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Genetic variability of soybean accessions for yield and yield attributing traits through using multivariate analysis

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Abstract— *Soybean (Glycine max L. Merril) is the second most important food legume of Nepal, grown either as sole or intercrop with maize or in paddy bund. It has immense potential to increase the area and production due to its yield stability and wider adaptation trait. Its importance increases due to the burgeoning of the poultry and cattle's farming. Genetic variability is under threat not only in the field but also in the national commodity programs that are meant to be safe heavens. It is the basic requirement for a successful breeding programme. Collection and evaluation of accessions of any crop is a pre-requisite for any programme, which provides a greater scope for exploiting genetic variability. Considering the truths, soybean cultivars were collected from IITA, Nigeria, NAGRC gene bank and local collections studied in depth for morphological characterization using multivariate analyses. An investigation was carried out in the forms of regeneration and observation screening nurseries to assess the variability quantitative traits at Rampur environment and over the years 2012 to 2013. Screening nurseries was carried out in rod row design. Yield and yield contributing traits were analyzed to understand the extent of variability for yield and yield attributing traits. The present study revealed the presence of high levels of variations for nine different morphological traits including yield attributes and seed yield among the soybean accessions. A total of forty diverse accessions of local landraces and exotic lines were evaluated in the subtropical rainfed system of Rampur in the year 2012.Some of high yielding accessions of soybean were 272W, Cobb, G-758, and Puja. Likewise a total of hundred one accessions were evaluated for grain yield and yield parameters during 2013. The research results revealed that high yielding soybean accessions were G-18428, TGX 1990-67F, G-757, V9 (B/pur-9, TGX1990-5F. Under cluster analysis using all the seven morphological traits grouped the 40 accessions into five major groups at the genetic distance of 202.63. It was also found that, among the five clusters, cluster I was the largest and consisted of 32 accessions and the second largest group was the clusters II and IV, and each consisted of three accessions. Likely cluster analysis using all the seven morphological traits grouped the 101 accessions collected from National Agricultural Genetic Resources Centre (Gene Bank) and exotic lines from IITA, Nigeria into five major groups at the genetic distance of 267.82. Among the five clusters, cluster I was the largest and consisted of eighty four accessions and the second largest group was the clusters II consisted of fourteen accessions. The accessions from cluster I and cluster II could be used for hybridization program with the soybean accessions of clusters III, IV and V in order to develop high yielding soybean varieties for further improvement. The first seven principal components were extracted which accounted for about 100% variability among the 104 soybean accessions for all morphological characters. There was rich diversity found in seed coat color of the soybean local landraces. Flower color and pattern of flower were also found diverse among the collected accessions. This study indicated the presence of high levels of genetic variability among the soybean accessions in terms of evaluated characters*

Keywords— ***soybean, accessions, genetic variability, cluster analysis, principal component analyses (PCA).***

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I. INTRODUCTION

Soybean (*Glycine max L. Merril*) is the second most important food legumes of Nepal, have a diverse adaptability to varied agro-ecological zones with an altitude ranging from 200-2000 m asl either as sole or intercrop with maize in upland or on paddy bund in low land conditions. It alone shared about 23757 ha area and 28237 MT productions out of total legumes (MOAD, 2013).Soybean is a crop which can provide complete protein, containing eight amino acids essential for human. That means it can play a major role in enriching nutritional standard of foods in developing countries, where human beings are facing protein deficiencies (Samia, 2013).The genetic diversity can be analyzed by morphological, biochemical traits, and molecular marker polymorphisms, analysis of gene marker data enables estimation of the mating system and monitoring of genetic changes caused by factors affecting the reproductive biology of a species. As we know, phenotypic traits are controlled by polygenes and affected by environment, but large numbers of accessions can adapt to environments. The phenotypic data has more polymorphism in genetic diversity and reveal genetic variation indirectly. On the contrary, the molecular data reveal genetic variation directly, but fewer markers have less polymorphism. It is very difficult to obtain molecular data for a large number of accessions that has enough polymorphism to show the genetic diversity of germplasm. So, the morphological traits are the suitable and practical tools for studying the genetic diversity on large numbers of accessions. Agro-morphological variation in shape of plants has always been an important means of (i) distinguishing individuals; (ii) controlling source seed production; and (iii) identifying the negative traits those effects on yield, the genetic diversity centers of annual wild soybean and the soybean lines resistance to pod shatter, drought, pests or disease (Truong et al.,2005; Malik et al.,2006, 2007). The soybean germplasm show a wide range of phenotypic variation in terms of flower color, days to maturity, plant height, number of pod per plant, seed number per pod, and seed yield. Pod shape is one of the important descriptors for evaluating soybean genetic resources (IPGRI, 1998). Truong et al., 2005 tested the applicability of elliptic Fourier method for evaluating genetic diversity of pod shape in soybean accessions and concluded that principal component scores based on elliptic Fourier descriptors yield seemed to be useful in quantitative parameters not only for evaluating soybean pod shape in a soybean breeding program but also for describing pod shape for evaluating soybean germplasm. For an effective breeding program for crop variety development, the analysis of genetic diversity is one of the useful tools and plays a vital role in identification of superior lines. Moreover, better knowledge on genetic variability could help to achieve long-term selection gain. In the present study, genetic variability of the available soybeans accessions was investigated through using morphological traits. The objective of this study is to understand the genetic variability of soybean germplasm derived from IITA, IVRDC and local landraces. This information will be very useful for rational management and allow breeders to better understand the evolutionary relationships among accessions and to develop strategies to integrate useful variability into their breeding programs.

II. MATERIALS AND METHODS

2.1 Experimental Site: The experiment was carried out at the experimental field of Grain Legume Research Program, Rampur, during June/July to November/December 2012-2014. Geographically, the place is located at about 27°40' N latitude, 84°19' E longitude and 228 m altitude. The soil of the experimental site is generally acidic (pH 4.2-5.7), light textured and sandy loam

2.2 Climate: It is low-lying and has humid, subtropical climate. The winter is started from November to February, December and January are the coldest months with temperatures dropping to 2-3°C, while the hot summer is from March to May with temperatures rise up to 43°C. Total rainfall is over 1500 mm with monsoon (>75% of rain) period from mid-June to mid-September

2.3 Plant Materials: In observation screening nursery, a total of forty soybean accessions in the year 2012 and one hundred four soybean accessions in 2013 including local collections were used as the experimental materials to evaluate the genetic diversity. A total of forty accessions in observation screening nursery and a total of one hundred four local landraces in regeneration screening nursery were morphologically characterized to determine the biodiversity within the local collections. The soybean genetic resources were received from IITA, Nigeria, AVRDC, Taiwan, IARI, IIPR, Govinda Ballav Agricultural University, Pantanagar, India and local collections from National Agricultural Genetic Resources Centre (Gene Bank), Khumaltar, Nepal.

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2.4 Experimental Design and Setting the Experiment: The experiments regeneration nursery, observation screening nursery were laid out in rod-row design with non-replicates. Seeds were sown at the spacing of 50 cm between rows and 10-15 cm between plant to plant in a row. Each entry was grown in 2 rows in screening nurseries keeping plant-to-plant distance of 8–10 cm in rows.

