

Soybean canonical nutraceutical interrelations and their reflections on breeding

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Abstract – In recent years, questionings on the behavior of genotypes in different environments are frequent, especially those seeking to disclose the commercial and nutritional value of soybean genotypes. Consequently, this study – which is linked to the IRC Soybean Breeding Program located in Campos Borges, Rio Grande do Sul, Brazil – sought to analyze the physiological and nutritional aspects of S5 Soybean Segregating Families. Research design consisted of complete randomized blocks containing 40 soybean genotypes arranged in four repetitions, corresponding to F5 generation genotypes tested in 2018/2019. This generation was obtained via artificial hybridizations of F1s plants carried out in 2014/2015, F2s in 2015/2016, F3 segregating families in 2016/2017 and F4 in 2017/2018. Traits were evaluated by a statistical model, verifying normality and homogeneity of variances. Behavioral explanation of the F5 Soybean Segregating Families was calculated using analysis of variance, grouping of means, and linear and canonical correlation. Analysis of variance showed a significant difference ($p < 0.01$) for all variables, indicating the existence of genetic variability. F5 Segregating Families IRC8_130 and IRC31_102 show promising results in breeding programs involving physiological and nutritional aspects. Crude protein, crude fiber, first pod insertion height, plant height and number of pods with 4 grains, are dominant and determining characteristics for establishing segregating generations, and can be used in breeding programs.

Index terms: *Glycine max*; Plant genetics; Segregating families; Multivariate analysis.

Inter-relações nutracêuticas canônicas da soja e suas reflexões sobre o melhoramento genético

Resumo – Nos últimos anos foram frequentes os questionamentos sobre o comportamento dos genótipos em diferentes ambientes, sobretudo aqueles que buscam revelar o valor comercial e nutricional dos genótipos de soja. Diante do exposto, o objetivo deste estudo foi analisar os aspectos fisiológicos e nutricionais das Famílias Segregantes S5 da soja. Este trabalho está vinculado ao Programa de Melhoramento de Soja do IRC localizado em Campos Borges, Rio Grande do Sul, Brasil. O delineamento utilizado foi de blocos casualizados completos, contendo 40 genótipos de soja dispostos em quatro repetições, correspondentes aos genótipos da geração F5 testados em 2018 e 2019. Esta geração foi obtida por meio de hibridizações artificiais de plantas F1s ocorridas em 2014 e 2015, F2s em 2015 e 2016 e famílias segregantes F3 em 2016 e 2017 e F4 em 2017 e 2018. Os caracteres foram avaliados e submetidos aos pressupostos do modelo estatístico, verificando a normalidade e homogeneidade das variâncias. Análise de variância, agrupamento de médias, correlação linear e canônica foram utilizadas para a explicação comportamental das Famílias Segregantes de Soja F5. A análise de variância revelou diferença significativa ($p < 0,01$) para todas as variáveis, indicando a existência de variabilidade genética. As famílias segregantes da geração F5 IRC8_130 e IRC31_102 são promissoras em programas de melhoramento que envolvem aspectos fisiológicos e nutricionais. As características de proteína bruta, fibra bruta, altura de inserção da primeira vagem, altura de planta e número de vagens com 4 grãos, são dominantes e determinantes para o estabelecimento de gerações segregantes, podendo ser utilizadas em programas de melhoramento.

Termos para indexação: *Glycine max*; Genética de plantas; Famílias segregantes; Análise multivariada.

Introduction

Considered one of the main commodities grown in southern Brazil, the history of soybean as an extensive crop began in the 1940s in the state of Rio Grande do Sul, where its adaptation

was facilitated by a species originating from a temperate climate (GAVIRAGHI et al., 2018). Developing new genotypes adapted to different edaphoclimatic conditions is undoubtedly one of the technologies that most contribute to increasing national productivity,

being relevant from an economic and environmental standpoint (DARONCH et al., 2019). In unfavorable environments, soybean genotypes efficient in taking advantage of the environmental stimulus show better productive performance. Gaviraghi et al. (2018)

Recebido em 12/4/2021. Aceito para publicação em 8/6/2021.

<http://dx.doi.org/10.52945/rac.v34i3.1155>

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state that research on adapting cultivars to different microclimates is important for awareness of the best productive material and its behavior against environmental variations.

Consequently, knowledge about the relations between traits, as estimated by correlations, has been of great relevance in plant breeding, as it provides useful information to breeders who assist in the selection process (NOGUEIRA et al., 2012). Monteiro et al. (2018) report several methods to analyze adaptability and stability when evaluating genotypes, which are tested in different environments representative of their recommendation locations that significantly interact with them. The correlation between two traits, however, can be phenotypic, genotypic or environmental, and only those genotypic correlations involving a heritable association are of greater interest for breeding (NOGUEIRA et al., 2012).

In recent years, questionings on the behavior of genotypes in different environments are frequent, especially those seeking to disclose the commercial and nutritional value of soybean genotypes (SZARESKI et al., 2015). Although research on the physiological and nutritional aspects of soybean segregating families, besides their adaptability and stability, is insufficient. Some studies touch upon this topic. Szarecki et al. (2015) evaluated the agronomic performance of soybean genotypes and their linear morphological and bromatological relations, seeking gains via breeding. Daronch et al. (2019) evaluated the environmental efficiency and genetic divergence of seventeen soybean genotypes, grown during sowing season. Nogueira et al. (2012) observed that the connection between traits of the total number of pods per plant and the number of nodes on the main stem can be used to indirectly select soybean grain yield, and Gaviraghi et al. (2018) analyzed the adaptation of soybean cultivars in the Upper Middle Uruguay region of the state of Rio Grande do Sul. Such information, however, does not meet the demand of producers and researchers for soybean

genotypes whose beans have potential for environmental adaptation and qualitative and quantitative responses. Based on the above, the study sought to analyze the physiological and nutritional aspects of S5 Soybean Segregating Families.

