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ESTIMATION OF VARIABILITY PARAMETERS FOR YIELD AND ITS COMPONENT TRAITS IN GROUNDNUT (*ARACHIS HYPOGAEA* L.)

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ABSTRACT
In the present investigation 58 Spanish bunch groundnut genotypes were used for variability studies in 16 plant characters. Analysis of variance revealed significant differences among the genotypes for all the characters studied. Maximum broad sense heritability was recorded for days to 50% flowering (97.1% (S1), 97.3% (S2), 98.0% (S3) followed by plant height (96.7% (S1), 97.1% (S2), 97.1% (S3) and 100-kernels weight (96.0% (S1), 96.0% (S2), 96.4% (S3). The maximum genetic advance was found for seed dormancy (36.9% (S1), 39.2% (S2), 40.8% (S3) followed by 100-kernels weight (29.3% (S1), 32.1% (S2), 32.2% (S3) and plant height (33.3% (S1), 32.9% (S2), 27.5% (S3). In general, moderate to high heritability coupled with moderate to high genetic advance for days to 50% flowering, plant height, 100-pods weight, 100-kernels weight, shelling percent and harvest index, indicated the involvement of additive gene action and scope of improvement in these traits through selection.

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is a self-pollinated, annual, herbaceous, allotetraploid legume with 2n = 40 chromosomes and belongs to the family *Fabaceae*. The total oilseed production in India during the year 2011-12 was 26.44 million tonnes, of which groundnut production was 6.93 million tonnes, from 5.31 million hectare area with an average productivity 1305 kg per hectare (DAC). Groundnut has to play a major role in bridging the vegetable oil gap in the country. The current average yield level of 1305 kg per hectare is deplorably low as compared 3568 kg per hectare in China and 4699 kg per hectare in USA (FAO). Genetic diversity in crop plants is essential to sustain level of high productivity (Tripathi *et al.*, 2013). The existence of genetic variability is prerequisite for any crop improvement programme; however, loss of locally adapted variable material has been rapid which, need to be maintained (Harlan, 1975). A critical analysis of the genetic variability is a prerequisite for initiating any crop improvement programme and for adopting of appropriate selection techniques (Dhanwani *et al.*, 2013). The genetic variability is determined with the help of certain genetic parameters viz. genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and heritability estimates. For predicting the effect of selection, heritability estimates along with genetic advance are more useful than the heritability estimates alone (Johnson *et al.*, 1955; Cholin *et al.*, 2010; Shinde *et al.*, 2010 and Meshram *et al.*, 2013). The present investigation was carried with objective to estimate the variability parameters for yield and component traits in some of newly developed groundnut genotypes which have not been reported earlier by researchers and this study will be helpful for harnessing present variability among them which in turn can support the ongoing and future groundnut breeding programs.

MATERIALS AND METHODS

The material for present study comprised of 58 Spanish bunch genotypes including six checks (Table 1). The material was evaluated in randomized block design with three replications at Regional Research station, Anand Agricultural University, Anand, Gujarat during summer 2010 (S1) and 2010 (S2) and rainy seasons 2010 (S3). Each experimental unit consisted of a single row of 5 m length with 30 × 10 cm inter and intra row spacing in the environments S1, S2 and 45 × 10 cm inter and intra row spacing in S3. The recommended package of practices and plant protection measures were timely and uniformly applied to raise a good crop. Five plants were randomly selected from each experimental unit in all the three environments. Selected plants were used for recording the observations on days to 50% flowering, numbers of primary branches per plant, days to maturity, plant height (cm), number of mature pods per plant, dry pod yield per plant (g), kernel yield per plant (g),100-pod weight (g), 100-kernel weight (g), sound mature kernel (%), shelling (%), haulm yield per plant (g), harvest index (%), dormancy (days), oil content (%) and protein content (%) characters. For the characters days to 50% flowering and days to maturity, observations were recorded on

Table 1: List of genotypes used in present study, originating centre and plant types

