academicJournals

Vol. 8(49), pp. 6529-6536, 19 December, 2013
DOI: 10.5897/AJAR12.921
ISSN 1991-637X ©2013 Academic Journals
http://www.academicjournals.org/AJAR

African Journal of Agricultural Research

Full Length Research Paper

Genetic diversity in soybean genotypes under water stress and normal condition using factor analysis and cluster analysis

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Accepted 4 December, 2013

To study the relationships between morphological characters of soybean plant an experiment was conducted in randomized complete blocks design (RCBD) in two replications under drought stress condition at Agricultural College of Guilan University in 2008. Result of analysis of variance showed that there was significant difference among the studied soybean genotypes in the majority of traits. The result of factor analysis in under water stress condition showed that 7 independent factors for characters to explain 86.4% variation of all data and under normal condition 5 independent factors for characters to explain 82% variation of all data. A similarity factor was constructed using UPGMA method for morphological characters varieties were classified into 8 groups for water stress condition and 4 groups for normal condition. Classifying the results of the cluster analysis identified Hamilton genotype suitable for sown in water stress condition and majority genotypes suitable for sown in normal condition.

Key words: Cluster analysis, factor analysis, genetic diversity, normal condition, soybean, water stress.

INTRODUCTION

Soybean seed is a major source of high-quality protein and oil for human consumption (Katerji et al., 2001). The unique chemical composition of soybean has made it one of the most valuable agronomic crops worldwide (Thomas et al., 2003). Its protein has great potential as a major source of dietary protein. The oil produced from soybean is highly digestible and contains no cholesterol (Essa and Al-ani, 2001). Genetic diversity analysis reveals genetic backgrounds and relationships of germplasm, and also provides strategies to establish, unitize, and manage crop core collections (Brown-Guedira et al., 2000; Roussel et al., 2004). Soybean genetic diversity and relationships can be assessed by the differences in morphological and agronomic traits, pedigree information, geographic origins, isozymes and DNA markers (Dong et al., 2004; Guan et al., 2010; Wang et al., 2010). The importance of genetic diversity in plant breeding is obvious from the results obtained in different crops (Ghafoor et al., 2001; Smart, 1990; Upadhyaya, 2003; Upadhyaya et al., 2002). Water stress is considered one of the most important factors limiting plant performance and yield worldwide (Boyer, 1982). Water stress during reproductive development often decreases the seed size in soybean (Kadhem et al., 1985; Momen et al., 1979; Sionet and Kramer, 1977). Waterlogging is defined as prolonged soil saturation with water at least 20% higher than the field capacity (Aggarwal et al., 2006). Increasing soil water deficiency correlated with reduction in dry matter accumulation (Lopez et al., 1996; Lazcano-Ferrat and Lovatt, 1999; Grieu et al., 2001). The best option for crop production, yield improvement and yield stability under water stress conditions is to develop water tolerant crop varieties. One of the main goals in breeding programs is selection of the

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Table 1. Used genotypes.

S/N	Genotypes	Origin (country)	S/N	Genotypes	Origin (country)
1	Line 33	Iran	11	Zane	Iran
2	Hill	Iran	12	Hack	Iran
3	Union	Iran	13	Dw2	Iran
4	Bp	Iran	14	Line 32	Iran
5	Hamilton	Iran	15	Clark	Iran
6	Streslland	Iran	16	Gorgan 3	Iran
7	Williams	Iran	17	Talar	Iran
8	Tnh 56	Iran	18	Century	Iran
9	Dpx	Iran	19	Line 17	Iran
10	Williams 82	Iran			

Table 2. Analysis of variance (RCBD) for studied traits

S.O.V	MS									
	df	Plant height	Number of pod	Leaf area	Number of Seed on Pod	Number of seed on plant	100 grain weight	Day to 50% flowering	Day to maturity	Grain yield
Replication	2	0/013^{ns}	0/71^{ns}	0/02^{ns}	0/012^{ns}	0/87^{ns}	1/90^{ns}	1/28^{ns}	7/6*	0/05^{ns}
Genotype	18	0/031^{ns}	12/53^{ns}	1/22^{ns}	0/029^{ns}	12/70^{ns}	5/37**	170/21**	41/06**	2/77*
Error	18	0/032	5/84	0/97	0/03	6/25	10/31	0/34	1/38	1/19
%CV		8/64	22/38	13/98	8/49	16/72	7/96	**2**/42	**2**/77	17/83