Material and methods

This study is linked to the IRC Soybean Breeding Program located in Campos Borges, Rio Grande do Sul, Brazil, under the geographical coordinates: 28°53'10" South and 52°59'55" West, at an altitude of 513 meters. Research design consisted of complete randomized blocks containing 40 soybean genotypes arranged in four repetitions, totaling 160 experimental units, five meters long and one meter wide. Plant generations were obtained via artificial hybridizations of: F1s plants sown in 2014/2015, F2s plants sown in 2015/2016, F3 segregating families sown in 2016/2017, and F4 segregating families tested in 2017/2018. F5 generation was sown in the first half of November 2018 and harvested in March 2019. Table 1 summarizes the genealogical definitions.

The following traits were evaluated radicle length (RIZ in g); shoot length (SL in g); seedling dry mass (SDM in g); first germination count (FGC in %); germination (GER in %); crude protein (PTN in %); moisture (MOI in %); lipids (LIP in %); crude fiber (FIB in %); mineral matter (MM in %); non-structural carbohydrates (CHO in %); first pod insertion height (FPI in cm); plant height (PH in cm); number of pods on main stem (NPS in units); number of branches (NBR in units); number of pods on branches (NPB in units); number of pods with 1 grain (NP1 in units); number of pods with 2 grains (NP2 in units); number of pods with 3 grains (NP3 in units); number of pods with 4 grains (NP4 in units); and seed mass per plant (SMP in units).

These data were then entered into the statistical model to verify normality (SHAPIRO & WILK, 1965) and homogeneity of variances (STEEL et al., 1997). It was performed an analysis of variance and the Scott-Knott averaging

test at 5% probability. Subsequently, the variables underwent Pearson's linear correlation to understand the association trend, with its significance based on a 5% probability by t-test. Canonical groups were established based on vigor traits (group I), quality components (group II), and morphological components (group III). Group I comprised the RAD, SL, SDM, FGC, and GER traits; group II the PTN, MOI, LIP, FIB, MM, and CHO traits; and group III the FPI, PH, NPS, NBR, NPB, NP1, NP2, NP3, NP4, and SMP traits. Significance among the trait groups were calculated by Chi-square statistics. All analyzes were performed using Genes software (CRUZ, 2016).

Results and discussion

Analysis of variance showed a significant difference ($p < 0.01$) for all variables, indicating the existence of genetic variability, as also observed by Daronch et al. (2019), Pinheiro et al. (2013), Monteiro et al. (2016; 2017), Medeiros et al. (2004), Meotti et al. (2012), Nogueira et al. (2012) and Oliveira (2018). Gaviraghi et al. (2018) add that soybean cultivars, when subjected to different environmental conditions, may show different responses due to physiological alterations emerging mainly from changes in temperature and relative humidity between sites.

The Scott-Knott clustering test resulted in the formation of 5 groups for seedling dry mass (SDM) and first germination count (FGC); 6 groups for radicle length (RAD), shoot length (SL), moisture (MOI), and mineral matter (MM); 7 for germination (GER) and crude fiber (FIB); 8 groups for non-structural carbohydrates (CHO); and 9 groups for crude protein (PTN) and lipids (LIP) (Table 2). Morpho-agronomic data also gathered genetic groups in studies reported by Daronch et al. (2019). This result shows the great genetic variability found and the different behaviors of the soybean genotypes under study.

Among the segregating families, IRC8_130 showed promising results with high RAD, GER, PTN, and MM means. The IRC31 population also showed potential in the breeding

Table 1. Detailed genealogy showing the maternal parent (MP), paternal parent (PP), F2 segregating population (POP) and F3 (F), F4 and F5 segregating families

Tabela 1. Genealogia detalhada representando o progenitor materno (MP), progenitor paterno (PP), população segregante F2 (POP) e famílias segregantes F3 (F), F4 e F5

MP	x	PP	2014/2015	2015/2016	2016/2017	2017/2018	2018/2019
			F1_Generation	F2_Generation	F3_Generation	F4_Generation	F5_Generation
1	x	2	1	1	22	21	194
1	x	2	2	1	22	22	196
3	x	2	3	2	5	31	111
3	x	2	4	2	6	32	191
1	x	4	5	3	4	66	159
1	x	4	6	3	4	66	120
3	x	6	7	7	8	121	29
3	x	5	8	8	27	155	130
10	x	6	9	11	25	191	136
10	x	6	10	11	25	190	135
11	x	3	11	12	48	221	134
11	x	3	12	12	48	119	132
11	x	3	13	12	40	220	155
1	x	3	14	13	5	366	117
1	x	3	15	13	31	237	119
1	x	3	16	13	39	244	164
7	x	10	17	16	11	284	153
7	x	10	18	16	11	286	82
7	x	10	19	16	11	287	97
12	x	4	20	17	11	304	193
12	x	4	21	17	7	301	46
2	x	13	22	19	5	325	62
2	x	13	23	19	15	334	114
2	x	13	24	19	4	6	124
16	x	17	25	21	8	362	113
16	x	17	26	21	6	360	160
17	x	29	27	22	5	359	49
Mass selection			28	25	7	87	154
Mass selection			29	26	1	399	9
Mass selection			30	28	18	437	110
Mass selection			31	28	19	436	123
Mass selection			32	29	14	384	122
25	x	6	33	30	1	464	104
25	x	6	34	30	12	646	182
26	x	11	35	31	12	2	102
26	x	11	36	31	12	3	137
1	x	27	37	32	21	511	189
1	x	27	38	32	4	500	103
1	x	27	39	32	6	502	129
6	x	27	40	33	5	529	175
6	x	27	41	33	5	530	192
26	x	17	42	34	13	560	174
25	x	6	43	35	9	577	118
3	x	28	44	36	15	605	152
3	x	28	45	36	16	600	121
27	x	6	46	37	3	619	116
28	x	27	47	39	17	651	106
28	x	27	48	39	30	3	105
28	x	27	49	39	14	648	133
29	x	28	50	40	29	678	58

