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Genetic Divergence and Principal Component Analysis of Soybean [*Glycine max* (L.) Merrill] Genotypes in Northwestern Ethiopia

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Abstract: The quantity of Soybean produced and yield per given area in Ethiopia is small compared to the world average capability because of less varied soybean genotypes. The reason at the back of is due to a lack of various soybean genotype available and the genetic potential reduction of released varieties which have been in utilizing. Subsequently, genotypes that have not been characterized clustered and tested for their variability subjected for this observe. Approximately eighty-one (81) genotypes had been examined in a 9*9 easy lattice layout for his or her variability and relation of amongst trends using yield and yield related trends, qualitative, and first-class tendencies at Pawe Agricultural studies middle predominant station and Dibate substation in 2018-2019 cropping season. The analysis of variance discovered that all developments besides wide variety of nodules in line with plant, range of pods plant^{-1} and number of seeds pod^{-1} confirmed exceedingly substantial ($p<0.01$) differences at each tested places. Sixty three and sixty five percent of variations, from the entire, were revealed from the first 4 PCAs for Pawe and Dibate, respectively. Cluster evaluation confirmed about four specific clusters and the most inter cluster distance became determined among cluster I and cluster IV (D2=875.31) at Pawe and among cluster II and cluster IV (D2=1227.68) at Dibate. However, one season test might now not realize genotypes' variability in response of environment; due to the fact quantitative traits are polygenic and profoundly affected by the environment. As a consequence, an addition experiment on those genotypes in changed seasons is needed for more real estimation of polygenic traits.

Keywords: Cluster Distance, Genetic Divergence, Genetic Variability, Genotypes, Important Factor, Soybean

1. Introduction

Soybean (Glycine max (L.) Merrill) is a self-pollinated and leguminous crop with a chromosome quantity of 2n = 4x = 40 [1, 2]. Soybean is the most extensively grown leguminous crop in the international and is a crucial supply of protein and oil [3, 4] and also rich in unsaturated fatty acids, minerals (inclusive of Calcium and Potassium) and vitamins which meet the nutritional desires of human beings and different animals [5].

Winner crop improvement programs are severely subjected to the presence of excessive genetic range [6]. Similarly to this, genetic variety complements the opportunity of any species' life and being adaptable to fluctuating environmental situations [7, 8]. Subsequently, loss of genetic variety places vegetation at risk of sickness and negative weather exchange [9]. Consequently, correct expertise of the character and degree of genetic variety present in soybean germplasms can help in selecting dad and mom to develop the excellent sorts.

Programs consisting of the observe of genetic divergence among genotypes which lets in the identification and selection of the maximum promising genotypes for cultivation and improvement, and comparing the relative importance of characters within the overall variant to be had amongst genotypes are predicted through most important element evaluation (PCA) [10].

Despite the increment of soybean production and productiveness from 15824.4 tons with productivity of 1.4 tons ha^{-1} in 2010 [11] to 86467.9 tons with a productivity of 2.27 tons ha^{-1} in 2017 [12] in countrywide level, it stays low

compared to the global productiveness capacity of 2.7 tons ha^{-1} [12]. The cause in the back of is because of a lack of diverse soybean genotypes and released varieties genetic potential reductions [13]. However, growing of population boom, agro-processing factories and urbanization have led to high demand for soybean raw materials and products in Ethiopia [14]. Consequently, genotypes have never yet characterized systematically need to be examined for its variableness at ground that quantitative traits are strongly altered by environmental influences [15].

2. Materials and Methods

2.1. Description of Experimental Areas

The experiments were conducted at Pawe Agricultural research center main station and Dibate sub-station in 2018/19. Pawe Agricultural studies middle is located at (11018`49.6``N and 036024`29.1``E) in Metekel sector. The altitude of the location levels from 1150 meters above sea level (m.a.s.l). This site receives 1586 mm rainfall annually. The annual maximum and minimum temperatures are 32.6°C and 16.5°C, respectively. The soil type of the test site is characterized by way of properly drained clay soil with pH value 4.3-5.5. Dibate substation is placed at (10°30′ 0″ N, 36° 10′ 0″ E) with an altitude of 1572 m.a.s.l. The mean annual maximum and minimal temperatures are 29°C and 15°C, respectively and it receives 1650 to 1700mm rainfall annually. The soil type of the substation is characterized by nitosol or loam [16].

