

Genetic variability studies in high oleic advanced breeding lines in groundnut (*Arachis hypogaea* L)

OM PRAKASH PATIDAR and HL NADAF

Department of Genetics and Plant Breeding
University of Agricultural Sciences, Dharwad 580005 Karnataka, India
Email for correspondence: oppatidar28@gmail.com

@ Society for Advancement of Human and Nature 2018

Received: 16.3.2018/Accepted: 20.3.2018

ABSTRACT

Investigations were done at main agriculture research station of University of Agricultural Sciences, Dharwad, Karnataka in two seasons viz summer 2013-14 and kharif 2014 on 125 high oleic advanced breeding lines of groundnut along with 5 checks to study genetic variability present in them. Analysis of variance revealed significant variations among the high oleic advanced breeding lines, seasons and genotype x season interactions for all the traits evaluated. The phenotypic coefficient of variation was higher in magnitude than the genotypic coefficient of variation in respect of all the characters studied.

Keywords: Oleic acid; heritability; oil; protein; variability; oleic-linoleic acid ratio

INTRODUCTION

Groundnut (*Arachis hypogaea* L) also known as peanut is an important oilseed crop in tropical and subtropical regions of the world. Oleic acid, a monounsaturated fatty acid and linoleic acid, a polyunsaturated fatty acid both account for 75-80 per cent of the total fatty acids in groundnut oil. The higher ratio of oleic-linoleic acid in groundnut oil which ranges from 0.75 to 5.5 imparts stability and improves its shelf-life by delaying the development of rancidity (Mozingo et al 2004) and thus improves its keeping quality. Oleic acid can also be beneficial in preventing heart problems, cancer, increasing insulin sensitivity and ameliorating some inflammatory diseases (Chong et al 2006).

High oleic mutants of GPBD-4 have been developed at University of Agricultural Sciences, Dharwad, Karnataka (Kavera et al 2008). But they were either low yielding or less resistant to foliar diseases compared to GPBD-4. Limited backcrosses followed by selections have been practiced to remove these defects in high oleic mutants. The present study was aimed at evaluation of backcross-derived high oleic

advanced breeding lines for important nutritional quality traits (proteins and oil), yield contributing traits and their association patterns for the improvement of low heritable traits through the indirect selection of the highly heritable traits.

MATERIAL and METHODS

The experimental material used in the present study consisted of advanced BC_2F_5 and BC_1F_7 generations of backcrosses of (GPBD 4 \times GM 4-3)-34 \times GPBD 4; (GPBD 4 \times GM 4-3)-38 \times GPBD 4; (TMV 2 \times GM 6-1)-98 \times TMV 2 and (TMV 2 \times GM 6-1)-104 \times TMV 2 that were evaluated along with checks for fatty acid composition and yield contributing traits. High oleic advanced breeding lines (125) with checks (5) were subjected to phenotypic evaluation to study genetic variability. The experiment was carried out in a randomized complete block design with two replications during summer 2013-14 and kharif 2014 at the main agriculture research station of University of Agricultural Sciences, Dharwad, Karnataka. The data were subjected to statistical analysis using statistical software Indostat 8.0.

RESULTS and DISCUSSION

Analysis of variance revealed significant variations among the high oleic advanced breeding lines, seasons and genotype x season interactions for all the traits evaluated (Table 1). A relative comparison of the magnitude of genotypic and phenotypic coefficients of variation for different traits revealed that moderate to high genotypic (GCV) and phenotypic (PCV) variabilities among genotypes studied were present for pod weight per plant, pod weight per plot, kernel yield and oil yield in both the seasons indicating greater scope for improvement in a desirable direction. The results are in conformity with the findings of Sarvamangala (2009). In reaction to foliar diseases like rust and late leaf spot both GCV and PCV were very high indicating a wide range of variability for these characters in the population. The results are in accordance with the findings of Khedikar (2008).

High heritability estimates were recorded for days to 50 per cent flowering, pod weight per plant, pod weight per plot, per cent sound matured kernels, kernel yield, oil yield, late leaf spot and rust disease reaction (Table 2). High heritability for 50 per cent flowering was also reported by Makinde and Ariyo (2013). Pod yield per plant and pod yield per plot are in accordance with the observations of Gangadhar (2013). High heritability for late leaf spot and foliar disease reaction is in confirmation with Khedikar (2008).