Table 2. Means for radicle length (RAD), shoot length (SL), seedling dry mass (SDM), first germination count (FGC), germination (GER), crude protein (PTN), moisture (MOI), (LIP), crude fiber (FIB), mineral matter (MM), and non-structural carbohydrates (CHO)

Tabela 2. Médias para comprimento da radícula (RAD), comprimento do caule (SL), massa seca da muda (SDM), primeira contagem de germinação (FGC), germinação (GER), proteína bruta (PTN), umidade (MOI), lipídios (LIP), fibra bruta (FIB), matéria mineral (MM) e carboidratos não estruturais (CHO)

Genotype	RAD		SL		SDM		FGC		GER		PTN		MOI		LIP		FIB		MM		CHO	
	g										%											
IRC1_194	6.95	d	10.45	d	0.63	c	18.50	d	25.50	c	35.82	d	10.74	c	18.32	e	5.30	g	4.85	c	3.56	d
IRC1_196											37.25	a	10.84	b	17.34	f	5.68	d	4.92	b	2.30	g
IRC1_136	10.70	b	9.50	d	0.61	c	23.75	c	36.25	b	34.66	f	10.98	b	19.32	c	5.22	f	4.81	c	3.41	d
IRC2_111	9.40	b	10.85	c	0.58	d	15.25	d	28.75	c	34.82	e	10.68	c	19.12	c	5.52	f	4.77	c	3.67	c
IRC2_191	2.60	f	5.42	f	0.54	d			4.75	g	35.26	e	10.53	d	17.75	f	5.34	g	4.81	c	3.51	d
IRC3_120	9.82	b	11.62	c	0.56	d	36.25	b	39.00	b	36.15	c	10.31	e	16.76	g	5.63	e	4.81	c	3.68	c
IRC3_159	11.25	b	10.50	d	0.57	d	35.00	b	43.75	a	34.07	g	10.68	c	20.79	a	5.55	f	4.57	e	4.26	a
IRC7_29											34.30	g	9.91	f	18.35	e	5.36	g	4.83	c	3.48	d
IRC8_130	13.05	a	9.52	d	0.64	c	26.50	c	41.00	a	37.21	a	10.38	e	14.99	i	5.90	b	4.99	a	2.29	g
IRC11_135	13.40	a	11.67	c	0.45	e	30.00	c	39.25	b	33.73	h	10.77	c	19.69	c	5.34	g	4.73	d	3.84	c
IRC12_155	13.20	a	12.80	b	0.62	c	36.00	b	38.50	b	35.67	d	10.27	e	18.95	d	5.62	e	4.84	c	3.18	d
IRC12_134											34.01	g	9.93	f	18.77	d	5.31	g	4.90	b	2.39	g
IRC12_132	12.92	a	10.72	c	0.55	d	33.75	b	39.75	b	34.84	e	10.27	e	18.62	d	5.57	e	4.90	b	3.14	d
IRC13_117	9.12	c	8.15	e	0.61	c	25.00	c	30.25	c	35.60	d	10.93	b	18.53	d	5.63	e	4.79	c	3.29	d
IRC13_119	13.85	a	12.60	b	0.49	d	41.50	a	45.25	a	32.97	i	10.74	c	19.64	c	5.51	f	4.52	e	4.09	b
IRC13_164	13.47	a	10.12	d	0.53	d	24.25	c	32.25	b	35.91	d	10.91	b	18.31	e	5.52	f	4.28	f	4.41	a
IRC16_82											35.77	d	10.00	f	18.23	e	5.51	f	4.97	b	2.54	f
IRC16_153											34.58	f	9.93	f	17.41	f	5.38	g	4.79	c	2.67	f
IRC16_97											33.28	i	9.99	f	19.26	c	5.48	f	5.05	a	2.30	g
IRC17_193											37.64	a	11.08	a	17.91	e	5.50	f	4.70	d	2.84	e
IRC17_46	10.20	b	8.47	e	0.73	a	34.25	b	37.25	b	36.82	b	10.99	b	17.72	f	5.68	d	4.66	d	3.90	b
IRC19_62	11.07	b	8.25	e	0.78	a	24.75	c	27.50	c	37.24	a	10.52	d	17.10	g	5.82	c	4.93	b	2.44	g
IRC19_124											35.47	d	10.50	d	17.39	f	5.58	e	4.96	b	2.29	g
IRC19_114											36.70	b	10.59	d	17.01	f	5.60	e	4.83	c	2.97	e
IRC21_160											33.16	i	10.57	d	19.96	b	5.24	g	4.87	c	2.39	g
IRC21_113											34.44	f	10.52	d	19.58	c	5.34	g	4.88	c	2.22	g
IRC22_49	10.27	b	10.47	d	0.56	d	32.75	b	37.50	b	35.50	d	11.05	a	18.62	d	5.53	f	4.66	d	3.68	c