2.2. Plant Materials and Experimental Field Layout

81 acquired soybean genotypes from various sources (Nigeria, America and Brazil) have been used for the experiment. The experiment becomes laid out in 9*9 simple lattice layouts with plot size of 7.2meter square (2.4m*3m). Each plot consisted of 4 rows with 60 cm inter row and 5 cm intra row spacing. The spacing between plots, blocks and replications had been 0.6m, 1m and a couple of m, respectively. The overall internet harvestable experimental place for every area changed into 583.2 m^2. The amounts of seed and DAP fertilizer charge in line with plot have been 54g and 72g, respectively.

2.3. Data Gathered

Data on days to flowering, days to maturity, protein and oil contents (in %) and grain yield ($kgplot^{-1}$) have been recorded on plot bases. While, number of nodule, branches, plant height and pods $plant^{-1}$ had been recorded from ten randomly selected plants in line with [17].

Protein and oil contents were determined through the usage of 150 grams of dried seed samples per genotype and grinded in the nice studies laboratory. A small cup with inner diameter of 35 millimeter and depth of eight millimeter turned into used to take two to three soybean seed powder. NIRS (close to Infrared spectroscopy) FOSS 6500 version was used for scanning the oil and protein contents. Worldwide calibration for proximate composition (listing of parameters) changed into predicted as of [18].

2.4. Statistics Analyses

Analysis of variance (ANOVA) was performed using proc GLM for the traits analyzed primarily based on RCBD and proc-lattice methods of SAS version 9.3 [19] for the traits analyzed primarily based on lattice design.

2.5. Cluster Analysis and Genetic Divergence

Cluster analysis was performed using the SAS proc cluster procedure [19]. D square statistics (D^2) developed by [20] was used to cluster genotypes into different groups. The average intra and inter cluster D2 values were computed by the formulae $\frac{\sum D^2 i}{n}$ where, $\sum^D 2_i$ stands the summation of distances between all possible groupings (n) of the genotypes involved in the group. Genetic difference was estimated by the generalized Mahalanobis's statistics $D^2ij = (Xi - Xj)S(Xi - Xj)$, where, D^2ij = the distance between two groups i and j. Xi and Xj = the two vectors mean i^{th} and j^{th} genotypes, respectively; S = is the inverse of the pooled divergence matrix. The D2 values obtained for sets of groups were measured as per the computed values of chi - square ($\chi 2$) and were tested for significance at (1% and 5%) probability levels contrary to the tabulated value of $\chi 2$ for 'P' degree of freedom, where P stands for the number of parameters considered [21]. Cubic clustering criteria (CCC), Pseudo F statistic and pseudo t^2 statistic generated by SAS were examined to decide the number of optimum clusters.

2.6. Principal Component Analysis

Principal components were estimated based on original data using the SAS PRINCOMP procedure [19] based on formulae given by [22]. The first and second PCAs' values (Y1) and (Y2) is given by the linear combination of the variables X1, X2…Xp. Y1=a11X1+a12+…a1pXp and Y2=a21X1+a22X2+…a2pXp, respectively. Principal components with Eigen values > 1 considered as a significant in the result.

3. Results and Discussion

3.1. Genetic Divergence Analysis

The distribution of genotypes by way of cluster from the biggest to the bottom is cluster I, II, IV and III with 44 (44.3%), 19 genotypes (23.5%), 10 (12.3%) and 8 (9.9%) genotypes at Pawe, respectively (Table 1). Whereas at Dibate, cluster I, II, III and IV with 38 (46.9%), 29 (35.8%), III eight (9.9%) and IV 6 (7.4%) genotypes, respectively (Table 2).

