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Research Paper

Evaluation of genetic diversity of cultivated and spontaneous accessions of cowpea (*Vigna unguiculata* Walp) in BURKINA FASO

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Abstract

In Burkina Faso, cowpea *[Vigna unguiculata (L.)* Walp*]* is the fourth largest crop after sorghum, maize and millet and the first interest economic food legume. Its techniques of cultivation and its yields experienced a substantial improvement in recent years. Nevertheless, recurrent attacks of fungi including *Macrophomina phaseolina* constitute a serious threat to the continuous improvement of its performance. In order to support sustainable way, cowpea production making the most of its genetic resources, an evaluation of the primary gene pool was performed. The objective of the study is to determine the level and structure of agro-morphological diversity and to identify characters and accessions of interest that could be used in breeding programs for the fight against fungal diseases *Macrophomina phaseolina*. Thus, 89 entries of cowpea consisting of 26 wild forms, 16 local ecotypes and 47 cultivars were characterized during raining season 2014 in a device of blocks of Fisher with three replications using 16 quantitative and 8 qualitative traits. The results showed that all quantitative traits discriminate accessions and that most accessions appreciated by cowpea producers and consumers have crawling ports (52.81%) with scarce to abundant foliage (87.53%), white beans (51.69%) and kidney-shaped (65.17%). Diversity was also observed between biological types and within each biological type. The 89 accessions were distributed into 4 groups based essentially on the characteristics of the vegetative system, cycle and performance. Group I consists of accessions with the lowest yields (PGP = 6,61 g and PCG = 4.1 g) and the longer cycles (74.82 JAS) while Group II contains the smallest accessions size (9.75 cm) and late flowering (47.9 JAS). Group III consists of the earlier accessions (39 j) and the highest yields (CG = 17.34 g). The fourth group consists of the highest accessions to the longest pod (136.54mm), the broader seed and long cycle (73.94 JAS). Groups II disease resistant and III and IV groups could be used in cowpea breeding programs.

Keywords: *Vigna unguiculata,* cowpea, agro-morphological variability, Burkina Faso.

Introduction

Cowpea *[Vigna unguiculata* (L.) Walp*] i*s a leading global food legume. It provides more than half of the protein consumed in some tropical countries [1]. Burkina Faso is the third largest producer of cowpea after Nigeria and Niger[2]. This crop is cultivated in all agro-ecological regions of the country in pure culture or in association with cereals such as sorghum and millet. Cowpea is the fourth crop after sorghum, maize and millet[3]. Annual production ranged from 376,225 tons in 2001 to 626,113 tons in

2010 [4]. Despite yield and production performance observed that culture is confronted to many abiotic and biotic constraints which greatly reduce its performance. Among the abiotic constraints of cowpea, there is drought, high temperatures, acidity and poverty of soil[5]. As for biotic constraints, it retains weeds like Striga[6,7], virus diseases[8,9], insect attacks[10], brown spots[11] and charcoal rot[12]. The resolution of certain biotic constraints necessarily involves the exploitation of interest genes in wild forms of cowpea. Indeed, alongside the cultivated forms, there is wild cowpea. The study of genetic diversity of cowpea appears as one of the best ways for the collection, conservation and use for crop improvement[13]. In Burkina Faso, all previous studies were based only on the cultivars and local ecotypes[7]. No study has integrated the wild forms.

To complement the knowledge about the state of the genetic diversity of the primary gene pool of cowpea culture in Burkina, it appeared necessary to extend the study to the wild forms of cowpea *[Vigna unguiculata* (L.) Walp]*.*The study is well conducted to determine the level and structure of the agro-morphological diversity between biological types and within each biological type.

Materials and Methods

Experimental site

The study was conducted in 2014 in the experimental station of Environment and Agricultural Research Institute (INERA) to Kamboinse. The village is located at 7 km north of Ouagadougou (12° 45 north latitude, 1° 53 west longitude and 290.56 m of sub- Sudan zone). During 2014, the cumulative annual rainfall was 790.5 mm (Figure 1).

