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#### Memon JT

Dept. of Genetics and Plant  
Breeding, College of Agriculture,  
JAU, Junagadh Gujarat, India

#### Kachhadia VH

Assistant Research Scientist,  
Main Oilseeds Research Station,  
JAU, Junagadh, Gujarat, India

#### Vachhani JH

Research Scientist (G & O),  
Vegetable Research Station,  
JAU, Junagadh, Gujarat, India

#### Dedaniya AP

Dept. of Genetics and Plant  
Breeding, College of Agriculture,  
JAU, Junagadh Gujarat, India

#### Correspondence

#### Memon JT

Dept. of Genetics and Plant  
Breeding, College of Agriculture,  
JAU, Junagadh Gujarat, India

## Genetic variability, heritability and genetic advance for quantitative characters in F<sub>2</sub> generation of groundnut (*Arachis hypogaea* L.)

Memon JT, Kachhadia VH, Vachhani JH and Dedaniya AP

#### Abstract

In the present investigation, estimates of genetic variability, heritability and genetic advance were assessed for eight different characters in the F<sub>2</sub> population derived from six groundnut crosses *viz.*, JL-24 x GJG-22 (Cross-1), ICGV-05155 x R-33-1 (Cross-2), AK-343 x TPG-41 (Cross-3), JL-501 x TG-36 (Cross-4), TG-26 x GG-20 (Cross-5), JL-1085 x TPG-41 (Cross-6). The mean sums of squares due to genotypes, parents as well as F<sub>2</sub>s were highly significant for all the characters indicating thereby sufficient variability in the materials studied. The estimates of GCV and PCV were found moderate to high in magnitude in most of the crosses for all the characters except in days to appearance of first flower and days to maturity. High heritability along with high genetic advance and high value of GCV and PCV for pod yield per plant in Cross 1 and Cross 6. Thus, it can be concluded that Cross 1 and Cross 6 for pod yield per plant was mainly under the influence of additive gene actions and selection would be effective for improving these traits.

**Keywords:** Genetic variability, heritability, genetic advance

#### Abbreviation

**GCV:** Genotypic Coefficient of Variances

**PCV:** Phenotypic Coefficient of Variances

**GAM:** Genetic advance as per cent of mean

#### Introduction

Groundnut is a rich source of edible oil (47-54%), high quality protein (22-30%), starch (6-24%), cellulose (1-2%), minerals (2-3%) and calories (5-6%). It has a distinct position among the oilseeds, as it can be consumed and utilized in diverse ways. It is valued both for edible oil and confectionery purposes. The groundnut kernels are consumed as raw, boiled, roasted or fried products and also used in a variety of culinary preparations like peanut butter, peanut milk and chocolates. Cake left after extraction of the oil is an excellent feed for livestock. Vegetative parts of groundnut like leaves and stems are good source of nutritionally high-quality fodder for farm animals. Dry roasted, salted peanuts are also marketed in significant quantities. Boiled peanuts are a preparation of raw, unshelled green peanuts boiled in brine and typically eaten as a snack. Groundnut is also used in cosmetics, nitroglycerin, plastics, dyes and paints.

In groundnut crop, it is obligatory to accumulate information on the variability existed among the polygenic characters. Since the economic part of groundnut known as pod is developed under the soil, prediction of its performance based on aerial morphological characters is almost difficult. Therefore, the critical assessment of nature and magnitude of genetic variability is pre-requisite in groundnut breeding programme.

The yield is a complex character which is highly influence by environmental variation, information on nature and magnitude of variability present in the population due to genetic and non-genetic causes is an important prerequisite for a systemic breeding programme (Prabhu *et al.* 2015a) [19]. Genetic variability is essential for initiating and effective and successful breeding programme and it became imperative to study the level of genetic variability available in the existing genotype. Study of genetic advance with heritability estimate further clarify the nature of character which can be improve through selection (Savaliya *et al.* 2009). Therefore, present investigation was undertaken to study variability, heritability and genetic

advance in six segregating F<sub>2</sub> generations of groundnut. The objective of the present study is to evaluate groundnut cross derivatives for yield and yield attributes and to assess genetic parameters among them.

### Materials and Methods

The present investigation is carried out to assess the genetic variability in F<sub>2</sub> generations of groundnut (*Arachis hypogaea* L.). The required quantity of seeds of F<sub>2</sub> populations and parents of six crosses were obtained from the Main Oilseeds Research Station, Junagadh Agricultural University, Junagadh (Gujarat) and was sown in the summer of 2017 at the Main Oilseeds Research Station, Junagadh Agricultural University, Junagadh (Gujarat).

