Electronic Journal of Plant Breeding, 10 (4): 1405-1414 (Dec 2019) DOI: 10.5958/0975-928X.2019.00180.7
ISSN 0975-928X

Research Article

Genetic variability and multivariate analysis in sorghum (*Sorghum bicolour*) under sodic soil conditions

A. Subramanian[1]*, R. Nirmal Raj[1] and M. Elangovan[2]
[1]Dept. of Plant Breeding and Genetics, Anbil Dharmalingam Agricultural College and Research Institute, TNAU, Trichy – 620 027, Tamil Nadu
[2]Principal Scientist, Indian Institute of Millets Research (IIMR), Hyderabad, Telangana
***E-Mail**: subbi25@yahoo.com

(Received: 20 May 2019; Revised: 28 Oct 2019; Accepted: 20 Nov 2019)

Abstract
A field study was conducted using 31 sorghum landraces and two improved varieties as yield checks under natural sodic soil conditions at Anbil Dharmalingam Agricultural College and Research Institute, Trichy during *Kharif,2018*. The study was aimed to assess the mean performance, genetic variability, heritability and diversity of key traits that would aid the selection of genotypes for sodicity tolerance. The experiment was laid out in randomized block design with two replications. Eight biometric traits *viz.,* days to 50 percent flowering, plant height, number of tillers, number of leaves, leaf length, leaf width, panicle length and yield per plant were observed. The genotype ES1 was identified to be sodicity tolerant as it based on its overall *per se* performance. Based on PCA analysis, the characters panicle length, number of leaves and yield per plant were identified to contribute more towards the total divergence. These traits also showed higher PCV and GCV coupled with higher heritability and genetic advance as percent of mean. Hence, indirect selection for sodicity tolerance can be carried out through these traits for selection of genotypes with sodicity tolerance. Cluster analysis revealed the diverse genotypes (Cluster I and VI) that could be used in hybridization programmes for exploiting the maximum heterotic potential.

Key words
Sodicity, PCA, Heritability, Cluster analysis.

Introduction

Sorghum (*Sorghum bicolour* L.) is the fifth prime cereal crop of the world, after wheat, rice, maize and barley (Cuevas *et al.*, 2014; Sabiel *et al*., 2015). It is the staple food in 30 countries in the tropics and semi-tropics and in contrast to many other cereal grains, sorghum grains are gluten-free. The crop can be successfully grown in the majority of soil types and performs well in a wide range of temperatures (Nguyen *et al.*, 2013). Moreover, it is a multipurpose crop exploited for its grain, fodder and biofuel potential (Elangovan *et al.,* 2014). Globally, sorghum is cultivated over an area of 40.67 million hectares with average production and productivity of 57.60 million tonnes and 1416.2 Kg/ha respectively. In India, the crop is cultivated over an area of 5.86 million hectares with production and productivity of 4.57 million tonnes and 779.6 kg/ha respectively (FAOSTAT, 2017). It is often grown by small farmers with not greater than two hectares of land (Kudadjie *et al.,* 2004). India contributes about 16 percent of the total global sorghum production (Rao and Parwez, 2003).

Both sodicity and salinity affected soils account for around 7-8 percent reduction in crop productivity and these soil types cover about 953 mha of land across 120 countries (Yadav, 2003; Singh, 2018). Sodicity is the dominant factor in salt-affected soils (>50%) and Australia has the largest area under sodic condition (Singh, 2018). In India, Uttar Pradesh has the largest area under sodicity (1.35 mha) followed by Gujarat (0.54 mha) (Mandal *et al.,* 2010). Sodic soils are characterized by low electrical conductivity (EC < 4 dS m-1), high pH (>8.2), high Sodium Absorption Ratio (SAR >13) and high Exchangeable Sodium Percentage (ESP >15). In comparison to saline soils, sodic soils have excess of CO_3^{2-} and HCO_3^- salts (Sharma *et al.,* 2016). Due to dissolved organic matter in soil solution, sodic soils are often known as "black alkali" or "slick spots" (Ogle, 2010). Sodic soils, upon drying forms compact crust which acts as a physical barrier hindering crop germination and root penetration (Upadhyay *et al.,* 2012). Sodic condition also results in poor soil structure and reduced water movement which in turn degrades available nutrients, when coupled with high pH (Sharma *et al.,* 2016). Sorghum has been reported to thrive well under moderately sodic soils (Bhat, 2019) and hence assessment of genetic variability among the germplasm accessions could pave way for crop improvement of sorghum under for sodic condition.

