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RESEARCH ARTICLE

Evaluation of the newly developed soybean cultivar for the Nepal region based on agro-morphological traits

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Abstract

The present investigation was conducted at Rampur chitwan region of the Napal during 2015. The objectives of the study were to assess the genetic variability in agro-morphological characters of newly developed soybean accessions and to identify the accession with high yield potentials. Fifteen soybean accessions including six released varieties obtained from National Grain legume Research Program, Nepalgunj were carried out in Randomized Complete Block Design (RCBD) with three replications. Number of nodules, days to flowering, days to maturity, plant height, numbers of fruiting nodes/plant, number of branches/plant, numbers of pods/plant, numbers of seeds/plant, seed diameter, test weight and grain yield were recorded. There exists a wide range of variation in agro-morphological characters and yield performance of fifteen soybean accessions. Among the different characters plant height, days to flowering, days to maturity, no of fruiting nodes plant-1 the number of pods plant-1, test weight grain yield and protein content (%) mostly contributed in classifying fifteen accessions into different groups. These characters are important for selecting desirable accession. Accession under cluster 4 i.e. Tarkari-Bhatmas-1 was comparatively early maturing although accessions under cluster 2 were better yielder compared to remaining clusters. The accession Iang-beakong is the best in regards to seed yield (3.36.ton/ha) in that locality.

Key words: Protein, soybean, nodule, morphology, diversity

Introduction

Soybean (*Glycine max* (L.) Merrill) is a species of legume native to East Asia. It is a versatile and fascinating crop of the 21st century because of its innumerable possibilities of not only improving soil health but also supporting industries and medicinal sectors worldwide (Figueiredo, 2014). Soybean provides cholesterol-free oil, high quality protein, and carbohydrate (Rahman *et al.*, 2011).As the world population expands, there will be a greater pressure for the consumption of plant products (Kinsella, 1979). Today soybean is considered one of the most economical and valuable agricultural commodity because of its unique chemical composition and multiple uses as food, feed and industrial materials.

Soybeans have the highest protein content among cereal and other legume species, and the second highest oil content among all food legumes. Soy protein contains the essential amino acids, which closely match the requirements for humans or animals. Furthermore, soybean also contains many biological active components like isoflavones, lecithin, saponins, oligosaccharides and phytosterols. Many of these components act as anti-cancer agents and antioxidants (Yao, Jiang, SHI, Tomas, Datta, Singanusong, and Chen, 2004). Considering the facts there is increasing interest towards the health benefits of soy-containing foods, particularly the role of soy protein helps to lowering the incidences of certain cancers. It has been suggested that the high intakes of soy may lower incidence of certain cancers in Asian countries, where soy consumption is high, as compared to Europe or United State of America (Davies, Netto, Glassenap, Gallaher, Labuza, and Gallaher, 1998). Due to its nutritional value along with its affordable low cost, soy protein is the largest commercially available vegetable protein in the world, and it is an important alternative to existing animal derived proteins. Soy proteins are also of particular interest because they impart high functionality in food systems and being used to obtain better quality products. Because of these advantages (economic, nutritive, dietetics, etc.) it is important to develop new soy protein foods or a range of new food formulations with new textures (Molina, Defaye, and Ledward, 2002).

Due to the health consciousness of the people increase in nutritionally reached natural food products are in high demand. The health benefits of soy-protein related to the reduction of cholesterol levels and reduction in risk for several chronic disease i.e., cancer, heart disease and osteoporosis have been reported (Aditya and Bhartiya, 2011). The cholesterol lowering effects of soybean has been attributed to isoflavones. The isoflavones namely daidzein and genistien found in soybean may reduce the risk of a number of cancers and also may help prevent and treat osteoporosis. Soy hull contains approximately 65 % dietary fiber and offer a good source of fiber when used in various food applications. Being legume it also fixes atmospheric nitrogen into soil making it available to plants. As the best source of protein it truly claims the title “the meat that grows on plant”.

