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Agronomic characterization and interaction of genotype by environment of quinoa under conditions of Brazil and Colombia

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ABSTRACT

Quinoa is a highly adaptable crop due to its considerable genetic variability, making it an important trait for cultivation under different soil and climatic conditions. To achieve crop-wide adaptation, it is essential to identify variability based on morpho-agronomic differences and genotype x environment (GxE) interaction. This study aimed to characterize eight quinoa progenies in Brazil and Colombia. The experiments in Brazil were conducted in an irrigated area of the Fazenda Água Limpa, Universidade de Brasília, at 1,100 m, on two dates: March to July 2018 and May to August 2019. In Colombia, experiments were carried out in Santander de Quilichao and Popayán at 1,100 and 1,800 m, respectively. The treatments consisted of five progenies selected in Brazil, one from Colombia, and two from Ecuador. The experiments followed a complete randomized block design, with eight progenies and four replications. For statistical analysis, the F test was used with $p \leq 0.01$ and $p \leq 0.05$. Means were grouped by the Scott-Knott test. The AMMI (Additive Main effects and Multiplicative Interaction) analysis was performed, combining analysis of variance and analysis of principal components, to adjust the main effects of genotypes (G) and environments (E) and the GxE interaction. Significant differences were found at $p \leq 0.01$ and $p \leq 0.05$ for environments, genotypes, and the interaction of GxE. The progenies with wide adaptation to environments were BRX2, BRX5, BRX6 (selected from BRS Syetetuba) and PRIX (selected from Piartal), with average yields above 3,151.95 kg/ha. The genotypes showed differences at the same location in different periods, expressing the need to carry out selection for specific periods and locations. Genotypes BRX5 and BRX6 showed high agronomic potential in all evaluated environments, being promising for future genetic improvement programs.

Keywords: *Chenopodium quinoa*, AMMI, adaptation, selection, tropicalized quinoa.

RESUMO

Caracterização agrônômica e interação genótipo ambiente de quinoa nas condições do Brasil e da Colômbia

A quinoa é uma cultura altamente adaptável devido à sua considerável variabilidade genética, tornando-se uma característica importante para cultivo em diferentes condições edafoclimáticas. Para conhecer a adaptação da cultura, é essencial identificar a variabilidade com base nas diferenças morfo-agronômicas e interação genótipo x ambiente (GxE). Este estudo teve como objetivo caracterizar oito progênies de quinoa no Brasil e na Colômbia. Os experimentos no Brasil foram conduzidos em área irrigada da Fazenda Água Limpa, Universidade de Brasília, a 1.100 m, em duas datas: março a julho de 2018 e maio a agosto de 2019. Na Colômbia, os experimentos foram realizados em Santander de Quilichao e Popayán a 1.100 e 1.800 m, respectivamente. Os tratamentos consistiram de cinco progênies selecionadas no Brasil, uma da Colômbia e duas do Equador. Os experimentos seguiram o delineamento em blocos casualizados, com oito progênies e quatro repetições. Para análise estatística foi utilizado o teste F com $p \leq 0,01$ e $p \leq 0,05$. As médias foram agrupadas pelo teste de Scott-Knott. Foi realizada a análise AMMI (Additive Main effects and Multiplicative Interaction), combinando análise de variância e análise de componentes principais, para ajustar os principais efeitos dos genótipos (G) e ambientes (E) e da interação GxE. Diferenças significativas foram encontradas em $p \leq 0,01$ e $p \leq 0,05$ para ambientes, genótipos e interação GxE. As progênies com ampla adaptação aos ambientes foram BRX2, BRX5, BRX6 (selecionadas em BRS Syetetuba) e PRIX (selecionadas em Piartal), com rendimentos médios acima de 3.151,95 kg/ha. Os genótipos apresentaram diferenças no mesmo local em diferentes períodos, expressando a necessidade de realização de seleção para períodos e locais específicos. Os genótipos BRX5 e BRX6 apresentaram elevado potencial agrônômico em todos os ambientes avaliados, sendo promissores para futuros programas de melhoramento genético.

Palavras-chave: *Chenopodium quinoa*, AMMI, adaptação, seleção, quinoa tropicalizada.

