Character Association Among Vegetative and Reproductive Traits in Advanced Generation of Intersubspecific and Intrasubspecific Crosses in Peanut[1]

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ABSTRACT

Character association studies among various vegetative and reproductive trains in groundnut (*Arachis hypogaea* L.) are important, because of the subterranean nature of pod development. Ninety-seven advanced generation selections derived from intersubspecific and intrasubspecific crosses were grown under high and low fertility environments for two years at ICRISAT to study the association among sixteen vegetative and reproductive traits. Only weight per mature seed with most of the vegetative traits and mature pods per plant, mature pod weight, mature seed per plant, and mature seed weight with height of the main axis and nodes with pegs showed significant positive association. Reproductive traits were significantly and positively associated among themselves. Correlation and path coefficient analyses further revealed that selection for increased mature seed yield per plant would be possible by selecting the component characters such as mature pods per plant, mature pod weight, and mature seeds per plant individually or in combination.

Key Words: Groundnut, *Arachis hypogaea,* correlations, Path coefficient.

Association among morphological and reproductive traits including pod yield in peanut (*Arachis hypogaea* L.) are of special interest because of the subterranean nature of pod development. Morphological traits are often highly heritable and if directly associated with pod yield, would help to accelerate the selection of high yielding plants in segregating populations before harvest. Character association studies in peanut are, in general, based on observations from a limited number of genotypes/segregating populations grown in one season (1,3,5,8,9,10,13,14), and as such may not be of much practical significance to applied breeding programs. It is therefore essential to grow a large number of genotypes/breeding lines over seasons to get meaningful results. Such studies on character association in peanut are very limited (6,7,12), and further, no attempt has been made to introduce fertility levels while testing genotypes over seasons. Studies of this nature would be of greater significance to breeders in formulating appropriate selection procedures.

Ninety-seven bulk selections from intersubspecific and intrasubspecific crosses in F_5 and F_7 generations were grown under high and low fertility environments over two years. Various vegetative and reproductive traits were measured to study correlations and path coefficients.

Materials and Methods

The parentage of the ninety-seven bulk selections derived from twenty-five intersubspecific and fifty-two intrasubspecific crosses are detailed in Table 1. These selections were derived from crosses involving sixty-nine different cultivars. Of these, fourty-eight belong to *A. fastigiata.* viz., Ah 65, Ah 8254, Argentine, Chico, Comet, Dh 3-20, FSB7-2, Faizpur 1-5, Goldin-1, Gangapuri, HG 1, J 11, JH 89, JH 171, Manfredi, MGS 7, MGS 9, NC Ac 400, NC Ac 2608 NC Ac 2945, NC Ac 475, NC Ac 580, NC Ac 2741, NC Ac 980, NC Ac 529, NC Ac 741, NC Ac 17142, NG 268, OG-69-6-1, OG-1-13-3, Pol. 2, Sm 5, Spancross, TG 3, TG 7, TG 14, TMV 2, TMV 7, Tifspan, Var. 2-2, Var. 2-5, Var. 47-16, VA 72 R, X9-2-B-25-B, X14-4-B-19-B, 55-437, 99-5 and 148-7-4-3-12-B and the remaining twenty-one to *A. hypogaea.* viz., Ah 2105, GA 207-3, G 37, JH 62, M 13, MK 374, NC Ac 962, NC Ac 2158, NC Ac 2698, NC Ac 2750, NC Ac 2821, NC Ac 2938, NC Ac 2944, NC Ac 2945, NC 2, NC 17, RS 138, Robut 33-1, TMV 4, TG 18 and USA 20. These crosses were advanced by bulk pedigree method in early generation. No individual plant selections were made at any stage. However, selection for growth habit and other pod and seed traits was done and the selected bulks were evaluated.

