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Inheritance of morphological traits and pod features in groundnut (*Arachis hypogaea* L.)

S. K. Pattanashetti[1], M. V. C. Gowda and Girija

Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad 580 005

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Abstract

TMV-2, a commercially cultivated Spanish bunch (ssp. *fastigiata*) variety on treatment with ethyl methane sulphonate (0.2%) had earlier resulted in a subspecific mutant i.e. narrow leaf mutant (NLM) with Virginia type (ssp. *hypogaea)* habit and narrow leaflets. TMV-2 and its mutant NLM differ from one another in many morphological traits. To know the inheritance of morphological traits, both direct (TMV-2 x NLM) and reciprocal (NLM x TMV-2) crosses were made during the rainy season 2001 and studied for their behaviour in subsequent generations *viz*., F_1, F_2 and F_3 during the post-rainy 2001, rainy 2002 and post-rainy 2002 seasons, respectively. The results indicated that growth habit, main-stem flowering, branching pattern, leaflet shape are under the control of two genes each, while albinism, pod beak, pod constriction and pod size are under the control of three genes each with different gene action.

Key words: Inheritance, morphological traits, pod features, groundnut (*A. hypogaea* L.)

Introduction

A thorough knowledge of the genetics of characters will help the plant breeder to choose the best breeding scheme in attaining desired objectives. In case of groundnut (*Arachis hypogaea* L.), both continuous and discontinuous variations have been observed for agronomically important characters. Although most of the traits were shown to exhibit inheritance suggestive of nuclear control, a few traits have been observed to show cytoplasmic inheritance. The work on genetics of groundnut was initiated by Van der Stock [1], since then the genetics of numerous traits has been analyzed. In the present study, an effort was made to know the inheritance of several morphological traits for which the parent, TMV-2 and its mutant, narrow leaf mutant (NLM) differed.

Materials and methods

TMV-2, a commercially cultivated Spanish bunch (ssp. *fastigiata*) variety on treatment with ethyl methane sulphonate (0.2%) had earlier resulted in a subspecific mutant with Virginia type (ssp. *hypogaea*) habit and narrow leaflets called 'Narrow leaf mutant' (NLM) [2]. TMV-2 and its mutant NLM differ from one another for many morphological traits (Table 1). To know the inheritance of morphological traits, both direct (TMV-2 x NLM) and reciprocal (NLM x TMV-2) crosses were made and studied for their behavior in subsequent generations *viz*., F_1, F_2 and F_3. Both direct and reciprocal crosses were made during the rainy season of 2001 and their F_1, F_2 and F_3 generations were grown during the post-rainy 2001, rainy 2002 and post-rainy 2002 seasons, respectively.

Table 1. Distinguishing features of TMV-2 and NLM

Features	TMV-2	NLM
Botanical variety	Spanish bunch	Virginia runner
Origin	Mass selection from 'Gudhiatham bunch'	EMS mutant of TMV-2
Morphological traits		
Growth habit	Erect	Semi-spreading
Branching pattern	Sequential	Alternate
Main-stem flowering	Present	Absent
Leaflet shape	Elliptic	Linear lanceolate
Pod features		
Pod beak	Slight	Moderate
Pod reticulation	Slight	Moderate
Pod constriction	Slight	Moderate
Pod size	Small	Medium

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[1] Present address: Assistant Professor, Department of Genetics and Plant Breeding, College of Agriculture, P. B. No.18, Bijapur 586 101; e-mail: skpshetty@rediffmail.com

Observations on morphological traits namely, growth habit, branching pattern, main-stem flowering and leaflet shape were recorded according to 'Groundnut Descriptors' published by IBPGR [3] for F_1, F_2 and F_3 generations during their respective seasons. For pod features namely, pod beak, pod reticulation, pod constriction and pod size observations were recorded for F_1 and F_2 generations during their respective seasons, since the grouping was done in the F_3 based on the above mentioned morphological traits. Inheritance of morphological traits and pod features was studied by using the Chi-square test based on the information from their segregating generations.

