Generation mean analysis of yield and mineral nutrient concentrations in peanut (*Arachis hypogaea* L.)

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ABSTRACT

Present study was undertaken to study the inheritance pattern of yield and mineral nutrients (Iron, Phosphorus, Potassium and Zinc) using five parameter generation mean analysis (P_1, P_2, F_1, F_2 and F_3) in two peanut crosses (Girnar-3 × FDRS-10 and TG-37A × FDRS-10). Scaling and joint scaling tests were significant for most characters studied indicating that additive-dominance model alone is not enough to explain the inheritance of characters studied. Both additive and dominance variance played important role for most of the traits. Traits PY, HY, HKW, SHP and RDW are governed by additive gene whereas K_{shoot}, K_{root}, Fe_{shoot}, Fe_{root}, P_{shoot} and P_{root} were governed by both additive and non-additive gene effects. Positive estimates of 'i' for Zn, K and P in cross-1 (Girnar-3 × FDRS-10) indicates that parents employed were phenotypically diverse. Therefore cross-1 holds better chance for identifying genotypes with high mineral concentrations without compromising yield levels. Hence, pedigree method of breeding could be followed for improving yield and selection could be followed in later generation when population is stable to select genotypes with high mineral concentrations.

Keywords: Gene action, Generation mean analysis, Mineral elements, Peanut, Yield

In India, peanut shares 2.66 per cent of gross cropped area and producing 25 per cent of world peanut production. There are fluctuating trends in area and production of peanut in India; however, on an average it is grown in an area of 4.56 million hectare producing 6.77 million tons of pods (DAC, 2015). Peanut being a drought tolerant in nature suffers from nutrient deficiencies resulting in low yield. On an average peanut crop with 2.0 to 2.5 t/ha of yield requires 20-25 kg P, 80-100 kg K, 3-4 kg Fe and 150-200g zinc (Singh, 1999). Higher peanut yield was attributable to enhanced uptake of mineral elements such as N, P, K, etc. (Chang and Sung 2004; Dinh *et al.,* 2014). On the contrary peanut farmers in most part of semi-arid region use very less fertilizer resulting in severe nutrient deficiencies and yield loss. The iron and zinc deficiencies cause 14-40 per cent (Singh *et al.,* 2004) and 15-20 per cent (Singh, 2001) yield loss, respectively. Increasing phosphorus application increased leaves and stem weight/plant, pods and seeds per plant, as well as N, P and K contents (El-Habbasha *et al.,* 2005).

Large amount of variability has been reported in peanut genetic stocks for yield (Upadhyaya, 2003) and accumulation of mineral elements (Singh and Chaudhari, 2006; Singh *et al.,* 2011). Till date studies related to inheritance pattern of P, K, Zn and Fe in peanut are very scarce. Knowledge of gene action and heritability involved in several quantitatively inherited traits helps in deciding appropriate breeding schemes for crop improvement. To know genetic mechanism for accumulation of these mineral elements knowledge of gene action and genetic variance are important (Akhshi *et al.,* 2014). Generation mean analysis is one such useful tool for estimation of gene effects for polygenic traits which can estimate epistatic gene effects such as additive × additive, dominance × dominance and additive × dominance effects (Kearsey and Pooni, 1996). Hence, present study was designed to study genetic variability and inheritance pattern of mineral nutrients such as P, K, Zn and Fe concentrations in shoot and root tissues of peanut in addition to yield and yield contributing characters.

MATERIALS AND METHODS

Materials used for this study consisted of 5 generations, i.e. parents (P_1, P_2), F_1, F_2 and F_3, from two crosses of peanut namely Girnar-3 × FDRS-10 (Cross-1) and TG-37A × FDRS-10 (Cross-2). Girnar-3 is a high yielding variety released for west Bengal, Orissa and Manipur regions whereas TG-37A is a high yielding variety released for Rajasthan, Uttar Pradesh, Punjab, Gujarat, Orissa, West Bengal, Bihar and north-eastern regions (Rathnakumar *et al.,* 2013). FDRS-10 has the ability to absorb and translocate higher amount of P into seeds but yields are low (Krishna, 1997). Hence, genotypes were selected to combine high yielding and efficient in absorption and translocation of P.