IRC25_154	8.65	c	8.30	e	0.70	b	11.75	d	24.00	d	37.43	a	10.64	c	17.51	f	5.51	f	4.78	c	3.51	d
IRC26_9	9.97	b	9.65	d	0.52	d	32.25	b	35.75	b	34.50	f	10.52	d	19.96	b	5.55	f	4.60	e	4.01	b
IRC28_110											34.21	g	9.83	f	21.17	a	5.37	g	4.91	b	2.14	g
IRC28_123	10.75	b	8.05	e	0.61	c	10.75	d	21.00	d	35.17	e	11.27	a	18.99	d	5.71	d	4.74	d	3.75	c
IRC29_122	6.25	d	7.25	e	0.67	b	18.50	d	19.75	d	35.67	d	10.72	c	17.69	f	6.06	a	4.92	b	2.74	f
IRC30_182	11.55	b	7.62	e	0.55	d	16.50	d	35.25	b	36.07	c	10.56	d	18.87	d	5.72	d	4.85	c	2.82	e
IRC30_104	11.32	b	11.40	c	0.56	d	37.50	b	39.75	b	34.57	f	11.11	a	18.75	d	5.54	f	4.25	f	4.56	a
IRC31_102	12.22	a	10.82	c	0.52	d	41.00	a	42.25	a	35.10	e	10.58	d	18.62	d	5.52	f	4.54	e	4.29	a
IRC31_137	7.35	d	7.25	e	0.52	d	16.25	d	17.50	e	33.12	i	11.26	a	19.19	c	5.57	e	4.76	c	3.47	d
IRC32_103	9.77	b	10.20	d	0.68	b	29.50	c	37.75	b	35.71	d	10.79	c	18.01	e	5.49	f	4.78	c	3.51	d
IRC34_174	11.42	b	8.57	e	0.51	d	24.00	c	28.50	c	34.66	f	10.70	c	19.14	c	5.70	d	4.60	e	3.80	c
IRC32_129	9.47	b	10.85	c	0.52	d	28.50	c	34.50	b	36.65	f	11.09	a	19.02	d	5.50	f	4.73	d	3.69	c
IRC32_189	7.40	d	8.40	e	0.68	b	15.25	d	24.75	d	35.83	d	10.56	d	17.58	f	5.52	f	4.69	d	3.46	d
IRC33_175	8.90	c	11.65	c	0.64	c	31.75	b	38.75	b	36.08	c	10.59	d	18.31	e	5.46	f	4.74	d	3.59	c
IRC33_192	5.05	e	7.80	e	0.63	c	4.50	e	12.25	f	34.88	e	10.51	d	17.96	e	5.36	g	4.71	d	3.63	c
IRC35_118	13.10	a	9.67	d	0.54	d	23.25	c	28.75	c	36.28	c	10.19	e	17.39	f	5.83	c	4.57	e	4.22	a
IRC36_152	10.37	b	11.37	c	0.54	d	36.00	b	38.50	b	34.21	g	11.15	a	18.62	d	5.44	f	4.70	d	3.39	d
IRC36_121											36.70	b	10.05	f	18.26	e	5.45	f	4.97	b	1.44	h
IRC37_116	11.80	b	10.10	d	0.52	d	32.75	b	39.50	b	34.97	e	10.94	b	18.50	d	5.77	c	4.64	e	3.66	c
IRC39_133	11.15	b	10.10	d	0.61	c	23.25	c	35.25	b	34.53	f	10.29	e	19.34	c	5.58	e	4.87	c	3.38	d
IRC39_106											34.09	g	10.63	c	21.04	a	5.33	g	5.06	a	3.78	c
IRC39_105	11.80	b	10.52	d	0.62	c	30.00	c	37.50	b	36.38	c	10.45	d	18.83	d	5.82	c	4.62	e	3.94	b
IRC40_58	11.02	b	7.92	e	0.68	b	13.00	d	21.75	d	35.31	e	10.91	b	17.99	e	6.00	b	4.65	d	4.25	a
M6210IPRO	15.55	a	14.77	a	0.41	e	36.00	b	44.25	a	37.10	a	10.76	c	16.26	h	5.67	d	4.59	e	2.94	e
NAS5909RG	12.32	a	9.95	d	0.58	d	28.25	c	36.75	b	35.92	d	10.71	c	18.36	e	5.53	f	4.74	d	3.31	d
TMG7069IPRO	10.47	b	8.40	e	0.65	c	26.75	c	36.25	b	36.23	c	11.05	a	17.84	f	6.15	a	4.70	d	3.04	e
NS6601IPRO	12.50	a	13.12	b	0.53	d	42.75	a	45.00	a	36.42	c	10.58	d	16.98	g	5.64	e	4.60	e	3.62	c

Means followed by the same letter vertically do not differ, according to the Scott-Knott test at a 5% error probability.

process, with good RAD, GER, and CHO means in the IRC31_102 family and MOI in IRC31_137. Among the homozygous ideotypes, M6210IPRO stood out for showing relevant results in RAD, SL, GER, and PTN (Table 2).

