

Adaptability and stability of mungbean genotypes in the Mid-North of Mato Grosso, Brazil

Adaptabilidade e estabilidade de linhagens de feijão-mungo na região médio-norte de Mato Grosso, Brasil

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ABSTRACT

Evaluation of genotype x environment interactions is essential in plant breeding aimed at adapting crops to new settings. Considering the need for research on the adaptation of mungbean to grain-production regions of Brazil, this study evaluated the agronomic performance, adaptability, and stability of mungbean production in the mid-north of Mato Grosso using different genotypes. Two experiments (with and without fertilizer application) were carried out in Sorriso and Sinop in 2019 and 2020, totaling eight environments. The treatments were 10 mungbean lines and the control cultivar BRSMG Camaleão. In general, significant differences among the treatments were observed in the yield, mass of 100 grains, and value for cultivation. The genotype x environment interactions were significant for yield. On average, the yield was in the range of 734-1305 kg ha⁻¹, the mass of 100 grains was 4.63-6.56 g, and the value for cultivation was 2.08-3.56. Genotypes BRA-08654-1, BRA-000027, BRA-084654-2, and BG3 combined high average yield and mass of 100 grains. These genotypes also showed good adaptability for cultivation in the mid-north of Mato Grosso. The yellow seed-coated genotype BRA-084689 also showed good agronomic performance and adaptability. Genotypes BRA-08654-1, BRA-000027, BRA-084654-2, BRA-084689, and BG3 are promising for further experiments evaluating the value for cultivation and use, the final breeding stage consisting of tests at a national level.

Index terms: *Vigna radiata* L.; pulses; genotype x environment interactions.

RESUMO

A avaliação da interação genótipos x ambientes é essencial no melhoramento de plantas visando à adaptação de culturas a novos ambientes de cultivo. Considerando a necessidade de pesquisas para avaliar a adaptação da cultura do feijão-mungo em regiões produtoras de grãos do Brasil, este trabalho foi realizado com o objetivo de avaliar o desempenho agrônomo e a adaptabilidade e estabilidade de produção de genótipos de feijão-mungo na região médio-norte de Mato Grosso. Os experimentos foram conduzidos em Sorriso e Sinop em segunda safra nos anos de 2019 e 2020. Dois experimentos foram conduzidos em cada local, sendo um com aplicação de fertilizante e outro sem, totalizando oito ambientes. Foi utilizado o delineamento de blocos casualizados completos, com três repetições e 11 genótipos, incluindo 10 linhagens e a cultivar BRSMG Camaleão. Avaliou-se a produtividade de grãos, a massa de 100 grãos e o valor de cultivo. Em geral, observou-se diferença significativa entre os tratamentos. A interação genótipos x ambientes foi significativa para produtividade de grãos. Em média, a produtividade variou entre 734-1305 kg ha⁻¹, a massa de 100 grãos entre 4,63-6,56 g e o valor de cultivo entre 2,08-3,56. As linhagens BRA-08654-1, BRA-000027, BRA-084654-2 e BG3 associaram alta média de produtividade e alta massa de 100 grãos, além de apresentarem boa adaptabilidade para cultivo na região médio-norte de Mato Grosso. A linhagem de grãos amarelos, BRA-084689, também apresentou bom desempenho agrônomo e boa adaptabilidade. As linhagens BRA-08654-1, BRA-000027, BRA-084654-2, BRA-084689 e BG3 são recomendadas para avaliação nos experimentos de valor de cultivo e uso, etapa final do melhoramento, com avaliação nos ensaios da rede nacional.

Termos para indexação: *Vigna radiata* L.; pulses; interação genótipos x ambientes.

INTRODUCTION

Mungbean (*Vigna radiata* (L.) R. Wilczek) sprouts are occasionally consumed in Brazil, where a relatively

small amount of seeds is needed for sprout production (Vieira; Oliveira; Vieira, 2003). However, the cultivation of mungbean has intensified in Brazil, particularly in the

state of Mato Grosso, to supply the international market (Menezes Júnior; Silva; Rocha, 2019).

Mungbeans are widely used worldwide, especially in Asian cuisine (Nair et al., 2019), and belong to a subgroup of leguminous plants known as pulses whose dry seeds are used for human nutrition (Kumar et al., 2021). Pulses are important sources of protein and benefit the soil through nitrogen fixation (Cheng et al., 2019; Kumar et al., 2021).

