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INTERNATIONAL JOURNAL OF CURRENT RESEARCH

International Journal of Current Research
Vol. 8, Issue, 10, pp.39714-39718, October, 2016

ISSN: 0975-833X

RESEARCH ARTICLE

COMPETITION OF SOYBEAN GENOTYPES CULTIVATED IN LOWLANDS OF RIO GRANDE DO SUL, BRAZIL

[1]Vinícius Jardel Szareski, [*,1]Ivan Ricardo Caralho, [1]Maicon Nardino, [1]Alan Junior de Pelegrin, [1]Mauricio Ferrari, [2]Ronei Gaviraghi, [1]Gustavo Henrique Demari, [3]Diego Nicolau Follmann, [3]Cleiton Antônio Warths and [4]Velci Queiróz de Souza

[1]Federal University of Pelotas, Brazil
[2]Federal University of Santa Maria, Campus FredericoWestphalen, Brazil
[3]Federal University of Santa Maria, Brazil
[4]Federal University of Pampa, Brazil

ARTICLE INFO

Article History:
Received 27th July, 2016
Received in revised form
15th August, 2016
Accepted 08th September, 2016
Published online 30th October, 2016

Key words:

Multivariate and Univariate analyzes,
Agricultural experimentation,
Glycine max (L.) Merrill.

ABSTRACT

The objective of this study was to infer on yield performance through linear associations of traits and identify the genetic variation of soybean genotypes through canonical variables. The experiment was carried out during the 2013/2014 agricultural year in a randomized block design arranged in four replications. The following genotypes were utilized: NS 5445 IPRO, NS 6211 RR, TEC 6029 IPRO, TECS 13/03 RR, 6458 RSF IPRO, DON MARIO 5.8i, 6160RSF IPRO, DON MARIO 5.9i, CD 2611 IPRO, CD 2585 RR, and TMG 7161 RR. Genotypes 6160RSF IPRO, NS 5445 IPRO, and 6458RSF IPRO presented the greatest grain yield values, demonstrating potential use for cultivation in lowlands in Rio Grande do Sul. The traits grain weight of ten plants, number of pods in the main stem, number of pods in the branches, number of pods with one, two, and three grains have positive linear correlations with grain yield. The genotypes were clustered according to their genetic basis and maturation cycle, canonical variables explained 85.05% of existent genetic variation, and four genotype groups were formed.

Citation: Vinícius Jardel Szareski, Ivan Ricardo Caralho, Maicon Nardino *et al.* 2016. "Competition of soybean genotypes cultivated in lowlands of rio grande do sul, Brazil", *International Journal of Current Research*, 8, (10), 39714-39718.

INTRODUCTION

Soybean (*Glycine max* (L.) Merrill is one of the main oilseeds grown in the world, being used as raw material for food and feed. In the 2014/2015 agricultural year,about31.3 million hectares were sown in Brazil, with production of 93 million tonnes of grains (Conab, 2015). In Rio Grande do Sul,4.9 million hectares were sown, being 302,000 hectares of these area cultivated in lowland areas in succession to rice (IRGA, 2014). Currently, soybean breeding programsare seeking increased yield with direct and indirect reduction of production costs. Furthermore, the objective is to increase the genotypes adaptive capacity in relationto soil and climatic conditions and the incidence of insect pests and diseases (Nascimento *et al*, 2010; Gulluoglu *et al*., 2011). Among the factors that influence the soybean growth and development, photoperiod directly influences the crop yield potential (Vernetti, 1983). Research performed by Sanchez (2012) evidenced that the changes in soybean morphology may be due to altitude, latitude, texture and soil fertility, plant population, sowing date, spatial arrangement among rows, and genotype intrinsic traits. Rezende and Carvalho (2007) indicated that among these factors, the sowing date is closely related to the photoperiod response. Thus, soybean genotypes that will be introduced in a new region should undergo preliminary analysis, facing the cropping environment changes and their responses to environmental variations (Cruz and Regazzi, 2001). Canonical variables can be used in order to understand the existent genetic variation among genotypes cultivated in a particular environment. They provide the interpretation of measured traits in a simplified and combined mode, being presented through a two-dimensional or three-dimensional graphical dispersion of scores. This dispersion allows to visualize groups of similar genotypes and discriminate genetically dissimilar groups (Cruz *et al*., 2014). The shortage of information regarding the performance of soybean genotypes cultivated in lowlands in Rio Grande do Sul has been noticed. Thus, theobjective of this study was to infer on yield performance through linear associations of traits and identify the genetic variation of soybean genotypes through canonical variables.

