Agronomic evaluation and clonal selection of ginger genotypes (*Zingiber officinale* Roscoe) in Brazil

Evaluación agronómica y selección clonal de genotipos de jengibre (*Zingiber officinale* Roscoe) en Brasil

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ABSTRACT

The analysis of the genetic diversity of ginger based on agronomic traits is essential to know its performance and to design breeding programs. In this study, we analyzed the phenotypic variability of 61 accessions of the ginger germplasm collection of the "Luiz de Queiroz" College of Agriculture at the University of Sao Paulo (ESALQ/USP) in a complete randomized block design with four replications. An analysis of variance test was performed and genetic parameters such as heritability, genetic variance, environmental variance, genetic-environmental variation ratio (CVg/CVe) and genetic correlations were estimated. There were highly significant differences ($P \leq 0.01$) among the accessions for all the agronomic traits analyzed. The CVg/CVe ratio (>1), along with the high heritability (>80%), showed a significant contribution of genetic factors on the phenotypic expression of plant height, rhizome thickness and yield traits, favoring the clonal selection of genotypes. Accessions Gen-29, Gen-29, Gen-32, Gen-36, Gen-37, Gen-40, Gen-41, Gen-42, Gen-50 were selected due to the best agronomic performance when compared to the rest of the germplasm. The results obtained may be useful in future breeding programs in Brazil.

Key words: agronomic performance, germplasm, genetic parameters, selection, phenotypic variability.

RESUMEN

El análisis de la variabilidad genética del jengibre (*Zingiber officinale*) con base en características de importancia agronómica es esencial para conocer su potencial productivo y direccionar correctamente programas de mejoramiento genético. Este estudio evaluó la variabilidad fenotípica de 61 accesiones del banco de germoplasma de jengibre de la Escuela Superior de Agricultura Luiz de Queiroz/Universidad de Sao Paulo (ESALQ/USP), utilizándose un diseño experimental de bloques completos al azar (BCA) con cuatro repeticiones. Para orientar el proceso de selección se realizó un análisis de varianza y se estimaron algunos parámetros genéticos tales como heredabilidad, varianza genética, varianza ambiental, relación entre el coeficiente de variación genético y ambiental (CV_g/CV_e) y correlaciones genéticas. Se presentaron diferencias altamente significativas ($P \leq 0,001$) entre las accesiones para todas las características agronómicas analizadas; la relación CV_g/CV_e (>1), en conjunto con la alta heredabilidad (>80%), mostró que hubo una importante contribución de los factores genéticos en la expresión fenotípica de los caracteres altura de planta, espesor del rizoma y rendimiento, favoreciendo la selección clonal de genotipos. Las accesiones Gen-05, Gen-29, Gen-31, Gen-32, Gen-36, Gen-37, Gen-40, Gen-41, Gen-42, Gen-43, Gen-44 y Gen-50 fueron seleccionadas por presentar el mejor desempeño agronómico al ser comparadas con el resto del germoplasma. Los resultados obtenidos en este estudio podrán ser útiles en futuros programas de mejoramiento genético y promoverán la producción de este cultivo en Brasil.

Palabras clave: desempeño agronómico, germoplasma, parámetros genéticos, selección, variabilidad fenotípica.

Introduction

The *Zingiber* genre is an important member of the family *Zingiberaceae* due to its medicinal and seasoning properties. Among them, *Zingiber officinale* (cultivated ginger) is the most remarkable specie and including two subspecies known as: *Z. officinale* var *rubra* e *Z. officinale* var *rubrum* (Muda *et al.*, 2004). The *Zingiber officinale* specie was morphologically described by Silvestrini *et al.* (1996) as an herbaceous and perennial plant with erected stems, formed by many dystic leaves, zygomorphic flowers, hermaphroditic, and yellow to green color. In addition, it has vegetative propagation by an articulated septant rhizomes, fleshy, rough epidermis and brown color. This species exhibits self-incompatibility and a high sterility specifically from chromosomic origin as a result either of translocations and

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inversions (Adaniya, 2001; Adaniya and Shirai, 2001) or derived from the bounding of bivalent counterparts with irregular segregation of genomic complements which leads to the formation of sterile gametes which decreases the production of viable seeds (Das *et al.*, 1999). Consequently, it is possible that the cultivated ginger is a sterile hybrid which originally comes from the crossing between two distant species and it was able to survive because vegetative propagation is a successful survival strategy (Peter *et al.,* 2007).

