

Relationships of Soybean [*Glycine max* (L.) Merrill] Accessions Based on Physiological and Agro-morphological Traits

Sandar Moe. and Teerayoot Girdthai

Abstract—In breeding programme, genetic diversity evaluation among germplasm is an importance and a prerequisite. The objectives of this research were to evaluate the diversity of soybean accessions at morpho-physiological traits and to identify the correlations among the traits. The ANOVA showed that the variations due to genotypes were highly significance. For agro-morphological traits, 94 accessions were grouped into 7 different clusters at similarity coefficient (0.52) by using Unweighted Pair Group Method with Arithmetic Mean (UPGMA). Positive and significant correlations were observed between yield and other traits, except seeds/pod. In physiological traits, negative and significant correlations between specific leaf area (SLA) and yield was found while association with SPAD chlorophyll meter reading (SCMR) values was non-significance. Regarding of physiological traits, 4 major groups were divided by using UPGMA. Genetic patterns and the correlations obtained from this study can be helpful information for parental evaluation and selection in soybean breeding program.

Keywords—genetic diversity, morpho- physiological traits, soybean accessions, clusters analysis

I. INTRODUCTION

THE soybean [*Glycine max* (L.) Merrill] is one of the oldest cultivated crops. It originated in China where first written records date back to 2328 B.C. [1]. Cultivated soybean is under family Leguminosae, subfamily Papilionoidea, Genus *Glycine*. Among pulses, soybean is one of the commercially potential crops. Comparing to animal protein, it is the best and cheapest protein source and its demand is tremendous for food and feed supply. In nutritional point of view, the primary constituents of soybean seed contained about 40% protein, 21% oil, and 11% soluble carbohydrates on dry matter basic [2].

Soybean is usually grown for protein and oil. It can also be used as soy ink. Although demand for soybean has been increased, the genetic improvement for soybean cultivars is extremely narrow. There are several limitations for soybean production such as low yield, susceptibility to pest and disease

and adverse environmental conditions, etc. These limitations can be overcome in different ways. They are field selection, variety improvement, cultural practices, post harvest technology, etc. Among these, variety improvement program can be done by breeding techniques.

In plant breeding program of new cultivars, it is essential to properly characterize and evaluate in the germplasm. Genetic diversity evaluation among germplasm is an importance and a prerequisite in any hybridization program and, would promote the efficient use of genetic variations [3] [4]. To improve an efficient crop, it is essential to obtain the information on genetic diversity and relationships among breeding materials for a plant breeder.

To improve the chances of selection for various characters within the different parents, genetic diversity among genotypes regarding to agro-morphological and physiological characters can be expected to provide information about genetic relationships. The assessment of genetic diversity is important not only for crop improvement but also for efficient management and conservation of germplasm resources [5]. In the selection of diverse parental combinations, it is invaluable to estimate accurately in genetic diversity for generating segregated progenies with maximum genetic variability.

Since yield is influenced by different characters, selection for yield *per se* does not give sufficient confidence for selection of genotypes. Hence, agro-morphological and physiological traits and correlation analysis would provide important information about the degree of relationship among important crop traits and can be used as an index to predict the yield response in relation to the change of particular trait. Watson [6] indicated that indirect selection for seed yield was a function of selection towards the enlargement of the components of seed yield.

The study was conducted to evaluate the diversity of the tested soybean accessions at agro-morphological and physiological levels and to determine the correlations between yield and the other traits.

II. MATERIALS AND METHODS

A study was performed on 94 soybean accessions including thirteen released varieties and eighteen local varieties of Thailand. The experiment was conducted in June 2012 at the Suranaree University of Technology farm, Nakhon Ratchasima Province, Thailand by using a randomized complete block design with three replications. The entries were sown in

Sandar Moe is with the School of Crop Production Technology, Institute of Agricultural Technology, Suranaree University of Technology, Muang, Nakhon Ratchasima, 30000 Thailand (phone: 0848310082; e-mail: sandarmoe88@gmail.com).

Teerayoot Girdthai was with the School of Crop Production Technology, Institute of Agricultural Technology, Suranaree University of Technology, Muang, Nakhon Ratchasima, 30000 Thailand (e-mail:teerayoot@sut.ac.th).

spacing of 50 cm between rows and 20 cm between plants. The collected morphological data consisted of leaf shape, flower color, pubescence color, mature pod color, seed coat color and hilum color, days to 50% flowering, days to pod formation, days to maturity, plant height at maturity (cm), number of filled pods per plant, number of seeds per pod, 100 seed weight (g), seed yield (g) and harvest index (%). In physiological identification, SPAD chlorophyll meter reading (SCMR) and specific leaf area (SLA) were studied on 27 soybean accessions with maturity date of more than 100 days after sowing, among 95 accessions. Analysis of variance was performed for all traits in order to test the significance of variation among genotypes. The collected data was analyzed for mean, coefficient of variation (CV%). Agro-morphological traits and physiological traits were used for cluster analysis to study the relationship among the tested varieties. Moreover, the correlations between the yield and other traits were computed. These computations were done by using statistic 8, crop stat 7.2 and NTSYSpc version 2.2.

