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Agromorphological Evaluation of 44 lines of Mung Bean (*Vigna radiata* (L.) Wilczek) Introduced in Burkina Faso

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Abstract

Mung bean (Vigna radiata L. Wilczek) is an important annual legume which is well suited to dry areas, like Burkina Faso where it is still an orphan legume. The present study was conducted to evaluate 44 mung bean genotypes introduced in Burkina Faso and to determine genetic diversity in this collection using both quantitative and qualitative traits. A field experiment was conducted in an augmented bloc design with three blocks and an extra

early maturing cowpea variety as check. Data were recorded on six (06) quantitative traits and seven (07) qualitative traits. For qualitative traits, diversity was revealed in four parameters including hypocotyl's color, seed coat color, pods and stem pubescence. Significant genetic variability was revealed among genotypes for all the quantitative characters. Phenotypic coefficient of variation (PCV) was higher than Genotypic coefficient of variation (GCV) for all characters studied indicating the influence of environmental effect on the characters. The GCV and PCV estimates were high for number of pods per plant followed by plant height and hundred seeds weigh. The high heritability coupled with high genetic advanced as percent of mean observed for these traits suggest an important genetic gain in genetic improvement for these characters. The genetic diversity observed was grouped into five clusters. Mungbean lines were grouped into four clusters and the cowpea variety used as check crop in this trial was clustered apart. This genetic diversity, both qualitatively and quantitatively, will help enrich local biodiversity in terms of legumes in general and mung bean in particular and constitutes an important basis for a future mungbean breeding program

Keywords: Mung Bean, Genetic Diversity, Heritability, Genetic Advance

Introduction

Mung bean also known as green gram [*Vigna radiata* (L.) Wilczek] belongs to the family of *Leguminosae*, subfamily of *Papilionoideae* and genus *Vigna*. It is a diploïde crop with a number of chromosomes 2n = 22 (Karpechenko, 1925 ; Krishnan and De, 1965). This grain legume is native of Asia and mainly cultivated in India where it is of vital importance in terms of nutrition, ecology and economy. Mungbean seeds are rich in proteins (~24% easily digestible protein), fiber, antioxidants, and phytonutrients (Itoh et al., 2006). This crop is rich in lysine that is predominantly deficient amino acid in cereals (Baskaran et al., 2009). It is also a legume of major importance due to its short maturing cycle. Moreover, according to Shil and Bandopadhya (2007), mung bean is highly digestible and produces low flatulence factor. Though it is produced in many African countries, mung bean is not a major crop in this area (Mogotsi, 2006). Thus, in Burkina Faso, this legume is still a minor crop as compared to cowpea (*Vigna unguiculata*), groundnut (*Arachis hypogaea*) and Bambara-groundnut (*Vigna subteranea*) despite its remarkable ecological and nutritional importance in a context of climate change. Also, only one variety of Mung bean exists in Burkina Faso and is being promoted. In order to enhance local biodiversity regarding legume family and enrich

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nutrition of most undernourished people that live on a mono carbohydrate diet (e.g.maize or rice), fifty (50) accessions of mung bean was introduced in Burkina Faso from Australia in 2016. The objective of this study is to assess the genetic diversity within this collection of mung bean accessions in the ecological context of Burkina Faso. This study also aims to compare mung bean to cowpea, the major legume grown in the country.

Material and methods

The plant material used in this study was composed of forty-four (44) accessions of mung bean imported from the Australian gene bank collection (table 1) and an extra-early maturing cowpea variety (Sanzi) used as check. Initially, 50 accessions were introduced in 2016, assessed for their adaptability and multiplied to increase seed stock. Out of the 50 accessions, 44 showed adaptability to the local climate conditions and were therefore used in this genetic diversity study. The experiment was carried out in 2018 during the rainy season, from July to September, at INERA (*Institut de l'Environnement et de RecherchesAgricoles*) research station in Kamboinsé, located at 12 ˚ 27 North latitude and 1˚ 32 West longitude, 296 m above sea level. The annual rainfall was 723.8 mm.

