

GENETIC EVALUATION OF GROUNDNUT (*ARACHIS HYPOGAEA* L.) GENOTYPES FOR AGRONOMIC AND SEED QUALITY TRAITS IN ALLAHABAD REGION

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ABSTRACT

Eleven groundnut genotypes (including check) obtained from ICRISAT, Hyderabad evaluated for quantitative and quality traits. The crop was sown during Kharif 2014 at field experimentation center of the Department of Genetics and Plant Breeding, SHIATS, Allahabad, Uttar Pradesh. The experiment was laid out in Randomized Block Design with three replications. The components of variance revealed that the phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the traits. High estimates of GCV and PCV were observed for seed yield per plant (g), pod yield per plant (g), oil yield per hectare (q) and pods per plant. High heritability was exhibited for all the traits, highest heritability were recorded for seed yield per plant, plant height and days to maturity. High genetic advance was exhibited for plant height, days to maturity and pods per plant. However, high heritability coupled with high genetic advance as mean percent was observed for seed yield per plant, indicating that these traits could be used as selection indices for crop improvement.

KEY WORDS: Groundnut (*Arachis hypogaea* L.), GCV, PCV, heritability, genetic advance, quantitative and quality traits.

INTRODUCTION

The cultivated groundnut (*Arachis hypogaea* L.), is one of the important oilseed, annual, herbaceous, allotetraploid (AABB genome, $2n=4x=40$) with a genome size of 3×10^9 bp. All species, except the cultivated species (*A. hypogaea* and *A. monticola*) in Section *Arachis*, and certain species in Section *Rhizomatosae*, are diploid ($2n = 2x = 20$). The diploid progenitors, *A. duranensis* and *A. ipaensis*, contributed “AA” and “BB” genomes, respectively, to the cultivated groundnut (Kochert *et al.*, 1996).

Groundnut is a legume crop species and belongs to the sub-tribe *Stylosanthinae* of tribe *Aeschynomeneae* in family Fabaceae. The genus *Arachis* is native of South America, with all the species having originated in Brazil, Argentina, Uruguay and Paraguay (Singh & Simpson, 1994). The origin of this crop dates back to 350 B.C. and in India it has been introduced in recent past around 1650. Groundnut is an important edible cash crop and it ranks

13th among food crops and 6th among oilseed crops in the world. Today, it is commercially cultivated over 100 countries between 40 degrees South and 40 degrees north of the equator, where average rainfall is 500 to 1200 mm and mean daily temperatures are higher than 20°C. (Ramanathan, 2001).

Groundnut is a valuable cash crop for millions of small-scale farmers. Groundnut seed contains 44-56% oil and 22-30% protein on a dry seed basis and is a rich source of minerals (phosphorus, calcium, magnesium and potassium) and vitamins (E, K and B group) (Savage & Keenan, 1994). They provide 564 kcal of energy from 100 g of kernels (Jambunathan, 1991). Over 60% of global groundnut production is crushed for extraction of oil for edible and industrial uses, while 40% is consumed in food uses and others (such as seed for sowing the next season crop; BIRTHAL *et al.*, 2010).

The crop occupied about 25.4 million hectares worldwide with an annual production of 45.2 million tonnes and a productivity of 1.77 tonnes ha⁻¹ (FAO STAT 2014). India is largest grower and second producer after china. The area, production and productivity of groundnut were 5.53 million hectares, 9.67 million tonnes and 1.75 tonnes per hectare respectively. India had highest productivity during 2013-2014 when compared with previous years, since from 1950. The area, production and productivity of groundnut in Uttar Pradesh during 2013-2014 were 0.10 million hectare, 0.9 million tonnes and 896 kg per hectare respectively (Agricultural Statistics at a Glance, 2014).

Genetic variability is essential for initiating an effective and successful breeding programme and it became imperative to study the level of genetic variability available in the existing genotype (Ivanovici, 2016). If the variability in the population is largely due to genetic cause with least environmental effect, the probability of isolating superior genotypes is a pre requisite for obtaining higher yield, which is the ultimate expression of various yield contributing characters. The study of genetic advance with heritability estimates further clarify the nature of character which can be improved through selection. Therefore, the present investigation was undertaken to study variability, heritability and genetic advance in groundnut genotypes.