Results and discussion

Morphological traits

***Growth habit**:* TMV-2 is erect, while NLM is semi-spreading in growth habit. In the direct cross (TMV-2 x NLM), the F_1 was semi-spreading. In the F_2 generation, three phenotypes namely erect, semi-spreading and spreading were observed. Erect types were considered as one group, while semi-spreading and spreading types under another group. The segregation in the F_2 showed a good fit to the ratio of 11 spreading / semi-spreading: 5 erect (Table 2). Behaviour of the families in the F_3 generation was as expected. The results indicated that two genes with complimentary-duplicate action govern growth habit i.e. two or more dominant alleles in any combination at the two loci results in spreading/semi-spreading plants, while three or more recessive alleles at the two loci results in erect plants. Similar ratio was observed in the intersubspecific cross between two US cultivars *viz*., Argentine and Early runner [4].

In the reciprocal cross (NLM x TMV-2), the F_1 was semi-spreading, but segregation in the F_2 generation showed slightly higher Chi-square values for the expected ratio of 11 spreading/semi-spreading: 5 erect as compared to the direct cross (Table 3). Breeding behaviour in the F_2 and F_3 generation of the reciprocal cross indicated that growth habit deviates from the expected ratio of 11 spreading/semi-spreading: 5 erect and cytoplasmic effect was evident. It did not fit any other ratio as well. Earlier, reciprocal cross differences for growth habit have been reported and concluded that the G and V_4 plasmons are rare, O plasmon is widespread, being present in at least three of the four botanical varieties of cultivated groundnut [5, 6, 7]. Observed reciprocal cross differences for growth habit could be due to active cytoplasmic and/or nuclear modifying factors [4] as observed in the present study.

***Branching pattern**:* TMV-2 is sequential branching type, while NLM is alternate branching type. The F_1 was alternate branching in both the crosses *viz*., TMV-2 x NLM and NLM x TMV-2. In the F_2 generation, they showed a good fit to the ratio of 15 alternate: 1 sequential in both the crosses (Tables 2 and 3). Breeding behaviour of F_3 families was also as expected in both the crosses. This indicates that two duplicate dominant genes govern branching pattern and sequential branching type is duplicate recessive. Similar ratio for sequential branching was earlier reported by Mouli and Kale [8].

***Main-stem flowering**:* TMV-2 shows the presence of main stem flowering, while NLM shows its absence. The F_1 was showing absence of main stem flowering in both the crosses. Segregation in the F_2 generation showed a good fit to the ratio of 15 main-stem flowering absence: 1 main-stem flowering presence in both the crosses (Tables 2 and 3). Breeding behaviour of F_3 families was as expected. This indicates that two duplicate genes govern main-stem flowering and presence of flower is duplicate recessive. Similar ratio for sequential branching was earlier reported by Mouli and Kale [8].

***Leaflet shape**:* TMV-2 has leaflets which are elliptic in shape, while NLM shows linear-lanceolate shape. In addition to parental types, a new leaflet shape lanceolate which is an intermediate type was observed in high frequency in the segregating generations of both the crosses. The F_1 was lanceolate in shape in both the crosses. Segregation in the F_2 showed a good fit to the ratio of 5 elliptic: 10 lanceolate: 1 linear-lanceolate in both the crosses (Tables 2 and 3). In the F_3 generation, slightly higher chi-square values were observed in both the crosses, which is probably due to the lesser population size. Breeding behaviour in the F_2 and F_3 generations indicated that two genes whose alleles are acting in a quantitative manner govern leaflet shape. Three or four dominant alleles in any combination at the two loci results in elliptic shape, while one or two dominant alleles results in lanceolate shape and homozygous recessive at both the loci results in linear-lanceolate shape giving an F_2 ratio of 5 elliptic: 10 lanceolate: 1 linear-lanceolate. Earlier, leaflet size has been reported to be quasi-quantitatively inherited i.e., its inheritance may present distinguishable genotypes within continuous variation and may involve two types of alleles, one for large leaflet while other for small leaflet [9]. Similar case may be happening in the crosses of the present study.