The rapid global population growth, combined with changing patterns of food consumption and the effects of climate change, has posed a challenge to sustainably achieving worldwide food security (Kumar et al., 2021). In this scenario, pulses are considered key crops for achieving the UN Sustainable Development Goals concerning food security, improving protein consumption, and promoting sustainable agriculture by 2030 (Cheng et al., 2019; Kumar et al., 2021). Therefore, research attention and investment in pulse crops have grown considerably in recent years (Cheng et al., 2019; Menezes Júnior; Silva; Rocha, 2019; Nair et al., 2019; Sequeros et al., 2020).

In Sub-Saharan Africa and South America, the cultivation of mungbean as a short-cycle crop with efficient nitrogen-fixing capacity has increased over the past 20 years. However, in these regions, biotic and abiotic factors along with other production restrictions represent major challenges for the genetic improvement of this species (Nair et al., 2019). In Mato Grosso, mungbean is cultivated extensively without appropriate management practices. Thus, the establishment and adaptation of this crop remain to be improved for this region (Menezes Júnior; Silva; Rocha, 2019).

One of the major problems faced by mungbean farmers in Mato Grosso is the limited number of cultivars available. Registered cultivars are recommended for other regions of the country, such as the state of Minas Gerais (Vieira et al., 2002; Vieira et al., 2008; Vieira et al., 2022), but they are not commonly used in Mato Grosso. This, allied to the lack of information on management practices, led to farmers having uneven grains and lower harvest yield than desired.

Evaluation of the genotype \times environment interactions is essential for plant improvement and breeding, helping to develop cultivars more adaptable to diverse environments. In the case of mungbean, the evaluation of the agronomic performance, adaptability, and stability of production has advanced knowledge and adaptation of the culture in different regions (Sayão; Briosso; Duque, 1991; Lin; Alves, 2002; Thangavel; Anandan; Eswaran, 2011; Vieira et al., 2011; Asfaw et al., 2012; Win et al., 2018; Kumar et al., 2020;

Samyuktha et al., 2020). The objective of this study was to evaluate these same parameters in mungbean genotypes in the mid-north of Mato Grosso, Brazil.

MATERIAL AND METHODS

The experiments involved eight environments and 10 mungbean genotypes (lineages) developed in Northeastern Brazil by the Plant Breeding Program of Embrapa Meio-Norte (Teresina, PI, Brazil). In addition, the commercial cultivar BRSMG Camaleão (Vieira et al., 2022) was used as a control (Table 1). The seed teguments of the evaluated genotypes were green except for the yellow seed-coated G6.

Table 1: Mungbean genotypes and experimental environments.

Genotypes, color of seed tegument	Environment ¹
G1 (BRA-084638), green	Sinop2019WF
G2 (BRA-08654-1), green	Sinop2019NF
G3 (BRA-084671), green	Sinop2020WF
G4 (BRA-000027), green	Sinop2020NF
G5 (BRA-084654-2), green	Sorriso2019WF
G6 (BRA-084689), yellow	Sorriso 2019NF
G7 (BRA-084930), green	Sorriso2020WF
G8 (BRA-084981), green	Sorriso2020NF
G9 (BG2), green	
G10 (BG3), green	
G11 (BRSMG Camaleão; control), green	

¹Codes refer to location (Sinop or Sorriso), cultivation year (2019 or 2020), and fertilization scheme employed (WF - with fertilizer application; NF - no fertilizer applied).

Evaluations were performed in 2019 and 2020 in areas around the cities of Sinop and Sorriso, state of Mato Grosso, Brazil. In Sinop, the experiments were carried out at the experimental fields of the Regional Center for Research and Technology Transfer/ Mato Grosso Research, Assistance, and Rural Extension Company (EMPAER, Brazilian acronym) located at 11°51'02.97"S; 55°31'03.33"W (altitude 366 m) in a Cerrado-Amazon Forest transition zone. In Sorriso, the experiments were performed at the experimental farm of the Federal Institute of Education, Science, and Technology of Mato Grosso (IFMT, Brazilian acronym) located at 12°32'40.17"S; 55°43'24.29"W (altitude 365 m) in a biome that is predominantly Cerrado.

