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Original Article

Morpho-agronomic, molecular characterization, and resistance to pests and diseases of cowpea genotypes in the semi-arid of Brazil

Caracterização morfo-agronômica, molecular e resistência a pragas e doenças de genótipos de feijão-caupi no semiárido do Nordeste brasileiro

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Abstract

Semi-arid regions require the use of varieties adapted to local edaphoclimatic conditions. This study aimed to characterize landraces (Verde Ligeiro, Sempre Verde, Cariri, Azul, and Corujinha) and commercial cultivars (BRS-Pajeú, Novaera, and Guariba) of cowpea and evaluate the resistance to pests and diseases of the genotypes in irrigated (Lagoa Seca, PB) and non-irrigated (Esperança, PB) production fields. The genotypes were cultivated in an agroecological system, and morpho-agronomic analyses were performed according to the International Biodiversity descriptors of the species. Molecular characterization was performed by using ISSR markers. Pests and diseases were evaluated during the crop cycle. The genotypes had differences in qualitative characteristics (growth habit, flower color, seed color, seed shape, and mature pod color) and in quantitative characteristics (days to flowering, number of pods, pod length, number of seeds per pod, and yield). In irrigated field, the Corujinha landrace had the highest yield, and Cariri had the lowest. In non-irrigated field, the Sempre Verde landrace was the most productive, and the BRS-Novaera cultivar was the least. The 11 ISSR primers used for molecular characterization of the genotypes generated 123 bands, of which 65% were polymorphic. Intrapopulation genetic diversity was low, but cluster analysis separated the populations into two groups. Differences in the incidence of powdery mildew and cercospora leaf spot were found among the genotypes, as well as differences in pod bug infestation. The BRS-Novaera genotype was the most susceptible to diseases and pests in both irrigated and non-irrigated fields. It is concluded that the most productive genotypes with the lowest intensity of diseases and pests in irrigated fields were the Corujinha, Sempre Verde, and Azul landraces, and the BRS-Pajeú and BRS-Guariba commercial cultivars; and under rainfed conditions, the most adapted cultivar was the Sempre Verde landrace.

Keywords: *Vigna unguiculata*, ISSR markers, genetic diversity, landraces.

Resumo

Regiões semiáridas exigem o uso de variedades adaptadas as condições edafoclimáticas locais. Este trabalho teve como objetivo caracterizar variedades crioulas (Verde Ligeiro, Sempre Verde, Cariri, Azul e Corujinha) e cultivares comerciais (BRS-Pajeú, Novaera e Guariba) de feijão-caupi e avaliar a resistência a pragas e doenças dos genótipos em campo de produção irrigado (Lagoa Seca, PB) e sem irrigação (Esperança, PB). Os genótipos foram cultivados em sistema agroecológico e as análises morfoagronômicas realizadas de acordo com os decritores de Biodiversidade Internacional da espécie. A caracterização molecular foi realizada por meio de marcadores ISSR. As pragas e doenças foram avaliadas durante o ciclo da cultura. Os genótipos tiveram diferenças quanto as características qualitativas (hábito de crescimento, cor da flor, cor da semente, formato da semente e cor da vagem madura) e quantitativas (dias de floração, número de vagens, comprimento da vagem, número de sementes por vagem e produção). Em campo irrigado, a variedade crioula Corujinha obteve a maior produção e a Cariri, a menor. Em campo não irrigado, a variedade crioula Sempre Verde foi a mais produtiva, e a cultivar BRS-Novaera a menos. Os 11 primers ISSR utilizados para a caracterização molecular dos genótipos geraram 123 bandas, das quais 65% foram polimórficas.

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A diversidade genética intrapopulacional foi baixa, mas a análise de agrupamento separou as populações em dois grupos. Diferenças quanto a incidência do oídio, da cercosporiose e quanto a infestação por percevejos foram encontradas nos genótipos. O genótipo BRS-Novaera foi o mais suscetível as doenças e pragas no campo irrigado e sem irrigação. Conclui-se que os genótipos mais produtivos e com menor intensidade de doenças e pragas em campo irrigado foram as cultivares crioulas Corujinha, Sempre verde e Azul e as cultivares comerciais BRS-Pajeú e BRS-Guariba; e nas condições de sequeiro a cultivar mais adaptada foi a crioula Sempre verde.

Palavras-chave: *Vigna unguiculata*, marcadores ISSR, diversidade genética, variedades crioulas.

1. Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) has great worldwide socioeconomic importance. Besides Brazil, it is consumed in various places in Africa, Asia and Latin America (Kim et al., 2024). The world's largest cowpea producers are Nigeria and Niger (Faostat, 2025). In Brazil, cowpea is mainly grown in semi-arid regions of the Northeast. This region is characterized by high solar radiation, high average daytime air temperatures, and low atmospheric humidity and rainfall (Araújo et al., 2019; Scholes, 2020).

Cowpea is cultivated by family farmers and agribusinesses (De Ron et al., 2018; Araújo et al., 2025). In the state of Paraíba, many family farmers use seeds of landrace varieties, which have heterozygous components with specific environmental adaptability characteristics (Santos et al., 2016; De Ron et al., 2018). Landrace seeds are selected every production year by agroecological family farmers and are kept in familiar and community seed banks (Santos et al., 2016). In spite of incipient research, the cowpea agroecological cultivation is a very important system used by family farmers and has high socioeconomic importance.

Despite the limited availability of water and the presence of dry periods during the rainy season, most family farmers in semi-arid regions cultivate annual crops, such as cowpea, under rainfed conditions, without the use of irrigation. In order for cowpea production to meet the food security and economic needs of family farmers, it is important that genotypes be characterized in terms of their adaptability to biotic and abiotic stresses present in the region. Conducting experiments partially or entirely under drought conditions allows the selection of genotypes that are better adapted to the region as a strategy to achieve good productivity while maintaining agroecosystem stability (Riyaz et al., 2025).

Morphological and molecular characterization is a very important step in studies with species germplasm (Asma et al., 2024), as it identifies germplasm sources with characteristics of interest, such as production, resistance to pests, and diseases, efficient use of nutrients, and tolerance to abiotic stress, among others. All of these characteristics are important to integrate breeding programs (Alghamdi et al., 2019; Zafeiriou et al., 2023). Molecular characterization is an important support to complement phenotypic characteristics of individuals using DNA-based molecular markers (Pardey-Rodríguez et al., 2025). The Inter-Simple Sequence Repeats (ISSR) is one of the molecular markers recommended for use with cowpea, targeting various genomic loci and broadening DNA segments (Araújo et al., 2019).

Several pests and diseases can reduce cowpea production, such as pod bugs (*Crinocerus sanctus* and *Nezara viridula*) (Alves et al., 2022; Melo et al., 2024), powdery mildew (*Erysiphe polygoni*), and cercosporiosis (*Pseudocercospora cruenta* and *Cercospora canescens*) (Pio-Ribeiro et al., 2016). The resistance of genotypes to pests and diseases can be affected by the environment and is a crucial factor for agriculture, especially for family farmers, who often do not carry out spraying due to the cost of the products and the lack of availability.

The present work has the hypothesis that the selection of cowpea genotypes by generations of farming families under semi-arid edaphoclimatic conditions, with biotic and abiotic stress, furnishes productive genetics that are resistant to water stress conditions and are adapted to agroecological production systems. In this context, two production fields with landraces (Verde Ligeiro, Sempre Verde, Cariri, Azul, and Corujinha) and commercial varieties (BRS-Pajeú, BRS-Novaera, and BRS-Guariba) of cowpea were implemented in a field with (Lagoa Seca-PB) and without irrigation (Esperança-PB), to characterize morpho-agronomically and molecularly these genotypes in an agroecological system. The aim was to characterize cowpea genotypes cultivated in the Brazilian semi-arid region and to identify genotypes that are better adapted in terms of productive potential and resistance to pests and diseases in agroecological systems without water stress (irrigated field) and with water stress (non-irrigated field).

2. Materials and Methods

The experimental material consisted of eight cowpea genotypes, including five landraces provided by farmers from the state of Paraiba (PB), Brazil: Verde Ligeiro (Esperança-PB), Cariri (Queimadas-PB), Sempre Verde (Esperança-PB), Azul (Massaranduba-PB), and Corujinha (Esperança-PB), and three cultivars provided by Brazilian Agricultural Research Corporation - Embrapa Semi-arid: BRS-Pajeú, BRS-Guariba, and BRS-Novaera.

