Indian J. Genet., **57** (3): 229–232 (1997)

INHERITANCE OF POD BEAK AND POD CONSTRICTION IN GROUNDNUT

J. A. PATEL,* S. A. PATEL AND D. N. CHAUDHARY

Department of Plant Breeding
Gujarat Agricultural University, Anand

(Received: September 10, 1990; accepted: August 16, 1996)

ABSTRACT

Genetic study of pod beak and pod constriction was taken up in 14 and 8 crosses, respectively. The presence of pod beak was dominant over beakless and was inherited as a monogenic character. The F_2 phenotypic ratios indicated that pod constriction was governed by three pairs of independent nuclear genes, which interacted with cytoplasmic factor(s).

Key words: Inheritance, pod beak, pod constriction, nuclear genes, plasmon.

Groundnut, *Arachis hypogaea* L., is one of the main oilseed crops of India and the world. The presence or absence of pod beak and pod constriction are the markers of interest for the indentification of varieties. Pods without constriction have seeds with flat ends. Pods with deep constriction produce seeds with narrow and tapering ends. Varieties with deeply constricted pods are undesirable because soil adheres to the pods and they break during mechanical harvesting and shelling, reducing the market value of the crop. Hence an inheritance study was carried out about the pod shape.

MATERIALS AND METHODS

The material for the study of pod beak and pod constriction consisting of 12 varieties, 14 F_1s and 8 F_2 populations (Tables 1–3) was evaluated in randomized block design with three replications at the Plant Breeding Research Farm, Gujarat Agricultural University, Anand, during kharif 1987–88. Each F_2 population comprised 5 rows with 2.4 m row length and 60 x 15 cm spacing. Pods of each plants of the F_2 populations were classified into groups of with and without pod beak as well as pod constriction. The plants having pods with

---

*Present address: Department of Plant Breeding, Gujarat Agricultural University, Anand Campus, Anand 388110.

prominant or moderate beak/constriction were considered as the beaked/constricted and those with slight beak/constrictions or without beak/constriction were considered as beakless/straight. The data were subjected to χ^2 analysis to test the mode of inheritance of these traits.

RESULTS AND DISCUSSION

The phenotypes of the parents for pod beak and pod constriction are given in Table 1, and for F_1 and F_2 in relation to pod beak and pod constriction in Table 2 and 3, respectively.

The F_1 plants in all the crosses developed pods with prominent or moderate beak. In F_2 all crosses segregated in the ratio of 3 beaked : 1 beakless plants, indicating that the beaked character is dominant over beakless and inherited monogenically. The individual and pooled χ^2 tests for goodness of fit also confirmed the above hypothesis. The genotype of the parents with beaked pods is proposed as BB, and for beakless pods bb. These results are opposite to the findings of a previous study [1], in which beakless condition was reported to be dominant over beaked pods.

Table 1. Origin as well as pod beak and pod constriction characters of peanut genotypes used for hybridization

Parent	Origin	Pod beak	Pod constriction
GG 2	Gujarat	Prominent	Slight
J 11	Gujarat	Slight	Slight
Rajkot Valencia	Gujarat	Slight	Slight
JL 24	Maharashtra	Slight	Moderate
TMV 10	Tamil Nadu	Moderate	—
NcAc 17500	U.S.A.	Prominent	Prominent
NcAc 17278	U.S.A.	Prominent	Prominent
Chico	U.S.A.	Moderate	—
TGE 1	BARC, Trombay	Prominent	Slight
TG 17	BARC, Trombay	Prominent	Prominent
Kadiri 3 (R 33-1)	Andhra Pradesh	Slight	Slight
Kaushal (CG 201)	Uttar Pradesh	Moderate	Slight

In all the crosses analysed for pod constriction, the F_1 plants developed prominant or moderate constriction on the pods. The F_2 populations segregated into four different phenotypic ratios 3:1, 9:7, 54:10, and 27:37 (Table 3). These F_2 phenotypic ratios indicated that pod construction is governed by three pairs of independent nuclear genes, which are interacting with the plasmon. The χ^2 test for individual crosses and pooled over all crosses for goodness of fit also confirmed the above hypothesis. The results are in agreement with the hypothesis proposed by [2]. Using the same gene symbols as proposed earlier (P_{C1}/P_{c1}, P_{C2}/P_{c2} and P_{C3}/P_{c3}) for nuclear genes and A/a for plasmon [2], the probable genotypes of the parents are presented in Table 4.

Table 2. Segregation for pod beak in F_2 populations of different crosses in groundnut