The magnitude of genetic variability, heritability, and genetic advance are reliable estimates which essentially identifies important morphological traits for enhanced genetic gain under selection and are dependable during crop improvement programmes (Smalley *et al.,* 2004; Jimmy *et al.,* 2017). Greater knowledge about genetic diversity enables a breeder to carry out targeted and precise hybridization (Jain and Patel, 2016). Considering these facts a study was carried out to assess genetic components of variability and genetic diversity among sorghum landraces under sodic soil condition.

Materials and Methods

The study was carried out at Anbil Dharmalingam Agricultural College and Research Institute, Trichy during *Kharif,2018*. A total of 30 sorghum genotypes obtained from Indian Institute of Millets Research (IIMR), Hyderabad, Telangana state were raised along with three improved sorghum varieties (CO 30, K 12 and PY 2) as yield checks (Table 1) and the experiment was laid out in a randomized block design with two replications and two rows (ridge) per genotype per replication. Each ridge was of 4m length with a spacing of 45 cm between ridges and 15 cm between plants in ridge. All recommended agronomic practices were followed for better crop stand and expression. Observations pertaining to eight quantitative traits (days to 50 percent flowering, plant height, number of tillers, number of leaves, leaf length, leaf width, panicle length and yield per plant) were recorded in five random plants per genotype per replication as per the descriptors of sorghum (IBPGR, 1984) and the mean values were subjected to statistical analysis. The EC and pH of the research field were 0.95 ds/m and 9.07 respectively, while EC, RSC and pH for irrigation water was 4.9 ds/m, 12.528 mg/lit and 7.6 respectively.

The means for all the characters were subjected to Analysis of Variance (ANOVA) based on the model proposed by Panse and Sukhatme (1969). The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were analyzed by adopting the procedure suggested by Searle (1961). Heritability in broad sense h^2 (b) and genetic advance as percent of mean were estimated by the formula suggested by Allard (1960). The PCV and GCV estimates were classified as high (above 20%), medium (10-20%) and low (below 10%) (Sivasubramanian and Menon, 1973). Broad sense heritability estimates were classified as low (<30%), medium (31-60%) and high (>60%) (Robinson *et al.,* 1949) and the genetic advance was categorized as low (<10%), medium (10-20%) and high (>20%) (Johnson *et al.,* 1955)

The principal component analysis was carried out as suggested by Rao (1952) and was computed using the following formula:

PCA

$$PC1 = \sum_{1}^{p} a_{j} X_{j}$$

Where; PC = Principal component, a1j = Linear coefficient – Eigen vectors
Statistical analysis was carried out using TNAUSTAT and STAR 3.0 softwares.

Results and Discussion

The ANOVA for the eight morphological traits showed high significant mean sum of squares for all the characters among the genotypes (Table 2). Hence, the selection of genotypes from the existing variation could be possible under sodicity. Similar genotypic variation was revealed by Jimmy *et al.* (2017) in sorghum under normal growing conditions. The *per se* performance revealed that the genotype ES1 had highly significant yield per plant followed by EA7. These genotypes also showed significant mean values for panicle length and days to maturity, days to 50 percent flowering respectively. Thus the accessions can be deemed as sodicity tolerant based on its mean performance, whereas the accessions ES13 and ES3 could be susceptible towards sodicity as they recorded the least yield per plant (Table 3).

The extent of genetic variability present for various quantitative traits is essential for effecting precise selection and the response towards selection is dependent on the magnitude of heritable component of the variability (Panse, 1957). Genetic advance as percent of mean, when considered in conjunction with heritability is deemed to be more reliable in judging the heritable efficiency of a trait (Johnson *et al.,* 1955).The genetic variability estimates for the eight quantitative traits are presented in Table 4. High PCV and GCV values were observed for days to fifty percent flowering, plant height, number of leaves, leaf width and yield per plant indicating that selection could be effective in improving these traits. Similar results were reported for number of leaves (Bello *et al.,* 2007), plant height (Can and Yoshida, 1999; Jimmy *et al.,* 2017) and yield per plant (Shamini and Selvi, 2018) in sorghum. Moderate PCV and GCV values were recorded by the traits, number of tillers and leaf length whereas, the trait panicle length exhibited low PCV and GCV. Thus, selection for these traits would be less effective. Similar results were obtained by Jimmy *et al.,* (2017) for number of tillers and Shamini and Selvi, (2018) for panicle length. PCV values were found to be greater than GCV for the traits plant height, number of tillers and leaf length which indicated the influence of environment in the expression of these traits. Similar reports were obtained by Sankarapandian *et al.,* (1996) for leaf length and by