S.N.	Genotypes	Originating centre	Plant types
1	AG-2006-2	AAU, Anand(Gujarat)	Advanced breeding line
2	AG-2006-6	AAU, Anand(Gujarat)	Advanced breeding line
3	AG-2006-10	AAU, Anand(Gujarat)	Advanced breeding line
4	AG-2006-14	AAU, Anand(Gujarat)	Advanced breeding line
5	AG-2006-15	AAU, Anand(Gujarat)	Advanced breeding line
6	AG-2240	AAU, Anand(Gujarat)	Advanced breeding line
7	AG-2243	AAU, Anand(Gujarat)	Advanced breeding line
8	AG-2244	AAU, Anand(Gujarat)	Advanced breeding line
9	AG-2008-1	AAU, Anand(Gujarat)	Advanced breeding line
10	AG-2008-2	AAU, Anand(Gujarat)	Advanced breeding line
11	AG-2008-3	AAU, Anand(Gujarat)	Advanced breeding line
12	AG-2008-4	AAU, Anand(Gujarat)	Advanced breeding line
13	AG-2008-5	AAU, Anand(Gujarat)	Advanced breeding line
14	AG-2008-6	AAU, Anand(Gujarat)	Advanced breeding line
15	AG-2008-7	AAU, Anand(Gujarat)	Advanced breeding line
16	AG-2008-8	AAU, Anand(Gujarat)	Advanced breeding line
17	AG-2008-9	AAU, Anand(Gujarat)	Advanced breeding line
18	ICGV-00309	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
19	ICGV-00310	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
20	ICGV-00321	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
21	ICGV-00349	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
22	ICGV-00350	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
23	ICGV-00351	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
24	ICGV-00380	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
25	ICGV-00387	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
26	ICGV-00441	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
27	ICGV-01263	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
28	ICGV-95058	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
29	ICGV-95066	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
30	ICGV-95069	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
31	ICGV-95070	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
32	ICGV-95090	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
33	ICGV-96155	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
34	ICGV-96174	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
35	ICGV-96175	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
36	ICGV-96177	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
37	ICGV-96211	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
38	ICGV-99083	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
39	ICGV-99105	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
40	ICGV-99181	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
41	ICGV-99186	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
42	ICGV-99233	ICRISAT, Hyderabad (Andhra Pradesh)	Advanced breeding line
43	J-68	JAU, Junagadh (Gujarat)	Variety
44	J-69	JAU, Junagadh (Gujarat)	Variety
45	J-71	JAU, Junagadh (Gujarat)	Variety
46	J-72	JAU, Junagadh (Gujarat)	Variety
47	J-73	JAU, Junagadh (Gujarat)	Variety
48	JB-1136	JAU, Junagadh (Gujarat)	Variety
49	JB-1137	JAU, Junagadh (Gujarat)	Variety
50	JB-1142	JAU, Junagadh (Gujarat)	Variety
51	JB-1145	JAU, Junagadh (Gujarat)	Variety
52	JB-1152	JAU, Junagadh (Gujarat)	Variety
53	GG-2 (C)	JAU, Junagadh (Gujarat)	Variety
54	GG-6 (C)	JAU, Junagadh (Gujarat)	Variety
55	GG-7 (C)	JAU, Junagadh (Gujarat)	Variety
56	TAG- 24 (C)	BARC, Mumbai (Maharashtra)	Variety
57	TG-26 (C)	BARC, Mumbai (Maharashtra)	Variety
58	TPG-41 (C)	BARC, Mumbai (Maharashtra)	Variety

plot basis. The duration of dormancy was measured by days taken by culture to attain 50 per cent germination (G50). Per cent oil and protein content in groundnut seed was calculated by using Nuclear Magnetic Resonance (NMR- BRUKER make) (FT-NMR Spectrometer, 2001) and Nuclear Near Infra-red Magnetic Resonance (NIR- BRUKER make) (FT-NIR Spectrometer, 2011) apparatus, respectively. Analysis of variance (Panse and Sukhatme, 1985), genotypic coefficients of varia-

Table 2: ANOVA for sixteen characters of groundnut studied under three environments and pooled over environments

