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Genetic Variability and Estimates of Genetic Parameters in Burkina Faso's Pearl Millet Landraces

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Abstract Pearl millet (*Pennisetum glaucum (L.) R. Br.*) is an important cereal crop in the arid area in sub Saharan Africa. Most of the cultivated cultivars are landraces, with relatively stable and low grain yield. Understanding the variability and the estimates of genetic parameters in a collection of accessions on hand would be useful in developing appropriate breeding strategies. An experiment was conducted in 2011 at the research station of Gampela, agronomic research center of the Institute of Rural Development (IDR), to assess the genetic variability, and to estimate the broad sense heritability and the genetic advance expected from selection in a collection of 82 accessions collected from three agro-ecological zones in Burkina Faso. Analysis of variance revealed highly significant differences ($P<0.01$) between the genotypes for all the characters studied except the number of productive tillers. The 12 significant characters were into four principal components each having eigenvalues greater than 1.00 and explained 76% of the total variation. Hierarchical cluster analysis split the accessions of the collection into seven clusters with 64% dissimilarity between clusters. The phenotypic coefficient of variation (PCV) was moderately higher than the genotypic coefficient of variation (GCV). High estimates of broad sense heritability (52-98%) were recorded for all the characters. All the characters, except stem width, recorded moderate to high genetic advance as per cent of the mean expected from selection of 5% best lines, coupled with high broad sense heritability, indicating that the studied genotypes could be improved for these characters through a simple selection method.

Keywords Genetic Variability, Cluster, Broad Sense Heritability, Genetic Advance, Pearl Millet

1. Introduction

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is the major cereal crop in the arid and semi-arid zones in West Africa and India. It is usually cultivated under harsh conditions (low rainfall, infertile soils, low external input) where no other cereal crop can yield economically ([8],[10]). It constitutes an important staple crop in the marginal agricultural production environments in Sub-Sahara of West Africa, where it is primarily grown on 15 million ha[11], for grain production for human consumption. The stover is the main source of feed for livestock in this area ([9],[12]). In Burkina Faso, it is the second cereal crop after sorghum and it is grown throughout all agro-ecological zones of the country.

Most of pearl millet cultivars cultivated by farmers are landraces. Landraces grown in the harsh environment conditions show some adaption to abiotic stresses and often provide stable and modest grain yields[13]. Though these cultivars are adapted to the environments, the grain yields potential remain very low. Improvement of yield potential requires knowledge about estimates of genetic variability, heritability and genetic advance of the agronomic traits in regard to the material that is on hand[15]. Heritability is the proportion of a phenotype that is transmitted from parents to offspring[4]. But, since heritability is influenced by environment, its estimate alone may not be helpful for selection based on phenotype. Nevertheless, heritability along with genetic advance conjointly can lead to reliable conclusion[3]. Therefore it become necessary to have information about the genetic variability and the estimates of the heritable and none heritable components of the observed variability. Previous studies reported high heritability and low genetic advance for days to 50% flowering in pearl millet[15]. High broad sense heritability and high genetic advance for grain yield and panicle length were also reported[16], whereas plant height and panicle girth showed high heritability and low genetic gain[16]. The objective of this study was to assess the genetic variability based on agro-morphological characters and to estimate genetic parameters in a collection of pearl millet accessions of Burkina Faso.

2. Material and Methods

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2.1. Site of Experimentation

The experiment was conducted during the rainy season 2011 at the research station of Gampela, 12° 25' N and 1° 12' W, situated at 20 kilometres in the East of Ouagadougou. The soil is a Ferric Lixisol, and the texture is loamy-sand with low organic matter and nutrient availability[1]. The climate is soudano–Sahelian type, characterized by a short rainy season from June-July to September-October with an average annual rainfall about 750 mm, and a long dry season from November to May. The maximal temperature varies between 35-40°C and minimal temperature varies between 18 to 19°C.

2.2. Genetic Material

The genetic material was selected from accessions collected in three agro-ecological zones in Burkina Faso (Sahel, Sub-Sahel and North Soudan) in 2010 (Figure 1). Details on the origin of the genotypes are mentioned in (table 1). The collected material was first grown in nursery in 2010 for observation and seed regeneration. In total, material consisted of eighty two ecotypes along with one open pollinated variety (OPV), SOSAT-C88 as check, were evaluated in this experiment in the rainy season 2011.

2.3. Experimental Design

The trial was conducted in randomized complete block design (RCBD). Each entry was sown on one row of 6 m length with 60 cm between hills on the same row (10 plants per row). The space between rows was 80 cm. Thinning was done two weeks after emergence to reduce the number of plant to a single plant per hill. Weeding was done two times and fertiliser was applied at recommended doses 100 kg of NPK 14-23-14 (two weeks after emergence), and 50 kg of urea 46% N split into two application (two weeks after emergence and 35 days after emergence).