Table 2. Behaviour of morphological traits in the F_2 and F_3 generations of the cross TMV-2 x NLM

Trait	Generation	No. of progeny	Phenotype			Expected ratio	Chi-square	d.f.	Probability
Growth habit			Spreading/ semi-spreading	Erect					
	F_2	1	26	11		11:5(S/SS:E)	0.04^{NS}	1	0.70-0.90
	F_3	16	192	-		BT(S/SS)	-	-	-
		9	111	49		11:5(S/SS:E)	0.029	1	0.70-0.90
		6	23	76		1:3(S/SS: E)	0.165	1	0.50-0.70
		4	-	29		BT(E)	-	-	-
	Total	35	χ^2 for 7:4:4:1			7:4:4:1	2.398^{NS}	3	0.30-0.50
Branching pattern			Alternate	Sequential					
	F_2	1	34	3		15:1(Alt: Seq)	0.22^{NS}	1	0.50-0.70
	F_3	24	258	-		BT(Alt)	-	-	-
		6	64	18		3:1(Alt: Seq)	0.407	1	0.50-0.70
		2	39	3		15:1(Alt: Seq)	0.059	1	0.70-0.90
		2	-	71		BT(Seq)	-	-	-
	Total	35	χ^2 for 7:4:4:1			7:4:4:1	11.303*	3	0.01-0.05
Main-stem flowering			Absence	Presence					
	F_2	1	33	4		15:1(Ab: Pr)	1.32^{NS}	1	0.20-0.30
	F_3	24	240	-		BT(Ab)	-	-	-
		5	61	22		3:1(Ab: Pr)	0.100	1	0.70-0.90
		2	41	3		15:1(Ab: Pr)	0.024	1	0.70-0.90
		4	-	86		BT(Pr)	-	-	-
	Total	35	χ^2 for 7:4:4:1			7:4:4:1	13.242**	3	0.001-0.01
Leaflet shape			Elliptical	Lanceolate	Linear Lanceolate				
	F_2	1	15	18	4	5:10:1(E:L:LL)	3.40^{NS}	2	0.10-0.20
	F_3	13	207	-	-	BT(E)	-	-	-
		2	31	13	-	3:1(E:L)	0.485	1	0.30-0.50
		7	-	51	-	BT(L)	-	-	-
		1	-	3	1	3:1(L:LL)	0.000	1	1.00
		8	41	82	8	5:10:1(E:L:LL)	0.005	2	0.90-0.95
		4	-	-	26	BT(LL)	-	-	-
	Total	35	χ^2 for 1:4:2:4:4:1			1 :4:2f 4:4:1	68.571**	5	<0.001

BT = Breeding True; NS = Non-significant; *,** = Significant at 5% and 1% level of probability, respectively
S/SS = Spreading/semi-spreading, E = Erect; Alt-Alternate, Seq = Sequential; Ab = Absent, Pr = Present; E = Elliptical;
L = Lanceolate; LL = Linear lanceolate.

***Albinism**:* TMV-2, NLM and the F_1's of both the crosses were normal (green). Albinos were observed only in the segregating generations *viz*., F_2 and F_3 of the reciprocal cross (NLM x TMV-2) but not in the direct cross (TMV-2 x NLM). Frequencies of normal (green) and albino plants were recorded within seven days after emergence of seedlings. On advancing the normal F_2 plants, some of them segregated into green and albino plants. Segregation in the F_2 generation of the cross NLM x TMV-2 showed a good fit to the ratio of 60 green: 3 albino: 1 zygotic lethal (Table 3). In the F_3 generation, slightly higher Chi-square values were observed for the

Table 3. Behaviour of morphological traits in the F_2 and F_3 generations of the cross NLM x TMV-2

