Superiority index based on target traits reveals the evolution of Brazilian soybean cultivars over last half-century[1]

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ABSTRACT

The objective of this work was to assess the breeding influences in different agronomic and physiological traits in Brazilian soybean cultivars, released between 1965 and 2011, to identify traits associated with modern cultivars. A total of 29 cultivars were evaluated in two locations in the 2016/17 crop season. Genotype selection based on agronomic and physiological traits was determined using GYT (Grain Yield*Trait) methodology, which uses the Superiority Index to rank genotypes by mean of all traits. Grain Yield is combined with other target traits and shows the strengths and weaknesses of each genotype. Soybean breeding improved desirable traits during the 46 years of evaluation. Superiority index can be a powerful tool for breeders to obtain high genetic gains in the future. The cultivars DMario 58i, TMG 7161RR and TMG 7262 RR stand out as the best cultivars but present different sets of desirable traits. The traits grain yield, harvest index, number of pods per plant, reproductive-vegetative ratio, photosynthetic rate and transpiration rate are core traits which can be evaluated in soybean breeding programs.

Keywords: genotype selection; grain yield*trait biplot; multi-traits.

INTRODUCTION

Simultaneous selection for multi-traits is one of the key points for continuous genetic gain in soybean [*Glycine max* (L.) Merrill] breeding (Yan & Frégeau-Reid, 2008). The simultaneous improvement of agronomic and physiological traits and the selection by performance indexes can be a useful strategy to identify genotypes closer to ideotype (Cruz *et al*., 2012). In this way, predict genetic gains to each trait have a great importance to indicate to breeder choices, and focus on the main desirable traits (Paula *et al*., 2002).

A selection index is a method of artificial plant selection to many traits simultaneously. It's based on the linear combination between traits, allowing adjustment of multiple traits in a single variable. This index is composed by a weight for each trait, and a truncation point for each trait must be established a priori by the breeder (Yan & Frégeau-Reid, 2008).

For most crops with agronomic importance, the main target trait is grain yield (GY). However, a good performance in other traits in soybean crop is essential for release a new cultivar. Among these traits can be cited the life cycle, plant height, disease resistance and lodging resistance (Yan & Frégeau-Reid, 2008). Nevertheless, these traits are important only when associated with GY (Zhang *et al.*, 2015; Sharifi & Ebadi, 2018).

Genotype by grain yield*trait (GYT) methodology, proposed by Yan & Frégeau-Reid (2008), provide a Superiority Index (SI) which allows to evaluate genotypes in relation to multi-trait. Initially, each trait positively or negatively associated with the GY (main trait for soybean) is evaluated by the breeder for the correct decision to select the best genotype. The breeder has the responsibility for identifying if a trait is positively or negatively associated with GY, i.e., identify if GY should be multiplied or be divided by a specific trait. From this,

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indices are generated by multiplying the GY by the magnitudes of traits in question (positive selection) or by dividing the magnitude of traits by the GY (negative selection). This methodology uses GGE biplot analysis to verify the genotypes performance and to identify strengths and weaknesses of each genotype. The Superiority Index (SI) ranks genotypes by the mean of all traits.

Soybean genetic progress has been reported by innumerous studies. Therefore, the most of them highlighted the grain yield gains, and someone showed the agronomic and physiologic trait evolution, regardless to individual trait (Rogers et al., 2014; Zhang et al., 2015; Todeschini et al., 2019). Use the multi-traits indexes to quantify genetic gains could improve the acknowledgment about the relationship between traits and the main trait – grain yield – over the years. Thus, the objectives of this work were to assess the influence of soybean breeding in different agronomic and physiological traits of genotypes released between 1965 and 2011, and to identify traits associated to grain yield in the modern soybean genotypes.

MATERIAL AND METHODS

Conduction of experiments

The experiments were conducted in two locations in Brazil: Pato Branco-PR (26°13‘ S, 52°40‘W, 765 m a.s.l.) and Realeza-PR (25°46‘S, 53°32‘W, 520 m a.s.l.), in the 2016/17 crop season. The soil of both locations is classified as a Hapludox (Santos et al. 2013), and the climate, according to the Koppen classification, is a Cfb type, humid subtropical with temperate summer (Alvares *et al*., 2013).

Twenty-nine soybean genotypes, available for cultivation in Brazil between 1965 and 2011 (Table 1), were evaluated. Experiments were conducted in a randomized complete block design, with three replications. The sowing density was 35 plants m^{-2}. The experimental units consisted of four 5m rows, spaced 0.5 m between rows. The two central rows of each plot, totaling 5 m^2, were considered as useful area. Cultural practices were carried out according to the technical recommendations for soybean crop (Oliveira & Rosa, 2014).

Agronomic traits

Grain yield (GY) was obtained from harvest of two central rows of each plot, totalizing 5 m². The grain moisture was corrected to 130g kg^{-1}, and after that the GY was converted to kg ha^{-1}. In full maturity (R8) Fehr & Caviness (1977), 15 plants per plot were randomly collected and the following traits were evaluated: plant height (PH), measured in cm, from the soil to last pod of plant; first pod height (FPH), measured in cm, from the soil to first pod of plant; number of nodes per plant (NNP), obtained from counting of number of reproductive nodes of collected plants, and calculated average value; number of pods per plant (NPP), obtained from counting the number of pods per sampled plants, and calculating the average value; number of grain per pod (NGP), obtained from division between the number of grain and the number of pods of sampled plants. Biological yield (BY) was obtained by weighing the shoot of 15 sampled plants at random in plot. Straw yield (SY) was determined from the difference between BY and GY. Harvest index (HI) was calculated as HI = GY/BY.