The agronomic evaluation is essential for plant breeders in order to know the level of variability present in the germplasm collections aiming to promote their use in breeding programs (Cruz *et al.,* 2004). Therefore, an important part of the breeding program success is about the existence of genetic variability in the targeted population (Cruz *et al.*, 2011). In case that the agronomic trait variability exists, it could therefore be possible to obtain genetic progress during recombination and selection processes or even determine a favorable situation for the genotypes clonal selection in the case of vegetative propagation species such as ginger. Both characterization and agronomic evaluation of ginger has been studied worldwide, mainly in those countries where ginger is highly valued such as India, China, Japan, etc. Many studies have detected different levels of variability (Wicaksana *et al.*, 2011; Yeh *et al.*, 2012; Chongtham *et al.*, 2013; Jatoi and Watanabe, 2013; Wang *et al.*, 2014) and provided relevant information about the association degree among plant characteristics and its yield as well as their combined effect on genetic variability.

Knowledge regarding the association degree among different agronomic traits is important in plant breeding since it supports genetic selection. If two characters have shown a favorable genetic correlation, then is possible to get progress for one of them by indirect selection of the other one (Cruz *et al.*, 2004). There is a consensus in the literature that the phenotypic characteristics such as: plant height, leaf area, length and width of the leaves, and the number of tillers per plant, have shown direct and positive effects on the yield of ginger (Sing *et al.*, 2001; Manhomandas *et al.*, 2000; Abraham and Latha, 2003; Lincy *et al.*, 2008; Aragaw *et al.*, 2011). Studies including multiple regression analysis of morphological characteristics have shown that the yield per plant at 120 d after planting may be predicted by considering the following characteristics: plant height, number

of leaves, and the width of the last leaf completely opened (Ratnambal *et al.*, 1982; Rattan, 1989; Rai *et al.*, 1999).

Different commercial ginger varieties (local and genetic improved) with high potential yields and quality attributes, have been used extensively by farmers from India and China. Variations on growth habits, fiber and essential oils contents, flavor and yield have been observed. Most of them are named considering either their origin or domestication (Sasikumar *et al.*, 1996). Ginger is widely grown plant in both Southwest and Southern regions of Brazil. Nonetheless there is a lack of knowledge concerning the level of genetic variability and agronomic potential of this crop. The most commercialized ginger cultivar is the "Gigante" variety because of the better fit to the local market requirements. However, some regional clones are also cultivated despite of reduced rhizome sizes and these are not well accepted in the local market (Elpo and Negrelle, 2004).

In order to study the genetic diversity of ginger and promote its cultivation and commercialization, the Department of Genetics of the "Luiz de Queiroz" College of Agriculture, University of São Paulo, Brazil (ESALQ/USP) created a germplasm collection with accessions coming from different Brazilian states and some introduced accessions from Colombia. The aim of this study was to evaluate agronomic characteristics of the available germplasm in order to verify the existent genetic variability level in the cultivars, and by doing this, to select the best genotypes based on their agronomic performance for future plant breeding studies.

Material and methods

Planting and experimental design
Sixty-one accessions from the ginger germplasm collection of the Department of Genetics (ESALQ/USP) were planted and evaluated during 2013/2014 agricultural year in the Anhembi`s experimental station which is located in Piracicaba (São Paulo/Brazil) (Tab. 1).

Accessions were arranged in a complete randomized block design with four replications. The experimental unit was represented by plots of 1.0 m^2 with planting distance of 1.0 m between rows, and 0.3 m between plants, in total 10 plants per plot. Chemical fertilization was made 8 d before planting with 4-14-8 (N, P, K fertilizer at 100 g m^{-1}) following by three more fertilizations done along of the crop period with ammonium sulfate (23 g m^{-1}), potassium chloride (14 g m^{-1}) and triple superphosphate (64 g m^{-1}).

TABLE 1. Description of 61 Brazilian accessions of ginger (*Zingiber officinale*) kept in the germplasm collection of Department of Genetics, ESALQ/USP.