Table 1. Material Collected per Agro-ecological Zone and per Province

Agro-ecological zones	Provinces	number of accessions
Sahel	Seno	6
Sub-Sahel	Lorum	8
	Zondoma	5
	Yatenga	18
	Gnagna	4
	Nanmentenga	4
North Sudan	Passore	6
	Gourma	5
	Zoundweogo	23
	Kadiogo	3
Check (improved OPV)		1

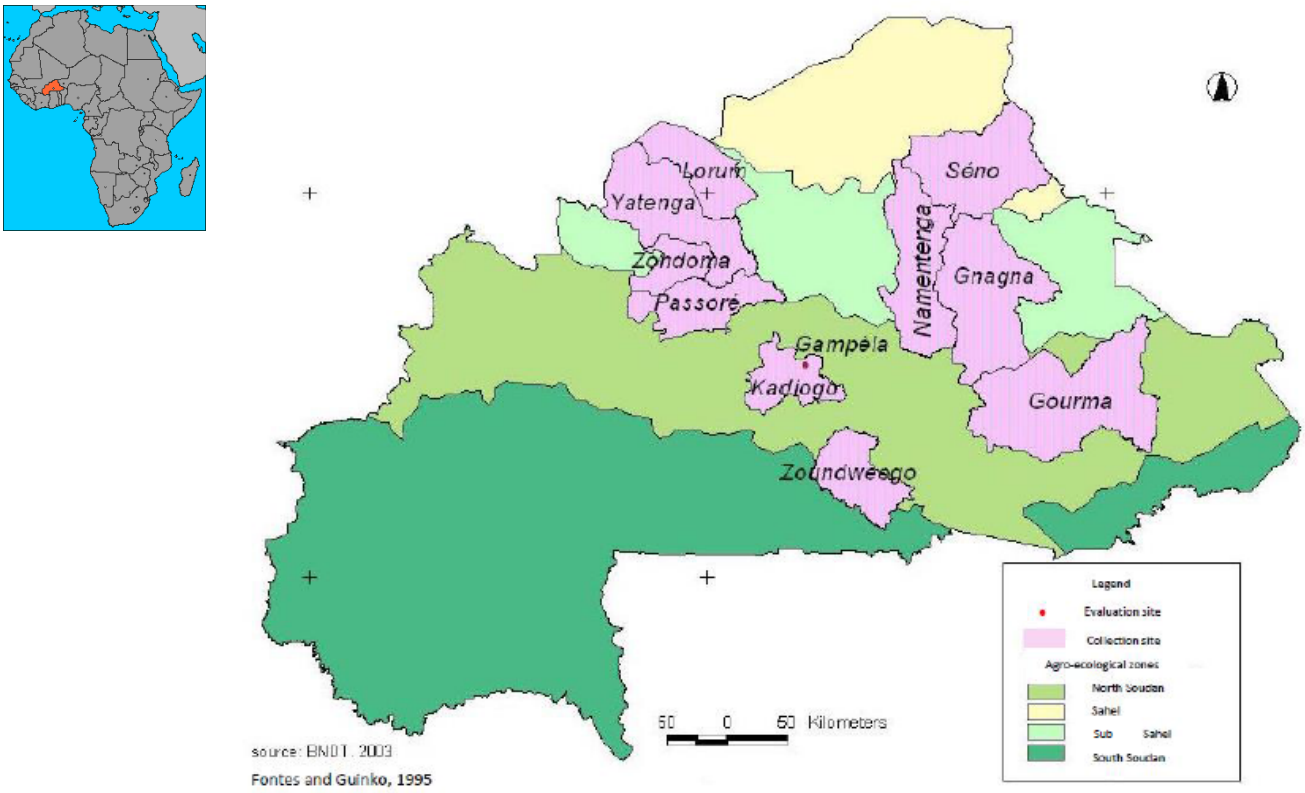

Figure 1. Agro-ecological zones sites of collection of the ecotypes, and experimentation site

2.4. Data Recording

Five plants per row were randomly selected by rejecting the border plants, to record quantitative data on characters *viz*., days to 50% flowering (days), panicle emerging duration (days), total number of tillers, total number of productive tillers, stem width (cm), plant height (cm), flag leaf length (cm), flag leaf width (cm), peduncle length (cm), peduncle width (cm), ear length (cm), ear width (cm) and hundred grains weight (g).