Hybridization was carried out during July, 2011 at ICAR-Directorate of Groundnut Research, Junagadh. Flowers were emasculated during evening hours and pollination was done next day early morning. Morphological

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traits such as plant type, flower colour and pod characters were used as markers to check the trueness of F_1 plants. Fifty per cent F_1 seeds generated by hybridization during *kharif* 2011 were raised during summer 2012 and rest were retained for sowing during summer 2013. F_2 population generated during summer 2012 were divided into two parts and 50 per cent of F_2 population were raised during *kharif* 2012 and rest were retained for summer 2013. F_3 population generated were raised during summer 2013. Families from two crosses were grown in randomised complete block design with two replications. A replication consisted of one row of P_1 and P_2 (Parental lines), one row of F_1 generation, two rows of F_2 (i.e. 8 plants of P_1, P_2 and F_1 families and 32 plants for F_2 family). F_3 generation consisted of 152 plants in cross Girnar-3 × FDRS-10 and 80 plants in TG-37A × FDRS-10. Crop was harvested at maturity, shoot and root samples were dried to a constant weight in hot air oven at 65°C. One gram sample of shoot and root were digested separately with 3:1 nitric and perchloric acid mixture. Concentration of P in digests was measured spectroscopically using Fiske and Subbarao (1925) blue colour method. Fe, K and Zn estimation was done using atomic absorption spectrophotometer (Perkin Elmer AA400).

Statistical analysis: The two crosses were analysed separately for components of means, variance, heritability and genetic advance as per cent mean (%). The presence of epistasis was detected using C and D scaling tests proposed by Mather (Mather, 1949) and Hayman and Mather (Hayman and Mather, 1955). Formulas used for calculating these scales are given in Table 1.

There are reports indicating the inadequacy of Mather's scaling test in explaining additive-dominance model (Deb and Khaleque, 2009). Hence joint scaling test was also employed to test the adequacy of additive-dominance model. Joint scaling test is based on 3-parameter model - *m* (mean of F_2 generation), *d* (pooled additive effects) and *h* (pooled dominance effects) - estimated from 5 generations using weighted minimum square method as proposed by Cavalli (Cavalli, 1952). The Chi-square (χ^2) test was employed to test the goodness of fit of observed generation means with expected means. If the 2 test was significant five generation mean analysis was performed to estimate other gene effects like 'i' (additive × additive) and 'l' (dominance × dominance) epistatic effects in addition to '*m*', '*d*', and '*h*'. The formulas used for five parameter model was given by Hayman (Hayman 1958) and are presented in Table 1 (Sharma, 1998). Dominance effect ('*h*') and dominance epistatic effect ('l') with the same sign the have complementary where as different signs indicated duplicate epistasis (Kearsey and Pooni, 1996).

Variance analysis: Heritable [additive (D)] and non-heritable [dominance (H) and Environment (E)] components of variance were derived as per the formula suggested by Mather and Jinks (Mather and Jinks, 1971). After solving the equation for total variance in F_2 and F_3 D and H components were obtained and are given below:

$$\text{Total variance in } F_2 = V_{F2} = \frac{1}{2}D + \frac{1}{4}H + E$$

$$\text{Total variance in } F_3 = V_{F3} = \frac{3}{4}D + \frac{3}{16}H + E$$

$$\text{Variance among } F_3 \text{ families} = V_{F3a} = \frac{1}{2}D + \frac{1}{16}H + E$$

$$\text{Variance within } F_3 \text{ families} = V_{F3W} = \frac{1}{4}D + \frac{1}{8}H + E$$

$$E = \bar{V}P_1 + \bar{V}P_2 + \bar{V}F_1$$

$$\text{Additive Variance (D)} = 4(V_{F3} - V_{F2} + \frac{1}{16}H)$$

$$\text{Dominance Variance (H)} = 16(3V_{F2} - 2V_{F3} - E)/6$$

$$\text{Average degree of dominance} = (H/D)^{1/2}$$

Heritability: Heritability in narrow sense ($h^{2n}{}_s$) was expressed as the ratio of additive variance to the phenotypic variance (h^2_n = D/(D+H+E)) in F_2 and F_3 generation. Heritability was classified into low (0-30%), moderate (30%-60%) and high (>60%) according to Robinson *et al.* (1949).