Id.	Accession name	Common name	Biological status	Country of origin[1]	Germplasm source
1	Gen-03	Variedad blanca	Landrace	Colombia	Genebank
2	Gen-04	Variedad amarilla	Landrace	Colombia	Genebank
3	Gen-05	Variedad jamaiquina	Landrace	Colombia	Genebank
4	Gen-07	Col-clone-europeo	Landrace	Colombia	Genebank
5	Gen-08	Jengibre	Landrace	SE-Brazil	Garden
6	Gen-10	Jengibre	Clonal selection	SP-Brazil	Market
7	Gen-11	Jengibre	Clonal selection	SP-Brazil	Market
8	Gen-12	Jengibre	Landrace	SP-Brazil	Garden
9	Gen-13	Jengibre	Clonal selection	AM-Brazil	Market
10	Gen-14	Jengibre	Clonal selection	ES-Brazil	Market
11	Gen-15	Jengibre	Clonal selection	SE-Brazil	Market
12	Gen-16	Jengibre	Clonal selection	SE-Brazil	Market
13	Gen-17	Jengibre	Clonal selection	SC-Brazil	Market
14	Gen-18	Jengibre	Clonal selection	SC-Brazil	Market
15	Gen-19	Jengibre	Clonal selection	AM-Brazil	Market
16	Gen-20	Jengibre	Clonal selection	SC-Brazil	Garden
17	Gen-21	Gigante	Clonal selection	SC-Brazil	Market
18	Gen-22	Jengibre	Landrace	SC-Brazil	Garden
19	Gen-23	Havai	Clonal selection	SP-Brazil	Field
20	Gen-24	Jengibre	Landrace	SP-Brazil	Garden
21	Gen-25	Jengibre	Clonal selection	SP-Brazil	Field
22	Gen-27	Jengibre	Clonal selection	SP-Brazil	Field
23	Gen-28	Gigante	Clonal selection	SP-Brazil	Field
24	Gen-29	Gigante	Clonal selection	SP-Brazil	Field
25	Gen-30	Havai	Clonal selection	SP-Brazil	Field
26	Gen-31	Jengibre	Clonal selection	SP-Brazil	Field
27	Gen-32	Dominica	Clonal selection	SP-Brazil	Field
28	Gen-33	Chinesse	Clonal selection	SP-Brazil	Field
29	Gen-34	Gigante	Clonal selection	SP-Brazil	Field
30	Gen-35	Gigante	Clonal selection	SP-Brazil	Field
31	Gen-36	Gigante	Clonal selection	SP-Brazil	Field
32	Gen-37	Gigante	Clonal selection	SP-Brazil	Field
33	Gen-38	jengibre	Clonal selection	SP-Brazil	Field
34	Gen-39	Jengibre	Clonal selection	SP-Brazil	Field
35	Gen-40	Jengibre	Clonal selection	SP-Brazil	Field
36	Gen-41	Gigante	Clonal selection	SP-Brazil	Field
37	Gen-42	Jengibre	Clonal selection	SP-Brazil	Field
38	Gen-43	Jengibre	Clonal selection	SP-Brazil	Field
39	Gen-44	Jengibre	Clonal selection	SP-Brazil	Field
40	Gen-45	Jengibre	Clonal selection	SP-Brazil	Field
41	Gen-46	Gigante	Clonal selection	PR-Brazil	Field
42	Gen-47	Paulista	Clonal selection	PR-Brazil	Field
43	Gen-48	Havai	Clonal selection	PR-Brazil	Field

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Id.	Accession name	Common name	Biological status	Country of origin[1]	Germplasm source
44	Gen-49	Gigante	Clonal selection	PR-Brazil	Field
45	Gen-50	Havai	Clonal selection	PR-Brazil	Field
46	Gen-51	Gigante	Clonal selection	ES-Brazil	Field
47	Gen-52	Gigante	Clonal selection	ES-Brazil	Field
48	Gen-53	Gigante	Clonal selection	ES-Brazil	Field
49	Gen-54	Jengibre	Landrace	ES-Brazil	Garden
50	Gen-55	Jengibre Incaper	Clonal selection	ES-Brazil	Field
51	Gen-56	Gigante	Clonal selection	ES-Brazil	Field
52	Gen-57	Gigante	Clonal selection	ES-Brazil	Field
53	Gen-58	Gigante	Clonal selection	ES-Brazil	Field
54	Gen-59	Gigante	Clonal selection	ES-Brazil	Field
55	Gen-60	Gigante	Clonal selection	ES-Brazil	Field
56	Gen-61	Gigante	Clonal selection	ES-Brazil	Field
57	Gen-62	Gigante	Clonal selection	ES-Brazil	Field
58	Gen-63	Jengibre Blanco	Clonal selection	SP-Brazil	Field
59	Gen-64	Jengibre Amarillo	Clonal selection	SP-Brazil	Field
60	Gen-65	Caipira	Landrace	SP-Brazil	Garden
61	Gen-66	Jengibre Azul	Clonal selection	SP-Brazil	Field

[1] Abbreviation of the names of the origin region of the accessions: SE: Sergipe; SP: São Paulo; AM: Amazonas; ES: Espirito Santo; SC: Santa Catarina; PR: Paraná; Id: Identification of the accessions.

Agronomic traits

Agronomic evaluation of the accessions was made according to phenotypic descriptors as suggested by Ahmad (2008). In this study, seven quantitative traits were evaluated as shown in Tab. 2. Mean values from 4 plants per plot were used for statistical analysis with the exception of the plot performance (PP), which was evaluated for the whole plot.

TABLE 2. Agronomic traits evaluated in ginger germplasm (*Z. officinale*).

Characteristic	Method and time of evaluation
Plant height (PH)	Measure from the soil surface to the end of the last leaf (cm), at maximum vegetative growth.
Leaf length (LL)	Measure from the base to the tip of the leaf (cm), at maximum vegetative growth.
Leaf width (LW)	Measured in three different parts of the leaf (cm), in the maximum vegetative growth.
Number of leaves per tiller (NLT)	Number of leaves per tiller after flowering.
Number of tillers per plant (NTP)	Number of tillers per plant after flowering
Rhizome thickness (RT)	Measured with pachymeter in 3 different rhizomes in postharvest (mm)
Yield per plot (YP)	Rhizomes weight of the plot (kg m^{-2}), corrected for the final number of plants per plot (7,184 plants) by the covarianza method.