During the crop development, phenological traits of data of emergence (VE), beginning flowering (R1), and complete maturation (R8) were evaluated in both locations as described by (Fehr & Caviness, 1977). Days to flowering (DTF) and days to maturity (DTM) were calculated by the number of days between VE and R1 stages, and between VE and R8 stages, respectively. The reproductive period, days flowering-maturation (DFM), was calculated as DFM = DTM – DTF. The ratio between reproductive (R) and vegetative (V) period (R/V) was calculated as R/V = DFM/DTF. Lodging was measured by visual evaluation, assigning a score from 1 to 9. In this scale, the grade 1 was attributed to the fully erect genotype and 9 to the fully lodging.

Physiological traits

Photosynthetic traits were evaluated between 9:00 to 11:00 h in sunny days, at beginning of grain filling stage (R5) Fehr & Caviness (1977), where the highest production of photoassimilates is required by plant. It was used a portable open system equipped with an infrared gas analyzer model LI-6400XT (LI-COR, Lincoln, Nebraska, USA), with automatic CO_2 injector, and artificial red and blue light sources. The evaluated traits were: photosynthetic rate (P_N, µmol CO_2 m^{-2}s^{-1}), stomatal conductance (G_S, mol H_2O m^{-2}s^{-2}), substomatal CO_2 concentration (C_I, mol H_2O m^{-2}s^{-2}), transpiration rate (E, mmol m^{-2}s^{-1}), and water use efficiency (WUE, %), obtained by the ratio P_N and E. The microclimatic conditions in the sample measurement chamber were adjusted at a constant rate with 200 µmol m^{-2}s^{-1} of PAR (Photosynthetic Active Radiation), and 400 ppm of CO_2, with a relative humidity between 50 e 80%.

The individual indices of chlorophyll A (Chl.A) and B (Chl.B), and total chlorophyll (Chl.A + B) were measured at the R1 stage. The readings were performed on fully expanded leaves, in the upper third of plants, in 15 plants per experimental unit. The readings were performed with an electronic chlorophyll apparatus, model ClorofiLOG CFL 1030 (Falker, Porto Alegre, Brazil).

Statistical analysis

The GYT was generated by the combination of each trait and GY, overall mean for each trait. The methodology developed by Yan & Frégeau-Reid (2008) indicates that each trait should be multiplied or divided by GY according the objectives of the breeder. FPH and PH are two traits where an intermediate ideal value is required, where very high or very low values are not desirable. FPH should be sufficiently high to allow mechanic harvest and sufficiently low to express ideal NNP. PH should be sufficiently high to plant have the maximum NNP, but sufficiently short to avoid lodging. Thus, the values of 0.125 m and 1.00 m were attribute for FPH and PH, respectively. In this way, the closer to this value the more desirable it is. The GYT biplot permits the selection for all traits combined in a different way with GY. GY values was multiplied by BY, NNP, HI, DFM, R/V, TGW, NGP, WUE, P_N, G_S, C_I, E, Chl.A, Chl.B and Chl.A+B, where increase these traits together to GY is expected. In the other hand, GY was divided by SY, Lod, DTF and DTM. For FPH and PH, GYT values were calculated by the follow equation: $GYT = \frac{GY}{(Ov - Iv) + 1}$, where GYT is the index response for a specific trait; GY is the data for genotype i, across environments and replicates; Ov is the observed value for a specific trait; Iv is the ideal value for a specific trait; and 1 is a correction factor to standard GYT when $Ov = Iv$.

The mean and stability biplot had SVP = 1 and is genotype-focused. The line with a single arrow (ATA) pass by biplot origin and point to high values of traits. The small circle indicates the “average yield-trait combination”. Genotype projection vectors in relation to ATC (double-arrow line) indicates if a genotype had an all-rounded or balanced trait profile. Genotypes closer to ATA (without projections in the direction of ATC) are more desirable because have balanced trait profiles (Yan & Frégeau-Reid, 2008). Analyses were performed using GGEbiplot software (Yan, 2001).

Table 1: Brazilian soybean cultivars evaluated for grain yield, agronomic and physiological traits, in two locations in the 2016/17 crop season