Eighty-six of these bulks belonged to the spanish type (*A. hypogaea* subsp. *fastigiata.* var. *vulgaris*) and the remaining 11 to the virginia type (*A. hypogaea* subsp. *hypogaea* var. *hypogaea*). These F_5 and F_7 selections were grown in a randomized complete block design with two replications in an alfisol (Udic Rhodustalfs) in two row plots, 9 meters in length, with 75 cm ridge x 10 cm intra ridge spacing under high and low fertility environments during the 1979 and 1980 rainy seasons at ICRISAT. The high fertility trail was grown under irrigated conditions with complete protection against pests, and single superphosphate was applied at 26.4 kg P/ha. The low fertility trial was grown under rain-fed conditions without any protection against pests, and single superphosphate was applied at 8.8 kg P/ha. A separate randomization was done for both the fertility regimes.

Data on the following vegetative and reproductive traits were recorded on ten plants per plot.

1. Height of the main stem axis (n) in cm (HMA)
2. Length of cotyledonary laterals in cm (LCL)
3. Number of (n + 1) primary branches (NOPRI)
4. Number of (n + 2) secondary branches (NOSEC)
5. Total number of nodes (TOTNOD)
6. Number of nodes with pegs (PEGNOD)
7. Total number of pegs (TOTPEG)
8. Pegs per node (PEG/NOD)
9. Total number of pods (TOTPOD)
10. Pods per peg (POD/PEG)
11. Mature pod per plant (MATPOD/PL)
12. Mature pod weight per plant (MATPODWT/PL)
13. Mature seed per plant (MATSD/PL)
14. Mature seed per pod (MATSD/POD)
15. Mature seed weight per plant (MATSDWT/PL)
16. Weight per mature seed (WT/MATSD)

Plot means were used to estimate correlations between characters. The phenotypic correlations were further partitioned into direct and indirect effects on seed yield by path coefficient analysis following Dewey and Lu (4).

Results and Discussion

Highly significant genotypic differences and genotype x year interactions were observed for all the characters except for MATSD/POD (Table 2). Nine of the sixteen characters showed significant fertility x year interactions both years. While ten traits showed significant genotype x fertility interactions in the first year, only four charac-

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Table 1. Parentage of the ninety-seven bulk selections of peanut.