RESULTS AND DISCUSSION

Results of two crosses analysed for genetic components of variance, gene action and heritability involved in inheritance of Zinc (Zn), Potassium (K), Iron (Fe), Phosphorus (P), shoot weight per plant (HY), root weight per plant (RDW), pod yield per plant (PY), shelling per cent (SHP) and 100 kernel weight (HKW) are furnished below:

Mean of Girnar-3 was higher for Zn_{shoot}, K_{shoot}, Fe_{shoot} Fe_{root}, RDW, PY and SHP over TG-37A and FDRS-10 whereas FDRS-10 was superior over other parents for K_{root}, P_{shoot} , P_{root}, HY (Table 2). The mean F_1 of the cross-1 was greater than both parents for Fe_{root}, PY and HKW and F_1 means of cross-2 was higher than parents for K_{root}, Fe_{shoot}, P_{shoot}, HY, RDW, PY, SHP and HKW. F_2 means for Zn_{root}, K_{root} was higher than both the parents in both crosses; lower than both the parents in cross-I for Zn_{shoot} and K_{shoot} and in cross-2 it was high and between two parents for K_{shoot} and Zn_{shoot} respectively. In cross-1 means values of Fe_{shoot}, Fe_{root}, P_{shoot} and P_{root} of F_2 generation were in between the parents, but in cross-2 F_2 mean values of Fe_{shoot} and P_{root} was higher than both the parents. F_3 means for Zn_{root}, K_{root} was higher than both the parents in both crosses; lower than both the parents in cross-I for Zn_{shoot} and K_{shoot} and was in between two parents in cross-2. F_3 mean values of Fe_{shoot}, Fe_{root}, P_{shoot} and P_{root} were in between two parents in both the crosses except for P_{shoot} in cross-1.

Scaling and joint scaling test: Results of scaling test revealed that C and D scales were significant for Zn_{shoot}, K_{shoot}, K_{root}, Fe_{root}, P_{shoot}, P_{root}, PY and SHP in both the crosses. In cross-1 only C test was significant for Zn_{root}, Fe_{root} and HY and both C and D were significant for Fe_{root} and HY in cross-2. For RDW and HKW both C and D scale test were significant in cross-2 and non-significant in cross-1. Significance of one and/or both the C and D scale test indicates the presence of epistasis for all the characters studied. Non-significant C and D indicate that additive-dominance model was adequate for the respective characters and crosses. The Cavalli's (1952) joint scaling (χ^2) test was done to test significance of observed generation means over expected means based on 3-parameter model (Table 3). 2 values were significant for all the characters indicating that epistasis is present and additive-dominance model alone is not sufficient.

Table 1 Formulae used for scaling test and five parameter model of generation mean analysis

Components	Estimate	SE	df
Scaling test			
C	$\bar{P}_1+\bar{P}_2+2\bar{F}_1-4\bar{F}_2$	$(\bar{V}_{P1}+\bar{V}_{P2}+4\bar{F}_1+16\bar{F}_2)^{0.5}$	df(P_1)+df(P_2)+ df(F_1)+df(F_2)
D	$4\bar{F}_3$- $2\bar{F}_2$ - $\bar{P}_1$- $\bar{P}_2$	$(16\bar{V}_{F3}+4\bar{V}_{F2}+\bar{V}_{P1}+\bar{V}_{P2})^{0.5}$	df(F3)+ df(F2)+ df(P1)+df(P2)
Genetic Variance			
m	$\bar{F}_2$	$(\bar{V}_{F2})^{0.5}$	df(F_2)
d	$(\bar{P}_1-\bar{P}_2)/2$	$[(\bar{V}_{P1}+\bar{V}_{P2})/4]^{0.5}$	df(P_1)+df(P_2)
h	$1/6(4\bar{F}_1+12\bar{F}_2-16\bar{F}_3)$	$[1/36(16\bar{V}_{F1}+144\bar{V}_{F2}+256\bar{V}_{F3}]^{0.5}$	df(F_1)+df(F_2)+ df(F_3)
i	$\bar{P}1-\bar{F}2-1/2(\bar{P}1-\bar{P}2)+$ ½$(4\bar{F}_1+12\bar{F}_2-16\bar{F}_3)/6$ ¼$(16\bar{F}_3-24\bar{F}_2+8\bar{F}_1)/3$	$[\bar{V}P1+\bar{V}F2+1/4(\bar{V}P1+\bar{V}P2)$ $+1/4(16\bar{V}_{F1}+144\bar{V}_{F2}+256\bar{V})/36$ $-1/16(256\bar{V}_{F3}+576\bar{V}_{F2}+64\bar{V}_{F1})/3]^{0.5}$	df(P_1)+ df(F_2)+ df(P_1)+df(P_2)+ df(F_1)+df(F_2)+ df(F_3)+ df(F_1)+ df(F_2)+ df(F_3)
l	$1/3(16\bar{F}_3-24\bar{F}_2+8\bar{F}_1)$	$[1/9(256\bar{V}_{F3}+576\bar{V}_{F2}+64\bar{V}_{F1})]^{0.5}$	df(F_1)+df(F_2)+ df(F_3)

