



Genetic parameters and gains with the selection of fig tree genotypes

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ABSTRACT. Fig tree (*Ficus carica* L., Moraceae), which originated in the Mediterranean Basin, is one of the many fruit trees grown in Brazil, with 'Roxo-de-Valinhos' being the exclusively used cultivar. In this context, research aimed at the improvement of this species to develop highly resistant and adaptable cultivars is paramount. Thus, the present study aimed to maintain fig accessions in an *in vivo* active germplasm bank (AGB) at the Faculty of Engineering of Ilha Solteira (FEIS), São Paulo State University (UNESP), as well as to characterize the agronomic traits of these accessions based on quantitative descriptors of genetic parameters and observe gains with the selection of specific genotypes to illustrate the AGB in terms of genetic variability. A total of 36 *F. carica* genotypes were evaluated in the field at the Teaching, Research and Extension Farm (FEPE) of the FEIS, UNESP. Qualitative traits, fruit parameters (e.g., insertion of the first fruit, fruit stalk length, fruit length, fruit diameter, and average fruit mass), and accumulated plant dry mass were measured. In addition, genetic parameters, variance components, and descriptive statistics, including genetic and environmental variances, heritability and average heritability of clones, coefficients of genotypic and environmental variation and their ratio ($CV_g\%/CV_e\%$), general average, and selection gain, were evaluated. The selected fig tree accessions showed genetic variability in the assessed traits, exhibiting good heritability and achieving selection gains. For instance, the first 10 classified clones exhibited a heritability of 80.2% and achieved a selection gain of 98% for accumulated plant dry mass. Therefore, the maintenance of *in vivo* AGBs allows agronomic studies, offering promising results for continuing the breeding programs and preserving the genetic variability of species.

Keywords: *in vivo* conservation; breeding; *Ficus carica* L.

Received on September 14, 2020.

Accepted on January 14, 2021.

Introduction

Fig tree (*Ficus carica* L.) is a perennial fruit species of the Moraceae family (Crisosto, Ferguson, Bremer, Stover, & Colelli, 2011). This species is distributed in both subtropical and temperate regions owing to its high adaptability to diverse climatic conditions (Flaishman, Rodov, & Stover, 2008; Pio, Souza, Kalcsits, Bisi, & Farias, 2018).

Fig tree cultivation is economically relevant in Brazil, with a gross revenue of approximately R\$ 184 million from an area under the cultivation of 2,591 hectares and annual production of 27,000 tons per year in the 2017–18 harvest (FAO, 2020). In addition, fig tree is popular as a healthy crop due to the medicinal properties its fruits, leaves, latex, stem, and roots against an array of diseases (Liu et al., 2019).

However, commercial fig cultivation in Brazil is based exclusively on a single cultivar, 'Roxo-de-Valinhos', which is characterized by high vigor, productivity, and rusticity as well as great acceptance among consumers and industry (Ferreira, Pasqual, & Tulmann Neto, 2009). However, the predominance of a single cultivar can result in severe problems related to pests and diseases, which may impair cultivation, depreciate fruits, and reduce profits (Rodrigues et al., 2019a).

Thus, genetic diversity of the fig cultivation must be evaluated and restored, as it is essential for species to adapt to and withstand diverse climatic conditions and environmental changes for development and survival over long periods (He, Wang, Li, & Yi, 2016). In this context, the genetic vulnerability of plant species can be minimized through conservation and maintenance of active germplasm banks (AGBs), which contain accessions for crop safety and diversity (Platt et al., 2010; Huang et al., 2014).

Simultaneously, a method for the correct estimation of genetic parameters must be established. For instance, the Residual or Restricted Maximum Likelihood/Best Linear Unbiased Prediction (REML/BLUP) is the most used method for perennial species, which accurately estimates genetic parameters to enable precise selection. Previous studies have shown that genotypes could be reliably selected based on the results of the REML/BLUP method (Resende, 2016; Casagrande, Mezzomo, Cruz, Borém, & Nardino, 2020).

Thus, we believe that research on accessions present in AGBs is crucial to understand the genetic structure of populations, enabling breeders to make decisions regarding the selection of suitable material for the establishment and/or enrichment of AGBs to guarantee crop sustainability over time and continuous genetic gains from the launch of improved cultivars combined with wide genetic variability to ensure genetic safety.

To this end, the present study aimed to maintain of fig accessions in an *in vivo* AGB of the Faculty of Engineering of Ilha Solteira (FEIS), São Paulo State University (UNESP), as well as to characterize their agronomic traits based on quantitative descriptors of genetic parameters and observe gains with the selection of genotypes to illustrate the AGB in terms of genetic variability.