The experimental material consisted of F<sub>2</sub> generations of 6 crosses derived from crossing among 11 parents. The crosses of the study were; JL-24 x GJG-22(cross-1), ICGV-05155 x R-33-1(cross-2), AK-343 x TPG-41(cross-3), JL-501 x TG-36 (cross-4), TG-26 x GG-20 (cross-5), JL-1085 x TPG-41 (cross-6), hereafter referred to as cross-1, cross-2, cross-3, cross-4, cross-5 and cross-6, respectively.

Six F<sub>2</sub> populations and 11 parental lines have been sown during summer season on 2<sup>nd</sup> February, 2017 in a Randomized Complete Block Design with 3 replications. Three rows of 3 meter length spaced at 60 x 15 cm distance were allotted to each F<sub>2</sub> population, while single row of same length and spacing was allotted to each parent. Soil of experimental area was fertilized with recommended dose of 25.00 kg N<sub>2</sub>, 50.00 kg P<sub>2</sub>O<sub>5</sub> and 50.00 kg K<sub>2</sub>O per hectare. The recommended agronomical and plant protection practices were followed for the successful raising of the crop.

The observations were recorded on 5 randomly selected plants from each parent and 50 plants from each F<sub>2</sub> per replication. Selected plants were tagged before the emergence of first flower and observations like days to appearance of first flower, days to maturity, number of matured pods per plant, kernel yield per plant (g), shelling outturn (%), pod yield per plant (g), biological yield per plant (g) and harvest index (%) were recorded. The data was analyzed to work out GCV, PCV, heritability and genetic advance as per cent of mean (GAM).

Analysis of variance was carried out as per methodology given by Panse and Sukhatme (1985). GCV, PCV and heritability (h<sup>2</sup>) in broad sense was calculated according to formula suggested by Mahmud and Kramer (1951), while genetic advance as per cent of mean (GAM) was calculated as suggested by Allard (1960) [1]. The range of coefficient of variation (CV) was categorized as per Sivasubramanian and Madhavamenon (1973): below 10% - low coefficient of variation; 10-20% - medium coefficient of variation and above 20% - high coefficient of variation. As suggested by Robinson *et al.* (1949), the heritability range was classified as: less than 30% - low heritability; 30-60% - moderate heritability and more than 60% - high heritability. Similarly, the range of genetic advance as per cent of mean (GAM) was grouped as: less than 10% low GAM, 10-20% - medium GAM and more than 20% - high GAM (Johnson *et al.* 1955) [10].

### Results and Discussion

Mean and genetic variability is the basic requirement for crop improvement as this provides wider scope for selection. Information on extent of genetic variability and role of important yield determining traits are paramount importance for their skilful engineering of new ideotype. The presence of variability in crop is important for genetic studies and

consequently used for improvement and selection. Thus, effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in material and the extent to which it is heritable. In present investigation, an attempt has been made to know the extent of genetic variability for quantitative characters in F<sub>2</sub> generations of groundnut. Six F<sub>2</sub>s along with their parents were evaluated and the results obtained on genetic variability for eight characters are presented and discussed in following paragraphs:

### Analysis of Variance

Mean squares due to various sources for eight characters are presented in Table 1. A perusal of the table indicated that mean squares due to genotypes were highly significant for all the characters suggesting presence of large amount of genetic variability in the material studied. The partitioning of genotypic variation into different sources like variation due to crosses, parents and parents *versus* crosses indicated that mean squares due to crosses were highly significant for all the characters depicting the existence of large amount of variation in the segregating F<sub>2</sub> generations. Likewise, variations due to parents were also significant for all the characters indicating that parents used in the crossing programme were diverse in nature. The significant mean squares due to parents *versus* crosses in all the characters indicated significant deviation of F<sub>2</sub> populations from the parents. According to Jayalakshmi *et al.* (2001) [6] the crosses showing higher mean would be relatively effective in identifying the superior segregants. Ramana *et al.* (2015) [20] also found highly significant differences among the F<sub>2</sub> populations.