Moderate to high broad sense heritability was recorded in days to maturity, shelling per cent, 100-kernel weight, protein content and oil content. Similar results were obtained by Rao et al (2012) for days to maturity and shelling per cent and Sarvamangala (2009) for 100-kernel weight, protein and oil content. Low to moderate broad sense heritability indicates the greater

Table 1. Pooled analysis of variance of yield, yield components and quality traits among 125 high oleic lines and 5 checks for summer 2013-14 and kharif 2014

Source of variation	Degrees of freedom	Days to 50% flowering	Days to maturity	Pod yield/ plant (g)	Pod yield (kg/ha)	Shelling (%)	Kernel yield (kg/ha)	100-seed weight (g)
Replication	1	8.38	0.62	1.19	878.8	1.15	257917.8	0.32
Genotype	129	14.51**	14.66**	9.99**	19946.64**	19.01**	563219**	11.85**
Season	1	1122.5**	4644.07**	0.54	2743409**	3307.75**	17169230**	4960.1**
Genotype x season	129	0.14	0.14	11.9**	20988.5**	18.13**	306040**	4.05**
Error	259	3.16	3.71	0.86	1832.5	3.35	219294.2	2.51
SEm \pm	-	0.89	0.96	0.46	21.4	0.91	234.14	0.79
CD _{0.01}	-	3.26	3.54	1.71	540	3.36	458	2.91
CV	-	5.62	1.74	8.28	9.62	2.61	17.8	4.56

**significant at 1% level

Table 1. Contd.....

Source of variation	Sound matured kernels (%)	Number of matured pods/plant	Protein content (%)	Oil content (%)	Oil yield (kg/ha)	Reaction to late leaf spot at 90 days (1-9 scale)	Reaction to rust disease at 90 days (1-9 scale)
Replication	0.32	0.39	0.37	1.92	83667.7	0.02	0.02
Genotype	39.51**	23.58**	6.75**	4.78**	125215.7**	0.33**	0.50**
Seasons	21880.2**	110.79**	21.24**	898.26**	1370532**	567.02**	518.00**
Genotype x season	48.21**	15.20**	4.08**	3.69**	78818**	0.33**	0.53**
Error	17.89	9.01	1.43	1.38	51496.7	0.01	0.01
SEm \pm	2.11	0.38	1.50	0.60	113.5	0.59	0.04
CD _{0.01}	7.76	1.38	5.51	2.2	222	2.16	0.14
CV	5.02	13.91	14.00	3.59	18.2	2.47	3.14

**significant at 1% level

Table 2 Mean range and genetic parameters of yield, yield components and quality parameters of 125 high oleic lines during summer 2013-14 and kharif 2014 and pooled analysis over two years