2.5 Intercultural Operations: Urea, Diammonium Phosphate(DAP) and Murat of potash (MOP) were used as basal dose during final land preparation at 9, 87 and 33 $kgha^{-1}$, respectively to supplement the recommended dose of chemical fertilizers @ 20:40:20 N: P_2O_5: K_2O kg/ha after final land preparation. Intercultural operations like weeding, thinning, application of pesticide, and so forth were done as recommended and when necessitated for proper growth and development of plants in each plot. Harvesting was done depending upon the maturity of the plants in each plot.

2.6 Data Collection: Agronomic traits yield and yield components data on days to flower, days to maturity, plant height, pods per plant, number of seeds per pod, hundred seed weight and seed yield per plant were taken from 5 randomly selected competitive plants from each plot. Plants of each plot were harvested when the plants and pods of each plot turned into yellowish brown colour and almost all the leaves shed. Pods were threshed and 3-4 days sun-dried for seed yield estimation. In addition, morphological traits such as seed coat, hilum colour, seed and pod shapes were recorded

2.7 Statistical Analyses: Statistical analysis for yield and yield attributing traits were carried out using R-program and Minitab. Mean and standard deviations for all quantitative traits were computed. Analysis of variance was performed for all traits in order to test the significance of variation among accessions. The data was analysed for mean, coefficient of variation (CV %), LSD value and correlation coefficient. UPGMA clustering was done using Minitab 14. For cluster analysis, the accessions were split into various groups on the basis of their performances which are displayed in a dendogram. Cluster analysis is a type of multivariate technique whose primary purpose is to group individuals or objects based on characteristics they possess, so that individuals with similar description are mathematically gathered into the same cluster. The resulting cluster of individuals should exhibit higher within clusters homogeneity and between clusters heterogeneity. Thus, if the classification is successful, individuals within cluster should be closer when plotted geometrically and different clusters shall be apart (Hair et al., 1995). Hierarchical clustering methods are commonly employed in analysis of genetic diversity in crop species. These methods proceeds either by a series of successive mergers or by a series of successive divisions of a group of individuals. Former, known as 'agglomerative hierarchical' methods, start with a single individual. Thus, initially there as many clusters as individuals (Mohammadi &Prasanna, 2003). The most similar individuals are first grouped and these initial groups are merged according to their similarities. Among various agglomerative hierarchical methods, the UPGMA (Un-weighted Paired Group Method using Arithmetic Averages).Panchen, 1992 is most commonly adopted clustering algorithm, followed by the Ward's minimum variance method(Ward, 1963). Data were analysed todetermine Euclidean distance based on paired group method to determine dissimilar groups of the soybean lines. Two-dimensional principal component analysis (PCA) graph was constructed using PAST-multivariate software.Agro-morphological traits were characterized as per the descriptors prepared by International Board for Plant Genetic Resources (IBPGR, 1984).

Annex i: List of different traits and their description of measurement

Morphological Traits	**Method of measurement**
Emergence	Seed emergence recorded when about 50% of the seedling emerged out of the soil
Days to flowering	The number of days from sowing to flowering of 50% plants
Days to maturity	The number of days from sowing until approximately 90% pod turned into brownish colour
Plant height (cm)	The height from the base of the plant to the tip of last leaf
Pods per plant (number)	Total number of pods with seed in a plant

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Seeds per pod (number)	Total number of seeds in a pod
100-seed wt (g)	One hundred seeds randomly counted and then weighed
Seed yield per plant (g)	Weighing the total number of seeds produced in a plant
Seed yield (kg per ha)	Weighing the seeds produced in a plot and then converted into kg per ha

III. RESULTS AND DISCUSSION

3.1 Genetic variability of soybean screening nurseries

A total of forty diverse accessions of local landraces and exotic lines were evaluated in the subtropical rainfed climate of Rampur chitwan in summer season of the year 2012. Variation was observed in agro-morphological traits like days to flower, days to maturity, plant height, seeds/pod, number of pods/plant, grain yield and hundred seed weight varied among accessions (Table 2). Days from sowing to flowering varied from 62 days in G8514 and G-757 to 39 days in TH227.Days from sowing to 90% maturity varied from 139 days in Gorkha local to 111 days in TH227.Number of pods per plant varied from 97 pods in Salyan-2 to 20 pods in Tandi collection # 1. Plant height ranged from 88 cm in PI200525 to 31 cm in Collection # 1 Mangal Bazar. Number of seeds per 10 pods ranged from 25 seeds in Gorkha local 1, Tandi collection no.1 and V-5 to only 13 seeds in TK-5. Hundred seed weight varied from 25.5 g of Tandi collection # 2 to 5.2 g of TH227. Some of high yielding accessions of soybean were 272W (2195 kg/ha), Cobb (1588kg/ha), G-758(1415 kg/ha) and Puja (1282 kg/ha). Early maturing accessions were TK-5, TH-227, V-3 and V-5(111 days).

Likewise a total of hundred one accessions including two checks (Puja and Cobb) were evaluated for grain yield and yield parameters during 2013. Early plant stand, days to flowering, days to maturity, plant height, seeds/pod, number of pods/plant, grain yield and two hundred seed weight varied among accessions (Table 5). Days from sowing to maturity varied from 108 days in the accessions CM9112, SJ-4, Co169, IPBSY1178, G-758, PI94159, Salyan-2, C2019 to 134 days in TGX1989-41F, V8 and V10. Plant height ranged from 10 cm in C2015 to 176 cm in C2017. Highest number of pods per plant was found in C2022 (263 pods) and lowest number of pods was found in TH227 (34 pods only). Hundred seed weight varied from 4 g of C2021, C2023, C2020 to 24 g of C2026. Table 5 revealed that some of high yielding soybean accessions were G-18428(5695 kg/ha), TGX 1990-67F (4895 kg/ha), G-757(4800 kg/ha), V9 (B/pur-9)[4550 kg/ha), TGX1990-5F(4080 kg/ha), Co 157(3900 kg/ha), Chatewan-9(3820 kg/ha), TGX1990-93F(3750 kg/ha), V7 (B/ pur-7)[3600 kg/ha), C2020(3550 kg/ha)and G-8514(3550 kg/ha). However mean yield performances of soybean accessions over the years (2012-2013) indicated that soybean cultivars G-757(3131 kg/ha), G-758(3108 kg/ha), G-8586(2329 kg/ha), V8 (B/pur-8)((1943 kg/ha)), 272 W (1928 kg/ha) produced the highest yielder than the check Cobb (1835 kg/ha).

Several investigators took interest in evaluating soybean genotypes and estimated the corresponding genetic parameters, such as Eisa et al (1998), Hassan et al (2001) and (2002), and Mohamed and Morsy (2005) who found that soybean genotypes differed significantly for most studied traits. Also, Hamdi et al (2008) evaluated most the studied genotypes for agronomic and seed technology characters. They found variability among genotypes for most studied characters. In the study large variation was found in days to maturity, pods per plant, plant height and grain yield. This data indicated that there is genetic and physical variability in soybean accessions and it is one of the best options to select the best lines for pre-breeding and hybridization program. The results are supported with the findings of Rasaily et al. (1986), which performed considerable genotypic variability for seed yield. Funnah and Mak (1978) also conducted field trials and found that some varieties yielded over 2000 kgha-1. Dadson (1976) also evaluated different cultivars of soybean and revealed highest seed yields of 2.0 - 2.46, 1.18 - 1.88, 1.29 - 1.59 and 1.21 - 1.24 t h-1 were given by cultivars Davis, Hardee, Improved Pelican and Williams, respectively. Ghatge and Kadu (1993) found the similar results and observed high variability for seed yield.