Corresponding author: Ivan Ricardo Caralho,
Federal University of Pelotas, Brazil

MATERIALS AND METHODS

The experiment was carried out during the 2013/2014 agricultural year in the municipality of Capão do Leão – RS, southern Brazil under the geographic coordinates of 31º52'00"S and 52º21'24"W and altitude of 13.24m. According to Köppen climate classification, the climate is subtropical *Cfa*. The soil is classified as dystrophicred-yellow Alfissolwith sandy loam texture (Santos *et al.*, 2006). The experimental design was randomized blocks arranged in four replications. The following genotypes were utilized: NS 5445 IPRO, NS 6211 RR, TEC 6029 IPRO, TECS 13/03 RR, 6458 RSF IPRO, DON MARIO 5.8i, 6160RSF IPRO, DON MARIO 5.9i, CD 2611 IPRO, CD 2585 RR, and TMG 7161 RR. Experimental units were composed by five rows of three meters long with spacing of 0.45 meters, totaling an area of 6.75 m². The useful area was 2.70 m², consideringthe three central rows and discarding 0.5 m from each end. Sowing procedure was based on no tillage system with basic fertilization of 300 kg ha^{-1} of NPK in the 02-25-25 formulation. Plant population density was 300,000 plants per hectare. The control of weeds, insect pests, and diseases were carried out according to the crop necessities. Ten representative plants were randomly sampled from each experimental unit in order to evaluate the yield components. The following traits were measured using the methodology proposed by Carvalho *et al.* (2015): number of pods in the main stem (NPS), in units; plant height (PH), in cm; first pod insertion height(FPIH), in cm; number of pods in the branches (NPB), in units; number of branches (NB), in units; number of pods with one grain (NP1G), in units; number of pods with two grains(NP2G), in units; number of pods with three grains (NP3G), in units; grain weight of ten plants (GW10P), in g; thousand grain weight (TGW), in g; and grain yield (GY), in kg ha^{-1}. Data were submitted to analysis of variance by F test. Traits that showed significance were submitted to further analysis by Tukey test with $p<0.05$ probability. Linear associations were performed by Pearson linear correlation and correlation coefficients followed the classification proposed by Carvalho *et al.* (2004). Subsequently, the analysis of canonical variables through the procedures proposed by Cruz *et al.* (2014) was performed. Statistical analyzes were performed using the Genes software (Cruz, 2013).

RESULTS AND DISCUSSION

The analysis of variance was significant ($p<0.05$) for the traits TGW, GY, GW10P, PH, NP1G, NP2G, and NP3G.Traits that were not statistically different among the tested genotypes were: NPS, FPIH, NPB, and NB. For the TGW, there was superiority of TEC 6029 IPRO genotype, differing of the genotypes ND 6211 RR, TEC S 13/03 RR, CD 2585 RR, and TMG 7161 RR. The same genotype presented superiority of 33% when compared to TEC S 13/03 RR genotype, which expressed the lower TGW. Research carried out by Navarro Júnior and Costa (2002) involving six soybean cultivars in the municipality of Eldorado do Sul – RS found that the genotype with the greatest TGW presented superiority of 22.5% in comparison to the genotype with lowest magnitude for this trait. Moreover, Brandt *et al.* (2006) worked with nine cropping succession systems in Dourados – state of Mato Grosso do Sul and they found superiority of 14.6% for the soybean genotype with the greatestmagnitudecompared to the genotype with the lowest magnitude, indicating that thistrait presents some variation.