2.1. Morpho-agronomic analysis of cowpea genotypes

The morpho-agronomic characterization was carried out in two fields in the Agreste region of the state of Paraiba. Field I in Lagoa Seca (7°15'75"S 35°87'33"W) and Field II in Esperança (6°59'19.2"S 35°52'50.4"W). The areas are characterized by hot and humid tropical conditions, and the Köppen and Geiger (1928) climate classification is As (Francisco et al., 2015). The average temperature during the months of the experiment was 24.5 °C in Field I (March to June 2018) and 23.8 °C in Field II (April to July 2018) (Agritempo, 2025).

The field areas used for agroecological cultivation of annual crops, did not have the use of chemical fertilizers and pesticides. After crops are harvested, the native vegetation is maintained in the area to cover the soil until the next crop is planted. In Field I, qualitative and quantitative analyses were carried out on campus II of the State University of Paraíba. In Field II, quantitative analyses were carried at the Advice and Services for Projects in Alternative Agriculture (AS-PTA).

The experiments were conducted in a system with irrigation (Lagoa Seca, Field I) and without irrigation (Esperança, Field II). Sprinkler irrigation was used for the experiment in Field I. Five sprinklers were installed between the plots. The irrigation system was activated, when necessary, since the region had considerable rainfall during the months of crop development (Figure 1). Annual precipitation data in the municipalities of Lagoa Seca and Esperança in the year 2018 is described in Figure 1.

A randomized complete block design with four replications and eight treatments was used. The experimental plots had dimensions of 2.8 m length and 2.4 m in width, each plot totaling an area of 6.72 m^2, with each experimental area of 12.6 m^2 width and 29.4 m^2 length, totaling an area of 370.44 m^2. The plots consisted of four rows with eight plants spaced 0.40 m apart and 0.80 m between rows, resulting in 32 plants per plot, distributed in 32 plots, with 1 m between plots. The two central rows were the useful area. Chemical characteristics of the soil were performed (Table 1) in the experimental areas (Lagoa Seca-PB and Esperança-PB).

The experiments were conducted in the agroecological production system used by ecologically based family farmers in the state of Paraíba. Control measures were not used for pests and diseases. Soil preparation consisted of plowing, harrowing (Campus II in Lagoa Seca-PB), and in AS-PTA the native vegetation was removed with the aid of a hoe. Native vegetation was preserved in the areas surrounding the experimental plots. The fertilization used in the experiments was organic, with the addition of 500 g of cured bovine manure (Table 1) per planting hole 25 days before planting. Three seeds were sown per pit, and at 28 days of sowing, thinning was performed, leaving one plant per pit.

Morpho-agronomic characterization of genotypes was carried out according to the descriptors of *V. unguiculata* by International Biodiversity (IBPGR, 2007) by using eight plants from the useful area of each plot. The evaluated qualitative characters were: growth habit (GH), flower color (FC), seed color (SC), and mature pod color (MPC) (IBPGR, 2007). The quantitative traits were: number of days to flowering (NDF) – observing the number of days from sowing to the stage when 50% of the plants are in flowering, pod length (PL), number of pods (NP), number of seeds per pod (NSP), and plant production (PROD).

2.2. Analysis of genetic diversity of cowpea genotypes

For molecular characterization, leaf samples were collected from eight individuals of each genotype (n = 64) in the experimental field. Molecular analyses were performed at the Biotechnology Laboratory from Brazilian Agricultural Research Corporation - Embrapa Cotton, located in Campina Grande, State of Paraiba,

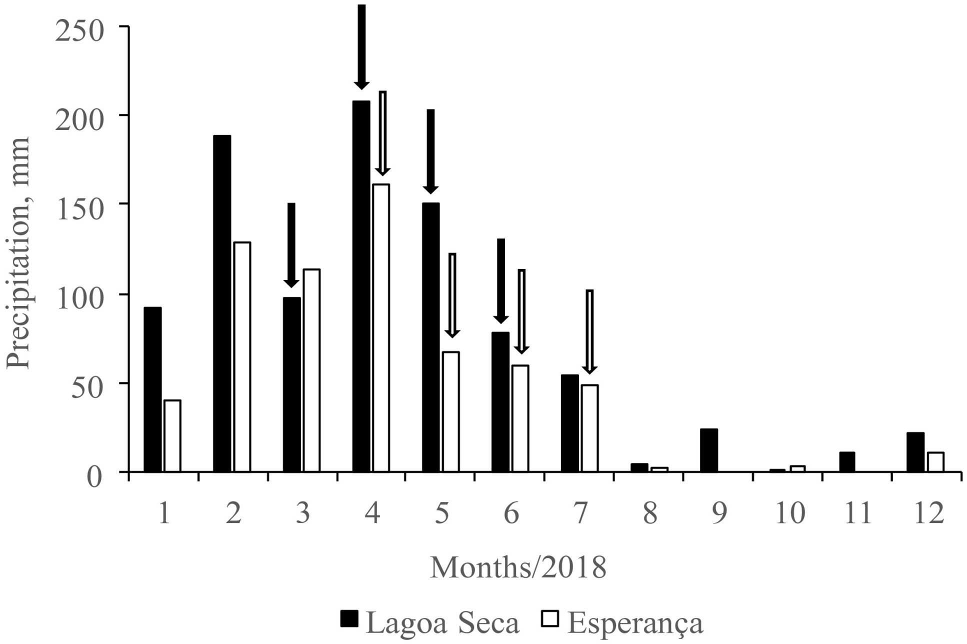

Figure 1. Annual precipitation data in the municipalities of Lagoa Seca-PB and Esperança-PB in the year of 2018. The arrows indicate the months in which the experiments were performed, March-June in Lagoa Seca-PB, and April-July in Esperança-PB, Brazil (AESA, 2019).

Table 1. Characteristics of the soil in Field I (Lagoa Seca, PB) and Field II (Esperança, PB) at a deph of 0 - 20 cm and of the bovine manure.

Soil type	pH	OM	P	B	Cu	Fe	Mn	Zn	Ca	K	Na	Mg	H+Al
	-	g dm^{-3}	---------------- mg dm^{-3} ------------------						-----------------cmol dm^{-3}--------------				
Field I													
Sandy loam	4.8	14	45	0.22	0.5	91	2.7	1.6	2.6	0.26	0	0.8	2.5
Field II													
Sandy	5.7	13	39	0.20	1.0	34	2.8	1.8	3.2	0.20	0	1.0	1.0
Manure													
Bovine	8.2	314.75	114.73	-	-	-	-	-	0.95	5.97	1.61	0.75	0.33

OM = Organic matter, pH $CaCl_2$ (soil); pH (H_2O) (bovine manure), P Extractor Mehlich; Cu, Fe, Mn, and Zn extraction in DTPA. Soil analyses were carried out in the Soil and Foliar Analysis Laboratory Ribersolo in Ribeirão Preto, SP. Bovine manure analyses were carried out at Federal University of Paraíba, Areia. B, Cu, Fe, Mn, and Zn were not determined in bovine manure.

Table 2. Sequence of ISSR oligonucleotides developed by the University of British Columbia Laboratory, total bands generated, polymorphic oligonucleotide bands, polymorphism rate and polymorphic information content (PIC), used to characterize cowpea genotypes.

Primer	Sequence (5`→ 3`)	Total Bands	Polymorphic Bands	Polymorphism Rate (%)	PIC
UBC 834	AGA GAG AGA GAG AGA GYT	14	8	57.14	0.224
UBC 808	AGA GAG AGA GAG AGA GC	11	2	18.18	0.102
UBC 809	AGA GAG AGA GAG AGA GG	11	7	63.63	0.352
UBC 826	ACA CAC ACA CAC ACA CC	11	8	72.72	0.312
UBC 827	ACA CAC ACA CAC ACA CG	6	5	83.33	0.269
UBC 846	CAC ACA CAC ACA CAC ART	9	7	77.77	0.307
UBC 847	CAC ACA CAC ACA CAC ARC	11	5	45.45	0.172
UBC 858	TGT GTG TGT GTG TGT GRT	9	7	77.77	0.280
UBC 866	CTC CTC CTC CTC CTC CTC	12	8	66.67	0.311
UBC 878	GGA TGG ATG GAT GGA T	9	6	66.67	0.303
UBC 888	BDB CAC ACA CAC ACA CA	20	17	85	0.451
Total		123	81		

Brazil. The leaf samples were three discs cut by the lid of the 2.0 mL microtube and collected in the vegetative phase of development (Campos et al., 2000) according to the CTAB method (Ferreira and Grattapaglia, 1998) with modifications. In the ISSR-PCR assays, 11 primers from the University of British Columbia (UBC, Vancouver, Canada) (Table 2) were used for the generation of polymorphism, and had the reactions optimized to obtain better quality amplification products.

