Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2017; SP1: 652-654

Ishu Kumar Khute
Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

S S. Rao
Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Nandan Mehta
Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Shrikant Sawargaonkar
Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Correspondence
Ishu Kumar Khute
Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Estimation of variability parameters for yield and its attributing traits in groundnut (*Arachis hyapogaea* L.)

Ishu Kumar Khute, S S. Rao, Nandan Mehta and Shrikant Sawargaonkar

Abstract
The present investigation was conducted to study the variability parameters in groundnut by using 21 genotypes including 6 parents. Analysis of variance revealed significant differences among the genotypes for all the characters studied. High heritability estimates were observed for days to 50 % flowering followed by 100 kernel weight, plant height at harvest cm, number of secondary branches per plant and all the traits. The heritability estimates for all the characters were high and none of the characters show moderate or low. Genetic advance as percentage of mean was recorded the highest for pod size followed by number of secondary branches per plant and seed weight per plant. The trend of high heritability coupled with high genetic advance and 100 kernel weight and harvest index showed high heritability with moderate genetic advance. The remaining two characters days to maturity and shelling percentage showed high heritability with low genetic advance.

Keywords: Genetic variability, heritability, genetic advance, groundnut.

Introduction

Groundnut (*Arachis hypogaea* L), chromosome no. 2n=40 is an important monoecious annual legume in the world mainly grown for oil seed, food and animal feed (Pande *et al*., 2003; Upadhyaya *et al*., 2006) [11]. Groundnut is an important food crop of the world. All parts of the peanut plant can be easily utilized. Besides income for farmers, groundnut provides an inexpensive source of high quality dietary protein and edible oil. The vast food preparations incorporating groundnut to improve the protein level has helped in no small way in reducing malnutrition in the developing countries. The special taste and flavour of foods containing groundnut is very important in the acceptance of these food preparations. It is estimated that the shell represents about 25% of the dry weight of unshelled peanut, and the kernel comprises 75%. Groundnut seeds contain high quality edible oil (50%), easily digestible protein (25%), carbohydrates (20%), vitamin E, niacin, folacin, calcium, phosphorus, magnesium, zinc, iron, riboflavin, thiamine and potassium (FAO, 2004) [1]. Worthington and Hammons (1971) [15] reported that the seed has several uses as whole seed or processed to make peanut butter, oil, soups, stews and other products. Nearly two thirds of all groundnuts are crushed for oil (Bunting *et al*., 1985) [4].

The major groundnut producing countries in the world are India, China, Nigeria, Senegal, Sudan, Burma and the United States of America. In India the total area under groundnut cultivation is 4.77 million hectare and production 7.40 million tones with productivity 1552 kg per hectare. Anonymous (2014-15) [3]. Gujarat leading position in production 3.0 million tones with area 1.4 million hectare and productivity 2154 kg per hectare. In Chhattisgarh the important districts for area and productions of groundnut, Raigarh 7,690 tones with area 6,080 thousand hectare and Surajpur 4,490 tones with 3,570 thousand hectare, Jashpur 3,890 tones with 2,670 thousand hectare, Raipur 1,200 tones with 910 thousand hectare, Janjgir860 tones with 700 thousand hectare, Mahasamund 760 tones with 590 thousand hectare and others. (Agricultural Department, Govt. of C.G. 2011) [2].

It is the third most important food crop and the fourth most important oilseed crop of the world. Groundnut seeds contain 40-50% fat, 20-50% protein and 10-20% carbohydrate. Groundnut seeds are a nutritional source of vitamin E, niacin, calcium, phosphorus, magnesium, zinc, iron, riboflavin, thiamin and potassium. Cultivated groundnut was originated from South America (Wiess, 2000) [16]. It is one of the most popular and universal crops cultivated in more than 100 countries in six continents (Nwokoto, 1996) [10].

The success of any breeding programme depends on the extent of variability creation. The selection, creation and maintenance of variable genotypes of a crop are the ultimate aims of any plant breeder. The presence of variability is thus prerequisite to undergo selection procedure for identification of diverse parents to be used in hybridization programme. Among the three kinds of variability i.e. Phenotypic, genotypic and environmental variability,

genotypic variability is of prime importance as directly contribute towards the improvement of crop plant.

For improvement of any crop, the breeder has to select superior individuals from their phenotypic expression. Selection based on the phenotypic expression is sometimes misleading, as the development of the character is the result of interaction of the heritable and non-heritable factors. It highlights the imperative need for partitioning the overall variability into its heritable and non-heritable components. Thus the components of variation such as genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were computed. The PCV was higher than the GCV for the characters under study.