Code	Genotype	Breeding Company	Year of Release	Modern (M) or Old (O)	Conventional (CV) or RR⁽¹⁾
M1	DMario 58i	GDM Seeds	2007	M	RR
M2	Dmario 70i	GDM Seeds	2007	M	RR
M3	BMX Potência RR	GDM Seeds	2007	M	RR
M4	BMX Titan RR	GDM Seeds	2007	M	RR
O5	BR 16	Embrapa	1987	O	CV
O6	BR 4	Embrapa	1979	O	CV
O7	Bragg	Embrapa (PI)⁽²⁾	1966	O	CV
O8	BRS 133	Embrapa	1997	O	CV
O9	BRS 184	Embrapa	2001	O	CV
M10	BRS 232	Embrapa	2003	M	CV
M11	BRS 284	Embrapa	2009	M	CV
O12	CD 202	Coodetec	1998	O	CV
O13	CD 206	Coodetec	1999	O	CV
O14	CD 208	Coodetec	1999	O	CV
M15	CD 214RR	Coodetec	2003	M	RR
O16	CD 215	Coodetec	2002	O	CV
O17	Davis	Embrapa (PI)	1965	O	CV
O18	Embrapa 48	Embrapa	1995	O	CV
O19	FT Abyara	FT Sementes	1988	O	CV
O20	IAS 5	Embrapa	1973	O	CV
O21	OCEPAR 4	Ocepar	1987	O	CV
O22	Paraná	Embrapa	1974	O	CV
M23	TMG 7161RR	TMG⁽³⁾	2010	M	RR
M24	TMG 7262 RR	TMG	2011	M	RR
M25	NK 7059 RR	Syngenta	2007	M	RR
M26	SYN1059 RR	Syngenta	2010	M	RR
M27	NA 5909 RG	Syngenta	2008	M	RR
O28	Nova Bragg (BR 6)	Embrapa	1981	O	CV
M29	NS 4823	Syngenta	2008	M	RR

⁽¹⁾RR: RoundUp Ready® technology; ⁽²⁾PI: Plant Introduction. ⁽³⁾TMG: TMG Tropical Melhoramento e Genética S.A.

The Pearson's correlation analysis was performed for the original data of all evaluated traits using function *correlation ()* in agricolae package (Mendiburu, 2017); and plotted using corrplot package, function *corrplot ()*, in R software (http://www.R-project.org).

RESULTS

The which-won-where biplot (Figure 1) allows to identify genotypes with higher values for each combination (GY*Trait) in the respective sector. Genotype M1 present high values for SY, Lod, HI and DTF. M23 had high values for PH, FPH, NNP, BY and NPP. M24 had high values for R/V, DTM, TGW, NGP, WUE, P_N, G_S, C_I, E, Chl.A, Chl.B and Chl.A+B. In this way, genotypes M24, M23, and M1 presented superior performance for different sets of traits. On the other hand, O17 and O6 do not have association with any GY*Trait, indicating that they are not desirable.

The genotypes M24, M23 and M1 presented the highest mean values for SI (Table 2). Among these genotypes, of these, M1 had negative values for FPH and for PH, indicating that this genotype had the best indexes; M23 had negative values for SY, indicating that this genotype produces a high amount of straw. M24 had negative values for FPH, and reveled low indexes. The modern genotypes M24 (2011), M23 (2010) and M1 (2007) may be considered the best genotypes, each with specific positive GY*traits associations. In the other hand, old genotypes, i.e., O17 (1965) and O6 (1979), were the worst genotypes in GYT biplot (Figure 1). In addition, M15 (2003) is exactly the "average genotype" between old and modern genotypes, with a SI = 0.00.

Agreeing with (Figure 2), the best grain yield was verified to genotypes M24, M23 and M1 and the worst genotypes were O17 and O6. Genotype M15 (1st genotype classified as a modern genotype) was the first genotype with RoundUp Ready® technology in the dataset. This genotype had a SI of 0.00, indicating that M15 had intermediate values. Some old genotypes had positive SI, e.g., O16 and O9, and a modern genotype presented negative values for SI, e.g., M4. Nevertheless, the biggest part of modern genotypes had positive values for SI and old genotypes had negative values for SI.