PCR-ISSR reactions were prepared with 25 µl final volume containing: 2.0 µl of template DNA (20 ng μl^{-1}) and 23 µl of PCR mix containing 1.0 mM primer, 0.25 mM dNTP's, 2.5 mM $MgCl_2$, PCR buffer 100 mM Tris-HCl (pH 8.5), 500 mM KCl], 1unit Taq DNA polymerase (Ludwig Biotec®), and ultrapure water. Samples were initially subjected to 94 °C for 5 minutes, and then to 30-35 cycles of amplification. Each cycle subjected the samples to 94 °C for 30 seconds, with annealing temperature ranging from 50 °C for 45 seconds, and finally 72 °C for 2 minutes. After the cycles, the samples were kept at 72 °C for 5 minutes for final extension (Melo et al., 2011; Dias et al., 2015).

One microlite of sample buffer (0.25% bromophenol blue and 40% sucrose) and 2.0 µL of SYBR® Gold (Invitrogen) were added to the reaction products, and then the samples were separated by horizontal gel electrophoresis (1.5% agarose) and photographed under UV light. The molecular-weight size marker (Kasvi 1 kb DNA Ladder RTU marker) was used to determine the molecular weight of fragments.

2.3. Pests and diseases

For the evaluation of pests and diseases, the eight plants of the useful area were analyzed weekly during the period of May/June at the Campus in Lagoa Seca-PB, and in the period of June/July at the ASPTA in Esperança-PB. The injuries of phytophagous insects were determined by using the methodology of Quintela (2001). Disease assessment was performed by severity. The following diagrammatic scales were used for the affected area of the plants for powdery mildew disease (Quintela et al., 2005) and cercosporiosis (Albert et al., 2008).

2.4. Statistical analysis

Statistical analysis for quantitative morpho-agronomic characters (PL, NSP, NP, and PROD) was done by fully integrated analyses of the experiments carried out in two different locations (Lagoa Seca and Esperança) and the data were organized into bar charts. The PL data did not follow a normal distribution and lacked homogeneity of variance; therefore, the medians were evaluated by using the non-parametric Aligned Rank Transform (ART) analysis via the ARTool package. The NSP data followed a normal distribution and had homogeneity of variances. The NP variables were transformed via Box-Cox ($\lambda = 0.5$) and had a normal distribution and homogeneity of variances. The PROD variables were transformed via Box-Cox ($\lambda = 0.3$) and met the assumptions of normality and homogeneity of variances. Mean comparisons were made by Tukey test at a significance level of 5% to the characters NSP, NP and PROD. PL median comparisons were made by ART analysis.

The data from the assessment of diseases (Field I and II) and pod bugs in Field II met the assumptions of normality and homogeneity of variances, and were evaluated by using Tukey's test at 5%. The pod bugs data from Field I did not meet the assumptions of normality and homogeneity of variances and were evaluated by using the generalized linear model (negative binomial distribution). Pest and disease data were organized into a table.

Quantitative morpho-agronomic, disease, and pest statistical analyses were performed by using Software R (version 3.5.3).

For molecular data analysis, the bands generated by each primer were counted and scored as binary data, considering 1 for presence and 0 for absence of the band in all genotypes (Yeh et al., 1999). Genetic diversity parameters were: Nei genetic diversity (He), percentage of polymorphic loci (P) effective number of alleles (Ne), observed number of alleles (Na), genetic distance, genetic identity (Nei, 1973), and Shannon index (I) (Kimura and Crow, 1964).

Dendrograms were constructed with the genetic identity values by analysis of Unweighted Pair Group Method using Arithmetical Averages (UPGMA) groupings using the NTSYS statistical software. In addition, the polymorphic information content (PIC) for each ISSR primer was determined by the following Expression 1, where Pij is the frequency of allele "j" in marker "i" (the sum extends across all alleles). The calculation was based on the number of alleles detected per marker for a given locus and the relative frequency of each allele in the eight cowpea populations analyzed, as follows:

$$PICi = 1 - \Sigma nj = 1P2ij \tag{1}$$

Data were organized into a figure (dendrograms) and tables.

3. Results

3.1. Morpho-agronomic analysis of cowpea genotypes

The cowpea genotypes had variability regarding the qualitative characteristics (Table 3). Among the eight genotypes evaluated, BRS-Pajeú, Sempre Verde, Corujinha, and Verde Ligeiro had semi-prostrate growth habit. The Cariri genotype had intermediate growth habit and the Azul, BRS-Novaera, and BRS-Guariba genotypes had semierect growth habit (Table 3).

Regarding the flower coloring, the genotypes produced violet, white, and yellow flowers. Violet flowers were produced by BRS-Pajeú cultivar and Azul landrace. Corujinha landrace produced a violet flower with yellow and Cariri landrace produced a white flower with violet hue. White flowers were produced by BRS-Novaera and BRS-Guariba cultivars, with lilac and yellow tones, and by Verde Ligeiro landrace with a yellow hue. Yellow flowers were produced only for the Sempre Verde landrace (Table 3).

The seed colors produced by the genotypes were white, dark brown, light brown, and blue to black. Most genotypes produced white seeds (BRS-Guariba, BRS-Novaera, Verde Ligeiro, and Cariri). The white seeds of the Cariri genotype had uniformly distributed spots.

Table 3. Qualitative characteristics: growth habit (GH), flower color (FC), seed color (SC), seed shape (SS) and mature pod color (MPC), observed in eight cowpea genotypes.

Genotypes	Qualitative characteristics				
	GH	FC	SC	SS	MPC
BRS-Pajeú	Semi-prostrate	Violet	Dark brown	Rhomboid	Straw-colored
BRS-Guariba	Semi-erect	White	White	Rhiniform	Dark purple
BRS-Novaera	Semi-erect	White	White	Rhiniform	Straw-colored
Sempre verde	Semi-prostrate	Yellow	Light brown	Rhiniform	Straw-colored
Azul	Semi-erect	Violet	Blue to black	Rhomboid	Dark purple
Corujinha	Semi-prostrate	Violet	Dark brown	Ovoid	Dark purple
Verde Ligeiro	Semi-prostrate	White	White	Rhiniform	Dark purple
Cariri	Intermediate	Violet	White	Rhiniform	Straw-colored

Biodiversity International [17].

The BRS-Pajeú and Corujinha genotypes produced dark brown seeds. The dark brown seeds of the Corujinha genotype had small, uniformly distributed spots. The Sempre Verde genotype produced light brown seeds, and the Azul genotype produced seeds with a mottled or marbled blue to black coloration (Table 3).

Three seed shapes were produced by the genotypes: riniform (BRS-Guariba, BRS-Novaera, Cariri, Verde Ligeiro, and Sempre Verde), rhomboid (Azul and BRS-Pajeú), and ovoid (Corujinha) (Table 3).

The genotypes produced mature pods with straw and dark purple coloration. BRS-Novaera, BRS-Pajeú, Cariri, and Sempre Verde produced straw-colored pods, while Verde Ligeiro, Azul, Corujinha, and BRS-Guariba produced dark purple pods (Table 3).

In irrigated Field I (Lagoa Seca), cultivars maintained their flowering standards ranging from 39 days (BRS-Pajeú and BRS-Guariba) to 40 days (BRS-Novaera). The Corujinha landrace was the earliest flowering variety, at about 47 days. The Sempre Verde variety bloomed at 53 days, Azul at 57 days, Verde Ligeiro at 59 days, and Cariri had the latest flowering, at 75 days.

In non-irrigated Field II (Esperança), the cowpea genotypes maintained their flowering standards ranging from 42 days for BRS-Pajeú and BRS-Guariba, and 40 days for BRS-Novaera. Among the landraces, Corujinha was the earliest flowering variety at 49 days, followed by Sempre Verde at 53 days, Azul at 57 days, and Verde Ligeiro at 55 days. Cariri had the latest flowering at 77 days.

Pod length and the number of seeds per pod did not differ between locations (Lagoa Seca and Esperança), therefore they were not influenced by the production field with irrigation (Field I) and without irrigation (Field II). However, there are differences between the genotypes with respect to the variables (Figure 2).

Regarding pod length, the BRS-Pajeú commercial cultivar and the Azul landrace produced the longest pods, which did not differ from Verde Ligeiro, Sempre Verde, and Cariri landraces. The BRS-Novaera commercial cultivars produced the shortest pods and did not differ from BRS-Guariba commercial cultivar and Corujinha landrace (Figure 2A).