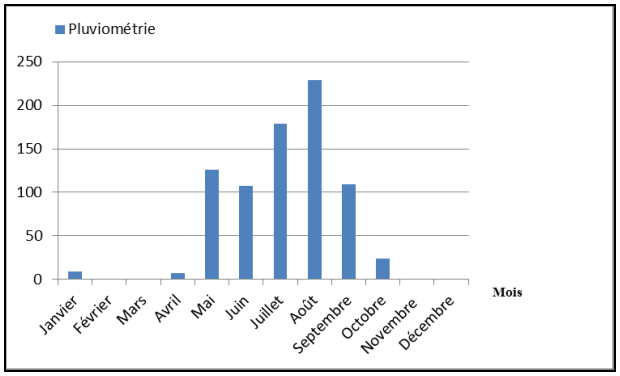

Figure 1: **Annual rainfall during 2014**

Plant material

Eighty- nine (89) entries of Cowpea consisted of 26 wild forms, 47 local ecotypes and 16 cultivars (Table 1) have been characterized. This material obtained from the INERA gene bank in Kamboinse. Entries come from several African countries (Botswana, Burkina Faso, Cameroon, Congo Brazzaville, Ghana, Malawi, Niger, Nigeria, Senegal, Sudan and Zambia) and USA.

Experimental device

Test was conducted in a Randomized Complete Block Design (RCBD) with three replications. Sowing took place during August 2014 and each variety was planted on a 4m line consisting of 21 bunches at the rate of one grain per hole (63 seeds per entry). The spacing between the planting holes and the lines were respectively 20 cm and 80 cm. No phytosanitary treatment of grain has previously been done before sowing. To facilitate germination, seeds of wild varieties have been scarified before sowing according to [14,15]. Two hoeing were done respectively 21 and 42 days after sowing. A manual weeding was done at 33 DAS.

Data collection

The agro-morphological study was done using 24 characters including 16 quantitative and eight (8) qualitative traits selected from the descriptor of cowpea[16]. Thus, in the vegetative stage, the quantitative traits measured are: height of plant (HP), length of the terminal leaflet (LTF), number of nodes on the main stem (NNS) and number of main branches by plant (NMB). The characters date of 50% flowering (DF), length of stalk per plant (LSt), date of 95% maturity (DM), number of pods per peduncle (NPPe) , weight of pods per plant (WPP), length of the pods (LP), number of boxes per pod (NBP), number of eggs per pod (NEP), number of seeds per pod (NSP), length of the seeds (LSe), width of the seeds (WSe) and weight of 100 seeds (W100) were measured at the flowering and maturity stages.

Table 1: List of accessions used for the cowpea genetic diversity evaluation

N°	Species	Type	Origin	N°	Species	Type	Origin
1	524B	A	USA	46	KVx525	A	BF
2	58-57	A	Sén	47	KVx61-1	A	BF
3	Apagbaala	A	Gh	48	KVx640	A	BF
4	B05 5a	S	BF	49	KVx65-114	A	BF
5	B07 13	S	BF	50	KVx745-11P	A	BF
6	B09-46	S	BF	51	KVx780-1	A	BF
7	B12-07a	S	BF	52	KVx780-3	A	BF
8	B16 1a	S	BF	53	KVx780-4	A	BF
9	B27 07a	S	BF	54	KVx780-6	A	BF
10	B28 02b	S	BF	55	KVx780-9	A	BF
11	B30 01	S	BF	56	MelaKH	A	Sén
12	B301	A	Bots	57	Moussa local	Loc	BF
13	Bambey-21	A	USA	58	N°2300 Profil 45	S	Cam
14	Bolga local	Loc	BF	59	N°3076 Profil 51b	S	Cam
15	CB27	A	USA	60	N°3076-Profil-22	S	Cam
16	CB46	A	USA	61	N°91 Prrofil 4	S	Cam
17	Djouroum local	Loc	BF	62	Nafi	A	BF
18	Gaoua local-2	Loc	BF	63	Nafi HT-1	A	BF
19	Goinkoro-2	Loc	BF	64	Nafi HT-2	A	BF
20	Gorom local	Loc	BF	65	Niizwé (IT98K-205-8)	A	IITA
21	Gourgou	A	BF	66	NS -1 BF	S	BF
22	HTR	A	Nig	67	Pâ local-2	Loc	BF
23	IT81D-994	A	IITA-	68	Pa local-GJ	Loc	BF
24	IT82D-849	A	IITA-	69	Pobé local	Loc	BF
25	IT84S-2049	A	IITA-	70	Pouytenga-3	Loc	BF
26	IT84S-2246	A	IITA-	71	Sakoula local	Loc	BF
27	IT93K-503-1	A	IITA-	72	SP118 Profil-24	S	Cam
28	IT93K-693-2	A	IITA-	73	SP130 Profil-19	S	Cam
29	IT95K-14 79	A	IITA-	74	SP17 Profil-30b	S	Cam
30	IT95K-627-4	A	IITA-	75	SP180	S	Con B
31	IT97K-207-15	A	IITA-	76	SP19A Profil-41	S	Cam
32	IT97K-499-35	A	IITA-	77	SP369A Profil-39B	S	Soud
33	IT98K-317-2	A	IITA-	78	SP5 Profil-51b	S	Cam
34	Kaya local	Loc	BF	79	SP88 Profil-13A	S	Cam
35	KN-1	A	BF	80	SP9 Profil-49a	S	Cam
36	Koakin local	Loc	BF	81	Tiligré	A	BF
37	Kolondura local	Loc	BF	82	TN88-63	A	Nig
38	Komkallé	A	BF	83	TV 365 Profil 41-b	S	Mal
39	Komsaré	Loc	BF	84	TV286b Profil-12	S	Bots
40	KVx295-2-124-61	A	BF	85	TV359 Profil-34	S	Zam
41	KVx30-309-6 G	A	BF	86	TV709 Profil-7	S	Zam
42	KVx396-4-5-2D	A	BF	87	TVU 14 676	A	IITA
43	KVx402-5-2	A	BF	88	Woango-1	A	BF
44	KVx404-8-1	A	BF	89	Yiisyandé (IT99K-573-2-1)	A	IITA
45	KVx414-22-2	A	BF				