Table 1: Entries name of mung bean accessions with country of origin

COUNTRY OF ORIGIN	ENTRY NAME
INDIA	PLM 944; IBS 3317; 13674; 13644; CPI 29755; V 2709; CO 1; 13584; M 9; 9154
INDONESIA	VC 1481A/VC 1560A
TAIWAN	CES 1d-21/PHLV 18; VC 1168D/VC1560A; Shanhua 1/VC1163A; NM 92; VC6372 (45-8-1); KPS1; VC 1131A/VC 1163B; KPS2; VC 1560 C /VC 1628 A; VC 1177B/VC 1647 A; VC 1301 /PHLV 18
PAKISTAN	22
PHILIPINE	V 2802
COLOMBIA	CPI 32968
SOUTH KOREA	Kyungkijaerae 16; Chunbukjaerae 7; Chunbukjaerae 2
VIETNAM	DAU XANH; EWVN (Commercial variety)
AUSTRALIA	Shantung; Emerald; Satin; King; White gold; Q14730; Q14731; Q14732; Q14726; Q14729; Q14724; Q14728; Q14723; Q14725

Experimental design and data analysis

In this study, the experimental design used was an "augmented block design" as described by Federer (1956). Each accession was sown on a 3-meter row with 60 cm within rows and 80 cm between rows. The trial consisted of three (03) blocks including two blocks of fifteen (15) entries and one bloc of fourteen (14) entries, and only the check crop (cowpea variety Sanzi) was repeated in each block. As mung bean is an orphan crop in Burkina Faso, the early maturing cowpea variety Sanzi was used as a control, in order to compare

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at the same time, the agronomic performances of the new accessions of mung bean with a variety of the local major legume. All the agronomic were done as required. Qualitative and quantitative data were collected on five plants chosen randomly on each plot and the average was analyzed so following parameters were evaluated for quantitative traits: Day to 50% flowering (50%Flw), day to 95% maturity (95%Mat), plant height (PH), number of pods per plant (PP) and hundred seed weight (HPW). For quantitative traits, analysis of variance (ANOVA) was performed using SPAD (Statistical package for augmented design) and XLstat 2016 software was used for cluster analysis. The mean squares of the genotype and error for each trait who shows significant difference were used to calculate the genotypic variance (**δ^2g**), phenotypic variance (**δ^2ph**). Broad sense heritability (H^2), Genotypic Coefficient of Variability (GCV), Phenotypic Coefficient of Variability (PCV) and Genetic Advance (GA) were calculated according to Jalata et *al*. (2011) procedure (Table 2).

Table 2. Mung bean calculated genetic parameters information and formulas

Parameters	Formula	terms Significance
Genotypic variance (δ^2g)	$\delta^2 g = \frac{(MSG - MSE)}{r}$	- **MSG**: Mean Square of Genotype
Phenotypic variance (δ^2p)	$\delta^2 p = \delta^2 g + \frac{MSE}{r} = \frac{MSG}{r}$	- **MSE**: Mean Square of error - **r**: Number of replications
Genotypic Coefficient of Variability (GCV)	$GCV\ (\%) = \frac{\delta g}{X} * 100$	**-X**: Mean of the character **-δg**: Genotypic standard deviations
Phenotypic Coefficient of Variability (PCV)	$PCV\ (\%) = \frac{\delta P}{X} * 100$	- **δp**: Phenotypic standard deviations
Heritability (Broad sense) (H^2)	$H^2\ (\%) = \frac{\delta_g^2}{\delta_p^2} * 100$	-**δ^2g: Genotypic variance** - **δ^2p: Phenotypic variance**
Genetic Advance (GA)	$GA = H^2 * \delta p * K$	**K** = 2,06 (Selection coefficient)

Results

Genetic diversity revealed by qualitative traits

Qualitative traits recorded in this trial showed different variants within the collection except plant growth habit, flower color and pod curvature (Table 3). This mung bean collection was characterized by yellow flowers, erect growth habit and slightly curved pods. For the other traits, existence of purple color was observed on the hypocotyl of 64% of the accessions. Presence of pubescence of varying density have also been observed on stems and pods. Thus, 57% of accessions have a strong pubescence while 36% have a light pubescence. On the other hand, pubescence was almost absent (glabrous) on 7% of accessions under study.