The TGW is genetically governed by many genes and highly influenced by the environment (Navarro Júnior and Costa, 2002). In addition, Rambo *et al.* (2004) observed that grain weight and size increase when the spacing between plants becomes equidistant, along with the reduction on plant population density, which directly affects the spatial arrangement and intra-specific competition of soybean plants. Water stress during grain filling period affect the grain weight, reduce photosynthetic capacity and tissue cooling, and harm assimilates accumulation, compromising the dislocation of them to the grains (Fontoura *et al.*, 2006). Another factor that influences this trait is the genotype precocity due to changes in photoperiod in low latitude regions, providing less vegetative growth and lower assimilate distribution, resulting in lighter grains with smaller dimensions (Maehler *et al.*, 2003). The GY exhibited greater magnitude for 6160RSF IPRO genotype, which differed only with Don Mario 5.9igenotype. This is a traitdependent of the interaction of various factors, including soil characteristics, mineral nutrition, climate, altitude, latitude, photoperiod, and all managements carried out from sowing to harvest. Currently, one of the main objectives in soybean breeding programs is to seek superior genotypes with high yield. However, this is a quantitative trait controlled by many genes and influenced by environmental conditions (Reis *et al.*, 2001). Medeiros *et al.* (1991) asserted that possible causes of the low soybean yield are attributed to soil and climatic characteristics of the region and the level of technology employed by the producer. The GW10P was similar to GY, with 6160RSF IPRO genotype being superior and differing from the genotypes NS 6211, Don Mario 5.9i, CD 2611 IPRO, and CD 2585 RR. Thus, the interpretation of this trait along with GY allows to infer greater reliability ingenotyperesponse, as the results of plant samplingin the experimental unit are consistent with those obtained by the total harvest per useful plot.

Table 1. Means for thousand grain weight (TGW, in g), grain yield (GY, in kg ha^{-1}), and grain weight of ten plants (GW10P, in g) for 11 soybean genotypes grown in lowland conditions during the 2013/2014 agricultural year

Soybean genotypes	TGW (g)	GY (kg ha^{-1})	GW10P (g)
NS 5445 IPRO	210.57 ab	3,293.60 ab	132.33 ab
NS 6211 RR	160.38 cd	2,407.30 ab	87.93 b
TEC 6029 IPRO	213.99 a	2,805.40 ab	140.89 ab
TEC S 13/03 RR	144.06 d	2,823.40 ab	141.80 ab
6458RSF IPRO	184.28 abcd	3,262.20 ab	163.84 ab
6160RSF IPRO	171.57 abcd	3,738.00 a	187.74 a
DON MARIO 5.8i	173.57 abcd	2,252.90 ab	113.15 ab
DON MARIO 5.9i	193.95 abc	2,002.00 b	100.55 b
CD 2611 IPRO	182.40 abcd	2,571.00 ab	108.74 b
CD 2585 RR	164.46 bcd	2,190.70 ab	92.65 b
TMG 7161 RR	166.63 bcd	2,242.40 ab	112.62 ab
CV (%)	10.39	24.59	24.65

*Means followed by the same lowercase letter in the column are not statistically different from each other by the Tukey test at 5% probability.

The PHexhibited similar behavior among genotypes, with the exception of NS 6211 RR genotype, which presented value 34.4% lower than the genotype with the greatest magnitude. The values oscillated in an amplitude of 65 to 102.13 cm, being considered ideal for mechanical harvesting. Further, the results are consistent with Rezende and Carvalho (2007), which stated that soybeans should present PHfrom 60 to 120 cm to reduce losses during mechanical harvesting. Changes in soybean growth habit are evidenced in the new genotypes, where the determined growth habit has lower preference by the producers when compared to genotypes with indeterminate growth habit.

Table 2. Means for plant height (PH, in cm), number of pods with one grain (NP1G, in units), number of pods with two grains (NP2G, in units), and number of pods with three grains (NP3G, in units) for 11 soybean genotypes grown in lowland conditions during the 2013/2014 agricultural year

Soybean genotypes	PH (cm)	NP1G	NP2G	NP3G
NS 5445 IPRO	82.18 ab	15.62 ab	33.50 ab	28.05bc
NS 6211 RR	65.00 b	17.12 ab	36.18 ab	25.52 c
TEC 6029 IPRO	98.37 ab	28.13 a	48.00 ab	47.93abc
TEC S 13/03 RR	94.83 ab	17.05 ab	54.88 ab	46.57abc
6458RSF IPRO	97.38 ab	16.39 ab	51.97 ab	66.13 a
6160RSF IPRO	89.33 ab	35.07 a	69.00 a	42.40 abc
DON MARIO 5.8i	74.86 ab	20.47 ab	45.00 ab	28.05 bc
DON MARIO 5.9i	88.95 ab	15.92 ab	40.33 ab	37.17 abc
CD 2611 IPRO	102.13 a	6.55 b	28.18 b	58.52ab
CD 2585 RR	80.96 ab	28.80 a	61.45 ab	26.71 c
TMG 7161 RR	89.35 ab	20.05 ab	61.85 ab	36.05 abc
CV (%)	16.5	42.95	30.00	31.38