Material and methods

The experiment was conducted at the Teaching, Research and Extension Farm (FEPE) of FEIS, UNESP, Ilha Solteira, São Paulo State, Brazil (20°22' S 51°22' W, 330 m a.s.l.), during 2018–2019.

The climate of the region is Aw according to the Köppen classification (Köppen, 1948), characterized by rainy summers and dry winters. Mean annual precipitation is ~1,300 mm, distributed between October and March; mean annual temperature is 23.5°C; and relative humidity is between 60 and 80% (Climate-Data.org, 2019).

The genetic material used was obtained from the fig (*Ficus*) AGB of the FEPE, a unit located in the municipality of Selvíria, Mato Grosso do Sul State, Brazil, which contains a collection of 50 accessions. Of these, seedlings of 36 genotypes were produced and planted in a randomized block design in two replicates with three plants per experimental plot and 3 × 2 m spacing between plants.

Table 1 lists the 36 genotypes used in the experiment, which were in field and in production, as well as their cultivars and origins. Clones without a defined cultivar are spontaneous or induced variants of 'Roxo-de-Valinhos'.

In the field, soil between planting rows was covered with plant material to conserve moisture and reduce weed infestation. When required, weeds were controlled using chemicals herbicides.

Irrigation was performed with a dripping tape (50-cm-wide in a planting row), three times a week, at an average rate of 2.0 mm h⁻¹ in the dry season. For rust control, the Bordeaux mixture was applied fortnightly. Plantation was in the formation of an open crown, composed of a main stem, three legs, and six arms, to increase aeration and light incidence between plants. First-production pruning was performed in the arms, yielding six productive branches per plant.

Following production pruning, fruits from the branches of the year were evaluated for the following characteristics of interest:

- a) Insertion of the first fruit (I1): distance between the branch bifurcation and the stalk of the first fruit of that branch, measured in centimeters.
- b) Fruit stalk length (CP), fruit length (CF), and fruit diameter (DF): measured in millimeters using a digital caliper.
- c) Average fruit mass (MMF): measured in grams using a 0.001 g precision scale.
- d) Accumulated plant dry mass (MSA): obtained after drying the shoots of third-production pruning in a forced air circulation oven, measured in grams.

Data were presented as the mean of every experimental plot. Estimates of variance components and genetic parameters were obtained for each variable using the REML/BLUP method with Selegen-REML/BLUP (Resende, 2016).

For analysis, one observation per plot was assumed to correspond to an unrelated clone, according to the model proposed by Resende (2016): $y = Xr + Zg + e$, where y is the vector of data, r is the vector of the block effects (assumed to be fixed) added to the general average, g is the vector of genetic effects (assumed to be random), and e is the vector of residual error (random); capital letters represent the incidence matrices for the aforementioned effects.

The genetic parameters, variance components, and descriptive statistics were as follows:

σ_g^2 : Genetic variance in the broad sense for clones;

σ_e^2 : Residual variance (environmental);
 h_g^2 : Heritability in the broad sense;
 h_{mc}^2 : Average heritability for clones;
 $CV_g\%$: Coefficient of genotypic variation;
 $CV_e\%$: Coefficient of environmental variation;
 R : $CV_g\%/CV_e\%$ ratio;
 MG : General average of the experimente;
 MPS : Average of the selected population;
 GS/GS (%): Selection gain percentage.

For selection gain, a selection intensity of 30% was adopted to select the best clones by study trait.

Table 1. *Ficus carica* L. genotypes from the active germplasm bank (Faculty of Engineering of Ilha Solteira, São Paulo State University, 2019) included in the experiment.

Treatment	Cultivar	Origin
1	'Calimyrna'	S. J. Rio Preto
2	'Nobile'	IAC
3	'Genoveso'	IAC
4	'Roxo-de-Valinhos'	S. S. Paraíso
5	'Stanford'	IAC
6	'White Adriatic'	IAC
7	'Bonato'	IAC
8	'White Genova'	S. J. Rio Preto
9	'White Genova'	IAC
10	'Smyrna'	IAC
11	'Brunswick'	IAC
12	'Caprifigo'	IAC
13	'Pingo de Mel'	-
14	'Palestino'	Campinas
15	'Turco'	Campinas
16	'Figo Vermelho'	Piracicaba
17	'PI 42'	ISA
18	'Gigante'	-
19	'FEIS – MA 01'	Monte Alto
20	'FEIS – MA 02'	Monte Alto
21	'FEIS – MA 03'	Monte Alto
22	'FEIS – MA 04'	Monte Alto
23	'FEIS – MA 05'	Monte Alto
24	'FEIS – MA 06'	Monte Alto
25	'FEIS – MA 07'	Monte Alto
26	'FEIS – MA 08'	Monte Alto
27	'FEIS – MA 09'	Monte Alto
28	'FEIS – MA 10'	Monte Alto
29	'FEIS – MA 11'	Monte Alto
30	'FEIS – MA 12'	Monte Alto
31	'FEIS – P 01'	Piracicaba
32	'FEIS – P 02'	Piracicaba
33	'FEIS – P 03'	Piracicaba
34	'FEIS – B 01'	Bahia
35	'Caprifigo'	IAC
36	'Figo Preto'	Piracicaba