Kamatar *et al.,* (2011) for plant height in sorghum. A closer GCV and PCV values were observed for other traits which suggested the low environmental impact on these traits. Similar reports were made by Yadav *et al.,* (2000) for grain yield of rice and reiterated the presence of adequate genetic variability among these traits.
High heritability coupled with high genetic advance as percent of mean were observed in six characters *viz.,* days to fifty percent flowering, number of tillers, number of leaves, leaf length, leaf width and yield per plant. This indicated that these traits would positively respond to selection as they are predominantly governed by additive gene action. Similar results were obtained by Arunkumar *et al.* (2004) for number of leaves, and Susmitha and Selvi, (2014) for grain yield in sorghum. In contrast, Bello *et al.* (2007), Tomar *et al.* (2012) and Kalpande *et al.* (2014) reported high heritability coupled with moderate genetic advance for days to fifty percent flowering. In the present study, panicle length recorded high heritability with moderate genetic advance as percent of mean indicating that the trait is governed by additive gene partially (Shamini and Selvi, 2018).

Principal component analysis condensed the eight quantitative traits into four major principal components which accounted for 77.00 percent of the total variation (Table 5 and Fig. 1). The first three principal component axis recorded eigenvalues greater than one whereas, the fourth principal component recorded a value less than one. Thus, the fourth one could be discarded to further shorten the set of data at disposal. PC1 accounted for around 35 percent of total variability and it was contributed predominantly by the traits plant height, panicle length and number of leaves. PC2 accounted for about 18 percent of total variability and the related traits were number of tillers, yield per plant and panicle length. PC3 contributed around 14 percent of total variability and it was contributed by yield per plant and number of leaves. The first two principal component axes explained more than half of the total variability (53.00%) hence, it indicated a high degree of correlation among the traits studied (Jain and Patel, 2016). The traits panicle length, number of leaves and yield per plant tend to remain together as they contributed in two principal components (Mohanlal *et al.,* 2018). As a whole, PCA analysis was able to identify the key traits that were responsible for the variability in a population. Similar studies were also conducted by Akatwijuka *et al.* (2016) in sorghum landraces and by Jain and Patel, (2016) in fodder sorghum. The biplot analysis (PC1 *vs* PC2) revealed that the trait panicle length had the maximum positive effect towards total divergence followed by number of tillers and yield per plant. All the sorghum genotypes were evenly distributed along the biplot indicating the diversity present among the materials studied (Fig. 2).

Cluster analysis was carried out using the ward's method and Euclidean distance measure was adopted for dendrogram construction (Fig. 3). A total of six clusters were formed of which cluster III was the largest grouping with nine genotypes followed by cluster I with eight genotypes. Cluster IV was a solitary cluster with EA10 as the lonely genotype. All clusters except for cluster IV had two sub-clusters each. The highest genetic distance was between cluster I and cluster VI hence, the genotypes from these clusters can be used as parents in hybridization programmes for sodicity. A similar estimation of genetic diversity using clusters was also done by Jain and Patel, (2016) in fodder sorghum. Though the sorghum genotypes were collected from different locations (Table 1) and the grouping pattern was not concordant with the geographical diversity pattern of the accessions. An interesting pattern was observed in the accessions collected from Kanpur district, as the genotypes *viz.,* ES1, ES 4, ES3, ES 6 and ES 8 were distributed in five different clusters indicating the variability and genetic distance existing between these genotypes. Similar patterns were observed for every other genotype except for ERS 1 and ERS 2 collected from Tuticorin as they were grouped in cluster I. The check varieties CO 30 and K12 were grouped under the same sub-cluster of cluster III, though the pedigree of these varieties revealed that the parents were of different kind. A similar study using morphological traits was conducted by Mujaju and Chakauya (2008) in sorghum landrace accessions. Hence, further evaluation of sorghum genotypes should be carried out at the molecular level using markers to understand the phylogenetic and genetic relationship among the accessions (Mace *et al.,* 2008).

The genotypes ES1 and EA7 were identified as sodicity tolerant based on mean performance. Genetic variability studies revealed that days to fifty percent flowering, number of leaves, leaf width and yield per plant as vital traits for selection in various generations. PCA analysis identified panicle length and yield per plant as key traits for divergence. Considering the above, traits *viz.,* number of leaves, panicle length and yield per plant could prove to be the major stakeholders of selection under sodic conditions. Cluster analysis identified two distant clusters (I and VI) from where the selection of parents for hybridization could yield more feasible dividends. A greater extent of variation was present in genotypes that were collected from the same location.

Acknowledgement
The authors gratefully acknowledge the receipt of seeds of sorghum germplasm from Indian Institute of Millets Research, Hyderabad, Telangana state, to carry out the study.

References

Akatwijuka, R., Rubaihayo, P.R. and Odong, T.L. 2016. Genetic diversity among sorghum landraces of southwestern highlands of Uganda. *Afr. Cr. Sci. J.,* **24(2):**179-190.