2.5. Statistical Analysis

Analysis of variance (ANOVA) was performed for the RCBD according to[2], by using GenStat (12 edition). Based on the variance component obtained from the ANOVA and the significance, the genetic parameters were estimated. Genotypic and phenotypic variances (V_G and V_P) were estimated according to[7], genotypic and phenotypic coefficient of variation (GCV and PCV), broad sense heritability (H^2) and expected genetic advance (GA) from the selection of the best 5% of genotypes were calculated as per the formula suggested by ([3],[4],[5] and[6]).

$$V_G = (MS_G - MS_E)/r \quad (1)$$

Where MS_G is the means squared of genotype, MS_E is the means squared of the residual (error), and r is the number of replication.

$$V_P = V_G + (MS_E/r) \quad (2)$$

$$H^2\,(\%) = (V_G/V_P)\ 100 \quad (3)$$

$$GCV\ (\%) = (\sigma_G/X)\ 100 \quad (4)$$

Where σ_G is the genotypic standard deviation and X is the trait mean

$$PCV\ (\%) = (\sigma_P/X)\ 100 \quad (5)$$

Where σ_P is the phonotypic standard deviation and X is the trait mean.

$$GA = H^2\ \sigma_P\ K \quad (6)$$

Where K is a constant, which at the selection intensity of 5% is 2.06.

$$GA\ (\%\ of\ trait\ mean) = (GA/trait\ mean)\ 100. \quad (7)$$

3. Results

3.1. Genetic Variability for Agro-morphological Characters

Analysis of variance (ANOVA) was performed on 13 agro-morphological characters and the result is reported in (table 2). The result revealed highly significant ($P < 0.01$) differences between genotypes for all the characters studied except total number of productive tillers. Hence further analyses were not carried out with the mean square of this character. The coefficient of variation (CV %) was large for panicle emergence duration (29.76%) followed by total number of tillers (22.84%). Days to 50% flowering, plant height, flag leaf length, flag leaf width, peduncle length, ear length, and ear width showed CV% less than 10%. The genotype means for all the characters were recorded in (table 3) and it showed a wide range of variation. For example days 50% flowering varied from extra-early (46 days) to late (81 days), the plant height varied from short (152 cm) to tall (300 cm), total number of tillers varied from 4 to 15 tillers per plant and the ear length varied from 17.3 to 82.3 cm.

Table 2. Analysis of Variance for Thirteen Characters in Pearl Millet

Source of variation	Replication	Genotypes	Error	CV (%)
df	2	82	164	-
Day_fl	52.964	76.09**	8.61	4.32
P_em_d	6.012	16.713**	4.896	29.76
TNT	15.042	6.386**	3.297	22.84
TNPT	5.206	2.004 ns	1.268	26.68
Plant_h	2299	994.6**	325.3	8.51
Flag_l	20.182	55.4**	9.347	6.81
Flag_w	0.392	0.3237**	0.1379	9.65
Ped_l	10.566	38.318**	4.579	5.13
Ped_w	0.032071	0.041633**	0.006906	11.66
Ear_l	28.16	339.08**	11.07	9.26
Ear_w	0.63042	0.18303**	0.05271	9.04
W_100	0.03498	0.05605**	0.02446	13.36
stem_w	0.22211	0.03212**	0.01551	11.25

** = significant at 1%, ns = non-significant (*P >0.05*), df = degree of freedom, Day_fl = days to 50% flowering, P_em_d = panicle emerging duration, TNT = total number of tillers, TNPT = total number of productive tillers, stem_w = stem width, plant_h = plant height, Flag_l = flag leaf length, Flag_w = flag leaf width, Ped_l = peduncle length, Ped_w = peduncle width, Ear_l = ear length, ear_w = ear width, w_100 = hundred grains weight

3.2. Structure of the Variability in the Collection

3.2.1. Principal Component Analysis

Table 3. Squared Cosines of 12 Characters on Four Factors and total variability explained of 12

Characters	Principal components			
	F1	F2	F3	F4
Day_Fl	0.051	**0.694**	0.000	0.002
Pan_em_D	0.005	0.260	0.127	**0.306**
TNT	0.065	**0.649**	0.003	0.036
TNPT	**0.435**	0.061	0.005	0.029
Plant_H	0.050	**0.707**	0.063	0.015
Flag_L	**0.347**	0.206	0.027	0.015
Flag_w	**0.541**	0.029	0.193	0.041
Ped_l	0.157	0.085	0.263	**0.283**
Ped_w	**0.802**	0.077	0.004	0.000
Ear_l	**0.758**	0.010	0.034	0.053
Ear_w	0.058	**0.378**	0.217	0.172
W_100	**0.308**	0.123	0.270	0.051
stem_w	**0.676**	0.002	0.056	0.054
Eigenvalue	4.939	3.318	1.313	1.070
Variability (%)	35.276	23.697	9.381	7.640
Cumulative %	35.276	58.972	68.354	75.994

