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Research Note

Induced genetic variability and correlation studies for yield and its component traits in Groundnut (*Arachis hypogaea* L.)

Channayya P. Hiremath* , H. L. Nadaf and Keerthi,C.M

Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad (Karnataka)
Email: chiremath18@gmail.com

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Abstract:
Groundnut is one of the principal economic oilseed crops of the world, which has been exposed extensively to mutagenic treatments for induction of genetic variability. In the present experiment, estimates of genetic variability, heritability and genetic advance were assessed for 12 different quantitative traits in the mutants derived from two Spanish Bunch groundnut cultivars, *viz.* TPG-41 and GPBD-4 with chemical and physical mutagenic agents. Wide genetic variations were observed for most of the quantitative traits studied as evidenced by higher mean, range, PCV and GCV values. Further genetic improvement through selection for yield improvement should rely on number of primary branches per plant, 100-kernel weight, SMK% and shelling per cent as these mutants recorded higher genetic variability, heritability and genetic advance for these quantitative traits. Pod yield was positively and significantly associated with number of primary branches, pod weight per plant, 100-kernel weight, sound matured per cent kernel and oil yield. These results clearly indicate that idirect selection for yield in groundnut is possible through simultaneous improvement of these yield components.

Key wards: Groundnut, variability, chemical and physical mutagen

Groundnut (*Arachis hypogaea* L.) is an important oilseed crop and grain legume grown worldwide. The groundnut seed has dual advantage of being important as a source of edible oil as well as protein. However, it is self pollinating and possesses limited variability. Despite its long history of cultivation, broad sub-specific variability and wide geographic distribution of the cultivated groundnut, defects in its genetic composition with respect to requirement of man are unwide spread and for many of these remedial resources are known to exist among its varietal forms. The exploitation of genetic resources from wild species is extremely difficult because of ploidy differences between cultivated tetraploid and diploid wild species coupled with compatibility barriers except with *Arachis* section. Although the conventional techniques have greatly helped to develop desirable types, induced mutagenesis might prove a potential tool to diversify the genetic variability, which could be valuable for selection of desirable types. Genetic variations induced by mutation represent a more efficient source of genetic variability than gene pools conserved by nature (Brock, 1977). Therefore, an attempt was made to create genetic variation for various characters by means of induced mutagenesis.

The experimental material for the present study comprised 180 mutant lines in M_5 generation of two improved Spanish bunch cultivars of groundnut, TPG-41 (confectionary, large seeded type) and GPBD-4 (resistant to foliar diseases) including ten checks were sown during *kharif* 2008 at Main Agricultural Research Station, Dharwad in 10 x 10 lattice design with two replications.

The entries were sown in three rows of 2 m length with a spacing of 30 cm between rows and 10 cm between plants. Data were recorded on different quantitative traits (Table 1 and 2) by randomly selecting five competitive plants/replication and data on the remaining plants were recorded on plot basis. Range, mean, genotypic and phenotypic coefficient of variation were computed using standard statistical methods (Burton and DeVane, 1953) whereas, heritability in broad sense and genetic advance was estimated by following the method suggested by Johnson *et al.*, (1955) and Allard, (1960) respectively and the correlation coefficients were calculated to determine the degree of association of character, with yield. Phenotypic correlation coefficients were estimated according to the formula of Al-Jibouri *et al.* (1958).

Lack of genetic variability even between the botanical groups of groundnut as evidenced by molecular analysis (Halward *et al.*, 1990) limits further improvement. An induced mutation significantly plays a vital role to improve few easily recognizable characters and widen the genetic base of the crop. Mutagenic treatment resulted in increased genetic variation for yield and its components characters (Gregory, 1955).

The effectiveness of the selection depends on the extent of genetic variability present in the population for different characters. Genetic parameters such as genotypic coefficient of variability, heritability and genetic advance serve as useful tools to quantify the genetic variability in the populations.

The estimation of genotypic and phenotypic coefficient of variation indicates the amount of genetic and non-genetic variation present for different desirable traits while heritability gives an insight into the proportion of the variation which is inherent. However, heritability estimate itself is not an indication of the amount of genetic progress that would result from selecting the best individual. Thus the study of heritability in conjunction with genetic advance was emphasized in predicting the resultant effect for selecting the best individuals (Johanson *et al.*, 1955).