Where VP_1, VP_2, VF_1, VF_2, VF_3 are the variances of P_1, P_2, F_1, F_2, F_3 populations respectively

Genetic components of variance and gene action: In cross-1 additive (D) component of variance was higher than dominance (H) component for most of the traits except K_{shoot}, SHP and HKW (Table 4). In cross-2 dominance (H) component of variance was higher than additive (D) component for most of the traits except K_{shoot}, Fe_{root}, and RDW. The H component was negative for most of the traits in cross-1. Average degree of dominance was more than unity and narrow sense heritability was low for most of the traits in both the crosses.

The gene actions such as mean (m), additive (d), dominance (h), additive × additive (i) and dominance × dominance (l) for different traits among cross-1 and 2 are presented in Table 5. In the inheritance of Zn_{shoot}, 'd' had significant influence in both the crosses whereas in epistatic interactions 'i' type of gene action was more predominant. Inheritance of Zn_{root} was mainly governed by additive type of gene action and epistatic interactions were not significant. In the inheritance of K_{shoot}, K_{root}, Fe_{shoot}, Fe_{root}, P_{shoot} and P_{root}, gene effects such as 'm', 'd', 'h' and 'l' had significant influence in both crosses whereas component 'i' had significant influence in Fe_{shoot}, Fe_{root}, P_{shoot} and P_{root} in cross-1 and in cross-2 'i' component was significant only in Fe_{root} and P_{root}. In the inheritance of Zn_{shoot} gene effects such as 'm', 'd' and 'i' were prominent in both crosses whereas inheritance of Zn_{root} was governed by 'm' and 'd' in cross-1 and by 'm', 'd' and 'l' in cross-2.

In the inheritance of HY, 'd' was significant in cross-1 whereas in cross-2 both 'd' and 'h' type of gene actions were significant. Among epistatic interactions, 'l' type gene effect was significant. For RDW only 'd' was significant and none of the epistatic interactions were significant in both crosses. For PY, 'd' and 'l' were significant in cross-1 whereas in cross-2 components 'm', 'd', 'i' and 'l' were found to be significant. For SHP, 'm', 'd', 'i' and 'l' components were significant in both the crosses. For HKW, 'd' component was significant in both the crosses and 'h' component was significant in cross-2. Among epistatic interactions both 'i' and 'l' were significant in cross-2 and in cross-1 only 'I' type of gene effects was significant. Duplicate type of gene action was more predominant for most of the traits in both the crosses except for Zn_{root}, K_{shoot} and Fe_{shoot} in cross-1 and Zn_{shoot}, K_{root} and RDW in cross-2.

Scaling and joint scaling tests were significant for most of the traits in both crosses (Table 1). This indicates that higher value interactions (inter-allelic interactions) play important role in the expression of characters and additive-dominance alone is not sufficient (Shahid, 1996; Ajay *et al.,* 2012). In such cases, populations have to be forwarded to next generations in order to arrive at the best fit model (Mather and Jinks, 1982).