The information as well as assessment of genetic variability in the existing germplasm of a particular crop is sought as prerequisite for crop improvement. Breeders select breeding material of his choice from the available variability present among germplasm accessions available with him. Heritability of a plant trait is very important in determining the response to selection because it implies the extent of transmissibility of traits into next generations. In addition, high genetic advance coupled with high heritability estimate offers the most effective condition for selection for a particular trait. Increased seed yield is the ultimate goal of the breeders. But seed yield itself is a product of interaction of many component traits which influence yield directly or indirectly. So, it is important to see the contribution of each of the traits in order to give more attention to those having the highest influence on yield. Moreover, understanding the relationship between yield and its component traits is of great importance to a breeder for making the best use of these relationships in selecting desirable genotypes for yield improvement programs. Therefore, objective of the study was to evaluate the performance of the newly developed soybean cultivars for the Nepal region based on the agro-morphological traits.

Materials and methods

Experimental site and material details

The experiment was carried out in Rampur chitwan in 2015.Geographically the place is located at 27^0 39′ 0.45″ North, 84^0 21′ 9.1″ East and 228 masl. The soil of the experimental site is sandy loam having PH value 6.5, 0.08% nitrogen, 1.56% soil organic matter,18.32kg/ha phosphorous and 65.32 kg/ha potash respectively. The seeds of 15 soybean accessions: six released varieties and nine pipeline varieties included in the study were obtained from National Grain legume Research Program (Nepal Agricultural Research Council).

Table 1: List of soybean accessions used

S.N.	Accession name	Accession type
1	Cobb	Released variety
2	Hardee	Released variety
3	AGS-376	Pipeline variety
4	Puja	Released variety
5	LS-77-16-16	Pipeline variety
6	Seti	Release variety
7	Ransom	Pipeline variety
8	Tarkari-Bhatmas-1	Release variety
9	PK-7394	Pipeline variety
10	PK-327	Pipeline variety
11	PI-94159	Pipeline variety
12	F-778817	Pipeline variety
13	IARS-87-1	Pipeline variety
14	Iang-beakong	Pipeline variety
15	TGX1485-1D	Pipeline variety

Experiment design and setting the experiment

Field experiment was conducted in Randomized Complete Block Design with three replication and fifteen treatments. In each replication there were fifteen plots of size 8 m2 (4m×2m) with 4 rows in each plot. The size of whole plot was 378 m^2. Soybean seed was planted on 15th June 2018 with maintaining space row to row 50 cm apart and plant to plant 10 cm. The plant population was 40 in each row and 160 plants in each plot. Soybean seed was sown on depth of 4 to 5 cm.. All the necessary agronomic practices as well as plant protection measures were taken up while growing the trials. The crop was sundried for two days to reduce moisture level of the grains. Sun drying was continued until the pods were dry enough for threshing. Manual threshing was made for separation of grains from the pods and winnowing was done to throw out the unwanted materials from the seed lot. After cleaning, all the grains were packed in a cotton sack separately. Eleven quantitative traits such as plant height, no of primary branches per plant, no of nodes per plant, no of pods per plant, no of seeds per pod, no of nodes per plant, seed diameter, days to flowering, days to maturity, test weight, grain yield, protein content and eight qualitative traits like flower color, hypocotyl color, leaf color and pubescence, pod color, seed coat color, surface lusture were recorded during the experiment Table 2.

Table 2: Different traits and their methods of measurement

S. N.	**Traits**	**Methods of measurement**
1	Plant height	The height from the base of the plant to the tip of last leaf
2	Days to flowering	The number of days from sowing to flowering of 50% plants
3	Days to maturity	The number of days from sowing until approximately 90% pod turned into brownish color
4	Branches per plant	Total number of pod bearing primary branches in a plant
5	Pods per plant	Total number of pods with seed in a plant
6	Seeds per pod	Total number of seeds in a pod
7	Seed diameter	Measured by digital vernier caliper
8	100 seed weight	Randomly selected 100 seed count and weighed
9	Nodule number	Total no of active nodule in a plant is counted
10	Protein content (%)	lab assays was done for the determination of nitrogen and protein content
11	Yield (ton/ha)	Weighing the seeds produced in a plot then converted to ton/ha

Data entry, processing and computation of mean standard deviation for all the quantitative traits were performed using Microsoft Office Excel. Data was analyzed by using R program 3.3 versions along with MS-excel 2013. Analysis of variance was performed for all traits in order to test the significance of variation among genotypes. The data was analyzed for mean, coefficient of variation (CV %), LSD value and correlation coefficient. UPGMA clustering was done using Minitab 17. Unweighted Paired Group Method using Arithmetic Averages (UPGMA) clustering method was used in clustering of soybean accessions. The accessions were clustered using days to flowering, days to maturity, plant height, no of nodules per plant, no of branches per plant, no of effective nodes per plant, no of pods per plant, 1000 seed weight, seed diameter, grain yield and protein content as variables.