3.2 Cluster Analysis

Cluster analysis using all the seven morphological traits grouped the 40 accessions into five major groups at the genetic distance of 202.63 (Table 2, 3 , Figure 1). It was also found that, among the five clusters, cluster I was the largest and consisted of 32 accessions (14 local landraces and 18 exotic lines). Under the cluster I characterized as the early flowering, early maturity and lower yield. This cluster represented 80 % of the total accessions i.e. Coll#3 Mangal bazar, Dhankuta , G-7959, Coll # 1 Mangalbazar, G-8754, SJ-4, IPBSY178, PI94159, Salyan-2, TGX311-23D, 7521-

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26-2, G-8513, SB0103, PI200451-2, 200525(Rampur), AGS-367, G-757, PI200525, PI368055, TK-5, TGX1925-1F, Gorkha Local-1, Coll#5 Sikre, Tandi Collection #1, TH227, V-1,V-2,V-3,V-5,V-6,V-8, Tandi Collection #2 and the second largest group was the clusters II and IV, and each consisted of three accessions. These two clusters II and IV represented 7.5% each. These groups had characterized as the moderate maturity and highest yielder. The smallest group was clusters III and V, and each cluster contained only one accessions. The dendrogram based on the quantitative traits of forty soybean accessions was constructed as presented in figure 1. Distances among different Cluster centroids of soybean accessions are presented in Table 3 & 4.

Likely cluster analysis using all the seven morphological traits grouped the 101 accessions collected from National Agricultural Genetic Resources Centre (Gene Bank) and exotic lines from IITA, Nigeria into five major groups at the genetic distance of 267.82 (Table 6, 7 Figure 2). It was also found that, among the five clusters, cluster I was the largest and consisted of eighty four accessions. Under the cluster I characterized as the medium maturity and lower yield. This cluster represented 82.69 % of the total accessions i.e.272 W,7521-26-2, AGS -367,C2014,C2015, C2016,C2017, C2021,C2022,C2023,C2024. C2026,C2027,Cina -2,CM-9112, Co 158, Co 159, Co 160, Co 161, Co 162, Co 164, Co 165, Co 166, Co 167, Co 168,Co 169,Co 170,Co 171,Co 172,Co 175, Co 176,Co 179, Co163, Co178, Cobb,Coll # 1 Mangalbazar, Coll#3 Mangalbazar, Coll#4 Ramechhap, COLL#5 Sikre, Dhankuta, G-758, G-7959, G8513, G-8514, G-8586, G-8754, IPBSY 178, PI 200451-2, PI 200525, PI 368055, PI 94159, Puja, Salyan -2,SB0103, SJ-4, Tadi Coll#2, Tandi Coll, TG X 1925-1F, TGX 1990-40F, TGX 1990-78F, TGX 1990-79F, TGX1835-10E, TGX1904-6F, TGX1987-10F, TGX1987-14F, TGX1988-3F, TGX1988-5F, TGX1989-20F, TGX1989-21F, TGX1989-41F, TGX1989-45F, TGX1990-101F, TGX1990-38F, TGX1990-47F, TGX1990-57F, TGX1990-94F, TGX1990-97F, TGX1991-10F,TGX311, TH-227, TK-5, V1 (B/pur-1),V10 (B/pur-10),V2 (B/pur -2),V5 (B/Pur-5),V8 (B/pur-8) and the second largest group was the clusters II consisted of fourteen accessions. This cluster II represented 13.46% and these groups comprised of G8514, V7, C2020, C0157, Chatewan-9, TGX1990-5F, TGX1990-93F, 200525 (Ramechap), C2019, V3, V4, TGX1835-10E, TGX1989-NF, and TGX1990-18F. These groups had characterized as the moderate maturity and medium yielder. The smallest group was clusters III, IV and V, and each cluster contained 1, 2, 1 accessions respectively.Cluster III groups were characterized as the late maturity and high yield while cluster V had early maturity, bolder seeds and medium yields. The dendrogram based on the quantitative traits of one hundred one soybean accessions was constructed as presented in figure 2. Distances among different Cluster centroids of soybean accessions are presented in Table 8

3.3 Principal component analysis for yield and yield attributing traits composition

Seven principal components were extracted which accounted for 21.9 to 100% variability among the 104 soybean accessions evaluated. PC1 accounted for 21.9% of the total variation and was correlated positively with the days to flower (0.036), pods per plant (0.19), Plant height (0.65 while days to maturity (-0.407) contributed negatively. PC2 accounted for 19.6% and mainly correlated with days to maturity, plant height and seeds per pod and negatively with days to flower, plant height, and seeds per pod. PC3 had 18.4% of the total variation. Pods per plant contributed 0.200, hundred seed weight (0.140). PC4 accounted for 13.7% of the variation and correlated with days to flower (0.033), pods per plant (0.329), plant height (0.173) and seeds per pod(0.070).PC5 accounted for 13.3% of the total variation and was correlated positively with the days to flower (0.320), days to maturity(0.259), seeds per pod(0.170) and hundred seed weight(0.147) while pods per plant, plant height and grain yield contributed negatively correlated. PC6 accounted for 7.4% of the total variation and was correlated positively with the pods per plant(0.19), seeds per pod (0.676) and grain yield(0.063) while days to flower, days to maturity, plant height, hundred seed weight contributed negatively.PC7 accounted for 5.7% of the total variation and was correlated positively with the days to maturity, pods per plant, plant height, seeds per pod, hundred seed weight and grain yield while days to flower (-0.560) contributed negatively (Table **9**).

Seven principal components were extracted which accounted for 21.9 to 100% variability among the 104 soybean accessions evaluated. PC1 accounted for 28.8% of the total variation and was correlated positively with pods per plant (0.062) while all others variable contributed negatively. PC2 accounted for 18.6% and mainly correlated with pods per plant (0.716), plant height (0.032) , seeds per pod (0.209) and grain yield(0.375) and negatively with days to flower, and days to maturity. PC3 had 17.7% of the total variation and the variables correlated positively with days to flower, days

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to maturity, pods per plant, seeds per pod, grain yield and hundred seed wt. and negatively contributed with plant height. PC4 accounted for 11.8% of the variation and positively correlated with days to flower, days to maturity and seeds per pod. PC5 accounted for 10.9% of the total variation and was correlated positively with the days to flower, seeds per pod(0.118) and grain yield(0.421) while remaining variables contributed negatively correlated. PC6 accounted for 6.6% of the total variation and was correlated positively with the days to flower, pods per plant, grain yield and hundred seed weight while days to maturity, plant height, and seeds per pod contributed negatively. PC7 accounted for 5.5% of the total variation and was correlated positively with the days to flower, pods per plant, plant height and seeds per pod, while days to maturity, grain yield (-0.614) and hundred seed weight contributed negatively(Table **10**).