*Means followed by the same lowercase letter in the column are not statistically different from each other by the Tukey test at 5% probability.

Table 3. Phenotypic linear correlations among morphological traits analyzed in 11 soybean genotypes cultivated in lowland conditions during the 2013/2014 agricultural year

	TGW	GY	GW10P	PH	FPIH	NPS	NPB	NB	NP1G	NP2G	NP3G
TGW**	-	0.186^{ns}	0.138^{ns}	0.244^{ns}	0.176^{ns}	0.214^{ns}	-0.199^{ns}	-0.256^{ns}	-0.019^{ns}	-0.224^{ns}	0.035^{ns}
GY		-	0.938*	0.219^{ns}	-0.039^{ns}	0.445*	0.391*	0.223^{ns}	0.433*	0.409*	0.471*
GW10P			-	0.312*	-0.068^{ns}	0.418*	0.502*	0.353*	0.471*	0.509*	0.536*
PH				-	0.651*	0.651*	-0.067^{ns}	-0.207^{ns}	-0.007^{ns}	-0.023^{ns}	0.342*
FPIH					-	0.369*	-0.364*	-0.409*	-0.241^{ns}	-0.416*	0.084^{ns}
NPS						-	0.068^{ns}	-0.235^{ns}	0.335*	0.301*	0.297*
NPB							-	0.876*	0.601*	0.826*	0.643*
NB								-	0.381*	0.643*	0.497*
NP1G									-	0.765*	0.114^{ns}
NP2G										-	0.334*
NP3G											-

n = 44;ns= not significant.

*Coefficients of Pearson linear correlation significant at 5% of probability.

**TGW: thousand grain weight; GY: grain yield; GW10P: weight of ten plants; PH: plant height; FPIH: first pod insertion height; NPS: number of pods in the main stem; NPB: number of pods in the branches; NB: number of branches; NP1G: number of pods with one grain; NP2G: number of pods with two grains; and NP3G: number of pods with three grains.