Allard, R. W. 1960. *Principles of Plant Breeding***.** John Wily and Sons. Inc., U.S.A. 485p.

Arunkumar, B., Biradar, B., D. and Salimath, P.M. 2004. Genetic variability and character association studies in *rabi* sorghum. *Karnataka J. Agric. Sci.,* **17(3):** 471-475.

Bello, D., Kadams, A.M., Simon, S.Y. and Mashi, D.S. 2007. Studies on genetic variability in cultivated Sorghum (*Sorghum bicolor* L. Moench) cultivars of Adamawa state Nigeria. *American-Eurasian J. Agric. Environ. Sci.,* **2(3):** 297-302.

Bhat, B.V. 2019. Breeding Forage Sorghum. **11:**175-191.

Can, N.D., Yoshida, T. 1999. Grain yield of sorghum cultivars in a double cropping system. *Pl. Prod. Sci.,* **2(2):** 121-124.

Cuevas, H.E., Prom, L.K., Erpelding, J.E., Brotons, V. 2014. Assessments of genetic diversity and anthracnose disease response among Zimbabwe sorghum germplasm. *Plt.Br.,* **133:**234-242.

Elangovan, M., Kiran Babu, P., Seetharama, N. and Patil, J.V. 2014. Genetic diversity and heritability characters associated in sweet sorghum [*Sorghum bicolor* (L.) Moench]. *Sugar Tech.,* **16(2):** 200-210.

FAOSTAT. 2017. Food and Agricultural Organization of the United Nations (FAO), FAO Statistical Database, 2017, from http: //faostat.fao.org

IBPGR/ICRISAT. 1984. Sorghum descriptors. IBPGR, Rome, Italy, pp. 49-70.

Jain, S.K. and Patel, P.R. 2016. Genetic diversity and principle component analyses for fodder yield and their component traits in genotypes of forage sorghum (*Sorghum bicolor* L. Moench). *A. Ar. Zone,* **55:**17-23.

Jimmy, M.L., Nzuve, F., Flourence, O., Manyasa, E. and Muthomi, J. 2017. Genetic variability, heritability, genetic advance and trait correlations in selected sorghum (Sorghum bicolor L. Moench) varieties. *Int. J. Agron. Agri. R.,* **5:** 47-56.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybean. *Agron. J.,* **47:** 314-318.

Kalpande, H.V., Chavan, S.K., More, A.W., Patil, V.S. and Unche, P.B. 2014. Character association, genetic variability and component analysis in sweet sorghum (*Sorghum bicolor* (L.) Moench). *J.Crop Weed.,* **10(2):**108-110.

Kamatar, M.Y., Kotragouda, M., Shinde, D.G. and Salimath, P.M. 2011. Studies on variability, heritability and genetic advance in F3 progenies of *kharif* × *rabi* and *rabi* × *rabi* crosses of Sorghum (*Sorghum bicolour* (L.) Moench). *Plant Arch.,* **11(2):** 899-901.

Kudadjie, C. Y., Struik, P. C., Richards, P. and Offei, S. K. 2004. Assessing production constraints, management and use of sorghum diversity in north-east Ghana: A diagnostic study. *NJAS-Wageningen J. Life Sci.*, ***52*(3-4)**: 371-391.

Mace, E.S., Xia, L., Jordan, D.R., Halloran, K., Parh, D.K., Huttner, E., Wenzl, P. and Kilian, A. 2008. DArT markers, diversity analyses and mapping in *Sorghum bicolour*. *BMC. Genom.,* **9:** 26-26.

Mandal, A.K., Sharma, R.C., Singh, G. and Dagar, J.C. 2010. Computerized database of salt affected soils in India. *Technical Bulletin*, CSSRI/Karnal, pp. 28.

Mohanlal, V.A., Saravanan, K., and Sabesan, T. 2018. Multivariate analysis in blackgram (*Vigna mungo* L. hepper) genotypes. *J. Pharm. Phyto.,* **7(6):** 860-863.

Mujaju, C. and Chakauya, E. 2008. Morphological variation of sorghum landrace accessions on farm in semi arid areas of Zimbabwe. *Int. J. Bot.,* **4(4):** 376-382.

Nguyen, C.T., Singh, V., Van Oosterom, E.J., Chapman, S.C., Jordan, D.R., Hammer, G.L. 2013. Genetic variability in high temperature effects on seed-set in sorghum. *Func. Plt. Biol.,* **40**: 439-448.

Ogle, D. 2010. Plants for saline to sodic soil conditions. USDA. Natural Resources Conservation Services. Boise, Idaho. Technical Note No.9A, p.10150.