3.4 Agro-morphological characteristics of soybean local landraces

3.4.1 Seed Coat Color

There was high diversity found in seed coat color of the soybean local landraces collected from seven districts namely Baitadi, Dadeldhura, Doti, Jumla, Kailali, Kalikot and Muguof mid and far western region of Nepal (Annex ii). The seed coat color was keenly documented after harvest of the crop. Out of thirty threeaccessions, thirteen of them had black seed coat color; two had buff, one grey, three imperfect black, two reddish brown, eight yellow and remaining four had yellowish white seed coat color.

3.4.2 Flower color and phenotypic traits

Flower color and pattern of flower were also found diverse among the collected accessions. Out of the thirty three local landraces, twenty one had white flower color, four had purple throats, and three had purple flower. Some of the five landraces had trailing type, typical little leaves like wild type along with purple flower colors (Annex ii).

IV. CONCLUSIONS

In plant breeding, generation of new genotypes from the existing ones with improvement in plant traits is the main objective. The present study revealed the presence of high levels of variations for nine different morphological traits including yield attributes and seed yield among the soybean accessions. A total of forty diverse accessions of local landraces and exotic lines were evaluated in the subtropical rainfed climate of Rampur chitwan in summer season of the year 2012. Variation was observed in agro-morphological traits. Some of high yielding accessions of soybean were 272W,Cobb, G-758, and Puja. Likewise a total of hundred oneaccessions were evaluated for grain yield and yield parameters during 2013. The research results revealed that high yielding soybean accessionswereG-18428, TGX 1990-67F, G-757, V9 (B/pur-9, TGX1990-5F, Co 157, Chatewan-9, TGX1990-93F, V7 (B/ pur-7), C2020and G-8514. However mean yield performances of soybean accessions over the years affirmed soybean cultivars G-757, G-758, G-8586, V8 (B/pur-8), 272 W were the better performer than the check Cobb. Under cluster analysis using all the seven morphological traits grouped the 40 accessions into five major groups at the genetic distance of 202.63. It was also found that, among the five clusters, cluster I was the largest and consisted of 32 accessions and the second largest group was the clusters II and IV, and each consisted of three accessions. The smallest group was clusters III and V, and each cluster contained only one accessions. Likely cluster analysis using all the seven morphological traits grouped the 101 accessions collected from National Agricultural Genetic Resources Centre (Gene Bank) and exotic lines from IITA, Nigeria into five major groups at the genetic distance of 267.82. Among the five clusters, cluster I was the largest and consisted of eighty four accessions and the second largest group was the clusters II consisted of fourteen accessions. The smallest group was clusters III, IV and V, and each cluster contained 1, 2, 1 accessions respectively. To obtain greater heterosis, accessions having distant clusters could be used as parents for hybridization program. The accessions from cluster I and cluster II could beused for hybridization program with the soybean accessions of clusters III, IV and V in order to develop high yielding soybean varieties for further improvement. The first seven principal components were extracted which accounted for about 100% variability among the 104 soybean accessions for all morphological characters. There was high diversity found in seed coat color of the soybean local landraces. Out of thirty three accessions, thirteen of them had black seed coat color; two had buff, one grey, three imperfect black, two reddish brown, eight yellow and remaining four had yellowish white seed coat color. Flower color and pattern of flower were also found diverse among the collected accessions. Out of the thirty three local landraces, twenty one had white flower color, four had purple throats, and three had purple flower. Some of the five

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landraces had trailing type, typical little leaves like wild type along with purple flower colors. This study indicated the presence of high levels of genetic variability among the soybean accessions in terms of evaluated characters

CONFLICT OF INTERESTS

The authors declare that there is no conflict of interests regarding the publication of the paper.

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Table 1: Agronomic performances of soybean accessions in observation nursery, 2012

SN	Cultivars	DF	DM	P/P	Plht(cm)	S/P	GY(kg/ha)	HSwt(g)
1	Coll#3 Mangal bazar	52	118	39	37	17	197.5	11.5
2	Dhankuta	52	114	55	39	22	265	14.5
3	G-7959	54	123	45	43	20	742.5	12.9
4	Coll # 1 Mangalbazar	55	112	26	31	18	220	14.6
5	G-8754	55	126	42	67	20	335	17.4
6	G-758	61	120	47	61	22	1415	10.5
7	SJ-4	52	114	30	55	17	170	11.7
8	IPBSY178	59	117	49	55	21	392.5	10.5
9	PI94159	57	117	25	46	16	122.5	12.6
10	Salyan-2	52	117	97	46	21	247.5	14.5

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11	TGX311-23D	57	128	38	41	21	135	16.2
12	G-8513	52	123	67	51	18	377.5	12.4
13	7521-26-2	57	123	89	54	20	435	9.6
14	SB0103	55	128	22	49	20	192.5	11.8
15	PI200451-2	57	123	63	57	21	167.5	13.3
16	200525(Rampur)	57	114	42	50	23	312.5	7.7
17	272 W	58	120	72	73	22	2195	9.7
18	AGS-367	57	118	55	51	21	732.5	6.5
19	CINA-2	57	123	46	81	19	1112.5	13.7
20	G-18428	61	120	40	56	19	1277.5	10.5
21	G-757	62	120	43	58	20	567.5	10.2
22	G-8514	62	114	48	61	19	995	8.8
23	G-8586	59	120	43	72	21	1107.5	11.3
24	PI200525	58	120	43	88	17	300	14.9
25	PI368055	57	115	50	65	23	832.5	10.8
26	TK-5	57	111	22	62	13	390	15.4
27	TGX1925-1F	59	126	28	62	20	580	11
28	Gorkha Local-1	62	134	21	46	25	547.5	9.5
29	Coll#5 Sikre	62	123	26	64	20	362.5	10.2
30	Tandi Collection #1	55	112	20	43	25	210	20.4
31	TH227	39	111	60	43	21	150	5.2
32	V-1	55	118	37	68	21	607.5	15.3
33	V-2	57	126	35	85	19	585	14.6
34	V-3	52	111	67	56	17	137.5	11.5
35	V-5	52	112	36	49	25	295	13.1
36	V-6	57	123	74	65	18	107.5	7.9
37	V-8	57	123	35	78	16	285	9.5
38	Tandi Collection #2	57	118	61	40	23	472.5	25.5
39	Cobb	57	124	54.6	61.6	20.4	1587.5	11.4
40	Puja	55	122	54.2	55.2	20.8	1282	14.34
	Mean	**56.2**	**119.5**	**46.2**	**56.6**	**20.1**	**561.2**	**12.3**
	Max	**62.0**	**134.0**	**97.0**	**88.0**	**25.0**	**2195.0**	**25.5**
	Min	**39.0**	**111.0**	**20.0**	**31.0**	**13.0**	**107.5**	**5.2**
	STDEV	**4.1**	**5.5**	**18.1**	**13.3**	**2.6**	**475.8**	**3.7**

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Table 2: Groups of 41 soybean accessions according to cluster analysis from seven phenological and morphological characters, yield attributes, and seed yield.

