckner and Dejong 2014, Reighard and Loreti 2008).

CONCLUSIONS

The estimates of the genetic parameters reveal the existence of genetic variability and selective potential among the studied peach genotypes.

The Mulamba and Mock selection index provides positive genetic gains in the rooting percentage, root number and mean root length.

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