Panse, V. G. and Sukhatme, P. V. 1967. Statistical methods of agricultural workers. *Indian Council of Agricultural Research*, New Delhi.

Panse, V.G. 1957. Genetics of quantitative characters in relation to Plant Breeding. *Indian J. Genet.,* **17:** 318-328.

Rao, B.D. and Parwez, S. Md. 2003. Analysis of growth in sorghum production in India. *Asian Econ. Rev*., **45(3):** 503-515.

Rao, C. R. 1952. Advanced statistical methods in biometrical research. *John Wiley and Sons Inc., New York*. 236-272.

Robinson, H.F., Comstock, R.E. and Harvey, P.H. 1949. Estimates of heritability and the degree of dominance in corn. *Agron. J.,* **41(8):** 353-359.

Salih, A. Sabielab, I., Noureldina, I., Balochb, S.K., Balochb, S.U. and Bashir, W. 2015. Genetic variability and estimates of heritability in sorghum (*Sorghum bicolor* L.) genotypes grown in a semiarid zone of Sudan. *Arch. Agr. and Soil Sci*. pp. 37-41.

Sankarapandian, Krishnadoss, D. and Devarathinam, A.A. 1996. Genetic parameters, correlations and path analysis among yield and yield characters in grain sorghum. *Madras Agric. J.,* **83:** 625-628.

Searle, S.R. 1961. *Biometrics,* **17:** 474-480.

Shamini, K. and Selvi, B. 2018. Genetic variability studies for stay green and different yield attributingtraits in Sorghum. *Elec. J. Pl. Br.*, **9(3):** 948 – 955.

Sharma, D.K., Anshuman Singh, Sharma, P.C., Dagar, J.C. and Chaudhari, S.K. 2016. Sustainable Management of Sodic Soils for Crop Production: Opportunities and Challenges. *J. Soil Sal. and W. Qual.* **8(2)**: 109-130.

Singh, G. 2018. Climate Change and Sustainable Management of Salinity in Agriculture. *Res Med Eng Sci.,* **6:**1-7.

Sivasubramanian, P. and Madhavamenon, P 1973. Genotypic and phenotypic variability in rice. *Madras Agric. J.,* **60:** 1093-1096.

Smalley, M.D., Fehr, W.R., Cianzio, S.R., Han, F., Sebastian, S.A., Streit, L.G. 2004. Quantitative trait loci for soybean seed yield in elite and plant introduction germplasm. *C. sci.,* 44(2): 436-442.

Susmitha, C.H and Selvi, B. 2014. Genetic variability for grain iron, zinc, other nutrients and yield related traits in sorghum (*Sorghum bicolor* (L.) Moench). *Int. J. Agri. Sci. Res.,* **4(3):** 91-99.

Tomar, S.S., Sivakumar, S. and Ganesamurthy, K. 2012. Genetic variability and heritability studies for different quantitative traits in sweet sorghum (*Sorghum bicolor* (L.) Moench) genotypes. *Electron. J. Plant Breed.,* **3(2):** 806-810.

Upadhyay, A., Tripathi, S. and Pandey, S.N. 2012. Effects of soil sodicity on growth, nutrients uptake and bio-chemical responses of *Ammi majus* L. *Res. J. Soil. Bio*., **4(3):** 69-80.

Watson, J.W. and Eyzaguirre, P.P.B. 2002. Homegardens and *in situ* conservation of plant genetic resources in farming systems. *Proceedings of the second international home gardens workshop*, 17-19th, July - 2001, Witzenhausen, Federal Republic of Germany. International Plant Genetic Resources Institute, Rome, Italy.

Yadav, J.S.P. 2003. Managing soil health for sustained high productivity. *J. Ind. Soc. Soil Sci.,* **51**: 448-485.

Yadav, R.K**.** 2000. Studies on genetic variability for some quantitative Characters in rice (*Oryza sativa* L). *Advances in Agric. Res.,* **13:** 205-207.