III. RESULTS AND DISCUSSIONS

A. Agro-morphological Traits Analysis

The mean sum of squares due to various sources of variation for 10 characters viz., days to emergence, days to 50% flowering, days to pod formation, days to maturity, plant height, number of filled pods per hill, number of seeds per pod, 100 seed weight, yield per hill and harvest index are presented in Table I. The variations due to genotypes were significant for all the characters under 5 and 1 per cent probability levels among 94 soybean accessions. Aravind [7] also found that the variation due to genotypes was significant for all the tested characters under the study both at 5 and 1 percent probability levels.

The germplasm exhibited high variability for the tested 10 traits. High CV percents were recorded in number of filled pods per hill (39.40%), yield per hill (45.6%) and harvest index (32.2%) respectively revealing a high level of diversity among the accessions for these traits. Therefore, selection on the basis of these traits can be useful. About this phenomenon, Malik et al [8] found that high CVs were recorded in leaf area (44.81%), pods per plant (29.47%), branches per plant (31.72%), 100-seed weight (39.01%) and grain yield per plant (46.55%) respectively indicating a high level of diversity among the accessions for these traits.

Unweighted Pair Group Method with Arithmetic Mean (UPGMA) procedure defined 7 clusters based on 7 morphological traits (flower color, leaf shape, plant type, pod color, pubescence color, seed coat color and helium color) at similarity coefficient (0.52). Cluster I consisted of 23 soybean accessions, cluster II of 37, cluster III of 5, cluster IV of 4, cluster V of 18, cluster VI of 5 and cluster VII of 2. The accessions in cluster IV were not only late maturity, high yielding and high number of seeds per pod but also had more plant height. Although the accessions in group VI and VII were early matured and high 100 seed weight, they showed low plant height and low yielding (Table III). In a similar phenomenon, Malik et al [8] reported that 98 soybean

accessions were clustered into 3 groups (6-subgroups) by using the UPGMA procedure regarding of morphological data. Yield is a complex quantitative character governed by large number of genes and is highly influenced by environment. Therefore, the selection of superior genotypes based on yield is very difficult. For a rational approach towards improvement of yield, selection has to be made for the components of yield. Association of yield components and yield may be assumed as special importance for the basis of indirect selection. Genetic correlation between different characters of plant often arises because of linkage or pleiotropy [9]. Positive and significant correlations were observed between yield and all other traits, except seeds per pod. The correlations among 9 characters are presented in Table II. In this study, most of the tested traits were positive and highly significantly correlated with the seed yield (days to 50% flowering, days to pod formation, days to maturity, plant height, number of filled pods per hill, 100-seed weight and harvest index). Although seed per pod was positively correlated with the seed yield, it is non-significant. Amaranath et al. [10], and Harer and Deshmukh [11] reported that yield was positively correlated with days to maturity. Dixit et al [12] indicated that yield was positively associated with number of pods per plant. Yield showed positive correlation with number of seeds per pod ([13], [14]). In the correlation between yield and HI, Sahu and Mishra [15], and Yao et al. [16] reported that these characters were positive associated.

B. Physiological Traits Analysis

SCMR, SLA and yield of 26 accessions were highly significant (Table IV). When the physiological traits were studied for correlation analysis, there were negative and significant correlations between SLA and yield (-0.54), while SLA showed negative and non-significant association with SCMR (-0.39). In the study, yield showed positive and non-significant association with SCMR (0.20) (Table V). Ahmed [17] indicated that SCMR showed significant positive correlation with chlorophylls at flowering stage. His result revealed that grain yield significantly correlated to the leaf chlorophyll.

In regarding of physiological traits (SCMR and SLA), 4 major groups were divided for 27 soybean accessions by using UPGMA method. Cluster I consisted of 11 soybean accessions, cluster II of 5, cluster III of 9 and cluster IV of 2. The accessions of cluster II showed low SCMR and high SLA.

IV. CONCLUSION

All tested agro-morphological characters were highly significant among the accessions. In the correlation analysis, seed yield showed positive and highly significant association with days to 50% flowering, days to pod formation, days to maturity, plant height, number of filled pods per hill, 100-seed weight and harvest index. It might be emphasized the importance of these characters to be considered for selection

TABLE I
MEAN SQUARES OBTAINED FROM THE ANALYSIS OF VARIANCE FOR THE TESTED 10 CHARACTERS IN 94 SOYBEAN ACCESSIONS (94 X 3) RCBD