Cross	Pod shape of F_1 plants	Pod beak character in F_2 plants				χ^2 (3:1)	P
		observed		expected			
		beaked	beakless	beaked	beakless		
GG 2 x Kadiri 3	Beaked	118	33	113.2	37.8	0.813	0.50–0.25
J11 x Chico	Beaked	91	36	95.3	31.7	0.778	0.50–0.25
J11 x TGE 1	Beaked	79	37	87.0	29.0	2.942	0.10–0.05
J11 x Kaushal	Beaked	128	45	129.8	43.2	0.099	0.90–0.75
J11 x TG 17	Beaked	136	32	126.0	42.0	3.170	0.10–0.05
JL24 x Chico	Beaked	130	34	123.0	41.0	1.593	0.25–0.10
JL24 x TGE 1	Beaked	117	33	112.5	37.5	1.070	0.50–0.25
JL 24 x Kaushal	Beaked	127	32	119.3	39.7	1.990	0.25–0.10
JL24 x TG 17	Beaked	137	35	129.0	43.0	1.980	0.25–0.10
TMV10 x J11	Beaked	141	43	138.0	46.0	0.195	0.75–0.50
NcAc 17500 x Raj. Val.	Beaked	47	18	48.8	16.2	0.266	0.75–0.50
NcAc 17500 x J11	Beaked	148	56	153.0	51.0	0.653	0.50–0.25
NcAc 17278 x Raj. Val.	Beaked	130	29	118.5	39.5	3.340	0.10–0.05
NcAc 17278 x J11	Beaked	142	49	143.3	47.7	0.011	0.95–0.90
Pooled over crosses	Beaked	2182	512	2020.5	673.5	2.909	0.25–0.10

Table 3. Segregation of pod constriction in F_2 populations of different crosses in groundnut

Cross	Pod constriction in F_1 plants	Pod constriction in F_2 plants				Ratio tested	χ^2	P
		observed		expected				
		present	absent	present	absent			
GG2 x TG 17	Present	66	95	67.9	93.1	27:37	0.092	0.90–0.75
J 11 x TG 17	Present	99	70	97.7	71.3	9:7	0.041	0.90–0.75
JL 24 x TGE 1	Present	118	32	112.5	37.5	3:1	1.070	0.50–0.25
JL 24 x Kadiri 3	Present	59	92	63.7	87.7	27:37	0.550	0.50–0.25
JL 24 x Kaushal	Present	66	93	67.1	91.9	27:37	0.031	0.90–0.75
NcAc 17500 x Raj. Val.	Present	40	32	40.5	31.5	9:7	0.014	0.95–0.90
NcAc 17500 x J 11	Present	99	90	106.3	82.7	9:7	1.140	0.50–0.25
NcAc 17278 x Raj. Val.	Present	135	23	133.3	24.7	54:10	0.138	0.75–0.50

Godness of fit test

Source	For 27:37 ratio			For 9:7 ratio		
	d.f.	χ^2	P	d.f.	χ^2	P
Total	2	0.673	0.75–0.50	2	1.195	0.50–0.25
Pooled	1	0.516	0.50–0.25	1	0.143	0.75–0.50
Heterogeneity	1	0.177	0.75–0.50	1	1.052	0.50–0.25

Table 4. Probable genotypes in respect of pod constriction of the groundnut strains used in crosses

GG 2 x TG 17	
a Pc1 Pc1 pc2 pc2 pc3 pc3	A Pc1 Pc1 Pc2 Pc2 Pc3 Pc3
	or
a pc1 pc1 Pc2 Pc2 pc3 pc3	A Pc1 Pc1 pc2 pc2 Pc3 Pc3
a pc1 pc1 pc2 pc2 Pc3 Pc3	A Pc1 Pc1 Pc2 Pc2 pc3 pc3
J 11 x TG 17	
A pc1 pc1 pc2 pc2 pc3 pc3	A Pc1 Pc1 Pc2 Pc2 pc3 pc3
–Do–	or A Pc1 Pc1 pc2 pc2 Pc3 Pc3
–Do–	or A pc1 pc1 Pc2 Pc2 Pc3 Pc3
JL 24 x TGE 1	
a Pc1 Pc1 Pc2 Pc2 Pc3 Pc3	a Pc1 Pc1 Pc2 Pc2 pc3 pc3
	or
–Do–	a Pc1 Pc1 pc2 pc2 Pc3 Pc3
	or
–Do–	a pc1 pc1 Pc2 Pc2 Pc3 Pc3
JL 24 x Kadiri 3	
a Pc1 Pc1 Pc2 Pc2 Pc3 Pc3	a pc1 pc1 pc2 pc2 pc3 pc3
JL 24 x Kaushal	
a Pc1 Pc1 Pc2 Pc2 Pc3 Pc3	a pc1 pc1 pc2 pc2 pc3 pc3
NcAc 17500 x Rajkot Valencia	
A Pc1 Pc1 Pc2 Pc2 pc3 pc3	xx pc1 pc1 pc2 pc2 pc3 pc3
or	
A Pc1 Pc1 pc2 pc2 Pc3 Pc3 or	–Do–
A pc1 pc1 Pc2 Pc2 Pc3 Pc3 or	–Do–
NcAc 17500 x J 11	
A Pc1 Pc1 Pc2 Pc2 pc3 pc3	A pc1 pc1 pc2 pc2 pc3 pc3
or	
A Pc1 Pc1 pc2 pc2 Pc3 Pc3	–Do–
or	
A pc1 pc1 Pc2 Pc2 Pc3 Pc3	–Do–
NcAc 17278 x Rajkot Valencia	
A Pc1 Pc1 Pc2 Pc2 Pc3 Pc3	x a pc1 pc1 pc2 pc2 pc3 pc3

REFERENCES

1. C. Balaiah, P. S. Reddy and M. V. Reddy 1977. Genetic analysis in groundnut. I. Inheritance studies on 18 morphological characters in crosses with Gujarat narrow leaf mutant. Proc. Indian Acad. Sci., **85B**: 340–350.

2. R. A. Coffelt and R. O. Hammons. 1974. Inheritance of pod constriction in peanuts. J. Hered., **65**: 94–96.