Cluster number	Number of accessions	Percent	Accessions
I	32	80	Coll#3 Mangal bazar, Dhankuta , G-7959, Coll # 1 Mangalbazar,G-8754,SJ-4,IPBSY178,PI94159,Salyan-2,TGX311-23D,7521-26-2,G-8513,SB0103,PI200451-2,200525(Rampur),AGS-367,G-757, PI200525,PI368055,TK-5,TGX1925-1F,Gorkha Local-1,Coll#5 Sikre, Tandi Collection #1,TH227,V-1,V-2,V-3,V-5,V-6,V-8,Tandi Collection #2
II	3	7.5	CINA-2,G-8586,G-8514
III	1	2.5	272W
IV	3	7.5	G-758,G-18528,Puja
V	1	2.5	Cobb

Table 3: Mean values of seven different agro morphological characters, yield attributes, and seed yield for five groups revealed by cluster analysis among 40 soybean accessions

Variable	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Grand centroid
DF	54.938	59.00	58.0	59.33	56.50	55.688
DM	119.313	120.67	120.0	119.00	124.00	119.525
P/P	45.063	47.07	72.0	45.67	54.60	46.170
Plht(cm)	54.500	57.40	73.0	71.33	61.60	56.620
S/P	19.969	20.60	22.0	19.67	20.40	20.055
GY(kg/ha)	354.375	1324.83	**2195.0**	1071.67	**1587.50**	557.800
HSwt(g)	12.584	11.78	9.7	11.27	11.43	12.324

Table 4: Distances between Cluster Centroids

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	0.00	970.475	1840.92	717.50	1233.19
Cluster II	970.47	0.000	870.67	253.56	262.84
Cluster III	1840.92	870.668	0.00	1123.65	607.88
Cluster IV	717.50	253.562	1123.65	0.00	516.04
Cluster V	1233.19	262.842	607.88	516.04	0.00

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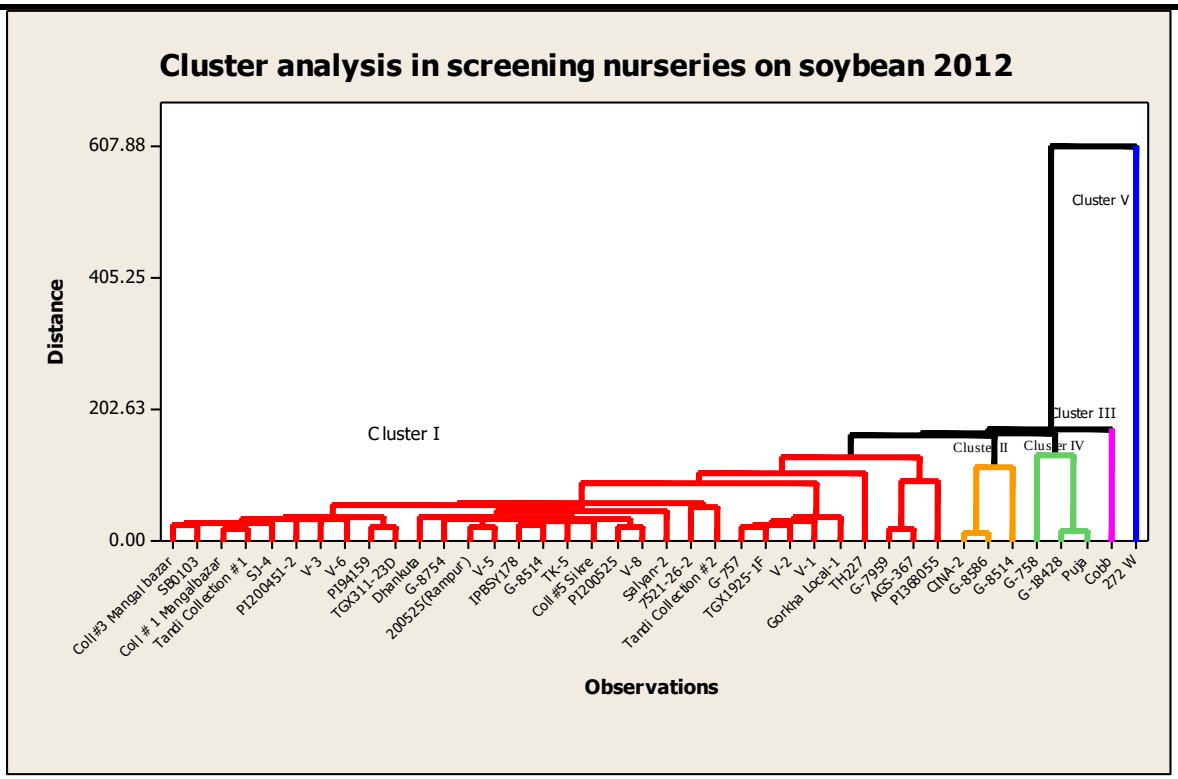

Fig 1. Dendrogram showing relationship among 41 soybean accessions using nine agro-morphological characters, seed yield, and yield traits.

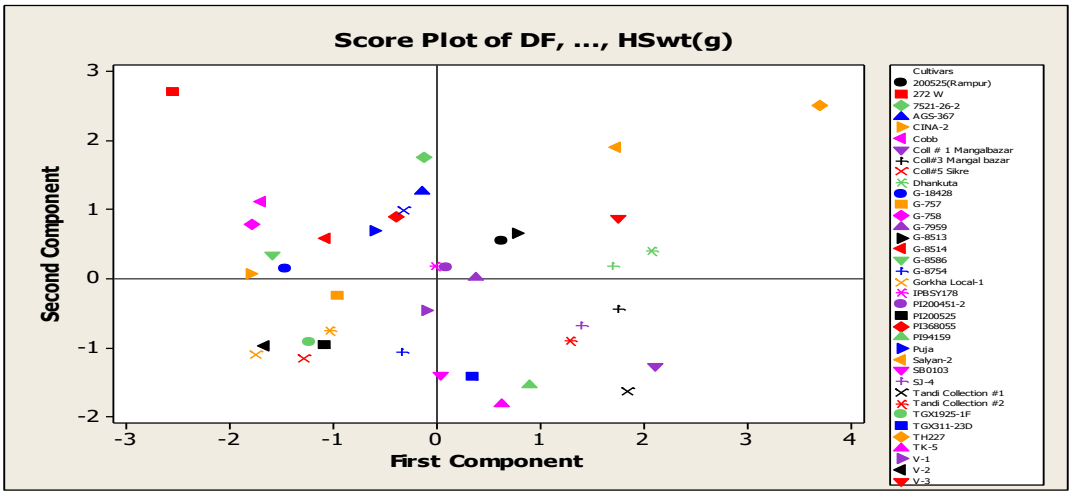

Table 5: Agronomic performances of soybean accessions in regeneration nursery, 2013

Entries	Cultivars	DF	DM	P/P	Plht(cm)	S/P	GY(kg/ha)	HSWT(g)
1	Coll#3 Mangalbazar	49	116	99.6	83.2	18.6	650	11.9
2	Dhankuta	49	126	80.4	35.4	14	650	11.5
3	G-7959	44	120	81.6	126.4	20.6	1285	10.2

