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Research Article

Estimation of genetic variability among different soybean genotypes for yield and quality traits under the agro-climatic condition of Rawalpindi –Pakistan

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Abstract

Soybean is one of the most valuable oil seed crop which is good source of protein and edible oil. Pakistan is facing acute shortage of edible oil and depends on import to satiate the requirement of country every year. Therefore present study was planned to identify promising soybean genotypes for yield and quality traits. The research was conducted in the department of Plant Breeding and Genetics at Pir Mehr Ali Shah-Arid Agriculture University Research Farm Chakwal Road, during Kharif season 2016. Ten exotic and one local soybean genotypes were evaluated in Randomized Complete Block Design (RCBD). Observations were recorded on the basis of morphological and biochemical characters. The collected data were subjected to statistical analysis for ascertaining the significance of traits. The results showed that an exotic genotype (19-2) performed best regarding yield per unit area (182.19 g/m^2), followed by genotype KD. For quality character, genotypeB-1(36.11%) performed best for higher protein content and also for oil contents (20.55 %) as compared to local check and other competitive exotic genotypes. Yield per unit area was showed significantly positive correlation with number of secondary branches, biomass yield per unit area, hundred grain weight, protein content, oil content and harvest index while it showed negative correlation with days to flower completion. This study is helpful in generating detailed information on yield and quality traits of soybean that can be used in future soybean breeding programs for the development of high yielding and better quality varieties.

Keywords: Correlation; Quality traits; Soybean; Yield

Introduction

Soybean (*Glycine max*) family leguminosea is an important oil seed crop which was introduced with sunflower in Pakistan few years before. Due to low yield per (average 1178kg ha^{-1}) [1], it could not make space in the country so its production remained low. It was grown in a very small area of Pakistan, majority in the Province Sindh and Khyber Pakhton Khan [2].Soybean is a big source of protein,

soya oil and soya meal, having highest protein contents (40 to 42%) as compared to others food and edible crops [3]. It is leguminous crop containing nitrogen fixing bacteria which are used to increase the fertility of soil. Due to its low production and competition with wheat it is considered as insignificant crop in Pakistan [4]. For the selection of any desirable genotype it is necessary to have information about yield parameters and their correlation. If the yield related traits are improved then grain yield could also be increased. To develop high yielding genotypes for plant breeder it is necessary to identify traits related to high yield [5]. Quality traits of soybean are affected by two factors like genetic and environment factor. To get high yield of soybean, cultivars selection is very important [6]. It has been reported that morphological traits and correlation of yield related traits play a vital role increasing soybean grain yield. Genetic variability is created through crossing between different elite lines. It is necessary to evaluate and conserve those elite lines germplasm which have high genetic variability [5-7]. Yield and quality traits are negatively correlated with each other if one is increased then other is decreased. So it is necessary to break negative correlation between these characters [8, 9].

Keepinginviewtheimportanceofsoybeanforyield anditsqualityattributes.Thepresentstudywasbeingcarriedoutwiththeobjective to determine the relationship between yield and quality traits in different local and exotic soybean genotypes.

Materials and methods

The present study was conducted at University Research Farm (URF), Chakwal road Rawalpindi during Kharif Season, 2016. For this purpose, eleven promising soybean genotypes (B-1, KD, 35, 19-2, 19-1, SEOTU, SANNING, SUNGMONG, JHUNGHWANG, KY and NARC-2) possessing good quality traits and yield were used for experiment. Soybean genotypes selected for this study were sown following Randomized Complete Block Design (RCBD) with three replications. Row to row distance was kept as 75cm and plant to plant distance was kept as 25cm. Five superior plants were selected to record data from each replication.

Allthenecessaryculturalpracticeswereperformeddduringthecroppingseason.Thedataregardingdifferentmorphological and biochemical traits such as germination percentage, plant population, number of primary branches/plant, number of secondary branches per plant, days to 50%flowering, days to flowering completion, plant height, number of pods per plant, hundred grain weight, biomass yield per unit area, yield per unit area, harvest index, protein content and oil content were recorded. The data were analyzed by using Analysis of Variance (ANOVA) technique and means were compared according to least significant difference (LSD) at 5% probability level among genotypes as described by Steel and Torrie [10]. To estimate the correlation between yield and quality traits was done by following [11].

Results and discussion

Evaluation of eleven soybean genotypes for different morphological and biochemical traits revealed that highly significant differences were found among all soybean genotypes for all parameters except germination percentage (Table 1). All the genotypes showed significant amount of variability, high range of variability was recorded in germination percentage, plant population, number of primary branches, number of secondary branches, days to 50 % flowering, days to flowering completion, plant height, number of pods per plant, 100 grain weight, biomass yield per unit area, yield per unit area, harvest index, protein and oil content. This high variability indicated that soybean could be improved if selection is made on the basis of these attributes. The results regarding mean square comparison indicated that genetic diversity was found in soybean genotypes for different traits.