Identity	Pedigree	Identity	Pedigree
Intersubspecific crosses		Intrasubspecific crosses	
BS 1	Ah 65 x Robut 33-1	BS 48	TG 3 x MGS 9
BS 2	Ah 2105 x M 13	BS 49	TG 3 x Sm-5
BS 3	Argentine x NC Ac 2944	BS 50	TG 7 x Sm-5
BS 4	FSB 7-2 x NC Ac 962	BS 51	TG-14 x Gangapuri
BS 5	JH 89 x NC Ac 962	BS 52	TMV 2 x NC Ac 171412
BS 6	JH 89 x NC Ac 2821	BS 53	TMV 7 x Chico
BS 7	MGS 7 x NC 2	BS 54	Manfredi x X14-4-B-19-B
BS 8	NC 17 x VA 72 R	BS 55	Var 2-5 x OG 69-6-1
BS 9	OG 69-6-1 x NC Ac 2938	BS 56	Var 2-5 x NC Ac 475
BS 10	RS 138 x OG 69-6-1	BS 57	99-5 x Faizpur 1-5
BS 11	RS 138 x Sm-5	BS 58	55-437 x MGS 9
BS 12	TG 18 x NC Ac 741	BS 59	55-437 x Spancross
BS 13	Tifspan x NC Ac 2944	BS 60	X14-4-B-19-B x NC Ac 400
BS 14	Var 2-2 x TG 18	BS 61	X14-4-B-19-B x NC Ac 980
BS 15	X9-2-B-25-B1 x MK 374	BS 62	X14-4-B-19-B x NC Ac 17142
BS 16	X14-4-B-19-B x NC Ac 2821	BS 63	X14-4-B-19-B x 99-5
BS 17	X14-4-B-19-B x NC Ac 2938	BS 64	X14-4-B-19-B x Goldin-1
BS 18	X14-4-B-19-B x NC Ac 2945	BS 65	Argentine x NC Ac 580
BS 19	Manfredi x M 13	BS 66	Argentine x NC Ac 580
BS 20	Argentine x NC Ac 2158	BS 67	Dh 3-20 x Manfredi
BS 21	Comet x USA 20	BS 68	Dh 3-20 x Manfredi
BS 22	Comet x USA 20	BS 69	Dh 3-20 x 55-437
BS 23	GA 207-3 x Chico	BS 70	Dh 3-20 x 55-437
BS 24	GA 207-3 x Chico	BS 71	OG 1-13-3 x NC Ac 2741
BS 25	TMV 4 x JH 89	BS 72	OG 1-13-3 x NC Ac 2741
BS 26	TMV 4 x JH 89	BS 73	Shulamit x NG 268
BS 27	Var. 47-16 x JH 62	BS 74	Shulamit x NG 268
BS 28	Var. 47-16 x JH 62	BS 75	TMV 7 x FSB 7-2
BS 29	Ah 8254 x Dh 3-20	BS 76	TMV 7 x FSB 7-2
BS 30	Dh 3-20 x FSB 7-2	BS 77	TMV 7 x 99-5
BS 31	Dh 3-20 x NC Ac 741	BS 78	TMV 7 x 99-5
BS 32	Dh 3-20 x NC Ac 2608	BS 79	Tifspan x NC Ac 529
BS 33	Dh 3-20 x 148-7-4-3-12-B	BS 80	Tifspan x NC Ac 529
BS 34	J 11 x Pol.2	BS 81	55-437 x MGS 7
BS 35	J 11 x TG 3	BS 82	55-437 x MGS 7
BS 36	J 11 x Faizpur 1-5	BS 83	J 11 x HG 1
BS 37	JH 171 x 55-437	BS 84	J 11 x HG 1
BS 38	MGS 7 x Sm-5	BS 85	J 11 x HG 1
BS 39	MGS 9 x X9-2-B-25-B	BS 86	VA 72 R x Comet
BS 40	MGS 9 x 2-5	BS 87	VA 72 R x Comet
BS 41	NC Ac 400 x MGS 7	BS 88	VA 72 R x Comet
BS 42	NC Ac 400 x Spancross	BS 89	G 37 x MK 374
BS 43	Pol. 2 x MGS 7	BS 90	RS 138 x Ah 2105
BS 44	Pol. 2 x NC Ac 2945	BS 91	RS 138 x Ah 2105
BS 45	Sm-5 x NG 268	BS 92	Robut 33-1 x NC Ac 2698
BS 46	Spancross x J 11	BS 93	Robut 33-1 x NC Ac 2698
BS 47	Spancross x J 11	BS 94	Robut 33-1 x NC Ac 2821
		BS 95	Robut 33-1 x NC Ac 2821
		BS 96	TG 1 x NC Ac 2750
		BS 97	TG 1 x NC Ac 2750

BS - Bulk selections

ters showed significant genotype x fertility interaction in the second year.

Estimates of phenotypic correlation coefficients for various vegetative and reproductive traits, HMA, LCL, NOPRI, NOSEC, TOTNOD and PEGNOD, were positively associated (P=0.01) among themselves except HMA with NOSEC. (Table 3). However, the vegetative traits, HMA and PEGNOD were significantly positively associated with MATSDWT/PL. It is interesting to note that all these vegetative traits were positively (P=0.01) associated with WT/MATDS. Sandhu and Khera (11), Balaiah *et al.* (2), and Yadava *et al.* (15) also observed positive association between number of secondaries, total nodes and peg nodes with length of cotyledonary laterals and number of primaries.

Some workers (2,6,7,9,11) have reported positive correlations between pod yield and number and length of primary and secondary branches and height of the main axis. While in this study most of the vegetative traits were positively associated with WT/MATSD, whereas only PEGNOD, TOTPEG and PEG/NOD were found positively associated with MATPOD/PL, MATPODWT/PL and MATSD/PL. Associations between vegetative and reproductive traits for most of the other combinations were either nonsignificant or low in magnitude and in general inconsistent over environment. Thus, indicating that none of them could be used reliably as an indicator of the productivity of the genotypes. It is also obvious that the results of character association studies based on one season's data should be interpreted cautiously.

