RESEARCH ARTICLE

GENETIC VARIABILITY ANALYSIS FOR AGRONOMICAL AND PRODUCTIVITY TRAITS IN INTROGRESSION POPULATION BETWEEN CULTIVATED AND SYNTHETIC AMPHIDIPLOIDS INGROUNDNUT (*ARACHIS HYPOGAEA* L.)

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Abstract: Introgression line (IL) population DH 86 × ISATGR 278-18 was developed by crossing cultivated variety of groundnut *viz.*, DH86 with the synthetic amphidiploids (ISATGR 278-18) and backcrossing twice with the recurrent parents to generate 51 BC_2F_4 ILs.Field evaluation of the ILs during *kharif* 2011and *kharif* 2012 showed considerable variability and heritability for most of the agronomic and productivity traits. ILs showed normal distribution agronomic and productivity traits. Most of the agronomic and productivity traits were positively correlated. Thus, indicating importance of these traits for enhancing the productivity in the populations.

Keywords: Agronomic traits, *Kharif*, Backcrossing, Synthetic amphidiploids

INTRODUCTION

Groundnut (*ArachishypogaeaL.*) is a self-pollinating crop with allotetraploid genome (2n = 4x = 40, AABB) having ten basic chromosomes (Stebbins, 1957 and Stalker and Dalmacio, 1986). It is amember of genus *Arachis*and belongs to the family *Leguminosae*, subfamily *Fabaceae*, tribe *Aeschynomeneae* and subtribe *Stylosanthenae* (Krapovickas and Gregory, 1994). It isoriginated in the Bolivian region of South America where the highest diversity isfound (Krapovickas, 1969). Groundnut is an important oilseed crop provides important sources of seed,oil and cakes (Kurrey*et al*., 2018). Wild diploid *Arachis*species are genetically very diverse and they represent an importantsource of genes that has been successfully tapped to improve productivity (Simpson, 2001). However, the genetic barrier between wild and cultivated peanut species arising due to ploidy differences has hampered the use of wild diploid relatives in peanut breeding programs. In this regard, development of synthetics is an effective option to overcome the genetic barrier. Many synthetic amphidiploids have been developed by crossing different diploid species followed by genome duplication through colchicine treatment (Stalker *et al*., 1991; Mallikarjuna*et al*., 2010). Such synthetic amphidiploids, ISATGR 278-18, ISATGR 5 and ISATGR 1212 provide an opportunity to introgress agronomically important traits in cultivated germplasm.

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MATERIALS AND METHODS

Introgression line was developed by crossing cultivated groundnutvariety(DH 8) with synthetic amphidiploids (ISATGR 278-18), and backcrossing the F_1s with the recurrent parent. The cross, DH 86 × ISATGR 278-18 waseffected to produce F_1 seeds. Hybrid plants were backcrossed to their respective recurrent parent to get BC_2F_1s. These plants were selfed twice to get BC_2F_3. Lines resembling the recurrent parents for most of the agronomic traits were selectedand advanced to BC_2F_4 (introgression lines).A total of fifty-one lines from DH 86 × ISATGR 278-18 were grown outin randomized block design (RBD) with two replications. Each genotype was sown in 2.5 m bed withspacing of 30 cm intra row and 10 cm inter plant and evaluated in the field for agronomic and productivity traits in two seasons, *viz. kharif* 2011and*kharif* 2012.Data on agronomic (plant height, leaf length, leaf width and number of branches) and productivity traits (total pod weight, shelling % and 100-seed weight) were recorded and subjected to analysis of variance (ANOVA) by method of Panse and Sukhatme (1964).Phenotypic and genotypic variances were estimated using the following formula (Singh andChaudhary, 1979). Heritability in broad sense was computed as the ratio of genetic variance to the total phenotypic variance as suggested by Hanson *et al.* (1956) and expressed as percentage. Genetic advance as per cent mean was categorized as low, moderate and high as given byJohnson *et al.* (1955). The correlation coefficients were worked out to determine the degree of association betweendisease resistance and agronomic and productivity traits using the formula given by Webber andMoorthy (1952).

RESULTS

Analysis of variance (ANOVA) for introgression population: The analysis of variance was carried out for the data collected from individual environmentsseparately and by pooling the data across the environments for agronomic and productivitytraits for ILs of two populations.Pooled analysis of variance for DH 86 × ISATGR 278-18 revealed significant differences among genotypes, seasons and genotype× season for agronomic and productivity traits except for number ofprimary branches (Table 1).

Components of variation for DH 86 × ISATGR 278-18 introgression population: The phenotypic and genetic coefficient of variation was high for agronomic andproductivity traits except for the leaf traits in two seasons indicating higher magnitude ofvariation.Among theagronomic and productivity traits, heritability was high for plant height, number of branches, total podyield, test weight and shelling percentage and moderate for leaf length and leaf width.Among the agronomic and productivity traits, genetic advance was high for plant height, leaflength, number of secondary branches, total pod yield, 100-seed weight and shelling percentage andlow to moderate for leaf width and number of primary branches. However, the components ofvariability were relatively less for all the traits when estimated across the seasons (Table 2).