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Quinoa is native to and has been cultivated for many years in South America and is now gaining popularity in other regions due to its exceptional nutritional value, with its high-quality

protein, containing essential amino acids, micronutrients, vitamins, minerals, and phenolic compounds (Pereira *et al.*, 2019). Additionally, it is adaptable to a range of climatic

conditions, making it a resilient crop. Quinoa is known to tolerate high salinity and to be grown in regions with a wide range of environmental variations, which makes it a promising crop in

areas with limited water resources and soils with high salinity (Anchico *et al.*, 2020; Zurita-Silva *et al.*, 2014).

Peru and Bolivia have been the main producers of quinoa, followed by Ecuador and Argentina (Perez-Rea & Antezana-Gomez, 2018). Due to genetic variability, quinoa may exhibit different physicochemical, antioxidant, and agronomic characteristics (Anchico-Jojoa *et al.*, 2023).

Research conducted at different locations and dates has shown that quinoa exhibits a strong genotype by environment interaction (GxE) for grain yield, dry mass yield, harvest index, grain size, grain weight, and phenological cycle (Ali *et al.*, 2018; Curti *et al.*, 2014). For instance, Bertero *et al.* (2004) evaluated the effects of genotype (G) and genotype by environment interaction (GxE) on grain yield, its physiological determinants, and grain size of quinoa, involving a diverse set of 24 cultivars tested at 14 locations under irrigation across three continents. The observed GxE interaction effects throughout the crop cycle had a significant influence on the average performance of cultivars and the patterns of interactions (GxE) observed for biomass and grain yield. On the other hand, Curti *et al.* (2014) assessed grain yield, its determinants, physiological components, and flowering days for 12 genotypes in six environments in Argentina. The results showed significant GxE interaction for grain yield, harvest index, and the number of grains. Additionally, Ali *et al.* (2018) conducted evaluations of five quinoa genotypes in ten environments, including irrigated and

rained conditions in Egypt. The results indicated significant interaction for grain yield, plant height, dry mass yield, grain size, and harvest index. They also determined the stability of genotypes in each location. Thiam *et al.* (2021) evaluated the adaptation of 14 quinoa varieties and lines from four different origins through 14 agromorphological traits at five contrasting agroclimatic locations in central Morocco. They found significant GxE interaction for grain yield, harvest index, 1000-grain weight, and tolerance to downy mildew caused by *Peronospora farinosa*. The high GxE interactions found in diverse environments have influenced the processes of advancing quinoa breeding (Bertero *et al.*, 2004). When different genotypes are evaluated in different environments, subsets can be formed between environments and genotypes to establish selection processes for specific conditions (Curti *et al.*, 2014).

The quinoa genetic variability is considered a critical characteristic for selecting and cultivating it in various regions and climatic conditions (Rezzouk *et al.*, 2020). The use of different genotypes allows quantifying intraspecific variability for different morpho-agronomic characters and their interactions. Genetic variability makes it possible to determine selection limits to obtain genotypes with desirable quality (Santis *et al.*, 2016). However, detailed research on quinoa variability concerning morpho-agronomic and qualitative aspects, as well as genotype by environment interaction, is necessary. This study aims to perform the morpho-agronomic characterization of eight quinoa progenies in Brazil and Colombia

for adaptability and interaction under conditions of 1,100/1,800 m in Colombia and 1,100 m altitude in Brazil.

MATERIAL AND METHODS

Experiment in Brazil

The experiments were conducted at Fazenda Água Limpa (FAL), Universidade de Brasília (UnB), in Distrito Federal (15°56'S, 47°55'W; 1,100 m altitude) and an Aw climate according to the Köppen classification. The climate features a rainy season from October to March and a dry season from April to September (Kottek *et al.*, 2006). Two cycles of quinoa were evaluated, the first from March to July 2018 and the second from May to August 2019, both irrigated. Soil water tension was maintained at 30-40 kPa, and it was monitored by tensiometers placed at 0-30 cm depth in the soil. Temperature and precipitation during the experimental cycles are described in Table 1.

Experiments in Colombia

In Colombia, two experiments were conducted. The first one took place from February to June 2020 in the Municipality of Popayán, Cauca (2°27'N, 76°37'W; 1800 m altitude). It had an average temperature of 19°C. The second experiment was conducted from March to July 2020 in the Municipality of Santander de Quilichao (3°0'N, 76°29'W; 1100 m altitude). It presented an average temperature of 26°C. Temperature and precipitation during the experimental cycles are described in Table 1.