Results and discussions

All the accessions were characterized based on the eight qualitative characters. Frequency distribution for 8 qualitative traits is presented in Table 3. Among the characterized soybean accessions, 53% accessions possessed hypocotyl with green color and remaining 47 % have purple color hypocotyl. Most of the accessions (74%) had intermediate type of leaflets shape followed by 13% and13 % narrow and broad type of leaflets shape respectively. For pubescence density, 53% accessions were having normal type of pubescence followed by 20% semi sparse, 20 % dense and remaining 7% have spare pubescence. Among the characterized accessions 73% had pubescence with brown color and remaining 27% have grey color pubescence. Similarly two types of flower observed among the accessions. Sixty percent accessions had white color flower and remaining 40 % had purple color flower. Result shows that there were four types of seed coat color observed among the accessions. Sixty six percent accessions had yellow seed coat color followed by 20 %, 7% and 7% had yellowish white, white and green color seed coat respectively.

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There were 40 % accessions which had brown color hilum and remaining 33 % had black and 27% had grey color hilum observed among the accessions. Among the characterized accessions, 87 % accessions had intermediate type of surface lusture and remaining 13% had shiny surface lusture. The extent of genetic diversity in accession can be accessed through morphological characterization and genetic markers. Then, the characterized material helps the plant breeders to select the accessions to be utilized in hybridization program (Ghafoor et al., 2002). For the management of collections and determining genetic diversity, phenotypic evaluation of soybean accessions is a fundamentally important step. The knowledge of the genetic variation within accessions from germplasm collection is essential to the choice of strategy to incorporate useful diversity into the program, to facilitate the introgression of genes of interest into commercial cultivars, to understand the evolutionary relations among accessions, to better sample germplasm diversity and to increase conservation efficiency (Fu, 2003).Edgar *et al.,* (1970) studied soybean morphological characters for growth habit, nature of stem hairiness, flower color and pubescence color. Szabo *et al.,* (1983) characterized 40 soybean cultivars and grouped on the basis of flower color, pubescence color and pod color at maturity.

Table 3: Morphological characterization through qualitative traits

S.N.	Characters	Description with code	Frequency	Frequency %
1.	Hypocotyl color	1-Green 2-Purple	8 7	53 47
2.	Leaflets shape	2-Narrow 3-Intermediate 5- Broad	2 11 2	13 74 13
3.	Pubescence density	1- Normal 2- Semi sparse 3-Sparse 4-Dense	8 3 1 3	53 20 7 20
3.	Pubescence density	1- Normal 2- Semi sparse 3-Sparse 4-Dense	8 3 1 3	53 20 7 20
4.	Pubescence color	1-Grey 2-Brown	4 11	27 73
5.	Flower color	1-White 2-Purple	9 6	60 40
6.	Seed coat color	1-Yellow 2-Yellowish white 3-White 4-Green	10 3 1 1	66 20 7 7
7.	Hilum color	1-Brown 2- Black 3-Grey	6 5 4	40 33 27
8.	Seed surface lusture	3- Shiny 5-Intermediate	2 13	13 87

Basic statistics for all the studied traits presented in Table 4. According to the result reasonably good amount of variation was measured for each trait. Number of nodules was ranged from 38-55. Among the accessions, range for plant height was 26.79-69.56. Fairly good amount of variation was recorded for grain yield which ranged between 1.72-3.36 ton/ha. Higher CV was recorded for each trait. Reddy *et al.*, (1989) recorded five soybean cultivar variations for days to maturity, period from flower initiation to maturity, plant height, and seeds per plant and yield per plant. Muhammad *et al.*, (2006) evaluated 33 soybean genotypes for days to flowering, days to maturity, pod length, number of branches, number of unfilled, filled pods and total pods, 100 seed weight and seed yield (kg/ha). Manjaya and Bapat (2008) grouped 55 soybean genotypes by using quantitative characters *viz,* days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of seeds per plant, 100 seed weight, yield per plant. Higher CV as well as diversity index indicating that selection based on these characters is expected to be effective (Zafar *et al.*, 2004).