*,** Significantly different at 5 and 1% probability level respectively; ns, non significant.

best genotypes under water stress conditions. Insufficient water, especially during emergence, flowering and pod-filling stages lower the yield of soybean (Abayomi, 2008). Optimally supplying water during different growth stages such as the early of growth season, flowering, pod set, and grain–filling improves crop yield and quality; and plants need more water from flowering to onset of grain–filling than any other times (Speeht et al., 2001). Narjesi et al. (2007) reported that 5 independent factors for characters 30 soybean genotypes to explain 80.2% variation of all data. The first factor alone 22.54 of the data changes can be justified and called the phonological properties. (Arshad et al., 2006) showed that cluster analysis the genotypes divided in 3 groups. The first group was involved 14 genotypes, second group 33 genotypes and third group involved 11 genotypes. The objectives of this study are to evaluate the genetic diversity of soybean cultivar using factor analysis and cluster analysis, to analyze and characterize population structure within soybean cultivars and compare effect traits on grain yield under water stress and normal condition.

MATERIALS AND METHODS

The present study was conducted to evaluate the effects of water stress and normal condition on soybean genotypes. To study the relationships between morphological characters of soybean plant an experiment was conducted in randomized complete blocks design (RCBD) with two replication sat water stress conditions and normal condition at Agricultural College of Guilan University, Iran during 2008. The material consisted of 19 soybean genotypes (Table 1). The seeds sown in the spring season and genotypes were grown in two row plots, each plot included four ridges, and each ridge was 3.5 m in length and 50 cm apart. Agronomic characteristics were including plant height, number of pod, leaf area, number of seed on pod, number of seed on plant, 100 grain weight, day to 50% flowering, day to maturity and grain yield. Data were recorded on 5 competitive plants of each plot and grain yield (kg/ha) was calculated for the entire plot. Data were statistically analyzed using ANOVA appropriate for RCBD with SAS ver. 9.1 and factor analysis and cluster analysis using SPSS 16 software's.

RESULTS AND DISCUSSION

Result of analysis of variance (Table 2) showed that there were significant differences among the studied soybean genotypes for yield and component yield traits. This illustrates the high potential of these genotypes to use the genetically source for breeding purposes.

Factor analysis

Factor analysis based principal component analysis and after varimax rotation under water stress condition

Table 3. Factor analysis of studied traits under water stress condition.

Parameter	PC1	PC2	PC3	PC4	PC5
Eigen values	6/155	3/506	2/842	2/011	1/952
Cumulative Eigen values	6/155	9/661	12/503	14/514	16/466
Proportion of variance	26/176	15/309	14/365	13/489	12/991
Cumulative variance	26/176	41/485	55/850	69/339	82/331
Traits					
Plant height	0/681	0/365	-0/403	0/215	0/216
Number of pod	-0/437	0/014	0/210	0/735	0/190
Leaf area	0/038	0/825	-0/115	0/241	00/145
Number of seed per pod	-0/228	-0/275	0/327	0/014	0/678
Number of seed per plant	0/392	-0/138	-0/193	0/364	0/128
100 grain weight	0/876	-0/774	-0/246	0/227	-0/169
Day to 50% flowering	0/868	0/061	0/097	0/2	-0/241
Day to maturity	0/109	0/19	0/058	0/868	-0/309
grain yield	0/203	0/254	0/101	0/804	-0/344
Oil content	0/034	0/88	-0/221	0/267	0/105
Protein content	0/346	0/486	0/442	0/045	0/132

Table 4. Factor analysis of studied traits under normal (non stress) condition.