Type : biological type, A : cultivars, Loc : local ecotypes, S : wild form, Origin : Bots : Botswana, BF : Burkina Faso, Cam : Cameroon, Con B : Congo Brazzaville, Gh : Ghana, Mal : Malawi, Nig : Niger, Nige : Nigeria, Sen : Senegal, Soud : Soudan, USA : United State of America, Zam : Zambia

Qualitative traits measured in the vegetative stage are abundance of vegetation (AV), shape of the terminal leaflet (STL), growth habit (GH), and leaf color (LC). The other qualitative characteristics such as color of the flower (CFl), texture of the seed (TSe), shape of the seed (SSe), color of eye of the seed (CES) and color of seed (CSe) were noted at flowering and maturity stages.

Statistical analysis

Four software (Excel, GenStat, Statistica version 6 and XLSTAT) were used for data analysis. Descriptive analysis of statistical data of the qualitative phenotypic variables, were obtained using EXCEL software.

An analysis of variance with Newman-Keuls (SNK) separation average test was done using the software GenStat V 4.10.3 in order to determine discriminating quantitative characters. Cluster analysis for divergence among genotypes was performed according to Ward method with Statistica version 6 from the interest's characters such as plant height (HP), date of 95% maturity (DM), length of seeds (LSe) and weight of 100 seeds (W100). The groups were then characterized through the factorial discriminating analysis (FDA) with XLSTAT Version 7.5.2.

Results and Discussion

Variation of qualitative traits and Characteristics of biological groups

According to the eight (8) characters related to vegetative port, flowering and seeds (Table 2), heterogeneity exists between accessions. An important variation is observed in the vegetative port. Cowpea plants are crawling (52.87%) or semi-erects (30.34%). They have the sparse (34.83%) to abundant foliage (42.70%) and white (47.19%) or dark-violet (41.57%) flowers. Thus, wild forms (100%) and 87.5% of the local ecotypes are crawling while cultivars are semi- erect (53.19%), erected (31.92%) or crawling (14.89%).