Qualitative and quantitative factors linked to GER, PTN, MOI, LIP, FIB, MM, and CHO are essential for commercializing the grain, or even the seed, often justifying the genotype's power in the field at the initial start – a period that includes the first 15 days after root protrusion. For Sedyama (2013), soybean cultivars can achieve 18-22% oil and 38-42% protein, some genotypes however can reach 13-18% oil and 43-54% protein, with an excellent balance of essential amino acids, minerals, fibers and carbohydrates. The variables under study were not accounted for in TACO 2011. Pinheiro et al. (2013) and Monteiro et al. (2017) observed other qualitative results, the latter pointing out that the behavior of genotypes concerning oil productivity, was influenced by changes in the environment.

Variables for NP4 and SMP were similar for all genotypes studied. Findings different from the research by Lima et al. (2012), who observed distinctions in SMP between parents, F2 and F3 generations. Families IRC3_159, IRC16_82, IRC19_62, and IRC36_152 satisfied the highest means for first pod insertion height (FPI), plant height (PH), and number of pods on main stem (NPS), whereas IRC1_194 satisfied the means for the number of pods on branches (NPB), number of branches (NBR), number of pods with 1 grain (NP1), number of pods with 2 grains (NP2) and number of pods with 3 grains (NP3) (Table 3). Plants with very low pods can lead to losses in mechanized harvesting or predisposition to pathogens, while high positioned pods can result in reduced reproductive nodes. Pod appearance between 10-15cm from the plant collection is a good indicator, as is plant height ranging from 80-100cm.

Reproductive node distribution and level of branching on the soybean stem result mainly from the genetic load of the genotype, but are also linked to

the final plant stand. High density can reduce such variables, and is sometimes offset by increased height, which can result in excessive energy expenditure or toppling of plants. Consequently, good positioning of the maturity group and a successful plant stand are critical for the soybean crop's success.

Characteristics such as plant height and pod distribution on the plant shoot are directly linked to the genotype's climatic adaptability, especially its photoperiodic and thermal response. As Daronch et al. (2019) argues, cultivars with long youth are needed because then, even if the crop receives the stimulus to bloom, it will continue to vegetate, promoting greater plant height.

Pearson's correlation coefficients of the characteristics under study ranged from -0.01 to 0.87 (Table 4), which according to Monteiro et al. (2016) and Pereira et al. (2017), show different levels of agreement in their order of classification. Al-Hadi et al. (2017) add that one can select promising soybean genotypes by analyzing morphological traits and their environmental interactions.

Research on the various correlations involving the physiological aspects of soybean crops can better elucidate the efficiency of crop production systems. As one of the main variables informing the producer's and or researcher's desire, income levels can be influenced by several other characteristics. Such observations help the decision-making of those involved in the production chain, like genetic choice and crop management positioning, as well as developing specific regional work, as observed by Hamawaki et al. (2019), who found soybean genotypes with high yield, high adaptability, good drought tolerance, and partial resistance to soybean rust.

Phenotypic correlations showed 71 significant pairs ($p < 0.05$) between the soybean cultivars variables, 24 of which were negative. Variables FPI and SMP were the most frequent, with 8 significant pairs each (Table 4). Medeiros et al. (2004), who sought to establish a methodology to select superior individuals and segregate generation

advances in soybean progeny tests with 51 genotypes, also observed positive and negative correlations between the variables obtained. Meotti et al. (2012), Nogueira et al. (2012) and Oliveira (2018) also reported correlations, when showing the increase in pod and node production, positively correlated with the potential to obtain high yield potential.

When interpreting correlations, Nogueira et al. (2012) mention three aspects to be considered: magnitude, direction and significance. Positive correlation coefficient estimates indicate the tendency of one variable to increase when the others increase, and negative correlations indicate the tendency of one variable to increase while the others decrease. Canonical correlations between Group I and Group II variables showed a significant canonical correlation ($p < 0.01$) in the first- and second-order canonical pairs, with a total correlation of $r = 0.58$ and 0.49 , respectively (Table 4). The first canonical pair showed that a reduction in SL and increase in SDM are determined by an increase in PTN, FIB, MM, and CHO; the second canonical pair, however, showed an increase in RAD, FGC and GER traits (Group I), correlating with high levels of FIB and CHO (Group II) (Table 5). These findings corroborate the study by Leamy et al. (2016), who also found correlations between soybean traits possibly attributed to gene flow between populations.

According to Pereira et al. (2017), the agronomic and physiological characteristics of seeds are not independent, as more productive plants, with greater number of pods and high oil content, are associated with seeds with high germination percentage and emergence rate. Szarecki et al. (2015) found contradictory results, finally concluding that bromatological traits do not show a significant difference between growth environments and soybean genotypes with an indeterminate growth habit. According to Monteiro et al. (2016), the recommendation of cultivars depends on the method used to analyze the adaptability and stability of the

Table 3. Means for first pod insertion height (FPI), plant height (PH), number of pods on main stem (NPS), number of branches (NBR), number of pods on branches (NPB), number of pods with 1 grain (NP1), number of pods with 2 grains (NP2), number of pods with 3 grains (NP3), number of pods with 4 grains (NP4) and seed mass per plant (SMP)

Tabela 3. Médias para a altura de inserção da primeira vagem (FPI), altura da planta (PH), número de vagens no caule principal (NPS), número de ramos (NBR), número de vagens nos ramos (NPB), número de vagens com 1 grão (NP1), número de vagens com 2 grãos (NP2), número de vagens com 3 grãos (NP3), número de vagens com 4 grãos (NP4) e massa de semente por planta (SMP)