Generally previous study showed that higher the seed diameter and grain yield of the soybean accession, lower protein concentration and vice versa. Substantial genotypic variation for seed protein concentration has been documented (Thorne and Fehr, 1970; Brim and Burton, 1979; Wehrmann *et al.,* 1987; Wilcox andCavins, 1995; Cober and Voldeng, 2000) and (Alt *et al.*, 2002). But high seed protein concentration is frequently associated with less yield (Wilcox and Zhang, 1997; Wilcox and Shibles, 2001; Carter *et al.,* 1982).High protein content is an important specialty trait which can be selected for soybean breeding program. Soybean contribute to more than 70% of the protein consumed by humans, its utilization as a protein source is demonstrated in its widespread use as a feed ingredient for livestock and poultry production (Krishnan, 2005). Additionally high protein content is one of the desired traits in food grade soybean. That is why high protein content trait can be utilized selection process and can develop soybean cultivars with high protein content which can help in increasing the nutritional security of the country.

Table 4: basic statistics of the quantitative characters

S.N.	Character	Mean±SE	Slandered deviation	Variance	CV (%)	Minimum	Maximum
1	Nodule number	46.53±1.84	5.78	33.40	12.46	38	55
2.	Days to flowering	43±0.86	3.34	11.21	7.83	40	50
3.	Days to maturity	112±2.67	10.35	107.17	9.23	94	127
4.	Plant height(cm)	42.67±2.56	9.90	97.97	23.19	26.79	69.56
5.	No of fruiting nodes	10±0.37	1.45	2.11	13.98	9	13
6.	No of branches	4±0.20	0.79	0.63	21.40	2	5
7.	No of pods /plant	47±3.14	12.15	147.57	25.85	30	72
8.	Seed diameter (cm)	4.94±0.06	0.27	0.07	5.48	4.39	5.38
9.	Test weight(gm)	130.89±4.47	17.31	299.50	13.22	100	170
10.	Protein content (%)	39.19±0.68	2.67	7.12	6.81	34.85	43.17
11.	Grain yield (ton/ha)	2.41±0.13	0.52	0.27	21.70	1.72	3.36

Clustering of soybean accessions

A dendrogram was constructed by using UPGMA clustering method based on average linkage and Euclidean distance (Fig.1). The cluster analysis grouped the landraces into four clusters for eleven quantitative traits Table 5. The accessions were clustered using days to flowering, days to maturity, plant height, number of nodules per plant, number of branches per plant, number of effective nodes per plant, number of pods per plant, 1000 seed weight, seed diameter, grain yield and protein content as variables.Distance between different cluster centroids of soybean accessions is presented in Table 6. The critical examination of the dendrogram revealed four clusters with minimum of 25.84% similarity level. Clusters were obtained on the basis of similarity percentage and related characters. Cluster 1, 2, 3 and 4 consist of 8, 4, 2 and 1 soybean accessions respectively.Cluster-1 had accessions that were having intermediate value for days to flowering, days to maturity, nodule number, plant height, number of nodes/ plant, and grain yield and protein content. Accessions in cluster-2 were higher yielder, late matured, having higher no of nodule, branches, nodes and pods/plant and intermediate value for test weight and protein content.Cluster-3 consist of accessions having lower plant height and grain yield and intermediate value for days to flowering, days to maturity, no of nodules per plant, no of pods/plant and lowest value for protein content. Cluster-4 consist of only one accession i.e. Tarkari-Bhatmas-1 which had lowest value for days to flowering, days to maturity, number of nodules per plant, number of branches per plant, no of pods/plant. This accession had intermediate value for plant height, number of nodes/plant, grain yield and having highest value for seed diameter and 1000 seed weight among the accessions. Average value of days to flowering, days to maturity, plant height, number of nodules per plant, no of branches per plant, no of effective nodes per plant, number of pods per plant, 1000 seed weight, seed diameter, grain yield and protein content is presented in Table 5. Plant height and grain yield were found high in cluster II (Table 6). Thus, cluster II was found to be high yield potentiality. Days to maturity was shortest in cluster IV. Thus cluster II and IV can be recommended for varietal development and crop improvement.