Table 2: Distribution of 89 accessions of cowpea based on eight qualitative traits

Traits	Modalities	Frequency	Traits	Modalities	Frequency
AV	Abundant	42,7	**CSe**	Black	7,87
	Scarce	34,83		Brown	14,61
	Very scarce	22,47		Brown-ocher	14,61
HG	Crawling	52,81		Cream	1,12
	Semi-erect	30,34		White	51,69
	Erected	16,85		Beige-brown	3,37
CFl	White	47,19		Red	4,49
	Dark-violet	41,57		Holstein	1,12
	Mallow	11,24	**SSe**	Kidney shape	65,17
CES	White	91,01		Rounded	6,74
	Black	6,74		Rhomboïd	21,35
	Eye absent	1,12		Egg-shaped	6,74
	Brown-wide-	1,12	**TSe**	Smooth	49,44
CL	Dark-green	48,31		Smooth to rough	2,25
	Green-intermediate	44,94		Rought to à wrinkled	4,49
	Pale green	6,74		Wrinkly	43,82

AV: abundance of vegetation, HG: habitus of growth, CFl: color of the flower, CL: color of leaf, CS: color of seed, CES: color of eye of the seed, SSe: shape of the seed, TSe: texture of the seed

The characteristics of seeds of accessions presented in Figure 2 show an important variability in many traits. Thus, colors of seeds are white (78.72%), brown (8.51%), red (4.26%) , cream (2.13%), beige-brown (2.13%), brown-ocher (2.13%) or black and white Holstein (2.13 %). the texture of the seeds clearly are wrinkled (61.70%), smooth (25.53%) , roughened to wrinkled (8.51%) and smooth to rough (4.26%).The shape of the seeds are kidney shape (87.23%), ovoid (6.38%), rounded (4.26%), or rhomboids (2.13%). Most of Seeds are kidney shaped (65.17%), white color (51.69%) with a smooth (49.44%) or wrinkled (43.82%) texture.

Wild forms (B12 07a, B27 07a, SP5 Profile 51b) have smaller seeds which are usually brown or brown-ocher (73.08%) and smooth while the seeds of cultivars (CB27, KVx61-1, *Apagbaala*) are more diverse. The shape of their seeds are often kidney (CB27 and KVx61-1) or rhomboids (*Apagbaala*) and the colors are white (CB27, KVX61-1) or red (*Apagbaala*). The texture of their seeds is wrinkled (61.70%), smooth (25.53%), roughened to wrinkled (8.51%) and smooth to rough (4.26%). The seeds of local ecotypes such as *Kaya local* are larger and white, but the size and color of some of them (B301 and *Kolondura* local) approach the wild forms.

Figure 2: Characteristics of seeds of cowpea accessions

Variation of quantitative traits of the whole collection
Results of analysis of variance (Table 3) performed on 15 variables reveal that all quantitative traits discriminate the accessions. Most of traits have low coefficient of variation (< 30%) except weight of pods per plant. The accessions have height ranging 5 to 40 cm and peduncles longs from 8 to 56 cm and a maturity cycle between 51 and 80 j after sowing. The average weight of pods per plant is 23.68 g while the average length of the seeds and the average weight of 100 seeds are respectively 7.35 mm and 13.1 g.

Variability within Biological groups based on quantitative traits
The analysis of variance within biological groups (Table 4) shows that all measured characters discriminate very significantly the accessions of each biological group. Therefore, an important diversity exists within cultivars, local ecotypes and wild forms.

Variability between biological groups based on quantitative traits
The results of Table 5 show the average of quantitative traits measured in the 3 biological types. Except the character maturity date, the results of analysis of variance of other data show a p-value<0.0001. These characters discriminate significantly the biological groups. The cultivars have the highest performances of following characters: plant height, length of the terminal leaflet, date of maturity, pod length, length and width of seeds and weight of a hundred seeds. Considering the same characters, the cultivars are followed respectively by the local ecotypes and the wild forms. The local ecotypes are distinguished by the highest number of nodes (5.514), number of branches per plant (5.829) and the weight of pods per plant while the wild forms are characterized by the highest values of date of 50 % flowering, length of stalk per plant, number of pods per peduncle, number of boxes

per pod, number of eggs per pod, number of seeds per pod and the lowest value of characters related to seeds and pod seeds.