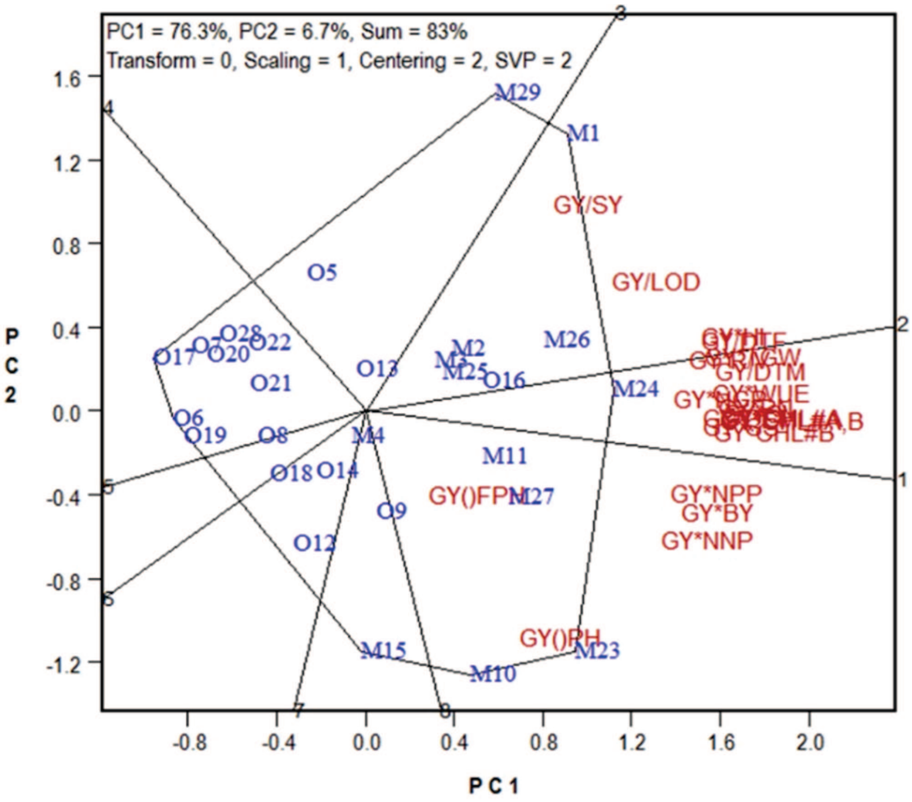

Figure 1: Which-Won-Where view of the genotype by grain yield*trait (GYT) biplot to highlight genotypes with outstanding profiles. The biplot was based on singular value decomposition of the standardized GYT table (Table 2) ("Scaling = 1, Centering = 2"). The trait-focused singular value partition ("SVP = 2") was used. Trait codes: GY: grain yield; BY: biological yield; SY: straw yield; FPH: first pod height; NNP: number nodes per plant; NPP: number of pods per plant; HI: harvest index; PH: plant height; LOD: lodging; DTF: days to flowering; DFM: days flowering-maturation; DTM: days to maturity; R/V: reproductive - vegetative ratio; TGW: thousand grain weight; NGP: number of grain per pod; WUE: water use efficiency; PN: photosynthetic rate; GS: stomatal conductance; CI: substomatal CO2 concentration; E: transpiration rate; Chl. A: chlorophyll A content; Chl. B: chlorophyll B content; Chl. A+B: chlorophyll A+B content. See Table 1 for a full description of genotypes.

Table 2: Superiority index using Genotype by grain yield*trait (GYT) methodology for 29 Brazilian soybean cultivars released between 1965 and 2011, evaluated for grain yield, agronomic and physiological traits in two locations in the 2016/17 crop season

Genotype	GY*[1] BY	GY()[2] FPH	GY/[3] SY	GY* NNP	GY* NPP	GY* HI	GY() PH	GY/ LOD	GY/ DTF	GY* DFM	GY* R/V	GY/ DTM
M1	0.61	-0.17	2.11	0.40	0.70	1.83	-0.79	1.80	1.80	1.31	1.62	1.68
M2	0.42	0.00	0.61	0.35	0.43	0.70	-0.03	0.61	0.69	0.59	0.64	0.67
M3	0.50	-0.53	0.22	0.27	0.42	0.57	-0.11	0.52	0.56	0.54	0.57	0.51
M4	0.34	-1.18	-0.79	-0.04	0.16	-0.11	-0.10	-0.08	-0.12	0.08	0.01	-0.18
O5	-0.80	0.01	0.58	-0.75	-0.68	-0.19	-0.83	0.08	-0.20	-0.48	-0.27	-0.29
O6	-0.96	-1.05	-1.20	-1.15	-1.04	-1.32	-0.68	-0.95	-1.32	-1.20	-1.19	-1.42
O7	-1.07	-1.04	-0.72	-1.26	-1.10	-1.08	-0.99	-0.65	-1.09	-1.12	-1.00	-1.22
O8	-0.61	-0.14	-0.57	-0.57	-0.61	-0.78	-0.21	-0.62	-0.78	-0.73	-0.73	-0.79
O9	-0.26	2.21	0.56	0.45	-0.02	-0.13	0.92	-0.36	-0.11	-0.16	-0.25	0.10
M10	1.07	1.49	-0.42	1.47	1.06	0.27	1.87	-0.29	0.31	0.67	0.31	0.57
M11	0.85	0.32	0.26	0.85	0.81	0.72	0.63	0.45	0.73	0.81	0.71	0.80
O12	-0.29	0.66	-0.66	-0.01	-0.26	-0.72	0.56	-0.78	-0.71	-0.53	-0.68	-0.60
O13	-0.06	-0.40	-0.01	-0.18	-0.08	0.01	-0.28	0.09	0.01	-0.03	0.02	-0.04
O14	-0.80	2.23	0.61	-0.03	-0.51	-0.48	0.54	-0.55	-0.46	-0.61	-0.62	-0.29
M15	0.57	0.43	-1.16	0.70	0.46	-0.42	1.25	-0.72	-0.39	0.03	-0.29	-0.23
O16	0.42	1.02	1.04	0.66	0.54	0.83	0.38	0.62	0.83	0.68	0.71	0.90
O17	-1.44	-0.51	-0.64	-1.43	-1.39	-1.36	-0.96	-0.91	-1.37	-1.45	-1.32	-1.47
O18	-0.30	-0.50	-0.93	-0.39	-0.38	-0.75	-0.04	-0.64	-0.74	-0.57	-0.65	-0.76
O19	-0.92	-0.74	-1.11	-1.02	-0.98	-1.27	-0.51	-0.96	-1.27	-1.16	-1.16	-1.34
O20	-1.28	0.14	-0.13	-1.10	-1.16	-1.01	-0.71	-0.67	-1.01	-1.16	-1.03	-1.06
O21	-0.62	-0.80	-0.63	-0.79	-0.67	-0.74	-0.59	-0.48	-0.75	-0.72	-0.67	-0.83
O22	-1.00	0.04	0.02	-0.89	-0.90	-0.70	-0.66	-0.41	-0.70	-0.86	-0.73	-0.76
M23	2.15	0.00	-0.70	1.97	1.89	1.05	1.81	0.39	1.07	1.59	1.19	1.25
M24	1.98	-1.15	0.33	1.40	1.73	1.77	0.44	1.39	1.75	1.90	1.81	1.72
M25	0.79	-1.26	-0.17	0.31	0.60	0.62	-0.16	0.57	0.61	0.70	0.69	0.52
M26	1.18	-0.56	0.67	0.86	1.08	1.35	0.11	1.13	1.34	1.30	1.32	1.30
M27	1.03	0.74	0.33	1.15	1.01	0.84	0.98	0.45	0.85	0.96	0.81	0.97
O28	-1.14	-0.26	-0.18	-1.10	-1.07	-0.88	-0.84	-0.52	-0.89	-1.03	-0.89	-0.98
M29	-0.33	0.97	2.67	-0.11	-0.02	1.38	-1.00	1.48	1.35	0.64	1.06	1.26
Mean	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Continue…