Table 1. List of Sorghum genotypes and their source

Sl.No.	List of Genotypes	Source
1.	EG 93	Veppandhattai, Perambalur
2.	EG97	Kunnam, Perambalur
3.	EG 101	Musiri, Karur
4.	EA 2	Dindigul
5.	EA 4	Dindigul
6.	EA 7	Dindigul
7.	EA 10	Dindigul
8.	EA 11	Vadipatti, Dindigul
9.	ES 2	Lucknow, Hardoi
10.	ES 3	Kanpur
11.	ES 13	Kanpur Nagar, Fatehpur
12.	EG 98	Kunnam, Perambalur
13.	ES 1	Kanpur
14.	ES 4	Kanpur
15.	ES 6	Kanpur
16.	ES 8	Kanpur
17.	ES 10	Kanpur Nagar, Fatehpur
18.	ES 11	Kanpur Nagar, Fatehpur
19.	EG 85	Virudhachalam, Cuddalore
20.	EG 92	Veppandhattai, Perambalur
21.	EG 96	Perambalur
22.	EG 99	Duraiyur, Karur
23.	EG 100	Karur
24.	EG 102	Musiri, Karur
25.	EG 103	Karur
26.	ERS 1	Kovilpatti, Tuticorin
27.	ERS 2	Kovilpatti, Tuticorin
28.	EA 1	Dindigul
29.	EA 3	Dindigul
30.	EA 6	Dindigul
31.	CO 30	TNAU, Coimbatore
32.	PY 2	Paiyur
33.	K12	Kovilpatti, Tuticorin

Table 2. Analysis of variance for eight quantitative traits

Source	df	Days to 50% flowering	Plant height	No. of tillers	No. of leaves	Leaf ln.	Leaf wd.	Panicle ln.	Yield per plant
Replication	1	2.97	2.47	0.23	0.92	67.61	1.07	0.53	8.78
Treatment	32	**89.59****	**7613.17****	**0.82****	**7.52****	**248.21****	**1.75****	**118.56****	**326.34****
Error	32	4.5	160.11	0.23	1.72	7.91	0.41	3.48	11.19

Table 3. Mean performance of thirty three sorghum genotypes

Sl. No.	Genotyes	Days to 50% flowering (Days)	Plant height (cm)	No. tillers	No. of leaves	Leaf length. (cm)	Leaf width (cm)	Panicle length (cm)	Yield per plant (g)
1	EG93	70.00	235.17	2.00	12.35	**83.20****	4.15	10.35	23.70
2	EG97	68.00	**161.83****	1.50	12.50	**58.50****	6.65	7.35	29.50
3	EG101	**66.00***	**168.24****	2.50	9.00	43.50	5.55	14.25	17.45
4	EA2	**64.50****	184.50	1.50	10.70	52.50	4.70	11.05	24.96
5	EA4	84.00	**139.33****	1.50	10.50	33.15	3.90	7.35	10.28
6	EA7	**63.50****	**169.00****	1.50	10.50	44.50	4.70	8.65	**43.68****
7	EA10	68.00	187.67	**4.50****	9.00	50.15	6.65	7.25	10.38
8	EA11	**66.00***	**159.50****	1.00	10.00	**61.00****	6.30	10.95	19.60
9	ES2	86.00	236.17	2.00	11.80	**63.35****	6.15	**24.50****	25.14
10	ES3	**65.00****	**147.00****	1.00	12.00	52.50	5.35	5.50	7.05
11	ES13	67.00	233.17	1.00	12.80	**66.50****	5.20	6.70	4.85
12	EG98	83.00	223.67	1.00	11.65	**62.20****	5.25	11.05	**35.02****
13	ES 1	69.50	195.00	1.80	12.50	42.80	5.85	**23.55****	**57.65****
14	ES 4	71.50	**144.25****	1.90	9.00	33.75	3.95	8.75	**37.47****
15	ES 6	83.00	**148.15****	1.70	10.00	43.50	**6.80***	19.65	19.45
16	**ES 8**	**72.50**	**208.90**	**1.95**	**9.50**	**46.35**	**5.45**	**19.80***	**9.29**
17	ES 10	78.00	216.50	1.75	12.00	37.55	5.90	19.15	25.05
18	ES 11	73.00	197.65	1.85	9.50	45.90	5.35	18.65	23.38
19	EG 85	76.00	332.25	1.70	**16.50****	52.75	**6.85***	17.10	9.48
20	EG 92	71.00	293.15	1.50	13.50	39.95	5.85	**21.90****	15.74
21	EG 96	76.00	297.15	1.95	13.50	47.10	6.00	**27.45****	**42.25****
22	EG 99	**63.00****	**159.65****	1.15	8.50	33.25	4.25	12.95	**40.69****
23	EG 100	72.00	328.20	2.05	13.00	47.50	6.05	**22.55****	**39.59****
24	EG 102	72.00	206.00	1.80	9.50	46.00	5.10	10.45	17.18
25	EG 103	76.50	253.15	2.45	11.50	45.55	6.45	**32.80****	**35.25****
26	ERS 1	73.50	312.40	1.75	13.00	54.20	5.85	**32.70****	**31.22***
27	ERS 2	73.50	340.35	2.00	**14.00***	**56.00***	6.20	**26.70****	**42.56****
28	EA 1	**60.00****	**146.35****	1.80	10.00	36.40	4.45	9.65	16.60
29	EA 3	61.00	**165.65****	2.15	10.50	34.55	4.80	16.60	23.80
30	EA 6	**65.00****	**133.10****	1.20	13.00	51.25	**7.60****	**23.75****	21.25
31	CO30	**63.50****	**181.00***	1.00	9.30	**64.50****	4.50	16.35	15.50
32	PY2	71.00	184.83	2.00	7.85	**56.35***	5.05	10.90	10.64
33	K12	72.50	**144.00****	2.00	13.15	50.65	4.45	10.40	18.86