MATERIALS AND METHODS

Eleven groundnut genotypes were received from International Crop Research Institute for the Semi Arid Tropics (ICRISAT), Patancheru, Hyderabad, Telangana, India were evaluated at field experimentation center, Department of Genetics and Plant Breeding, SHIATS, Allahabad, during kharif 2014. The experiment was laid out in randomized block design (RBD) having three replications with 35 cm inter and 10 cm intra row spacing. The observations were recorded on five randomly selected plants from each replication for various traits *viz.* field emergence percentage, plant height, primary branches/plant, pods/plant, pod yield/plant, pod yield (q/ha), seed yield/plant, hundred kernel weight, sound mature kernels, kernel uniformity, shelling percentage, kernel yield (q/ha) and 3 quality traits oil yield (q/ha), protein and oil content. Observations for days to 50% flowering and days to maturity were recorded on plot basis. Analysis of variance to test the significance difference among accessions for each character was carried out as per methodology suggested by Panse and Sukhatme (1967). Phenotypic Coefficient of Variance (PCV) and Genotypic Coefficient of Variance (GCV) were calculated by the formula given by Burton (1952), heritability in broad sense (h²) was worked

out by using formula suggested by Lush (1949) and Burton and Devane (1953) and genetic advance *i.e.* the expected genetic advance were calculated by using the procedure given by Lush (1949) and Johnson *et al.* (1955)

RESULTS AND DISCUSSIONS

The analysis of variance for different characters is presented in Table 1 & 2. Mean sum of squares due to genotypes showed significant difference for all 14 quantitative and 3 quality traits were studied. The mean sum of squares was suggesting that the selected genotypes were genetically variable and considerable amount of variability existed among them. Similar results were also reported by Patidar *et al.* (2014), Maurya *et al.* (2014), Shukla *et al.* (2014), Rai *et al.* (2014) and Rao *et al.* (2014).

TABLE 1. Analysis of variance for quantitative traits of 11 groundnut genotypes during Kharif 2014

S.No.	Traits	Mean Sum of Square		
		Replication (df= 2)	Treatment (df= 10)	Error (df= 20)
1	Field Emergence	63.796	83.942**	19.475
2	Days to 50 % flowering	0.364	23.352**	0.297
3	Plant height	0.205	368.536**	0.376
4	Primary branches per plant	0.147	6.857**	0.052
5	Days to maturity	0.758	228.067**	0.458
6	Pods per plant	0.884	150.092**	0.319
7	Pod yield per plant	0.469	86.829**	0.170
8	Pod yield	2.781	138.621**	0.964
9	Seed yield per plant	0.073	51.844**	0.030
10	Sound matured kernel	2.742	10.742**	2.303
11	Shelling percent	16.265	35.973**	5.926
12	Hundred Kernel weight	0.460	107.847**	0.375
13	Kernel yield	2.608	85.773**	0.787
14	Kernel uniformity	4.758	7.491**	1.691

** Significant at 1% level of significant respectively.

TABLE 2. Analysis of variance for quality traits of 11 groundnut genotypes during Kharif 2014

S.No	Traits	Mean Sum of Square		
		Replication (df=2)	Treatment (df=10)	Error (df=20)
1.	Protein content	0.156	2.254**	0.056
2.	Oil content	0.511	6.698**	0.204
3.	Oil yield	0.521	24.024**	0.182

** Significant at 1% level of significant respectively.

The genotypic coefficient of variation provides a measure to compare the genetic variability present in quantitative and quality traits. Indicating the existence of considerable genetic variation in the experimental material. A perusal of the components of variance revealed that the phenotypic coefficient of variation (PCV) were higher than Genotypic coefficient of variation (GCV) for all the characters studied (table 3 & 4). Coefficient of variation at both genotypic and phenotypic levels was relatively high for seed yield per plant followed by pods per plant, oil yield, plant height, kernel yield, pods per plant, pod yield per hectare and primary branches per plant, hundred kernels weight. Whereas days to 50%

flowering, days to maturity and field emergence showed moderate values. While the lowest value for GCV and PCV was observed for kernel uniformity followed by sound matured kernel, oil content, protein content and shelling percentage. Similar findings were in conformation with findings of Patidar *et al.* (2014), Maurya *et al.* (2014). High GCV and PCV for oil yield and kernel yield were also reported by Shukla and Rai (2014).

