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Study on genetic variability, heritability and genetic advance in groundnut (*Arachis hypogaea* L.)

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Abstract
Twenty four germplasm line and eight cultivar of groundnut were planted in three replication of RBD design with two different dates at research farm of COA Gwalior and KVK Ashoknagar each in kharif 2018. The pooled analysis of variance was significant for all characters, plant height (cm), days to 50% flowering, days to maturity, number of primary branches, number of secondary branches, number of pods per plant, pod yield per plant (g), kernel yield per plant (g), shelling (%), sound matured kernel (%), 100 pod weight (g), 100 kernel weight (g), biological yield per plant (g) and harvest index (%).High heritability estimates were observed for number of 100 pod weight (94.13%), moderate heritability estimates were expressed by kernel yield per plant (66.67%) and sound mature kernels (42.74%) exhibited low estimates of heritability. High value of genetic advance as percent of mean was observed for 100 pod weight (33.17%) while moderate value of genetic advance was observed for biological yield per plant (12.83%). The highest GCV and PCV was observed for 100 pod weight (767.91%) and (815.77%).

Keywords: Groundnut (*Arachis hypogaea* L.), genetic variability, heritability, PCV, GCV and genetic advance

1. Introduction
Groundnut or peanut is an allotetraploid (*Arachis hypogaea* L., AABB, $2n = 4x = 40$, a self-pollinated legume), crop. It is one of the five oilseeds, namely, soyabeans, sunflower seeds, cotton seed, and rapeseed. It is popularly known as the "King" of oilseeds or "Wonder nut" or "Poor man's cashew nut" (Thamaraikannan *et al.,* 2009) [18]. It is an important source of oil, food and feed legume, where kernels are rich in oil (48-50%), protein (25-28%) and 10–20% carbohydrates. The genus *Arachis* is native to South America, with all the species having originated in Brazil, Bolivia, Argentina, Uruguay and Paraguay. Groundnut is commercially cultivated over 100 countries between latitude 40º N and 40º S latitudes (Ramanathan, 2001) [15]. In year 2017-18 total oilseed production in india was 20.68 million tonnes in 17.42 million hectare area and yield of 1187 kg/ha of oilseeds has been achieved. Among oilseeds crop, in 2017-18 groundnut average production was 6.21 million tonnes.

Genetic diversity plays a pivotal role in survival and adaptability of a species. When a specific environment changes, slight genetic variation is necessary for it to adapt and survive. A species that has a large degree of genetic diversity among its population will have more variation. The genetic diversity is a crucial factor in determining the success of hybridization programme and its importance in crop improvement has long been recognized by breeder. The more diverse parents within overall limits of fitness, the greater are the chances of heterotic F₁'s and broad spectrum of variability in segregating generation (Arunachalum, 1981 and Falconer, 1989) [1, 6]. Therefore, the first step in any crop breeding programme is to assess genetic variability.

Evaluation of self pollinated crop like groundnut is normally done by obtaining information on variability and nature of gene action. Genetic parameters such as coefficient of variation, heritability, genetic advance would be of value to the groundnut breeder for identifying superior lines as well as superior plants.

Material and Methods
The experimental material comprised 24 germplasm line and 8 cultivar of groundnut (*Arachis hypogaea* L.). Experiments were conducted in two different dates at research farm of COA Gwalior and KVK Ashoknagar each in kharif 2018.

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32 genotypes of groundnut were sown in a Randomized Block Design (RBD) with three replications during kharif 2018. Each genotype was accommodated in a single row of 2 m length with a spacing of 30 cm between rows and 10 cm between plants within the row. The experiment was surrounded by two guard rows to avoid damage and border effects. The recommended packages of practices were adopted for optimum crop growth. The fertilizer was applied at the rate of 20:60:40 kg NPK/ha. The observations were recorded on 5 competitive plants selected at random on 14 morphological characters namely plant height (cm), days to 50% flowering, days to maturity, number of primary branches, number of secondary branches, number of pods per plant, pod yield per plant (g), kernel yield per plant (g), shelling (%), sound matured kernel (%), 100 pod weight (g), 100 kernel weight (g), biological yield per plant (g) and harvest index (%) were recorded.

The pooled data were subjected to statistical analysis to test the homogeneity for error variance was applied by utilizing the Barlletts method (Panse and Sukhatme, 1967) [13]. Heritability (broad sense and narrow sense) was estimated by formula given by Warner (1952) [19]. Genetic advance as percent of mean can be classified according to proposed by Johnson et al., (1955) [8] as low (0-10%); moderate (10-20%) and high (20% and above). The phenotypic and genotypic coefficients of variation were computed by the following formulae given by Burton (1952) [2].

Result and Discussion

Pooled analysis of variance for kernel yield per plant and its contributing traits is presented in table 1. The mean sum of square due to genotypes were significant for all the characters viz., plant height (cm), days to 50% flowering, days to maturity, no. of primary branches, no. of secondary branches, no. of pod per plant, pod yield per plant (g), selling %, sound mature kernel, 100 pod weight (g), 100 kernel weight (g), biological yield per plant (g), harvest index % and kernel yield per plant (g) in pooled analysis of four environmental data. It indicates that there was considerable variability for these characters in the present material of groundnut genotypes. Same result was seen by Choudhary et al. (2013) [3], Patidar et al. (2014) [14] and Devangan et al. (2015) [5].