Statistical analysis

Descriptive statistics (mean, rank and coefficient of variation) were calculated. The Shapiro-Wilk Test was used to verify the normality of the data ($P \leq 0.05$) and analysis of variance was performed to detect differences between the accessions. Once significance level was confirmed between the accessions, a Scott-Knott means comparison test was performed. To verify the association degree among traits, both genotypic and phenotypic correlations were calculated. The following genetic parameters were calculated based on the mean values obtained from the experimental plots:

- Phenotypic variance (σ_p^2): $\frac{GMS}{r}$

- Environmental variance (σ_e^2): $\frac{RMS}{r}$

- Genotypic variance (σ_g^2): $\frac{GMS - RMS}{r}$

- Heritability (h^2): σ_g^2 / σ_p^2

- Genetic coefficient of variation (CV$_g$, %): $\frac{(100 \sqrt{\sigma_g^2})}{\mu}$

- Genetic-environmental variation ratio (CV$_g$/CV$_e$): $\sqrt{\frac{\sigma_e^2}{\sigma_g^2}}$

Where:

GMS = genotypes mean square
RMS = residual mean square
r = number of experimental replications
μ = average mean for evaluated trait

The experimental data were analyzed by SAS (version 9.3; SAS Institute Inc., Cary, NC) and GENES software (Cruz, 2013).

Results

Shapiro-Wilk test which was performed to determine the normality of the residuals, confirmed that the seven traits followed a normal distribution. An example for NTP trait is presented (Fig. 1). Analysis of variance showed that there are highly significant differences ($P \leq 0.01$) among phenotypic means of the accessions for all of analyzed agronomical traits (PH, LL, LW, YP, RT, NTP and NLT) indicating that phenotypic variability exist (Tab. 3).

The mean comparison analysis for PH revealed that most of the accessions (54.10%) presented phenotypic values above of the average mean (>60 cm) being classified as high phenotypes and therefore gathered in one group (identified by letter a). The rest of the germplasm accessions showed an average plant height (between 54 and 59 cm; letter b), and low plant height (<54 cm; letter c) (Tab. 4).

Slightly less than a half of the accessions displayed longer leaves (>20 cm) and wider (>2.30 mm) compared to mean values for the other accessions. Similarly 66% of the accessions showed high density of foliage reaching up to 18.38 leaves per tiller whilst for the rest of the accessions, between 11.88 and 14.51 leaves per tiller were counted. The Gen-18 accession showed the lowest NLT (10) as presented in Tab. 4.

Approximately 35% of the accessions showed the highest YP ranging from 4.50 to 7.20 kg m^{-2}. In 20 accessions (32.79%), the NTP produced the greatest number of tillers (≥ 16) whilst in little bit more than a half (54.10%) of the
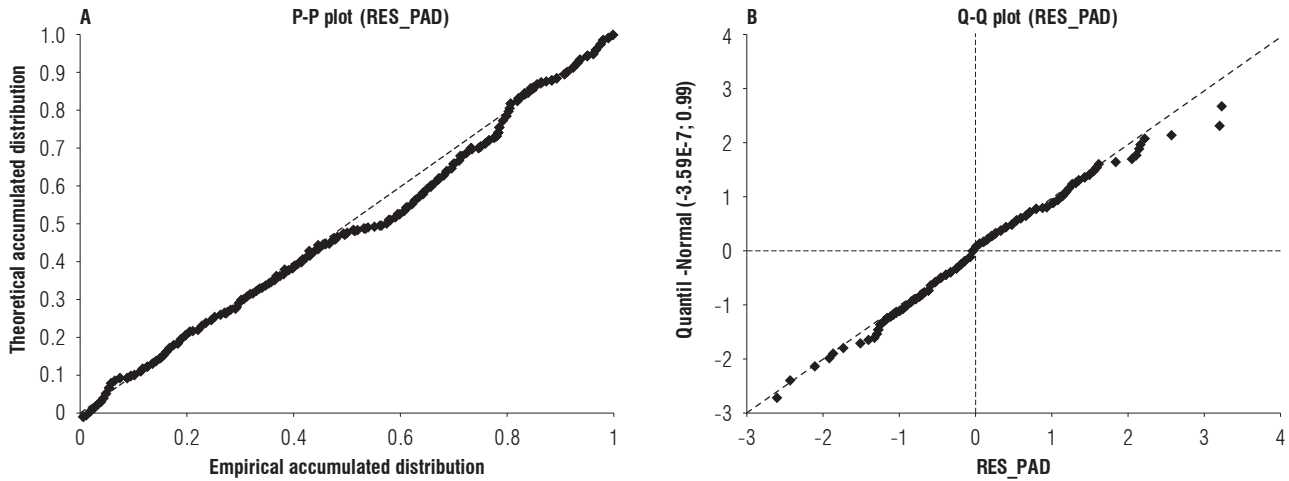

FIGURE 1. Normal distribution chart of standardized residuals for the NTP trait evaluated in 61 ginger accessions. Normality test Shapiro-Wilk = 0.078 ($P \leq 0.05$).