As observed for the pod length variable, the genotypes that produced the highest number of seeds per pod were the BRS-Pajeú commercial cultivar and the Azul landrace (Figure 2B). The number of seeds per pod did not differ between the Cariri, Corujinha, Sempre Verde, and Verde Ligeiro genotypes. Cariri landrace did not differ from the Azul landrace. BRS-Guariba and BRS-Novaera produced the lowest number of seeds per pod (Figure 2B).

The production fields with (Lagoa Seca) and without (Esperança) irrigation influenced the variables number of pods and production (grams per plant), with statistical analyses performed separately for location and genotype (Figure 3).

In the irrigated field (Field I), the BRS-Guariba cultivar produced the highest number of pods compared to the evaluated genotypes. Statistical differences were not found among BRS-Guariba and Corujinha, BRS-Novaera, BRS-Pajeú, and Sempre Verde genotypes. The Cariri landrace produced the lowest number of pods, with no differences compared to Verde Ligeiro and Azul genotypes (Figure 3A).

BRS-Novaera, BRS-Guariba, and Sempre Verde genotypes produced the greatest number of pods and did not differ from Verde Ligeiro, Azul, Corujinha, and BRS-Pajeú, in the non-irrigated Field II (Esperança). The Cariri genotype produced the lowest number of pods and did not differ from Verde Ligeiro, Azul, Corujinha, and BRS-Pajeú (Figure 3C).

In Lagoa Seca (irrigated Field I), Corujinha landrace had the highest production, and did not differ from the BRS-Pajeú, Sempre Verde, BRS-Guariba, Azul, and BRS-Novaera genotypes. Cariri landrace had the lowest production, and did not differ from Verde Ligeiro landrace (Figure 3B).

In Esperança (non-irrigated Field II), the Sempre Verde genotype had the highest production, and the BRS-Novaera genotype had the lowest. Azul, Verde Ligeiro, Corujinha, BRS-Pajeú, Cariri, and BRS-Guariba genotypes did not differ from Sempre Verde and BRS-Novaera genotypes (Figure 3D).

3.2. Analyses of genetic diversity of cowpea genotypes

The eleven primers generated 123 bands, of which 65.8% were polymorphic. The number of bands applied per primer ranged from 6 to 20 with the polymorphism rate ranging from 45.45 to 85.0% (Table 2). Primer Polymorphic

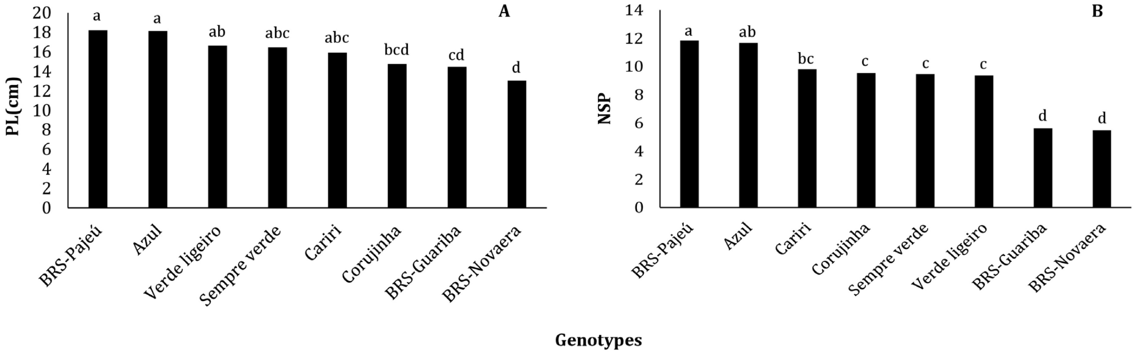

Figure 2. Pod length (PL) and number of seeds per pod (NSP) were determined by a joint analysis of experiments in Field I (Lagoa Seca-PB) and Field II (Esperança-PB). PL median values followed by the same letter do not differ according the non-parametric analysis. NSP followed by the same letter do not differ by 5% Tukey.

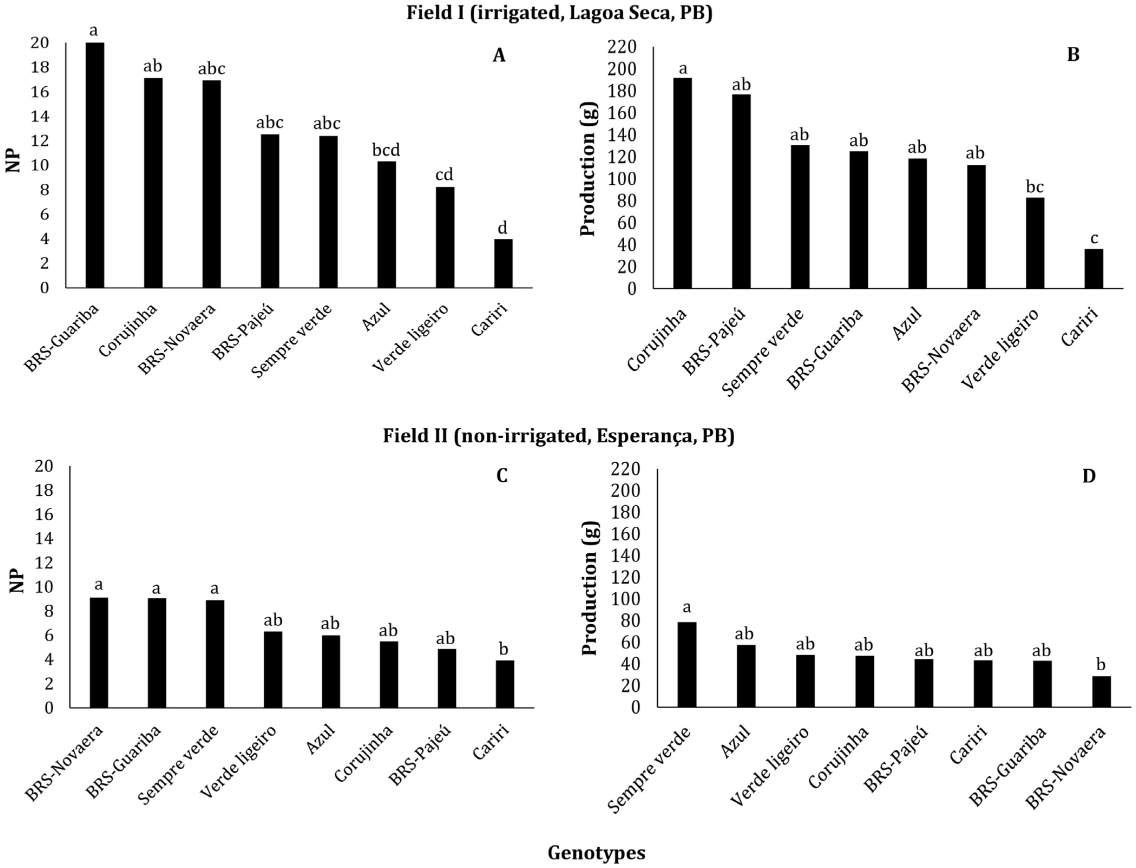

Figure 3. Number of pods (NP) and production (gram per plant) obtained from cowpea genotypes in the Lagoa Seca-PB (Field I, irrigated) and Esperança-PB (Field II, non-irrigated). Data followed by the same letter do not differ by 5% Tukey.

Information Content ranged from 0.102 to 0.451, most of which were classified as moderately informative (Table 2).

The total number of bands and the percentage of polymorphic bands (P) were obtained from the eight genotypes of cowpea. Verde Ligeiro genotype had the lowest values of number of bands generated and polymorphism, and BRS-Novaera genotype had the highest values, from 7-23 and 5.69-18.70, respectively (Table 4).

The genetic similarity matrix obtained from the Nei Identity Coefficient ranged from 0.0901 to 0.9360, suggesting that the germplasm evaluated has a narrow genetic basis. The highest value of genetic identity (0.93) and the shortest genetic distance (0.0661) were found between Sempre Verde and Verde Ligeiro genotypes, so they ended up being similar and genetically close genotypes (Table 5).

The pair of genotypes with the highest genetic identity and the shortest genetic distance were: BRS-Pajeú and Cariri; BRS-Guariba and BRS-Pajeú; BRS-Novaera and BRS-Pajeú; Sempre Verde and BRS-Novaera; Verde Ligeiro and Sempre Verde; Azul and Verde Ligeiro; Cariri and Sempre Verde; Corujinha and Cariri (Table 5).