Results for mean comparisons among different yield and quality related traits which are determined during the study as followed in (Table 2). Maximum germination percentage was recorded in genotype B-1 and KD with germination percentage (77 %).These findings were well supported with Chung *et al.* [8] and Boroomandan *et al.*[9] results that germination

percentages enhance crop production. Higher plant population was recorded in genotype 35(69.23) and minimum mean value was recorded in genotype SEOTU (32.77), these results are in line with findings of **[8, 9]**. The maximum number of primary branches plant^{-1} was observed in NARC-2 (5.3) and minimum for KY (1.86). Similarly, secondary branches (3.93-1.43) were observed for NARC-2 and SUNGMONG with respect to maximum and minimum values respectively. Our results were in line with the results of Islam *et al.* **[12]**and Rasaily *et al.***[13]**who evaluated different soybean genotypes on the basis of these attributes.

The data range for days to 50 % flowering (31-50.3) were observed for B-1 and KY whereas days to flower completion maximum was recorded for SEOTU (57.34) and minimum for B-1 (39) was observed (Table 2). These Results are in line with Arshad *et al.* **[5]** who concluded that most of the genotypes flowered at the optimum days of 30-35 days after sowing. The results for days to flower completion agree with the findings of Islam *et al*. **[12]**.Maximum plant height (43.90 cm) was recorded in genotype NARC-2 while minimum plant height (26.06) was recorded in genotype KD. Our results of this parameter are well supported by Khan *et al.* **[14]** who reported that reduction in plant height is occurred due to different genetic material and environmental conditions. The number of pods per plant showed high variability among different soybean genotypes. The range of number of pods per plant, genotypes KY (39.30) and genotype NARC-2 (68.10) were recorded minimum and maximum respectively. Our results are in agreement with Rasaily *et al.* **[13]** who showed that considerable genetic diversity is present in different soybean genotypes for number of pods per plant.

Data regarding biomass yield per unit area (278.60 gm) was maximum for genotype 19-2, while (145.17 gm) was recorded for both genotypes i.e. NARC-2 and KY as lowest (Table 2). The results observed for hundred grain weight among different genotypes indicated that there was high range of variability for hundred grain weight.It was recorded maximum (19.12 gm) for genotype 35, whereas minimum (9.71 gm) observed for genotype SANNING. The results were different on the basis of seed size in different genotypes. These results are comparable who conducted trials to compare different genotypes of soybean and recorded similar results were observed by Maestri*et al.* **[15]**. According to mean comparison (Table 2) maximum yield per unit area was recorded high in genotype 19-2 (183.81 gm) but it was observed very low for genotype SANNING (54.89). Similar results were reported by Ghatge and Kadu **[16]** high genetic variability for grain yield per unit area in studied soybean genotypes. Mean comparison for harvest index 48.85 % for genotype KY maximum, whereas 26.06 % subjected lowest for JHUNGHWANG. Our results showed similarity with results of Maestri *et al.* **[15]** for harvest index study.

As for soybean quality related trait, the protein contents and oil contents are highly demanding. Data regarding protein contents was recorded 36.11 % (B-1) to 34.06 % (NARC-2). Data recorded for oil content indicated that high range of genetic variability for oil content was exhibited 20.55 % to 17.94 % for genotype B-1 and 35 respectively. Results for quality traits such as protein and oil content varied among different soybean genotypes, showing similarity with the findings of Aditya *et al.* **[17]**. The results regarding phenotypic correlation (Table 3) showed that grain yield per unit area was highly positively significantly correlated with biomass yield per unit area, hundred grain weight and was positively significantly correlated with the number of secondary branches. Positive relationship among these characters revealed that selection on the basis of these attributes can increase the soybean yield. It was also negatively significantly associated with days to 50 % flowering and days to flower completion but it has positive relationship for protein and oil content. These findings are in line with the results of Khan *et al.* **[14]**. These results are contradicted with Arshad *et al.* **[5]** due to different genetic material constitution and environmental condition of soybean genotypes.

Table1. (ANOVA) for different soybean yield and quality traits

SOV	DF	GP	PP	NPB	NSB	FG	FC	PH	NPP	HGW	BM	YUA	HI	PC	OC
Replication	2	150.81	22.26	6.00	9.97	0.15	0.27	19.2	12.93	14.39	0.98	55.76	8.9	0.14	9.85
Genotypes	10	89.85*	188.8**	232.6**	77.6**	2.22**	1.68**	10458.9**	104.98**	102.75**	30.38**	4060.84**	1.40**	1.91**	135.03**
Error	20	19.51	18.31	13.30	8.15	0.09	0.14	103.8	3.406	2.59	0.20	13.29	0.43	0.46	14.91