TABLE 3. Summary of the analysis of variance of the agronomic traits evaluated in 61 accessions of ginger (*Z. officinale*).

FV	GL	MS						
		PH	**LL**	**LW**	**YP**	**RT**	**NTP**	**NLT**
Blocks	3	749,93	11,96	0,66	7,25	6,23	62,32	36,23
Accessions	60	137,14**	7,89**	0,11**	12,17**	104,08**	55,77**	8,41**
Residue	180	25,49	1,98	0,03	1,13	7,24	15,02	3,15
Mean		59,41	20,68	2,29	3,83	30,67	14,49	14,93
CV (%)		8,50	6,80	7,28	27,78	8,77	26,75	11,89
Máx.		68,92	24,69	2,75	7,15	41,88	24,20	18,38
(accesión)		(Gen-10)	(Gen-17)	(Gen-17)	(Gen-42)	(Gen-33)	(Gen-42)	(Gen-33)
Mín.		46.38	15.72	1.68	1.04	17.98	6.15	8.87
(accesión)		(Gen-24)	(Gen-18)	(Gen-24)	(Gen-22)	(Gen-24)	(Gen-04)	(Gen-18)

**: Significant to 1% (F test); PH: plant height (cm); LL: leaf length (cm); LW: leaf width (mm); YP: yield per plot (kg m^{-2}); RT: rhizome thickness (mm); NTP: number of tillers per plant; NLT: number of leaves per tiller; Max: maximum value; Min: minimum value; CV: coefficient of variation; FV: sources of variation; GL: degrees of freedom; MS: mean square.

accessions, this trait ranged from 11 to 15.50 tillers per plant. Ten tillers per plant were observed for the rest of the accessions (13.11%). Regarding to RT trait, 27.87 % of the accessions were characterized by large (33.89 to 41.88 mm); intermediate (28.73 to 33.59 mm); and small rhizomes (17.97 to 28.01 mm) respectively (Tab. 4).

Genetic parameters for evaluated traits are shown in Tab. 5. The CV_g/Cv_e ratio displayed greater values than 1.0 and high heritability values (>80%) indicating an advantageous genotype selection towards PH, RT, and YP. These results indicate that an important contribution of the genetic factors exist in the final expression of these agronomic traits. This most likely favors clonal selection of promissory genotypes.

The significance for the phenotypic (above of diagonal) and genotypic correlations (bellow of diagonal) among tested traits is shown in Table 6. Positive and highly significant correlations ($P \leq 0.01$) were detected among evaluated traits, except for LW and RT which correlations with NTP and NLT were non-significant. In general, YP showed higher correlations with PH (r = 0.69), NTP (r = 0.63), and RT (r = 0.54) compared with the other traits. High correlation between PH and LL was also detected (r = 0.75). Conversely, LW was higher correlated with LL and RT (r = 0.67 and 0.61, respectively). Finally, moderate correlations were observed between NLT and PH (r = 0.523), LL (r = 0.455), YP (r = 0.483) and NTP (r = 0.474).

TABLE 4. Means comparison analysis (Scott and Knott) for the seven agronomic traits evaluated in 61 accessions of ginger (*Z. officinale*).