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Table 3. Distribution frequency for qualitative traits of mung bean

Trait	Type	Frequency (%)
growth habit	Erect	100(44)
flower color	Yellow	100 (44)
pod curvature	Slightly curved	100 (44)
Hypocotyl color	Green	63.64 (28)
	Purple	36.36 (16)
Seed Coat Color	Green	93.18 (41)
	Black	4.54 (2)
	Yellow	2.27 (1)
Pod Pubescence	Densely pubescent	45.45 (20)
	Moderately pubescent	54.54 (24)
Stem Pubescence	Densely pubescent	56.81 (25)
	Glabrous	6.81 (03)
	Moderately pubescent	36.36 (16)

For seed coat color, three (03) types were observed within this collection: majority of the accessions (93.18%) have green seed coat color, while 4.54% showed black seeds and only one (2.27%) accession produced yellow seeds (Figure 1).

Black seeds **yellow seeds** **Green seeds**

Fig. 1: Different seeds coat color observed on mung bean genotypes

Genetic diversity revealed by quantitative traits

Genetic diversity revealed by quantitative traits' results presented in Table 4 shows that days to 50% flowering of tested mung bean accessions ranged from 29 to 48 days with an average of 36.46 days after planting. Number of days to 95% maturity varied between 44 and 67 days after sowing with an average of 54.43 days. With an average of 10.26 cm, the pod length varied between 6.5 and 12.66 cm whilst number of pods per plant value ranged from 17 to 145 with a mean value of 55.33 pods. Plant height ranged from 22 cm to 72 cm with an average of 66.33 cm. Hundred seed weight (HSW) varied between 2.4 and 7.1 g with an average of 4.5 gr. High values of coefficient of variation (CV> 30%) were recorded for plant height, while traits such as 50% flowering (2.89 %), 95% maturity (5.54), pod length (10.63%), and hundred seeds weight (13.03%) have low coefficient of variation.

Table 4. Descriptive statistics for quantitative traits of 44 mung bean lines

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Statistics	Mean	Range	CV (%)
50%F	36.46	29 – 48	2.89
95%M	54.43	44 – 67	5.54
PL (cm)	10.26	6.5 – 12.66	10.63
NPP	55.33	17 – 145	9.54
PH (cm)	66.33	22 – 72	31.48
HSW (gm)	4.5	2.4 – 7.1	13.03

Legend: Days to 50% flowering (50%Flw).Days to 95%maturity (95%Mat). pod length (PL) plant height (PH). number of pods per plant (NPP). and hundred seed weight (HSW). Coefficient of Variation (CV)

ANOVA

Analysis of variance revealed highly significant differences as shown in Table 5 among the accessions for all the characters under investigation: day to 50% flowering, day to 95% maturity (95%M) plant height (PH), pod length (PL), number of pods per plant (PP) and hundred seed weight (HSW). This significant variation for all the studied traits in this collection of mung bean suggests a large genetic variability within this germplasm.

Table 5: Mean squares values for different characters of mung bean

	MEANS SQUARES					
Sources of variation	**50%F**	**95%M**	**PL (cm)**	**NPP**	**PH (cm)**	**HSW (gm)**
Treatment	16.12**	27.07**	9.43**	1087.64**	2350.81**	5.19**
Error	**1.11**	**9.19**	**1.18**	**29.5**	**396.83**	**0.49**

*Legend:***: *highly significant*
Days to 50% flowering (50%Flw).Days to 95%maturity (95%Mat). pod length (PL) plant height (PH). number of pods per plant (NPP). and hundred seed weight (HSW).

Estimates of genetic parameters like phenotypic and genotypic coefficient of variation in addition to heritability and genetic advance are presented in Table 6.

Genetic variability (PCV and GCV)

The phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) for all the traits (Table 6). The magnitude of PCV and GCV was the highest for plant height (42.83; 39.05), number of pods per plant (33.47; 33.02), and hundred seeds weight (24.35; 23.06). Moderate PCV and GCV values were observed for pod length (17.3; 16.23) and Low estimates of PCV and GCV was observed for 50% flowering (6.38; 6.16) and 95% maturity (5.49; 4.46)