Values in bold correspond for each character to the factor for which the squared cosine is the largest and show the association of characters with the principal component

Characters which were significant in the analysis of

variance were used to perform a principal component analysis. These characters *viz* day to 50% flowering (Day_Fl), panicle emerging duration (P_em_d), total number of tillers (TNT), stem width (stem_w), plant height (plant_h), flag leaf length (Flag_l), flag leaf width (Flag_w), peduncle length (Ped_l), peduncle width (Ped_w), ear length (Ear_l), ear width (ear_w), and hundred grains weight (w_100), were grouped into 14 principal components or factors with eigenvalues laying between 0.073 and 4.939. By considering the first four factors with eigenvalues greater than 1.00, about 76% of the total variation could be explained (table 3). The squared cosines of the characters presented in table 3 revealed that factor one (F1) accounted for 35.28% of the total variation was associated with flag length and width, peduncle width, ear length, hundred grains weight and stem width. Factor (F2) consisted mainly of flowering time, tillering, plant height, and ear width explained 23.69% of the total variation. Factor three (F3) explained 9.38% of the total variation. Factor four explained 7.64% of the total variation and consisted of peduncle length and panicle emergence duration.

3.2.2. Cluster Analysis

Agglomerative hierarchical clustering based on the factor scores of the four factors (F1, F2, F3 and F4) and truncating the dendrogram at 12% revealed that all the collection of 82 accessions formed seven distinctive clusters (figure 2), displaying 64% dissimilarity between clusters and 34% dissimilarity within cluster from optimal classification. Accessions from the Sahel zone (cluster 5) were homogeneous and formed only one group whereas, those from the North-Soudan and Sub-Sahel formed several groups indicating the large diversity in these regions.

Mean values of the different characters per cluster presented in table 4 revealed that cluster 1 had the greatest grain weight. Panicle emergence duration was longest in accessions of cluster 2. Accessions of cluster 3 were mostly characterized by width panicles. Accessions of cluster 4 were predominantly tall and late maturing. Flag leaf length and flag leaf width, ear length, peduncle width and steam width made accessions of cluster 5 a very distinct group in the collection. This cluster was separated from the rest by the first bifurcation of the dendrogram (figure 2). Accession in cluster 6 and 7 were predominantly characterized by long peduncle and high number of tiller respectively.

3.3. Estimates of Genetic Parameters

In order to understand whether the observed variation was due to genetic factors, genotypic (V_G) and phenotypic(V_P) variances, genotypic (GCV) and phenotypic (PCV) coefficient of variation, broad sense heritability(H^2) and genetic advance (GA) expected from selection of best 5% of the genotypes were estimated and reported in (table 3).

