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Research Article

An assessment of genetic variability and traits association among high oleic advanced breeding lines for yield and quality traits in groundnut (*Arachis hypogaea* L.)

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Abstract
The present study is aimed at evaluation of backcross derived high oleic advanced breeding lines for important nutritional quality traits and their association pattern for the improvement of low heritable traits through the indirect selection of the highly heritable traits. The estimates of the phenotypic coefficient of variation were higher than the genotypic coefficient of variation signifying the influence of environmental factors, while in certain cases the low magnitude of difference observed indicated that these characters were less influenced by the environments.PCV and GCV for different traits revealed that moderate to high variability among genotypes for, pod yield, and kernel yield indicating greater scope for improvement. Low to medium variability for 100 kernel weight whereas low variability for shelling per cent, protein content and oil content was recorded indicating the narrow range of variability for these characters and restricting the scope of selection. Pod yield was recorded as positively correlated with 100 seed weight and shelling percent whereas negatively correlated with foliar disease resistance. No significant correlation was reported between pod yield and oil quality traits like oleic acid, linoleic acid and O/L ratio indicating that pod yield can be increased without affecting the oleic acid content. In addition, high oleic lines along with higher yield and other quality traits and foliar disease resistance compared to check, GM4-3 were also selected.

Key words
Groundnut, oleic acid, heritability, oil, protein, LLS, rust

Introduction

Groundnut (*Arachis hypogaea* L.), also known as peanut, is an important oilseed crop in tropical and subtropical regions of the world. About two-third of the world production of groundnut seed serves for the extraction of oil, which is used for the cooking, salad oil and margarine and lower grades of oil are used in soap manufacture. Groundnut seeds contain high-quality edible oil (35-55%) that varies depending on variety, season and maturity. Groundnut oil is composed principally of unsaturated fatty acids and major fatty acid components are oleic acid, C18:1 (35-72%), linoleic acid C18:2 (20-45%), palmitic acid C16:0 (6-18%), stearic acid 18:0 (1.3-6.5%) and arachidic acid C20:0 (1-3%) therefore, the total unsaturated fatty acid content of peanut oil can be as much as 90 per cent. Monounsaturated oleic acid is significantly more stable for oxidation (rancidity) than polyunsaturated linoleic acid. It can be heated to a higher temperature without smoking and has advantages like reduced cooking time, less oil is absorbed and fewer food impurities enter the oil. The high oleic acid in the diet can reduce blood cholesterol and aortic cholesterol accumulation thereby decreasing the risk of cardio-vascular diseases (Wilson *et al*., 2006). Renaud *et al.* (1995) reported a 70% decrease in recurrent myocardial effects when oleic acid levels are increased in plasma fatty acids. Oleic acid also can be beneficial in preventing cancer, increasing insulin sensitivity and ameliorating some inflammatory diseases (Garcia *et al*., 2006). Replacing partially hydrogenated oil by high oleic acid groundnut oil can minimize the consumption of trans fatty acids.

Foliar diseases in groundnut are major problems in groundnut production. The tikka leaf spots (early and late leaf spots) are the most important fungal diseases of groundnut. Cultivation of resistant/tolerant varieties is the best approach under for cost effective and sustainable agriculture. So evaluation of genetic materials for disease resistance is essential in any research work.

Some high oleic acid groundnut varieties (Lopez *et al.*, 2001) reported earlier couldn’t be released in China due to their undesirable agronomic features. Original undesirable attributes present in both F435 and F78-1339, such as the split pod characteristic and low yield, associated with the high oleic acid were overcome by backcross method and produced high yielding and agronomically acceptable lines (Knauft *et al.*, 1993). High oleic mutants of GPBD-4 have been developed at UAS, Dharwad (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 is aimed at evaluation of backcross derived high oleic advanced breeding lines for important nutritional quality traits (proteins and oil) and their association pattern for the improvement of low heritable traits through the indirect selection of the highly heritable traits.