Heritability and genetic advance

The heritability estimates were considered as low (5-10%), medium (10-30%) and high (> 30%) as per the classification of Dabholkar, 1992 . In this study, estimates of heritability for all six traits ranged between 66.00 and 97.29 per cent. The highest magnitude of heritability was observed for number of pods per plant (97.29), followed by 50% flowering (93.11), hundred seeds weight (90.75), Pod length (87.58), plant height (83.12) and then 95% maturity (66). According to Johnson et *al*. (1955), heritability values in addition with estimates of genetic advance were more useful than heritability alone in predicting study effect of selection. In consequence, the estimate of genetic advance has shown its highest value with plant height (73.34) followed by number of pods per plant (67.09), hundred seeds weight (45.57), pod length (31.18), 50% flowering (12.23) and 95% maturity (7.46). High heritability coupled with high genetic advance as per cent of mean was observed for number of pods per plant (97.29; 67.09), hundred seeds weights (90.75; 45.57), Pod length (87.58; 31.18), and Plant height (83.12; 73.34). High heritability with low genetic advance were observed for 50% flowering (93.11; 12.23). Medium heritability coupled with low genetic advance were observed for 95% maturity (66; 7.46).

Table 6. Estimates of heritability and genetic advance parameters of 44 mung bean lines

Statistics	δ^2g	δ^2p	GCV	PCV	H2	GA	Gam
50%F	5	5.37	6.16	6.38	93.11	4.45	12.23
95%M	5.96	9.03	4.46	5.49	66	4.08	7.46
PL (cm)	2.75	3.14	16.23	17.3	87.58	3.19	31.18
NPP	352.71	362.55	33.02	33.47	97.29	38.16	67.09
PH (cm)	651.33	783.61	39.05	42.83	83.12	47.93	73.34
HSW(gm)	1.57	1.73	23.06	24.35	90.75	2.47	45.57

Legend: Days to 50% flowering (50%Flw).Days to 95%maturity (95%Mat). pod length (PL) plant height (PH). number of pods per plant (NPP). and hundred seed weight (HSW). Genotypic Coefficient of Variation (GCV).Phenotypic Coefficient of Variation (PCV).H2: Heritability, GA: Genetic Advance (GA), Genetic Advance by mean (Gam).Genotypic variance (δ^2g). Phenotypic variance (δ^2p)

Cluster analysis

Based on the six quantitative traits recorded, all tested genotypes were grouped into five (05) clusters including cowpea (*Vigna unguiculata*) variety Sanzi used as check crop, at 0.90 similarity threshold (Figure 2). Cluster I was the largest group which consisted of 20 accessions followed by cluster II with 12 accessions (Table 7) and Cluster IV consisted of 07 accessions. Cluster III was composed of 04 accessions and the check crop Sanzi felt in the Cluster V with the highest hundred seeds weight.

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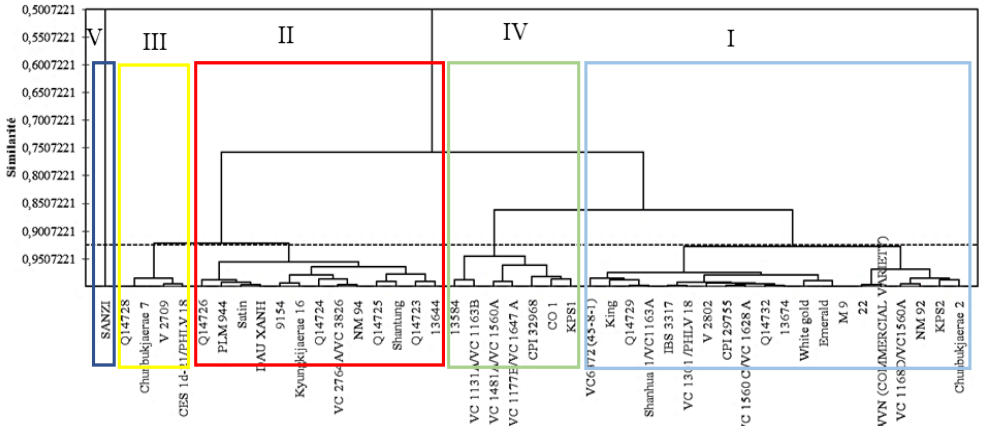

Fig. 2: Dendrogram of cluster analysis of 44 Mung bean accessions with check crop(Sanzi)