Accession	PH	LL	LW	YP	RT	NTP	NLT
Gen-03	63.67 a	21.39 a	2.35 a	3.05 c	23.13 e	12.40 b	17.62 a
Gen-04	66.92 a	21.64 a	2.25 b	2.54 d	23.14 e	6.15 c	12.87 b
Gen-05	60.67 a	21.34 a	2.23 b	6.84 a	21.22 e	13.90 b	14.37 b
Gen-07	50.13 c	19.35 b	2.15 b	2.48 d	23.83 e	11.88 b	15.44 a
Gen-08	60.00 a	20.58 b	2.27 b	4.56 b	25.92 d	20.13 a	16.63 a
Gen-10	68.92 a	22.04 a	2.24 b	2.54 d	23.61 e	13.40 b	16.62 a
Gen-11	61.44 a	20.42 b	2.17 b	2.83 d	29.83 c	15.75 a	14.94 a
Gen-12	50.92 c	18.89 b	2.18 b	1.80 d	22.55 e	14.65 b	14.62 a
Gen-13	63.41 a	21.78 a	2.35 a	3.27 c	35.49 b	13.84 b	15.51 a
Gen-14	58.19 b	21.58 a	2.37 a	3.21 c	32.07 c	15.00 b	15.56 a
Gen-15	48.67 c	20.41 b	2.48 a	2.36 d	26.82 d	7.57 c	13.54 b
Gen-16	68.17 a	23.14 a	2.30 a	5.23 b	35.34 b	20.15 a	15.12 a
Gen-17	66.42 a	24.69 a	2.75 a	2.93 c	27.50 d	22.90 a	14.87 a
Gen-18	49.67 c	15.72 c	2.19 b	2.53 d	31.50 c	8.40 c	8.87 c
Gen-19	53.17 c	20.09 b	2.35 a	2.73 d	28.73 c	15.90 a	15.12 a
Gen-20	61.56 a	20.84 a	2.22 b	3.06 c	33.59 c	11.94 b	15.19 a
Gen-21	54.44 b	20.11 b	2.22 b	2.52 d	32.33 c	11.45 b	14.51 b
Gen-22	52.41 c	20.32 b	1.93 c	1.04 d	21.81 e	9.18 c	13.68 b
Gen-23	55.06 b	19.37 b	2.22 b	2.19 d	33.37 c	11.50 b	14.81 a
Gen-24	46.38 c	16.85 c	1.68 d	1.27 d	17.98 f	13.20 b	14.74 a
Gen-25	51.00 c	19.89 b	2.34 a	2.06 d	29.00 c	13.25 b	14.00 b
Gen-27	51.38 c	18.50 b	2.18 b	1.18 d	26.95 d	8.56 c	11.88 b
Gen-28	61.31 a	20.46 b	2.23 b	3.53 c	34.86 b	13.00 b	13.44 b
Gen-29	64.06 a	21.53 a	2.32 a	6.12 a	32.38 c	19.94 a	15.06 a
Gen-30	54.75 b	20.38 b	2.51 a	2.73 d	35.45 b	13.44 b	12.63 b
Gen-31	67.13 a	22.53 a	2.43 a	7.04 a	35.66 b	19.13 a	15.88 a
Gen-32	63.75 a	21.64 a	2.41 a	6.57 a	37.53 b	14.19 b	15.69 a
Gen-33	64.19 a	22.10 a	2.59 a	5.59 b	41.88 a	12.00 b	18.38 a
Gen-34	58.44 b	19.74 b	2.48 a	5.62 b	37.59 b	14.94 b	16.56 a

Accession	PH	LL	LW	YP	RT	NTP	NLT
Gen-35	58.88 b	21.03 a	2.35 a	3.69 c	30.15 c	14.38 b	14.81 a
Gen-36	63.63 a	21.39 a	2.20 b	6.36 a	32.14 c	18.31 a	15.94 a
Gen-37	65.69 a	20.28 b	2.30 a	6.24 a	40.01 a	16.81 a	15.69 a
Gen-38	51.31 c	19.68 b	2.23 b	2.18 d	24.92 d	11.06 b	13.44 b
Gen-39	65.94 a	22.58 a	2.45 a	4.49 b	33.16 c	13.63 b	15.56 a
Gen-40	65.69 a	20.46 b	2.27 b	6.80 a	35.30 b	18.38 a	16.19 a
Gen-41	64.25 a	21.19 a	2.34 a	7.14 a	32.67 c	19.44 a	16.31 a
Gen-42	64.63 a	19.18 b	2.20 b	7.15 a	31.21 c	24.20 a	17.06 a
Gen-43	64.06 a	21.30 a	2.36 a	6.19 a	34.81 b	17.25 a	16.31 a
Gen-44	67.25 a	21.39 a	2.37 a	6.46 a	34.41 b	15.50 b	14.81 a
Gen-45	59.56 a	20.88 a	2.32 a	4.97 b	32.30 c	18.06 a	14.38 b
Gen-46	58.25 b	20.44 b	2.38 a	3.28 c	35.45 b	12.06 b	13.81 b
Gen-47	62.69 a	21.69 a	2.34 a	4.17 c	35.19 b	16.38 a	13.75 b
Gen-48	56.06 b	19.60 b	2.24 b	1.94 d	33.90 b	9.88 c	15.00 a
Gen-49	57.44 b	21.82 a	2.44 a	3.74 c	32.71 c	13.31 b	16.00 a
Gen-50	63.00 a	22.07 a	2.46 a	6.01 a	34.98 b	13.56 b	16.00 a
Gen-51	61.38 a	22.44 a	2.35 a	4.61 b	35.30 b	18.00 a	14.38 b
Gen-52	61.31 a	21.29 a	2.32 a	4.16 c	31.66 c	17.69 a	14.81 a
Gen-53	61.38 a	20.14 b	2.15 b	4.23 c	29.27 c	14.88 b	15.50 a
Gen-54	56.21 b	19.90 b	2.01 c	2.13 d	22.62e	7.74 c	15.15 a
Gen-55	52.44 c	19.46 b	2.17 b	1.67 d	28.01 d	11.63 b	13.63 b
Gen-56	53.25 c	19.89 b	2.08 b	2.57 d	30.21 c	13.69 b	14.81 a
Gen-57	53.19 c	19.71 b	2.22 b	2.60 d	30.25 c	12.00 b	14.31 b
Gen-58	55.96 b	21.15 a	2.42 a	2.67 d	29.53 c	14.77 b	14.23 b
Gen-59	65.31 a	20.56 b	2.33 a	3.83 c	30.69 c	19.94 a	15.69 a
Gen-60	55.75 b	20.59 b	2.28 a	2.72 d	32.03 c	10.50 c	14.06 b
Gen-61	57.50 b	20.05 b	2.34 a	3.67 c	30.28 c	14.19 b	12.94 b
Gen-62	54.92 b	20.18 b	2.21 b	3.09 c	31.62 c	15.04 b	14.17 b
Gen-63	66.63 a	22.06 a	2.44 a	5.70 b	33.02 c	18.13 a	16.50 a
Gen-64	67.56 a	21.95 a	2.45 a	5.25 b	33.52 c	15.06 b	15.69 a
Gen-65	53.19 c	18.75 b	1.88 c	2.47 d	18.31f	17.81 a	15.94 a
Gen-66	63.50 a	21.19 a	2.31 a	2.22 d	30.17 c	12.63 b	15.69 a