The genotypic coefficient of variation (GCV) helps to measure the range of genetic variability in character and provides measure to compare the genetic variability present in various quantitative characters. Burton (1952) suggested that genetic coefficients of variation along with heritability gives clear picture of amount of advance to be expected from selection. The character which exhibited high heritability indicates the presence of additive gene action and such character could be fixed by resorting to selection (Panse, 1957) [12] according to Johnson *et al*. (1955a) [5], heritability estimates could not be alone guideline for improvement work, since high heritability does not mean high expected genetic gain. Therefore, the heritability estimates appear to be more meaningful when accompanied by estimates of genetic advance. Thus the data of present investigation subjected to heritability in broad sense and genetic advance for all the characters under study. Estimates of heritability grouped into high (above 75 %), moderate (above 50 % but below 75 %) and low (below 50 %) as per Lush (1940). In the same way the estimates of genetic advance as percentage of mean grouped into high (above 20 %), moderate (above 10 % but below 20 %) and low (below 10 %) as suggested by Johnson *et al.* (1955a) [5]. The extent of genetic variability present in the material was analyzed with the help of statistical parameters namely, analysis of variance, range, phenotypic and genotypic coefficients of variation, heritability and genetic advance

Materials and methods

In crossing block six varieties Jyoti, Girnar-3, Kadiri-6, Kadiri-3, ICGV 91114 and JL-501 were sown during *Kharif* 2015 at Research Farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.). Selected six parents were crossed to generate a set of hybrids in a half diallel manner as proposed by Kempthorne (1957) [6]. Three lines of each variety are sown in spacing of 45 cm row to row and 25 cm plant to plant.

At the onset of flowering, for 1-2 days, all the flowers on the female parents should be removed to help stimulate profuse flowering. Removal of anthers from buds flowers before their dehiscence to avoid self-pollination. The leaf is pulled down gently to expose these buds. The bud is held gently between the thumb and index finger of the left hand. Using forceps held in the right hand, the single sepal opposite the standard petal is pulled down. The fused sepal is also folded down and held back. The standard is then gently and carefully opened with forceps and is held back by the thumb and index finger. The wing petals are pulled down locking them with the standard. The keel is pulled outwards by its ridge with forceps to expose the anthers. All the anthers are removed with the filaments from their bases (Nigam *et al*., 1990) [9].

Total 15 hybrids and their 6 parents were planted in Randomized Complete Block Design (RCBD) with three replications during *Kharif* 2016. Each entry was raised in single row of 3 m length with a row to row spacing 45 cm apart with 15-20 cm interplant distances.

Result and discussion

The analysis of variance indicated significant differences due to genotypes for all the characters (Table 1). Highly significant difference & were observed / exists among genotypes for all the characters under study indicating the existence of considerable amount of genetic variability. A wide range was observed for most of the characters, the highest being in days to maturity followed by shelling percentage and 100 kernel weight whereas, low range was observed for pod size cm and number of primary branches per plant. The range of remaining characters was moderate. The heritability estimates for all the characters were high and none of the characters show moderate or low. Genetic advance as percentage of mean was recorded the highest for pod size followed by number of secondary branches per plant and seed weight per plant. The characters days to 50 % flowering, plant height, number of primary branches per plant, number of secondary branches per plant, number of kernel per plant, pod size, pod yield per plant and seed weight per plant followed the trend of high heritability coupled with high genetic advance and 100 kernel weight and harvest index showed high heritability with moderate genetic advance. The remaining two characters days to maturity and shelling percentage showed high heritability with low genetic advance. The heritability (broad sense) estimates ranged between 83.58 for shelling percentage and 99.03 for days to 50% flowering and days to maturity (Table 2). The heritability estimates for all the characters were high. High heritability estimates were observed for days to 50 % flowering followed by 100 kernel weight g, plant height at harvest cm, number of secondary branches per plant and all the traits. Genetic advance as percentage of mean was recorded the highest pod size cm followed by number of secondary branches per plant, seed weight per plant and number of primary branches per plant. All the other characters showed high heritability with low genetic advance. On the contrary, high heritability estimates for days to 50 % flowering, followed by 100 kernel weight plant height at harvest, number of secondary branches per plant were associated with low value of genetic advance and those of genotypic and phenotypic coefficients of variation. Improvement for such characters is not easy and efforts should be made for increasing genetic variability in such cases. At the present investigation moderate heritability estimates for days to 50 % flowering, 100 kernel weight g, plant height at harvest cm, number of secondary branches per plant were associated with low value of genetic advance for most of the other traits. Improvement for such characters is not easy and efforts should be made for increasing genetic variability in such cases.

High heritability estimates coupled with low genetic advance observed for days to 50 % flowering, days to maturity and most of the other traits indicated contribution of dominance or epistatic variances in these characters. These findings are also reported by Patil *et al.*, (2014) [13] for days to 50% flowering, plant height, 100- pods weight, 100-kernels weight, shelling per cent and harvest index. Vekariya *et al*. (2011) [17], John *et al*. (2013), Mekonnen *et al*. (2014) [8] reported high heritability coupled with high genetic advance.