### Mean performance of parents

Mean performance is the important criteria to select an individual. The perusal of data indicated the significant differences were observed among the parents for all the characters. The parental values indicated that parent R - 33- 1 was early for first flowering and early maturing. Among the parents, JL - 24, GJG - 22, ICGV - 05155, R - 33- 1, AK - 343, TPG - 41, JL - 501 and TG - 36 recorded significantly superiority for number of matured pods per plant and pod yield per plant, while the parent GJG - 22, R - 33- 1 and TPG - 41 possessed higher mean values for kernel yield per plant and shelling outturn. Harvest indices per cent were the highest in the parents like; GJG - 22, ICGV - 05155, AK - 343, JL - 501, TG - 36 and JL - 1085. Thus, GJG - 22 was considered as desirable parent for yield improvement and R - 33- 1 early for first flowering and early maturing (Table 2).

### Mean performance of crosses

The perusal of data indicated the significant differences among the generations of all the crosses. Among the F<sub>2</sub> populations, the mean days to appearance of first flowering to occur and days to maturity were numerically lower than its early parent in the Cross 4. For the Cross 5 and Cross 6, mean of matured pods per plant, kernel yield per plant and pod yield per plant were numerically higher than its better performing parents, while the mean biological yield per plant was numerically higher than its higher parent in the Cross 5 and mean harvest index per cent was numerically higher than its higher parents in the Cross 1 and Cross 5. Similar results for variation were earlier reported by Patil and Bhapkar (1987) [17] and Sing *et al.* (2005) [22]. The range of these F<sub>2</sub> generations exceeded the range of their respective parents either in negative or positive directions indicated transgressive segregation. Thus, the results suggested that

sufficient amount of variability was existed for all the traits in F<sub>2</sub> populations of all the crosses studied. These variations provide good scope for further improvement in pod yield per plant (Table 3).

### Variability Parameters

In the present study, the PCV and GCV exhibited wide range for all the traits. The values of GCV and PCV were moderate to high in magnitude in most of the crosses for all the character except in days to appearance of first flower and days to maturity indicating that there would be a scope for selecting better segregants in the population on the basis of their phenotypic performance. The estimates of genotypic coefficient of variances were quite close to the phenotypic coefficient of variances for the characters; days to appearance of first flower and days to maturity indicating least influence of environmental variation. This suggested that phenotypic variation can be used reliably to judge genetic variation. Our results are akin to those obtained by Chauhan and Shukla (1985) [3] and Padmaja *et al.* (2013) [14]. The genetic parameters studies for various trait in F<sub>2</sub> generations (Table 3) are narrated below.

### Days to appearance of first flowering

The estimates of GCV, PCV and GAM were observed low for days to appearance of first flowering in all the crosses. Such results were earlier obtained by Vekariya *et al.* (2011) [23] and Ramana *et al.* (2015) [20] for this character. The magnitude of heritability for this trait was medium in all the crosses. Thus, direct selection for this character is not effective.

### Days to Maturity

For days to maturity the low GAM along with moderate heritability and low GCV and PCV as observed in all the crosses indicated that direct selection for this character is not effective. Such result was earlier obtained by John *et al.* (2012) for this character.

### Number of matured pods per plant

The GCV and PCV for matured pods per plant revealed that the GCV estimates ranged from the value of 38.44% (Cross 2) to 44.83% (Cross 4) and PCV varied from 54.29% (Cross 2) to 65.91% (Cross 4). In fact, the values of GCV and PCV were high in magnitude in all the crosses, indicating that there would be a scope for selecting better segregants in the population on the basis of phenotypic performance, in this situation selection could be possible to increase number of matured pods per plant. Our findings are in accordance with the results of John *et al.* (2007) [8] and Patil *et al.* (2015) [18]. Magnitudes of heritability were moderate in all the crosses. The estimates of genetic advance expressed as percentage of mean ranged from 54.34% (Cross 5) to 64.43% (Cross 6), indicating high magnitude of the genetic advance in all the crosses. Raut *et al.* (2010) [21] earlier reported high genetic advance in groundnut for this character. High values of genetic advance are helpful in identifying the appropriate character for selection and enabling the breeder to apply selection pressure on said character. John *et al.* (2011) [7] reported moderate heritability and high GAM for matured pods per plant.

### Kernel yield per plant (g)

The GCV and PCV for kernel yield per plant revealed that the GCV estimates ranged from the value of 51.61% (Cross 6) to 58.71% (Cross 1) and PCV varied from 72.31% (Cross 2) to

88.64% (Cross 1). In fact, the values of GCV and PCV were high in most of all the crosses, indicating that there would be a scope for selecting better segregants in the population on the basis of phenotypic performance. Our findings are in accordance with the results of John *et al.* (2007) [8].