3.2. Cluster Distance of Soybean Genotypes

Cluster I and IV (D2=875.3), Cluster I and III (D2=580.05) and cluster II and IV (D2=529.9) showed the greatest inter cluster distance at Pawe (Table 3). While between clusters II and IV (1227.7), clusters I and II (853.8) and cluster III and cluster IV (779.5) at Dibate (Table 4). The shortest squared distance changed into discovered between

clusters I and IV (373. 9) following with the aid of clusters I and III (405.7) and among cluster II cluster III (448.2). As a result, clusters with the most important distance indicate the variableness between genotypes that are blanketed among the ones clusters. The presence of the genetic distance between clusters maximizes the chance of bread wheat varieties improvement through wide crosses and high expression of heterosis had also reported by [23]. Besides, crossing of genotypes from distant inter clusters may also produce higher amount of wide range of variability in subsequent segregating populations [24].

Hence, crossing between genotypes related to among clusters I and IV at Pawe and between clusters II and IV at Dibate is suggested to expose better recombinants and could bring about segregates with better seed yield.

3.3. Cluster Mean Analysis

The cluster means for traits are shown in Tables 5 and 6 for Pawe and Dibate. Cluster I genotypes at Pawe had the second highest mean value for protein and the lowest mean value for oil content. Cluster II genotypes had the lowest mean values for nodule number, plant height, number of branches, number of pods, second highest a hundred seed weight, and lowest grain yield. Similarly, a cluster characterized by the lowest mean values of number of branches, number of pods, and grain yield in soybean genotypes were observed by [25]. Cluster III genotypes had the greatest mean values for days to blooming, days to maturity, number of nodules, plant height, and number of branches, as well as the second highest mean values for number of pods and grain yield. Cluster IV genotypes were distinguished by the lowest mean values for days to blooming, days to maturity, and protein content, as well as the highest mean values for number of branches, number of pods, number of seeds, a hundred seed weight, and grain yield. Similarly, several investigators have observed a cluster characterized by the lowest mean values of days to flowering and days to maturity with the greatest mean value of grain production in soybean genotypes [25-27]. There are situations that would bring contradict relationships between traits such as disease occurrence and moisture stress. These unfavorable conditions, in fact, were happened during this field experiment due to that planting time was being late. Frogeye leaf spot was also occurred at pod filling stage of the crop especially at Pawe. These might be caused that, consequently, most of genotypes could not attain their seed as expected.

At Dibate (Table 6), genotypes are characterized with the aid of the second least common values for wide variety of branches, range of pods, quantity of nodules and grain yield in cluster I; by way of the least common values for days to flowering, quantity of nodule, days to adulthood, wide variety pods and seeds, a hundred seed weight and yield in cluster II; through the most average values for days to adulthood, the highest plant height, 2nd biggest imply cost for wide variety of pods, the very best protein content material and second biggest yield in cluster III and with the aid of the most average values for days to flowering, wide variety of nodule, days to adulthood, department variety, pod variety, seed number, one hundred seed weight and grain yield in cluster IV. Further, cluster characterized by maximum values of days to flowering, days to maturity & grain yield of soybean has been reported by [28]. Genotypes in the 2nd cluster may be used for crossing with genotypes in cluster IV to develop past due maturing soybean genotypes with excessive wide variety of pods, excessive hundred seed weight and grain yield.