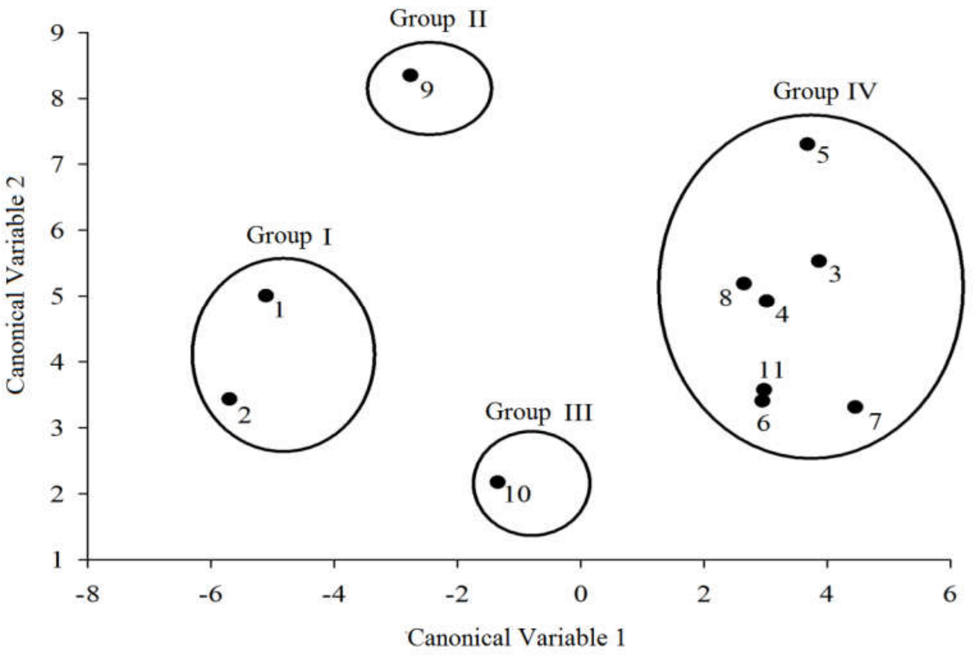

Figure 1. Graphic dispersion of scores obtained by the canonical variables analysis *CV1* (68.70%) e *CV2* (16.31%) obtained in 11 soybean genotypes, where *1*=(NS 5445 IPRO); *2*=(NS 6211 RR); *3*=(TEC 6029 IPRO); *4*=(TEC S 13/03 RR); *5*=(6458RSF IPRO); *6*=(6160RSF IPRO); *7*=(DON MARIO 5.8i); *8*=(DON MARIO 5.9i); *9*=(CD 2611 IPRO); *10*=(CD 2585 RR), and *11*=(TMG 7161 RR) evaluated during the 2013/2014 agricultural year

The last ones present a long juvenile period and higher PH, which enables early sowings and provide escape of water stress periods that occur frequently in the southern region (EMBRAPA, 2008).The PH is dependent oninternode elongation andnumber of nodes per stem (Taiz and Zeiger, 2004). Guimarães *et al.* (2008) claimed that even though with genotypes insensitive to photoperiod and not modifying their flowering, these genotypes presented modifications for the PH trait. Regarding the NP1G and NP2G, 6160RSF IPRO genotype presented the larger magnitudes, which differed of CD 2611 IPRO genotype. For the trait NP3G, there was a greater magnitude for 6458RSF IPRO genotype, differing with NS 5445 IPRO, NS 6211 RR, Don Mario 5.8i, and CD 2585 RRgenotypes. Results of Navarro and Costa (2002) identified the contribution of the number of pods and grains per pod to the soybean grain yield in Eldorado do Sul - RS. According to Rambo *et al.* (2004), the three soybean canopy portions are modified depending on the plant arrangement modification and water demand, where the grain number per pod (one, two, and three grains) are the most influenced traits.Considerable influences to the grain number perpod are attributed to interspecific and intraspecific competition and water deficits, which change the balance between the production of flowers per plant and the proportion of those that develop and form pods (Navarro and Costa, 2002). In agreement with Mundstock and Thomas (2005), the grain number per podpresented low phenotypic variation, showing a uniformity of genetic breeding searching for plants with formation of two and three grains per pod. The most productive genotype in this study presented more pods with two grains, corroborating the results found by Pípolo *et al.* (2005).