Parameter	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Eigen values	6/155	3/246	2/407	1/608	1/456	1/294	1/128
Cumulative Eigen values	6/155	9/401	11/808	13/416	14/872	16/166	17/294
Proportion of variance	15/685	14/891	14/406	11/346	11/312	10/023	8/833
Cumulative variance	15/685	30/549	44/955	56/300	67/612	77/635	86/468
Traits							
plant height	0/109	-0/037	0/331	-0/241	0/744	-0/107	0/068
Number of pod	0/114	0/257	0/151	-0/123	-0/180	0/839	0/116
Leaf area	0/049	-0/157	-0/017	0/194	0/793	0/120	0/097
Number of seed per pod	-0/271	0/046	-0/009	-0/740	-0/087	-0/224	0/041
Number of seed per plant	0/383	0/595	-0/048	-0/137	0/195	0/138	0/756
100 grain weight	0/009	0/154	0/330	0/155	0/386	0/337	0/716
Day to 50% flowering	0/920	-0/335	0/369	0/261	0/361	0/372	0/304
Day to maturity	0/919	0/060	0/206	0/107	0/050	0/134	0/042
grain yield	0/123	0/049	0/213	0/177	0/080	0/061	0/034
Oil content	-0/092	0/023	-0/002	0/010	-0/128	0/030	-0/028
Protein content	0/059	0/964	0/793	0/034	0/157	-0/003	0/128

showed (Table 3) that 7 independent factors for characters to explain 86.4% variation of all data. The first factor because of high day to 50% flowering and day to maturity alone 15.68% of the data changes can be justified and called the phonological factor properties. The second factor because high number of seed per plant and protein content was called quality factor and alone 14.89% of the data changed can be justified and total 86.4% variation of all data under water stress condition. Factor analysis under normal (non stress) condition showed (Table 4) that 5 independent factors for characters to explain 82% variation of all data. The first factor because of high plant height, 100 grain weight and Day to 50% flowering alone 26.17% of the data changes can be justified and called yield and yield component factor properties. The second factor because high oil content was called quality factor and alone 15.3% of the data changed can be justified and total 82% variation of all data under normal condition (non stress) condition. Figures 1 and 2 showed projection of the agro-morphological and seed quality traits on the planes defined in water stress and normal condition by principal

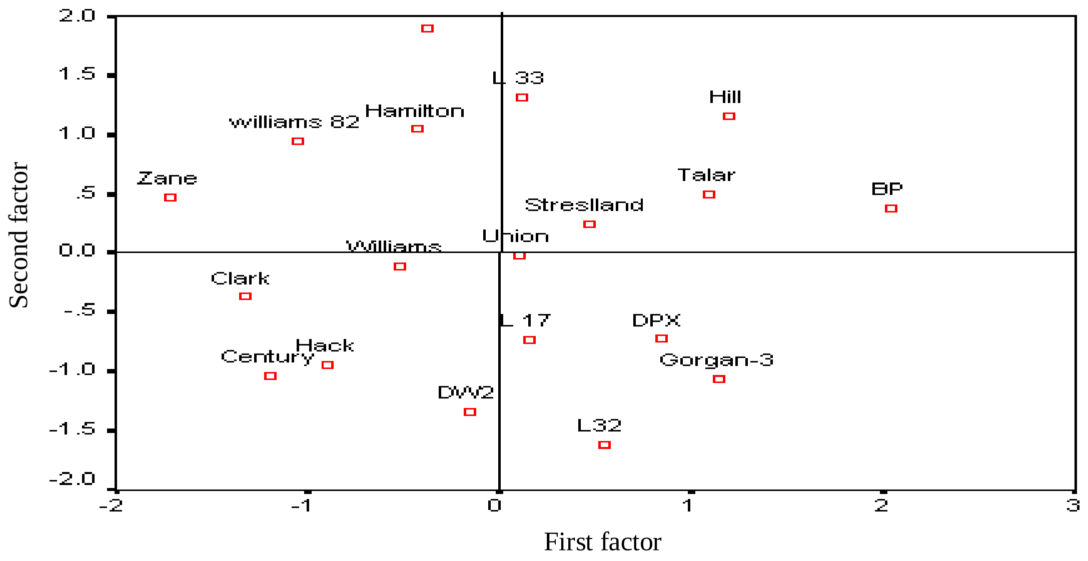

Figure 1. Plot of graph first factor (phonological properties) and second factor (quality properties) in soybean.