Genotype	FPI		PH		NPS		NPB		NBR		NP1		NP2		NP3		NP4		SMP	
	-----cm-----										-----Unit-----								g	
IRC1_194	13.20	b	81.60	b	81.60	b	82.70	a	5.00	a	10.80	a	45.50	a	45.33	a	0.00	a	45.01	a
IRC2_111	22.00	a	80.10	b	80.10	b	7.40	d	1.20	b	2.00	d	15.40	c	15.60	c	0.00	a	11.01	a
IRC2_191	8.50	c	68.00	c	68.00	c	26.60	c	3.40	a	8.50	c	19.25	c	18.00	c	0.60	a	19.08	a
IRC3_120	4.87	c	49.87	d	49.87	d	38.25	b	3.75	a	9.25	b	29.00	b	18.00	c	1.25	a	26.97	a
IRC3_159	22.80	a	90.40	a	90.40	a	1.80	d	0.80	b	1.40	d	8.40	d	13.20	d	0.20	a	6.12	a
IRC12_134	18.40	a	67.80	c	67.80	c	4.40	d	1.00	b	2.40	d	9.40	d	7.60	d	0.40	a	6.76	a
IRC13_117	11.60	b	74.40	c	74.40	c	21.00	c	2.60	a	5.00	c	14.80	c	19.20	c	1.18	a		
IRC13_164	14.80	b	61.90	c	61.90	c	21.00	c	2.20	b	1.40	d	22.25	b	18.00	c	0.80	a	21.83	a
IRC16_82	29.00	a	101.80	a	101.80	a	1.00	d	0.40	b	4.40	c	13.20	c	23.40	c	0.00	a	16.36	a
IRC16_97	23.80	a	87.60	b	87.60	b	20.40	c	2.40	a	2.00	d	15.80	c	18.75	c	0.00	a	18.02	a
IRC17_46	12.62	b	91.40	a	91.40	a	52.25	b	4.40	a	12.40	a	31.00	b	5.20	d	2.00	a	51.55	a
IRC19_62	25.00	a	93.40	a	93.40	a	0.00	d	0.00	b	1.40	d	6.00	d	9.60	d	0.00	a	4.01	a
IRC19_114	13.00	b	65.20	c	65.20	c	0.00	d	0.00	b	3.00	d	13.40	c	51.67	a	0.20	a	8.03	a
IRC22_49	10.20	c	86.00	b	86.00	b	49.00	b	3.20	a	9.00	b	30.80	b	11.40	d				
IRC25_154	19.60	a	73.20	c	73.20	c	0.80	d	0.40	b	1.20	d	6.40	d	8.00	d	0.40	a	7.99	a
IRC26_9	15.50	b	58.00	d	58.00	d	1.40	d	0.80	b	1.60	d	7.20	d	4.80	d	0.20	a	6.17	a
IRC28_110	15.20	b	48.20	d	48.20	d	1.80	d	0.60	b	4.20	c	11.50	c	21.00	c	0.00	a	5.79	a
IRC30_182	14.80	b	59.20	d	59.20	d	17.00	c	2.20	b	2.60	d	2.60	d	31.00	b	1.20	a	20.00	a
IRC30_104	18.20	a	67.80	c	67.80	c	34.40	b	4.00	a	8.80	b	23.20	b	3.60	d	0.20	a	21.44	a
IRC31_102	18.40	a	82.20	b	82.20	b	0.00	d	0.00	b	1.40	d	5.25	d	12.60	d	0.00	a	4.94	a
IRC31_137	13.00	b	57.80	d	57.80	d	20.00	c	2.00	b	2.25	b	8.75	d	11.20	d	0.00	a	12.35	a
IRC32_103	17.20	b	63.00	c	63.00	c	11.20	c	1.40	b	4.20	c	11.25	c	2.50	d	0.00	a	9.23	a
IRC34_174	22.20	a	69.60	c	69.60	c	0.00	d	0.00	b	3.00	d	3.20	d	8.60	d	0.00	a	2.73	a
IRC32_129	17.40	b	68.60	c	68.60	c	12.00	c	2.00	b	4.40	d	16.50	c	7.20	d	0.00	a	9.34	a
IRC32_189	24.40	a	86.20	b	86.20	b	3.20	d	1.00	b	1.80	d	8.00	d	11.33	d	0.00	a	5.50	a
IRC33_192	15.80	b	66.20	c	66.20	c	3.00	d	4.20	a	2.40	d	7.50	d	27.60	b	0.40	a	12.35	a
IRC36_152	22.00	a	90.40	a	90.40	a	9.60	d	1.80	b	4.40	c	13.80	c	9.25	d	0.60	a	14.40	a
IRC36_121	13.00	b	91.40	a	91.40	a	1.40	d	0.40	b	1.60	d	9.20	d		d	0.20	a	7.40	a

Means followed by the same letter vertically do not differ, according to the Scott-Knott test at a 5% error probability.