At each year and location, the experiments were conducted with and without the application of fertilizers (Table 1). The fertilizer dose was based on the physicochemical characteristics of the top soil layer (0-0.20 m) and information from the literature (Duque; Pessanha, 1990; Vieira; Oliveira; Vieira, 2003). The availability of P in the soil at the experimental sites in the 2019 and 2020 seasons (15.2 and 11.8 mg dm⁻³, respectively, at Sinop and 1.4 and 2.5 mg dm⁻³ at Sorriso) were also important for defining the fertilizer dose employed. Other soil characteristics were: pH (CaCl₂) 5.2; organic matter = 41 g dm⁻³; K = 82 mg dm⁻³; V = 27%; clay = 340 g kg⁻¹; silt = 160 g kg⁻¹ and sand = 500 g kg⁻¹ in Sinop 2019; pH (CaCl₂) 4.52; organic matter = 19.56 g dm⁻³; K = 82 mg dm⁻³; V = 39.68%; clay = 502.5 g kg⁻¹; silt = 100 g kg⁻¹ and sand = 397.5 g kg⁻¹ in Sinop 2020; pH (CaCl₂) 4.8; organic matter = 2.83 dag kg⁻¹; K = 40.8 mg dm⁻³; V = 35.40%; clay = 428 g kg⁻¹; silt = 104 g kg⁻¹ and sand = 468 g kg⁻¹ in Sorriso 2019; pH (CaCl₂) 4.7; organic matter = 1.6 dag kg⁻¹; K = 55.4 mg dm⁻³; V = 37.7%; clay = 270 g kg⁻¹; silt = 55 g kg⁻¹ and sand = 675 g kg⁻¹ in Sorriso 2020.

In Sinop, the soil was harrowed and the sowing furrows were opened mechanically. In Sorriso, the soil was prepared using two different approaches. In 2019, harrowing was followed by mechanical rotary hoeing and the furrows opened with the aid of hand hoes. In 2020, the experiments were conducted under a no-tillage system, after the soybean harvest. The spacing between furrows was first marked with a seeder and the furrows were opened with the aid of hand hoes.

At the sowing of the fertilized experiments, 200 kg ha⁻¹ of a formulated fertilizer 00-20-20 (N-P₂O₅-K₂O) was used in Sinop and 400 kg ha⁻¹ in Sorriso. Urea (45 kg ha⁻¹) was surface applied on soil 35 days after seedling emergence. The experiments without fertilization were conducted by simply distributing the seeds in the sowing furrows. In Sinop, sowing was carried out on 8th March 2019 and 13th March 2020, and in Sorriso on 9th March 2019 and 6th March 2020. Average precipitation during the crop cycle in Sinop was 347 and 438 mm in 2019 and 2020, respectively, and 234 and 318 mm in Sorriso. Insecticide was applied whenever the insect infestation caused approximately 5% damage to mungbean plants. Weeds were eliminated using hand hoes. Fungicides were not applied during the development of mungbean plants.

The experiments were carried out in a complete randomized block design with three repetitions. Each plot had two 3 m-long rows, spaced 0.5 m apart, with a rate of 18 seeds/m along the rows. Before harvesting, values for cultivation (VC) of each genotype were determined

visually by taking into account the general conditions of the plants (i.e., pod and seed characteristics, pod loading, phytosanitary aspects, plant size, and lodging) based on Silva et al. (2018). VC scores were attributed as follows: 1 - no desired traits, 2 - few desired traits, 3 - many desired traits, 4 - most of the desired traits, and 5 - all desired traits. Yield (g m⁻²) was determined by weighing the total mass of grains produced in each of the plots and the values were subsequently extrapolated to kg ha⁻¹. The mass of 100 grains (g) was also determined for each plot.

The assumptions of normality of errors and homogeneity of variance were tested (Ramalho; Ferreira; Oliveira, 2012) before subjecting the data to analysis of variance (ANOVA) using GENES software (Cruz, 2013). The mean values of the agronomic characteristics (yield, mass of 100 grains, and VC scores) of genotypes were compared using Tukey test at 5% probability.