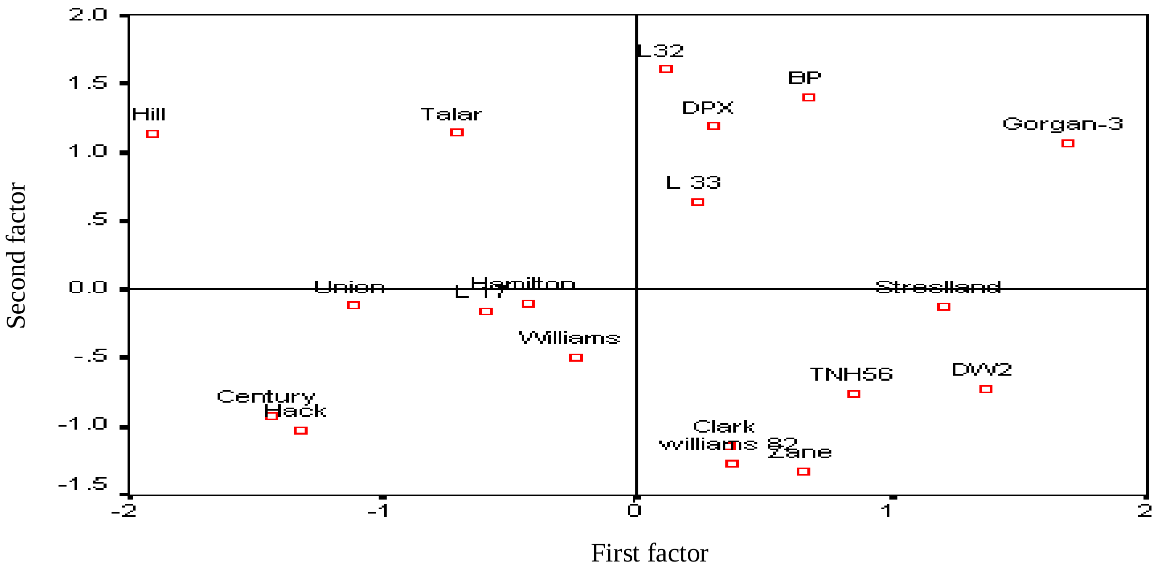

Figure 2. Plot of graph first factor (yield and yield component properties) and second factor (quality properties) in soybean.

components. In water stress condition first factor determined according to high day to 50% flowering (0/92) and day to maturity (0/919) and called phonological factor properties and second factor determined according to high number of seed per plant (0/595) and protein content (0/964) was called quality factor (Figure 1) and in normal condition first factor determined according to high plant height (0/681), number of seed per plant (0/868) and grain yield (0/876) called yield and yield component factor properties and second factor determined according to high oil content (0/88) and 100 grain weight (-0/774) was called quality factor (Figure 2). Principal component analysis is useful as it gives information about the groups where certain traits are more important allowing the breeders to conduct specific breeding programs. The results of present studies are in line with those of Narjesi et al. (2007). Principal component analysis is useful as it gives information about the groups where certain traits are more important allowing the breeders to conduct specific

Table 5. Means value and variance of 7 cluster of studied traits under water stress condition.