Fig1: UPGMA clustering of 15 soybean accessions

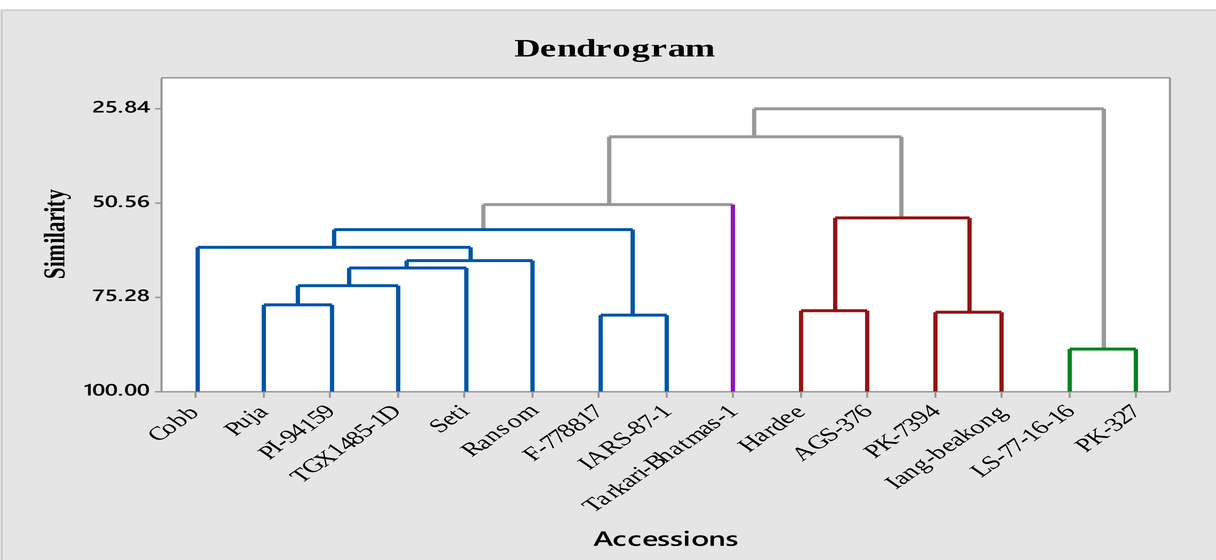

Table 5: Number of accessions with average of major agronomic traits in each cluster

S.N	Variables	Cluster-1	Cluster-2	Cluster-3	Cluster-4
1	Days to flowering	42	47	40	40
2	Days to maturity	115	119	101	94
3	Nodule number/plant	45	50	46	42
4	Plant height (cm)	41.29	55.56	27.34	32.97
5	No of nodes/plant	10	12	9	9
6	No of branch/plant	4	4	4	2
7	No of pods/plant	40	64	46	35
8	Test weight (gm)	140	121.5	102.5	153
9	Seed diameter	5.10	4.84	4.39	5.17
10	Grain yield(Ton/ha)	2.26	3.05	1.89	2.15
11	Protein content (%)	38.71	39.78	42.02	35

The inter cluster distance (Table 6) was maximum in between cluster II and IV (55.61) and minimum in between cluster I and IV (26.51). The range of inter-cluster values ranged from 26.51 to 55.61 showed medium range of diversity. The intra-cluster distance between cluster I and II was 34.21, cluster I and III was 42.82, cluster II and III was 43.43, and cluster III and IV was 53.05. The intra-cluster values in all the four clusters were low indicating the genotypes within the same clusters were closely related. Genotypes of distant clusters were preferred to obtain wide spectrum of variation among the segregation and to execute maximum heterosis in crossing (Hosan *et al.,* 2010).

Table 6: Distance between cluster centroid

	Cluster-1	Cluster-2	Cluster-3	Cluster-4
Cluster-1	0.00	34.21	42.82	26.51
Cluster-2	34.21	0.00	43.43	55.61
Cluster-3	42.82	43.43	0.00	53.05
Cluster-4	26.51	55.61	53.05	0.00

Conclusion

There exists a wide range of variation in agro-morphological characters and yield performance of fifteen soybean accessions. Among the different characters plant height, days to flowering, days to maturity, no of fruiting nodes plant-1 the number of pods plant-1, Test wt., grain yield and protein content (%) mostly contributed in classifying fifteen accessions into different groups. These characters are important for selecting desirable accession. Accession under cluster 4 i.e. Tarkari-Bhatmas-1 was comparatively early maturing although accessions under cluster 2 were better yielder compared to remaining clusters. The accession Iang-beakong is the best in regards to seed yield (3.36.ton/ha) in that locality.

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