GP= Germination Percentage, PP= Plant Population, NPB=Number of Primary Branches, NSB= Number of Secondary Branches per Plant, FG=50%Days50%Flowering, FC=Days to flowering completion, PH=Plant Height, NPP=Number of Pods per Plant, HGW= Hundred grain weight, BM= Biomass yield per unit area, YUA= Yield per unit area, HI =Harvest Index, PC = Protein Content, OC = Oil content

Table2. Means of different yield and quality traits of 14 characters studied in 11 soybean genotypes

Genotypes	GP	PP	NPB	NSB	FG	FC	PH	NPP	HGW	BM	YUA	HI	PC	OC
B-1	77	53.77	3.62	2.93	31	39	31.83	49.66	17.24	149.22	108.53	42.62	36.11	20.55
KD	77	42.86	3.30	2.30	38.67	46.33	26.06	51.93	18.78	244.41	152.11	37.66	35.88	18.36
35	67.33	69.33	3.43	3.10	40	46.33	32	58.30	19.12	282.77	130.57	38.30	35.71	17.94
19-2	61.33	46.30	3.30	2.62	44.67	50.67	32.30	55.40	17.23	278.60	183.81	42.11	35.62	18.44
19-1	68	46.03	3.31	1.80	46.67	54.67	34.69	48.20	18.78	168.49	75.67	36.95	35.55	19.91
SEOTU	67	32.77	3.13	1.73	49.66	57.33	29.20	50.86	15.24	151.09	83.28	27.72	35.41	18.80
SANNING	61	40.46	3.63	1.80	48	57	28.23	62.06	9.71	208.57	54.89	38.72	35.49	19.31
SUNGMONG	67	34.80	3.06	1.43	41	46	38.60	60.43	17.15	179.67	85.00	34.32	35.32	19.72
JHUNGHWANG	70.33	50.83	2.30	1.80	47.33	53	36.30	68.06	17.17	191.52	97.97	26.06	34.81	19.99
KY	67	51.40	5.3	2.30	50.30	55.33	30.30	39.30	10.27	145.17	92.16	48.85	34.07	18.63
NARC-2	62	45.53	5.3	3.93	48	56	43.92	68.10	14.97	145.17	107.55	31.13	34.06	19.71
Error	19.51	18.31	0.09	0.14	3.406	2.59	8.15	13.30	0.20	103.8	13.29	14.91	0.43	0.46

GP= Germination Percentage, PP= Plant Population, NPB=Number of Primary Branches, NSB= Number of Secondary Branches per Plant, FG=50%Days50%Flowering, FC=Days to flowering completion, PH=Plant Height, NPP=Number of Pods per Plant, HGW= Hundred grain weight, BM= Biomass yield per unit area, YUA= Yield per unit area, HI =Harvest Index, PC = Protein Content, OC = Oil content.

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Table 3. Phenotypic Correlation coefficient among indicated traits in soybean genotypes

Traits	GP	PP	NPP	PH	NPB	NSB	BM	HGW	FG	FC	YUA	PC	OC
PP	0.039												
NPP	-0.271	-.072											
PH	-0.073	-0.06	0.46										
NPB	-0.269	-.008	0.454**	0.276									
NSB	-0.123	0.434*	0.165	0.339	0.562**								
BM	-0.230	0.182	0.506**	0.293	0.577**	0.61**							
HGW	0.321	0.175	0.138	0.174	0.100	0.10	0.23						
FG	-0.54**	-0.258	0.057	0.06	-0.117	-0.228	-0.02	-0.52**					
FC	-0.55**	-0.302	0.069	0.026	0.001	-0.185	-0.01	-0.54**	0.96**				
YUA	0.102	0.296	-0.037	-0.103	0.104	0.418*	0.59**	0.48**	-0.34*	-0.40*			
PC	0.360*	0.275	.098	-0.210	0.191	0.071	0.10	0.49**	-0.83**	-0.75**	0.19		
OC	0.130	-0.052	0.252	0.397*	0.171	0.085	-0.24	-0.07	-0.24	-0.20	0.33	0.12	
HI	-0.084	0.365*	-0.533**	-0.441*	-0.138	0.115	-0.13	-0.24	-0.20	-0.22	0.21	0.13	0.26

* Significant at 5% level of probability level
**Highly Significant at 1% level of probability level

Conclusion

The present study is useful in generating detailed information about soybean genotypes that can be used in improving yield and quality traits. On the basis of the results for grain yield per unit area genotypes (19-2), (35) and (KD) performed best while genotype (B-1), JHUNGHWANG and (KD) gave good performance for protein and oil content. Based on these results it is suggested that these genotypes should be used for future soybean hybridization programs for the development of high yielding and better quality local varieties.

Authors' contributions

Conceived and designed the experiments: Z Akram & G Shabbir, Performed the experiments: Q Ahmad, Analyzed the data: M Ilyas & G Rasool, Contributed materials/ analysis/ tools: SS Ijaz, Wrote the paper: Q Ahmad, A Ullah & M Naeem.

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