Cluster analysis (UPGMA) allowed the separation into two groups considering a cutoff point in the genetic divergence percentage of 0.81 (Figure 4). Despite the genotype's low diversity, it was possible to identify similar and divergent groups. Group I was constituted by the BRS-Pajeú, BRS-Guariba, BRS-Novaera, Sempre Verde, Verde Ligeiro, and Azul populations, and cluster group II had the Cariri and Corujinha populations (Figure 4). Group I gathered most of the cowpea genotypes, cultivars BRS-Guariba and BRS-Novaera and Azul variety with semi-erect growth habit, and BRS-Pajeú, Sempre Verde, and Verde Ligeiro with semi-prostrate growth.

As for the color of the seed, cluster Group I gathered seeds of white (BRS-Guariba, BRS-Novaera), light brown (Sempre Verde), dark brown (BRS-Pajeú), white (Verde Ligeiro), and blue to black (Azul). Group II had dark brown seeds with equally distributed pigments (Corujinha) and white seeds with equally distributed pigments (Cariri) (Figure 4, Table 3).

Group I (Figure 4) had genotypes with higher pod length (BRS-Pajeú and Azul) (Figure 2A), number of seeds per pod (BRS-Pajeú) (Figure 2B), pod number averages (BRS-Guariba) (Figure 3A and 3C), and higher production (Sempre Verde) in Esperança (Field II). In group II (Figure 4), Corujinha had higher production in Lagoa Seca (Field I) (Figure 3B). Cariri had lower pod number (Figure 3A and 3B), intermediate pod length (Figure 2A), and number of seeds per pod (Figure 2B).

Table 4. Measures of genetic diversity for the eight cowpea populations generated by the 11 ISSR primers.

Genotypes	*TNB*	*P(%)*	*Na*	*Ne*	*He*	*I*
BRS Pajeú	12	9.76	1.0976±0.30	1.0741±0.24	0.0407±0.13	0.0587±0.18
BRS Guariba	8	6.50	1.0650±0.25	1.0527±0.21	0.0279±0.11	0.0399±0.15
BRS Novaera	23	18.70	1.1870±0.39	1.1462±0.33	0.0786±0.17	0.1128±0.24
Sempre Verde	13	10.57	1.1057±0.31	1.0577±0.20	0.0336±0.11	0.0510±0.16
Verde Ligeiro	7	5.69	1.0579±0.23	1.0378±0.17	0.0216±0.09	0.0319±0.13
Azul	13	10.57	1.1057±0.31	1.0731±0.24	0.047±0.12	0.0596±0.18
Cariri	18	14.63	1.1463±0.35	1.1202±0.30	0.0646±0.15	0.0923±0.22
Corujinha	21	17.07	1.1707±0.38	1.1129±0.28	0.0637±0.15	0.093±0.22

TNB = total number of bands; P (%) percentage of polymorphic loci (polymorphism); Na = Observed number of alleles; Ne = Effective number of alleles; He = Genetic diversity of Nei [23]; I = Shannon Index.

Table 5. Impartial measures of Genetic Identity and Nei Genetic Distance to cowpea.

Genotypes	BRS Pajeú	BRS Guariba	BRS Novaera	Sempre Verde	Verde Ligeiro	Azul	Cariri	Corujinha
BRS Pajeú	****	0.8579	0.9145	0.8823	0.8889	0.9047	0.7749	0.7771
BRS Guariba	0.1533	****	0.8903	0.8254	0.8489	0.8034	0.7473	0.7323
BRS Novaera	0.0893	0.1162	****	0.9122	0.9042	0.9036	0.7976	0.7818
Sempre Verde	0.1253	0.1919	0.0919	****	0.9360	0.8786	0.8099	0.7895
Verde Ligeiro	0.1177	0.1639	0.1007	0.0661	****	0.9139	0.7645	0.7548
Azul	0.1002	0.2189	0.1013	0.1294	0.0901	****	0.7551	0.7708
Cariri	0.2551	0.2913	0.2262	0.2109	0.2685	0.2810	****	0.8901
Corujinha	0.2521	0.3116	0.2461	0.2363	0.2813	0.2603	0.1165	****

Values above the matrix refer to Genetic Identity, values below the matrix refer to Nei Genetic Distance.

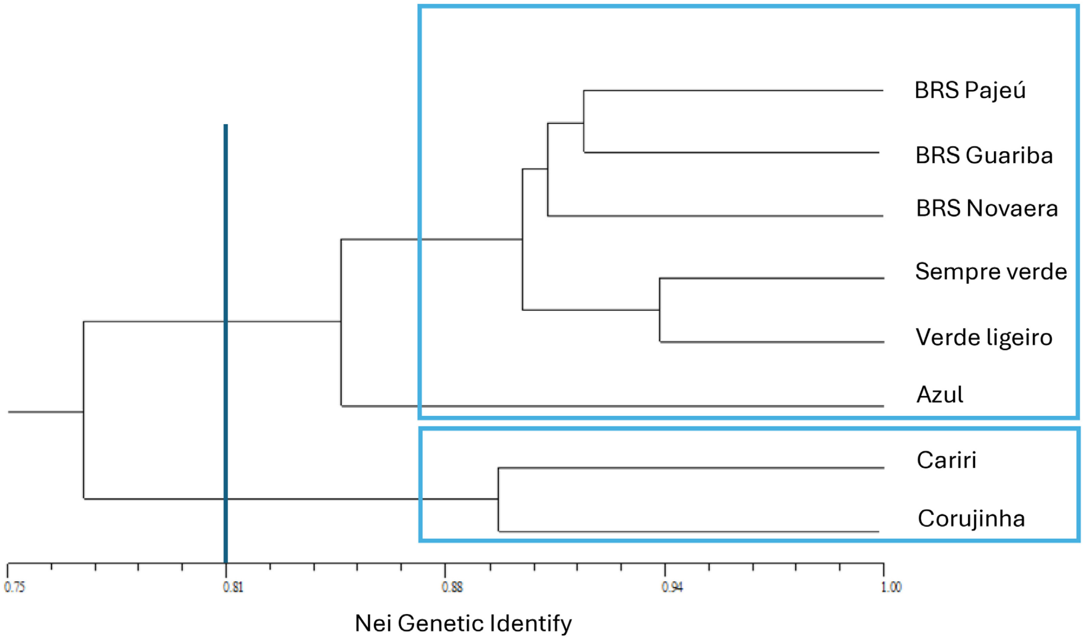

Figure 4. UPGMA dendrogram based on Nei genetic identity for eight cowpea genotypes.

3.3. Diseases and pests

Powdery mildew (*Oidium* sp.), cercosporiosis (*P. cruenta* and *C. canescens*), rough mosaic (*Bean rugose mosaic*), anthracnose (*Colletotrichum lindemutianum*), and rust (*Uromyces appendiculatus*) plant diseases were identified in both experiments (Field I and Field II). Nevertheless, statistical differences between genotypes were only observed for powdery mildew and cercosporiosis.

In Field I (irrigated field), BRS-Novaera had the highest susceptibility to powdery mildew when compared to the other genotypes tested. Regarding the severity of cercosporiosis, the BRS-Novaera cultivar and the Sempre Verde landrace were the most susceptible when compared to the other genotypes. In Field II (non-irrigated field), BRS-Novaera and Verde Ligeiro were the most susceptible to the powdery mildew, but did not differ from Cariri, Sempre Verde, and Azul genotypes. The genotypes that presented the lowest disease intensity were Corujinha, BRS-Pajeú, and BRS-Guariba. Genotypes did not differ among cercosporiosis severity in Field II (Table 6).

The plants were infested by pod bugs (*Crinocerus sanctus* and *Nezara viridula*), aphids (*Aphis craccivora, Aphis gossypii* e *Aphis fabae*), leafminer (*Liriomyza sativae*), hemipterans (*Crinocerus sanctus* and *Nezara viridula*), and beetles *(Diabrotica speciosa* and *Cerotoma arcuatus*). However, differences among genotypes were observed for pod bug infestation. In the irrigated crop grown in Lagoa Seca (Field I), the genotype with the highest infestation was BRS-Novaera, followed by BRS-Pajeú and Corujinha. The genotypes with the lowest infestation were Sempre Verde, Azul, Verde Ligeiro, Cariri and BRS-Guariba. In the non-irrigated Field II (Esperança), the BRS-Novaera genotype had the highest infestation, differing only from the Azul genotype, where there was no infestation by pod bugs (Table 6).