Continuação Tabela 2

Genotype	**GY* TGW**	**GY* NGP**	**GY* WUE**	**GY*** $\mathbf{P_N}$	**GY*** $\mathbf{G_S}$	**GY*** $\mathbf{C_I}$	**GY*** ***E***	**GY* Chl.A**	**GY* Chl.B**	**GY* Chl.A+B**	**SI (Mean)**
M1	1.70	1.33	1.53	1.46	1.26	1.43	1.39	1.40	1.30	1.38	1.23
M2	0.67	0.56	0.64	0.63	0.58	0.63	0.62	0.62	0.59	0.61	0.54
M3	0.61	0.40	0.45	0.49	0.50	0.51	0.50	0.50	0.42	0.48	0.40
M4	0.04	-0.20	-0.23	-0.12	0.02	-0.07	-0.08	-0.08	-0.21	-0.11	-0.14
O5	-0.29	-0.30	-0.33	-0.41	-0.49	-0.45	-0.46	-0.45	-0.45	-0.45	-0.36
O6	-1.22	-1.28	-1.44	-1.40	-1.25	-1.37	-1.37	-1.38	-1.44	-1.40	-1.23
O7	-1.03	-1.14	-1.28	-1.27	-1.17	-1.26	-1.27	-1.27	-1.34	-1.29	-1.12
O8	-0.77	-0.69	-0.77	-0.78	-0.73	-0.78	-0.77	-0.77	-0.75	-0.77	-0.67
O9	-0.31	0.24	0.26	0.13	-0.03	0.06	0.10	0.09	0.35	0.16	0.18
M10	0.30	0.68	0.74	0.77	0.78	0.79	0.82	0.82	0.98	0.86	0.72
M11	0.74	0.73	0.82	0.84	0.82	0.86	0.86	0.86	0.86	0.86	0.73
O12	-0.72	-0.44	-0.50	-0.51	-0.48	-0.52	-0.49	-0.50	-0.39	-0.47	-0.41
O13	0.03	-0.07	-0.08	-0.07	-0.05	-0.06	-0.07	-0.07	-0.12	-0.08	-0.07
O14	-0.70	-0.12	-0.13	-0.30	-0.48	-0.39	-0.35	-0.35	-0.08	-0.28	-0.19
M15	-0.31	-0.08	-0.11	-0.03	0.08	0.00	0.03	0.02	0.10	0.05	0.00
O16	0.72	0.83	0.93	0.87	0.72	0.83	0.83	0.84	0.91	0.86	0.77
O17	-1.38	-1.33	-1.49	-1.52	-1.47	-1.54	-1.54	-1.54	-1.54	-1.54	-1.32
O18	-0.66	-0.66	-0.75	-0.70	-0.58	-0.67	-0.66	-0.67	-0.69	-0.68	-0.61
O19	-1.20	-1.19	-1.34	-1.31	-1.18	-1.30	-1.29	-1.29	-1.32	-1.31	-1.14
O20	-1.09	-0.94	-1.05	-1.13	-1.15	-1.17	-1.16	-1.16	-1.11	-1.15	-0.97
O21	-0.69	-0.77	-0.87	-0.84	-0.76	-0.83	-0.83	-0.84	-0.90	-0.85	-0.75
O22	-0.77	-0.69	-0.76	-0.83	-0.86	-0.86	-0.86	-0.86	-0.83	-0.85	-0.71
M23	1.26	1.19	1.31	1.48	1.61	1.57	1.58	1.57	1.54	1.57	1.29
M24	1.93	1.43	1.61	1.76	1.82	1.84	1.81	1.81	1.61	1.76	1.47
M25	0.75	0.37	0.42	0.53	0.62	0.58	0.56	0.56	0.39	0.52	0.41
M26	1.40	1.07	1.21	1.27	1.25	1.31	1.28	1.28	1.16	1.26	1.07
M27	0.84	0.92	1.03	1.04	1.00	1.05	1.06	1.06	1.11	1.08	0.92
O28	-0.93	-0.89	-1.00	-1.05	-1.05	-1.07	-1.07	-1.07	-1.07	-1.08	-0.91
M29	1.07	1.02	1.18	0.98	0.65	0.88	0.85	0.87	0.91	0.88	0.85
Mean	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-

[1] GY combined with the other traits in different ways, according to the ideal combination of traits, for example: GY*BY, where GY values were multiplied by BY; [2] GY()FPH, where a central value is considered as optimal; [3] GY/SY, where GY was divided by SY. Trait codes: GY: grain yield; BY: biological yield; SY: straw yield; FPH: first pod height; NNP: number nodes per plant; NPP: number of pods per plant; HI: harvest index; PH: plant height; LOD: lodging; DTF: days to flowering; DFM: days flowering-Maturation; DTM: days to maturity; R/V: reproductive - vegetative ratio; TGW: thousand grain weight; NGP: number of grain per pod; WUE: water use efficiency; PN: photosynthetic rate; GS: stomatal conductance; CI: substomatal CO_2 concentration; E: transpiration rate; Chl. A: chlorophyll content; Chl. B: chlorophyll content; Chl. A+B: chlorophyll contente; SI: Superiority index. See Table 1 for a full description of genotypes.