The heritability estimates for kernel yield per plant revealed that the heritability ranged from 43.87% (Cross 1) to 52.95% (Cross 2). Magnitudes of heritability were moderate. The estimates of genetic advance expressed as percent of mean varied from 72.83% (Cross 6) to 82.66% (Cross 5), indicating high magnitude of genetic advance in all the crosses. Moderate heritability along with high genetic advance and high GCV and PCV were observed in all the crosses indicated that the character was least influenced by the environmental effects and under the control of additive gene action, thereby suggesting that the phenotypes were the true representative of their genotypes for this trait and selection based on phenotypic value could be reliable. Similar results for kernel yield per plant were also earlier observed by Nandini *et al.* (2011) [13] and Gupta *et al.* (2015) [5].

### Shelling Outturn (%)

The estimates of GCV and PCV for shelling outturn revealed that the GCV values were observed to vary from 12.11% (Cross 4) to 14.89% (Cross 2). Magnitudinally, moderate GCV were recorded in all the crosses. The values of PCV varied from 17.85% (Cross 5) to 21.02% (Cross 2), which were moderate in magnitude for this character in all the crosses. Such results were earlier obtained by Kumar (2004) [11]. The heritability estimates for shelling outturn ranged from low value of 40.80% in the Cross 4 to high value of 54.52% in the Cross 5. Magnitudinally, moderate heritability were recorded in all the crosses. The estimates of genetic advance percentage of mean for this character varied from 15.93% (Cross 4) to 21.73% (Cross 2), which were moderate in magnitude for this character in all the crosses. Dewangan *et al.* (2015) [4] found similar results for this character.

### Pod yield per plant (g)

A perusal of the values of GCV and PCV for pod yield per plant revealed that the GCV were observed from the value of 39.62% (Cross 1) to 54.49% (Cross 2) and PCV varied from 50.32% (Cross 1) to 72.31% (Cross 2). In fact, the values of GCV and PCV were high in magnitude in most of all the crosses, indicating that there would be a scope for selecting better segregants in the population on the basis of phenotypic performance. Our results are akin to those reported earlier by Bhargavi *et al.* (2016) [2] and Padmaja *et al.* (2015) [15].

The heritability estimates for pod yield per plant revealed that heritability ranged from 49.68% in the Cross 5 to 63.04% in the Cross 6. The magnitudes of heritability were found moderate to high suggested that differences among the F<sub>2</sub> plants within the cross were mostly genetic. The estimates of genetic advance expressed as percentage of mean for pod yield per plant showed the value of 61.95% in the Cross 5 to 86.16% in the Cross 6, which were high in magnitude. Similar observations were also reported by Nandini *et al.* (2011) [13]. All F<sub>2</sub> populations showed wider range, which is indicating scope for improvement of this trait.

High heritability along with high genetic advance and high value of GCV and PCV for pod yield per plant in Cross 1 and Cross 6. Thus, it can be concluded that this Cross 1 and Cross 6 for pod yield per plant was mainly under the influence of additive gene action and improvement in this traits would be possible through selection in the subsequent generations to

isolate high yielding genotypes with desirable traits.

### Biological yield per plant (g)

The GCV and PCV for biological yield per plant revealed that the GCV estimates ranged from the value of 41.79% (Cross 4) to 53.84% (Cross 1) and PCV varied from 59.86% (Cross 4) to 66.35% (Cross 1). In fact, the values of GCV and PCV were high in all the crosses, indicating that there would be a scope for selecting better segregants in the population on the basis of phenotypic performance. Our findings are in accordance with the result of Ramana *et al.* (2015) [20].

The heritability estimates for biological yield per plant revealed that heritability ranged from 44.65% in the Cross 2 to 67.47% in the Cross 6. The magnitudes of heritability were found moderate to high suggested that differences among the F<sub>2</sub> plants within the cross were mostly genetic. The estimates of genetic advance expressed as percentage of mean for biological yield per plant showed the value of 58.48% in the Cross 2 to 90.00% in the Cross 1, which were high in magnitude. Similar observations were also reported by Bhargavi *et al.* (2016) [2]. All F<sub>2</sub> populations showed wider range, which is indicating scope for improvement of this trait.