Table 3: Results of Analysis of variance from all accessions for 16 quantitative traits

Variable	Minimum	Maximum	mean	CV (%)	F
HP (cm)	5,0	40,0	15,5	19,0	28,08**
LTF (mm)	4,8	14,5	9,118	8,3	33,49**
NNS	2,0	13,0	4,386	22,0	16,32**
NMB	2,0	10,0	5,389	20,0	6,89**
LSt (mm)	8,0	56,0	24,65	20,3	8,91**
DM (j)	51,0	80,0	67,6	3,9	69,26**
NPPe	1,0	5,0	2,348	18,8	13,13**
WPP (g)	1,5	129,0	23,68	36,0	26,14**
LP (cm)	15,62	219,9	119,4	12,2	28,69**
NBP	7,0	21,0	13,25	13,5	7,19**
NEP	1,0	25,0	11,91	15,2	6,6**
NSP	1,0	25,0	11,92	15,3	6,54**
LSe (mm)	3,28	11,88	7,395	8,5	80,53**
WSe (mm)	1,38	11,07	5,215	10,4	74,18**
W100 (g)	3,0	23,2	13,1	0,3	3,234E+0**5

*HP: height of plant, LTF: length of the terminal leaflet , NNS: number of nodes on the main stem, NMB: number of main branches by plant, DF: date of 50 % flowering, LSt: length of stalk per plant, DM: date of 95% maturity, NPPe: number of pods per peduncle, WPP: weight of pods per plant, LP: length of the pods, NBP: number of boxes per pod, NEP: number of eggs per pod, NSP: number of seeds per pod, LSe: length of the seeds, WSe: width of the seeds, W100: weight of 100 seeds F: coefficient of Fisher, **: significant at 1%.*

Table 4: **Analysis of variance within biological groups**

	Cultivars	Local ecotypes	Wild forms
	F	F	F
HP	19,665**	20,808**	17,207**
LTF	**35,073****	21,830**	7,774**
NNS	8,344**	36,194**	5,102**
NMB	6,704**	17,415**	3,872**
LSt	9,399**	15,615**	5,422**
DM	**56,054****	**86,807****	**144,182****
NPPe	4,558**	5,370**	**13,348****
WPP	12,347**	22,811**	12,012**
LP	9,439**	11,244**	3,264**
NBP	5,283**	13,938**	4,697**
NEP	5,935**	10,472**	3,686**
NSP	6,010**	9,603**	3,488**
LSe	17,688**	**35,820****	**2,241****
WSe	27,209**	14,363**	4,054**

*HP: height of plant, LTF: length of the terminal leaflet, NNS: number of nodes on the main stem, NMB: number of main branches by plant, LSt: length of stalk per plant, DM: date of 95% maturity, NPPe: number of pods per peduncle, WPP: weight of pods per plant, LP: length of the pods, NBP: number of boxes per pod, NEP: number of eggs per pod, NSP: number of seeds per pod, LSe: length of the seeds, WSe: width of the seeds,; F : coefficient of Fisher, **: significant at 1%*

Structure of the agro-morphological variability

The dendrogram (Figure 3) resulting from the Agglomerative Hierarchical Clustering shows at the truncation on the level of inertia 125 a distribution of the 89 accessions in 4 groups I, II , III and IV. The test of Lambda of Wilks in discriminant factorial analysis gives a value of F observed of 0.011

with a p-value <0.0001 at the threshold 5% confirming that these groups are separate entities. An Analysis of the squares of Mahalanobis distances between groups (Table 6) reveals that the 4 groups are very significantly different at the threshold 1%. The closest groups are I and II and the farthest are II and IV.

Table 5: Analysis of variance between biological types

Traits	Cultivars	Local	Wild	M	F	CV (%)	Pr.
HP	18,279a	11,822b	12,253b	15.5	155,607	38.92	<0,0001
LTF	9,871a	8,095b	8,245b	9,118	147,573	18.35	<0,0001
NNs	4,569b	5,514a	3,429c	4,386	99,987	37.07	<0,0001
Nmb	5,319b	5,829a	5,282b	5,389	8,287	26.15	0,000
DF	40,163b	39,500b	48,220a	42,406	274,974	14.24	<0,0001
Lst	24,676b	21,576c	26,244a	24,648	21,098	28.36	<0,0001
DM	68,160a	67,607ab	66,529b	67,597	3,522	11.86	0,030
Nppe	2,118b	2,164b	2,880a	2,348	143,172	29.47	<0,0001
WPP	30,441a	30,719a	7,104b	23,678	282,791	71.98	<0,0001
LP	136,149a	125,397b	84,434c	119,351	576,550	25.34	<0,0001
NBP	12,708c	13,471b	14,162a	13,252	35,724	17.74	<0,0001
NEP	11,438c	11,979b	12,761a	11,909	29,077	19.57	<0,0001
NSP	11,408c	12,064b	12,819a	11,922	33,161	19.68	<0,0001
LSe	8,616a	8,108b	4,705c	7,395	1214,248	27.42	<0,0001
WSe	6,247a	5,593b	3,043c	5,215	991,761	32.44	<0,0001
W100	17,674a	13,866b	4,039c	13,097	2225,932	49.88	<0,0001