Disease and pest occurrence directly influences cowpea productivity. In Lagoa Seca, the cultivar with the highest productivity was Corujinha (5,990.26 kg ha^{-1}), and BRS Pajeú (5,519.2 kg ha^{-1}) had the lowest severity of powdery mildew and cercosporiosis and average infestation of pod bugs. In Esperança, the intensity of powdery mildew and bed bug infestation was similar to that in Lagoa Seca for Corujinha (1,483.39 kg ha^{-1}) and BRS Pajeú (1,387.54 kg ha^{-1}) genotypes. The BRS Guariba genotype had a productivity of 3,907.6 kg ha^{-1} in Lagoa Seca and low infestation of powdery mildew in both municipalities; and low infestation of pod bugs in Lagoa Seca and average infestation in Esperança. Sempre Verde genotype, with a productivity of 4,077.9 kg ha^{-1} in Lagoa Seca and 2,454.54 kg ha^{-1} in Esperança, had low intensity of powdery mildew in Lagoa Seca, medium intensity in Esperança and high intensity of cercosporiosis in Lagoa Seca. Regarding pod bug infestation, Sempre Verde had a low infestation in Lagoa Seca and medium infestation in Esperança. The Azul genotype had a

Table 6. Comparison of means for the severity of powdery mildew (*Oidium* sp.) and cercosporiosis (*Cercospora* sp.), and number of pod bugs obtained from the eight cowpea genotypes concerning Field I (Lagoa Seca, PB) and Field II (Esperança, PB), 2018.

Field I (Lagoa Seca, PB)			
Genotypes	**Powdery mildew**	**Cercosporiosis**	**Pod bugs**
Sempre Verde	3.90 b[1]	10.89 a[1]	2.5 c[2]
Azul	0.70 b	4.75 b	2.5 c
Corujinha	0.79 b	5.29 b	3 bc
Verde Ligeiro	4.31 b	5.61 b	1.75 c
Cariri	7.39 b	5.64 b	1 c
BRS-Novaera	35.47 a	11.38 a	17.75 a
BRS-Guariba	3.51 b	5.52 b	0.75 c
BRS-Pajeú	1.44 b	5.20 b	8 b
Field II (Esperança, PB)			
Genotypes	**Powdery mildew**	**Cercosporiosis**	**Pod Bugs**
Sempre Verde	2.59 ab[1]	2.45^{ns}	1.50 ab[1]
Azul	2.13 ab	4.21	0 b
Corujinha	0.61 b	3.01	2.75 ab
Verde Ligeiro	10.29 a	2.46	1.00 ab
Cariri	6.53 ab	2.93	1.75 ab
BRS-Novaera	10.4 a	3.03	3.75 a
BRS-Guariba	0.63 b	2.75	1.00 ab
BRS-Pajeú	0.48 b	4.24	1.25 ab

[1]Data followed by the same letter differ by Tukey teste (p ≤ 5%). ^{ns}Data do not differ by the F test. [2]Analysis performed by using a generalized linear model (negative binomial distribution).

productivity of 3,695.3 kg ha^{-1} in Lagoa Seca, low intensity of diseases (powdery mildew and cercosporiosis) and pod bug infestation in both locations. Despite the similar productivity of the BRS Novaera genotype (3,516.89 kg ha^{-1}) and the Azul genotype in Lagoa Seca, the BRS Novaera genotype had greater susceptibility to powdery mildew (Lagoa Seca and Esperança), cercosporiosis (Lagoa Seca) and pod bug infestation (Lagoa Seca and Esperança). The genotypes with the lowest productivity in Lagoa Seca, Cariri (1,125.85 kg ha^{-1}) and Verde Ligeiro (2,588.35 kg ha^{-1}), had low intensity of powdery mildew and cercosporiosis in Lagoa Seca, higher intensity of powdery mildew in Esperança, low pod bug infestation in Lagoa Seca and intermediate infestation in Esperança (Figure 3 and Table 6).

4. Discussion

Morphological characterization of genetic resources is essential for the knowledge of phenotypic variations among genotypes (Alghamdi et al., 2019; Morillo et al., 2023). The evaluated cowpea genotypes had variability regarding the morpho-agronomic characteristics evaluated (Table 3, Figure 2, and Figure 3). Morphological analyses, such as growth habitat, flower color, and pod characteristics are considered important elements to evaluate the level of genetic variability of cowpea genotypes (Onuminya et al., 2023). Qualitative characteristics are considered the most appropriate in determining a cultivar or variety, since they are mostly genetically controlled and independent of the growing environment (Carvalho et al., 2017). Among the growth habit of the eight genotypes evaluated (Table 3), the results showed similarity to the results obtained by Torres et al. (2016).

The Sempre Verde landrace produced yellow flowers. The yellow flower color is not listed by *V. unguiculata* International Biodiversity (IBPGR, 2007) and is a different color produced by the landrace. Differences in phenotypic characters such flower color and seed coat color were also reported by Mafakheri et al. (2017) and Onuminya et al. (2023).

Flowering days were similar among the genotypes in both production fields (irrigated and non-irrigated). In Lagoa Seca, genotypes had flowering days between 40 and 75 days after sowing, and in Esperança they flowered between 40 and 77 days after sowing. The cultivars had the earliest cycle, compared to the landraces. The landrace with the earliest cycle was Corujinha and the one with the latest cycle was Cariri. According to Hamidou et al. (2007), early cycle genotypes have more advantages for the producer.

Except for Cariri landrace, all genotypes decreased production in Field II (Esperança) without irrigation (Figure 3). The better performance of Cariri landrace in Esperança, with production increase of 16.5%, can be explained by genotype adaption to the drier region. According to family farmers, Cariri landrace is resistant to drought. Lagoa Seca and Esperança are located in the Agreste mesoregion of Paraíba, which is characterized by a rainfall reaching 800 mm per year, with a dry summer (Nascimento et al., 2022). During the development of the experiments, the plants grown in Lagoa Seca did not have water stress, since Lagoa Seca had 533.10 mm of rainfall and irrigation was carried out on dry days. The rainfall in Esperança was 352.5 mm and since irrigation was not carried out, the plants were subjected to water stress until the end of the cycle on the dry days (Figure 1).

Landrace seeds had a production equivalent to the Embrapa cultivars. There is a lack of research involving the production of landrace genotypes in the Paraíba region, and there is a need for more research on the subject. Landrace seeds have the value and responsibility of those who worked with them for generations, guaranteeing the recovery of culture and preservation of local biodiversity (Paulino and Gomes, 2015).

The molecular characterization analysis showed that ISSR molecular markers were efficient to detect genetic polymorphism in cowpea, because the eleven primers were used, as they generated polymorphic, clear, and consistent bands. Although nonspecific, the ISSR molecular markers have a high reproducibility and low cost, and are widely used in studies to evaluate the diversity of genotypes of the species (Araújo et al., 2019). The UBC-808, UBC-834, UBC-858, UBC-826, and UBC-888 primers have already been used in other cowpea studies and have shown good quantity, quality, and reproducibility of amplified bands (Ferreira and Grattapaglia, 1998; Melo et al., 2011).

According to Montalván et al. (2015), the genetic basis of the Brazilian cowpea is considered narrow. In the present study, the intra-population genetic diversity indices were low, and among the evaluated genotypes. The genetic diversity in the BRS Novaera population was identified as the highest (P = 18.70%; Na = 1.1870 ± 0.39; Ne = 1.1462 ± 0.33; He = 0.0786 ± 0.17, and I = 0.1128 ± 0.24) (Table 4). The values were low, indicating that the loci are homozygous high, which was expected, since it is an autogamous specie. According to Egbadzor et al. (2014), high genetic diversity is related to the largest number of accessions tested, but in contrast to this, Chen et al. (2017) evaluated 33 cowpea genotypes from Niger and 27 from China and a lower genetic diversity level in Niger (0.23) was found than in the genotypes from China (0.31), confirming that the number of populations does not interfere with genetic diversity. In this context, it is important to observe that, among the populations of landrace varieties, Corujinha was the one that presented the highest number of alleles 1.1707 ± 0.38, a value only below BRS-Novaera cultivar.

Despite the socioeconomic importance of cowpea for many populations, the characterization of the genetic diversity and germplasm of the specie is still incipient. Such characterizations are important for use in cowpea genetic improvement programs, for the selection of genotypes with desired characteristics (Patel et al., 2022). According to Asare et al. (2010), generally, genetic distances among the cowpea genotypes are low, reflecting the initial obstruction during the domestication process, and are maintained by the inherent self-pollination system in the crop, although it has great phenotypic variability for some morphological characters (Gajera et al., 2014; De Ron et al., 2018), such as seed coat color, visualized in this study.