Identification of superior ILs: Superior ILs was selected from the introgression population based on their yield performance across the seasons.Twelve from DH 86 × ISATGR 278-18 were selected as superior over respective parents. For example, ILs AB-ICGS DH86-47-3 and AB-ICGSDH86-47-4were superior to DH 86and ISATGR 278-18 for yield and attributing traits (Table 3; Plate 1).

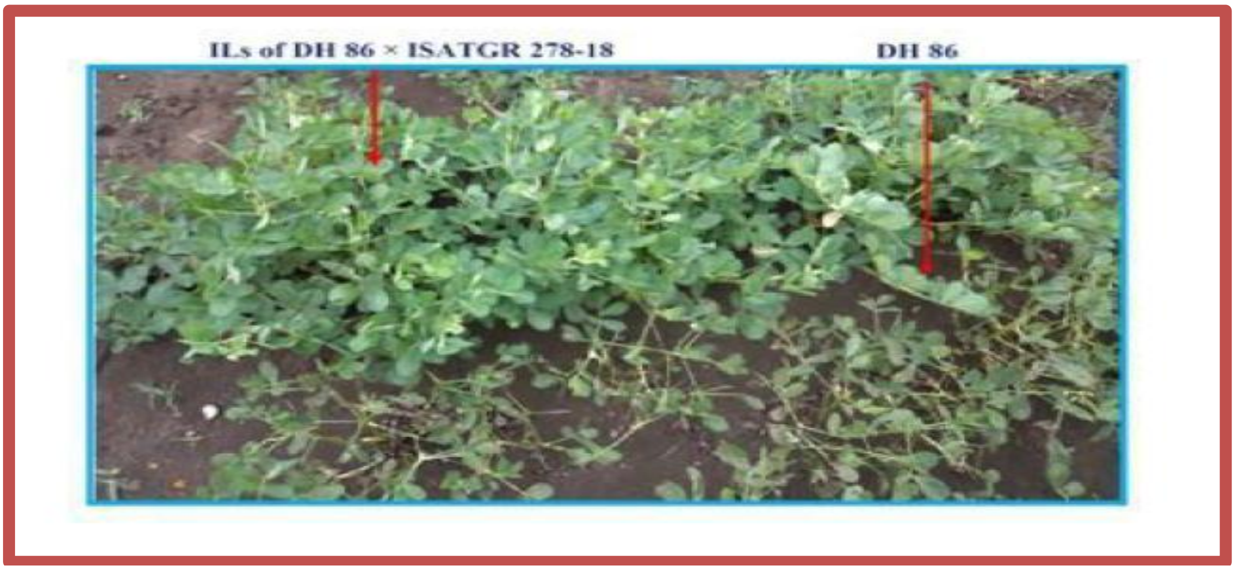

Plate 1: Comparison between DH86 and introgression lines

Correlation studies for DH 86 × ISATGR 278-18 introgression population

Agronomic and productivity traits: Correlation among the agronomic and productivity and traits has been studied in *kharif*2012 and*kharif* 2011. Plant height was positively correlated with leaf length, leaf width,number of secondary branches, total pod yield and negatively correlated with number of primarybranches, 100-seed weight and shelling per cent.Leaf length was positively correlated with leaf width, number of primary branches, total podyield and negatively correlated with number of secondary branches, 100-seedweight and shelling per cent.Leaf width had a positive association with number of secondary branches, total pod yield,100-seed weight and shelling per cent and had a negative association with number of primarybranches. Number of primary branches was positively correlated with total pod yield, 100-seed weightand shelling per cent and negatively correlated with number of secondary branches. Number of secondary branches was negatively correlated with total podyield, 100-seed weight and shelling per cent.Total pod yield had a positive association with 100-seed weight and shelling per cent.Test weight was positively correlated with shelling per cent. In general, the association was strong among the different morphological traits and the productivity traits. (Table 4).

DISCUSSION

Phenotypic evaluation of ILs: Two years of phenotyping was undertaken on morphological and productivity traits during*kharif* 2011 and *kharif* 2012. Analysis of variance for the ILs of DH 86 × ISATGR

278-18 revealed significant differences among genotypes, seasons and genotype ×season for all the traits except for number of primary branches suggesting the need to screen in multiple seasons/locations. The magnitude of variation as revealed by GCV and PCV was moderate to high for all thetraits except for leaf traits. But higher heritability and GAM indicated higher heritable variation for mostof these traits except for leaf length and leaf width, which was recorded as low to moderate. Ascompared to season-wise estimates, pooled analysis resulted in lower heritable variation, revealingthe predominance of G × E interaction for the populations.