*HP: height of plant, LTF: length of the terminal leaflet , NNS: number of nodes on the main stem, NMB: number of main branches by plant, DF: date of 50 % flowering, LSt: length of stalk per plant, DM: date of 95% maturity, NPPe: number of pods per peduncle, WPP: weight of pods per plant, LP: length of the pods, NBP: number of boxes per pod, NEP: number of eggs per pod, NSP: number of seeds per pod, LSe: length of the seeds, WSe: width of the seeds, W100: weight of 100 seeds, F : coefficient of Fisher, M: mean of character, CV: coefficient of variation, **: significant at 1%, Pr.: probability*

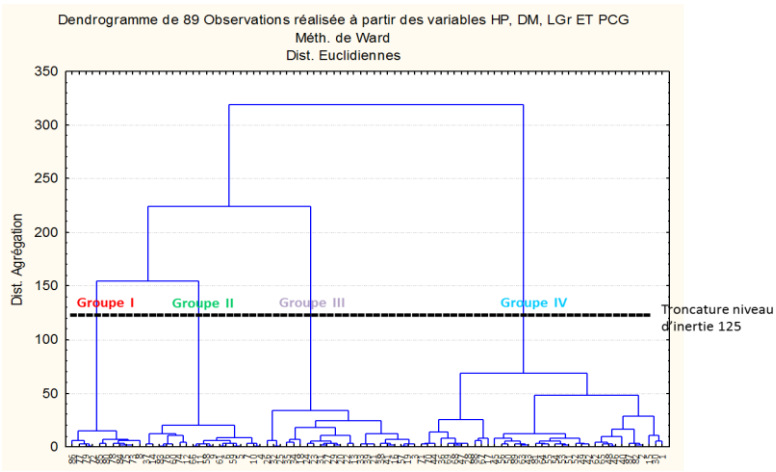

Figure 3 : Dendrogram showing the clustering pattern in Cowpea accessions based on Quantitative traits

The structuring of groups is strongly influenced by biological group. Thus, Group I consists exclusively of 11 wild forms (100 %), while Group II consists of 15 wild forms (84.4%) and 3 local ecotypes (15.6%). Group III includes 18 cultivars (75%) and 6 local ecotypes (25%).

Table 6: Squares of Mahalanobis distances between groups

	1	2	3
1			
2	25,408**		
3	66,990**	41,231**	
4	48,751**	70,360**	25,690**

The group 4 is constituted of 29 cultivars (80.56 %) and 7 local ecotypes (19.44%). The groups I and II are those that seeds are rhomboids and smooth while groups III and IV have essentially kidney-shaped and wrinkled seeds.

Characteristics of the groups

Eleven of the 16 characters discriminate very significantly the 4 groups. These characters are related to vegetative, cycle and weight. The position of individuals and gravity centers of groups in the canonical system of axes 1 and 2 with 98.90% of inertia in the factorial discriminant analysis is presented in figure 4. The coordinates of the variables show that characters, height of plant, length of the pods, weight of pods per plant, width of the seed, length of the seeds, weight of 100 seeds are strongly and positively correlated with axis 1 while, date of 50% flowering is negatively correlated to the same axis. However, the axis 2 is explained by the date of 95% maturity trait. The comparison of groups (Table 7) reveals that except number of main branches per plant and length of stalk per plant, the other characters discriminate significantly the four groups.