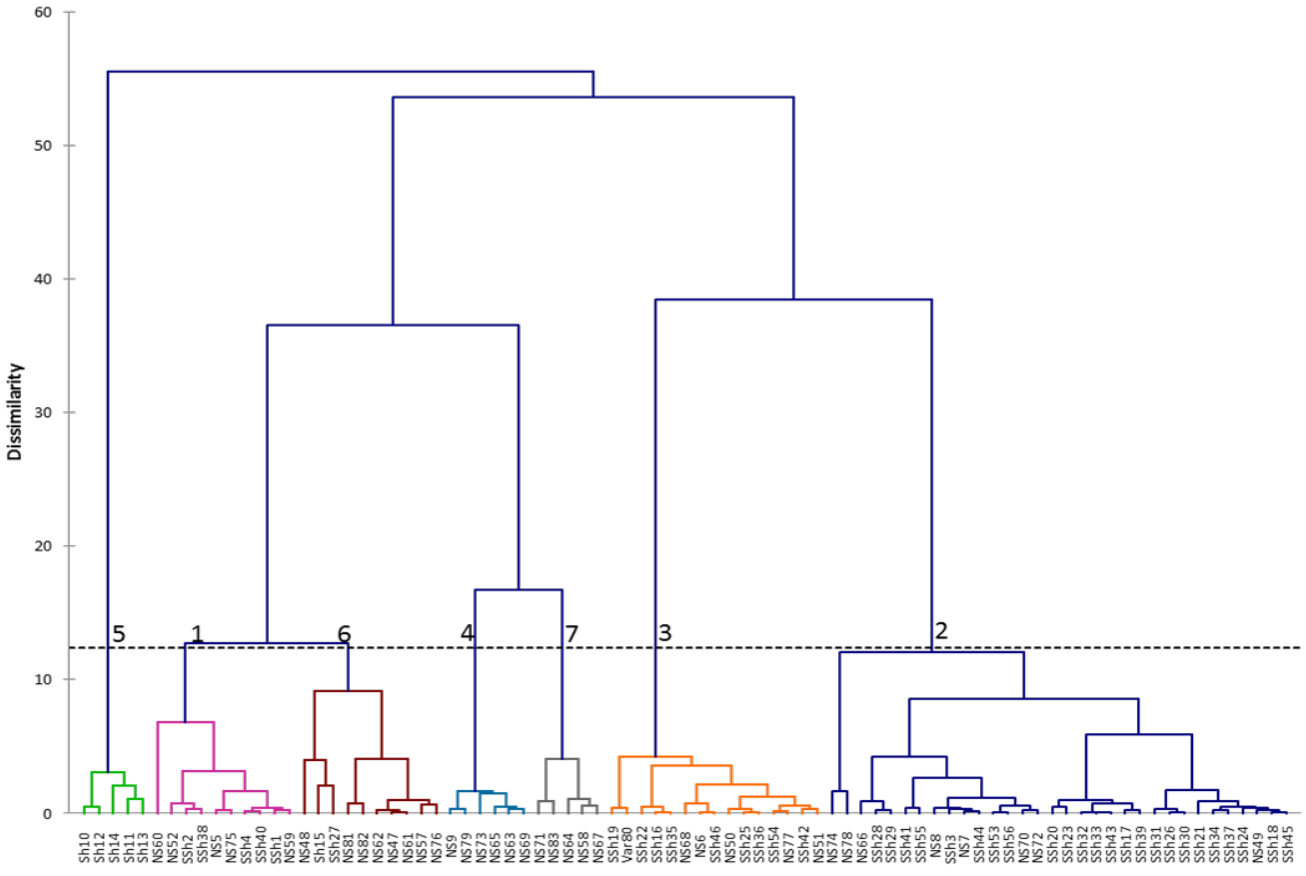

Figure 2. Dendrogram of Dissimilarity among 82 Accessions of Pearl Millet using Ward's Minimum Variance Method of Cluster Analysis

Table 4. Mean values of Characters per Cluster for Pearl Millet Collection in Burkina Faso

Character	Collection			Cluster						
	Mean	Range	SD	1	2	3	4	5	6	7
Day_Fl	67.9	49.0 -78.7	5.0	68.0	65.1	66.8	**75.4**	71.3	70.2	72.7
Pan_em_D	7.4	2.7 -13.7	2.4	6.9	**8.8**	6.2	4.2	8.5	7.8	5.4
TNT	8.0	5.2 -12.0	1.5	8.0	7.3	7.5	10.4	7.3	8.2	**10.6**
Plant_H	211.8	173.3 -259.4	18.2	222.3	199.3	203.6	**245.5**	225.3	219.9	225.8
Flag_L	44.9	34.4 -55.4	4.3	45.5	42.8	44.7	49.9	**52.7**	45.4	43.2
Flag_w	3.8	3.2 -4.7	0.3	4.0	3.7	4.1	3.9	**4.3**	3.6	3.5
Ped_l	41.7	32.7 -52.2	3.6	44.3	40.4	39.7	45.2	37.6	**46.8**	40.4
Ped_w	0.7	0.5 -1.1	0.1	0.7	0.7	0.8	0.6	**1.0**	0.7	0.6
Ear_l	36.0	19.9 -77.2	10.6	34.8	33.0	35.2	33.2	**71.6**	35.2	28.9
Ear_w	2.5	2.0 -3.3	0.2	2.6	2.5	**2.8**	2.4	2.5	2.3	2.3
W_100	1.2	0.7 -1.5	0.1	**1.3**	1.2	1.2	1.1	0.8	1.2	1.0
stem_w	1.1	0.9 -1.5	0.1	1.1	1.1	1.2	1.1	**1.3**	1.1	1.0
No of accessions	82	-	-	10	32	15	6	**5**	10	5

Values in bold are the most greater for each character, SD = standard deviation

Table 5. Estimates of Mean, Genotypic and Phenotypic Variances, Genotypic and Phenotypic Coefficient of Variation, Broad Sense Heritability, Expected Genetic Advance and Expected Genetic Advance as Percentage of Mean for Twelve Characters in Pearl Millet