Traits	Cluster I		Cluster II		Cluster III		Cluster IV		Cluster V		Cluster VI		Cluster VII		Cluster VIII	
	Mean	Variance	Mean	Variance	Mean	Variance	Mean	Mean	Variance	Variance	Mean	Variance	Mean	Variance	Mean	Variance
plant height	99	32/16	87/62	318/7	93	84/5	95/75	70	690/75	1/12	85/66	72/3	101/75	21/12	70	690/75
Number of pod	139/7	988/07	130/72	1028/18	209/23	4387/5	121	171/53	136/1	551/12	132/8	2263/93	112/5	5325/1	171/53	136/1
Leaf area	55/71	40/98	50/17	64/68	55/55	6/91	60/22	41/95	213/08	121/13	53/83	76/27	48/84	111/52	41/95	213/08
Number of seed on pod	2/07	/008	2/03	0/038	1/93	0/00	2/13	2/19	0/001	0/002	2/12	0/004	2/2	0/008	2/19	0/001
Number of seed per plant	17/55	6/29	17/28	7/78	19/09	16/84	17/28	17/67	3/7	0/01	16/19	6/62	19/55	6/26	17/67	3/7
100 grain weight	43/76	84/52	38/31	137/32	53/98	8/16	39/18	46/71	3/43	66/52	36/56	25/18	44/49	139/36	46/71	3/43
Day to 50% flowering	255/2	879/56	222/27	1797/6	296/45	4077/04	228/05	286	571/59	3353/8	233/46	2012/7	221/2	1897/2	286	571/59
Day to maturity	68	40/66	64/5	23	71/5	0/5	62/5	66	21	12/5	67	36	67	0/00	66	21
grain yield	141/7	128/25	134/5	144/33	148	8	134/5	138	112/3	24/5	137/67	156/33	138	0/00	138	112/3
Oil content	14/13	3/55	15/006	1/75	14/83	7/5	12/59	16/52	3/64	0/55	15/49	9/96	14/26	0/77	16/52	3/64
Protein content	80/71	116	85/68	57/06	84/73	244/74	71/89			17/91	88/48	324/8	81/43	25/17	118/7	94/36

Table 6. Mean value and variance of 4 cluster of studied traits under normal (non stress) condition.

Traits	Cluster I		Cluster II		Cluster III		Cluster IV	
	Mean	Variance	Mean	Variance	Mean	Variance	Mean	Variance
Plant height	95/83	203/37	93	249	83	0/5	57/5	690/75
Number of pod	121/25	492/59	134/22	895/68	169/6	4493/5	164	136/1
Leaf area	58/13	136/91	51/73	119/43	79/25	300/61	34/42	213/08
Number of seed on pod	2/06	0/005	2/16	0/02	2/09	0/019	2/19	0/001
Number of seed per plant	17/76	5/41	18/81	7/24	16/88	0/89	15/59	3/7
100 grain weight	54/48	99/47	42/73	150/22	28/66	0/13	12/13	3/43
Day to 50% flowering	307/12	1042/51	235/56	3328/41	161/7	92/48	81/3	571/5
Day to maturity	66/33	22	68/14	22/47	65/5	40/5	61	21
Grain yield	139	74/25	141/28	87/57	135/5	220/5	125	112/3
Oil content	14/47	5/07	15/2	1/63	13/92	6/66	13/28	3/64
Protein content	82/65	165/4	86/79	53/25	79/48	217/2	75/85	118/7

breeding programs.

Cluster analysis

Cluster analysis based on nine agro-morphological and two seed quality traits during 2008, divided 19 genotypes of glycin max into 8 clusters in water stress condition and 4 cluster in normal condition. Mean values and variance for each of 8 and 4 clusters are presented in (Tables 5 and 6). In water stress condition Cluster I consisted of 4 genotypes (6, 9, 10 and 14) and these genotypes were medium early in flowering, medium early in maturity, tall, medium number of seed per plant, medium grain yield, medium oil content and medium protein contents (Figure 3). Cluster II comprised of 4 genotypes (2, 11, 12 and