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4	Coll # 1 Mangalbazar	48	129	66.6	43.4	14.2	600	7
5	G-8754	50	126	116.2	57.2	14.4	640	10.2
6	G-758	51	108	116.4	138.8	19.8	1400	14.1
7	CM-9112	48	108	109.2	83.6	18.2	800	17.4
8	SJ-4	48	108	99.6	113	19.6	940	12.2
9	IPBSY 178	50	108	122.8	76	21.8	810	13.2
10	PI 94159	52	108	103	108.6	19.2	905	23.4
11	Salyan -2	52	108	99.6	123.8	18.8	1330	9
12	TGX311	54	117	146.2	96	20.4	710	13.2
13	G-8514	54	126	95.4	42.2	21.2	3550	14.5
14	7521-26-2	52	126	92.8	136.8	19.6	1775	9.2
15	Coll#4 Ramechhap	54	126	105.6	79	18.8	710	12.8
16	SB0103	54	126	97.8	82.6	20	740	8.3
17	PI 200451-2	54	117	98.8	110.4	20	1225	14.5
18	200525 (Ramechhap)	54	118	91.8	54.4	14.8	3200	9.7
19	272 W	59	116	119.8	110.4	20.4	1660	13.4
20	AGS -367	55	116	93.4	91.2	16.2	515	16.7
21	Cina -2	60	116	102	74.6	19	620	16.3
22	G-18428	59	131	133.4	57.4	8.8	5695	11.6
23	G-757	60	126	137	72.2	19.8	4800	15.4
24	G8514	65	113	123.8	121	20.4	800	10.8
25	G-8586	61	123	127	98	20.6	905	16.1
26	PI 200525	60	123	152	92.6	19.8	680	14.5
27	PI 368055	60	119	132.4	56.2	20.8	690	15.2
28	TK-5	61	117	106.8	87.6	20.6	1860	15.4
29	TG X 1925-1F	59	113	116.2	85.8	21.6	705	13.9
31	COLL#5 Sikre	63	117	107.6	62.8	17.6	1005	11.4
32	Tandi Coll	54	119	63.6	26.8	18	1010	12.6
33	TH-227	40	131	34	42.6	13	650	10.7
34	V1 (B/pur-1)	54	126	105.4	52	18.8	635	9
35	V2 (B/pur -2)	62	126	121	31.8	19.6	1000	9.7
36	V3 (B/Pur-3)	52	129	60.2	39	17.8	2750	18
37	V4 (B/Pur -4)	50	119	59.4	43.4	17.4	2900	13.3
38	V5 (B/Pur-5)	59	132	126.4	33	18.6	795	4.5

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39	V7 (B/ pur-7)	50	113	68.8	52.8	18.8	3600	13
40	V8 (B/pur-8)	54	134	80	26.8	16	650	8.1
41	V9 (B/pur-9)	44	111	90.2	44.4	22.6	4550	7.9
42	V10 (B/pur-10)	60	134	130	32.2	19.2	710	14.6
43	Tadi Coll#2	54	123	76.2	84.2	19.6	1010	10
44	C2014	44	119	194.4	27	18.6	800	12.5
45	C2015	58	111	152.8	10.2	11	1000	10.4
46	C2016	52	116	72.6	86	21.4	2210	8.3
47	C2017	45	120	80.4	175.8	21.6	2020	13
49	C2019	54	108	155.4	18.25	13.5	3200	15.7
50	C2020	59	112	218	126	20	3550	4
51	C2021	60	111	243	61.6	18.4	2150	9.7
52	C2022	63	111	263.2	58.6	18.2	790	13.6
53	C2023	54	111	174	65.2	20.2	1750	5.4
54	C2024	45	124	71.6	86.6	21	2490	7.5
55	C2026	45	126	78.6	102.6	21.2	2425	10.2
56	C2027	50	129	68.4	88.2	22.6	2125	17.4
57	Co 157	65	119	96.2	44.8	18.6	3900	23.5
58	Co 158	44	119	73.6	31.4	22	1350	14.1
59	Co 159	60	119	90.8	42.4	20	895	13
60	Co 160	47	116	64.4	56.6	14.4	825	3.5
61	Co 161	50	111	114.6	51.2	17	635	15.1
62	Co 162	50	111	73.6	33.8	17.4	1045	11.3
63	Co163	54	114	63.4	52.6	19.2	770	7
64	Co 164	47	119	59	68.8	20	805	21.1
65	Co 165	41	111	104	39.6	19.4	500	13.5
66	Co 166	40	126	70.8	62.8	20.2	1280	10.9
67	Co 167	40	111	154.6	70.4	19.6	1075	11.4
68	Co 168	45	118	55.4	62.8	21.6	1105	13.5
69	Co 169	49	108	92	45.8	17.8	775	19.5
70	Co 170	65	111	138	64	19.4	1750	14
71	Co 171	50	111	51	80.4	20.8	1700	5.8
72	Co 172	59	129	127.4	30.4	15.8	1800	10
73	Co 175	60	119	74.6	53	19.8	570	3.8

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74	Co 176	50	116	73.2	60.8	18.8	1190	6.5
75	Co178	53	129	91	38	18.4	520	11.7
76	Co 179	65	129	123.2	43.6	21	660	15.2
77	TGX 1990-78F	65	131	106	22.8	16	1065	9.9
78	TGX 1990-79F	56	131	101.2	70.4	20.6	1025	10.5
79	TGX1989-45F	61	127	99.4	93.8	18.8	970	11.2
80	TGX1990-47F	54	118	70.6	84	22.6	1895	12
81	TGX1989-NF	60	127	95.6	46.6	20.4	3050	11.8
82	TGX 1990-67F	54	120	98.8	120.6	23.4	4895	10.5
83	TGX1991-10F	60	127	102.2	94.2	19.2	1355	16.2
84	TGX1990-38F	59	127	105.8	110	22.6	885	8.4
85	TGX1990-93F	65	129	72.6	18.8	17.6	3750	9.3
86	TGX1990-94F	64	129	106.6	91.6	20.6	1960	14
87	TGX1987-14F	65	126	83.6	86	20	1130	16.8
88	TGX1990-101F	60	130	84	43.2	21	575	9.7
89	TGX1987-10F	54	118	92.2	91	22.8	1930	9.5
90	TGX1904-6F	60	127	94.8	95.6	21.4	1975	17.4
91	TGX 1990-40F	54	119	74	67.6	18.8	945	11.5
92	TGX1989-21F	67	129	94	112.6	22.2	1895	11
93	TGX1990-5F	60	128	98.6	46.6	21	4080	9.7
94	TGX1989-41F	50	134	60.8	54.2	21.8	1245	4.4
95	TGX1990-57F	59	124	102.8	109.4	18.6	1105	9.4
96	TGX1988-5F	60	129	96	71.4	19.2	2270	8.9
97	TGX1990-18F	60	116	92.6	107.6	20.2	3360	9
98	TGX1989-20F	54	125	71.2	50.8	20	1000	5.9
99	TGX1988-3F	59	131	71.8	72.6	20.4	1450	10.7
100	TGX1835-10E	50	126	102	56.2	16.8	2955	8.8
101	TGX1990-97F	52	126	77.4	50	21.4	1350	10.9
102	Chatewan-9	59	131	78.6	85	21	3820	16.3
103	Puja	49	121	86	49	19	1468	15.3
104	Cobb	48	124	97	78	20	2082	11.2
	Mean	54	121	102	70	19	1620	12
	MIN	40	108	34	10	9	500	4
	MAX	67	134	263	176	23	5695	24

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	MS	42.70	56.39	1356	982.64	6.28	1.32197E+06	15.16
	S D	6.53	7.510	36.82	31.31	2.50	1149.77	3.89

Table 6 : Groups of 104 soybean accessions according to cluster analysis from seven morphological characters, yield attributes, and seed yield.