In the present study, an attempt has been made to partition the total variability into genetic and non-genetic and their magnitude for different groups which has been compared by computing genotypic and phenotypic coefficient of variation. Other genetic parameters *viz.,* heritability in broad sense and genetic advance were also calculated and the results obtained are discussed below.

The range for a particular trait can provide a preliminary idea about the variability. However, the extent of variability as measured by PCV and GCV gives information regarding the relative amount of heritable variation in different populations. The phenotypic and genotypic coefficient of variation showed wide variation for most of the characters in both the mutant populations. Phenotypic coefficient of variation (PCV) was marginally higher than the genotypic coefficient of variation (GCV) for all the characters studied in the two mutant groups.

A relative comparison of the magnitude of genotypic and phenotypic coefficients of variation for different traits revealed that induced genotypic and phenotypic variability for pod weight per plant was higher in both the two sets of mutants, indicating that there is greater scope for improvement of pod weight per plant in desirable direction. These results are in conformity with the findings of Mensah and Obadoni (2007) for pod weight per plant.

In the present investigation, plant height had moderate genotypic and phenotypic variability in both the mutant groups *viz.,* GPBD-4 and TPG-41. These results are in accordance with the results of Ganesan and Sudhakar (1995). Both the mutant groups had moderate genotypic and phenotypic variability for number of primary branches per plant, 100-kernel weight, oil yield, pod yield and kernel yield for which there would be only moderate response to selection. Similar results were earlier reported by Venkataramana *et al.* (2001) for kernel yield and by Purnima *et al*. (2008) in soybean for 100- kernel weight.

The quality traits like shelling per cent, sound matured kernel, protein content and oil content recorded low genotypic and phenotypic variability indicating the narrow range of variability induced for these characters and restricting the scope of selection. Such results are in agreement with the earlier reports of Deshmukh *et al.* (1986) for sound matured kernel, Venkataramana (2001) for shelling percentage, and Kaveri *et al.* (2008) for oil content and protein content.

Heritability in broad sense is the ratio of genotypic variance to the phenotypic variance which is heritable. High heritability in broad sense does not always mean better response to selection, since it is also inclusive of non-additive genetic factors. Thus, estimate of genetic advance further narrow down the response of selection.

In the present study, high heritability estimates were recorded for plant height, number of primary branches, pod weight per plant, 100-kernel weight, shelling per cent, sound matured kernel per cent, protein content, oil content, oil yield, pod yield and kernel yield in both the mutant groups studied. A high genetic gain along with the high heritability would suggest suitable conditions for making effective selection. The estimated genetic advance was high for the traits like plant height, pod weight per plant, 100-kernel weight, oil yield, pod yield and kernel yield in both the mutant groups studied as also reported by the earlier workers (Manoharan *et al,.* 1990, Abhay Darshora *et al.* , 2002, Venkataramana *et al.* ,2001).

The high genetic advance coupled with high heritability estimates for these traits suggested the importance of additive gene action and improvement of these characters could be made possible by simple phenotypic selection. Even though, shelling per cent, sound matured kernel per cent and oil content recorded high heritability in both mutant groups, had low genetic advance which suggested that improvement of these characters is not possible by simple phenotypic selection. These findings confirm the results of Uddin *et al.* (1995) for shelling per cent and Kavera (2009) for sound matured kernel per cent and oil content.

The other characters like number of primary branches per plant, protein content and kernel uniformity recorded high heritability in both the mutant groups with moderate expected genetic advance indicating the substantial contribution of additive genetic variance in the expression of these characters. These findings were in agreement with the results of Kavera (2009).

The present study clearly indicated that the identified superior mutants for each of traits including pod, kernel and oil yield and quality traits can be further evaluated on large scale to confirm their superiority over different environments for their direct adoption or they can be used in breeding programmes for genetic improvement of respective traits.

Yield is a complex quantitative character governed by large number of genes and is greatly affected by environment. Hence, the selection of superior genotypes based on yield will not give a fruitful result. Association of yield components and yield thus, assumed special importance as the basis for selecting desired strains. Genetic correlation between different characters often arises due to its tight linkage or pleiotropy.