Table 4. Simple phenotypic correlation matrix of soybean cultivars concerning the variables: radicle length (RAD), shoot length (SL), seedling dry mass (SDM), first germination count (FGC), germination (GER), crude protein (PTN), moisture (MOI), lipids (LIP), crude fiber (FIB), mineral matter (MM), non-structural carbohydrates (CHO), first pod insertion height (FPI), plant height (PH), number of pods on main stem (NPS), number of branches (NBR), number of pods on branches (NPB), number of pods with 1 grain (NP1), number of pods with 2 grains (NP2), number of pods with 3 grains (NP3), number of pods with 4 grains (NP4) and seed mass per plant (SMP)

Tabla 4. Matriz simples de correlação fenotípica de cultivares de soja nas variáveis: comprimento da radícula (RAD), comprimento da parte aérea (SL), massa seca da muda (SDM), primeira contagem de germinação (FGC), germinação (GER), proteína bruta (PTN), umidade (MOI), lipídios (LIP), fibra bruta (FIB), matéria mineral (MM), carboidratos não estruturais (CHO), altura de inserção da primeira vagem (FPI), altura da planta (PH), número de vagens no caule principal (NPS), número de ramos (NBR), número de vagens nos ramos (NPB), número de vagens com 1 grão (NP1), número de vagens com 2 grãos (NP2), número de vagens com 3 grãos (NP3), número de vagens com 4 grãos (NP4) e massa de semente por planta SMP

Variable	RAD	SL	SDM	FGC	GER	PTN	MOI	LIP	FIB	MM	CHO	FPI	PH	NPS	NPB	NBR	NP1	NP2	NP3	NP4	SMP	
RAD	1	0.54*	-0.32*	0.52*	0.62*	0.07 ^{ns}	-0.10 ^{ns}	-0.01 ^{ns}	0.16 ^{ns}	-0.29*	0.11 ^{ns}	0.19 ^{ns}	-0.01 ^{ns}	-0.08 ^{ns}	-0.16 ^{ns}	-0.19 ^{ns}	-0.09 ^{ns}	-0.12 ^{ns}	0.01 ^{ns}	-0.03 ^{ns}	-0.10 ^{ns}	
SL		1	-0.34*	0.65*	0.67*	-0.05 ^{ns}	-0.09 ^{ns}	0.02 ^{ns}	-0.18 ^{ns}	-0.23*	0.15 ^{ns}	0.11 ^{ns}	0.04 ^{ns}	0.11 ^{ns}	0.03 ^{ns}	-0.01 ^{ns}	0.08 ^{ns}	0.25*	0.12 ^{ns}	-0.14 ^{ns}	0.01 ^{ns}	
SDM			1	-0.25*	-0.22*	0.38*	-0.08 ^{ns}	-0.21*	0.25*	0.31*	-0.22*	0.15 ^{ns}	0.43*	0.07 ^{ns}	-0.06 ^{ns}	0.01 ^{ns}	0.09 ^{ns}	-0.05 ^{ns}	-0.06 ^{ns}	-0.02 ^{ns}	0.16 ^{ns}	
FGC				1	0.87*	0.03 ^{ns}	0.10 ^{ns}	0.06 ^{ns}	0.10 ^{ns}	-0.28*	0.13 ^{ns}	-0.01 ^{ns}	0.12 ^{ns}	0.05 ^{ns}	0.04 ^{ns}	0.04 ^{ns}	0.16 ^{ns}	0.12 ^{ns}	0.09 ^{ns}	0.02 ^{ns}	0.06 ^{ns}	
GER					1	0.09 ^{ns}	0.14 ^{ns}	0.05 ^{ns}	0.14 ^{ns}	-0.19*	0.05 ^{ns}	0.06 ^{ns}	0.15 ^{ns}	0.08 ^{ns}	0.04 ^{ns}	0.01 ^{ns}	0.12 ^{ns}	0.08 ^{ns}	0.11 ^{ns}	0.02 ^{ns}	0.08 ^{ns}	
PTN						1	0.09 ^{ns}	-0.68*	0.38*	-0.02 ^{ns}	-0.16*	-0.03 ^{ns}	0.17 ^{ns}	0.13 ^{ns}	-0.03 ^{ns}	-0.05 ^{ns}	0.04 ^{ns}	-0.00 ^{ns}	-0.02 ^{ns}	0.10 ^{ns}	0.11 ^{ns}	
MOI							1	0.01 ^{ns}	0.26*	-0.42*	0.39*	-0.09 ^{ns}	0.01 ^{ns}	0.14 ^{ns}	0.24*	0.26*	0.31*	0.18 ^{ns}	0.28*	0.13 ^{ns}	0.17 ^{ns}	
LIP								1	-0.42*	-0.05 ^{ns}	0.17*	0.14 ^{ns}	-0.12 ^{ns}	-0.17 ^{ns}	-0.08 ^{ns}	-0.08 ^{ns}	-0.14 ^{ns}	-0.07 ^{ns}	-0.04 ^{ns}	-0.06 ^{ns}	-0.18 ^{ns}	
FIB									1	-0.06 ^{ns}	0.05 ^{ns}	0.08 ^{ns}	0.08 ^{ns}	-0.06 ^{ns}	-0.17 ^{ns}	-0.09 ^{ns}	0.05 ^{ns}	-0.28*	0.01 ^{ns}	0.17 ^{ns}	-0.03 ^{ns}	
MM										1	-0.70*	-0.01 ^{ns}	0.13 ^{ns}	0.04 ^{ns}	-0.03 ^{ns}	-0.06 ^{ns}	-0.08 ^{ns}	-0.06 ^{ns}	-0.19 ^{ns}	0.04 ^{ns}	0.06 ^{ns}	
CHO											1	-0.03 ^{ns}	-0.15 ^{ns}	0.01 ^{ns}	0.12 ^{ns}	0.16 ^{ns}	0.19 ^{ns}	0.11 ^{ns}	0.16 ^{ns}	-0.01 ^{ns}	0.11 ^{ns}	
FPI												1	0.37*	-0.27*	-0.40*	-0.40*	-0.36*	-0.34*	-0.17 ^{ns}	-0.19*	-0.35*	
PH													1	0.27*	0.01 ^{ns}	-0.11 ^{ns}	0.02 ^{ns}	0.08 ^{ns}	0.22*	-0.06 ^{ns}	0.12 ^{ns}	
NPS														1	0.64*	0.53*	0.61*	0.75*	0.84*	0.03 ^{ns}	0.74*	
NPB															1	0.84*	0.70*	0.89*	0.78*	0.22*	0.92*	
NBR																1	0.61*	0.79*	0.56*	0.25*	0.67*	
NP1																	1	0.69*	0.59*	0.14 ^{ns}	0.70*	
NP2																		1	0.74*	0.19*	0.87*	
NP3																			1	0.19*	0.87*	
NP4																				1	0.39*	
SMP																						1