Table 1. Temperature and precipitation in the cycles of quinoa, in Santander de Quilichao and Popayán – Colombia, 2020 and Fazenda Água Limpa, University of Brasília – Brazil, 2018/2019. Brasília, UnB, 2018-2020.

Environment	T (°C)	P (mm)						
	Month 1		Month 2		Month 3		Month 4	
location 1	24.2	212.0	24.6	138.0	24.2	189.0	24.3	138.0
location 2	19.0	361.5	19.7	289.0	19.0	317.5	19.2	142.0
location 3	22.8	251.2	22.3	143.0	20.8	58.2	18.2	0.5
location 4	19.9	58.2	17.7	0.5	16.7	0.0	19.3	0.0

¹T: Average ambient temperature; P: precipitation. ²Location 1: Santander de Quilichao - Colombia, 2020 (1,100 m altitude); Location 2: Popayán - Colombia, 2020 (1,800 m altitude); Location 3: Brasília - Brazil, 2018 (1,100 m altitude); Location 4: Brasília - Brazil, 2019 (1,100 m altitude).

Experimental design

The experiments were conducted in a randomized block design, with 8 genotypes and 4 replicates for the 4 environments. The useful area of each plot was 1 m², with 60 plants. The soil was prepared 30 days before sowing with the application of organic fertilizer and lime. Planting and topdressing fertilizations at each location and year of cultivation were performed according to soil analysis (Table 2) and following Spehar's *et al.* (2011) recommendations, 60 kg/ha N, 60 kg/ha P, and 60 kg/ha of K.

Statistical analyses

The original data was subjected to the analysis of variance using the F-test at a $p \leq 0.05$ level, and the means were grouped using the Scott-Knott test with the SISVAR® software. In addition, the AMMI analysis (Additive Main effects and Multiplicative Interaction) was used, which combines the analysis of variance and principal component analysis to adjust the main effects of genotypes (G) and environments (E), as well as the effects of the GxE interaction (Varela & Castillo, 2005).

Evaluated progenies

BRS Syetetuba, average weight of 1,000 grains of 2.5 g and 3.3 g in summer and winter crops, respectively, containing up to 18 g/100 g of protein (Spehar *et al.*, 2011). The quinoa progenies used in this experiment, selected from this cultivar, were: BRX 1, BRX 2, BRX 5, BRX 6, and BRX 4 [BRS Syetetuba (control)] (Anchico *et al.*, 2020).

Piartal presents adaptability in locations between 2,400 and 3,200 m altitude. The plant has a purple color, reaches 240 cm height, and is susceptible to mildew. The grain is opaque white, with an approximate diameter of 2 mm (Alvarez *et al.*, 1990). The progeny PR1X was used in this experiment (Anchico *et al.*, 2020).

Aurora is adapted to altitudes between 2,300 and 3,000 m, with plant heights ranging from 90 to 130 cm and a yield of 1,800 to 2,400 kg/ha. The seeds are small and white, with a diameter of less than 2 mm (Sañudo, 2005). The progeny used in this experiment was AURX (Anchico *et al.*, 2020).

Tunkahuan is adapted to altitudes up to 3,000 m, similar to Aurora. In Colombian areas, it presents 144 cm height, with a cycle of 150 to 210 days, purple color, and yellow-orange glomerulate panicle, white grain, grain size ranging from 1.7 to 2.1 mm, low saponin content of 0.06%, and 15.73% protein with an average yield of 2,200 kg/ha (Nieto, 1992). The progeny used in this experiment was TUNK (Anchico *et al.*, 2020).

Agronomic assessments

Plant height: measurement from ground level to the apex of the inflorescence (cm), in 10 randomly sampled plants per plot, before harvesting. For the remaining plants, height was measured by sighting from the center of the plot using a measuring tape.

Panicle length: 10 plants were used to evaluate the panicles, measured from the apex of the main panicle to the base

of insertion. Results were expressed in cm/panicle.

Dry matter yield: the plants cut at their base were placed in woven polypropylene bags, kept open and suspended until they reached a constant weight, evaluated by sample weighing of the entire aboveground part, with values expressed in kg/ha.

Harvest index (HI): determined by dividing the grain yield per plant by the aboveground biomass per plant (dry mass of plants). Results were expressed as percentage.