The Pearson linear correlation presentsatrend among measured traits and the coefficient magnitudes vary from -1 to 1, with positive and negative coefficients. In this way, the closer to 1 or -1, stronger is the degree of linear association between the two variables and the closer to zero, the lower is the linear association (Cruz *et al.*, 2012). According to Carvalho *et al.* (2004), the coefficient interpretation is based on the following: r=0 indicates zero correlation; r=0 to 0.3 indicates weak or low correlation; r=0.3 to r=0.6 indicates moderate or intermediate correlation; r=0.6 to r=1.0 indicates a strong or high correlation. The same interpretations serve to negative associations. The Pearson linear correlation was carried out among 11 traits, with 55 associations and 32 significant pairs (Table 3). The GY presented high and positive linear correlation with GW10P (r=0.93), and moderate and positive correlation with NPS (r=0.44), NPB (r=0.39), NP1G (r=0.43), NP2G (r=0.40), and NP3G (r=0.47), indicating that the greater the magnitude of these traits, possibly greater increment of yield will be found. The same can be extended to the trait GW10P, which exhibited a moderate positive linear correlation with the PH (r=0.31), NPS (r=0.41), NPB (r=0.50), NB (r=0.35), NP1G (r=0.47), NP2G (r=0.50), and NP3G (r=0.53). The PH demonstrated strong positive correlation with FPIH traits (r=0.65) and NPS (r=0.65) and moderate and positive with the trait NP3G (r=0.34). This indicates that the greater the PH, possibly the FPIH will increase, as there will be greater NPS. Regarding the FPIH, there was moderate and positive correlation with the NPS trait (r=0.36). On the other hand, it presented moderate and negative correlation with the traits NPB (r=-0.36), NB (r=-0.40), and NP2G (r=-0.41). StudiesofMauad *et al.* (2010) indicated that soybean expresses ability to morphologically modify according to the croppingenvironment. This is a trait of great importance at harvest because plants with very near ground level pods have greater losses due to the combine header height does not allow the total harvest of the plant pods. According to Sediayama *et al.* (1999), the minimum FPIHto minimize losses should be of 10 to 12 cm on flat terrains and of 15 cm in soils with accentuated slope. The trait NPS presented moderate and positive correlation with NP1G (r=0.33), LDG (r = 0.30), weak and positive with LTG (r=0.29), which demonstrated that increasing the magnitude of this trait will possibly result in greater number of grains per plant. The NPBexhibited strong and positive correlation with NB (r=0.87), NP1G (r=0.60), NP2G (r=0.82), and NP3G (r=0.64). Meanwhile, the NB trait was positive strongly correlated with NP2G(r=0.64)and positive moderately correlated with NP1G(r=.38) and NP3G (r=0.49). This indicates that the increased NB possibly will result in greater number of pods per plant. Several studies demonstrated that the number ofpods is characterized as one of the most dynamic components, which can be the differential to increased yield especially in situations with changes in plant density and reduced spacing between rows (Peixoto *et al.* 2000). Thus, this trait along with the length of branches has relation with yield potential since they represent greater photosynthetic area with more flowers and pods. On the other hand, thelength of branchescan deviate assimilates and represent an additional demand for reproductive structures fixation in plants (Navarro and Costa, 2002).The trait NP1G was positive and very strongly correlated with NP2G (r=0.64) and the trait NP2G presented positive and moderate correlation with NP3G (r=0.33). Clustering genotypes based on agronomically important traits can be performed using the analysis of canonical variables (Cruz *et al*., 2012). The analysis of canonical variables was performed for the traits TGW, GY, GW10P, PH, NP1G, NP2G, and NP3Gassessed in 11 soybean genotypes grown during the 2013/2014 agricultural year. The variation of genotypes was expressed through the first two canonical variables, which CV1 was responsible for 68.70% and CV2 for 16.31% of the total variation. Graphically expressed scores through the canonical variables CV1 and CV2 are exhibited in Figure 1, with the formation of four groups. Thus, the first group was composed by the genotypes 1 (NS 5445 IPRO) and 2 (NS 6211 RR); the second group was composed by the genotype 9 (CD 2611 IPRO), which presents early maturity cycle, indeterminate growth habit and belongs to the maturity group 6.1; the third group was composed by the genotype 10 (CD 2585 RR), which presentssuper-early cycle, indeterminate growth habit, maturity group 5.8, and it is indicated for high and cold regions;andthe fourth group was composed by the genotypes 3 (TEC 6029 IPRO), 4 (TEC S 13/03 RR), 5 (6458RSF IPRO), 6 (6160RSF IPRO), 7 (DON MARIO 5.8i), 8 (DON MARIO 5.9i), and 11 (TMG 7161 RR).

The obtained canonical variables explain 85.01% of the variation involved in the study. Hence, the reliable interpretation in this multivariate analysis must be based on minimum estimates of 80% through the traits set (Cruz *et al*., 2006). Therefore, the combined use of univariate and multivariate analyzes becomes feasible to identify which genotypes were superior in a competition trial. This results in adequate responses regarding which genotypes are superior and genetically closest to each other and supports the determination of the interest traits for grain yield. This genetic variability obtained among genotypes is essential for plant breeders because it enables effectively select the genotypes that are more suitable for certain crops (Bernardo, 2002).

Conclusion

Genotypes 6160RSF IPRO, NS 5445 IPRO, and 6458RSF IPRO presented the greatest grain yield values, demonstrating potential use for cultivation in lowlands in Rio Grande do Sul. The traits grain weightof ten plants, number of pods in the main stem, number of pods in the branches, number of pods with one, two, and three grains have positive linear correlations with grain yield. The genotypes were clustered according to their genetic basis and maturation cycle, canonical variables explained 85.05% of existent genetic variation, and four genotype groups were formed.

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