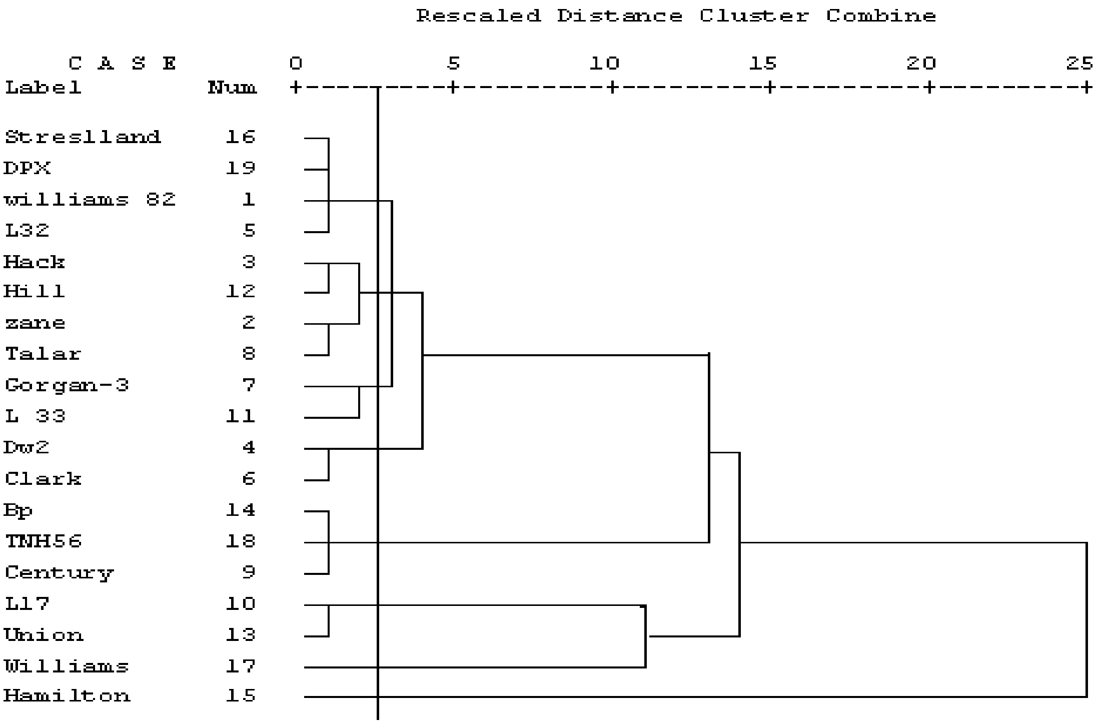

Figure 3. Dendogram of cluster analysis of soybean genotypes classified according to all the traits studied in water stress condition.

17) and these genotypes were early in flowering, early in maturity, short, low number of seed per plant, low grain yield, medium oil contents and medium protein contents. There were 2 genotypes (1 and 16) in Cluster III and these genotypes were late in flowering, late in maturity, medium height, high number of seed per plant, high grain yield, medium oil contents and medium protein contents. Cluster IV consisted of 2 genotypes (13 and 15) and these genotype were early in flowering, early in maturity, tall, low number of seed per plant, low grain yield and low oil contents and very low protein contents. There were 3 genotypes (4, 8 and 18) in cluster V and these genotypes were medium in flowering, medium in maturity, short, low number of per plant, low grain yield, high oil contents and high protein contents. Cluster VI had 2 genotypes (3 and 19) and these genotypes were characterized by medium in flowering, medium in maturity, tall, low number of seed per plant, high grain yield, medium oil contents and medium protein contents. Cluster VII comprised of Williams genotype characterized as medium in flowering, late in maturity, medium very tall, medium number of seed per plant, medium grain yield, medium oil contents and low protein contents. Cluster VIII comprised of Hamilton genotype characterized as medium in flowering, medium in maturity, very short, high number of seed per plant, high grain yield, high oil contents and high protein contents (Figure 4). In normal (non stress) condition Cluster I consisted of 9 genotypes (1, 6, 7, 8, 10, 14, 15 and 16) and these genotypes were medium in flowering, medium in maturity, tall, very high number of seed per plant, very high grain yield, medium oil content and medium protein contents. Cluster II comprised of 7 genotypes (3, 4, 5, 9, 11, 17 and 19) and these genotypes were medium in flowering, medium in maturity, medium height, very low number of seed per plant, medium grain yield, medium oil contents and medium protein contents. There were 2 genotypes (2 and 18) in cluster III and these genotypes were medium in flowering, medium in maturity, short, very low number of seed per plant, very low grain yield, medium oil contents and medium protein contents. Cluster IV consisted Hack genotype and this genotype were early in flowering, early in maturity, very short, very low number of seed per plant, very low grain yield and medium oil contents and medium protein contents. Classifying the results of the cluster analysis identified Hamilton genotype suitable for sown in water stress condition and majority genotypes suitable for sown in normal (non stress) condition and Hamilton genotype in water stress condition which confirm the results of the compared means yield. This genotype could be used as source of germplasm for breeding for water tolerance. The results of cluster analysis suggested that there is variation among the genotypes for different agro-morphological and seed quality traits. Genotypes with greater similarity for agro-morphological and seed quality traits were placed in the same cluster. Results of present studies are in agreement with those of Chang et al. (1998).