Table 4. Genetic variability, heritability and GAM for eight quantitative traits

Character	Mean	PCV %	GCV %	Heritability %	Genetic advance as percentage of mean %
Days to 50% flowering	71.06	30.11	29.48	95.88	59.47
Plant height	207.26	40.87	30.56	55.91	47.08
Number of tillers	1.77	19.07	15.11	62.77	24.66
No. of leaves	11.28	22.81	22.10	93.82	44.09
Leaf length	49.6	18.92	14.89	61.91	24.13
Leaf width	5.49	48.94	47.52	94.30	95.06
Panicle length	15.96	9.65	9.18	90.43	17.98
Yield per plant	24.38	53.29	51.49	93.37	102.49

Table 5. Eigen vectors, percentage variation, eigen values and cumulative variance of eigth quantitative traits

Characters	Eigen Vectors			
	PC1	PC2	PC3	PC4
Days to 50% flowering	0.304	0.039	-0.218	0.885
Plant height	0.498	-0.105	0.056	0.015
Number of tillers	0.12	0.496	-0.58	-0.177
Number of leaves	0.436	-0.34	0.151	-0.126
Leaf length	0.118	-0.658	-0.139	-0.079
Leaf width	0.4	0.013	-0.373	-0.396
Panicle length	0.484	0.254	0.14	-0.039
Yield per plant	0.218	0.36	0.643	-0.069
Eigen Value	2.81	1.43	1.13	0.83
% Variance	0.35	0.18	0.14	0.1
Cumulative %	0.35	0.53	0.67	0.77