Values with the same letter are not significantly different ($P \leq 0.05$) and belong to the same group.

TABLE 5. Estimation of the genetic parameters for the agronomic traits evaluated in 61 accessions of ginger (*Z. officinale*).

Charateristic	σ_p^2	σ_e^2	σ_g^2	h^2 (%)	CV_g (%)	CV_g/CV_e
PH	34.28	6.37	27.91	81.41	8.89	1.05
LL	1.98	0.49	1.48	74.93	5.88	0.86
LW	0.03	0.01	0.02	74.38	6.20	0.85
YP	3.04	0.28	2.76	90.69	43.35	1.56
RT	26.02	1.81	24.21	93.05	16.04	1.83
NTP	13.94	3.75	10.19	73.07	22.04	0.82
NLT	2.10	0.79	1.32	62.54	7.68	0.65

TABLE 6. Phenotypic (above the diagonal) and genotypic correlations (below the diagonal) between the agronomic traits evaluated in 61 accessions of ginger (*Z. officinale*).

Characteristic	PH	LL	LW	YP	RT	NTP	NLT
PH	1	0.748**	0.476**	0.697**	0.449**	0.518**	0.523**
LL	0.788**	1	0.671**	0.443**	0.350**	0.386**	0.455**
LW	0.518**	0.705**	1	0.401**	0.606**	0.246^{ns}	0.189^{ns}
YP	0.730**	0.483**	0.457**	1	0.543**	0.626**	0.483**
RT	0.472**	0.376**	0.696**	0.564**	1	0.245^{ns}	0.166^{ns}
NTP	0.591**	0.446**	0.299^{ns}	0.697**	0.285^{ns}	1	0.474**
NLT	0.598**	0.558**	0.240^{ns}	0.566**	0.189^{ns}	0.657	1

**: Significant to 1%; ns: not significant.

Discussion

Variability and genotypes selection

A well known method to determine the genetic variability of crops is by the analysis of agro-morphological traits (phenotypic characteristics) which are relevant to establish their productive performance to improve the success of crop breeding programs (Mohammadi and Prasanna, 2003). In the present study, the evaluation of 61 accessions of a ginger germplasm bank (ESALQ/USP) indicates that there was moderate genetic variability for the evaluated agronomic traits.

The variables that contributed more to the germplasm variability were yield per plot, rhizome thickness, number of tillers per plant and lift width. Moderate genetic variability in ginger was also reported recently in accessions grown in Burkina Faso for 13 quantitative traits (Nandkangre *et al.*, 2016). In that study, the analysis of variance highlighted the presence of some discriminatory traits such as number of leaves per tiller, leave length, plant height, and both length and width of the rhizome. Similar results were reported two decades ago by Ravindran *et al.* (1994) in India and more recently by Jatoi and Watanabe (2013) in Japan who found moderate variability for plant height, number of leaves per plant, yield per plant and associated traits. The number of tillers per plant and yield per plant were the most divergent traits among the evaluated accessions. The results of the present study are consistent based on the fact that the genetic variability in plant species with an exclusive vegetative propagation system such as ginger tends to be either moderated or limited, unless that the evaluated genotypes come from geographic areas with constant agroecology conditions. The long history of ginger domestication and its adaptation to several eco-geographic niches has been the main evolutionary driving force of this plant, therefore moderate to low variability exist among collected or planted accessions in nearby areas

with similar environmental conditions. Conversely, large variation is observed when the accessions come from areas with contrasting eco-geographic conditions because of being influenced by different selection pressures (Ravindran and Nirmal-Babu, 2005; Bosseti *et al.,* 2011).

