Assessment of genetic variability, heritability and genetic advance for nutrients and antinutrients in soybean genotypes

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ABSTRACT

Seventeen soybean genotypes were evaluated for phenotypic and genotypic variability, heritability and genetic advance for fourteen quality characters viz., protein, oil, sucrose, trypsin inhibitor activity, total phenols, tannins, saponin, tocopherol, phytic acid and fatty acid composition (Palmitic, stearic, oleic, linoleic and linolenic acid) under three different sowing dates (March 1, June 5 and August 7) at Punjab Agricultural University, Ludhiana. High amount of genetic variability was possessed by saponin content, tocopherol content and linolenic acid in all the sowings except for linolenic acid in March sowing. Considerable amount of genetic variability was exhibited by other biochemical characteristics. Heritability estimates were high for saponin, tocopherol, phytic acid content and all fatty acids in all the environments. High heritability with high genetic advance was observed for saponin content, tocopherol content, palmitic acid and linolenic acid indicating the presence of additive gene action in their inheritance, providing rapid genetic improvement through simple selection.

Keywords: Genetic advance, heritability, sowing dates, soybean, variability

Soybean (*Glycine max* (L.) Merrill) is considered as one of the important grain legumes containing 37 to 42 per cent high quality protein, 6 per cent ash, 29 per cent carbohydrate and 17-24 per cent oil (composed of about 85 per cent poly-unsaturated fatty acids) (Balasubramaniyan and Palaniappan, 2003; Malik *et al*., 2006) owing to its use in food, feed, and industrial applications. However, it contains many anti-nutritional factors, such as trypsin inhibitors, phytic acid, saponins, tannins and lipoxygenase affecting the nutritional value, utilization and digestibility of soybean protein, carbohydrates and minerals. Human demand for high quality soybean is increasing continuously. Hence, in breeding programs, improvement of seed quality has been a major concern to meet the consumer preference and market demand. Knowledge of nature and magnitude of variability before starting any selection programme are helpful in carrying out a successful breeding programme because breeding techniques generally exploit the availability of genetic variability present in the germplasm for crop improvement. Thus, determining genetic variability and partitioning the observed variability into its heritable and non heritable components with the help of suitable genetic parameters such as phenotypic variance, genotypic variance, heritability *etc*. is essential for understanding the genetic nature of traits. The heritability of the traits determines the extent of its transmission from one generation to the next. The response to selection will be higher if the heritability for the characters is higher (Sabu *et al.,* 2009). But the estimates of heritability alone fail to indicate the amount of progress expected from selection. Heritability

coupled with high genetic advance would be more useful in predicting the resultant effect from selecting the best individuals (Johnson *et al.,* 1955). The knowledge of these parameters is essential for proper understanding and their manipulation in any crop improvement programme. A wide range of genetic variability has been reported for quality traits earlier.

Different workers have reported medium to high heritability with moderate genetic advance for oil and protein content (Ramteke *et al.,* 2010; Malik *et al.,* 2006; Aravind, 2006; Recker, 2010). However, limited information is available regarding studies for heritability and genetic advance for other nutrients and antinutrients present in soybean seed under different environmental conditions. Medium to high heritability has also been reported for tocopherol (Dwiyanti *et al.,* 2007), sucrose (Yoshikawa *et al.,* 2014), oleic acid (Bachlava *et al.,* 2008) in soybean. In recent years, there is need for increasing nutritional and decreasing antinutritional components which adds to the overall quality improvement of soybean making it a significant area of research. The present investigation was thus carried out to estimate genetic variability, heritability and genetic advance of some quality characters under different environments as soybean seed composition varies with environmental factors, especially occurring during the seed filling period when accumulation of the seed chemical components occurs (Wolf *et al.,* 1982; Wilson, 2004; Carrera *et al.,* 2009, 2011). The present results would provide a reference for breeding of soybean varieties with low-levels of anti-nutritional factors.