GY was positively correlated with BY, FPH, NPP, HI, R/V, NGP, P_N, *E*, and Chl.A, Chl.B and Chl.A+B (Figure 3). This indicates that higher values for these traits help to improve GY. Otherwise, traits PH, Lod, DTF and DTM are negative related with GY, where lower values are desirable to improve GY.

A minimum number of traits may be evaluated by soybean breeding programs. Among these traits are: GY, HI, NPP, R/V, P_N and *E*. HI is related to grain yield and biomass production, through the traits GY, BY and SY (Figure 3). HI shows similar correlations to those obtained by GY for the remaining traits and has even more negative correlation with DTM than GY/DTM. In addition, it has a higher correlation with NGP than GY*NGP and is the only trait showed a positive correlation with the yield component TGW. NPP consists of one of the major yield components and is correlated to NNP. Already, R/V is a trait which encompasses in all crop cycle traits, i.e., DTF, DFM and DTM. Physiological traits P_N and *E* indicate the capacity of photoassimilates production, maintenance of the metabolic processes and are determinant traits in water use by plants, through WUE trait. In addition, these traits show a high correlation with all chlorophyll indexes (Chl. A, Chl. B and Chl. A + B).

DISCUSSION

The main trait improved by soybean breeding companies is GY. In Brazil, the annual genetic gain was in order of 39 kg ha^{-1} yr^{-1} (Todeschini *et al*., 2019). The GY is selected *per se* many times. However, an indirect selection is realized for many traits along the breeding process. Many traits need to be increased such as TGW, and others need to be reduced, e.g., lodging. A third group of traits need be in an ideal value, not very high nor very low, e.g., FPH and PH.

The modern genotypes M24 (2011), M23 (2010) and M1 (2007) may be considered the best genotypes, each with specific positive GY*traits associations. In the other hand, old genotypes, i.e., O17 (1965) and O6 (1979), were the worst genotypes in GYT biplot. In addition, M15 (2003) is exactly the "average genotype" between old and modern genotypes, with a SI = 0.00. These results corroborate to Todeschini et al. (2019), that evaluated the same set of soybean genotype performance, and a revealed positive genetic progress of 2.4% $year^{-1}$.

The M24 had high values for many traits, especially for physiological traits. The increment of P_N consist in the increase of assimilation rate of CO_2, which increases the amount of photoassimilates and, consequently, growth

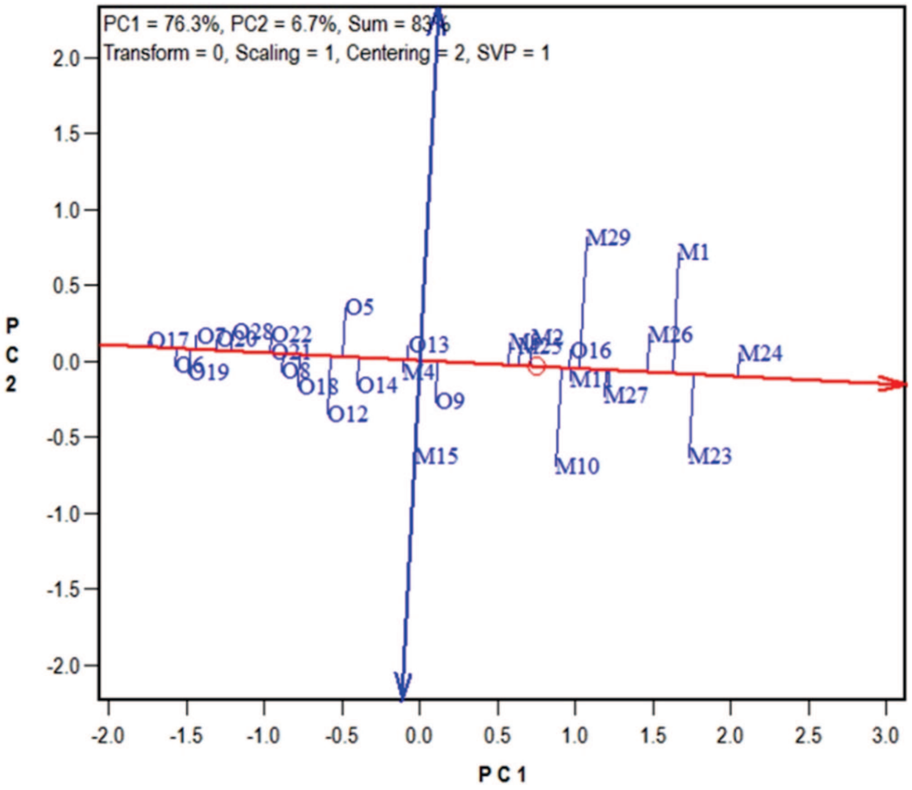

Figure 2: Average tester coordination for 29 Brazilian soybean cultivars released between 1965 and 2011, evaluated for grain yield, agronomic and physiological traits, in two locations in the 2016/17 crop season. Average of the genotype by grain yield*trait (GYT) biplot to rank the genotypes based on their overall superiority and stability of genotypes. The biplot was based on singular value decomposition of the standardized GYT table ("Scaling = 1, Centering = 2"). The genotype focused singular value partition ("SVP = 1") was used. See Table 1 for a full description of genotypes.