Trait	Generation	No. of progeny	Phenotype			Expected ratio	Chi-square	d.f.	Probability
Growth habit			Spreading/ semi-spreading	Erect					
	F_2	5	231	62		11:5(S/SS:E)	13.88**	1	<0.001
	F_3	122	1329	-		BT(S/SS)	-	-	-
		100	1258	471		11:5(S/SS:E)	12.932	1	<0.001
		23	84	205		1:3(S/SS: E)	2.548	1	0.10-0.20
		29	-	221		BT(E)	-	-	-
	Total	274	χ^2 for 7:4:4:1			7:4:4:1	52.99**	3	<0.001
Branching pattern			Alternate	Sequential					
	F_2	5	271	22		3:1(Alt: Seq)	0.79^{NS}	1	0.30-0.50
	F_3	150	1755	-		BT(Alt)	-	-	-
		65	713	237		3:1(Alt: Seq)	0.002	1	0.95-1.00
		41	758	56		15:1(Alt: Seq)	0.552	1	0.30-0.50
		18	-	289		BT(Seq)	-	-	-
	Total	274	χ^2 for 7:4:4:1			7:4:4:1	18.832**	3	<0.001
Main-stem flowering			Absence	Presence					
	F_2	5	272	21		3:1(Ab:Pr)	0.42^{NS}	1	0.50-0.70
	F_3	156	1719	-		BT(Ab)	-	-	-
		61	693	223		3:1(Ab:Pr)	0.209	1	0.50-0.70
		39	738	53		15:1(Ab:Pr)	0.273	1	0.50-0.70
		18	-	304		BT(Pr)	-	-	-
	Total	274	χ^2 for 7:4:4:1			7:4:4:1	24.454**	3	<0.001
Leaflet shape			Elliptical	Lanceolate	Linear lanceolate				
	F_2	5	97	179	17	5:10:1(E:L:LL)	0.51^{NS}	2	0.70-0.90
	F_3	60	793	-	-	BT(E)	-	-	-
		33	399	150	-	3:1(E:L)	1.579	1	0.20-0.30
		68	-	733	-	BT(L)	-	-	-
		30	-	335	109	3:1(L:LL)	0.048	1	0.70-0.90
		67	322	646	71	5:10:1(E:L:LL)	0.607	2	0.70-0.90
		16	-	-	121	BT(LL)	-	-	-
	Total	274	χ^2 for 1:4:2:4:4:1			1:4:2:4:4:1	178.52**	5	<0.001
Albinos			Green	Albino	Lethal				
	F_2	5	293	10	-	60:3(Gr: Alb)	1.43^{NS}	-	0.20-0.30
	F_3	214	2797	-	-	BT(9r)	-	1	-
		17	111	32	-	3:1(Gr: Alb)	0.523	1	0.30-0.50
		17	312	74	-	12:3(Gr: Alb)	0.166	1	0.50-0.70
		18	471	22	-	60:3(Gr: Alb)	0.098	1	0.70-0.90
		8	101	9	-	15:1(Gr: Alb)	0.704	4	0.30-0.50
	Total	274	χ^2 for 32:8:8:8:4			32:8:8:8:4	73.24**		<0.001

BT = Breeding True; NS = Non-significant; *,** = Significant at 5% and 1% level of probability, respectively
S/SS = Spreading/semi-spreading, E = Erect; Alt = Alternate, Seq = Seqential; Ab = Absent, Pr = Present; E = Elliptical;
L = Lanceolate; LL = Linear lanceolate; Gr = Green, Alb = Albino

Table 4. Behaviour of pod features in the F_2 and F_3 generations of the crosses TMV-2 x NLM and NLM x TMV-2

Cross	Character	No.of F_1 progeny	F_2 phenotype		Expected ratio	Chi-square	d.f.	Probability
TMV-2 x NLM	Pod beak		Beaked	Non-beaked				
		1	34	3	57:7 (B: NB)	0.301^{NS}	1	0.50-0.70
	Pod reticulation		Reticulated	Non-reticulated				
		1	35	2	15:1(R:NR)	1.445^{NS}	1	0.20-0.30
	Pod constriction		Constricted	Un-constricted				
		1	32	5	54:10(C:UC)	0.125^{NS}	1	0.70-0.90
	Pod size		Medium/Large	Small				
		1	32	5	54:10(M/L:S)	0.125^{NS}	1	0.70-0.90
NLM x TMV-2	Pod beak		Beaked	Non-beaked				
		5	263	30	57:7 (B: NB)	0.147^{NS}	1	0.70
	Pod reticulation		Reticulated	Non-reticulated				
		5	280	13	15:1(R:NR)	1.642^{NS}	1	0.20-0.30
	Pod constriction		Constricted	Un-constricted				
		5	249	44	54:10(C:UC)	0.082^{NS}	1	0.70-0.90
	Pod size		Medium/Large	Small				
		5	257	36	54:10(M/L:S)	2.476^{NS}	1	0.10-0.20