Table 1: ANOVA for pod yield and component characters in groundnut

S.N.	Name of character	Mean square values F_1+parents		
		Replications df=2	Genotypes df=20	Error df =40
1	Days to 50% flowering	38.111*	67.782**	0.227
2	Days to maturity	55.111**	204.351**	0.661
3	Plant height (cm)	57.925*	66.288**	0.561
4	Number of primary branches per plant	3.683	1.414*	0.057
5	Number of secondary branches per plant	24.105*	41.365*	0.591
7	Number of kernel per plant	95.085*	46.710**	1.348
8	100 kernel weight (gm)	49.374**	120.818**	0.498
9	Pod size (cm)	0.375*	0.250**	0.006
10	Pod yield per plant (gm)	14.755	15.379*	0.301
11	Harvest index (%)	82.917*	90.656**	2.252
12	Seed weight per plant	17.127**	9.528**	0.253
13	Shelling percentage (%)	296.327	127.112**	7.81

*, ** significant at 5 and 1 per cent levels, respectively.

Table 2: Genetic parameters of variation for pod yield and its components in groundnut

S.N.	Name of the character	mean	range		PCV (%)	GCV (%)	h^2bs	GA	GA % mean
			Min.	Max.					
1	Days to 50% flowering	31.12	23.67	38.22	8.54	8.50	99.03	9.73	31.27
2	Days to maturity	112.12	98.33	130.67	7.81	7.78	99.03	5.69	5.07
3	Plant height (cm)	28.59	22.20	36.00	8.87	8.75	97.51	5.99	20.95
4	Number of primary branches per plant	4.29	2.97	5.27	3.34	3.20	91.67	3.46	80.65
5	Number of secondary branches per plant	6.94	2.98	14.85	14.29	13.99	96.45	7.51	108.21
7	Number of kernel per plant	15.40	9.67	23.00	10.34	9.90	91.80	6.09	39.54
8	100 kernel weight (gm)	40.93	26.91	55.12	9.96	9.89	98.74	6.43	15.70
9	Pod size (cm)	2.03	1.27	2.50	2.07	2.0	93.10	2.76	135.96
10	Pod yield per plant (gm)	8.68	5.07	14.54	7.83	7.60	94.30	5.44	62.67
11	Harvest index (%)	30.40	23.26	41.56	10.05	9.85	92.91	6.07	19.97
12	Seed weight per plant (gm)	5.83	3.19	9.78	7.56	7.28	92.51	5.24	89.88
13	Shelling percentage (%)	66.05	55.06	77.74	8.48	7.76	83.58	5.01	7.59

References

1. Anonymous. Food and Agricultural Organisation, 2004.
2. Anonymous. Agricultural Department, govt. of C.G, 2011
3. Anonymous. Ministry of Agriculture and Farmers Welfare, Govt. of India, 2014-15.
4. Bunting AH, Gibbons RW, Wynne JC. Groundnut (*Arachis hypogaea* L.), 1985, 747-800.
5. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal 1955; 47:314-318.
6. Kempthorne O. An introduction to Genetic Statistics. John Wiley and Sons Inc., New York, 1957.
7. Lush JL. Heritability of quantitative characters in farm animals. Proceeding 8th congress Genetics Herediates (suppl.) 1949, 356-375.
8. Mekonnen TW, Wakjira A, Genet T. Correlation and path coefficient analysis among yield component traits of Ethiopian mustard (Brassica carinata a. Brun) at Adet, Northwestern, Ethiopian Journal of Plant Science. 2014; 2(2):89-96.
9. Nigam SN, Vasudeva Rao MJ, Gibbons RW. Artificial Hybridization in Groundnut. Information Bulletin no. 29.Patancheru, A.P. 502 324, India: International Crops Research Institute for the Semi-Arid Tropics, 1990.
10. Nwokoto E. Peanut (*Arachis hypogaea* L.). In: Food and Fee from Legumes and Oilseeds. E. Nwokolo and J. Smartt, Eds, 1996, 49-63.
11. Pande S, Bandyopadhyay R, Blümmel M, Rao NJ, Thomas D, Navi SS. Disease management factors influencing yield and quality of sorghum and groundnut crop residues. *Field Crops Res*. 2003; 84(1-2):89-103.
12. Panse AV. Genetics of quantitative characters in relation to plant breeding. Indian Journal of Genetics. 1957; 17:318-328.
13. Patil S, Shivanna S, Irappa BM, Shweta. Genetic variability and character association studies for yield and yield attributing components in groundnut (*Arachis hypogaea L.).* International Journal of Recent Scientific Research Research. 2014; 6(6):4568-4570.
14. Upadhyaya HD, Reddy LJ, Gowda CLL, Singh S. Identification of diverse groundnut germplasm: Sources of early maturity in a core collection. Field Crops Res. 2006; 97(2-3):261-271.
15. Worthington RE, Hammons RO. Genotypic variation in fatty acid composition and stability of *Arachis hypogaea L*. oil. Oleagineaux. 1971; 26:695-700.
16. Weiss EA. Oilseed Crops. London: Blackwell Science, 2000.
17. Vekariya HB, Khanpara MD, Vachhani JH, Kachhadia VH, Madariya RB, Jivani LL. Variability and heritability studies in bunch groundnut (*Arachis hypogaea* L.).International Journal of Agricultural Sciences. 2011; 7:32-34.