Cluster number	Number of accessions	Percent	Accessions
I	86	82.69	272 W,7521-26-2,AGS -367,C2014,C2015, C2016, C2017, C2021, C2022, C2023, C2024 C2026, C2027, Cina -2 ,CM-9112,Co 158,Co 159, Co 160,Co 161,Co 162,Co 164,Co 165,Co 166,Co 167,Co 168,Co 169, Co 170, Co 171, Co 172, Co 175, Co 176, Co179, Co163, Co178, Cobb, Coll # 1 Mangalbazar, Coll#3 Mangalbazar, Coll#4 Ramechhap, COLL#5 Sikre, Dhankuta, G-758, G-7959, G8513, G-8514, G-8586, G-8754, IPBSY 178,PI 200451-2,PI 200525,PI 368055,PI 94159, Puja, Salyan -2,SB0103,SJ-4,Tadi Coll#2, Tandi Coll, TG X 1925-1F,TGX 1990-40F,TGX 1990-78F,TGX 1990-79F, TGX1835-10E, TGX1904-6F, TGX1987-10F, TGX1987-14F, TGX1988-3F, TGX1988-5F,TGX1989-20F, TGX1989-21F, TGX1989-41F, TGX1989-45F, TGX1990-101F, TGX 1990-38F, TGX1990-47F, TGX1990-57F, TGX1990-94F, TGX1990-97F, TGX1991-10F, TGX311, TH-227,TK-5,,V1 (B/pur-1),V10 (B/pur-10),V2 (B/pur -2),V5 (B/Pur-5),V8 (B/pur-8)
II	14	13.46	G8514, V7, C2020, C0157, Chatewan-9, TGX1990-5F, TGX1990-93F, 200525 (Ramechap), C2019, V3, V4, TGX1835-10E, TGX1989-NF, TGX1990-18F
III	1	0.96	V9
IV	2	1.92	G-757, TGX1990-67F
V	1	0.96	G18428

Table: 7 Mean values of seven different agro morphological characters, yield attributes, and seed yield for five groups revealed by cluster analysis among 104 soybean accessions

Variable	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Grand centroid
DF	54.10	56.57	59.0	57.0	44.0	54.44
DM	120.63	121.50	131.0	123.0	111.0	120.80
Pod/Plant	101.49	98.94	133.4	117.9	90.2	101.66
Plht(cm)	72.05	55.83	57.4	96.4	44.4	69.89
S/P	19.30	18.51	8.8	21.6	22.6	19.17
GY(kg/ha)	**1162.56**	**3404.64**	**5695.0**	**4847.5**	**4550.0**	**1620.20**
HSWT(g)	11.87	11.45	9.7	11.3	16.7	11.83

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Table: 8 Distances between Cluster Centroids

	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5
Cluster1	0.00	2242.15	4532.60	3685.06	3387.61
Cluster2	2242.15	0.00	2290.66	1443.56	1145.58
Cluster3	4532.60	2290.66	0.00	848.68	1146.27
Cluster4	3685.06	1443.56	848.68	0.00	303.84
Cluster5	3387.61	1145.58	1146.27	303.84	0.00

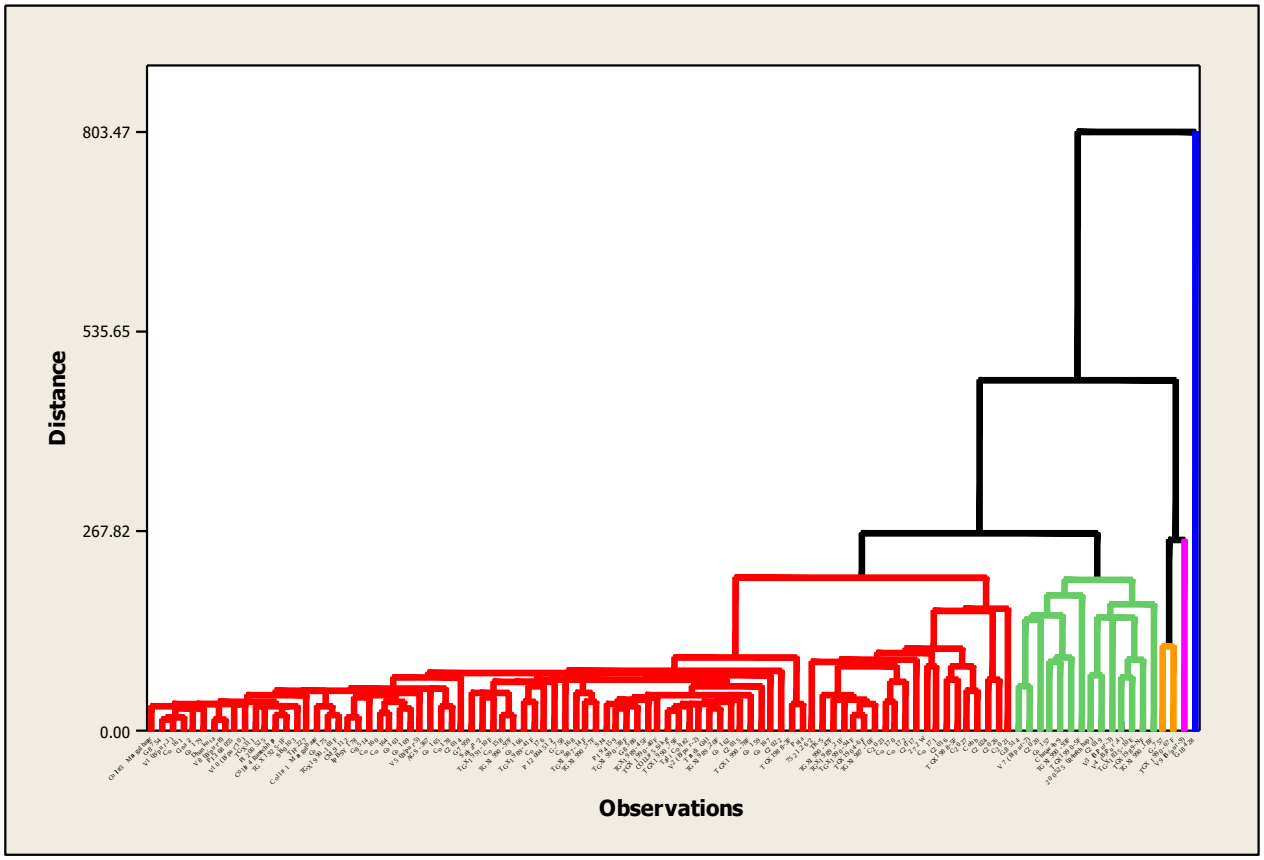

Fig 2. Dendrogram showing relationship among 104soybean accessions using nine agro-morphological characters, seed yield, and yield traits, 2013.