### Harvest Index (%)

A perusal of the values of GCV and PCV for harvest index revealed that the GCV was observed from the value of 46.84% (Cross 4) to 58.81% (Cross 6) and PCV varied from 70.24% (Cross 1) to 81.64% (Cross 5). In fact, the values of GCV and PCV were high in magnitude in most of all the crosses, indicating that there would be a scope for selecting better segregants in the population on the basis of phenotypic performance. Our results are akin to those reported by Bhargavi *et al.* (2016) [2] and Ramana *et al.* (2015) [20].

The heritability estimates for harvest index revealed that heritability ranged from 42.75% in the Cross 4 to 52.66% in the Cross 2. The magnitudes of heritability were found moderate suggested that differences among the F<sub>2</sub> plants within the cross were mostly genetic. The estimates of genetic advance expressed as percentage of mean for harvest index showed the value of 69.16% in the Cross 1 to 87.27% in the Cross 6, which were high in magnitude. Similar observations were also reported by Bhargavi *et al.* (2016) [2]. All F<sub>2</sub> populations showed wider range which is indicating scope for improvement of this trait.

**Table 1:** Analysis of variance showing mean square for twelve characters in parents and F<sub>2</sub> generation of six groundnut crosses

Source	Replication	Genotypes	Parents	Crosses	Crosses vs Parents	Error
DF	2	17	11	5	1	34
Days to appearance of first flowering	0.19	77.17**	103.07**	31.62**	19.99**	0.27
Days to maturity	0.99	78.53**	84.78**	70.15**	51.64**	0.40
No. of matured pods/plant	3.09	15.57**	20.33**	6.84**	6.75**	1.61
Kernel yield/plant (g)	1.59	9.82**	11.48**	2.30**	29.21**	0.29
Shelling outturn (%)	0.52	130.95**	148.22**	5.95**	565.99**	2.95
Pod yield/plant (g)	5.41	32.88**	43.75**	5.75**	48.89**	0.80
Biological yield/plant (g)	122.81	453.21**	584.13**	34.80**	1105.13**	11.60
Harvest index (%)	3.08	37.78**	43.23**	30.37**	14.84**	1.40

\*, \*\* Significant at p=0.05 and 0.01 levels, respectively.

**Table 2:** Mean performance of parents for various traits in F<sub>2</sub> generation of groundnut

Parents	Days to appearance of first flower	Days to maturity	Number of matured pods per plant	Kernel yield per plant (g)	Shelling outturn (%)	Pod yield per plant (g)	Biological Yield per plant (g)	Harvest Index (%)
JL - 24	39.07	109.33	8.27*	6.71	54.09	12.44*	61.73*	20.53
GJG - 22	42.27	108.93	10.33*	9.29*	70.16*	13.24*	50.87*	26.02*
ICGV - 05155	45.40	101.73	8.33*	6.72	52.43	12.26*	49.02	25.33*
R - 33-1	30.40*	95.00*	9.40*	9.08*	73.94*	12.28*	59.60*	20.60
AK - 343	49.60	108.00	9.27*	6.98	56.98	12.24*	43.28	27.85*
TPG - 41	39.60	111.73	9.33*	8.27*	72.86*	11.35*	54.96*	20.60
JL - 501	38.50	109.87	8.53*	5.65	59.29	9.77*	35.74	27.43*
TG - 36	46.80	109.38	7.47*	4.11	57.62	7.04	25.68	26.60*
TG - 26	52.20	115.53	5.73	5.00	67.83	7.33	34.55	21.14
GG - 20	45.80	108.00	5.87	4.87	66.34	7.34	35.52	20.60
JL - 1085	40.17	107.67	5.60	4.96	67.49	7.20	28.06	25.65*
TPG - 41	39.27	112.73	5.80	4.76	63.79	7.48	35.96	20.48
SE	1.76	2.12	4.27	1.80	5.79	3.00	11.46	3.98

\*significant @ 5% level of probability

**Table 3:** Estimate of genetic parameters in F<sub>2</sub> population of groundnut

Character	Cross	Mean	GCV (%)	PCV (%)	H <sup>2</sup> (%)	GA as (%) of mean
Days to appearance of first flower	C 1	39.62	3.58	5.24	46.68	5.04
	C 2	36.27	4.89	6.38	58.75	7.72
	C 3	41.75	4.64	7.01	43.81	6.33
	C 4	43.52	5.31	7.61	48.69	7.63
	C 5	45.63	3.89	5.64	47.57	5.53
	C 6	40.37	4.94	7.21	46.94	6.97
Days to maturity	C 1	109.73	2.99	4.21	50.44	4.37
	C 2	101.89	3.91	5.21	56.32	6.04
	C 3	110.93	3.08	4.61	44.64	4.24
	C 4	109.03	2.82	3.81	54.78	4.30
	C 5	116.52	3.18	4.21	57.05	4.95
	C 6	111.48	3.68	5.03	53.53	5.55