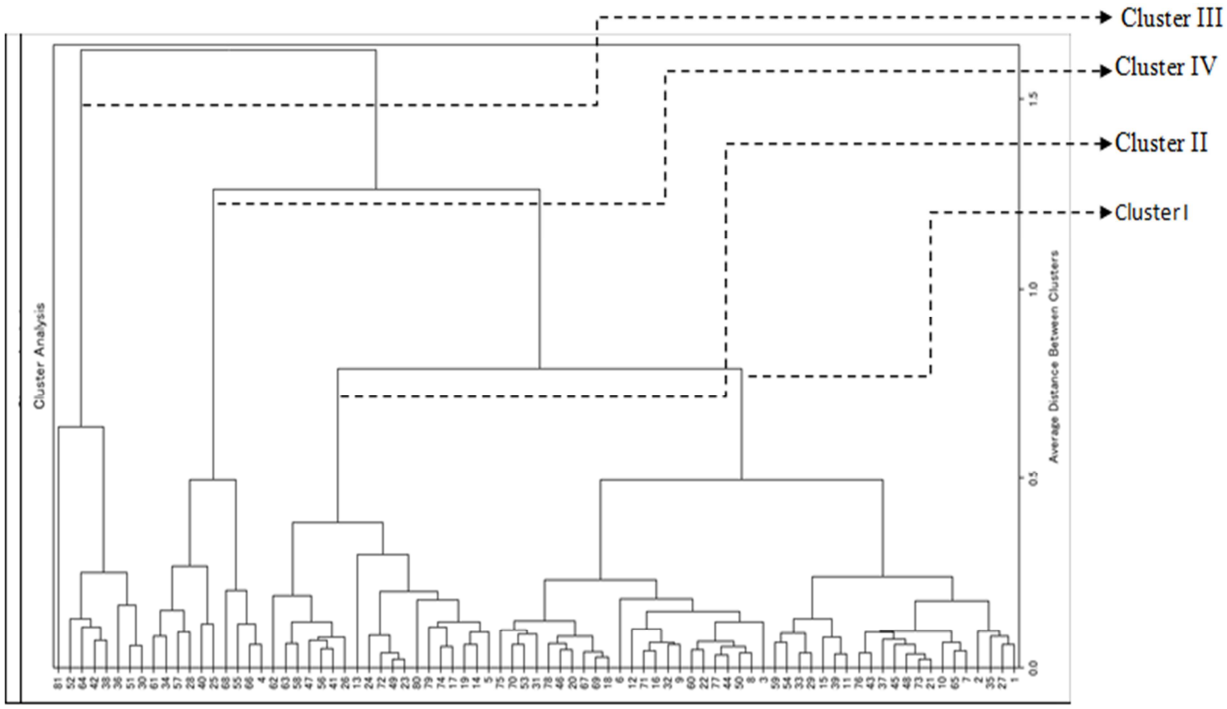

Figure 1. *Dendrogram for 81 Soybean genotypes at Pawe.*

Table 1. *The distribution of 81 genotypes based on D^2 analysis at Pawe.*

Cluster	Number of genotypes	Genotypes included
I	44	Tgx-1448-2e, Tgx-2010-11f, Tgx-1989-19f, Tgx-2010-12f, Tgx-2004-10f, Tgx-1485-1d, Tgx-2007-8f, Tgx-2008-2f, Tgx-2004-13f, Tgx-2007-11f, Tgx-2010-3f, Tgx-2004-3f, Tgx-1987-10f, Tgx-1987-45f, Tgx-1990-101f, Tgx-1990-47f, H3-15-SE-1, ALM-15-SB, PR142-1-SE, G99-15-SE-2, CLK-15-SA-1, G99-15-SA, Tgx-1990-78f, Tgx-1904-6f, Tgx-1989-11f, Tgx-1989-42f, Tgx-1989-45f, Tgx-1990-106fn, Tgx-1990-110fn, Tgx-1990-87f, Tgx-1990-8f, Tgx-1990-78f, Tgx-1990-57f, Tgx-1987-6f, Tgx-1987-64f, Tgx-1987-35f, Tgx-1987-38f, Tgx-1987-15f, Tgx-1986-3f, Tgx-1740-2f, pb12-1, pb12-6, pb12-7.
II	19	Tgx-2008-4f, Tgx-2010-15f, Tgx-2011-3f, Tgx-2011-7f, Tgx-1987-42f, Tgx-1990-70f, Tgx-1990-73f, H3-15-SG, Tgx-1989-75f, Tgx-1990-107fn, Tgx-1993-4fn, Tgx-1989-68f, Tgx-1995-5f, Tgx-1987-20f, Tgx-1987-19f, Tgx-1987-40f, pb12-8, pb12-4.
III	8	CRFD-15-SC, H3-15-SB-2, SCS-1, Tgx-1991-10f, Tgx-1990-111fn, Tgx-1990-114fn, Tgx-1987-23f, pun11-4.
IV	10	Tgx-2006-3f, pr142-15-SG, CLK-15-sb-1, CRFD-15-SB, Tgx-1990-80f, Tgx-1990-95f, Tgx-1989-48fn, Tgx-1835-10f, Tgx-1987-65f, Tgx-1987-37f.