* S: significant at 5% probability by F test; NS: not significant at 5% probability by F test.

Table 5. Estimates of correlations and canonical pairs between radicle length (RAD), shoot length (SL), seedling dry mass (SDM), first germination count (FGC), germination (GER), crude protein (PTN), moisture (MOI), lipids (LIP), crude fiber (FIB), mineral matter (MM), non-structural carbohydrates (CHO), first pod insertion height (FPI), plant height (PH), number of pods on main stem (NPS), number of branches (NBR), number of pods on branches (NPB), number of pods with 1 grain (NP1), number of pods with 2 grains (NP2), number of pods with 3 grains (NP3), number of pods with 4 grains (NP4) and seed mass per plant (SMP)

Tabela 5. Estimativas das correlações e pares canônicos entre comprimento da radícula (RAD), comprimento do caule (SL), massa seca da muda (SDM), primeira contagem de germinação (FGC), germinação (GER), proteína bruta (PTN), umidade (MOI), lipídios (LIP), fibra bruta (FIB), matéria mineral (MM) e carboidratos não estruturais (CHO), altura de inserção da primeira vagem (FPI), altura da planta (PH), número de vagens no caule principal (NPS), número de ramos (NBR), número de vagens nos ramos (NPB), número de vagens com 1 grão (NP1), número de vagens com 2 grãos (NP2), número de vagens com 3 grãos (NP3), número de vagens com 4 grãos (NP4) e massa de semente por planta (SMP)

Group I		
TRAITS	Canonical pairs	
	1 st	2 nd
RAD	0.0199	0.4334
SL	-0.2293	0.1631
SDM	0.4916	-0.1770
FGC	-0.0699	0.3059
GER	-0.0050	0.2282
Group II		
PTN	0.3996	0.0127
MOI	-0.0611	-0.0265
LIP	-0.1802	0.0507
FIB	0.3968	0.1934
MM	0.2269	-0.3764
CHO	-0.2055	0.1843
r	0.58	0.49
p	<0.0001	0.0030
Group I		
TRAITS	Canonical pairs	
	1 st	
RAD	0.2498	
SL	0.5253	
SDM	0.2217	
FGC	0.4380	
GER	0.2855	
Group III		
FPI	0.3058	
PH	0.3623	
NPS	-0.1509	
NPB	-0.0656	
NBR	-0.0289	
NP1	0.0852	
NP2	0.1279	
NP3	0.0758	
NP4	-0.3432	
SMP	-0.1951	
r	0.7212	
p	0.0253	

genotype, highlighting the relations that point to significant correlations and of greater magnitude.

The canonical correlations between Group I and Group III variables showed a significant canonical correlation ($p < 0.05$) in the first-order canonical pair, with a total correlation of $r = 0.72$ (Table 5). Concerning the traits related to Group I, the canonical loads increased for SL and FGC, while in Group III, this increase was verified for FPI, PH, and NP4, indicating that these are the traits of greater importance in their respective groups. Thus, the coefficients of the first canonical pair evince the establishment of intergroup associations. The relationship between plants with higher FPI, PH, and NP2, with reduced NPS, NP4, and SMP are determinant in adding RAD, SL, SDM, FGC, and GER (Table 5).

For Gaviraghi et al. (2018), such characteristics depend on each cultivar, especially regarding the length of the cycle that directly influences the flowering season and, consequently, coupled with the environmental conditions of the moment and the reduction or not of the plant size. Nogueira et al. (2012) found that the total number of pods per plant and the number of nodes on main stem can be used to indirectly select for soybean grain yield.

Distinctions between segregating genotypes and homozygous ideotypes were first diagnosed by analysis of variance and clustering of means by t-test and Scott-Knott test at 5% probability, respectively. Pearson's phenotypic correlation between the analyzed traits showed the interaction between them, and the dependency relationships were proven by evaluating the canonical correlations. Although knowing the correlations is of great importance, Nogueira et al. (2012) argue for some precautions, since these are not measures of cause and effect, and the direct interpretation of their magnitudes may result in errors during strategy selection because the high correlation between two traits can result from the indirect effect of a third trait or a group of them.

Conclusion

The F5 generation segregating families IRC8_130 and IRC31_102 are promising in breeding programs involving physiological and nutritional aspects. Crude protein, crude fiber, first pod insertion height, plant height, and the number of pods with 4 grains are dominant and determining characteristics for establishing segregating generations and can be used in breeding programs.

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