Trait	Season	Mean	Range		PCV (%)	GCV (%)	h^2_{bs} (%)	Genetic advance	Genetic advance as per cent mean
			Minimum	Maximum					
Days to 50% flowering	Summer 2013-14	30	26	34	6.4	5.1	64.4	2.5	8.5
	Kharif 2014	33	29	37	5.8	4.5	61.5	2.4	7.3
	Pooled	31	25	34	8.7	5.3	36.9	2.1	6.6
Days to maturity	Summer 2013-14	113	95	118	2.0	1.2	37.3	1.8	1.6
	Kharif 2014	107	92	112	2.2	1.2	39.4	1.9	1.7
	Pooled	110	100	113	2.1	1.6	58.1	2.8	2.5
Pod weight/plant (g)	Summer 2013-14	12.15	4.7	17.5	18.6	17.5	88.6	4.1	33.9
	Kharif 2014	12.1	4.4	24.4	21.5	19.6	83.2	4.4	36.8
	Pooled	12.1	7	17.08	20.0	10.6	28.2	1.4	11.6
Pod weight/plot (kg/ha)	Summer 2013-14	3600	1783	5241	20.7	18.3	78.4	1203	33.4
	Kharif 2014	3849	1693	5863	19.4	18.0	85.7	1317.3	34.2
	Pooled	3724	2603	4957	20.0	10.6	27.8	427.7	11.5
Shelling percentage	Summer 2013-14	67.6	54	74.5	5.5	4.8	77	5.9	8.7
	Kharif 2014	72.7	63	78	3.9	2.9	56.2	3.3	4.5
	Pooled	70.1	63.1	73.6	5.9	4.3	53.1	4.5	6.5
Kernel yield (kg/ha)	Summer 2013-14	2437	1284	3770	22	19.4	77.8	861.5	35.34
	Kharif 2014	2801	1137	4319	20.2	18.7	85.4	997.4	35.6
	Pooled	2619	1718	3594	21.1	11.2	28.2	320.6	12.2
100-kernel weight (g)	Summer 2013-14	37.2	32	49	6.0	4.1	47	2.2	5.9
	Kharif 2014	31	24	43	7.5	5.7	58.1	2.8	9.0
	Pooled	34.1	30.2	45.4	11.3	9.2	66.4	5.3	15.4
Sound matured kernels (%)	Summer 2013-14	77.7	66.7	90.6	6.6	6.1	86.7	9.1	11.7
	Kharif 2014	91	81.9	95.4	6.6	1.9	81.6	1.1	1.2
	Pooled	84	63.6	89.78	10.2	8.0	62.6	11.0	13.1
Number of matured pods/plant	Summer 2013-14	24	15	39	18.5	4.7	6.5	0.6	2.5
	Kharif 2014	25	12	34	13.9	6.8	23.8	1.7	6.8
	Pooled	24	17	29	15.6	6.3	16.6	1.3	5.3
Protein content (%)	Summer 2013-14	36.06	30.1	40.9	6.1	4.2	47.3	2.2	6.0
	Kharif 2014	35.6	30.8	39.6	3.9	3.6	85.5	2.5	6.9
	Pooled	35.8	32.0	38.1	5.1	2.0	15.4	0.6	1.6
Oil content (%)	Summer 2013-14	48.8	44.5	53.9	4.2	2.7	40.6	1.7	3.5
	Kharif 2014	46.2	43.2	49.5	2.6	2.3	79.8	2.0	4.3
	Pooled	47.5	44.8	50.3	4.5	3.3	54	2.4	5.0
Oil yield (kg/ha)	Summer 2013-14	1190.8	617.2	1804	22.5	19.64	75.9	419.7	35.2
	Kharif 2014	1293	524	2012	20.1	18.5	84.5	453.1	35.0
	Pooled	1242	830	1699	21.3	10.9	26.4	143.6	11.6
Late leaf spot score	*Summer 2013-14	1	1	1	-	-	-	-	-
	Kharif 2014	3.1	3	8	18.4	18.2	97.6	1.1	36.9
	Pooled	2	2	4	55.0	52.5	91	2.1	71.3
Rust disease score	*Summer 2013-14	1	1	1	-	-	-	-	-
	Kharif 2014	3.09	3	9	21.2	21.1	99.1	1.3	43.4
	Pooled	2.08	2	4.2	53.9	50.0	85.8	2.0	95.4

*Incidence of late leaf spot and rust disease was very less during summer 2013-14, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation

influence of environment in the expression of these traits. Genetic advance can help to predict the extent of genetic improvement that can be achieved for the traits. A high genetic gain along with the high heritability suggest that the characters are governed by additive gene action which is suitable for making an effective selection. The genetic advance as per cent mean was

high for pod weight per plant, pod weight per plot, late leaf spot and rust. These results are supported by the study of Rao et al (2012). The high genetic advance coupled with high heritability estimates for these traits suggest that the importance of additive genetic variance and improvement of these characters could be made by simple phenotypic selection.

REFERENCES

Chong EW, Sinclair AJ and Guymer RH 2006. Facts on fats. *Clinical and Experimental Ophthalmology* **34(5)**: 464-471.

Gangadhar K 2013. Genetic enhancement of oleic acid content in groundnut (*Arachis hypogaea* L). PhD thesis, University of Agricultural Sciences, Dharwad, Karnataka, India.

Kavera SB, Nadaf HL, Vijayakumar AG and Salimath PM 2008. Fatty acid profile of groundnut (*Arachis hypogaea* L) cultivars. *Crop Improvement* **35(1)**: 61-65.

Khedikar YP 2008. Molecular tagging and mapping of resistance to late leaf spot and rust in groundnut (*Arachis hypogaea* L). PhD thesis, University of Agricultural Sciences, Dharwad, Karnataka, India.

Makinde SCO and Ariyo OJ 2013. Genetic divergence, character correlations and heritability study in 22 accessions of groundnut (*Arachis hypogaea* L). *Journal of Plant Studies* **2(1)**: 7-17.

Mozingo RW, O'keefe SF, Sanders TH and Hendrix KW 2004. Improving shelf-life of roasted and salted inshell peanuts using high oleic fatty acid chemistry. *Peanut Science* **31(1)**: 40-45.

Rao VT, Bhadru D, Murthy KGK and Bharathi D 2012. Genetic variability and association among the various characters in groundnut (*Arachis hypogaea* L). *International Journal of Applied Biology and Pharmaceutical Technology* **3(3)**: 337-341.

Sarvamangala 2009. Construction of genetic linkage map and QTL analysis for foliar disease resistance, nutritional quality and productivity traits in groundnut (*Arachis hypogaea* L). PhD thesis, University of Agricultural Sciences, Dharwad, Karnataka, India.