Materials and methods

The present investigation was carried out at Department of Genetics and Plant Breeding, Main Agricultural Research Station, University of Agricultural Sciences, Dharwad in *Kharif* 2014. The experimental material used in the present study consisted of advanced BC_2F_6 and BC_1F_8 generations of backcrosses of (GPBD 4 × GM 4-3)-34 × GPBD 4, (GPBD 4 × GM 4-3)-38 × GPBD 4, (TMV 2 × GM 6-1)-98 × TMV 2 and (TMV 2 × GM 6-1)-104 × TMV 2 that were evaluated along with checks for fatty acid composition and yield component traits. The experiment was laid out in a Randomized Complete Block Design (RCBD) with two replications. The 130 entries (125 high oleic advanced lines and 5 Checks) were sown during *kharif* 2014 as two rows of 2.5 m length each with a spacing of 30 cm between rows and 10 cm between the plants.

Observations were recorded on five randomly tagged plants for different characters in each line in for morphological traits. The mean value for the line was computed by taking an average. Analysis of data was done using statistical software, INDOSTAT version 8.0. Quality traits were estimated using Near-Infrared spectrometer 6500 (Foss NIR system, France) with a diffused reflectance range of 400-2500 nm. Disease score for both late leaf spot and rust taken based on the 1-9 scale by Subbarao (1985).

Results and discussion

Analysis of variance showed significant variation among the advanced breeding lines and checks for all the traits evaluated suggesting the existence of high genetic variability among the genotypes (Table 1).

Components of variation: It is also essential to have knowledge regarding the amount of genetic variability created through back cross hybridization method for various economic characters since information on nature and magnitude of variability present for traits of interest is a prerequisite for crop improvement. The phenotypic expression of the plant character is mainly controlled by the genetic makeup of the plant and the environment. So it is necessary to partition the recorded phenotypic variability into heritable and non-heritable components with suitable parameters such as phenotypic and genotypic coefficient of variation, heritability and genetic advance. Moderate to high PCV and GCV associated with high heritability and high genetic advance as per cent mean was recorded in pod yield, LLS score, rust score, linoleic acid and O/L ratio (Table 2). Hence, there is a better option for selection in these traits. These results were in conformity with the findings of Kavera *et al.* (2008) and Sunday and Omolayo (2013). Moderate to high heritability but low PCV and GCV lead to the low genetic advance in shelling percent, 100 kernel weight, protein content and oil content indicating low availability of variation for the selection of traits and is in confirmation with Azharudheen (2010), and John *et al.* (2005). Oleic acid content has low PCV and GCV but very high heritability that leads to moderate genetic advance as percent mean indicating a chance for the selection to be made in oleic acid content among the lines.

Correlation analysis: Correlation coefficients measure the mutual relationships among various characters, which help in devising efficient strategies for indirect selection using component traits and in simultaneous selection for multiple traits. It also reveals favorable associations, which could be exploited and unfavorable associations that should be modified by employing appropriate breeding strategies. Pod yield was recorded as positively correlated with 100 seed weight and shelling percent (table 3). These results were in confirmation with reports of Venkataramana *et al.* (2001), and Narasimhulu *et al.* (2012) for pod yield per plant, 100 seed weight, kernel yield and shelling per cent; Pod yield was reported to be significantly and negatively correlated with LLS and rust. These results were in accordance with the earlier reports of John *et al.* (2005) for LLS and rust as expected since these foliar diseases reduce the photosynthetic area of the plant.

No significant correlation was reported between pod yield and oil quality traits like oleic acid, linoleic acid and O/L ratio indicating that pod yield can be increased without affecting the oleic acid content. A similar association between these traits was reported by Kavera *et al.* (2008) and Ashish (2013). Hence, genotypes with high pod yield combined with high oleic acid can be selected in oleic acid improvement breeding programmes. Trait 100 seed weight was negatively correlated with oleic acid content and O/L ratio, whereas it was positively correlated with linoleic acid indicating that increase in oleic acid content reduces seed mass and this result was in accordance with Kavera *et al.* (2008).An inverse relationship observed between linoleic acid and O/L ratio has been noted by Braddock *et al.* (1995) and O'Keeffe *et al.* (1993). The strong negative correlation between oleic acid and linoleic acid results from these being the chief acyl desaturation of oleic acid leads to linoleic acid accumulation in the oil. From these correlations, it can be concluded that breeding for increased oleic acid normally results in reduced linoleic acid. The late leaf spot also showed a positive association with rust indicating that some of the genotypes have resistance to both the diseases. The negative association of oleic acid with foliar disease scores indicates that superior lines having high oleic acid content and higher disease resistance can be selected from the population. Thus it can be concluded from the above trait association studies that from this population superior lines having high pod yield along with high oleic acid with high foliar disease resistance can be selected.