Table 2 Average Zinc (Zn), Potassium (K), Iron (Fe), Phosphorus (P) and yield related traits among five generations in two peanut crosses

Sample	Zn Conc (ppm)		K Conc (ppm)		Fe Conc (ppm)		P conc (ppm)		HY (g/plt)	RDW (g/plant)	PY (g/plant)	SHP (%)	HKW
	Shoot	Root	Shoot	Root	Shoot	Root	Shoot	Root					
Cross-1: Girnar-3 × FDRS-10													
Girnar-3 (P1)	67.0	14.3	22420.0	10400.0	1431.0	918.3	1180.0	500.0	19.3	3.3	14.5	71.5	33.8
FDRS-10 (P2)	61.4	10.1	16350.0	13850.0	249.2	344.2	1820.0	1000.0	30.4	2.1	9.0	63.0	35.3
F_1	16.1	22.4	10390.0	9325.5	1087.8	1022.5	928.0	827.5	24.8	2.9	16.6	71.2	36.8
F_2	21.0	19.4	14554.5	21740.0	714.1	665.0	1400.0	1040.0	44.5	3.4	6.0	64.4	34.8
F_3	19.4	18.0	13705.4	14282.1	798.1	827.4	964.6	695.3	37.6	3.1	16.0	68.1	36.7
Cross-2: TG-37A × FDRS-10													
TG-37A (P1)	18.6	18.7	11690.0	9057.0	162.8	723.8	1140.0	560.0	16.1	2.7	6.9	66.5	35.9
FDRS-10 (P2)	61.4	10.1	16350.0	13850.0	249.2	344.2	1820.0	1000.0	30.4	2.1	9.0	63.0	35.3
F_1	31.2	15.7	9104.0	14030.0	283.3	374.9	830.0	1130.0	34.9	7.3	13.8	68.4	38.7
F_2	23.8	31.6	17295.0	16830.0	785.8	283.0	1810.0	1385.0	39.4	3.8	9.4	63.8	29.1
F_3	25.2	22.1	14708.5	18060.7	543.5	446.1	1292.0	1040.0	27.1	4.3	17.4	66.4	36.3

Table 3 Scaling and joint scaling test (χ^2) for Zinc (Zn), Potassium (K), Iron (Fe), Phosphorus (P) and yield related traits in two peanut crosses

Sample	Zn Conc (ppm)		K Conc (ppm)		Fe Conc (ppm)		P conc (ppm)		HY (g/plt)	RDW (g/plant)	PY (g/plant)	SHP (%)	HKW
	Shoot	Root	Shoot	Root	Shoot	Root	Shoot	Root					
Cross-1: Girnar-3 × FDRS-10													
C	76.6*	-8.2*	-1332.0*	-44059*	999.5*	647.5*	-744.0*	-1005.0*	-78.8*	-2.2	32.6*	19.2*	3.3
D	-92.8*	9.0	-13057*	-10601*	84.0	717.1*	-1941.7*	-798.8*	11.9	0.4	28.3*	9.0*	8.2
χ^2	22686**	83103**	10452**	1278.1**	178418**	2472.3**	2459**	1325.2**	85961**	853289**	1308.3**	4335.2**	2946.3**
Cross-2: TG-37A × FDRS-10													
C	47.2*	-66.1*	-22932.0*	-16353.0*	-2164.8*	685.7*	-3220.0*	-1400.0*	-41.3*	2.1*	5.9	10.9*	32.0*
D	-26.8*	-3.6	-3795.9*	15675.9*	190.4*	150.3*	-812.0*	-490.0*	-17.1*	3.8	35.2*	8.5*	15.8*
χ^2	21375**	514**	10903**	339856**	231144**	155182**	49938**	12954**	1116071**	4016.5**	553**	33689**	2639**

C and D Mather's Scaling test *,** Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

Table 4 Genetic variance components and allied parameters for Zinc, Potassium (K), Iron (Fe), Phosphorus (P) and yield related traits in two peanut crosses