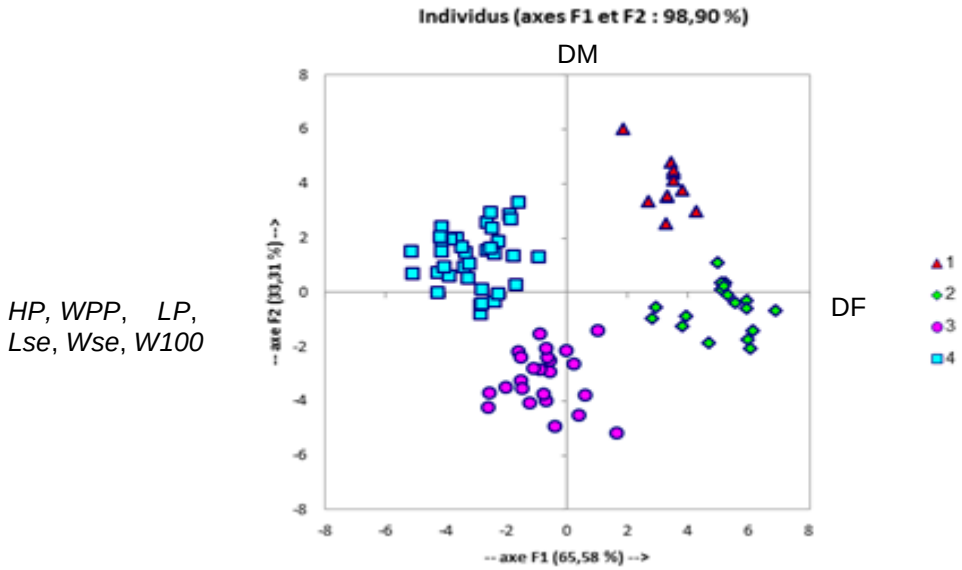

Figure 4: Discriminant analysis performed on two axes (F1&F2) on the 4 classes obtained through hierarchical clustering

Table 7: average performance of four cowpea groups present in Burkina Faso for the discriminating characters

Group	I	II	III	IV	F	PR.
Frequency	11	18	24	36		
HP	15,781	9,759c	13,864b	19,398a	25,345	<0,0001
LTF	8,313b	7,992b	9,556a	9,627a	7,768	0,000
NNS	3,573b	3,398b	4,579a	4,994a	9,112	<0,0001
NMB	5,191a	5,246a	5,481a	5,458a	0,405	0,750
DF	47,909	48,389a	39,500b	39,694b	22,732	<0,0001
LSt	27,291	25,067a	25,417a	23,094a	0,329	0,08
DM	74,827	60,667b	59,958b	73,940a	141,775	<0,0001
NPPe	3,136a	2,608b	2,113c	2,133c	19,502	<0,0001
WPP	6,613b	9,679b	29,308a	32,124a	28,240	<0,0001
LP	85,579	89,342b	131,557a	136,546b	56,376	<0,0001
NBP	13,709	14,550a	13,479b	12,314c	10,782	<0,0001
NEP	12,555	13,035a	11,688bc	11,292c	6,600	0,000
NSP	12,573	13,085a	11,667bc	11,314c	6,831	0,000
LSe	4,757b	4,919b	8,639a	8,610a	135,536	<0,0001
WSe	3,139c	3,295c	5,845b	6,371a	79,757	<0,0001
W100	4,109b	4,769b	17,345a	17,150a	141,663	<0,0001

HP: height of plant, LTF: length of the terminal leaflet , NNS: number of nodes on the main stem, NMB: number of main branches by plant, DF: date of 50 % flowering, LSt: length of stalk per plant, DM: date of 95% maturity, NPPe: number of pods per peduncle, WPP: weight of pods per plant, LP: length of the pods, NBP: number of boxes per pod, NEP: number of eggs per pod, NSP: number of seeds per pod, LSe: length of the seeds, WSe: width of the seeds, W100: weight of 100 seeds F : coefficient of Fisher, Pr : probability

These results reflect the existence of morphological diversity among groups. Thus, group I consists of accessions to the lowest yields (WPP = 6.61 g, LP = 85.57 mm, LSe = 4.75 mm, W100 = 4.10 g) and a long cycle (DF = 47.90 JAS) and group II contains smaller accessions (HP = 9.75 cm) which have a very long cycle (DF = 48.38 JAS). The group III consists of the earlier accessions (DF = 39.5 JAS) with highest grain yield (W100 = 17.34 g) while group IV is characterized by larger accessions (HP = 19.39 cm) with short cycles and higher yields pods (LP = 136.54 mm, WPP = 32.12 g).

Genetic diversity of cultivated and spontaneous forms of cowpeas in Burkina Faso

Cowpea is an important crop and a power source of food in Burkina Faso. Despite the significant variation observed within each group of biological cowpea, it remains low compared to crops such as sweet grains sorghum[17]. These results could be explained by the generally low level of polymorphism in the genus *Vigna*[18-22].