Weight of 1000 grains: a defined methodology for quinoa (Souza *et al.*, 2017) was used, evaluating eight replicates of 100 seeds. The weight of thousand seeds can vary depending on the moisture content. Thus, 100 seeds were randomly collected with eight replicates. The seeds from each replicate were weighed on a precision scale of 0.001 g. Variance, standard deviation, and coefficient of variation of the obtained values were calculated from the measurements. Results were expressed in grams.

Grain yield: After being air-dried in a shaded and ventilated environment, the panicles were subjected to mechanical threshing, and the seeds were cleaned using sieves and a fan, keeping them in paper bags. Before weighing, the water content was determined and adjusted to 13%. The mass of the grains was determined using a precision balance at 0.001 g, and the results were expressed in g/plant and later extrapolated to kg/ha.

RESULTS AND DISCUSSION

The analysis of variance demonstrated significant differences ($p \leq 0.05$) between environments, genotypes, and the genotype x environment interaction in the agronomic traits evaluated (Table 3). Quinoa progenies presented variability in all locations, demonstrating their potential to adapt to different environments (Anchico *et al.*, 2020). The genotype x environment interaction, when compared to genotype, showed a variance ratio of 14:1 in plant height evaluation (PH), 1.5:1 in panicle length (PL), 2:1 in grain yield (GY), 3:1 in dry

Table 2. Results of soil analysis in the experimental area at four evaluation sites at a depth of 0-20 cm. Brasília, UnB, 2018-2020.

Location	pH	P (mg/dm ³)	Al	Ca	Mg	K
			(meq/100g)			
Brazil						
2018, 1100m	5.50	2.2	0.0	3.2	1.3	0.46
2019, 1100m	5.20	4.0	0.0	1.8	0.8	0.20
Colombia						
S. Quilichao, 1100 m	4.87	2.30	2.20	1.95	0.85	0.25
Popayán, 1800 m	5.74	3.16	0.20	5.02	0.87	0.22

matter yield (DM), 3:1 in 1,000-grain weight (WTG), and 1:1.2 in harvest index (HI) (Table 3).

Yield components such as grain yield (GY) and harvest index (HI) showed a strong relationship between genotype x environment interaction and genotype component (Table 3). Bertero *et al.* (2004) found similar data in studies carried out with 24 genotypes in 14 environments. Significant interaction between genotypes and environments was found in the evaluation of grain yield, and this data is recurrent in different studies of genotype adaptation processes to different environments (Santis *et al.*, 2016). The constant presence of genotype x environment interactions in quinoa highlights the need to structure breeding strategies that allow obtaining genotypes adapted to specific regions (Curti *et al.*, 2014).

Of all the evaluated traits, only harvest index (HI) presented a lower variance

ratio in the genotype x environment interaction than the genotype component (Table 3). In studies carried out in the Northeast Argentina, higher genotype x environment interaction relationships were found on the genotype evaluation of traits such as grain yield, harvest index, and number of grains (Curti *et al.*, 2014).

The Scott-Knott test, with $p \leq 0.05$, determined the significant differences observed when grouping the means of the variables in different locations (Table 4). For the plant height (PH) characteristic, the mean was 137.70 cm, with location 2 standing out at 161.46 cm. The panicle length (PL) presented mean values of 31.49 cm, with location 4 being the most suitable, with 34.24 cm. For the grain yield (GY) and dry mass yield (DM) characteristics, the means were 2,956.29 kg/ha and 9,882.20 kg/ha, respectively, with location 2 showing the highest values at 5377.69 kg/ha and

15468.62 kg/ha, respectively (Table 4). The mean weight of 1000 grains (WTG) was 2.55 g, with location 3 being the most representative for this characteristic at 2.73 g. However, the lowest values were observed in location 4, probably due to high temperature conditions, a factor that influences grain size (Maliro *et al.*, 2017).

The harvest index (HI) had mean values of 29.45%, with location 2 standing out at 34.66% (Table 4). According to the data (Table 4), location 2 (Fazenda Água Limpa, 2019) presented the highest values for the following characteristics: PH, GY, DM, and HI. These results can be explained, in part, by the irrigation carried out during the planting cycle, which can help reduce heat stress and its use in critical growth stages, such as germination, initial flowering, and seed formation, which would help ensure maximum yield (Walters *et al.*, 2016). In addition, water supply through irrigation leads to stability in quinoa grain yield (Maliro *et al.*, 2017).