In the irrigated system (Lagoa Seca), all commercial cultivars exceeded the average productivity described by

Rocha et al. (2017). Powdery mildew and cercosporiosis affect the aerial part of the plants, impairing photosynthesis and consequently production (Pio-Ribeiro et al., 2016). Regarding pod bug infestation, the damage is direct to production, since the insects suck the seeds (Silva, 2016). Studies on the identification of pests and diseases in agricultural practices favor the choice of control measures, reducing the cost of chemical products, contributing to the environment and to the identification of resistant genotypes that can be used locally, mainly by agroecological and organic farmers.

5. Conclusion

The morpho-agronomic and molecular characterization of Verde Ligeiro, Sempre Verde, Cariri, Azul, and Corujinha landraces and BRS-Pajeú, BRS-Novaera, and BRS-Guariba commercial cultivars, in irrigated and non-irrigated production fields, under agroecological cultivation conditions and without disease and pest management, allowed the identification of the genotypes that are best adapted to the studied edaphoclimatic conditions of the semi-arid region of Paraíba. Morpho-agronomic differences were identified among the genotypes. Regarding molecular differences, the genotypes had low intrapopulation genetic diversity and were separated into two groups by cluster analysis. Group I included BRS-Pajeú, BRS-Novaera, BRS-Guariba, Sempre Verde, Verde Ligeiro, and Azul genotypes. Group II included Cariri and Corujinha genotypes. Differences in the incidence of powdery mildew and cercospora leaf spot were found among the genotypes, as well as differences in pod bug infestation. The most productive genotypes with the lowest intensity of diseases and pests in irrigated fields were Corujinha, Sempre Verde, and Azul landraces, and BRS-Pajeú and BRS-Guariba commercial cultivars; and under rainfed conditions, the most adapted cultivar was the Sempre Verde landrace. Corujinha, Sempre Verde, and Azul landraces showed equivalent or superior production to the commercial cultivars in irrigated fields, and Sempre Verde landrace in non-irrigated fields, confirming the hypothesis that the selection of cowpea genotypes by generations of farming families under semi-arid edaphoclimatic conditions, with biotic and abiotic stress, furnishes productive genetics that are resistant to water stress conditions and adapted to agroecological production systems.

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Data Availability Statement

All the data supporting the results of this study were published in the manuscript itself.

References

AGÊNCIA EXECUTIVA DE GESTÃO DAS ÁGUAS – AESA, 2019 [viewed 10 December 2019]. Available from: https://www.aesa.pb.gov.br/chuvas/

ALBERT, I.C.L., NORONHA, M.A., MARTINS, R.B. and MICHEREFF, A.J., 2008. Escala diagramática para avaliação da severidade da cercosporiose em caupi. *Ciência Rural*, vol. 38, no. 7, pp. 2029-2032. http://doi.org/10.1590/S0103-84782008000700036.

ALGHAMDI, S.S., KHAN, M.A., MIGDADI, H.M., EL-HARTY, E.H., AFZAL, M. and FAROOQ, M., 2019. Biochemical and molecular characterization of cowpea landraces using seed storage proteins and SRAP marker patterns. *Saudi Journal of Biological Sciences*, vol. 26, no. 1, pp. 74-82. http://doi.org/10.1016/j.sjbs.2018.09.004. PMid:30622409.

ALVES, A.S.S.C., ACIOLI, A.N.S., FERREIRA, G.S.L. and SILVA, N.M., 2022. Effect of cowpea (*Vigna unguiculata* L. Walp.) sowing season on population dynamics of pest insects. *Arquivos do Instituto Biológico*, vol. 89, no. 1-8, pp. e00322021. http://doi.org/10.1590/1808-1657000322021.

ARAÚJO, L.B.R., PINHEIRO, M.S., FIEGE, L.B.C., BERTINI, C.H.C.M. and DOVALE, J.C., 2019. Agronomic potential and genetic diversity of landraces of cowpea of the state of Ceará. *Revista Caatinga*, vol. 32, no. 3, pp. 698-708. http://doi.org/10.1590/1983-21252019v32n314rc.

ARAÚJO, L.B.R., TOMAZ, F.L.S., FREITAS, L.M., BERTINI, C.H.C.M. and DOVALE, J.C., 2025. Recommendation of cowpea genotypes based on adaptability, stability and grain darkening. *Revista Ciência Agronômica*, vol. 56, pp. e202292875. http://doi.org/10.5935/1806-6690.20250002.

ASARE, A.T., GOWDA, B.S., GALYUON, K.A., ABOAGYE, L.L., TAKRAMA, J.F. and TIMKO, M.P., 2010. Assessment of the genetic diversity in cowpea (*Vigna unguiculata* L. Walp) germplasm from Ghana using simple sequence repeat markers. *Plant Genetic Resources*, vol. 8, no. 2, pp. 142-150. http://doi.org/10.1017/S1479262110000092.

ASMA, HUSSAIN, M., ALI, N., MASOOD, R., AKBAR, N., SHAFQAT, N. and SHAD, N., 2024. Agro-morphological characterization of Pakistani maize accessions using qualitative and quantitative traits. *Brazilian Journal of Biology = Revista Brasileira de Biologia*, vol. 84, pp. e259729. http://doi.org/10.1590/1519-6984.259729.

CAMPOS, F.L., FREIRE FILHO, F.R., LOPES, A.C.A., RIBEIRO, V.Q., SILVA, R.Q.B. and ROCHA, M.M., 2000. Phenological cycle in cowpea (*Vigna unguiculata* L. Walp.): a proposal of development scale. *Revista Científica Rural*, vol. 5, no. 2, pp. 110-116.

CARVALHO, M., BEBELI, P.J., PEREIRA, G., CASTRO, I., EGEA-GILABERT, C., MATOS, M., LAZARIDI, E., DUARTE, I., LINO-NETO, T., NTATSI, G., RODRIGUES, M., SAVVAS, D., ROSA, E. and CARNIDE, V., 2017. European cowpea landraces for a more sustainable agriculture system and novel foods. *Journal of the Science of Food and Agriculture*, vol. 97, no. 13, pp. 4399-4407. http://doi.org/10.1002/jsfa.8378. PMid:28419490.

CHEN, H., CHEN, H., HU, L., WANG, L., WANG, S., WANG, M. and CHENG, X., 2017. Genetic diversity and a population structure analysis of accessions in the Chinese cowpea (*Vigna unguiculata* (L.) Walp.) germplasm collection. *The Crop Journal*, vol. 5, no. 5, pp. 363-372. http://doi.org/10.1016/j.cj.2017.04.002.

DE RON, A.P., BEBELI, P.J., NEGRI, V., PATTO, M.C.V. and REVILLA, P., 2018. Warm season grain legume landraces from the south of Europe for germplasm conservation and genetic improvement. *Frontiers in Plant Science*, vol. 9, pp. 1524. http://doi.org/10.3389/fpls.2018.01524. PMid:30405662.

DIAS, F.T.C., BERTINI, C.H.C.M., SILVA, A.P.M. and CAVALCANTI, J.J.V., 2015. Genetic variability in early-cycle erect cowpea analyzed with RAPD and ISSR markers. *Revista Ciência Agronômica*, vol. 46, no. 3, pp. 563-572. http://doi.org/10.5935/1806-6690.20150039.

EGBADZOR, K.F., OFORI, K., YEBOAH, M., ABOAGYE, L.M., OPOKU-AGYEMAN, M.O., DANQUAH, E.Y. and OFFEI, S.K., 2014. Diversity in 113 cowpea [*Vigna unguiculata* (L) Walp] accessions assessed with 458 SNP markers. *SpringerPlus*, vol. 3, no. 1, pp. 541. http://doi.org/10.1186/2193-1801-3-541. PMid:25332852.

FERREIRA, M.E. and GRATTAPAGLIA, D., 1998. *Introdução ao uso de marcadores moleculares em análise genética*. 3rd ed. Brasília: Embrapa-Cenargen. 255 p.

FOOD AND AGRICULTURE ORGANIZATION DATABASE – FAOSTAT, 2025 [viewed 23 January 2026]. Available from: https://www.fao.org/faostat/en/#data

FRANCISCO, P.R.M., MEDEIROS, R.M., SANTOS, D. and MATOS, R.M., 2015. Classificação Climática de Köppen e Thornthwaite para o Estado da Paraíba. *Revista Brasileira de Geografia Física*, vol. 08, no. 04, pp. 1006-1016. http://doi.org/10.5935/1984-2295.20150049.

GAJERA, H.P., DOMADIYA, R.K., PATEL, S.V. and GOLAKIYA, B.A., 2014. Appraisal of RAPD and ISSR markers for genetic diversity analysis among cowpea (*Vigna unguiculata* L.) genotypes. *Journal of Crop Science and Biotechnology*, vol. 17, no. 2, pp. 79-88. http://doi.org/10.1007/s12892-013-0062-1.