High heritability estimates were observed (table 2) for number of 100 pod weight (94.13%) followed by days to 50% flowering (89.98%), no. of secondary branches (89.41%), 100-kernal weight (86.60%), days to maturity (83.07%), plant height (80.17%), biological yield per plant (79.56%), harvest index (76.63%), pod yield per plant (76.38%), no. of pod per plant (73.27%) and no. of primary branches (73.17%). Moderate heritability estimates were expressed by kernel yield per plant (66.67%) and shelling % (51.62%). The sound mature kernels (42.74%) exhibited low estimates of heritability. Similar findings were also reported by Mothilal et al. (2004) [11], Golakia et al. (2005) [7] and Rao et al. (2015) [6].

The estimation of genetic advance expressed as percentage of mean (table 2) were found high for 100 pod weight (33.17%) followed by no. of secondary branches (28.33%), 100 kernel weight (19.66%), no. of pod per plant (15.08%), pod yield per plant (15.02%) and no. of primary branches (14.57%) same as work done by Dashora and Nagda (2002) [4] and Korat et al. (2009) [9]. The values were moderate for biological yield per plant (12.83%), plant height (12.11%) and kernel yield per plant (11.47%) (Mothilal et al. 2004 [11] and Suneetha et al. 2004) [17]. It was low for harvest index (8.14%), days to 50% flowering (6.36%), selling % (5.25%), sound mature kernels (3.48%) and days to maturity (1.67%).

The highest phenotypic coefficient of variation was observed (table 2) for 100 pod weight (815.77%) followed by biological yield per plant (203.56%), 100 kernel weight (132.51%), plant height (72.51 %), no. of secondary branches (46.88%) and no. of pod per plant (40.10%). The selling% (36.42%), pod yield per plant (36.05 %) and sound mature kernel (32.94%) exhibited moderate values for phenotypic coefficient of variation. The highest genotypic coefficient of variation was observed for 100 pod weight (767.91%) followed by biological yield per plant (161.95%), 100 kernel weight (114.75%), plant height (58.14%) and no. of secondary branches (41.91%). The no. of pod per plant (29.38%), pod yield per plant (27.53%) and selling% (18.80%) had moderate values. Similar work was done by Nath and Alam (2002) [12], Kumar and Rajamani (2004) [10], Mothilal et al. (2004) [11] and Korat et al. (2009) [9].

Conclusion

Analysis of variances showed highly significant differences for all the traits indicating the presence of considerable variability among the entries. High heritability estimates was associated with high estimates of genetic advance as per cent of mean for 100 pod weight followed by no. of secondary branches, 100 kernel weight, no. of pod per plant, pod yield per plant and no. of primary branches, thereby, indicating the presence of additive variances. The highest genotypic coefficient of variation and phenotypic coefficient of variation was observed for 100 pod weight, biological yield per plant, 100 kernel weight, plant height and no. of secondary branches whereas pod yield per plant and selling% showed moderate genotypic coefficient of variation and phenotypic coefficient of variation.

Table 1: Pooled analysis of variance in groundnut for 14 characters over four environments.

Sources	df	Plant height (cm)	Days to 50% flowering	Days to maturing	No. primary branches	No. secondary branches	No. of pod per plant	Pod yield per plant (g)	Selling %	Sound mature Kernel %	100 Pod weight (g)	100 Kernel weight (g)	Biological yield per plant (g)	Harvest Index %	Kernel yield per plant (g)
Environment	3	24137.1**	564.7**	28.2**	4.3*	1295.0**	3112.2**	1260.2**	8655.1**	219642.4**	573.9**	131.2**	53088.3**	327.4**	115.8**
Genotype	31	332.9**	41.0**	41.0**	14.7**	34.2**	51.5**	46.9**	373.3**	158.1**	8695.1**	519.9**	2290.3**	45.2**	10.6**
G X E	93	303.6	16.4	12.7	13.5	18.6	71.8	38.0	427.3	136.9	489.3	162.0	1341.9	34.1	9.6
pooled error	248	19.4	1.1	2.0	1.2	1.0	4.3	3.4	68.4	39.7	133.4	19.4	138.2	3.1	1.2
Total	127	873.8	35.4	19.9	13.6	52.6	138.7	69.1	608.4	5327.2	2494.3	248.7	2795.8	43.7	12.3

*, ** significant at 5 and 1 percent levels, respectively,

Table 2: Estimation of mean squares, genotypic and phenotypic coefficient of variability, heritability and genetic advance of 14 characters of 32 groundnut genotypes tested over four environments in pooled data.

Characters	Mean ±SE	GCV(%)	PCV(%)	h^2B	GA(%mean)
Plant height (cm)	2.20	58.14	72.51	80.17	12.11
Days to 50% flowering	0.53	10.28	11.42	89.98	6.36
Days to maturity	0.70	2.78	3.35	83.07	1.67
No. of primary branches	0.55	15.15	20.70	73.17	14.57
No. of secondary branches	0.50	41.91	46.88	89.41	28.33
No. of pod per plant	1.04	29.38	40.10	73.27	15.08
Pod yield per plant (g)	0.92	27.53	36.05	76.38	15.02
Selling (%)	2.57	18.80	36.42	51.62	5.25
Sound mature kernel (%)	3.15	14.08	32.94	42.74	3.48
100 pod weight (g)	5.77	767.91	815.77	94.13	33.17
100 kernel weight (g)	2.20	114.75	132.51	86.60	19.66
Biological yield per plant (%)	5.88	161.95	203.56	79.56	12.83
Harvest index (%)	0.76	12.36	16.13	76.63	8.14
Kernel Yield per plant(g)	0.54	10.45	15.68	66.67	11.47

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