Initially, individual ANOVA was performed for each environments and year of study, following the statistical model presented in Equation 1.

$$Y_{ij} = m + t_i + r_j + e_{ij} \quad (1)$$

in which Y_{ij} is the value obtained for the plot planted with genotype i within block j , m is the average value of the experiment, t_i is the effect of treatment related to genotype i ($i = 1, 2, 3, \dots, 11$), r_j is the effect of block j ($j = 1, 2, \text{ and } 3$), and e_{ij} is the experimental error associated with the observation Y_{ij} , assuming that the errors were independent and normally distributed with a mean of zero and variance σ_e^2 .

Subsequently, combined ANOVA was performed for each variable considering the eight environments and using a fixed effect model for genotypes and a random effect model for environments (Equation 2).

$$Y_{ijk} = m + t_i + b_{(j)k} + a_k + (ta)_{ik} + \bar{e}_{jki} \quad (2)$$

in which, Y_{ijk} is the value obtained for the plot planted with genotype i within block j and environment k , m is the average value of the experiment, t_i is the effect of treatment related to genotype i ($i = 1, 2, 3, \dots, 11$), $b_{(j)k}$ is the effect of the block j ($j = 1, 2, \text{ and } 3$) within environment k ; a_k is the effect of the environment k ($k = 1, 2, \dots, 8$), $(ta)_{ik}$ is the effect of the interaction between genotype i and environment k , and \bar{e}_{jki} is the experimental error associated with observation Y_{ijk} assuming that the errors were independent and normally distributed with a mean of zero and variance σ_e^2 .

When the ratios between the largest and smallest mean squared residual values obtained in the individual analyses were greater than seven (Pimentel-Gomes, 2009), the method described by Cochran (1954) was used to adjust the degrees of freedom of residues and to enable the inclusion of all eight environments in the combined analysis. Thus, the possible effects of environmental heterogeneity on the significance were minimized by adjusting the degrees of freedom of residues and interactions.

The adaptability and stability of production were assessed using the method described by Lin and Binns (1988) with modifications (Cruz; Carneiro, 2006). The P_i index was submitted to decomposition analysis to identify the genotypes that better suited favorable (P_{ij}) and unfavorable (P_{ii}) environments. The environmental indices, the genetic and interaction deviations, and the contribution of genotype \times environment interactions were estimated as proposed by Cruz and Carneiro (2006).

RESULTS AND DISCUSSION

Individual ANOVA tests showed differences ($P < 0.05$) in the genotypic source of variation concerning yield in the Sinop2020WF environment and all four environments in Sorriso (Table 2). The mean yield of genotypes in Sinop was generally lower than in Sorriso, indicating that the Sinop environments were less favorable to mungbeans. In addition, the lower yield in

Sinop may be attributed to the conventional soil tillage employed and to the high rainfall events during the first three days after sowing in both years. These factors hampered germination and seedling emergence, thereby reducing stand and yield.

The mass of 100 grains differed among genotypes ($P < 0.01$) in all eight environments (Table 2), ranging from 4.98 g (Sorriso2020NF) to 6.38 g (Sinop2019WF). On average, grains of the evaluated genotypes were within the standard of commercial cultivars (Vieira et al., 2002; Vieira et al., 2008; Khattak et al., 2021; Kim et al., 2020;). Regarding the VC scores, there were significant differences ($P < 0.05$) among the tested genotypes in Sinop2020WF and in all four Sorriso environments (Table 2).

Combined ANOVA showed differences ($P < 0.01$) in the genotypic source of variation for the three traits evaluated (Table 3), suggesting that it is possible to select genotypes suitable for the growing conditions in Mato Grosso. The genotype \times environment interactions were significant ($P < 0.05$) only for yield, indicating that the genotypes presented different responses in the experimental environments. Although the occurrence of genotype \times environment interactions in mungbean has been previously reported (Thangavel; Anandan; Eswaran, 2011; Asfaw et al., 2012; Win et al., 2018; Samyuktha et al., 2020), this is the first study evaluating these interactions in the state of Mato Grosso, Brazil.

Table 2: Means, coefficients of variation (CV), and probabilities (P value) for the genotypic source of variation obtained in the individual analysis of variance for grain yield, mass of 100 grains, and value for cultivation (VC) of 11 mungbean genotypes grown in eight environments in Sinop and Sorriso, Mato Grosso, Brazil, in 2019 and 2020.