Variable	Range	Mean	Genotypic variance	Phenotypic variance	H^2 (%)	GCV (%)	PCV (%)	GA	GA (% of mean)
Day_fl	46 - 81	67.9 ± 2.9	33.740	36.610	92.16	8.55	8.91	11.49	16.91
P_em_d	2 - 16	7.4 ± 2.2	5.909	7.541	78.36	32.70	36.94	4.43	59.63
TNT	4 - 15	8.0 ±1.8	1.545	2.644	58.43	15.63	20.45	1.96	24.61
Plant_h	152 - 300	211.8 ± 18.	334.650	443.083	75.53	8.64	9.94	32.75	15.46
Flag_l	32 - 59	44.9 ± 3.1	23.027	26.142	88.08	10.68	11.38	9.28	20.66
Flag_w	3 - 5	3.8 ± 0.4	0.093	0.139	66.90	7.92	9.68	0.51	13.34
Ped_l	29 - 53	41.7 ± 2.1	16.870	18.396	91.70	9.85	10.28	8.10	19.43
Ped_w	0.4 - 1	0.7 ± 0.1	0.017	0.020	88.29	18.49	19.68	0.26	35.79
Ear_l	17 - 82	36.0 ± 3.3	164.005	167.695	97.80	35.62	36.02	26.09	72.56
Ear_w	2 - 4	2.5 ± 0.2	0.065	0.083	78.76	10.05	11.32	0.47	18.37
W_100	0.6 - 1.7	1.2 ± 0.2	0.011	0.019	56.36	8.77	11.68	0.16	13.56
stem_w	0.6 - 1.6	1.1 ± 0.1	0.006	0.011	51.71	6.72	9.35	0.11	9.96

H^2= broad sense heritability, GCV = genotypic coefficient of variation, PCV= phenotypic coefficient of variation, GA = genetic advance, GA (% of mean) = genetic advance as per cent of the mean

3.3.1. Phenotypic and Genotypic Variances

Plant height had expressed high genotypic and phenotypic variances (334.65 and 443.08) followed by earl length (164.00 and 167.69) and days to 50% flowering (33.74 and 36.61). Stem width, hundred grains weight, ear width, peduncle width, flag leaf width, total number of tillers and panicle emergence duration recorded low genotypic variance (0.006 to 5.909) and low phenotypic variance (0.011 to 7.541). Peduncle length and flag leaf length showed moderate genotypic variance (16.870 to 23.027) and phenotypic variance (18.396 to 26.142).

3.3.2. Phenotypic and Genotypic Coefficient of Variation

Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the characters, but the differences between them were low. GCV and PCV were classified into high, medium and low according to[19]. The GCV was high (>20%) for ear length (35.62%) followed by panicle emergence duration (32.70%). Low (<10%) GCV was recorded for stem width (6.70%), flag leaf length (7.90%), days to 50% flowering (8.55%), plant height (8.64%), and hundred grains weight (8.77%). Estimate of PCV was maximum for panicle emergence duration (36.90%), followed by ear length (36.02%) and total number of tillers (20.45%). Moderate (11-20%) GCV and PCV were recorded for the other characters.

3.3.3. Broad Sense Heritability

As per the classification according to[3], the genotypes studied showed high heritability (>50%) for all the characters. Ear length (97.80%), days to 50% flowering (92.16%), peduncle length (91.70%), peduncle width (88.29%), flag leaf length (88.08%), ear width (78.76%), panicle emergence duration (78.36%), and plant height (75.53%) were the characters which recorded very high (>70%) broad sense heritability. Moderate (50-70%) broad sense heritability was recorded for flag leaf width (66.90%), total number of tillers (58.43%), hundred grains weight (56.36%), and stem width (51.71%).

3.3.4. Expected Genetic Advance

Among the characters, high (>20%) genetic advance as per cent of mean expected from selection of best 5% of the

genotypes was recorded for ear length (72.56%), panicle emergence duration (59.63%), peduncle width (35.79%), total number of tillers (24.61%), and flag leaf length (20.66%). The lowest estimate genetic advance was recorded for stem width (9.96%). The other characters viz., peduncle length, ear width, days to 50% flowering, plant height, hundred grains weight, and flag leaf width had recorded moderate (10 to 20%) genetic advance as per cent of mean.

4. Discussion

Variability is the key in crop improvement since it offers possibility for selection to develop desired genotype. The more the variability in the basic population, the more is the chance of improvement[17]. In the present study, analysis of variance revealed highly significant ($P < 0.01$) differences for all the characters except for total number of productive tillers (table 2), indicating huge genetic variability existing among the accessions. This observed significant variability among the accessions could be attributed to their diverse agro-ecological provenances.[22] also demonstrated high variability among genotypes collected from divers geographical zone in Burkina Faso. The observed wide range of variability suggests ample scope for selection within the genotypes for development of desirable cultivars. The hierarchical cluster analysis was useful by sorting the pearl millet accession collection from three agro-ecological areas in Burkina Faso into meaningful groups. According to[23], hierarchical cluster analysis is preferred for examining relationship between pearl millet landraces because of their heterogeneity and heterozygosity nature. The Sahel area is the driest agro-ecology in Burkina Faso with an annual rainfall less than 400 mm. Landraces grown in this harsh condition, have eventually developed some specific adaptation measures which make them distinct from the rest of accessions of the collection. Sub Sahel and Northern Soudan areas form a large agro-ecological region, 'soudano-sahelien', with an annual rainfall lying between 500 mm and 800 mm. This condition offers a large scope of adaptability which could explain the diverse groups formed by accessions from these areas. The current result confirms that of[23] who studied the diversity of landraces collected in central Burkina Faso which correspond to the 'soudano-sahelien' area. The study revealed up to 10 clusters of landraces in this region. Identification of clusters of morphological diversity among the accessions will allow an efficient use of this collection in a breeding program. However molecular characterization should be done to validate this phenotypic diversity.