Sources of Variation	df	Days to 50% flowering				Numbers of primary branches per plant			
		S1	S2	S3	Pooled	S1	S2	S3	Pooled
Genotypes	57	44.0607**	59.301**	46.153**	82.829**	1.649**	0.837**	1.372**	1.514
Environments	2	0.121	0.224	0.868	13058.57**	0.224	0.368	0.282	8.626**
Geno. x Env.	114				33.616**				1.172**
Error	114 (342)	0.442	0.546	0.318	0.435	0.242	0.245	0.264	0.250
Sources of Variation	df	Days to maturity				Plant height (cm)			
		S1	S2	S3	Pooled	S1	S2	S3	Pooled
Genotypes	57	9.087**	16.665**	51.047**	26.467	245.467**	235.837**	200.601**	537.335**
Environments	2	0.213	0.868	0.040	7312.202**	5.937	0.971	0.276	1699.209**
Geno. x Env.	114				25.166**				72.285**
Error	114 (342)	0.312	0.312	0.485	0.370	2.720	2.340	1.983	2.348
Sources of Variation	df	Number of mature pods per plant				Dry pod yield per plant (g)			
		S1	S2	S3	Pooled	S1	S2	S3	Pooled
Genotypes	57	16.447**	12.313**	25.017**	29.290**	3.195**	5.625**	5.387**	7.494**
Environments	2	0.557	1.385	0.207	45.761**	0.493	0.285	0.314	85.522**
Geno. x Env.	114				12.244**				3.357**
Error	114 (342)	2.324	2.233	2.394	2.317	0.435	0.615	0.467	0.506
Sources of Variation	df	Kernel yield per plant (g)				100 pod weight (g)			
		S1	S2	S3	Pooled	S1	S2	S3	Pooled
Genotypes	57	2.004**	3.065**	1.909**	4.160**	378.692**	404.768**	431.066**	1197.998
Environments	2	0.221	0.037	0.525	50.169**	2.461	8.002	0.391	2.400**
Geno. x Env.	114				1.409**				8.264**
Error	114 (342)	0.180	0.312	0.225	0.239	7.502	9.675	10.725	9.300

Table 2: Cont....................

Sources of Variation	df	100 kernel weight (g)				Sound mature kernel (%)			
		S1	S2	S3	Pooled	S1	S2	S3	Pooled
Genotypes	57	134.348**	157.628**	161.422**	439.758**	17.777**	19.800**	32.296**	23.715
Environments	2	0.885	0.306	0.959	15.164**	13.301	15.593	14.579	101.608**
Geno. x Env.	114				6.806**				23.079**
Error	114 (342)	1.843	2.166	1.967	1.992	6.528	6.143	4.896	5.856
Sources of Variation	df	Shelling (%)				Haulm yield per plant (g)			
		S1	S2	S3	Pooled	S1	S2	S3	Pooled
Genotypes	57	48.092**	65.750**	49.956**	144.601**	17.461**	11.826**	7.787**	20.474**
Environments	2	0.571	4.367	2.152	27.042**	0.054	1.205	3.805	174.386**
Geno. x Env.	114				9.598**				8.300**
Error	114 (342)	3.684	2.489	4.641	3.605	1.044	0.941	1.305	1.097
Sources of Variation	df	Harvest index (%)				Dormancy (Days)			
		S1	S2	S3	Pooled	S1	S2	S3	Pooled
Genotypes	57	56.025**	67.074**	49.449**	132.708**	14.272**	13.604**	12.411**	28.996**
Environments	2	6.102	6.151	5.430	706.094**	1.126	1.310	0.483	139.088**
Geno. x Env.	114				19.920**				5.646**
Error	114 (342)	4.331	8.196	7.050	6.526	0.419	0.433	0.354	0.402
Sources of Variation	df	Oil content (%)				Protein content (%)			
		S1	S2	S3	Pooled	S1	S2	S3	Pooled
Genotypes	57	8.422**	8.072**	7.944**	18.098**	4.774**	3.276**	2.720**	4.213
Environments	2	0.117	0.481	0.482	35.316**	0.063	0.244	0.329	43.872**
Geno. x Env.	114				3.170**				3.278**
Error	114 (342)	0.222	0.217	0.192	0.210**	0.104	0.180	0.157	0.147

*, ** significant at 5% and 1% levels, respectively. Figures in parenthesis indicate the d.f. for pooled error.

tion (Burton, 1952), phenotypic coefficients of variation (Burton, 1952), broad sense heritability (Lush, 1949), genetic gain (Allard, 1960), and genetic advance (Johnson *et al.,* 1955) were estimated by using SAS 9.4 software (SAS, 2004).