Environment ¹	Yield (kg ha ⁻¹)			Mass of 100 grains (g)			VC (score)		
	Mean value	CV %	P value	Mean value	CV %	P value	Mean value	CV %	P value
Sinop2019WF	899	26.35	0.082	6.38	5.98	0.000	2.86	19.19	0.263
Sinop2019NF	576	32.01	0.097	6.16	8.81	0.000	2.46	27.27	0.239
Sinop2020WF	895	27.12	0.012	5.44	8.49	0.000	3.09	9.59	0.000
Sinop2020NF	781	47.41	0.293	5.36	8.55	0.002	2.98	21.74	0.283
Sorriso2019WF	1464	10.17	0.000	5.21	3.87	0.000	3.95	7.19	0.000
Sorriso2019NF	851	15.82	0.006	5.13	3.86	0.000	3.19	9.81	0.000
Sorriso2020WF	2055	11.39	0.001	5.36	9.24	0.004	3.33	8.69	0.000
Sorriso2020NF	1656	16.22	0.048	4.98	6.06	0.000	3.21	10.28	0.001

¹ Description of environments is available in Table 1.

Table 3: Summary of combined ANOVA of the grain yield, mass of 100 grains, and value for cultivation (VC) of 11 mungbean genotypes grown in eight different environments in Sinop and Sorriso, Mato Grosso, Brazil, in 2019 and 2020.

Source of variation	DF ¹	Mean square yield	DF ¹	Mean square 100-grain mass	DF	Mean square VC
Block within environment	16	469732.67	16	0.295	16	0.535
Genotype	10	599283.60**	10	8.044**	10	3.619**
Environment	7	8753011.99**	7	8.239**	7	5.946**
Genotype × environment interactions	53	115752.57*	55	0.214 ^{ns}	70	0.157 ^{ns}
Mean Error	115	78904.97	122	0.209	160	0.204
Mean		1147		5.50		3.13
CV% ²		24.48		8.32		14.41

¹Degrees of freedom were adjusted using the Cochran (1954) method; ² Coefficient of variation; ^{ns} not significant, * significant at 5% probability, and ** significant at 1% probability according to *F* test

The mean yield of genotype G4 (1305 kg ha⁻¹) was higher compared with the genotypes G1, G7, and G9 (Table 4). However, the yields of the other seven genotypes were higher than 1150 kg ha⁻¹ indicating good yield potential for cultivation in the mid-north of Mato Grosso, with averages above 1000 kg ha⁻¹. In Mato Grosso, yield estimates for mungbean grown in the off-season ranged from 298.40 kg ha⁻¹ to 1163 kg ha⁻¹ (Menezes Júnior; Silva; Rocha, 2019). It is noteworthy that yield in the Sorriso2020WF environment was 2055 kg ha⁻¹, demonstrating that the genotypes respond to the improvement of the environment.

Besides high yield, genotypes G10, G4, G2, G5, and the control G11 had a mass of 100 grains above 5.5 grams (Table 4). Moreover, the mass of 100 grains of G10 (6.56 g) stood out, higher than that of other genotypes (Table 4). Grain size is important for the commercial acceptance of a mungbean cultivar and, in Brazil, successful cultivars such as MGS Esmeralda exhibit masses of 100 grains ranging from 5.5 to 6.8 g (Vieira et al., 2008).

For cultivation value, G6 had the highest average score (3.56), similar to other six genotypes (Table 4). G6 is the only genotype with yellow seed coat color and also showed high productivity (1162 kg ha⁻¹) and mass of 100 grains. Thus, G6 is promising for cultivation in the mid-north region of Mato Grosso, Brazil. The market for green seed coat grains is most common for mungbean. However, yellow seed coat cultivars have been selected for regions with a preference for this grain color (Biswas et al., 2016; Kim et al., 2019; Kim et al., 2020). Exception for G9, the VC scores of the genotypes were equal to or greater than three (Table 4), which corresponds to most of the traits suitable for commercial cultivation.

Table 4: Means of yield, mass of 100 grains, and value for cultivation (VC) of 11 mungbean genotypes grown in eight environments in Sinop and Sorriso, Mato Grosso, Brazil, in 2019 and 2020.