Table 1. Pooled ANOVA for agronomic and productivity traits in DH 86 × ISATGR 278-18 introgression population

Source of variation	D.F.	F value							
		PLHT	LL	LW	NOPB	NOSB	TPW(g)	TW(g)	SP%
Season	2	751.81**	138.90**	3.30**	0.46	8.50**	38843.3**	1450.12**	1458.23**
Replication × Season	3	73.61	29.14	31.77	3.42	30.60	217.70**	10.98	2.65
Genotype	52	121.70**	21.63**	6.17**	3.93**	43.58**	1041.24**	12.72**	7.08**
Season × Genotype	104	5.51**	8.99**	4.72**	2.80**	5.80**	756.97**	9.15**	3.22**
Pr > F		<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
CV		14.21	6.55	10.35	16.13	27.21	3.22	12.08	18.87
$S.E_d$		2.28	0.26	0.21	1.25	1.05	6.33	3.39	7.55

*, **: Significant at 5% and 1% level of probability respectively

PLHT- Plant height
LL-Leaf length
LW-Leaf width
NOPB-Number of primary branches
NOSB-Number of secondary branches
TPW-Total pod weight (g)
TW-Test weight or 100-seed weight
Sp-Shelling per cent

Table 2. Mean, range and genetic variability components for agronomic and productivity traits in DH 86 × ISATGR 278-18 introgression population

Traits	MEAN	Range	PCV	GCV	h^2b.s %	GAM
			***Kharif* 2012**			
PLHT	15.31	7.00-19.58	56.43	58.30	65.06	24.68
LL	4.01	3.05- 5.13	7.60	4.90	38.41	22.19
LW	2.18	1.81-2.73	4.22	2.61	25.22	7.21
NOPB	6.45	4.00-9.00	37.62	26.92	61.08	15.43
NOSB	4.25	1.50-31	46.72	40.53	62.91	20.01
TPW(g)	95.24	21.75-272.62	31.50	30.98	79.18	21.72
TW(g)	32.67	8.75-46.00	25.88	20.59	70.05	36.29
Sp%	48.60	15.50-71.25	42.11	35.20	72.35	53.18
			***Kharif* 2011**			
PLHT	22.05	11.27-31.75	56.07	56.02	69.95	20.36
LL	4.41	2.63-6.23	15.40	15.22	59.40	38.20
LW	2.14	1-3.275	9.04	8.88	39.10	11.89
NOPB	6.42	2.5-10.0	57.37	52.00	65.09	18.43
NOSB	4.75	1.0-31.0	39.29	38.58	79.08	28.53
TPW(g)	242.76	25.00-726.60	67.74	67.70	69.98	23.04
TW(g)	17.98	5.25-38.69	46.79	46.05	79.20	20.40
Sp%	20.99	6.73-40.68	43.33	42.03	78.48	52.01

Table 3. Superior lines identified for productivity traits in DH 86 × ISATGR 278-18 introgression population

ILs/ Parents	Total pod wt (g)	100-seed wt (g)	Shelling per cent
DH 86	109.50	31.00	60.75
ISATGR 278-18	25.00	8.50	15.50
AB-ICGS DH86-47-1	154.12	38.85	62.00
AB-ICGS DH86-47-3	272.62	44.00	67.00
AB-ICGS DH86-47-4	248.62	40.00	69.00
AB-ICGS DH86-47-5	117.38	36.50	62.00
AB-ICGS DH86-47-8	221.25	44.50	66.00
AB-ICGS DH86-47-10	203.63	46.00	66.00
AB-ICGS DH86-47-11	141.00	40.50	63.00
AB-ICGS DH86-47-14	127.50	41.50	68.00
AB-ICGS DH86-8-2	136.50	36.50	70.25
AB-ICGS DH86-8-4	136.00	34.75	62.00
AB-ICGS DH86-8-6	162.50	35.25	71.25
AB-ICGS DH86-8-9	133.00	35.00	68.50

Table 4. Phenotypic correlation among agronomic and productivity traits pooled across the seasons in DH 86 × ISATGR 278-18 introgression population

Traits	PLHT	LL	LW	NOPB	NOSB	TPW(g)	TW(g)	SP
PLHT	1.00	0.003	0.248**	-0.197**	0.761**	0.071	-0.419**	-0.379**
LL		1.00	0.620**	0.050	-0.208**	0.422**	-0.036	-0.093
LW			1.00	-0.054	0.140	0.147	0.123	0.092
NOPB				1.00	-0.111	0.296**	0.268**	0.160**
NOSB					1.00	-0.155	-0.281**	-0.215**
TPW(g)						1.00	0.028	0.116
TW(g)							1.00	0.912**
SP								1.00

* Significance at 0.05 level of probability, ** Significance at 0.01 level of probability

Several ILs superior to the better parents were identified for yield performance, across the seasons (Table 3). Twelve ILs for DH 86 × ISATGR 278-18 introgression population were selected as superior over respective parents for yield traits. Since, most of the agronomic traits,*viz.* plant height and leaf length possess direct association with productivity traits, *viz.* pod yield,shelling per cent and 100-seed weight, the superior ILs were selected for each trait.As more height leads to more branches and foliage which leads to more yield because foliageare the places of photosynthesis in plants so the superior ILs could be exploited in futurebreeding programs. Many of the ILs exhibited high yield and superior for agronomic traits whichreflects positive correlations between the traits. Based onthe earlier reports, pod yield possessed significant positive association with kernel yield, number ofpods per plant and test weight at both genotypic and phenotypic levels (Sah*et al.*, 2000;Lakshmidevamma *et al.*, 2004 and Upadhyaya and Nigam, 1998).

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