Estimates of phenotypic coefficient of variation were higher than genotypic coefficient of variation for all the characters. Similar results were reported by ([16],[18], and[19]). Though the estimates of genotypic coefficient of variation was less than phenotypic coefficient of variation, the differences was closed for all the traits, indicating that the expression of characters was less influenced by environment. Similar results have been reported by[16] and[20] in pearl millet. Ear length and panicle emergence duration recorded high GCV, and hundred grains weight, days to 50% flowering recorded low GCV estimates, and total number of tillers expressed moderate GCV. This result is in line with the findings of ([18],[19]).

The coefficient of variability is an indication of the amount of variability existing among genotypes for a character. However it does not indicates the heritable and the non-heritable portion of this variability. Estimate of heritability indicates the proportion of the variability which could be transmitted from parent to offspring[4]. All the characters studied recorded high broad sense heritability. Similar result was reported by[16] for days to flowering, earl length, ear width, plant height, number of tillers, hundred grain weight, and grain yield per plant.[19] also demonstrated in his findings similar result except for number of tillers per plant which recorded moderate heritability. The high broad sense heritability recorded for all the characters studied could be an indication that the environment had less influenced the genotypes in the expression of the phenotype. Thus, phenotype could be a good predictor of genotype for these accessions[4].

The gain in mean value of population due to selection depends on the heritability of the character, phenotypic variation and the selection pressure per the formula of genetic advance[5]. Therefore, heritability alone may not be informative whether selection could make substantial improvement. In spite of that, heritability estimate along with expected genetic advance may give more reliable information[18]. High broad sense heritability coupled with high genetic advance as per cent of mean expected from selection of 5% of best genotypes, was recorded for ear length, panicle emergence duration, total number of tillers per plant, flag leaf length, and peduncle width, indicating additive gene action. Similar findings have been reported by[19] for ear length,[21] for ear length and total number of tillers per plant. Except stem width which recorded high heritability and low genetic advance, suggesting non-additive gene action, the other characters studied recorded high broad sense heritability associated with moderate genetic advance.[19] reported similar result for plant height, and demonstrated high heritability combined with low genetic advance for days to 50% flowering.

5. Conclusions

This study has confirmed the existence of broad genetic variability in the collection of pearl millet accessions of Burkina Faso. It could also be concluded that pearl millet landraces from the Sahel area were less diverse and strictly distinct from landraces from the Sub Sahel and Northern Soudan which were highly diverse. This study revealed also that estimates of PCV was moderately higher than GCV for all the characters studied, indicating the lesser environmental effect in the expression of the phenotype, which mean that

the phenotype could be a reliable predictor of the genotype in these accessions. Broad sense heritability estimates were high for all the traits. High heritability (broad sense) coupled with moderate to high expected genetic advance as per cent of mean was observed for all the characters studied except stem width, showing that all the characters studied were governed by additive genes effect, except stem width which was controlled by non-additive gene effect. Characters which were controlled by additive genes could be improved through direct selection. However for the characters controlled by non-additive gene, simple selection procedure may not be effective in improving for these traits. This study should be validated by molecular characterization.

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REFERENCES

[1] E. Ouédraogo L. Stroosnijder, A. Mando, L. Brussaard, and R. Zougmoré "Agroecological Analysis and Economic Benefit of Organic Resources and Fertiliser in till and No-till Sorghum Production after a 6-year Fallow in Semi-arid West Africa," Nutrient Cycling in Agroecosystems 77, no. 3 (2007): 245–256

[2] K. A. Gomez and A. A. Gomez, Statistical Procedures for Agricultural Research (Wiley, 1984).

[3] H. W. Johnson, H. F. Robinson, and R. E. Comstock, "Estimates of Genetic and Environmental Variability in Soybeans," Agronomy Journal 47, no. 7 (1955): 314–318.