Table 2. *The distribution of 81 genotypes based on D^2 analysis at Dibate.*

Cluster	Number of genotypes	Genotypes included
I	38	Tgx-1989-19f, Tgx-2010-12f, Tgx-2008-4f, tgx-2004-10f, Tgx-1485-1d, Tgx-2008-2f, Tgx-2004-13f, Tgx-2007-11f, Tgx-2010-15f, Tgx-2010-3f, Tgx-1987-10f, Tgx-1987-45f, Tgx-1990-47f, H3-15-SG, CLK-15-sb-1, PR142-1-SE, CRFD-15-SB, CLK-15-SA-1, H3-15-SB-2, G99-15-SA, Tgx-1990-78f, Tgx-1990-80f, Tgx-1991-10f, Tgx-1989-45f, Tgx-1989-75f, Tgx-1990-107fn, Tgx-1990-110fn, Tgx-1990-111fn, Tgx-1990-114fn, Tgx-1990-87f, Tgx-1990-8f, Tgx-1993-4fn, Tgx-1989-48fn, Tgx-1990-78f, Tgx-1987-64f, Tgx-1987-38f, Tgx-1987-19f, pb12-4.
II	29	Tgx-1448-2e, Tgx-2010-11f, Tgx-2007-8f, Tgx-2011-3f, Tgx-2004-3f, Tgx-1990-101f, Tgx-1990-73f, ALM-15-SB, CRFD-15-SC, G99-15-SE-2, CLK-15-SA-1, Tgx-1990-95f, Tgx-1989-42f, Tgx-1990-106fn, Tgx-1989-68f, Tgx-1990-57f, Tgx-1835-10f, Tgx-1995-5f, Tgx-1987-20f, Tgx-1987-65f, Tgx-1987-6f, Tgx-1987-37f, Tgx-1987-35f, Tgx-1986-3f, Tgx-1987-40f, Tgx-1740-2f, pb12-1, pb12-6, pun11-4.
III	8	Tgx-2011-7f, Tgx-1990-70f, pr142-15-SG, H3-15-SE-1, SCS-1, Tgx-1904-6f, Tgx-1989-11f, Tgx-1987-23f.
IV	6	Tgx-2006-3f, Tgx-1987-42f, Tgx-1990-95f, Tgx-1987-15f, pb12-7, pb12-8.