Number of matured pods per plant	C 1	6.17	43.28	62.35	48.18	61.89
	C 2	7.39	38.44	54.29	50.13	56.07
	C 3	7.61	41.38	60.94	46.11	57.88
	C 4	7.40	44.83	65.91	46.26	62.81
	C 5	9.64	39.51	59.18	44.57	54.34
	C 6	10.11	42.68	58.24	53.70	64.43
Kernel yield per plant (g)	C 1	5.46	58.71	88.64	43.87	80.11
	C 2	4.04	52.62	72.31	52.95	78.88
	C 3	4.13	57.39	82.11	48.85	82.63
	C 4	5.85	53.34	79.65	44.85	73.58
	C 5	6.13	55.92	77.93	51.49	82.66
	C 6	5.60	51.61	75.34	46.93	72.83
Shelling outturn (%)	C 1	48.90	3.49	7.60	21.09	3.30
	C 2	49.26	3.46	6.68	24.57	3.53
	C 3	49.06	2.98	5.84	26.04	3.13
	C 4	47.84	2.32	5.11	20.61	2.17
	C 5	49.37	4.31	8.37	26.52	4.57
	C 6	49.80	4.18	8.49	24.22	4.24
Pod yield per plant (g)	C 1	9.50	39.62	50.32	61.99	64.26
	C 2	7.28	54.49	72.31	56.79	84.59
	C 3	8.10	42.30	59.24	50.99	62.22
	C 4	8.95	50.94	71.68	50.50	74.57
	C 5	10.84	42.67	60.54	49.68	61.95
	C 6	7.86	52.68	66.35	63.04	86.16
Biological Yield per plant (g)	C 1	35.22	53.84	66.35	65.85	90.00
	C 2	37.21	42.48	63.57	44.65	58.48
	C 3	31.79	51.6	64.32	64.36	85.27
	C 4	33.77	41.79	59.86	48.74	60.10
	C 5	41.02	52.85	65.38	65.34	88.01
	C 6	33.74	52.67	64.12	67.47	89.13
Harvest Index (%)	C 1	26.88	48.56	70.24	47.80	69.16
	C 2	20.15	57.62	79.40	52.66	86.14
	C 3	26.41	51.64	76.94	45.05	71.40
	C 4	26.50	46.84	71.64	42.75	63.09
	C 5	26.06	54.09	81.64	43.90	73.82
	C 6	22.23	58.81	81.61	51.89	87.27