Treatment (genotype)	Yield ¹ (kg ha ⁻¹)	Mass of 100 grains ¹ (g)	VC ¹ (score)
G1 (BRA-084638)	1048 b	5.44 de	3.20 ab
G2 (BRA-08654-1)	1239 ab	5.71 cd	3.06 b
G3 (BRA-084671)	1204 ab	5.14 ef	3.00 b
G4 (BRA-000027)	1305 a	5.96 bc	3.35 ab
G5 (BRA-084654-2)	1216 ab	5.69 cd	3.02 b
G6 (BRA-084689)	1162 ab	5.38 de	3.56 a
G7 (BRA-084930)	1057 b	4.63 g	3.22 ab
G8 (BRA-084981)	1161 ab	5.00 fg	3.35 ab
G9 (BG2)	734 c	4.88 fg	2.08 c
G10 (BG3)	1250 ab	6.56 a	3.35 ab
G11 (control)	1243 ab	6.13 b	3.29 ab

¹Significant differences among treatments, using Tukey test at the 5% level of significance, are indicated by letters.

Based on the results of the adaptability and stability analysis, the G4 genotype presented the lowest estimate of overall P_i (Table 5). The G2 and G10 genotypes also showed low P_i estimates, indicating good adaptability of these genotypes to the evaluated environments. In addition, these three genotypes had the highest grain yield means. The combination of low P_i index and high yield has been reported previously (Cruz; Carneiro, 2006), including a study with cowpea lines in Mato Grosso, Brazil (Alves et al., 2020).

Decomposition of the P_i indices into the genetic and interaction components revealed that genetic deviation contributed substantially ($> 50\%$) to the magnitude of the P_i values of all genotypes except for the control G11 (Table 5). According to Daros and Amaral Júnior (2000), the combination of low P_i index with a high percentage of genetic deviation is an important criterion for the selection of genotypes. On this basis, G4, G2, and G10 are the most promising genotypes for cultivation in the mid-north of Mato Grosso, since they showed high mean yield and low percentage contributions to the genotype \times environment interactions.

As shown by the mean environmental indices (Table 6), all four Sinop environments were classified as unfavorable (negative values) regardless of the application of fertilizer. In contrast, three of the four Sorriso environments were classified as favorable (positive indices). By the minimum and maximum values, one can see the divergence between the genotypes for yield. The lowest yield amplitude was observed in Sinop2019NF (461 kg ha⁻¹), whereas the largest was recorded in Sorriso2020WF (997 kg ha⁻¹). The practical meaning of these results is that the most productive genotype yielded approximately 1000 kg ha⁻¹ more than the least productive. In general, the yield amplitude in fertilized environments was higher in comparison with

those cultivated in the absence of fertilizer, suggesting that the tested genotypes responded well to the environmental improvement.

Table 7 shows the adaptability and stability indices of the tested genotypes under environments considered favorable and unfavorable. G10 had the lowest P_{if} index and was, therefore, the most adaptable to favorable environments. G2, G4, and G6 also exhibited low P_{if} indices. Our results suggest that these four genotypes were the most responsive to environmental improvement. G4 showed the lowest P_{iu} index (22.03), indicating that this genotype has good production performance in unfavorable environments (Table 7). G3 and G5 combined high yield and good adaptability under unfavorable environments, indicating a stable behavior in the evaluated environments.

The method proposed by Lin and Binns (1988) with modifications (Cruz; Carneiro, 2006) allowed efficient identification of the most adaptable genotypes for cultivation under favorable and unfavorable environments. Pereira et al. (2009) have previously highlighted that the method is simple whilst allowing straightforward interpretation of the results and logical classification of genotypes. This methodology is commonly used in research with other types of beans, such as common bean and cowpea (Ribeiro et al., 2008; Pereira et al., 2009; Silva et al., 2013; Alves et al., 2020).

Table 5: Mean yield, adaptability and stability indices (P_i) of mungbean genotypes grown in eight environments in Sinop and Sorriso, Mato Grosso, Brazil, in 2019 and 2020.