Sample	Zn Conc (ppm)		K Conc (ppm)		Fe Conc (ppm)		P conc (ppm)		HY (g/plt)	RDW (g/plant)	PY (g/plant)	SHP (%)	HKW
	Shoot	Root	Shoot	Root	Shoot	Root	Shoot	Root					
Cross-1: Girnar-3 × FDRS-10													
D	21.0	14.3	-8464.3	6085.6	877.9	1713.8	210.0	129.3	12.4	0.5	1.0	-1.7	-11.5
H	-40.9	-28.4	41942.7	-12435.9	-1320.7	-3720.9	-403.2	-256.6	-24.2	-0.1	24.7	10.4	54.2
E	0.0	0.04	337.9	450.7	3.0	73.2	4.8	6.3	0.5	0.0	0.3	0.0	0.0
$(H/D)^{0.5}$	1.4	1.44	2.3	1.4	1.6	1.5	1.6	1.9	1.4	1.4	5.0	2.5	2.2
h^2_{ns} (%)	34.0	32.5	16.2	35.0	25.1	31.0	27.0	19.5	33.2	33.9	2.6	13.8	17.6
Cross-2: TG-37A × FDRS-10													
D	-20.0	-12.4	6251.0	-2544.9	-361.3	467.2	-1646.9	-37.1	-4.5	2.1	-20.6	-1.8	-4.1
H	67.6	69.2	-6047.2	12256.2	1443.3	-847.9	6717.5	645.1	31.0	-4.6	105.0	8.5	25.1
E	6.7	0.2	51.3	734.1	70.0	0.6	61.4	23.8	0.3	0.1	0.4	0.0	0.1
$(H/D)^{0.5}$	1.8	2.4	1.0	2.2	2.0	1.3	2.0	4.2	2.6	1.5	2.3	2.2	2.5
h^2_{ns} (%)	21.2	15.2	50.6	16.4	19.3	35.5	19.5	5.3	12.7	30.6	16.3	17.4	13.9

D - additive variance; H - dominance variance; E - environmental variance; h^2ns - narrow sense heritability; $(H/D)^{0.5}$ - degree of dominance

Table 5 Gene effects and epistasis for Zinc, Potassium (K), Iron (Fe), Phosphorus (P) and yield related traits in two peanut crosses

Sample	Zn Conc (ppm)		K Conc (ppm)		Fe Conc (ppm)		P conc (ppm)		HY (g/plt)	RDW (g/plant)	PY (g/plant)	SHP (%)	HKW
	Shoot	Root	Shoot	Root	Shoot	Root	Shoot	Root					
Cross-1: Girnar-3 × FDRS-10													
m	21.0*	19.4*	14554.5	21740.0*	714.1*	665.0*	1340.0*	1040.0*	44.5*	3.4*	6.0*	64.4*	34.8*
d	2.8*	2.1*	3035.0*	-1725.0*	590.9*	287.1*	-320.0*	-250.0*	-5.6*	0.6*	2.8*	4.3*	-0.8*
h	0.9	5.55	-513.2*	11634.6*	25.2*	-195.1*	848.2*	779.1*	5.2	0.3	-19.5	-5.2	-3.7
i	49.1*	-4.67	8468.2*	14314.8*	-221.2*	-583.8*	1413.2*	696.1*	5.1	0.1	-24.2	-9.1*	-5.9*
l	-21.4	1.2	-15477.3*	-72151.9*	1430.3*	1801.3*	-2545.1*	-2381.1*	-88.3*	-2.4	80.5*	37.2*	15.1
Epistasis	D	C	C	D	C	D	D	D	D	D	D	D	D
Cross-2: TG-37A × FDRS-10													
m	23.8*	31.6*	17295.0*	16830.0*	785.8*	283.0*	1810.0*	1385.0*	39.4*	4.3*	9.4*	63.8*	29.1*
d	40.0*	14.4*	14020.0*	11453.5*	206.0*	534.0*	1180.0*	940.0*	23.3*	2.4*	7.9*	64.8*	35.6*
h	1.2	14.7	1439.5*	-5158.9*	311.8*	-374.4*	729.5*	751.5*	30.0*	2.0	-18.6*	-3.8	-12.8*
i	-51.4*	3.2	-10035.9*	-21565.7*	-18.6	-556.8*	-148.8	-764.0*	-12.2	-5.0	-33.3*	-70.4*	-51.1*
l	27.0	-92.0*	-35280.8*	-893.7*	-2606.2*	1103.6*	-5322.2*	-2494.8*	-77.1*	7.8	54.2	25.6*	63.2*
Epistasis	C	D	D	C	D	D	D	D	D	C	D	D	D

M - mean of the F_2 generation; d - additive gene effect; h - dominance gene effect; I - additive × additive gene effect; l - dominance × dominance gene effect; C - complementary gene action and D - duplicate gene action.
*, ** Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