Table 7. Mungbean genotypes grouping with check crop (cowpea) according to dendrogram into five clusters

Cluster	I	II	III	IV	V
Lines names	Q14732; 22; Q14729; Emerald; CPI 29755; M 9; V 2802; White gold; King; 13674; VC 1168D/VC1560A;Shanhua 1/VC1163A; NM 92; VC6372 (45-8-1); KPS2;VC 1560 C /VC 1628 A;VC 1301 /PHLV 18; EWVN (COMMERCIAL VARIETY); Chunbukjaerae 2	Q14726; Q14724; Q14723; Q14725; Shantung; Satin; PLM 944, 13644; VC 2764A/VC 3826; NM 94; DAU XANH;9154; Kyungkijaerae 16;	Q14728; V 2709; CES 1d-21/PHLV 18; Chunbukjaerae7	CPI 32968; CO 1; 13584; VC 1481A/VC 1560A; KPS1; VC 1131A/VC 1163B; VC 1177B/VC 1647A	SANZI (cowpea)

Mean value of quantitative traits by cluster is presented in Table 8 which presents the characteristics of each group of genotypes. Cluster I was composed of late maturing mung bean accessions with medium pod length and high seed weight. This cluster gathered the larger number of accessions of mung bean reflecting the diversity of origin for these accessions. These accessions come from seven different countries including Taiwan (most represented with 7 accessions) from where comes the accession 1177B/VC 1647 A with the highest hundred seeds weight (6.98gm). Taiwan is followed by Australia with 5 accessions, India with 4 accessions, then Pakistan, South Korea, Philippine and Vietnam represented by one accession each. In addition to this diversity of origin, this cluster is characterized by the third longer pods (with a mean value of 9.65 cm) and the third higher mean value of hundred seeds weight (5.04 gm). In cluster II, genotypes were tall, medium maturing with high number of pods per plant and low hundred seeds weight. Cluster II is also rich in terms of country of origin as his accessions come from five countries among which Australia is mostly represented with six (06)

accessions out of thirteen (13). The Cluster III is the smallest cluster with four accessions and is characterized by late maturing genotypes with highest average number of pods per plant (134.76), and the lowest hundred seeds weight in average (3.11gm). This cluster is composed of one accession originating from each of the following countries: Australia, India, Taiwan and South Korea. Cluster IV grouped accessions that are early matured (average of 50.51 days to reach 95% maturity) with the average longest pods (10.02 cm) and the average higher hundred seeds weight (5.93 gm)

Table 8: Mean value of the different traits of mung bean and check crop by cluster

Cluster	50%F	95%Mat	PL (cm)	NPP	PH (cm)	HSW (gm)
1	36.47	56.20	9.65	46.88	43.87	5.04
2	34.97	53.29	8.15	78.06	47.77	3.49
3	38.54	56.39	7.09	134.76	46.48	3.11
4	33.74	50.51	10.02	22.11	34.02	5.93
5	38.67	55.58	14.63	44.83	145.17	8.48

Legend: Days to 50% flowering (50%Flw).Days to 95%maturity (95%Mat). pod length (PL). number of pods per plant (NPP). plant height (PH)and hundred seed weight (HSW)

Discussion

Genetic diversity among the assessed germplasm was revealed through both qualitative and quantitative traits. However, any variability was observed for plants growth habit, flower color and pods shape. This characterizes cultivated forms of mung bean, the wild relatives tending to be prostrate (Lambrides and Godwin, 2006).

The erect growth habit of our germplasm confirms their cultivated nature as it is stated by GenBank of origin (Australian Grains GeneBank). Hypocotyl were purple for 36.64% of the accessions and green (no pigmentation) for 63.36%. Poehlman (1990) has reported that the purple coloration in hypocotyl and various parts of the mungbean plant is due to the presence of a class of water-soluble pigments or anthocyanins. In mungbean, hypocotyl color is either purple or green (no pigmentation) and may be used as a genetic marker at the seedling stage. Stem and pods pubescence could be used as morphological marker. It can be dense or moderate, with the existence of accessions presenting a glabrous stem. Khattak et *al*., (2000) have reported that presence or absence of pubescence on mung bean plant can easily be detected at the late seedling. For these authors, this trait is dominantly inherited. In addition, Murty and Patel (1973) asserted that dense pubescence is conferred by a single gene over moderate pubescence. Genetic variability was also observed among accessions for seed color. According to Trustinah et *al*. (2014), in Indonesia, each region has a typical preference for utilizing