Genotype	Mean yield (kg ha ⁻¹)	Overall $P_i^1/1000$	Genetic deviation/1000	Interaction deviation/1000	Genetic deviation (%)	Contribution to the interaction (%)
G1 (BRA-084638)	1048	91.88	83.14	8.74	90.48	4.39
G2 (BRA-08654-1)	1239	36.20	23.55	12.65	65.03	6.35
G3 (BRA-084671)	1204	41.84	31.84	10.00	76.08	5.02
G4 (BRA-000027)	1305	20.38	11.45	8.93	56.16	4.48
G5 (BRA-084654-2)	1216	54.00	28.75	25.25	53.23	12.67
G6 (BRA-084689)	1162	65.38	43.24	22.14	66.13	11.11
G7 (BRA-084930)	1057	105.99	79.57	26.42	75.06	13.26
G8 (BRA-084981)	1161	65.59	43.50	22.09	66.32	11.08
G9 (BG2)	734	276.15	260.28	15.87	94.25	7.97
G10 (BG3)	1250	36.40	21.15	15.25	58.10	7.65
G11 (control)	1243	54.54	22.61	31.93	41.46	16.02

¹ P_i was calculated according to the method described by Lin and Binns (1988) with modifications (Cruz; Carneiro, 2006).

Table 6: Environmental indices and yield of mungbean genotypes grown in eight environments in Sinop and Sorriso, Mato Grosso, Brazil, in 2019 and 2020.

Environment ¹	Mean environmental index	Yield (kg ha ⁻¹)			
		Mean	Minimum	Maximum	Amplitude
Sinop2019WF	-248	899	578	1227	649
Sinop2019NF	-572	576	366	827	461
Sinop2020WF	-252	895	460	1341	881
Sinop2020NF	-366	781	498	1262	764
Sorriso2019WF	317	1464	913	1774	861
Sorriso2019NF	-296	851	477	993	516
Sorriso2020WF	908	2055	1411	2408	997
Sorriso2020NF	509	1656	1020	1816	796
Mean	-	1147	-	-	-

¹Description of environments is available in Table 1.

Table 7: Adaptability and stability indices under favorable (P_{if}) and unfavorable (P_{iu}) environments of the mungbean genotypes grown in eight environments in Sinop and Sorriso, Mato Grosso, Brazil, in 2019 and 2020.

Genotype	$P_{if}/1000$	$P_{iu}/1000$
G1 (BRA-084638)	95.73	89.58
G2 (BRA-08654-1)	9.27	52.35
G3 (BRA-084671)	38.13	44.06
G4 (BRA-000027)	17.64	22.03
G5 (BRA-084654-2)	67.88	45.68
G6 (BRA-084689)	9.90	98.67
G7 (BRA-084930)	103.03	107.76
G8 (BRA-084981)	33.65	84.75
G9 (BG2)	394.84	204.94
G10 (BG3)	2.98	56.44
G11 (control)	9.73	81.42

From the field evaluations, the genotypes had a short cycle and high productivity in the mid-north region of Mato Grosso, Brazil. Even in environments without any fertilizer application and sowing at the end of the rainy season (March), yields above 1000 kg ha⁻¹ were obtained (Table 6). It was possible to identify genotypes with stable behavior, good adaptability to unfavorable environments, and that respond to environmental improvement. In general, the genotypes are promising for further experiments testing the value for cultivation and use.

CONCLUSIONS

Genotypes G2 (BRA-08654-1), G4 (BRA-000027), G5 (BRA-084654-2), and G10 (BG3) combine high yield and large grains. These four genotypes show good general adaptability for cultivation in the mid-north region of Mato Grosso, Brazil. The yellow grain genotype G6 (BRA-084689) also shows high productivity and good adaptability in this region. Genotypes BRA-08654-1, BRA-000027, BRA-084654-2, BRA-084689, and BG3 are indicated for further experiments evaluating cultivation value and use.

AUTHOR CONTRIBUTION

Conceptual idea: Menezes Júnior, J.A.N.; Silva, K.J.D.; Methodology design: Menezes Júnior, J.A.N.; Olibone, D.; Data collection: Menezes Júnior, J.A.N.; Noleto, M.P.; Olibone, D.; Gobbi, S.D.; Pivetta, L.G.; Data analysis and interpretation: Menezes Júnior, J.A.N.; Noleto, M.P.; Pivetta, L.G., and Writing and editing: Menezes Júnior, J.A.N.; Noleto, M.P.; Gobbi, S.D.; Olibone, D.; Pivetta, L.G.; Silva, K.J.D.

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