Our results showed also a variation between biological groups. Thus, the crawling port observed in all the wild forms is reduced when switching to local ecotypes whereas at the cultivars, the dominant port is semi-erect. Indeed, there is a strong genetic diversity within the genus *Vigna* including wild forms [23]. In general, the cowpea plants were crawling ports, abundant or scarce foliage and white flowers. These results are confirmed by those of[24] which showed that vegetative erect ports, semi-erect and crawling discriminate ecotypes of cowpea. The crawling port is characteristic of local ecotypes[7] and wild forms. The seeds are frequently kidney shape, white with a smooth or wrinkled texture.[7,24] showed also that the seeds of the cutlivars are often kidney-shaped and white. Previous studies already revealed a net polymorphism in wild forms of cowpea of [25], local ecotypes[7,21,26] and cultivars [27].

Highly significant differences were too observed in the accessions except the maturity date. These results are similar to[28]. Thus, the size and length of seeds oppose wild forms to local ecotypes and cultivars. These results have been shown in previous studies[29]. This would be related to the selection criteria. Indeed, most of the characters of interest used in the selection are oriented to the grains[7].

Organization of agro-morphological diversity

Despite the net diversity observed within biological groups, agro-morphological groups can be constituted according to the characters of interest. The structuring into 4 groups is closely linked to the biological group. Thus, Group I consists exclusively of wild forms characterized by dehiscent pods, seeds and small pods and seed dormancy that distinguish them to cultivars[1,30]. This result confirms that these accessions are not still exploited by farmers. They retain their primitive characteristics. The great variability in wild forms of cowpea reflects a broad genetic base. The cultivated forms were domesticated and have lost part of the genetic diversity[25]. Low yields are due to the length of their cycle which does not allow the plants to be mature before the end of the rainy season. The late implementation of the test had probably a negative impact on the performance of late varieties. Indeed, that was shown in previous studies. According to[31], drought is a one of performance reduction factors in cowpea. Group II constituted of wild forms and local ecotypes could reveal the existence of similitude between these biological groups. The distinction of this group would be linked to the dehiscence of pods [32]. The results of[15], already showed a strong genetic proximity between local ecotypes and wild forms of cowpea. Indeed, other studies about genetic diversity of *Vigna* gender [19] using microsatellite markers confirmed that the contribution of within-population genetic diversity to the total diversity is greater than the inter- population genetic diversity. The results of [15], already have shown a strong genetic proximity between local ecotypes and wild forms of cowpea. Indeed, other studies about genetic diversity of *Vigna* gender[19] using microsatellite markers confirmed that the contribution of the genetic diversity in each population to the total diversity is greater that the genetic diversity between populations. Group III including cultivars and local ecotypes has the high performance such as seed yield and pod length. These results are explained by the fact that the pod length proves a combination of seed length and the number of ovum[33]. Finally the group IV consists also of cultivars and local ecotypes. This group has the largest number of local ecotypes. This is the group that has the highest plant (with pods and seeds the longest. This group is also distinguished by its kidney-shaped seeds. Considering their response to the attack of insects and diseases, the Group I and II appear to those who adapt most compared to groups III and IV. This suggests that the groups I and II resistance traits can be transferred to other groups (III and IV).

Conclusion

This study revealed important agro-morphological diversity within biological groups and between them. This diversity was then structured into 4 groups based on the weight of seeds per pod, pod length, weight of pods per plant and stage maturity. Except group I, the other groups contain the accessions of different biological types showing the existence of some proximity between them. The groups I and II are those of the rhomboids and smooth seeds while groups III and IV have essentially kidney-shaped and wrinkled seeds and early flowering. These preliminary results showed the importance of the existing potential in Burkina. These accessions could constitute a reservoir of genes. Future research should continue in the direction of improvement and valorization of these plants genetics resources. The characters of interest such as early of cycle, white color and wrinkled texture and kidney-shaped of seeds observed in the groups III and IV could be combined with disease resistance observed in Group II. The disease resistance genes could be transferred by crossing from

local ecotypes and cultivars. A characterization of these accessions using microsatellite markers or SNPs could help supplement the results of this study and better understand the level and structure of genetic diversity of material.

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