mungbean based on qualitative traits such as seed coat color. Seed colors in addition to presence or absence of a rough layer are used to distinguish different types of mung bean (Lambrides and Godwin, 2006; Mogotsi, 2006). Cultivated types are generally green or golden and can be shiny or dull depending on the presence of a texture layer (Lambrides and Godwin, 2006). Same authors have reported that golden gram which has yellow seeds seems to have low seed yield and pods that shatter at maturity, and is often grown for forage or green manure, point that should be taken into account in breeding process. Diversity of seed coat color is also linked to a variability of phytic acid (PA) content, an anti-nutritional factor that strongly inhibits trypsin and absorption of nutrients including iron, zinc, calcium and magnesium in monogastric animals according to Singh et *al*. (1982). Dhole et *al*. (2015) has reported that there are no significant differences in PA content between yellow and green seed coat genotypes, and in the meantime the author reported significantly greater PA content in black genotypes than yellow and green seed coat genotypes. Genotypes with low phytic acid (lpa) in seed as found in yellow and green seed may show increased assimilation of nutrients and be useful in breeding lpa cultivars. In addition to the genetic variability observed through qualitative traits, important genetic diversity was revealed by quantitative traits for which highly significant differences were observed. Important genetic variability among mung bean genotypes was also reported by Hemavathy et *al*. (2015), Dhoot et *al*. (2017) and Garg et *al*. (2017). Bhist et *al*. (1998) and Pandiyan et *al*. (2012) mentioned that pod length, number of pods per plant and hundred seeds weight have a maximum contribution to the genetic diversity as it was the case in the present study. Moreover, the mean values of the different observations of the present study are in concordance with those reported in previous works (Shyamalee et *al*., 2016; Garg et *al*., 2017; Muthuswamy et *al*., 2019).

Estimates of phenotypic and genotypic coefficient of variation (PCV and GCV), broad sense heritability (H2) and genetic advance (GA) revealed that all the six measured traits are mostly controlled by genotypes as reported by Venkateswarlu (2001) and Muthuswamy et *al*. (2019). In addition, the high values of PCV and GCV for number of pods per plant (33.47; 33.02), plant height (42.83; 39.05) and hundred seeds weight (24.35; 23.06) suggested that best genotypes for these traits could be determined based on the observed diversity. Similar assertion was made by Natarajan et *al*. (1988) and Muthuswamy et *al*. (2019). Srivastava and Singh (2012) and Khajudparn and Tantasawat (2011) reported that good breeding progress can be achieved for pod length even though moderate magnitude of PCV and GCV was observed. In contrast, 50% flowering and 95% maturity which exhibited low estimate of PCV and GCV will be more influenced by environmental factors according to Venkasteswarlu (2001) and Gadakh et *al*. (2013)

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Heritability and genetic advance

High broad sense heritability (H^2) coupled with high genetic advance (Gam) was observed for all traits under study (except for 50% flowering and 95% Maturity where the magnitude of genetic advance was low). Hence the high magnitude of heritability and genetic advance for Pod length (87.58; 31.18), number of pods per plant (97.29; 67.09), Plant height (83.12; 73.34) and hundred seed weight (90.75; 45.57) suggest preponderance of additive and fixable gene governing these traits expression with low influence of environment and could be exploited in breeding for early generation. Similar observation was previously reported by Venkateswarlu, (2001b) and Hemavathy et *al*., (2015) for plant height and number of pods per plant. Heritability of character number of days to 50% flowering was high (93.11) and similar to the one reported by Nair et *al*. (2004) and Sriphadet et *al*. (2014), but the low genetic advance recorded for this trait as well as for 95 % maturity were similar to Shah and Patel (1981) report. So, the low heritability with low genetic advance we observed for 95% flowering indicating probable effect of non-additive gene action as suggested by Singh (2009). Heritability estimates which provide the amount or ratio of transmissible genetic variation from parents to offspring, appear to be the most important basic factor that determines genetic improvement or response to selection. The estimate of genetic advance as percentage of mean provides more reliable information on selection effectiveness because it is determined from heritability, phenotypic standard deviation and selection intensity. Therefore, heritability and genetic advance are very important to plant breeders for developing suitable selection strategy.