The results on phenotypic and genotypic correlation between yield and its components in the present investigation are presented in Table 3 and 4. The correlation analysis revealed that the genotypic correlation coefficient were higher than phenotypic values indicating that strong intrinsic association are reduced at phenotypic level due to environmental effects. Higher genotypic correlation coefficients compared to phenotypic correlation coefficients have been reported by Nadaf and Habib (1989).

Pod yield was positively and significantly associated with number of primary branches, pod weight per plant, 100-kernel weight, sound matured per cent kernel and oil yield. These results clearly indicate that indirect selection for yield in groundnut can be based on these traits. The results are in consonance with those of Rosemary Francis and Ramalingam (1997) for number of primary branches per plant, Lakshmidevamma *et al.* (2004) for 100-kernel weight and Vasanthi *et al.* (1998) for sound matured kernel per cent.

Plant height was significantly and negatively associated with 100-kerenel weight. Negative association between 100-kernel weight and plant height was reported by Lambana *et al.* (1980). Days to 50 per cent flowering positively and significantly associated with days to maturity indicating that if the number of days taken for 50 per cent flowering is less, it indicates the earliness in maturity.

Number of primary branches per plant is the important component which showed negative association with 100-kernel weight and shelling percentage. It indicate that as the number of primary branches increased there was significant reduction in 100-kernel weight, may be attributed to uneven distribution of available sink to the more number of pods produced. This is in agreement with the findings of Lambana *et al.* (1980), who observed negative association between numbers of primary branches and100-kernel weight.

It was evident that with increase in 100-kernel weight and sound matured kernel percentage, there was significant increase in total kernel yield as indicated by the positive significant association of both 100-kernel weight and sound matured kernel with kernel yield. Positive correlation between kernel yields with 100-kernel weight was reported by Venkataramana (2001). Hundred kernel weight was positively associated with shelling percentage and sound matured kernel per cent. There was highly significant association between shelling per cent and sound matured kernel per cent and oil yield. Similar findings were reported by Ramnathan and Raman (1968).

The correlation studies indicated that pod weight per plant, number of primary branches per plant, 100-kernel weight, shelling per cent and plant height indicate greater weightage during selection for pod yield improvement in groundnut.

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Table 1. Mean, range and genetic parameters for different quantitative traits in mutants of cv. GPBD-4

Traits	Mean	Range	GCV (%)	PCV (%)	$h^2_{(BS)}$ (%)	Genetic advance	Genetic advance as per cent mean
Plant height (cm)	25.61	15.93 - 39.36	18.80	19.56	92.39	9.89	37.24
Number of primary branches per plant	6.37	4.80 - 8.05	10.19	12.91	62.33	1.06	16.57
Pod weight/plant(g)	29.19	15.43 -43.93	21.54	23.03	87.52	12.12	41.52
100-Kernel Weight (g)	40.10	24.29 - 52.20	12.04	12.53	92.43	9.57	23.85
Shelling (%)	67.19	60.60 -73.66	4.70	5.04	86.94	6.06	9.02
Sound Matured Kernel (%)	87.79	80.00 -92.00	2.66	3.08	74.52	4.15	4.73
Protein content (%)	31.98	25.72 - 34.47	7.86	8.26	90.43	4.92	15.39
Oil content (%)	47.69	46.15 - 49.80	1.82	2.23	66.78	1.46	3.07
Oil yield (kg/ha)	806.12	429.105-1124.36	16.65	19.01	76.74	24.22	30.04
Kernel uniformity (%)	72.35	57.79 - 81.00	7.79	8.20	90.22	11.02	15.24
Pod yield (q/ha)	25.23	14.27- 33.39	15.95	18.83	71.76	6.41	27.83
Kernel yield (q/ha)	16.95	8.815 -23.77	16.50	18.80	77.08	5.06	29.84

Table 2. Mean, range and genetic parameters for different quantitative traits in mutants of cv. TPG-41