and GY (Rao & Chaitanya, 2016; Müller *et al*., 2017). According to Morrison *et al*. (1999), the increase of P_N in the modern genotypes occurs due to reduction in leaf area and the increase in photoassimilates demand. Leaf area reduction together with architecture modification provides greater interception of the photosynthetically active radiation (PAR) on vegetative canopy. Thus, more efficient photosynthetic soybean genotypes present a higher number of fertile nodes in the lower third of plant, resulting GY increase (Müller *et al*., 2017).

Transpiration rate (E) is positively associated with GY, and most productive genotypes present the higher transpiration rates (Figure 1, Figure 3). G_S consists of the rate of passage of CO_2 entering the leaf stomata. A large G_S can correlate with improved crop yield (Prashar *et al*., 2013). Liu *et al*. (2012) observed a significant increase in G_S over the years. According to these authors, genotypes increased P_N, G_S and *E* through the release year, and the selection for high-yielding genotypes led to higher photosynthetic ability. In relation to WUE, M24, M23 and M1 presented positive values for this trait.

Increased WUE can improve productivity and reduce water stress under drier environmental conditions (Han *et al*., 2013; Franks *et al*., 2015). In thermal and/or drought stress conditions, response mechanism is started involving stomata regulation. In this process, stomata are fast closed in stresses conditions, to reduce water losses by plant (Reynolds-Henne *et al*., 2010). Battisti *et al*. (2017) evaluating soybean yield under climate changes in Southern Brazil, observed that reduction of transpiration