Selection of superior lines: Five superior lines with high pod yield compared to best check, G2-52 were identified during *kharif* (data not shown). Two superior lines selected for high shelling percent compared to best check, GPBD-4. Ten superior lines were selected for high oleic acid and O/L ratio compared to best check, GM4-3. All these superior lines selected were having equal foliar disease resistance and is comparable to check, GPBD-4.

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Table 1. Analysis of variance for yield and yield components and quality traits among 125 high oleic lines and checks evaluated during *kharif* 2014

Source of variation	Degrees of freedom	Pod yield (kg/ha)	Shelling (%)	100 seed weight (g)	Protein content (%)	Oil content (%)	LLS at 90 DAS	Rust at 90 DAS	Oleic acid (18:1)	Linoleic acid (18:2)	O/L ratio
Replication	1	2844	0.12	0.12	0.16	0.94	0.01	0.003	7.31	4.01	6.43
Genotype	129	1034732.8**	12.57**	8.49**	3.66**	2.59*	0.63*	0.85*	58.61**	46.59**	4.11**
Error	129	79934.3	3.53	2.36	0.29	0.29	0.007	0.003	2.02	1.48	0.40
CD (5%)		394	2.62	2.14	0.74	0.75	0.15	0.15	1.98	1.69	0.88
CV (%)		7.3	2.58	4.96	1.5	1.17	3.45	3.46	2.20	8.23	13.09

*, ** Significant at 5 and 1 per cent levels of probability, respectively; LLS- late leaf spot; O/L oleic to linoleic ratio

Table 2. Mean range and genetic parameters for yield, yield components and quality parameters among 125 high oleic lines during *kharif* 2014

Traits	Mean	Range		PCV (%)	GCV (%)	h^2_{bs} (%)	Genetic advance	Genetic advance as per cent mean
		Minimum	Maximum					
Pod yield (kg/ha)	3849	1693	5863	19.4	18.0	85.7	13.3	34.2
Shelling percent	72.7	63	78	3.9	2.9	56.2	3.3	4.5
100 kernel weight (g)	31	24	43	7.5	5.7	58.1	2.8	9.0
Protein content (%)	35.6	30.8	39.6	3.9	3.6	85.5	2.5	6.9
Oil content (%)	46.2	43.2	49.5	2.6	2.3	79.8	2.0	4.3
LLS score (1-9 scale)	3.1	3	8	18.4	18.2	97.6	1.1	36.9
Rust score (1-9 scale)	3.09	3	9	21.2	21.1	99.1	1.3	43.4
Oleic acid (%)	64.8	40.0	73.1	8.5	8.3	95.5	10.8	16.6
Linoleic acid (%)	14.8	7.5	35.4	33.0	32.3	95.6	9.6	65.1
O/L ratio	4.8	1.2	9.3	30.9	28.4	84.7	2.6	53.8

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Table 3. Correlation analysis for yield, yield components and quality parameters

Traits	Shelling (%)	100 seed weight (g)	Protein content (%)	Oil content (%)	LLS score at 90 DAS	Rust disease score at 90 DAS	Oleic acid (%)	Linoleic acid (%)	O/L ratio
Pod yield (kg/ha)	0.19*	0.18*	0.13*	0.11	-0.19*	-0.19*	0.06	0.01	0.02
Shelling (%)	1.00	0.12*	-0.05	0.07	-0.05	-0.05	0.11	-0.12*	0.04
100 seed weight (g)		1.00	-0.36**	0.22*	0.41**	0.40**	-0.44**	0.46**	-0.29**
Protein content (%)			1.00	0.12*	-0.33**	-0.33**	0.41**	-0.40**	0.36**
Oil content (%)				1.00	0.02	0.02	0.29*	0.22*	0.17*
Late leaf spot score					1.00	0.82**	-0.54**	0.48**	-0.29**
Rust disease score						1.00	-0.54**	0.48**	-0.29**
Oleic acid (%)							1.00	-0.98 **	0.88**
Linoleic acid (%)								1.00	-0.91**
Oleic/Linoleic ratio									1.00

*, ** Significant at 5 and 1 per cent levels of probability, respectively; LLS- late leaf spot; O/L oleic to linoleic ratio