The forty-four (44) mungbean accessions and the cowpea variety used as check in this study were grouped into five clusters suggesting the existence of high level of genetic diversity. Larger genetic diversity was obtained by Bisht et *al*., (1998); this could be explained by the relatively high number (111) of accession used by these authors. In current study, cluster V consisted exclusively of the cowpea variety is completely distinct from the rest of mung bean accessions. The difference between the mung bean accessions and the cowpea line was mainly related to traits such as plant height and hundred seeds weight that was higher for the cowpea line as compared to mung beans. Seed's weight is certainly one of the most important yield components and large seeds usually command consumer preference. However, similarities exist between the lines of these two species for maturity cycle and also for pod length (especially with the accessions of cluster IV).

More similarities were found between Vigna radiata (mung bean) genotypes and other species including Vigna unguiculata (cowpea) that

clustered together when more morphological markers were used (Pandiyan et al., 2012). In addition, Fatokun et al., (1992) reported that a QTL identified in cowpea is orthologous to QTL governing seed weight in mung bean suggesting that this genomic region has remained conserved through evolution between these two species. This information on cowpea genome represent an opportunity that can help improve mung beans traits especially seed size. Waldia et al., (1993) and Khattak et al., (2001) mentioned that large seed size is a major component of grain yield due to its importance in breeding as seed size is reported to be stable and highly heritable in comparison with other quantitative traits.

According to Prasanna, 2012 and Tripathy et al., 2016 n mung bean, seed size in terms of test weight i.e. 100 or 1000 grain-weight is very important character as it directly influences productivity and, as reported by Santha and Veluswamy 1997 and Misiak, et al., 2017, seed weight along with seed colors determine grain quality for marketing. This cluster is dominated by accession from Taiwan with three accessions out of seven (07), the other accessions comes from Indonesia, Colombia and India. Collection of India possess the greater diversity, since it has a representative in every cluster, confirming with Rishi (2009) and also Singh et al., (2013) that India is the leading green gram cultivator, with up to 55% of the total world acreage and 45% of total production. In addition, in this study, accessions from India, Taiwan and Australia are the most represented. Indeed, as an example, according to Shyamalee et al. (2016), Sri Lanka imports about 33% of domestic requirement from Australia, Myanmar, Thailand and India.

Cluster analysis of these 44 lines shows that genotypes from different countries of origin grouped together in several clusters rise the fact that a close genetic relationship may exist, which might be due to their narrow genetic bases. This could also be related to the movement of genetic material between these countries inferring that the different genetic cluster do not reflect the geographical origin of the accessions as reported by Lestari et *al*. in 2014 . Similar conclusion was drawn by Hapsari et *al*., (2018). Earlier investigations reported that there is no association between variations in geographical areas with genetic diversity of mung bean (Bisht et *al*., 1998). However, Zhang et *al*., (1999) asserted that collections of diverse germplasm from different centers of diversity and other sources may broaden the genetic basis of a plant collection. Therefore, the relatively high genetic diversity observed in this study may be exploited for breeding activities in Burkina Faso whilst broadening local mung bean collection.

Conclusion:

This study revealed genetic diversity both in terms of qualitative and quantitative traits for this collection of mung bean introduced in Burkina Faso. Despite the very diverse origins of the accessions of this collection of mung bean, they have been shown to be adapted to the ecological conditions of Burkina Faso and therefore suitable for introduction into the agricultural systems of the country. In addition, genetic parameters such as heritability and genetic advance (GA) open up prospects for improving this legume for further breeding program. Cluster's analysis revealed groups of accessions with agronomic performance similar or sometime superior to the main grain legume specie grown in the country which is cowpea. Also, this clustering pattern can be used for the selection of parental materials with interesting characteristics useful in the development of new varieties of mung bean. These results, as first investigation on mung bean agromorphological characterization and evaluation in Burkina Faso will contribute to the popularization of this legume in the country, while mung bean accessions used in this study will serve to enrich the local genetic diversity in terms of pulses and thus contribute to resilience of population in a context of climate change.

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