In all four locations, the eight progenies demonstrated satisfactory performance in terms of their agronomic characteristics, possibly due to selection that capitalized on the existing genetic variability in the genotypes (Jojoa *et al.*, 2021; Anchico-Jojoa *et al.*, 2021). The genotypes displayed PH values ranging from 115.68 cm to 149.82 cm, corresponding to BRX 1 and PRIX, respectively (Table 5).

The PRIX genotype had the highest values for PL (34.98 cm) and the lowest value was from BRX5 with 28.89

Table 3. Analysis of variance of agronomic traits of quinoa genotypes at the four experimental sites. Brasília, UnB, 2018-2020.

Characteristic	Mean values	Environment	Genotype	Genotype x Environment
		F	F	F
PH (cm)	137.7	181.409*	38.253*	2.723*
PL (cm)	31.49	77.799*	19.156*	12.931*
GY (kg ha ⁻¹)	2956.29	69367.982*	535.701*	264.544*
DM (kg ha ⁻¹)	9882.2	4157.095*	413.434*	133.055*
WTG (g)	2.55	525.742*	19.657*	5.762*
HI (%)	29.45	2763.644*	131.295*	163.270*

*Significant in the F test at $p \leq 0.05$. PH: plant height; PL: panicle length; DM: dry mass yield; GY: grain yield; WTG: weight of 1000 grains; HI: harvest index.

Table 4. Scott-Knott grouping test of the four experimental sites in the evaluation of quinoa agronomic characteristics. Brasília, UnB, 2018-2020.

Id	Environment	PH (cm)	PL (cm)	GY (kg/ha)	DM (kg/ha)	WTG (g)	HI (%)
1	FAL1/2018	112.63 c	31.70 b	2,485.15 b	8,752.11 c	2.54 c	28.65 c
2	FAL2/2019	161.46 a	29.72 c	5,377.69 a	15,468.62 a	2.69 b	34.66 a
3	Popayán.	140.23 b	30.29 c	1,971.35 c	5,983.33 d	2.73 a	32.73 b
4	S. Quilichao.	136.47 b	34.24 a	1,990.97 c	9,324.76 b	2.24 d	21.75 d
Mean		137.7	31.49	2956.29	9882.2	2.55	29.45
CV (%)		6.1	4.11	1.19	3.55	2.14	2.09

Mean followed by the same letters in each column do not differ from each other by the Scott-Knott Test at $p \leq 0.05$. PH: plant height; PL: panicle length; DM: dry mass yield; GY: grain yield; WTG: weight of 1000 grains; HI: harvest index. CV (%): Coefficient of variation.

cm (Table 5). All genotypes showed yield values above 2,000 kg/ha, with BRX6 and BRX2 standing out with 3,480.70 kg/ha and 3,465.13 kg/ha, respectively (Table 5). Referencing the comparison of grain yield between BRX 4 (control) and the selected genotypes from BRS Syetetuba, it can be stated that there were superior results for all the selections (BRX 1, BRX 2, BRX 5, and BRX 6), demonstrating a gain in selection (Table 5). The genotypes showed differences in the same location in different periods, indicating the need to perform selection for specific periods (Soares *et al.*, 2019). Regarding the characteristic DM, the most suitable genotypes were BRX6 with 11,321.57 kg/ha, PRIX with 11,147.04 kg/ha, and BRX5 with 11,097.13 kg/ha. The extreme climatic conditions in which quinoa evolved presumably contributed to the high levels of adaptation to different environments, generated by its characteristic of being an allotetraploid species (Zurita-Silva *et al.*, 2014).

The highest values of WTG were observed in the BRX1 genotype with 2.69 g and BRX6 with 2.66 g (Table 5). BRX2 and AURX genotypes showed the highest HI percentages with 31.43% and 30.83%, respectively (Table 5). Genotypes BRX6, BRX2, BRX5 from Brazil, and PRIX from Ecuador exhibited superior values in most of the evaluated characteristics (Table 5), highlighting their potential adaptability

to different environments. Due to its wide adaptability, quinoa can be grown in unfavorable conditions (Ali *et al.*, 2018).