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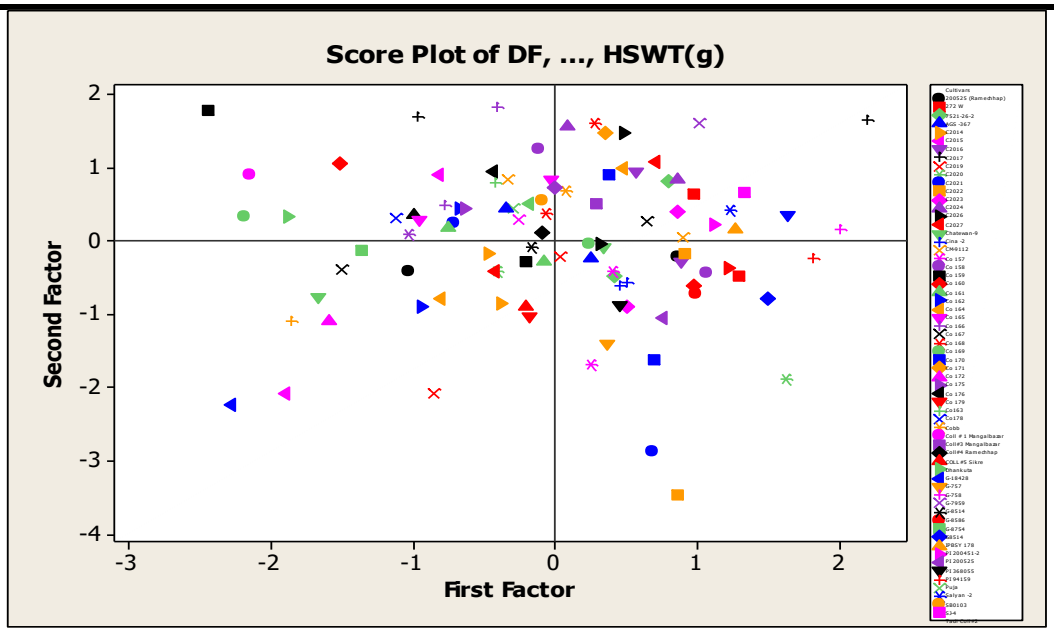

Fig.3: Two-dimensional plot of PCA showing relationships among 104 soybean accessions using morphological and yield related traits.

Table 9: Principal Components (PCs) Analysis for seven Yield and Yield attributing traits in 104soybean accessions

Yield and yield related traits	**Component matrix**						
	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Eigen value	1.5328	1.3734	1.2911	0.9603	0.9278	0.5162	0.3984
Proportion of variation	**0.219**	**0.196**	**0.184**	**0.137**	**0.133**	**0.074**	**0.057**
Cumulative variance	0.219	0.415	0.600	0.737	0.869	0.943	1.000
Variables	Eigen factors						
DF	0.036	-0.591	-0.479	0.033	0.320	-0.064	-0.560
DM	-0.407	0.110	-0.636	-0.056	0.259	-0.165	0.566
P/P	0.192	-0.688	0.200	0.329	-0.003	0.132	0.570
Plht(cm)	0.652	0.158	-0.152	0.173	-0.013	-0.700	0.087
S/P	0.552	0.274	-0.354	0.070	0.170	0.676	0.073
GY(kg/ha)	0.032	-0.162	-0.409	-0.146	-0.883	0.063	0.003
HSWT(g)	0.256	-0.199	0.104	-0.912	0.147	-0.035	0.172

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Table 10: Principal Components (PCs) Analysis for seven Yield and Yield attributing traits in 41 soybean accessions

Yield and yield related traits	**Component matrix**						
	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Eigen value	2.0138	1.3036	1.2402	0.8243	0.7661	0.4655	0.3865
Proportion of variation	**0.288**	**0.186**	**0.177**	**0.118**	**0.109**	**0.066**	**0.055**
Cumulative variance	0.288	0.474	0.651	0.769	0.878	0.945	**1.000**
Variable	Eigen factors						
DF	-0.551	-0.262	0.126	0.056	0.156	0.638	0.421
DM	-0.439	-0.170	0.184	0.265	-0.748	-0.115	-0.319
P/P	0.062	0.716	**0.017**	**-0.333**	**-0.457**	**0.344**	**0.213**
Plht(cm)	-0.500	0.032	**-0.378**	**-0.362**	**-0.014**	**-0.567**	**0.391**
S/P	-0.013	0.209	0.798	0.178	0.118	-0.371	0.370
GY(kg/ha)	-0.477	0.375	0.177	-0.214	0.421	0.027	-0.614
HSwt(g)	0.145	-0.453	0.373	-0.779	-0.130	0.031	-0.098

Annex ii: Local name and morphological characterization (seed coat and flower color) of soybean local collections in regeneration nursery, 2013

Reg #	**Collection District**	**Local name**	**Seed coat color**	**Flower color with Phenotypic trait**
C2014	Mugu	Muse Bhatmas	Buff	Purple Throat
C2015	Mugu	Kalo Bhatmas	Black	Purple
C2016	Mugu	Seto Bhatmas	Yellowish white	White flower
C2017	Mugu	chhyasmise bha	Imperfect black	White flower
C2018	Jumla	Seto Bhatmas	Creamy white	Purple Throat
C2019	Jumla	Muse Bhatmas	Imperfect black	Trailing and little leaf, purple flower
C2020	Jumla	kalo Bhatmas	Black	Trailing and little leaf, purple flower
C2021	Jumla	chhyasmise bha	Imperfect black	Trailing and little leaf, purple flower
C2022	kalikot	kalo Bhatmas	Black	Trailing and little leaf, purple flower
C2023	kalikot	Muse Bhatmas	Yellowish white	Trailing and little leaf, purple flower
C2024	kalikot	Thulo seto Bha	Yellow	White flower
C2026	kalikot	Kalo Bhatta	Black	White flower
C2027	kalikot	Bhatta	Yellow	White flower
C0157	Doti	Kalo Bha	Black	Purple Throat

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C0158	Doti	Moto Bhatta	Yellow	White flower
C0159	**Doti**	Kalo Bhatta	Black	Purple Throat
C0160	Baitadi	Seto Bhatta	Yellowish white	White flower
C0161	Baitadi	Kalo Bhatta	Black	White flower
C0162	Baitadi	Seto Bhatta	Yellow	White flower
C0163	Baitadi	Seto Bhatta	Yellow	White flower
C0164	Baitadi	Seto Bhatta	Yellow	White flower
C0165	Dadeldhura	Kalo Bhatta	Black	White flower
C0166	Dadeldhura	Rato Bhatta	Reddish brown	White flower
C0167	Dadeldhura	Kalo Bhatta	Black	White flower
C0168	Dadeldhura	Seto Bhatta	Yellow	White flower
C0169	Dadeldhura	Nepali Bhatta	Buff	White flower
C0170	Dadeldhura	Seto Bhatta	Yellowish white	White flower
C0171	Dadeldhura	Khairo Bhatta	Grey	White flower
C0172	Kailali	Kalo Bhatta	Black	White flower
C0175	Kailali	Seto Bhatta	Yellow	Purple
C0176	Kailali	Kalo Bhatta	Black	White flower
C0178	Kailali	Kalo Bhatta	Black	Purple
C0179	Kailali	Khairo Bhatta	Reddish brown	White flower

Source : Gene Bank, Khumaltar