Results and discussion

According to Couto, Peternelli, and Barbosa (2013), a $CV_e\%$ of greater than 20% is considered high. Based on this, for most traits evaluated in this study, $CV_e\%$ was high or very high, with I1 showing the highest value (104%) (Table 2).

The high $CV_e\%$ values obtained in the present study may primarily be attributed to the high rust incidence (*Cerotelium fici*), which resulted in the abortion of some leaves and subsequently of some fruits, lowering the fruit quality and number of fruits that persisted despite the disease. Thus, to efficiently improve fig trees for cultivation in tropical climates, resistance to rust and the direct and indirect effects of this disease on production must be taken into account. However, studies targeting diseases are difficult to conduct; therefore,

indirect assessment via productivity is the best approach, since more resistant plants tend to be more productive (Mezzalira, Piva, Nava, Paulus, & Santin, 2015).

Table 2. Genetic parameters (PG) and variance components (CVar) of *Ficus carica* L. clones for the following traits: insertion of the first fruit (I1), fruit stalk length (CP), fruit length (CF), fruit diameter (DF), average fruit mass (MMF), and accumulated plant dry mass (MSA). (Faculty of Engineering of Ilha Solteira, São Paulo State University, 2019).

PG and CVar	I1	CP	CF	DF	MMF	MSA
σ_g^2	33.21	0.219	16.99	2.443	12.08	0.028
σ_e^2	64.58	11.97	46.96	38.99	170.6	0.007
$h_g^2\%$	34.0±23.3	1.8±5.4	26.6±20.6	5.9±9.7	6.6±10.3	80.2±35.8
$h_{mc}^2\%$	50.70	3.52	41.98	11.13	12.40	88.98
$CV_g\%$	75.14	5.456	10.23	4.333	13.28	81.57
$CV_e\%$	104.8	40.38	17.00	17.31	49.89	40.59
r	0.717	0.135	0.601	0.250	0.266	2.010
MG	7.67	8.57	40.30	36.07	26.18	0.205

σ_g^2 : genetic variance; σ_e^2 : environmental variance; $h_g^2\%$: heritability; $h_{mc}^2\%$: average heritability of clones; $CV_g\%$: coefficient of genetic variance; $CV_e\%$: coefficient of experimental variance; r : $CV_g\%/CV_e\%$ ratio; MG : general average.

The genetic variation coefficient (deviation from the genetic standard), expressed as a percentage of the mean, is an indicator of the relative magnitude of changes in a trait through selection during a breeding program (Lopes et al., 2018).

Rust control appears to be an environmental factor that significantly affects I1. Fig trees with early fruiting tended to show a lower incidence of rust and higher I1, as they escaped the most rainy and hot season, which is conducive to infection. However, in fig trees with late fruiting coinciding with the beginning of the rainy season, rust incidence was high, resulting in the abortion of leaves and first fruits.

Traits related to fruit morphology, such as fruit length (17.00%) and diameter (17.31%), showed a relatively low $CV_e\%$, demonstrating that fruit shape is a genetic parameter with a weaker environmental effect than other traits.

However, these $CV_e\%$ values did not show high heritability, with MSA showing the highest $h_g^2\%$ value (80.2%). High $h_g^2\%$ values indicate highly effective selection in the initial generations (Cazzola, Bermejo, & Cointry, 2020). Therefore, MSA is a promising selection trait for cultivation. Low heritability for other fruit morphological characteristics due to low genetic variability may be a consequence of previous selection before being deposited in the AGB.

Typically, cultivars with acceptable fruit morphology or genotypes that have undergone spontaneous or induced mutations are deposited in AGBs, because they present desirable fruit characteristics. Specifically, fruit stalk length is a vital characteristic related to shelf life (Rodrigues et al., 2019b).