Phenotypic variability found among accessions is the result of the interaction of genetic and environmental factors. So, agronomic traits such as plant height, yield per plant/plot, etc., usually have polygenic inheritance due to be controlled by several genes highly influenced by the environment (Ceballos, 2000; Vallejo and Estrada, 2002). However, unlike this consensus, genetic parameters such as heritability, CV_g/CV_e ratio, etc., indicate that environmental variance had little influence on the final expression of the yield of ginger, despite of it is one of the traits with greatest contribution to the phenotypic variability of the analyzed accessions. These results suggest that phenotypic differences observed during the evaluated agricultural period were more related to genetic than environmental variables, thus is possible to perform clonal selection for ginger plant yield as recently done by Ravishanker *et al.* (2014) using 25 Indian *Z. officinale* genotypes. In the present study, 35% of the germplasm showed a higher yield related to the mean value and the following accessions are highlighted: Gen-05, Gen-29, Gen-31, Gen-32, Gen-36, Gen-37, Gen-40, Gen-41, Gen-42, Gen-43, Gen-44, and Gen-50 (yield per plot above 6.0 kg m$^{2-1}$). Most of the accessions originally come from the most highly productive ginger region in the São Paulo state ("Tapiraí" and "Piedade" municipalities), and they could be selected once the existent phenotypic variability indicates, in a considerable extent, their genetic potential. One of the advantages of clonal selection is that enables the capture of genetic superiority of the cultivars perpetuating it throughout the generations. Clonal propagation permits the fixation of favorable genetic combinations maintaining a high level of heterozygosity for one or more characteristics of agronomic interest (Mckey *et al.,* 2010; Bisognin, 2011).

Genetic variance, heritability and CV_g/CV_e ratio, among other genetic parameters were studied in 90 Indian ginger genotypes (Islam *et al.,* 2008). Similarly to the results obtained in the present study, the authors found little environmental effect on the phenotypic expression of the associated yield traits with high heritability values (>90%) for both height and yield per plant. In a study conducted in Ethiopia, genetic variability of 36 ginger accessions was evaluated. High heritability values (>90%) were reported for yield per plant, plant height, rhizome thickness, among other traits (Aragaw *et al.,* 2011). Most of the accessions evaluated in the present study are commercial cultivars or varieties which are widely adapted to the agro-ecological areas where they are cultivated. This broad adaptation capacity in addition to the favorable conditions for plant growth and crop management may contribute to the high heritability of the agronomic traits evaluated. High heritability values for these traits have been reported in *Curcuma Longa* (Singh *et al.*, 2003; Chattopadhyay *et al.*, 2004; Sasikumar, 2005), an specie characterized by its vegetative propagation and it is also a member of the *Zingiberaceae* family.

Genetic correlations

The study on the nature and magnitude of the existent relationships among traits is crucial for breeding purposes. In case that two characters present favorable genetic correlation is possible to obtain genetic gains for one of them by the indirect selection of the second one (Vencovsky and Barriga, 1992). As confirmed recently in the studies by Kumar *et al.* (2016) and Ravishanker *et al.* (2013); in the present study, yield per plant showed a positive and highly significant correlation with plant height, number of tillers per plant and rhizome thickness. Also, the magnitude of genetic correlations was more expressive than for phenotypic correlations (Tab. 6). These findings confirm the hypothesis towards that the variability found among the analyzed accessions is mainly genetic. In such scenario, may be plausible the early selection of superior genotypes for agronomic traits such as: plant height, number of tillers per plant, rhizome thickness, etc., and it leads to expressive productive gains taking into account that in some cases indirect selection based on correlated response could lead to faster progress compared with direct selection on the desired trait (Cruz *et al.*, 2004).

Conclusions

There was moderate genetic variability among 61 accessions of the ESALQ/USP ginger germplasm collection. Among the studied agronomic traits, yield per plot, rhizome thickness, number of tillers per plant, and leaf width were the most variable characters. The present study identified the following accessions as the most promissory genotypes based on their agronomic performance: Gen-05, Gen-29, Gen-31, Gen-32, Gen-36, Gen-37, Gen-40, Gen-41, Gen-42, Gen-43, Gen-44 and Gen-50 because of that they were selected as a potential clones. However, it is important to emphasize that genetic superiority and adaptation of these accessions must be confirmed by conducting new agronomic studies at different environments and seasons in order to validate the obtained results in this study. So far, ginger phenotypic variability in Brazil has not been studied, for that reason the results of the present study may be useful in future ginger plant breeding programs and also to promote its cultivation and further study at national level.

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