RESULTS AND DISCUSSION

The analyses of variances for sixteen characters in each environment revealed that the mean squares due to genotypes were significant indicating the presence of sufficient amount of variability in the material studied (Table 2).The pooled analysis over the three environments revealed that mean squares due to genotypes were significant for all the characters under study except, number of primary branches per plant, days to maturity, 100 pod weight, sound mature kernel (%) and protein content. The significant mean square for all the characters revealed the presence of substantial amount of variation (John *et al.,* 2013) in the material studied except for five characters. Further, the mean squares due to environments were significant for all the characters under study, which indicated the significant effect of the environment on the expression of all the traits and also suggested the presence of

Table 3: Range, mean, phenotypic and genotypic coefficient of variation, heritability, genetic gain and genetic advance for different characters in groundnut

S.N.	Characters		Range	Mean	PCV(%)	GCV (%)	h^2 (%)(broad sense)	Genetic gain	Genetic advance K = 2.06 (% of mean)
1	Days to 50% flowering	S1	39.3-54.3	46.3	8.4	8.3	97.1	7.8	16.8
		S2	36.7-54.3	44.9	10.0	9.9	97.3	9.0	20.0
		S3	22.7-40.3	30.6	12.9	12.8	98.0	8.0	26.1
2	No. of primary branches perplant	S1	4.3-8.3	6.0	14.1	11.4	66.0	1.2	19.2
		S2	4.7-7.0	5.6	11.9	8.0	44.6	0.6	10.9
		S3	5.0-8.3	5.9	13.4	10.3	58.3	1.0	16.3
3	Days to maturity	S1	120.3-126.7	124.0	1.5	1.4	90.4	3.4	2.7
		S2	114.1-124.3	120.1	2.0	1.9	94.6	4.7	3.9
		S3	102.0-119.3	111.3	3.7	3.7	97.2	8.3	7.5
4	Plant height (cm)	S1	31.7-75.7	54.7	16.7	16.5	96.7	18.2	33.3
		S2	30.4-74.3	54.5	16.4	16.2	97.1	17.9	32.9
		S3	37.7-76.3	60.0	13.8	13.7	97.1	16.5	27.5
5	Number of mature pods per plant	S1	10.7-22.3	15.2	17.5	14.3	67.0	3.7	24.1
		S2	10.1-20.0	14.4	16.4	12.7	60.1	2.9	20.4
		S3	9.7-22.3	15.3	20.5	17.9	75.9	4.9	32.2
6	Dry podyield per plant (g)	S1	7.7-11.9	9.8	11.8	9.8	67.9	1.6	16.6
		S2	5.8-11.2	8.5	17.7	15.1	73.1	2.3	26.8
		S3	6.0-14.4	8.7	16.7	14.7	77.8	2.3	26.8
7	Dry Kernelyield per plant (g)	S1	4.4-7.9	6.0	14.7	12.9	77.1	1.4	23.5
		S2	3.5-7.3	5.1	21.6	18.7	74.6	1.7	33.3
		S3	3.4-7.0	5.1	17.4	14.7	71.4	1.3	25.5
8	100 -pods weight (g)	S1	57.4-100.6	74.8	15.3	14.9	94.3	22.3	29.8
		S2	56.9-101.1	74.6	15.9	15.4	93.2	22.8	30.6
		S3	55.0-102.8	74.6	16.5	15.9	92.9	23.5	31.5
9	100- kernels weight (g)	S1	35.0-62.7	45.7	14.8	14.5	96.0	13.4	29.3
		S2	34.0-65.4	45.3	16.2	15.9	96.0	14.5	32.1
		S3	35.0-64.6	45.8	16.2	15.9	96.4	14.8	32.2
10	Sound mature kernel (%)	S1	81.0-95.5	92.2	3.5	2.1	36.5	2.4	2.6
		S2	83.6-95.2	91.6	3.6	2.3	42.5	2.9	3.1
		S3	82.6-96.0	90.7	4.1	3.3	65.1	5.0	5.5
11	Shelling (%)	S1	53.3-69.7	61.3	7.0	6.3	80.1	7.1	11.6
		S2	46.7-70.6	61.0	8.0	7.5	89.5	9.0	14.7
		S3	51.4-69.3	61.8	7.2	6.3	76.5	7.0	11.3
12	Haulm yield per plant (g)	S1	11.1-21.7	15.1	17.0	15.5	84.0	4.4	29.3
		S2	10.5-20.2	13.7	15.6	13.9	79.4	3.5	25.6
		S3	12.0-19.4	15.6	11.9	9.4	62.3	2.4	15.3
13	Harvest index (%)	S1	32.7-50.5	39.8	11.7	10.4	79.9	7.6	19.2
		S2	30.8-49.8	38.4	13.7	11.5	70.5	7.7	20.0
		S3	24.0-47.5	35.8	12.9	10.5	66.7	6.3	17.7
14	Dormancy (Number of days)	S1	7.7-17.7	11.5	19.5	18.7	91.7	4.2	36.9
		S2	6.0-16.0	10.5	21.0	20.0	91.0	4.1	39.2
		S3	5.7-14.3	9.7	21.5	20.6	91.9	4.0	40.8
15	Oil content (%)	S1	46.4-54.7	50.3	3.4	3.3	92.5	3.3	6.5
		S2	47.1-54.6	50.6	3.3	3.2	92.4	3.2	6.3
		S3	46.8-54.8	51.2	3.3	3.1	93.1	3.2	6.3
16	Protein content (%)	S1	24.4-29.7	27.2	4.7	4.6	93.8	2.5	9.2
		S2	25.3-30.1	28.2	3.9	3.6	85.1	1.9	6.8
		S3	26.2-29.6	27.8	3.6	3.3	84.5	1.8	6.3