MATERIALS AND METHODS

Experimental material consisted of seventeen photo and thermotolerant soybean genotypes (Table 1) which were sown in randomized complete block design with three replications at Pulse Research area of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana. The experiment was conducted under three different planting dates *i.e.* March $1(D_1)$, June 5 (D_2) and August $7 \text{ (D}_3)$ to expose seed development stage to varying temperature and photoperiod conditions. Each genotype was planted in four rows of 3m length with row to row spacing of 22.5 cm and plant to plant spacing of 5 cm within the rows. Data were recorded on ten randomly taken plants of each genotype in each replication in all the three dates of sowing and observations were recorded for fourteen quality characters including protein content, oil content, sucrose content, trypsin inhibitor activity, total phenols, tannins, saponin, tocopherol, phytic acid and fatty acid composition (Palmitic, stearic, oleic, linoleic and linolenic acid). Protein content was determined by macro Kjeldahl method (AOAC, 2000) while oil content was estimated by solvent extraction system using Socsplus AS Series 4. Fatty acids were estimated through gas liquid chromatography (model NUCON 5700, AIMIL India). Other quality characters *i.e*. sucrose content (sucrose extraction procedure by Dubois *et al*., 1956; estimation of sucrose by Roe, 1934); Trypsin Inhibitor Activity (TIA) (Kakade *et al*., 1974); total phenols and tannins (Swain and Hillis, 1959); saponin content (extraction procedure by Fenwick and Oakenfull, 1983, estimation procedure by Baccou *et al*., 1977) ; tocopherol content (Kayden *et al*., 1973) and phytic acid (Wheeler and Ferrel, 1977) were also estimated for all the genotypes. The genotypic and phenotypic coefficient of variability were estimated according to Burton and Devane (1953). This is given by

$$
GCV = \frac{G_g}{x} \times 100
$$
, where, σ_g = genotypic

standard deviation; \bar{x} = general mean of population

$$
PCV = \frac{\sigma_p}{x} \times 100
$$
, where, σ_p = phenotypic standard

deviation; $x =$ general mean of population

Heritablity was calculated by the formula given by Lush (1949)

Genetic advance (GA) was calculated by the formula used by Miller *et al* (1958).

 $GA = h^2 \cdot k \cdot \sigma_p$

where, $k =$ Selection differential, at 5% selection intensity. It is 2.06

GA (%) of mean) =
$$
\frac{GA}{x} \times 100
$$

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Table 1: List of photo and thermotolerant soybean genotypes used in the study.

S. No.	Entry	S. No.	Entry	S. No.	Entry
	SL(E)1		$SL(E)$ 22	13	$SL(E)$ 40
2	$SL(E)$ 14	8	SL (E) 27	-14	$SL(E)$ 42
3	SL (E) 14A	9	$SL(E)$ 28	15	$SL(E)$ 44
4	$SL(E)$ 18	10	$SL(E)$ 32	16	$SL(E)$ 45
5	SL (E) 20	11	SL (E) 38	17	MACS 330
6	$SL(E)$ 21	12.	SL (E) 39		

RESULTS AND DISCUSSION

The Analysis of variance pooled over the three environments (sowing dates) is given in table 2 & 3. The variance due to genotypes was significant for all the characters indicating the existence of significant amount of variability among the genotypes for all the fourteen quality characters studied. Similar trend was shown by variance due to sowing dates. Genotype x sowing date interaction was also significant for all the characters except for oil content. Highly significant variance due to interaction between sowing dates and genotypes suggested that response of different genotypes was not uniform in direction and magnitude. Sowing dates increased the difference among genotypes for certain characters, while in others, both genotypes and environment were more or less equally responsible for the variance observed. Highly significant G x E interaction for protein and oil content had also been earlier observed (Arslanoglu *et al.,* 2011; Zargar *et al.,* 2011).

The estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as percent of mean are presented in table 4. Phenotypic coefficient of variation was higher in magnitude than genotypic coefficient of variation in respect to all the characters studied but these differences were generally low for almost all the characters implied that traits are mostly governed by genetic factors with little role of environment in the phenotypic expression of these characters. Thus phenotypic performance could be used as an effective criteria for selection for the improvement in these characters.