Reproductive traits, in general, were significantly positively associated (P=0.01) among themselves. Selection for increase in any of these traits, particularly, MATPOD/PL, MATPODWT/PL, MATSD/PL, MATSD/POD, and MATSDWT/PL would result in a corresponding increase in the other characters. Similar results have been reported earlier (1,3,6,7,11,13,14).

It was interesting to observe that while WT/MATSD showed a significant, positive association with all the vegetative traits, only two of the reproductive traits were significant. Such significant but low positive correlation between WT/MATSD and MATSD/POD and MATSDWT/PL revealed that selection for increased seed size and higher yield would be possible in segregating populations. Coffelt and Hammons (3) also reported significant but low positive correlations between seed yield, 100 seed weight, and seeds/pod.

Path coefficient analyses were used to determine the direct and indirect effects of those characters that showed significant positive correlations with MATSDWT/PL (Table 4). MATSD/PL had a higher degree of direct effect (0.88) on MATSDWT/PL. The indirect effects of other characters were negligible except for MATPODWT/PL. The direct effect of MATPODWT/PL was low (0.25) compared to the indirect effect of this character via MATSD/PL (0.69). Similarly MATPOD/PL showed an extremely low direct effect (0.03), whereas, a high indirect effect via MATSD/PL and a lower but significant effect via MATPODWT/PL was observed. Earlier studies using path coefficient analyses indicated that number and length of secondary branches and mature pod were the most important characters contributing direct effects on pod yield (8,9).

From the correlations, it was clear that MATPOD, MATPODWT, and MATSD were positively associated (P=0.01) among themselves and also with MATSDWT.

Table 2. Pooled analysis of variance for various vegetative and reproductive traits in peanut.

Source	d.f.	HMA	LCL	NOPRI	NOSEC	TOTNOD	PEGNOD	TOTPEG	PEG/NOD	TOTPOD	POD/PEG	MATPOD/PL	MATPODWT/PL	MATSD/PL	MATSD/POD	MATSDWT/PL	WT/MATSD
Year	1	9644**	3318**	13.3	2523.0**	29712*	4432*	113052**	8.23**	14601**	0.93**	11441**	3925*	11.2	0.29	13.6	0.11*
Fertility within Ist year	1	20419**	24255**	90.3**	1985.0**	171774**	9685**	51249*	0.52	25621**	1.28**	30595**	15520**	20952**	10.71*	2200.6**	0.22**
Fertility within IInd year	1	1319**	1233**	118.9**	64.5	8981	1494	17364	5.57**	7436*	0.53**	7047*	2651*	8307**	2.52	839.4**	0.04
Error	4	10	21	2.9	13.4	1948	253	2574	0.16	363	0.02	505	208	288	1.27	37.2	0.01
Genotype	96	34**	40**	3.7**	37.6**	2527**	139**	469**	0.09**	91**	0.05**	75**	21**	60**	0.25	4.8**	0.007**
Genotype x year	96	27**	36**	2.7**	52.2**	3167**	123**	463**	0.09**	130**	0.05**	85**	23**	61**	0.25	4.8**	0.012**
Genotype x fertility in Ist year	96	10**	19**	2.2**	14.0**	1044**	60	280	0.03	45**	0.01	55**	22**	53**	0.07	5.4**	0.003
Genotype x fertility in IInd year	96	18**	12	1.3	4.7	294	107*	379	0.07**	31	0.04**	12	5	26	0.49	2.8	0.003
Error	384	12	12	1.3	3.9	308.0	75	249	0.04	27	0.02	19	7	23	0.24	2.4	0.003

*, ** - Significant at 0.05 and 0.01 probability level.

Table 3. Phenotypic correlation coefficients for various vegetative and reproductive traits in peanut over all environments.