Knowledge of the heritability coefficient (h^2) allows for the estimation of genetic gains and helps the selection of the best strategy in genetic breeding programs (Baldissera, Valentini, Coan, Guidolin, & Coimbra, 2014). h^2 values vary with different traits and are generally considered high when greater than 0.7 (Tsagkrasoulis, Hysi, Spector, & Montana, 2017). Moreover, according to Sturion, Stuepp, and Wendling (2017), heritability in the broad sense is sufficient to achieve selection gains when the plants of interest are vegetatively propagated, while heritability in the strict sense is relevant to sexual propagation.

Traits related to growth and production, despite being affected by the environment, show wide genetic variability, which allows for achieving greater selection gains by selecting genotypes with a higher growth capacity in tropical climates and lower I1, resulting in longer harvest and better yield at the end of the productive cycle (Sayd, Amabile, Faleiro, Coelho, & Montalvão, 2019). In this context, MSA is a significant trait for the selection of figs trees in the initial stage of production, since more vigorous plants tend to achieve greater production and longer harvest; however, the evaluation of productivity in the initial period may neglect the potential of genotypes with a young appearance but prolonged harvest (Pinheiro et al., 2013). Moderate-to-high h^2 values and genetic variation are associated with high genetic variability and selective accuracy as well as the possibility of the successful selection of accessions with agronomic traits of interest (Sayd et al., 2019).

The average heritability of clones was also high for MSA; therefore, considering both $CV_g\%$ and average heritability, MSA appears to be a significant trait for breeding programs, as it can offer a complementary selection gain among clones (Moraes et al., 2014).

The ratio of coefficient of genetic variation (CV_g) and coefficient of environmental variation (CV_e) can be used as another parameter indicative of significant genetic gains by selecting superior genotypes (Cruz, Regazzi, & Carneiro, 2012).

The $CV_g\%/Cv_e\%$ ratio for MSA was greater than 1, indicating that the trait is favorable for selection (Cruz, 2005). When the estimated $CV_g\%/Cv_e\%$ ratio is greater than or equal to 1, the available genetic variation explains most of the estimated variation in the experimental data. Thus, the CV_g/Cv_e ratio can be used as an index of ease of genotype selection for a specific trait (Leite et al., 2016).

Based on the best numerical data, accumulated dry mass was the most promising trait among genetic parameters based on variance components. It represents the extent to which the plant grew before and after pruning. Based on this trait, the genotype that shows better development between pruning intervals can be selected and plant production can be estimated.

However, selection based on a single characteristic is unreliable, because despite achieving a superior final product in terms of that characteristic, it can lead to unsatisfactory performance for other traits (Cruz et al., 2012). One way to increase selection success is through simultaneous selection for several characteristics based on selection indices.

To estimate genetic gains, the 36 accessions studies here were evaluated for each of the six characteristics of interest (Table 3) based only on the first 10 classified clones. Clone 14 ('Palestine') presented satisfactory results for all six traits. This index classifies accessions in terms of each trait favorable to breeding (Yadav et al., 2020).

Table 3. Classification (CLASS) of clones (CL) and respective genetic values (VG) for insertion of the first fruit (I1), fruit stalk length (CP, mm), fruit length (CF, mm), fruit diameter (DF, mm), average fruit mass (MMF, g), and accumulated plant dry mass (MSA, g), along with selection gain (GS), percentage gain (GS%) for the first 10 classified clones, general average (MG), and average of the selected population (MPS). (Faculty of Engineering of Ilha Solteira, São Paulo State University, 2019).