Good estimate of heritability is a useful tool that helps the researcher to determine traits that can serve as criteria for selection of superior genotypes in evaluation program. According to Allard (1960), heritability is the proportion of the genetic variation that can be attributed to genetic causes. When considered alongside with genetic advance, heritability estimates give a better assessment of the reliability of the traits and allows for easy prediction of the genetic progress to be achieved in a breeding program (Johnson *et al.*, 1955). Heritability in broad sense was observed higher in all the traits (table 3 & 4). In the traits high heritability recorded for seed yield per plant (99.94) followed by plant height (99.90) days to maturity (99.80), pod yield per plant (99.80), pods per plant (99.79), hundred kernel weight (99.65), primary branches per plant (99.25), oil yield per hectare (99.25), days to 50% flowering (98.74), protein content (97.57) and oil content (97.02). High value of heritability in broad sense indicates that the character is least influenced by environmental effects. Similar observations were made by Shukla and Rai (2014). A perusal of genetic advance for different traits revealed that it varied from 3.08 (protein content) to 39.54 (plant height). High genetic advance was recorded for plant height (39.54) followed by days to maturity (31.10), pods per plant (25.13) and pod yield (24.23). Lowest genetic advance was observed for protein content (3.08) and oil content (5.30). Similar observations were made by Shukla and Rai (2014) for protein content and oil content and Rao *et al.* (2014) for plant height and pod yield.

TABLE 3. Estimation of mean, range, GCV, PCV, heritability, genetic advance and genetic advance as % of mean of 14 quantitative traits in groundnut genotypes

No	Characters	Mean	Range		GCV %	PCV %	h ² (BS) %	GA	GG=GA%
			Min.	Max.					
1	Field emergence	68.58	61.40	78.95	12.83	14.36	79.91	18.13	26.43
2	Days to 50% flowering	27.25	24.33	32.33	17.56	17.68	98.74	9.93	36.18
3	Plant height	30.61	19.33	45.20	62.70	62.73	99.90	39.54	129.16
4	Primary branches per plant	6.24	4.07	9.60	41.89	42.05	99.25	5.39	86.30
5	Days to maturity	116.67	107.33	130.67	12.94	12.95	99.80	31.10	26.66
6	Pods per plant	20.30	9.99	31.27	60.33	60.39	99.79	25.23	124.28
7	Pod yield per plant	13.07	8.14	23.67	71.25	71.32	99.80	19.19	146.77
8	Pod yield	21.68	12.85	33.78	54.26	54.44	99.31	24.23	111.77
9	Seed yield per plant	9.16	4.95	17.31	78.59	78.61	99.94	14.83	161.89
10	Sound mature kernel	81.76	77.84	83.83	3.86	4.29	81.24	6.51	7.96
11	Shelling percent	69.30	61.61	73.12	8.41	9.12	85.16	12.01	17.33
12	100 kernel weight	36.67	27.63	48.11	26.48	26.53	99.63	19.22	54.55
13	Kernel yield	15.24	7.96	24.69	60.66	60.94	99.09	19.05	124.97
14	Kernel uniformity	81.15	78.67	83.67	3.24	3.62	80.38	5.42	6.68

TABLE 4. Estimation of mean, range, GCV, PCV, heritability, genetic advance and genetic advance as percent of mean of 3 quality traits in groundnut genotypes

No	Characters	Mean	Range		GCV %	PCV %	h ² (BS) %	GA	GG=GA %
			Min.	Max.					
1	Protein content	24.75	23.37	26.10	6.04	6.12	97.57	3.08	12.45
2	Oil content	48.53	46.88	51.73	5.31	5.39	97.02	5.30	10.93
3	Oil yield	7.45	3.75	12.54	65.67	65.92	99.25	10.08	135.28

Genetic advance as percent of mean for various characters are presented in table 3 & 4 and noticed that high genetic advance as percent of mean was recorded for seed yield per plant (161.89) followed by pod yield per plant (146.77), oil yield per hectare (135.28), plant height (129.16), kernel yield per hectare (124.97) pods per plant (124.28), pod yield per hectare (111.77), primary branches per plant (86.30), hundred kernel weight (58.31), days to 50% flowering (36.18), days to maturity (26.66), filed emergence (26.43). The values were moderate for oil content (12.45) and shelling percentage (17.33). It was low for sound matured kernel (7.96) followed by kernel uniformity (6.68), protein content (6.68). High heritability coupled with high genetic advance as percent of mean were recorded for seed yield per plant, plant height, days to maturity, pod per plant, hundred kernel weight and oil yield, indicating the role of additive genes in expressing these traits and revealed better scope for improvement of these traits through direct selection. The present findings were in conformation with findings of Nath and Alam (2002), Rao *et al.* (2014). High heritability and high genetic advance as percent of mean for oil yield and kernel yield reported by Shukla and Rai (2014).

The results from the present study were outcome of one year evaluation. It is generally believed that evaluation carried out across year (at least two year) derived reliable conclusions on the range of quality traits measured from each entry. Our results provide some useful information for genetic improvement of the cultivated groundnut.

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