HAMIDOU, F., ZOMBRE, G. and BRACONNIER, S., 2007. Physiological and biochemical responses of cowpea genotypes to water stress under glasshouse and field conditions. *Journal Agronomy & Crop Science*, vol. 193, no. 4, pp. 229-237. http://doi.org/10.1111/j.1439-037X.2007.00253.x.

INTERNATIONAL BOARD FOR PLANT GENETIC RESOURCES SECRETARIAL – IBPGR, 2007. *Descriptors for Phaseolus vulgaris*. Rome: IBPGR. 32 p.

KIM, D.-K., IWAR, K., OCHAR, K., PARK, S.-Y., GO, E.-B., LEE, K.-D. and KIM, S.-H., 2024. Cowpea (*Vigna unguiculata*) cultivation and breeding in the Republic of Korea: advances and future perpectives. *Agronomy*, vol. 14, no. 11, pp. e2679. http://doi.org/10.3390/agronomy14112679.

KIMURA, M. and CROW, J.F., 1964. The number of alleles that can be maintained in a finite population. *Genetics*, vol. 49, no. 4, pp. 725-738. http://doi.org/10.1093/genetics/49.4.725. PMid:14156929.

KÖPPEN, W. and GEIGER, R., 1928. *Klimate der Erde*. Gotha: Verlag Justus Perthes.

MAFAKHERI, K., BIHAMTA, M.R. and ABBASI, A.R., 2017. Assessment of genetic diversity in cowpea (*Vigna unguiculata* L.) germplasm using morphological and molecular characterization. *Cogent Food & Agriculture*, vol. 3, no. 1, pp. e1327092. http://doi.org/10.1080/23311932.2017.1327092.

MELO, R.A., ALMEIDA, C.M.A., SILVA, M.V. and MELO, P.C.T., 2011. Caracterização molecular de genótipos de feijão-caupi. *Horticultura Brasileira*, vol. 29, pp. S84-S91.

MELO, A.S., SILVA, S.S.S., SILVA, J.W.P., OLIVEIRA, P.H.A., SUÁREZ, N.D.L.P., CALVET, E.C. and RIBEIRO, J.E.S., 2024. Induced resistance to *Crinocerus sanctus* (Hemiptera: Coreidae) in cowpea through silicon application. *Journal of Crop Protection*, vol. 13, no. 4, pp. 321-332.

MONTALVÁN, R., MAIA, J.P., MACIEL, S.V.P.A., RAMOS, S.R.R. and FREIRE FILHO, F.R., 2015. *Base genética das cultivares brasileiras de feijão-caupi*. Belém: Embrapa Meio-Norte.

MORILLO, A.C., MANJARRES, E.H. and PEDREROS, M.C., 2023. Characterization of yellow pitahaya (*Selenicereus megalanthus* Hae.) genotypes under two productive systems in Colombia. *Brazilian Journal of Biology = Revista Brasileira de Biologia*, vol. 83, pp. e274152. http://doi.org/10.1590/1519-6984.274152. PMid:37377291.

NASCIMENTO, R.L.X., SOUZA, C.C., GRASSI, G. and OLIVEIRA, M.A.N., 2022. *Caderno de caracterização: estado da Paraíba*. Brasília: Codevasf. 129 p.

NEI, M., 1973. Analysis of gene diversity in subdivided populations. *Proceedings of the National Academy of Sciences of the United States of America*, vol. 70, no. 12, pp. 3321-3323. http://doi.org/10.1073/pnas.70.12.3321. PMid:4519626.

ONUMINYA, T.O., OGUNKANMI, M.A. and OGUNKANMI, L.A., 2023. Morphological characterization of selected cowpea [*Vigna unguiculata* (L.) Walp.] accessions from International Institute of Tropical Agriculture, Ibadan, Nigeria. *Nigerian Journal of Basic and Applied Sciences*, vol. 31, pp. 65-72. http://doi.org/10.4314/njbas.v31i1.8.

PARDEY-RODRÍGUEZ, C., RIVERA MESA, B.J., MORILLO, A.C. and MORILLO, Y., 2025. Molecular characterization of creole inbred lines from Magdalena, Colombia using Inter Simple Sequence Repeats (ISSRs). *Brazilian Journal of Biology = Revista Brasileira de Biologia*, vol. 85, pp. e298945. http://doi.org/10.1590/1519-6984.298945. PMid:41172530.

PATEL, C.G., PATEL, P.T., DHARAJIYA, D.T., PATEL, A.B., ZALA, H.N., KHATRI, A.B. and TIWARI, K.K., 2022. Morphological and molecular characterization of cowpea (*Vigna unguiculata* L. Walp.) genotypes. *Genetika*, vol. 54, no. 2, pp. 633-648. http://doi.org/10.2298/GENSR2202633P.

PAULINO, J.S. and GOMES, R.A., 2015. Sementes da Paixão: agroecologia e resgate da tradição. *Revista de Economia e Sociologia Rural*, vol. 53, no. 3, pp. 517-528. http://doi.org/10.1590/1234-56781806-9479005303008.

PIO-RIBEIRO, G., ASSIS FILHO, F.M. and ANDRADE, G.P., 2016. Doenças do feijão-caupi. In. L. AMORIM, J.A.M. REZENDO, A. BERGAMIN FILHO and L.E.A. CAMARGO, eds. *Manual de Fitopatologia.* Viçosa: Agronômica Ceres, pp. 373-381.

QUINTELA, E.D., 2001. *Manejo integrado de pragas do feijoeiro*. Goiás: Embrapa Arroz e Feijão, 46 p.

QUINTELA, E.D., SARTORATO, A., LOBO JÚNIOR, M. and COBUCCI, T., 2005. *Manejo fitossanitário do feijoeiro*. Goiás: Embrapa. 73 p.

RIYAZ, I., ZAFFAR, A., FATIMA, S., SHAFI, S., BHAT, R., SHOWKAT, S., KHAN, T., WANI, F.J., ZARGAR, S.M., PRASAD, P.V.V. and SOFI, P.A., 2025. Identification of water deficit stress tolerant genotypes of common bean using adaptive root and shoot traits under different screening systems. *Scientific Reports*, vol. 15, no. 1, pp. 19888. http://doi.org/10.1038/s41598-025-04635-8. PMid:40481126.

ROCHA, M.M., SILVA, K.J.D., FREIRE FILHO, F.R. and MENEZES JUNIOR, J.A.N., 2017. Cultivo de feijão-caupi. In: C. B. MATTOS and J. I. S. BARBOSA. *Sistemas de Produção*. Teresina: Embrapa Meio Norte.

SANTOS, A.S., SILVA, E.D., TAVARES, E.D., CURADO, F.F., SALES, J.F.S. and PEREIRA, L., 2016. *Desempenho de variedades crioulas e comerciais de feijão-macassar ou feijão-caupi no Agreste Paraibano*. Alagoas: Embrapa Tabuleiros Costeiros.

SCHOLES, R.J., 2020. The future of semi-arid regions: a weak fabric unravels. *Climate*, vol. 8, no. 3, pp. e43. http://doi.org/10.3390/cli8030043.

SISTEMA DE MONITORAMENTO AGROMETEREOLÓGICO – AGRITEMPO, 2025 [viewed 9 April 2025]. Available from: https://www.agritempo.gov.br/br/

SILVA, P.H.S., 2016. Pragas da cultura do feijão-caupi. In: E.A. Bastos, ed. *A cultura do feijão-caupi no Brasil*. Alagoas: Embrapa, 40 p.

TORRES, E.B., NÓBREGA, R.S.A., FERNANDES-JÚNIOR, P.I., SILVA, L.B., CARVALHO, G.S., MARINHO, R.C.N. and PAVAN, B.E., 2016. The damage caused by *Callosobruchus maculatus* on cowpea grains is dependent on the plant genotype. *Journal of the Science of Food and Agriculture*, vol. 96, no. 12, pp. 4276-4280. http://doi.org/10.1002/jsfa.7639. PMid:26800228.

YEH, F.C., YANG, R.C. and BOYLE, T., 1999. *POPGENE Version 1.32: Microsoft Window-Based Freeware for Population Genetics Analysis* [software]. Canada: University of Alberta.

ZAFEIRIOU, I., SAKELLARIOU, M. and MYLONA, P.V., 2023. Seed phenotyping and genetic diversity assessment of cowpea (V. unguiculata) germplasm collection. *Agronomy*, vol. 13, no. 1, pp. e.274. http://doi.org/10.3390/agronomy13010274.