Additive variance indicates average effects of individual alleles at segregating loci whereas dominance variance represents summation of variance due to interaction effects between two alleles at different loci. If the trait has high additive variance it may not follow strictly additive model. There is a possibility that traits may follow dominance model even when additive variance is high. Though additive variance is a major factor it is not always the best measure in the inheritance of a trait (Abney *et al.,* 2001; Ajay *et al.,* 2012). Hence it is possible, for instance, to have a trait that is heavily influenced by genetics but has a relatively low additive variance. In the present study, additive variance (D) was more prominent than dominance variance (H) for most of the traits (Table 3) in cross-1 whereas in cross-2 'H' was predominant than 'D'. Predominance of additive variance indicates that there is difference between homozygotes at a locus with positive and negative alleles being distributed between parents. Dominance genetic variance for these mineral nutrients have been reported in peanut kernels (Ajay *et al.,* 2016). For some of the traits negative H component have been observed. Previously negative H component have been reported in many crops like chickpea (Deb and Khaleque, 2009), bread wheat (Aglan and Farhat, 2014), soybean (Ribeiro *et al.,* 2009) and pigeonpea (Ajay *et al.,* 2012). Mather (1949) has inferred that this negative value of H arises due to sampling error and/or genotype and environment interactions (Robinson *et al.,* 1955).

Estimates of 'D' and 'H' components for the characters studied were not free from bias due to the presence of epistatic gene effects as indicated by scaling and joint scaling test (Table 2). Under such circumstances 'D' is affected by the presence of 'i' which often inflates the variance of F_2 and its subsequent generations (Mather and Jinks, 1982). H is also affected by 'j' and 'l' when genes interact and 'l' increases the variance of F_2 when having the same sign with 'h' and decreases it when it is in the opposite sign. For yield related traits such as PY, HY, RDW, SHP and HKW and for Znshoot and Znroot residual effect 'm' and additive effect 'd' was significant and dominance effect 'h' was non-significant. Significance of additive effect suggests that effective selection for PY could be practiced even in the early generations (Venuprasad *et al.,* 2011). To exploit additive effect simple selection techniques or hybridization followed by pedigree method is suggested for improvement of yield. For K_{shoot}, K_{root}, Fe_{shoot}, Fe_{root}, P_{shoot} and P_{root} all the gene effects were significant though some of the gene effects were negative indicating that both additive and non-additive gene effects are present for these traits. Improvement of such traits requires recombination breeding followed by postponing selection to later generations.

Positive 'i' estimates suggest that the sum of the interactions from dispersed pairs of genes is less than half the sum of all interactions. Conversely, when the contribution from dispersed pairs is more than half, 'i' will have negative sign (Mather and Jinks, 1982). For PY estimates of 'i' was negative in both crosses indicating that parents were in dispersed form and phenotypically parents are not contrasting. For Zn_{shoot}, K_{shoot}, K_{root}, P_{shoot}, P_{root} and HY estimates of 'i' was positive in cross-1 than in cross-2. This indicates that parents employed in cross-1 were phenotypically contrasting and genes were in associated form for zinc, phosphorus and potassium concentrations. Hence cross-1 holds better chance for identifying genotypes with high mineral concentrations without compromising yield levels.

Gene interaction is considered to be complementary when the 'h' and 'l' estimates have the same signs and duplicate when the signs differ (Mather and Jinks, 1982). Both patterns were found among these results, with duplicate gene action being more prominent. Peanut being an allo-tetraploid with two genomes and four sets of chromosomes (Seijo *et al.,* 2004; 2007) most of the characters were controlled by duplicate gene factors. Previous studies have also indicated duplicate gene action among tetraploid crops such as Eragrostis tef (Tefera and Peat, 1997) and cotton (Nidagundi *et al.,* 2012). This is further supported by the fact that most of the traits were governed by over-dominance type of gene action with low to moderate narrow sense heritability. As selection based on progeny performance exploits only additive component of genetic variances, bi-parental mating followed by recurrent selection or diallel selective mating, which allows inter-mating among the selected segregates in the different cycles, would be useful to recover superior homozygote in later generations (Eshighi and Akhundovoa, 2010). Selection intensity and progress in improving population performance may be greater under complementary interaction than under duplicate interaction (Ajay *et al.,* 2012).

Present study concludes the presence of additive variance in the inheritance of mineral concentrations and yield related traits. Additive gene effect governed yield traits and Fe, K and P contents were governed by both additive and non-additive gene effects. Hence, pedigree method of breeding could be followed for improving yield and selection could be followed in later generation when population is stable to select genotypes with high mineral concentrations.

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