Source of Variation	Degree of Freedom	Days to emergence	Days to 50% flowering	Days to pod formation	Days to maturity	Plant height	No. of filled pods/hill	No. of seeds/pod	100 seed weight	Yield/hill	Harvest index
Replication	2	25.77	11.77	6.93	2.63	11.02	2722.13	1.08	2.16	421.18	4107.34
Genotypes	93	4.29**	109.66**	276.76**	249.27**	1200.89**	4285.97**	0.40**	71.29**	555.41**	1073.70**
Error	186	2.39	4.62	8.48	2.66	7.99	578.63	0.19	0.98	110.99	370.41
Total	281	3.18	39.43	97.23	84.27	402.81	1820.87	0.27	24.26	260.29	629.77
CV%		24.90	5.81	6.12	1.62	6.03	39.38	18.96	5.68	45.60	32.21

**highly significant

TABLE II
CORRELATION COEFFICIENTS OF 9 TRAITS STUDIED IN NINETY-FOUR ACCESSIONS OF SOYBEAN

Characters	DF	DP	DM	PH	NF	SP	SW	PY
DP	0.90**							
DM	0.64**	0.74**						
PH	0.54**	0.58**	0.56**					
NF	0.63**	0.70**	0.50**	0.53**				
SP	0.00 ^{ns}	0.02 ^{ns}	0.04 ^{ns}	0.18**	0.01 ^{ns}			
SW	-0.43**	-0.48**	0.31**	0.25**	0.44**	0.01 ^{ns}		
PY	0.62**	0.71**	0.56**	0.51**	0.82**	0.09 ^{ns}	0.27**	
HI	0.31**	0.32**	0.19**	0.23**	0.48**	0.05 ^{ns}	0.18**	0.62**

*=significant, **=highly significant, ^{ns}=non-significant, DF=days to 50% flowering, DP=days to pod formation, DM=days to maturity, PH=plant height, NF=number of filled pods per hill, SP=no. of seeds per pod, SW=100 seed weight, PY=yield per hill, HI=harvest index (%)

TABLE III
CLUSTER MEANS OF 9 MORPHOLOGICAL TRAITS STUDIED IN 94 SOYBEAN ACCESSIONS

Sr.No.	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
1.	Days to 50% flowering	37	39	34	42	37	31	29
2.	Days to pod formation	47	51	43	53	48	38	36
3.	Days to maturity	96	103	102	105	102	95	94
4.	Plant height (cm)	33.81	54.01	51.28	73.89	50.75	24.41	20.90
5.	No. of filled pods per plant	45	75	58	70	69	20	8
6.	Seeds per pod	2	2	2	3	2	2	2
7.	Harvest index	59.51	65.46	61.91	59.12	56.26	39.44	35.14
8.	100 seed weight (g)	18.70	16.51	17.73	17.60	15.18	23.76	23.19
9.	Yield per hill (g)	17.71	27.64	27.99	30.41	23.46	8.50	7.72

TABLE IV
MEAN SQUARES OBTAINED FROM THE ANALYSIS OF VARIANCE FOR SCMR, SLA AND YIELD
IN 26 SOYBEAN ACCESSIONS

Source of Variation	Degree of Freedom	SCMR	SLA	yield
Replication	1	1.41	45.27	0.520
Genotypes	25	20.58**	2368.93*	505.72**
Error	25	3.94	1154.61	60.64
Total	51	12.05	1728.12	277.64
CV%		4.69	17.11	20.22

*-significant, **- highly significant

TABLE V
CORRELATION COEFFICIENTS OF PHYSIOLOGICAL TRAITS STUDIED IN TWENTY-SEVEN
SOYBEAN ACCESSIONS

Characters	SCMR	SLA	No. of pods/hill	No. of seeds/pod	100 seeds wt.
SLA	-0.39 ^{ns}				
No. of pods/hill	-0.02 ^{ns}	0.35 ^{ns}			
No. of seeds/pod	0.30 ^{ns}	0.27 ^{ns}	0.74 ^{**}		
100 seeds wt.	0.20 ^{ns}	-0.32 ^{ns}	-0.43 [*]	-0.29 ^{ns}	
Yield	0.20 ^{ns}	-0.54 ^{**}	-0.69 ^{**}	-0.47 [*]	0.20 ^{ns}

*-significant, **- highly significant, ^{ns} -non-significant

programmes. Diversity studies at morphological level suggest that there is a large amount of diversity present in the materials. Hence, diverse germplasm lines possessing desirable characters may be used in future breeding programmes.

The physiological study mentioned that negative and significant correlations between SLA and yield, while the SLA showed negative and non-significant association with SCMR. The yield was positive and non-significantly correlated with SCMR.

Diversity studies at both agro-morphological and physiological levels suggest that there is high amount of diversity present in the materials. Hence, diverse germplasm lines possessing desirable characters may be used in future breeding programmes to get maximum spectrum of variability for wide range of characters. There is a need to utilize diverse germplasm lines in breeding programmes to widen the genetic base in the crop. The correlation information of the tested traits can be provided for the breeders in the indirect selection programmes.

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