[4] M. Peter Visscher, G. H. William, and R. W. Naomi, "Heritability in the Genomics Era—concepts and Misconceptions," Nature Reviews Genetics 9, no. 4 (2008): 255–266.

[5] K. Assefa, H. Tefera, A. Merker, T. Kefyalew and F. Hundera "Variability, Heritability and Genetic Advance in Pheno - Morphic and Agronomic Traits of Tef[Eragrostis Tef (Zucc.) Trotter] Germplasm from Eight Regions of Ethiopia," Hereditas 134, no. 2 (2001): 103–113

[6] R. K. Singh and B. D. Chaudhary, "Biometrical Genetics," Kalyani Publishers, New Delhi India (1985).

[7] Rex Bernardo, Breeding for Quantitative Traits in Plants (Stemma press Woodbury, 2002),

[8] B. Ouendeba G.Ejeta, W.E. Nyquist, W. W. Hanna and A. Kumar "Heterosis and Combining Ability Among African Pearl Millet Landraces," Crop Science 33, no. 4 (1993): 735–739.

[9] K. M. Devos, W. W. Hanna, and P. Ozias-Akins, "Pearl Millet," Cereals and Millets (2006): 303–323.

[10] J. M. J. De Wet, "Pearl Millet (Pennisetum Glaucum) in Africa and India," in Proceedings of the International Pearl Millet Workshop, 1987, 3–4,

[11] FAOSTAT, "Statistical Database of the Food and Agricultural of the United Nation. FAO Statistics Division 2013,"

[12] O. P. Yadav, "Heterosis in Crosses Between Landraces and Elite Exotic Populations of Pearl Millet[Pennisetum Glaucum (L.) R. Sr.] in Arid Zone Environments," Indian Journal of Genetics and Plant Breeding 66, no. 4 (2006): 308–311.

[13] O. P. Yadav, E. Weltzien-Rattunde, F.R. Bidinger and V Mahalakshmi, "Heterosis in Landrace-based Topcross Hybrids of Pearl Millet Across Arid Environments," Euphytica 112, no. 3 (2000): 285–295.

[14] Jawahar R. Sharma, Statistical and Biometrical Techniques in Plant Breeding (New Age International (P) Limited, 2003).

[15] M. Govindaraj, P. Shanmugasundaram, and A. R. Muthiah, "Estimates of Genetic Parameters for Yield and Yield Attributes in Elite Lines and Popular Cultivars of India's Pearl Millet," African Journal of Agricultural Research 5, no. 22 (2010): 3060–3064.

[16] M. Vetriventhan and A. Nirmalakumari, "Studies on Variability Parameters in Pearl Millet (Pennisetum Glaucum (L.) R. Br.).," Madras Agricultural Journal 94, no. 1/6 (2007): 118–120.

[17] B. Vidyadhar et al., "Genetic Variability and Character Association in Pearl Millet ${$Pennisetum Glaucum (L.) R. Br.$}$ and Their Implications in Selection," Indian Journal of Agricultural Research 41, no. 2 (2007): 150.

[18] Mahalingam Govindaraj et al., "Genetic Variability and Heritability of Grain Yield Components and Grain Mineral Concentration in India's Pearl Millet (Pennisetum Glaucum (L) R. Br.) Accessions," African Journal of Food, Agriculture, Nutrition and Development 11, no. 3 (2011),

[19] P. Sumathi, Sumanth Madineni, and P. Veerabadhiran, "Genetic Variability For Different Biometrical Traits In Pearl Millet Genotypes (Pennisetum Glaucum LR BR.)," Electronic Journal of Plant Breeding 1, no. 4 (2010): 437–440.

[20] D. Lakshmana, B. D. Biradar, and R. L. Ravikumar, "Genetic Variability Studies for Quantitative Traits in a Pool of Restorers and Maintainers Lines of Pearl Millet (Pennisetum Glaucum (L.))," Karnataka Journal of Agricultural Sciences 22, no. 4 (2009): 881–882

[21] Shashi Kant et al., "Variability, Heritability and Genetic Advance in Pearl Millet (Pennisetum Glaucum L.) for Implications of Selection.," Environment and Ecology 30, no. 4 (2012): 1378–1380.

[22] R. G. Zangre, M. Sawadogo, M. Ouedraogo and D. Balma, Caractérisation et stratification d'une collection de mil (Pennisetum glaucum (L.) R. Br.) du Burkina Faso. Int. J. Biol. Chem. Sci. 3:5 (2009): p 1042-105

[23] J. P. Wilson, G. W. Burton, J. D. Zongo, and I. O. Dicko. Diversity Among Pearl Millet Landraces Collected in Central Burkina Faso. Crop Sci. 30 (1990) 40-43.