Cross 1 = JL - 24 x GJG - 22

Cross 2 = ICGV - 05155 x R - 33-1

Cross 3 = AK - 343 x TPG - 41

Cross 4 = JL - 501 x TG - 36

Cross 5 = TG - 26 x GG - 20

Cross 6 = JL - 1085 x TPG - 41

## References

- Allard RW. Principles of Plant Breeding. John Willey and Sons, New York, 1960.
- Bhargavi G, Satyanarayana Rao VR, Narasimha Rao KL. Genetic variability, heritability and genetic advance of yield and related traits of Spanish bunch groundnut (*Arachis hypogaea* L.). Agric. Sci. Digest. 2016; 36(1):60-62.
- Chauhan RM, Shukla PT. Variability, heritability and genetic advance in bunch and spreading types of groundnut. Indian J agric. Sci. 1985; 55:71-74.
- Dewangan H, Kumar NJ, Gabriel M, Kumar PR. Study on genetic variability in groundnut (*Arachis hypogaea* L.) germplasm. Inter. J Agril. Sci. Res. 2015; 5(1):19-22.
- Gupta RP, Vachhani JH, Kachhadia VH, Vaddoria MA, Reddy P. Genetic variability and heritability studies in Virginia groundnut (*Arachis hypogaea* L.). Electron. J. Plant Breed. 2015; 6(1):253-256.
- Jayalakshmi V, Reddy PV, Reddy G, Haritha S. Heritability and genetic advance in segregating populations of groundnut (*Arachis hypogaea* L.). Legume Res. 2001; 24:141-147.
- John K, Raghava PR, Hariprasad PR, Sudhakar P, Eswar NP. Genetic variability for morphological, physiological, yield and yield traits in F<sub>2</sub> populations of groundnut (*Arachis hypogaea* L.). Int. J App. Bio. Pharm. Tech. 2011; 2(4):463-469.
- John K, Vasanthi RP, Venkateswarlu O. Variability and correlation studies for pod yield and its attributes in F<sub>2</sub> generations of six Virginia x Spanish crosses of groundnut (*Arachis hypogaea* L.). Legume Res. 2007; 30:292-296.
- John K, Vasanthi RP, Venkateswarlu O. Estimates of genetic parameters and character association in F<sub>2</sub> segregating populations of Spanish x Virginia crosses of groundnut (*Arachis hypogaea* L.). Legume Res. 2012; 31(4):235-242.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic variability and environmental variability in soybeans. Agron. J, 1955; 47:314-318.
- Kumar PR, Rajamani S. Genetic variability and heritability in groundnut (*Arachis hypogaea* L.). Indian J agric. Res. 2004; 16:61-64.
- Mahmud I, Kramer HH. Segregation for yield, height and maturity following a soybean cross. Agron. J, 1951; 43:605-609.
- Nandini C, Savithamma DL, Nareshbabu N. Genetic variability analysis for surrogate traits of water use efficiency in F<sub>8</sub> recombinant inbred lines of the cross NRCG12568 x NRCG12326 in groundnut (*Arachis hypogaea* L.). Electron. J Plant Breed. 2011; 2(4):555-558.
- Padmaja D, Eswari KB, Brahmeswara Rao MV, Madhusudhan RS. Genetic variability parameters for

- yield components and late leaf spot tolerance in BC<sub>1</sub>F<sub>2</sub> population of groundnut (*Arachis hypogaea* L.). Int. J. Inn. Res. Dev. 2013; 2(8):348-354.
15. Padmaja D, Eswari KB, Brahmeswara Rao MV, Shiva PG. Genetic variability studies in F<sub>2</sub> populations of groundnut (*Arachis hypogaea* L.). Helix. 2015a; 2:668-672.
  16. Panse VG, Sukhatme PV. Statistical Methods for Agricultural Workers (Second edition), ICAR, New Delhi. Oxford & IBH Publishing Co. Pvt. Ltd. New Delhi, 1985, 244-257.
  17. Patil PS, Bhapkar DG. Estimates of genotypic and phenotypic variability in groundnut. J Maharashtra agric. Univ. 1987; 12:319-321.
  18. Patil S, Shivanna S, Irappa BM, Shweta HM. Genetic variability and character association studies for yield and yield attributing components in groundnut (*Arachis hypogaea* L.). Int. J Rec. Sci. Res. 2015; 6(6):4568-4570.
  19. Prabhu R, Divyadharsini R, Manivannan N. Genetic variability analysis in F<sub>3</sub> populations of groundnut (*Arachis hypogaea* L.). Inter. J Agri. Envi. Biotech. 2015a; 8(4):819-825.
  20. Ramana EV, Vasanthi RP, Reddy KH, Bhaskara RBV, Ravindra RB. Studies on genetic variability for yield, yield components and resistance to kalahasti malady in groundnut (*Arachis hypogaea* L.). Intn. J App. Bio. Pharma. Tech. 2015; 6(1):72-74.
  21. Raut RD, Dhaduk LK, Vachhani JH. Studies on genetic variability and direct selections for important traits in segregating materials of groundnut (*Arachis hypogaea* L.). Internat. J agri. Sci. 2010; 6(1):234-237.
  22. Sing RV, Khedar OP, Chaudhary SPS, Ved Prakash. Genetic variability, correlation and path coefficient study in groundnut under drought condition. National symposium on stress management in arid and semi-arid ecosystem for productivity enhancement in agriculture on sustainable basis (Abstact), held at SDAU, Sardae Krushinagar (Gujarat) on 11-13<sup>th</sup> April-2005, 2005.
  23. Vekariya HB, Khanpara MD, Vachhani JH, Kachhadia VH, Madariya RB, Jivani LL. Variability and heritability studies in bunch groundnut (*Arachis hypogaea* L.). Internat. J agri. Sci. 2011; 7(1):32-34.