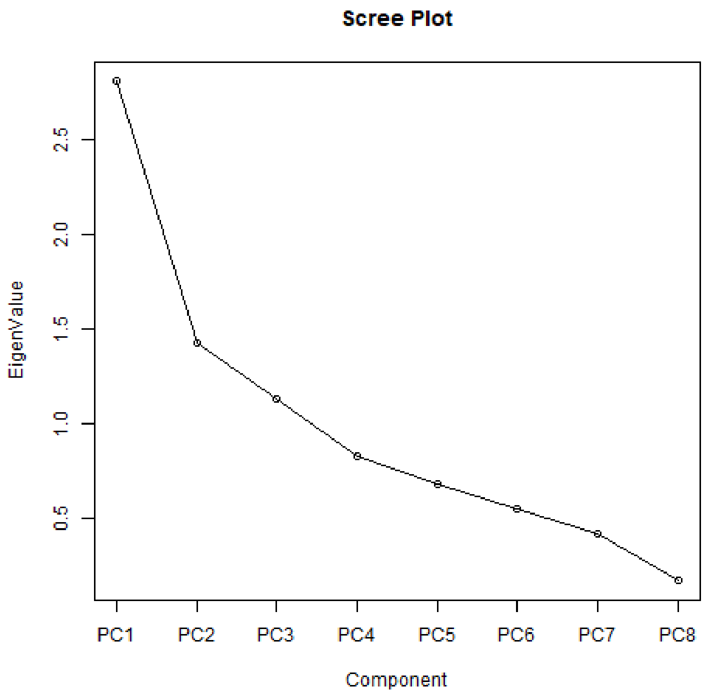

Fig. 1. Scree plot for eight principal component axes

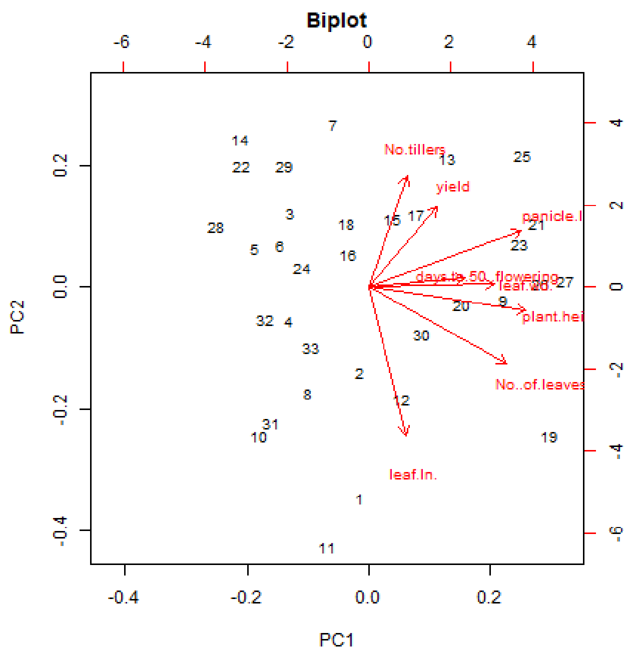

Fig. 2. Biplot between PC1 and PC2

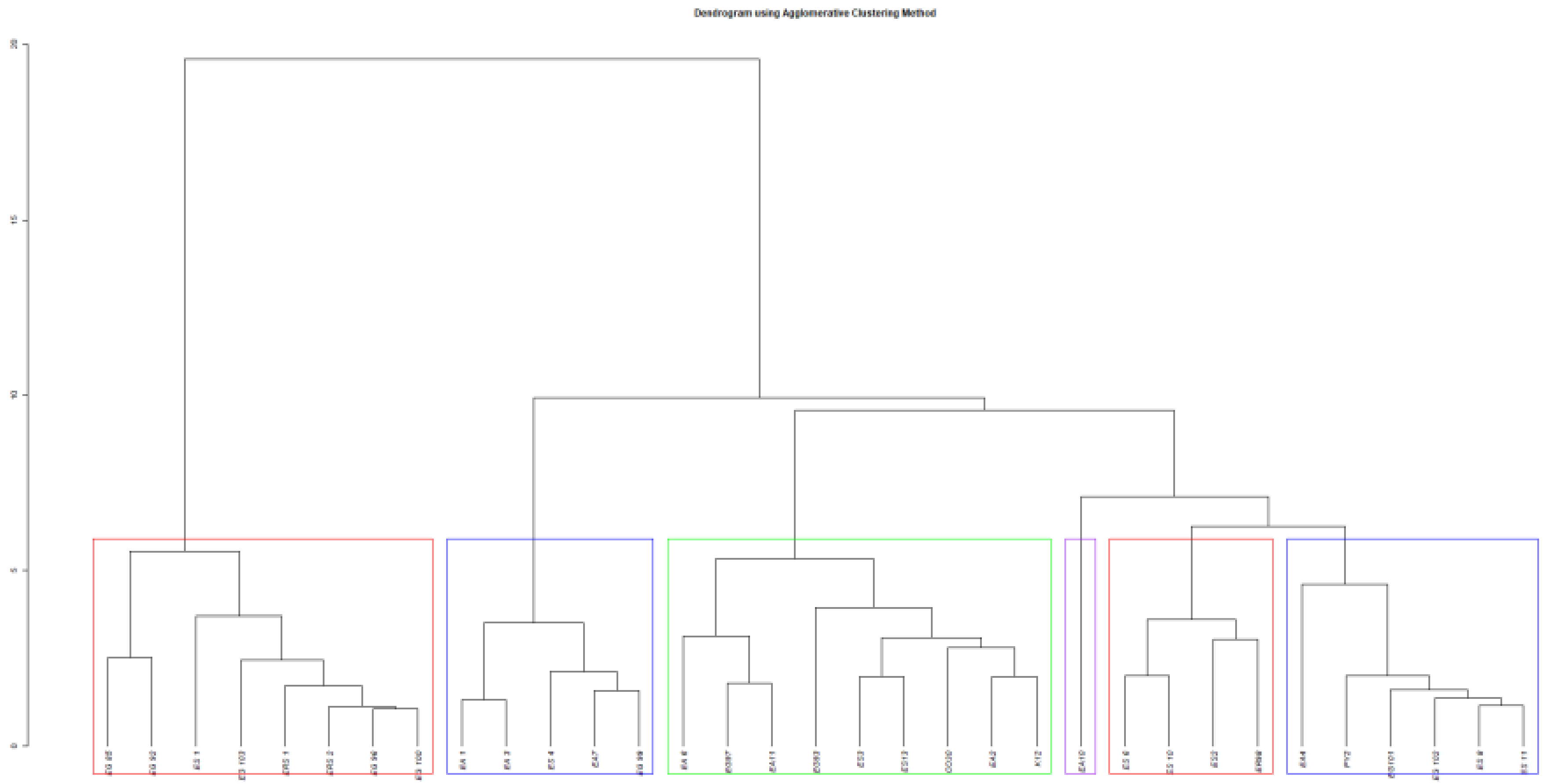

Fig. 3. Cluster analysis of thirty three genotypes using ward's method