expected ratio, which could be probably due to lesser population size. The results suggest that chlorophyll production is controlled by duplicate loci (*A* and *B*) interacting with a third locus (*L*) in an epistatic manner. The presence of one dominant allele at either *A* or *B* locus ensures normal chlorophyll development independent of recessiveness/dominance of *L* locus. The double recessive condition of both *A* and *B* and at least one dominant allele at the *L* locus (*aabbL_*) results in albino seedlings, while triple recessive (*aabbll*) are zygotic lethal giving an F_2 ratio of 60 green: 3 albino: 1 zygotic lethal. Same ratio has been earlier reported for albinism by Coffelt and Hammons [10] but they did not observe reciprocal cross differences.

Reciprocal cross differences for various agronomic traits have been reported in intersubspecific crosses of groundnut [11, 12, 13, 14]. Based on these observations, Wynne and Hal ward [15] suggested that cytoplasmic genomes are different for Virginia and Spanish parents. Reciprocal cross differences observed for growth habit and albinism in the present study could be due to cytoplasm factors *per se* or nuclear genes governing the constitution or expression of cytoplasmic genome.

Pod features

Pods of TMV-2 are slightly beaked, slightly reticulated, slightly constricted and small in size, while NLM pods are moderately beaked, moderately reticulated, moderately constricted and medium in size. The pods of F_2's of both the crosses were beaked, reticulated, constricted and medium/large in size. In the segregating generations of both the crosses, a gradient of phenotypes were observed for the pod features namely, pod beak (absent/slight/moderate/prominent/very prominent), pod constriction (none/slight/moderate/deep/very deep) and pod size (small/medium/large).

***Pod beak**:* Pods with absence of beak/slightly beaked were grouped as non-beaked, while those with moderate/prominent/very prominent beak as beaked for fitting genetic ratios. In the F_2 generation, pod beak showed a good fit to the ratio of 57 beaked: 7 non-beaked in both the crosses (Table 4). The results suggest that pod beak is under trigenic control i.e. one independent dominant gene and two complementary genes govern pod beak. Dominance of beaked pods over non-beaked has been reported earlier by Patel *et al.* [16].

***Pod reticulation**:* Pods which are smooth / slightly-reticulated were grouped as smooth, while those with moderate / prominent / very prominent reticulation as reticulated for fitting genetic ratios. Segregation in the F_2 generation of both the crosses fit well to the ratio of 15 reticulated: 1 non-reticulated pods (Table 4). The results indicated that two duplicate genes govern pod reticulation. Similar ratio was earlier observed by Manoharan and Ramalingam [17].

***Pod constriction**:* Pods with none / slight constriction were grouped as un-constricted, while those with moderate / deep / very deep constriction as constricted for fitting genetic ratios. Segregation in the F_2 generation of both the crosses showed a good fit to the ratio of 54 constricted: 10 un-constricted pods (Table 4). The results suggest that pod constriction is under trigenic control i.e. any two of the three complementary genes lead to constricted pods. It has been earlier reported that three pair of independent nuclear genes interacting with plasmon govern pod constriction [16, 18].

***Pod size**:* The medium/large pods were considered as one group, while small pods as another group for fitting genetic ratios. Segregation in the F_2 generation of both the crosses showed a good fit to the ratio of 54 medium / large: 10 small pods (Table 4). The results indicate that pod size is under trigenic control i.e. any two of the three complimentary genes lead to medium / large pods. Earlier, trigenic dominant nature of large pods over small pods was reported by Badami [19].