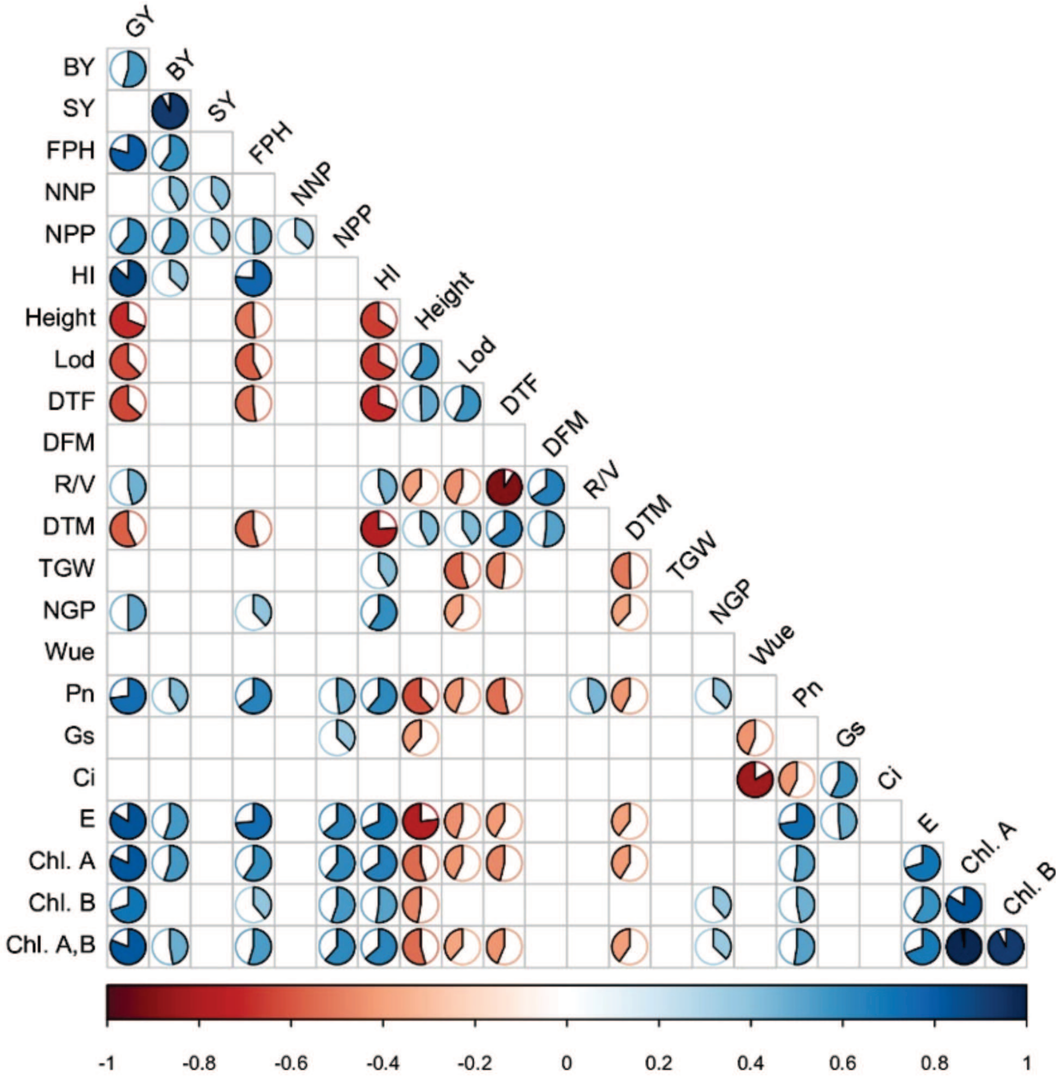

Figure 3: Pearson correlations between 29 Brazilian soybean cultivars released between 1965 and 2011, evaluated for grain yield, agronomic and physiological traits, in two locations in the 2016/17 crop season. Correlations shown are significant ($P<0.05$) according to the t-test. Trait codes: GY: grain yield; BY: biological yield; SY: straw yield; FPH: first pod height; NNP: number nodes per plant; NPP: number of pods per plant; HI: harvest index; PH: plant height; LOD: lodging; DTF: days to flowering; DFM: days flowering-Maturation; DTM: days to maturity; R/V: reproductive - vegetative ratio; TGW: thousand grain weight; NGP: number of grain per pod; WUE: water use efficiency; P_N: photosynthetic rate; G_S: stomatal conductance; C_I: substomatal CO_2 concentration; *E*: transpiration rate; Chl. A: chlorophyll A content; Chl. B: chlorophyll B content; Chl. A+B: chlorophyll A+B content.

index collaborates with tolerance induction to drought stress and reduces cultivar sensibility. Thus, WUE increase may be related to how modern genotypes keep metabolism in stress conditions (Blum, 2009).

M24 genotype had high values for R/V ratio and GY/DTM, two important traits in soybean breeding. A large R/V ratio is desirable, since genotypes with a longer reproductive stage have more time for grain filling grains and pod development. Although, a low DTM is desirable because genotypes with a shorter life cycle reduces the incidence of pest attacks and allows, in Brazil and tropical regions, the cultivation of a second crop in the same crop season. Bodner *et al.* (2018) highlighted the best yielding genotypes to faba bean, belong to the same family of soybean, include phenological pattern combining earliness with prolonged duration of reproductive period. Xavier *et al*. (2017) conclude that optimal soybean grain yield occurs when growing environment favors faster canopy closure and extend reproductive length.

GY is arguably the most important trait in soybean crop. Except for soybean for specific purposes (like as human food), selection methods and indices are valid only if they give GY its proper importance. The standardized multiple selection index (SMSI), proposed by Gesteira *et al*. (2018), considers each trait individually, i.e., do not contrast each evaluated trait with GY. These authors evaluated 39 soybean inbred lines and four traits (grain yield, absolute maturity, protein and oil contents). This index indicated a line as the most prominent by SMSI, i.e., associated with early cycle, good yield and grain quality (high oil and protein contents). However, when evaluated at ten locations for two years, this inbred line presented a GY near 3,500 kg ha^{-1}. This line was preferred over another inbred line with produced near 4,500 kg ha^{-1}. These results can be misleading in plant breeding since GY is the most important trait. Otherwise, the Superiority Index avoid this mistake, once “genotypes are evaluated by their levels in combining yield with other traits as opposed to by their levels in individual traits” (Yan & Frégeau-Reid, 2008).

M24, M1 and M23 genotypes highlighted to specific group of traits. In this way, the next step in soybean breeding is to seek the union of all the favorable traits into a single genotype. Among the main practical information presented in this article, it is that soybean breeding companies may evaluate set of core traits (GY, HI, NPP, R/V, P_N and E) in their germplasm bank and identify strengths and weaknesses of each genotype. Subsequently, crosses for new lineages development may be schematized to join the strengths of each parent in a single genotype.

Positive correlation between chlorophyll content and grain yield is showed in cultivated plants as soybean (Ergo *et al*., 2018, Sakowska *et al*., 2018), wheat, barley, and oat (Sid’Ko *et al*., 2017). Ergo *et al.* (2018) studying heat and drought stressed field-grown soybean, reveled thought principal component analysis complemented with multiple regression models that physiological and biochemical traits may be include as powerful explanatory variables of yield.

Over the years, soybean breeding aimed to get an optimal combination of morphological and physiological traits that results in an efficient plant material, known as the ideotype by (Martre *et al*., 2015). Researches about traits association certainly helped to obtain the ideotype and genetic progress. Cui *et al*. (2015) reported increase in GY by increase in number of grains per pod. Regarding to physiological traits, over more than 80 years of breeding, Koester *et al*. (2014); Koester *et al*. (2016) showed positive linear association of light interception, energy conversion with increase in grain yield gains. Also, the modern lines presented lodging resistance that is related to radiation use efficiency and yield potential (Koester *et al*., 2014; Rogers *et al*., 2014), that corroborate to results of this study and show the traits association importance to soybean breeding.

CONCLUSIONS

1. Soybean breeding improved desirable traits in brazilian cultivars.

2. Some cultivars present interesting sets of favorable traits: DMario 58i,TMG 7161RR TMG 7262.

3. Grain yield, Harvest index, number of pods per plant, the ratio between reproductive and vegetative period, photosynthetic rate and transpiration rate are core traits which can be evaluated in soybean breeding to obtain future gains.

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CONFLICT OF INTEREST

The authors declare no conflict of interest.

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