Considering all the three sowing dates, high genotypic and phenotypic coefficient of variation were recorded for saponin content, tocopherol content and linolenic acid in all the sowings except for linolenic acid in D_1 . The estimates of PCV and GCV were medium for TIA, phenol, tannin, phytic acid content and all fatty acids except linolenic acid in all the sowings. For sucrose content, these estimates were high in D_1 and medium in

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Table 3: Mean Squares for phytic acid, tocopherol and fatty acids in soybean over different sowing dates.

Source of	d.f.	Phytic acid $(mg g-1)$	Tocopherol $(mg g-1)$	Fatty acids $(\%)$				
variation				Palmitic acid	Stearic acid	Oleic	Linoleic	Linolenic acid
						acid	acid	
Replications								
(in env.)	6	0.18	0.22	0.40	$0.17*$	0.16	0.22	0.12
Sowing Dates								
(D)	2	$159.07**$	$15.69**$	$3.63**$	$0.24*$	2741.98**	663.28**	75.88**
Genotypes								
(G)	16	$38.63**$	$11.64**$	$19.74**$	$1.67**$	39.82**	$217.90**$	48.59**
(GXD)	32	$6.83**$	$8.58**$	$8.30**$	$0.57**$	$115.27**$	$140.73**$	34.48**
Error	96	0.09	0.13	0.07	0.05	0.78	0.05	0.17

*** Significant at P = 0.01 level; *Significant at P = 0.05 level*

 D_2 and D_3 . Low PCV and GCV were recorded for protein and oil content. Thus, results revealed considerable amount of phenotypic and genotypic variances among the genotypes for most of the traits studied. Earlier workers also revealed low GCV and PCV values for oil content and protein content (Dhillon *et al.,* 2005; Parameshwer, 2006 and Bhat and Basavaraja, 2011). However limited data is available for other quality traits.

Information of heritability estimates along with genotypic coefficient of variation determines the effectiveness of selection in the breeding program. High heritability was observed for saponin, tocopherol, phytic acid content and fatty acids in all the environments. Moderate heritability estimates were obtained for TIA,

sucrose, oil, phenol and tannin content**.** For protein content, heritability estimates were medium for D_1 and D_2 and low for D_3 sowing. On the contrary, Malik *et al.* (2006) and Ramteke *et al.* (2010) reported high heritability for protein and oil content. Knowledge of genetic advance along with heritability estimates are more useful as it helps in understanding the type of gene action involved in the expression of quantitative characters. Saponin content, tocopherol content, linolenic acid, palmitic acid, TIA and sucrose were the quality traits that had shown high genetic advance in all environments. High heritability with high genetic advance as per cent of mean was observed for saponin content, tocopherol content, palmitic acid and linolenic acid. This indicates the lesser influence of environment

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in expression of characters and prevalence of additive gene action in their inheritance, which is advantageous for simple selection. High heritability with moderate genetic advance as percent of mean was recorded for phytic acid, phenol content, tannin content, oleic acid and linoleic acid indicating that these characters were less influenced by environment but governed by both additive and non additive gene action. The characters *viz*., protein content and oil content showed moderate heritability with lower genetic advance, there by indicating that expression of these characters may be due to non additive gene action. It may be noted that the characters *i.e*. protein and oil content showing low genetic advance also had lower GCV and PCV values.

Thus, the present study concludes that most of the traits had shown the presence of sufficient genetic variability. High GCV values recorded for tocopherol, saponin content and linolenic acid, suggests the existence of genetic variability that could be exploited for better improvement of these traits. As heritability along with genetic advance gives the idea of expected gain in the next generation, maximum heritability with high genetic advance as percent of mean is the powerful tool used in selection process as it contributes towards the reliability in the selecting genotypes for a particular trait. High heritability with high genetic advance as per cent of mean was observed for plant saponin content, tocopherol content, palmitic acid and linolenic acid. These traits suggests the existence of additive gene action in their inheritance and provide reliability during selection process for the development of elite genotypes of soybean with high nutritional and low antinutritional factors.

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