Analysis of Genotype (G) x Environment (E) interaction by the AMMI model

The GxE interaction, measured by AMMI (Additive Main effects and Multiplicative Interaction Analysis), in the evaluation of grain yield (GY), dry mass yield (DM), harvest index (HI), and weight of 1000 grains (WTG), was followed by a graphical representation (Biplot, Figure 1).

The main components (PC1 and PC2) presented values above 80% of the GxE interaction variance of each characteristic (Figure 1). These component (PC1 and PC2) percentages in each characteristic are relevant as they represent values above 75%. Studies on several crops using the AMMI model have reported values above 80% in the same components (Ceballos-Aguirre *et al.*, 2021).

The biplot of grain yield showed a greater contribution to the interaction at the FAL2 location. This is possibly due to the greater distance found at the end of the vector from the coordinates of its origin point. Additionally, this location provided the highest grain yield (Table 4), indicating a positive correlation in the evaluation of PC1 and PC2 components (Figure 1a). In this

sense, it was confirmed that the variable GY exhibited a strong dependence on environmental conditions, as mentioned by Thiam *et al.* (2021).

The progenies BRX2, BRX5, BRX6, and PRIX exhibited grain yield values above the mean, as evidenced by the angles formed between the genotypes and the environments vectors, which were less than 90° (Figure 1a). It is not always possible to find consistently superior genotypes in all environments when GxE interaction is significant (Wardofa *et al.*, 2019). Nevertheless, the progenies that showed angles larger than 90° (BRX1, TUNX, and AURX) had values below the mean (Figure 1a and Table 5). Additionally, associations between genotypes and environments were identified, with them being located in the same quadrants and positively correlated (Silva & Benin, 2012). Thus, the genotypes BRX6 and PRIX exhibited a positive association with FAL2 and Popayán, while BRX2 and BRX5 showed a positive association with FAL1 and Santander (Figure 1a). In the graphical representation, genotypes with very narrow angles were correlated with each other (Yan & Kang, 2002). In this sense, the angle resulting from the vectors of the progenies BRX2 and BRX5 showed a significant correlation, exhibiting less dissimilarity between them.

A strong positive association between dry matter yield (DM) and

Table 5. Scott-Knott clustering test of eight quinoa genotypes in the evaluation of agronomic characteristics. Brasília, UnB, 2018-2020.

Genotype	PH (cm)	PL (cm)	GY (kg/ha)	DM (kg/ha)	WTG (g)	HI (%)
BRX 1	115.68 d	29.22 c	2,794.40 d	8525.34 d	2.69 a	29.85 c
BRX 2	142.80 b	30.26 b	3,465.13 a	10888.10 b	2.59 b	31.43 a
BRX4 (control)	137.97 b	30.43 b	2,738.17 e	9356.07 c	2.60 b	29.54 d
BRX 5	144.96 b	28.89 c	3,151.95 c	11097.13 a	2.61 b	29.13 e
BRX 6	143.95 b	30.61 b	3,480.70 a	11321.57 a	2.66 a	30.02 c
AURX	123.53 c	34.05 a	2,248.70 g	7283.57 e	2.42 d	30.83 b
PRIX	149.82 a	34.98 a	3,206.65 b	11147.04 a	2.37 d	28.78 e
TUNX	142.88 b	33.44 a	2,564.60 f	9438.82 c	2.48 c	25.97 f
Mean	137.7	31.49	2956.29	9882.2	2.55	29.45
CV (%)	5.55	6.75	2.58	2.94	4.12	1.95

Mean followed by the same letters in each column do not differ from each other by the Scott-Knott Test at $p \leq 0.05$. CV (%): Coefficient of variation. PH: plant height; PL: panicle length; DM: dry mass yield; GY: grain yield; WTG: weight of 1000 grains; HI: harvest index.