significant variation among the environments (Shukla and Rai, 2014).

The mean dry pod yield per plant in different environment ranged from 5.8 g (S2) to 14.4 g (S3) indicated variability of the test environments under study. Maximum dry pod yield was exhibited by genotype TG- 26 (12.2 g), followed by AG-2008-7 (10.6 g) and AG-2008-9 (10.5 g) on pooled basis. The dry pod yield per plant varied from 7.7 g (JB-1142; ICGV-95058) to 11.9 g (TG-26) in S1, 5.8 g (JB-1136) to 11.2 g (ICGV-99083) in S2 and 6.0 g (ICGV-00310) to 14.4 g (TG-26) in S3. Considerable influence of environmental factors was observed for expression of all the traits as depicted by higher values of phenotypic coefficient of variation than corresponding genotypic coefficient of variation (Table 3.)(Rao *et al.*, 2014). The estimates of genotypic parameters revealed that differences between the values of GCV and PCV were least for most of the characters (Thakur *et al.*, 2013 and Rao *et al.*, 2014). Higher estimates of GCV were observed for seed dormancy, 100-kernels weight and 100-pods weight. The present findings of higher GCV for these traits were in accordance with the findings of Nath and Alam (2002), Makhan Lal *et al.* (2003), Mothilal *et al.* (2004), John *et al.* (2006) and Jakkeral *et al.*, (2014).

Whereas, PCV estimates were higher for seed dormancy, number of mature pods per plant and kernel yield per plant. Similar results of higher PCV were observed for these traits by Patil and Bhapkar (1987), Mothilal *et al.* (2004), Mahalaxmi *et al.* (2005), John *et al.* (2006), Kadam *et al.* (2007) and Jakkeral *et al.* (2014). Both GCV and PCV were estimated the minimum for days to maturity among the characters studied.

Maximum heritability was observed for days to 50% flowering followed by plant height and 100-kernels weight (Table 3). While maximum genetic gain was observed for 100-pods weight followed by plant height and 100-kernels weight. The findings of higher broad sense heritability, genetic gain and genetic advance for these traits were in accordance with the finding of Parmeshwarappa *et al.* (2004), Mahalaxmi *et al.* (2005) and Jakkeral *et al.* (2014). The maximum genetic advance was found for seed dormancy followed by 100-kernels weight and plant height. In general, moderate to high heritability was coupled with moderate to high genetic advance for days to 50% flowering, plant height, 100-pods weight, 100-kernels weight, shelling percent and harvest index. Similar results of moderate to high heritability coupled with moderate to high genetic advance were observed earlier for these traits by Azad and Hamid (2000), Dashora and Nagda (2002), Golakia *et al.* (2005) and Mahalaxmi *et al.* (2005), Cholin *et al.* (2010) Shinde *et al.* (2010) and Jakkeral *et al.* (2014). indicated the involvement of additive gene action and there is a scope for improvement in these traits through selection.

In conclusion, the success of plant breeding programs relies heavily on the existence of genetic variability in plants for a particular trait (Arunkumar, 2013). More variability coupled with heritability and genetic gain gives a better idea about the efficiency of selection. Looking to the present findings, it seems that there is a substantial scope for improvement of characters; days to 50% flowering, plant height, 100-pods weight, 100-kernels weight, shelling percent and harvest index.

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