Traits	Mean	Range	GCV (%)	PCV (%)	$h^2_{(BS)}$ (%)	Genetic advance	Genetic advance as per cent mean
Plant height (cm)	22.30	17.14 - 27.34	13.11	14.90	77.40	5.30	23.76
Number of primary branches per plant	5.59	3.89 - 7.04	10.48	13.56	60.01	0.93	16.69
Pod weight /plant (g)	28.58	16.89 - 38.25	15.65	17.19	82.82	8.38	29.33
100-Kernel Weight (g)	57.61	45.67 - 75.61	15.55	16.20	92.18	17.72	30.76
Shelling (%)	64.81	53.97 - 71.32	5.73	6.32	82.30	6.95	10.72
Sound matured kernel (%)	86.55	80.00 -92.00	3.26	3.52	85.79	5.38	6.22
Protein content (%)	25.66	20.88 – 28.72	9.24	9.83	88.36	4.59	17.88
Oil content (%)	46.70	43.42 - 48.43	2.43	2.72	80.10	2.09	4.48
Oil yield (kg/ha)	683.31	453.23 -1051.84	18.95	20.91	82.11	24.12	35.36
Kernel uniformity (%)	60.15	38.00 - 79.00	14.14	14.94	89.62	16.59	27.58
Pod yield(q/ha)	22.59	15.62 – 31.05	16.06	18.14	78.45	6.75	29.31
Kernel yield (q/ha)	14.67	9.85-21.37	18.96	20.88	82.48	5.20	35.47

Table 3. Phenotypic and genotypic correlations among different quantitative traits in GPBD-4 mutants

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches	Pod weight/ plant	100-kernel weight (g)	Shelling (%)	Sound matured kernel (%)	Protein content (%)	Oil content (%)	Oil yield (kg/ha)	Kernel uniformity (%)	Pod yield (q/ha)	Kernel yield (q/ha)
Days 50% flowering	P	1.00	0.44**	0.11	0.10	-0.16	-0.06	0.06	-0.02	0.07	-0.17	0.13	0.11	0.10	0.14
	G	1.00	0.79**	0.27**	0.10	-0.41**	-0.11	0.05	0.03	0.16	-0.39**	0.15	0.28**	0.13	0.15
Days to maturity	P		1.00	0.26**	0.03	-0.09	-0.23**	0.16	-0.04	0.24**	-0.02	0.16	0.03	0.16	0.17
	G		1.00	0.29**	0.01	-0.14	-0.25**	0.21*	-0.05	0.27**	-0.07	0.18	0.03	0.20*	0.19
Plant height (cm)	P			1.00	0.25**	-0.07	-0.29**	-0.05	-0.14	0.35**	0.02	0.11	0.33**	0.11	0.10
	G			1.00	0.33**	-0.09	-0.32**	-0.06	-0.19**	0.38**	0.01	0.13	0.35**	0.15	0.13
No. of primary branches per plant	P				1.00	-0.06	-0.18	-0.07	-0.02	0.16	0.13	0.11	0.22*	0.16	0.10
	G				1.00	-0.07	-0.19*	-0.13	-0.08	0.27**	0.17	0.21**	0.32**	0.26**	0.19*
Pod weight/plant (g)	P					1.00	-0.06	0.06	-0.07	-0.12	0.02	0.23**	-0.10	0.29**	0.31**
	G					1.00	-0.08	0.07	-0.10	-0.13	0.01	0.24**	-0.11	0.27**	0.33**
100-kernel weight (g)	P						1.00	0.22*	0.36**	-0.29**	-0.05	0.26**	-0.12	0.27**	0.28**
	G						1.00	0.23**	0.43**	-0.33**	-0.06	0.30**	-0.13	0.33**	0.32**
Shelling (%)	P							1.00	0.12	0.05	0.05	0.51**	-0.20*	0.28*	0.51**
	G							1.00	0.17	0.06	0.02	0.62**	-0.23**	0.37**	0.61**
Sound Matured Kernel (%)	P								1.00	-0.19*	-0.15	0.08	0.05	0.11	0.09
	G								1.00	-0.24**	-0.19*	0.06	0.01	0.18	0.08
Protein content (%)	P									1.00	0.10	0.01	0.32**	-0.04	-0.01
	G									1.00	0.12	0.02	0.35**	-0.04	-0.01
Oil content (%)	P										1.00	0.11	-0.10	0.08	-0.02
	G										1.00	0.11	-0.11	0.12	-0.03
Oil yield (kg/ha)	P											1.00	-0.03	0.94**	0.99**
	G											1.00	-0.04	0.94**	0.98**
Kernel uniformity (%)	P												1.00	0.04	0.08
	G												1.00	0.05	0.09
Pod yield (q/ha)	P													1.00	0.95**
	G													1.00	0.96**
Kernel yield (q/ha)	P														1.00
	G														1.00