	HMA	LCL	NOPRI	NOSEC	TOTNOD	PEGNOD	TOTPEG	PEG/NOD	TOTPOD	POD/PEG	MATPOD/ PL	MATPOD WT/PL	MATSD /PL	MATSD /POD	MATSD WT/PL	WT/MATSD
HMA	-	0.71**	0.34**	0.14	0.36**	0.47**	0.44*	0.34**	0.38**	0.27**	0.27**	0.35**	0.17	0.27**	0.27**	0.41**
LCL		-	0.63**	0.51**	0.67**	0.53**	0.46**	0.13	0.18	0.08	0.11	0.13	0.02	0.19	0.13	0.52**
NOPRI			-	0.54**	0.65**	0.53**	0.48**	0.20*	0.19	0.08	0.03	0.02	-0.01	0.05	0.06	0.42**
NOSEC				-	0.84**	0.35**	0.27**	-0.31**	-0.28**	-0.42**	-0.22*	-0.19	-0.20*	0.05	-0.11	0.38**
TOTNOD					-	0.67**	0.57**	-0.10	-0.01	-0.27**	0.06	0.14	0.05	0.21*	0.18	0.53**
PEGNOD						-	0.78**	0.39**	0.42**	0.03	0.44**	0.46**	0.38**	0.36**	0.46**	0.38**
TOTPEG							-	0.67**	0.55**	0.03	0.43**	0.49**	0.32**	0.17	0.37**	0.31**
PEG/NOD								-	0.71**	0.44**	0.44*	0.40**	0.32**	0.11	0.25**	0.04
TOTPOD									-	0.78**	0.69**	0.56**	0.55**	0.09	0.45**	-0.06
POD/PEG										-	0.49**	0.35**	0.42**	0.09	0.28**	-0.13
MATPOD/PL											-	0.83**	0.77**	0.63**	0.71**	0.03
MATPODWT/PL												-	0.78**	0.58**	0.82**	0.14
MATSD/PL													-	0.55**	0.90**	-0.08
MATSDWT/POD														-	0.55**	0.21*
MATSDWT/PL															-	0.23*
WT/MATSD																-

*, ** - Significant at 0.05 and 0.01 probability level.

Table 4. Path coefficient analysis of eleven characters on mature seed yield (pooled over locations) in peanut.

	HMA	PEGNOD	TOTPEG	PEG/NOD	TOTPOD	POD/PEG	MATPOD/ PL	MATPOD WT/PL	MATSD/ PL	MATSD/ POD	WT/MAT SD	MATSD WT/PL
HMA	.013	.030	-.069	.001	-.003	-.037	.007	.087	.156	-.039	.124	.27**
PEGNOD	.006	.062	-.123	.001	-.004	-.004	.011	.113	.335	-.052	.114	.46**
TOTPEG	.006	.049	-.155	.001	-.005	-.005	.011	.121	.282	-.025	.093	.37**
PEG/NOD	.004	.025	-.104	.002	-.006	-.059	.011	.100	.280	-.016	.012	.25**
TOTPOD	.005	.026	-.086	.001	-.008	-.105	.017	.139	.488	-.014	-.017	.45**
POD/PEG	.004	.002	-.005	.001	-.007	-.135	.012	.087	.373	-.014	-.040	.28**
MATPOD/PL	.004	.027	-.067	.001	-.006	-.067	.025	.207	.683	-.091	-.009	.71**
MATPODWT/PL	.005	.028	-.076	.001	-.005	-.047	.021	.247	.690	-.084	.044	.82**
MATSD/PL	.002	.024	-.050	.001	-.005	-.057	.019	.194	.881	-.079	-.026	.90**
MATSD/POD	.004	.022	-.028	.000	-.001	-.013	.016	.145	.485	-.143	.062	.55**
WT/MATSD	.005	.024	-.048	.000	.000	.018	-.001	.036	-.075	-.030	.301	.23*

Path coefficient analyses also revealed a high contribution of these traits (directly or indirectly) in determining the MATSDWT/PL. Selection of either trait or a combination of these traits for increased yield should be possible in segregating generations. Emphasis should be given to evaluate the genotypes/breeding lines under diverse environments over years.

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