CLASS	I1		CP		CF		DF		MMF		MSA	
	CL	VG	CL	VG	CL	VG	CL	VG	CL	VG	CL	VG
1	16	9.4	11	0.16	4	4.0	20	0.77	11	2.1	28	0.40
2	27	9.0	25	0.15	31	3.4	11	0.56	20	1.9	7	0.38
3	14	7.9	17	0.15	28	3.4	31	0.53	12	1.7	20	0.31
4	20	5.1	12	0.11	12	3.2	7	0.52	31	1.4	14	0.28
5	10	4.5	19	0.10	11	3.1	12	0.51	4	1.3	35	0.18
6	21	3.6	27	0.09	14	2.9	32	0.45	32	1.1	15	0.15
7	13	3.4	10	0.08	3	2.0	34	0.45	34	1.1	27	0.11
8	6	3.3	14	0.07	25	2.0	14	0.40	5	0.83	6	0.08
9	35	1.3	16	0.06	20	1.9	4	0.39	1	0.76	21	0.07
10	3	1.2	31	0.06	22	1.9	9	0.30	14	0.74	2	0.05
11	19	1.0	35	0.01	32	1.8	8	0.27	8	0.64	8	0.04
12	4	0.5	20	0.01	19	1.5	6	0.25	25	0.50	16	0.03
13	8	0.5	28	0.01	7	1.1	25	0.18	9	0.39	5	0.03
14	1	0.4	18	-0.01	34	1.0	3	0.18	7	0.37	4	0.03
15	32	-0.1	9	-0.01	1	0.7	5	0.17	33	0.30	18	-0.01
16	2	-0.4	33	-0.02	9	0.4	28	0.17	23	0.20	10	-0.01
17	34	-0.5	5	-0.02	35	0.2	33	0.16	28	0.12	31	-0.04
18	24	-1.4	4	-0.02	36	0.2	23	0.09	6	-0.01	26	-0.05
19	9	-1.6	32	-0.02	27	-0.1	36	0.08	36	-0.12	9	-0.06
20	30	-2.0	3	-0.03	33	-0.2	1	0.04	35	-0.23	1	-0.07
21	5	-2.0	23	-0.04	5	-0.2	19	0.01	19	-0.31	12	-0.07
22	12	-2.0	34	-0.04	16	-0.2	27	-0.14	3	-0.42	19	-0.08
23	15	-2.0	29	-0.04	2	-1.0	22	-0.14	27	-0.43	30	-0.08
24	22	-2.0	24	-0.05	8	-1.0	29	-0.16	16	-0.46	3	-0.08
25	23	-2.0	2	-0.05	23	-1.0	16	-0.21	2	-0.50	34	-0.10
26	28	-2.0	22	-0.05	6	-1.5	35	-0.24	22	-0.72	24	-0.10
27	31	-2.0	15	-0.05	30	-1.5	24	-0.24	30	-0.87	36	-0.11
28	33	-2.6	30	-0.05	21	-2.2	15	-0.31	26	-0.91	22	-0.12
29	18	-3.2	21	-0.06	29	-2.4	2	-0.35	15	-1.0	23	-0.12
30	7	-3.3	13	-0.06	10	-2.6	10	-0.50	10	-1.0	25	-0.13
31	36	-3.3	36	-0.07	15	-2.6	30	-0.52	29	-1.1	13	-0.13
32	29	-3.6	1	-0.07	13	-3.2	13	-0.56	24	-1.1	11	-0.15
33	17	-3.9	26	-0.07	18	-3.2	18	-0.63	21	-1.2	32	-0.15
34	25	-3.9	6	-0.07	24	-3.3	26	-0.66	13	1.3	29	-0.16
35	26	-3.9	8	-0.08	17	-4.0	21	-0.68	18	-1.5	17	-0.17
36	11	-3.9	7	-0.10	26	-4.8	17	-1.14	17	-2.2	33	-0.17
MG	7.67		8.57		40.30		36.07		26.18		0.205	
MPS	12.54		8.67		43.08		36.56		27.46		0.406	
GS	4.87		0.103		2.78		0.486		1.28		0.201	
GS%	63.6		1.20		6.91		1.35		4.88		98.0	

I1 showed the highest selection gain (4.87) based on the first 10 classified clones (Table 3). Selection gain refers to the increase in the general average of the original population, and it depends on heritability and selection differential (Viana, Faria, & Silva, 2009). Thus, despite the high *CV*, I1 seems to be a trait with the most genetic variability, and selection for this trait combined with rust resistance can lead to genotypes with early production, which would enable fruit supply to the consumer market before the production peak, resulting in greater returns to producers and satisfaction to consumers in terms of quality.

Based on the classification in Table 3, the new genotypes (mutants of ‘Roxo-de-Valinhos’) #20 (‘FEIS – MA 02’), #27 (‘FEIS – MA 09’), and #31 (‘FEIS – P 01’) were selected for specific characteristics, demonstrating that such derivations may be superior to the precursor genotype in terms of cultivation in tropical regions. Such derivations create variability that allows the expansion of cultivation to regions other than the conventional ones (Pereira & Kavati, 2011). Strategies aimed at increasing genetic variation within a crop species can dramatically improve breeding efficiency (Amri-Tiliouine et al., 2018).

Among the mutant genotypes, ‘FEIS – MA 02’ showed the greatest potential, since it was superior to ‘Roxo-de-Valinhos’ in terms of five traits in six of the first 10 classified clones. The remaining genotypes were selected for three or four traits and outperformed the precursor in at least three of the first 10 classified clones.

Conclusion

The present study demonstrates that genetic variability in *F. carica* L. can allow for the selection and breeding of this species for specific traits, and this, combined with the cutting-edge plant biotechniques, can offer opportunities to expand the cultivation of fig trees in tropical regions and improve fruit yield. Therefore, maintenance of *in vivo* AGBs of fig accessions can facilitate research on agronomic traits and fruit quality to promote crop breeding programs.

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