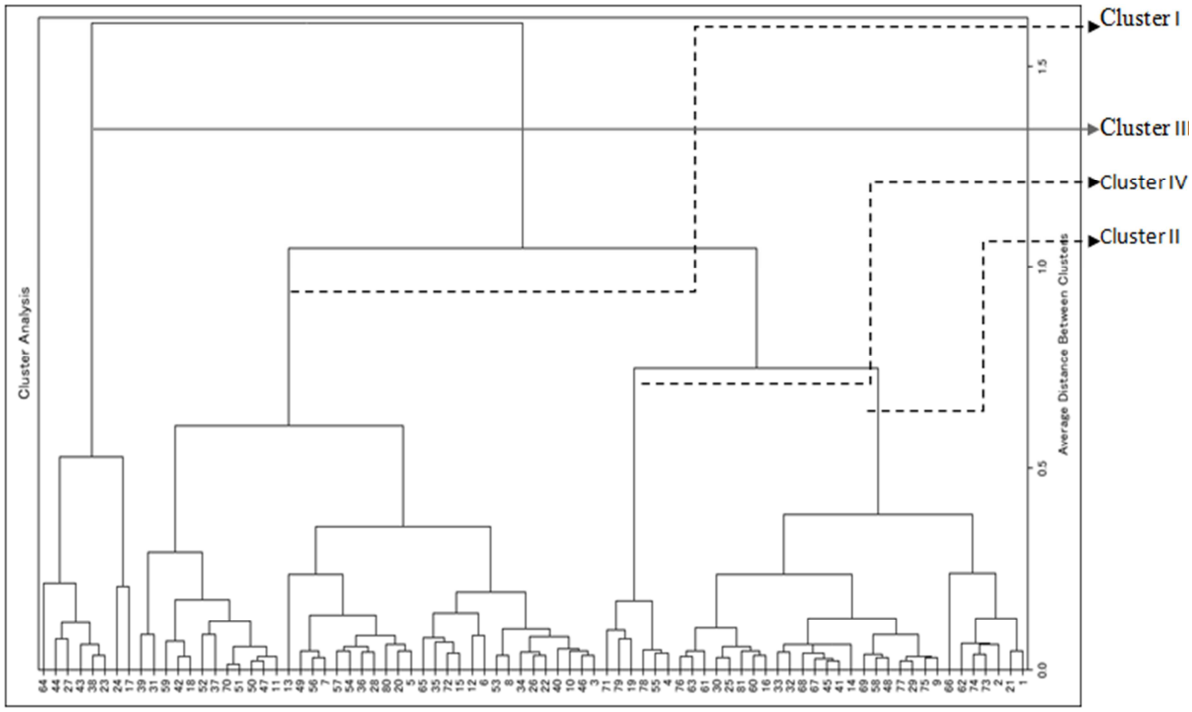

Figure 2. *Dendrogram for 81 Soybean genotypes at Dibate.*

Table 3. *Intra (bold diagonal) and inter Mahalanobis distance among genotypes at Pawe.*

Cluster	I	II	III	IV
I	50.9	345.5**	580.05**	875.31**
II		76.5	234.69**	529.96**
III			71.7	295.29**
IV				81

Table 4. *Intra (bold diagonal) and inter Mahalanobis distance among genotypes at Dibate.*

Cluster	I	II	III	IV
I	102.8	853.8**	405.7**	373.9**
II		131.7	448.2**	1227.7**
III			135	779.5**
IV				111

Table 5. *Cluster mean for eleven traits in soybean traits at Pawe.*

Traits	Clusters			
	I	II	III	IV
DF	58.1	56.9	59.4	53.2
DM	114.1	111.4	114.5	113.2
NN	17.4	16.5	18.2	17.4
PH	82	76.2	82.1	76.7
BrP	4.2	3.9	4.5	4.5
PdP	53.9	48.7	60.1	64.2
SdP	1.92	1.91	1.87	2.1
HSW	12.7	13.1	12.7	13.9
Protein	35.7	35.9	35.9	34.2
Oil	21	21.4	21.1	22
Yield	2094.4	1812.1	2361.3	2631.4

Table 6. *Cluster mean for 11 traits in soybean tested at Dibate.*

Traits	Cluster			
	I	II	III	IV
DF	69	68	70	70.5
NN	12.6	12.2	14.1	16.3
DM	124	123	126	125.2
PH	62.6	59.9	63.6	61.4
BrP	4	4.1	4	4.4
PdP	30.9	28.7	32.3	36.4
SdP	1.78	1.7	1.8	1.8
HSW	12.2	11	12.1	13
Oil	21	20.6	20.7	20.5
Protein	36	36	36.6	36.3
Yield	1484.6	1110.4	1842.9	2324.2

DF=days to 50% flowering, NN=number of nodule per plant, DM=days to 95% maturity, PH= plant height, BrP= number of branches per plant, PdP=number of pods per plant, SdP=number of seeds per pod, HSW=hundred seed weight.