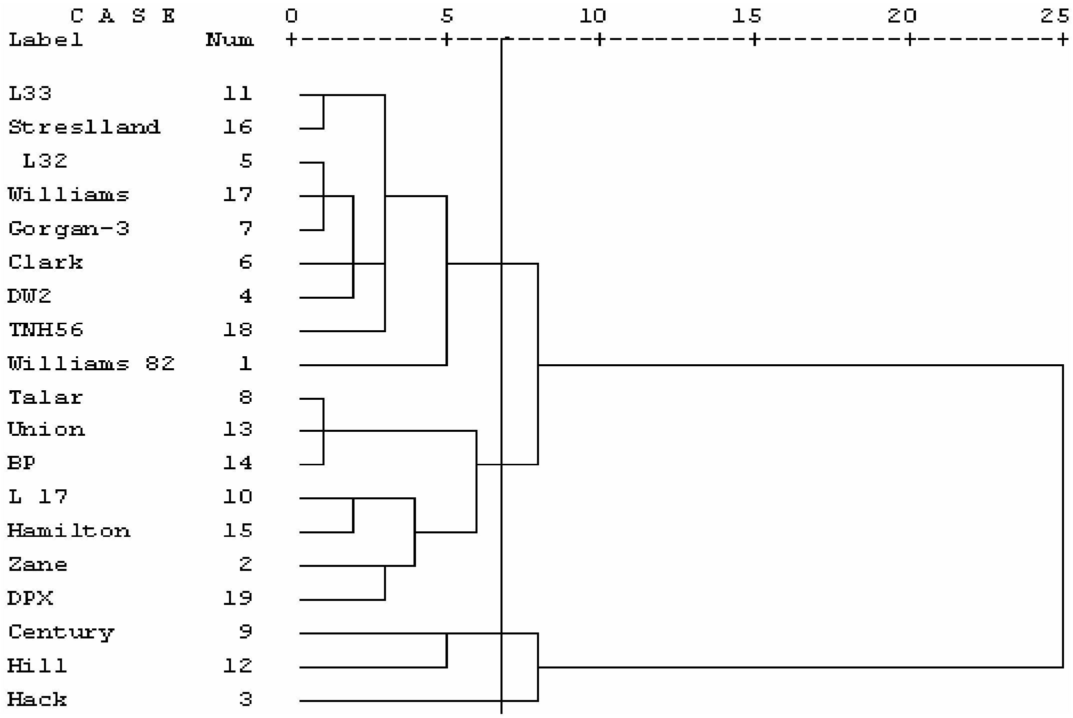

Figure 4. Dendogram of cluster analysis of soybean genotypes classified according to all the traits studied in normal (non stress) condition.

Conclusions

Result of analysis of variance showed that there was significant difference among the studied soybean genotypes in the majority of traits. Principal component analysis is useful as it gives information about the groups where certain traits are more important allowing the breeders to conduct specific breeding programs. Classifying the results of the cluster analysis identified Hamilton genotype suitable for sown in water stress condition and majority genotypes suitable for sown in normal condition. Identifying a genetic structure within soybean genotypes is useful for establishing strategies for sampling and managing germplasm. Crosses between the Hamilton genotype with other genotypes could be used to create genotype resistant under stress condition.

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