*Significant at 5 per cent level of probability **Significant at 1 per cent level of probability

Table 4. Phenotypic and genotypic correlations among different quantitative traits in TPG-41 mutants

Traits		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches	Pod weight/ plant	100 seed weight (g)	Shelling (%)	Sound matured kernel (%)	Protein content (%)	Oil content (%)	Oil yield (kg/ha)	Kernel uniformity (%)	Pod yield (q/ha)	Kernel yield (q/ha)
Days 50% flowering	P	1.00	0.06	-0.08	0.17	-0.08	-0.24**	-0.03	0.07	0.13	0.01	0.10	0.07	0.04	0.06
	G	1.00	-0.03	-0.11	0.25**	-0.24**	-0.60**	-0.12	0.16	0.32**	0.01	0.11	0.12	0.10	0.08
Days to maturity	P		1.00	-0.17	-0.15	-0.06	0.15	0.01	-0.01	-0.20*	-0.09	0.15	-0.21*	0.003	0.08
	G		1.00	-0.28**	-0.15	-0.16	0.31**	0.14	-0.09	-0.52**	-0.30**	0.16	-0.55**	0.07	0.10
Plant height (cm)	P			1.00	0.24**	0.03	-0.28**	0.02	-0.24**	0.37**	0.00	0.02	0.04	0.01	0.02
	G			1.00	0.33**	0.08	-0.35**	0.01	-0.29**	0.46**	-0.01	0.04	0.04	0.04	0.04
No. of primary branches per plant	P				1.00	-0.14	-0.26**	0.18	0.09	0.27**	0.15	0.23**	0.27**	0.20**	0.23**
	G				1.00	-0.16	-0.32**	0.27**	0.17	0.39**	0.21*	0.34**	0.38**	0.31**	0.33**
Pod weight (g)	P					1.00	-0.01	-0.15	0.01	0.03	0.02	0.29**	0.13	0.30**	0.28**
	G					1.00	-0.03	-0.17	0.01	0.03	0.04	0.31**	0.15	0.28**	0.23**
100 seed weight (g)	P						1.00	0.04	-0.12	-0.60**	-0.15	-0.04	-0.27**	-0.19*	0.33**
	G						1.00	0.06	-0.15	-0.66**	-0.21*	-0.06	-0.28**	-0.22*	0.35**
Shelling (%)	P							1.00	0.11	0.02	0.02	0.49**	0.07	0.22**	0.49**
	G							1.00	0.15	0.02	0.05	0.56**	0.06	0.29*	0.55**
Sound Matured Kernel (%)	P								1.00	0.15	0.30**	0.18	0.15	0.12	0.15
	G								1.00	0.17	0.33**	0.19*	0.18	0.13	0.15
Protein content (%)	P									1.00	-0.30**	0.14	0.44**	0.14	0.13
	G									1.00	-0.36**	0.16	0.49**	0.18	0.14
Oil content (%)	P										1.00	0.11	0.34**	-0.01	-0.01
	G										1.00	0.09	0.41**	-0.04	-0.02
Oil yield (kg/ha)	P											1.00	0.25**	0.93	0.99**
	G											1.00	0.28**	0.95	0.99**
Kernel uniformity (%)	P												1.00	0.24**	0.22**
	G												1.00	0.28**	0.25**
Pod yield (q/ha)	P													1.00	0.95**
	G													1.00	0.96**
Kernel yield (q/ha)	P														1.00
	G														1.00

*Significant at 5 per cent level of probability **Significant at 1 per cent level of probability