3.4. Principal Components Analysis

The major components which had the highest contribution for the total variability of the eighty-one genotypes are given in Table 7. Variations explained by the first four PCAs from total variations were 63% and 65% at Pawe and Dibate, respectively. In the first principal components, traits with positive and high value were days to flowering (0.48), days to maturity (0.44), plant height (0.33) and protein content (0.30) at Pawe and days to maturity (0.46), plant height (0.42), protein content (0.38) and days to flowering (0.36) at Dibate.

The major contributing traits in the second principal component with high and positive component loading were number of branch (0.51), number of pods (0.5) and plant height (0.29) at Pawe and number of branch (0.6), pod number (0.46) and oil content (0.31) at Dibate. Traits with high and positive component loading were yield (0.59) and number of nodule (0.47) from the third PCA at Pawe and number of seeds (0.61), nodule number (0.47) and a hundred seed weight (0.38) at Dibate. The same finding reported that numbers of pods per plant, total seeds per pod & grain yield were the major contributing traits in PCA of soybean genotypes [25]. Traits loaded with high positive or negative values accounted more to the variability and they considered that are the most differentiated the cluster [29].

Table 7. *Eigen vectors, variance explained and Eigen values of PCs of soybean genotypes evaluated at Pawe and Dibate.*

Eigen vectors								
Traits	Pawe				Dibate			
	PC1	PC2	PC3	PC4	PC1	PC2	PC3	PC4
DF	0.48	0.17	-0.04	-0.05	0.36	0.17	0.11	-0.34
NN	0.05	0.22	0.47	-0.32	0.28	0.00	0.47	-0.11
DM	0.44	0.21	0.10	0.07	0.46	0.04	-0.09	-0.07
PH	0.33	0.29	0.23	-0.16	0.42	0.09	-0.08	0.01
BrP	-0.24	0.51	-0.11	0.07	0.05	0.60	0.06	-0.15
PdP	-0.22	0.50	-0.06	0.01	0.22	0.46	-0.19	0.40
SdP	-0.17	-0.19	0.22	-0.19	-0.08	-0.06	0.61	-0.35
HSW	0.10	-0.19	0.28	0.78	-0.15	0.10	0.38	0.31
Oil	-0.43	-0.08	0.08	0.00	-0.41	0.31	0.04	-0.05
Protein	0.30	0.00	-0.29	0.19	0.38	-0.32	0.06	0.07
Yield	-0.15	0.24	0.59	0.29	0.11	0.18	0.43	0.54
Eigen Values	3.25	1.87	1.28	1.11	3.40	1.83	1.43	1.21
Variance %	27.00	16.00	11.00	9.00	28.00	15.00	12.00	10.00
Cumulative	0.27	0.43	0.54	0.63	0.28	0.43	0.55	0.65

PCs= Principal components, DF=Days to 50% flowering, NN=Number of nodules per plant, DM= Days to 95% maturity, PH=Plant height, BrP= number of branches per plant, PdP=Number of pods per plant, SdP=number of seeds per pod and HSW= Hundred seed weight.

4. Conclusions

The soybean genotypes grouped into four grand clusters at both locations. The first four PCAs have been observed to be significant (with Eigen values greater 1) and accounted for about 63% and 65% from the overall variability at Pawe and Dibate, respectively.

Genotypes from distant inter cluster (cluster I and cluster IV) at Pawe and cluster II and IV (1227.7) at Dibate and genotypes with major variability contributor traits having high value which include days to flowering, days to maturity, plant height and protein content at both locations from the first principal component could be used as a parental material

for crossing.

However, one season test might now not realize genotypes' variability in response of environment; due to the fact quantitative traits are polygenic and profoundly affected by the environment. As a consequence, an addition experiment on those genotypes in changed seasons is needed for more real estimation of polygenic traits.

Conflict of Interest

Writer ensures that not any opposing profits occur. The materials and inputs used for this research are commonly and predominantly from the employer institution in I am working for. There is absolutely not any clash of importance between the author and of the institution. Also, the research was funded only by the institution.

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