The inheritance studies indicated that the traits namely, growth habit, main stem flowering, branching pattern, leaflet shape are under the control of two genes each, while albinism, pod beak, pod constriction and pod size are under the control of three genes each with different gene action. In addition to the parental types, new phenotypes like spreading growth habit, lanceolate leaflet shape, albinism, prominent / very prominent pod beak, prominent / very prominent pod reticulation and deep / very deep pod constriction were observed in the segregating generations of both direct and reciprocal crosses. Plants with new combinations of characters compared to parental types were also observed.

References

1. **Van der Stock J. E.** 1910. Onderzockingen omterent ryst en tweed gewassen. Mededelingen ven het. Department van Landbouw, **12**: 176-221.
2. **Prasad M. V. R., Kaul S. and Jain H. K.** 1984. Induced mutants of peanut (*Arachis hypogaea* L.) for canopy and pod bearing characters. Indian J. Genet., **44**: 25-34.
3. **IBPGR.** 1981. Groundnut Descriptors. International Board for Plant Genetic Resources and International Crops Research Institute for Semi-Arid Tropics, IBPGR Secretariat, Rome.
4. **Coffelt T. A.** 1974. Inheritance of growth habit in an infraspecific cross population of peanuts. J. Hered., **65**: 160-162.
5. **Ashri A.** 1964. Intergenic and genic-cytoplasmic interactions affecting growth habit in peanuts. Genetics, **50**: 363-372.
6. **Ashri A.** 1968. Genic-cytoplasmic interactions affecting growth habit in peanuts *A. hypogaea* II. A revised model. Genetics, **60**: 807-810.
7. **Ashri A.** 1976. Frequencies of plasmon types in a germplasm sample of peanuts *Arachis hypogaea.* Euphytica, **25**: 777-785.
8. **Mouli C. and Kale D. M.** 1982. Gamma ray induced Spanish bunch mutant with large pod groundnut. Oleagineux, **37**: 583-588.
9. **Essomba N. B., Coffelt T. A., Branch W. D. and Van Scoyoc S. W.** 1993. Inheritance in leaflet size in peanut (*Arachis hypogaea* L.). Peanut Sci., **20**: 90-93.
10. **Coffelt T. A. and Hammons R. O.** 1971. Inheritance of an albino seedling character in *Arachis hypogaea* L. Crop Sci., **11**: 753-755.
11. **Wynne J. C. and Emery D. A.** 1974. Response of interspecific peanut hybrids to photoperiod. Crop Sci., **14**: 878-880.
12. **Emery D. A.** 1983. Reproductive efficiency of cultivated peanuts V. Response of parental and Virginia (NC4) x Spanish (C_2) hybrid families to changes in photoperiod. Peanut Sci., **10**: 8.
13. **Phillips T. D.** 1987. Genetics of symbiotic nitrogen fixation in peanuts (*Arachis hypogaea* L.). M.S. Thesis, North Carolina State University, Raleigh, USA.
14. **Mercer L. C.** 1988. Inheritance of fatty acid content in peanut (*Arachis hypogaea* L.). M.S. Thesis, North Carolina State University, Raleigh.
15. **Wynne J. C. and Halward T. M.** 1989. Cytogenetics and genetics of *Arachis.* Critical Rev. Plant Sci., **8**: 189-220.
16. **Patel J. A., Patel S. A. and Choudhary D. N.** 1997. Inheritance of pod beak and pod constriction in groundnut. Indian J. Genet., **55**: 229-232.
17. **Manoharan V. and Ramalingam R. S.** 1992. Inheritance of testa colour and pod reticulation in groundnut. Madras Agril. J., **79**: 646-648.
18. **Coffelt T. A. and Hammons R. O.** 1974. Inheritance of pod constriction in peanut. J. Hered., **65**: 94-96.
19. **Badami V. K.** 1928. *Arachis hypogaea* (The groundnut). Ph.D. Thesis, Cambridge University, U.K., pp. 297-374.