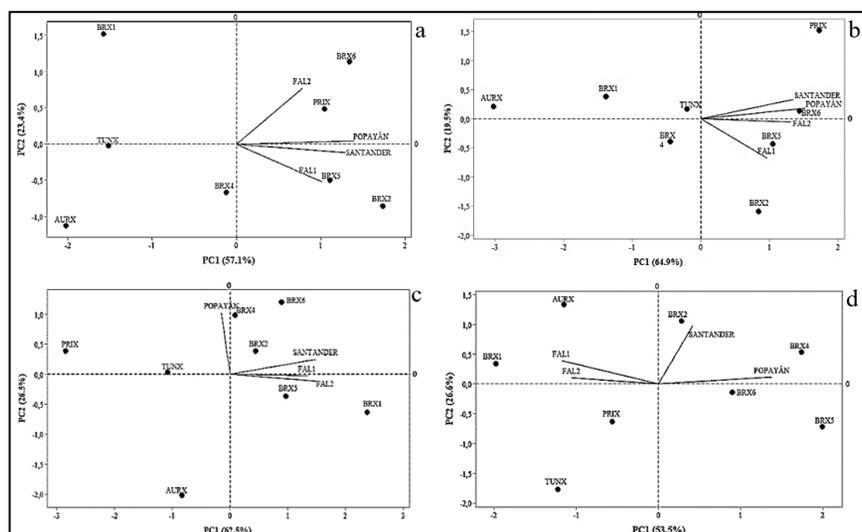


Figure 1. Biplot of principal components (PC1 and PC2) of eight quinoa progenies grown in four locations for: a: grain yield (GY); b: dry mass yield (DM); c: weight of 1000 grains (WTG) and d: harvest index (HI). Progenies are represented by points and environments correspond to vectors. Brasília, UnB, 2018-2020.

BRX6 and Popayán, located in the same sector (Figure 1b) was observed, while BRX5 showed a positive association with the FAL1 and FAL2 locations. The progenies AURX, BRX1, BRX4 (control), and TUNK, located to the left of the biplot center, presented values below the mean, as related by Silva & Benin (2012) (Figure 1b). Considering the resulting angle of the vectors of the progenies BRX6 and BRX5, a significant correlation was observed, exhibiting lower dissimilarity between them in this characteristic (Figure 1b). The grain yield and dry matter yield of AURX were more unstable, confirmed by the greater distance from the biplot center (Figures 1a and 1b).

The biplot (Figure 1c) describes the interactions of the weight of thousand grains characteristic, where the progenies BRX1 and BRX5 exhibit a strong interaction with the FAL2 site, indicated by the narrow angle formed between their vectors. The sites of Santander, FAL1, and FAL2 showed a strong correlation, demonstrated by the angle formed between their vectors (Figure 1c). The control (BRX4) was the most stable due to its location between the two axes of the PC1 and PC2 interaction. The absence of association between environments or genotypes was detected by the right angle between

vectors, and negative association by the obtuse angle (Yan & Kang, 2002). Thus, the progenies BRX1 and PRIX exhibited a strong absence of association in the weight of thousand grains characteristic, as did BRX6 and AURX.

The harvest index (HI) showed variability among locations and progenies, demonstrating sensitivity to plant cycle and environmental conditions (Bertero & Ruiz, 2010). In the HI biplot, low association between locations in Brazil and Colombia was confirmed by the vectors with angles greater than 90° (Figure 1d). Progenies AURX and BRX1 showed positive association in locations FAL1 and FAL2. Genotype BRX2 presented positive association with Santander, while BRX6 and BRX4 (control) were associated with Popayán. The angles below 90° formed by the vectors of genotypes BRX6 and BRX5 determine their high correlation (Figure 1d). Progeny TUNK had higher instability, with the greatest distance from the coordinate zero. Considering that stability measured by grain yield (GY) can be an important selection criterion (Thiam *et al.*, 2021), progenies BRX6 and BRX5 were considered as potential for inclusion in experiments in different environments. The GxE interactions in quinoa lead to the need for structured

breeding strategies that allow the development of genotypes adapted to specific regions. The genotype x environment interaction allowed for the determination of increased response to selection. Realizing selections of genotypes aiming for yield under specific conditions does not ensure its conservation in other environments. The plant height, panicle length, dry matter yield, grain yield, weight of 1000 grains, and harvest index were relevant traits in the selection of quinoa progenies adapted to tropical agricultural systems. The AMMI model allowed for the identification of quinoa genotypes with greater stability across different environments.

In conclusion, the genotypes showed differences at the same location in different periods, expressing the need to carry out selection for specific periods and locations. The AMMI model allowed the identification of quinoa genotypes with greater stability in different environments. Finally, genotypes BRX5 and BRX6 showed high agronomic potential in all evaluated environments, being promising for future genetic improvement programs.

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