

## Genetics of Fertility Restoration and Variability for Nodulation and Yield Traits in Pigeonpea

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**ABSTRACT:** Genetics of fertility restoration conducted with four back crosses along with their restores revealed monogenic to digenic ratios for the material under study. Wide range of variability was observed for plant height followed by number of pods per plant, seed yield per plant, number of secondary branches, days to maturity and days to 50 per cent flowering. The crosses ICPA 2092 x ICPR 10934, ICPA 2092 x ICPR 3473, ICPA 2092 x ICPR 10650 and ICPA 2092 x ICPR 87119 showed better performance for nodulation as well as yield and yield contributing characters. Correlation studies revealed that number of secondary branches; number of pods per plant and per cent pod setting has significant positive correlation with yield per plant at both genotypic and phenotypic levels. Among nodulation characters, number of nodules per plant and shoot dry weight recorded significant positive association with yield per plant.

**Key words:** Fertility restoration, variability, nodulation, pigeonpea

### INTRODUCTION

The pigeonpea area, production and productivity trends in India in last five decades shows that, there was about 2% increase in the area per year, but the yield levels are stagnated around 600-700 kg/ha (Saxena, 2005). Efforts have been made in past to increase the average productivity by developing high yielding varieties. In spite of release of over 100 good varieties, yield levels did not increase significantly. Perhaps, the other reason for low yields of pigeon pea was susceptibility to diseases and pod borer complex. Although India produces 2.4 million tonnes of pigeonpea, the per capita availability of pigeonpea is gradually declining and one of the main reasons for this is widening of demand and supply gap due to mismatch in the growth of human population and production of protein rich pulses. In order to maintain self-sufficiency in pulses production for the ever-increasing population, a proportionate increase in their production is essential. In this endeavour, the use of hybrid pigeon pea technology has potential.

Considering the limitations in large scale hybrid seed production encountered due to genetic nature of male-sterility and the prospects of hybrids in yield enhancement through breeding, the development of

an efficient cytoplasmic nuclear male sterility (CMS) system became necessary. It is also essential to study nodulation behaviour in inter specific crosses in pigeonpea.

### MATERIALS AND METHODS

The present investigation was carried out to study the genetics of fertility restoration and variability for nodulation, yield and yield contributing characters and correlation. The experiment consists of four back crosses and their restores and 14 fertile F<sub>1</sub>s along with GTH1 and BSMR 736 as standard checks. Four back crosses along with their restorers were tested for above observations during *Kharif* 2009 at Experimental Farm of Department of Agricultural Botany, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani. Further, 14 fertile F<sub>1</sub>'s along with two checks *viz.*, GTH 1 and BSMR 736 were separately tested for genetic variability, nodulation and yield traits. Observations recorded were fertility restoration per cent, days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g), per cent pod

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setting, grain yield per plant (g), number of nodules per plant, nodules fresh weight (mg), nodules dry weight (g), main root length (cm) shoot dry weight (g), seed protein (%) and straw protein content (%).

## RESULTS AND DISCUSSION

### Mean Performance

Analysis of variance showed significant differences among the treatments for all the characters. This indicated the wide range of variability among the genotypes for yield and yield contributing characters as well as nodulation characters. Maximum number of pods per plant were observed in ICPA 2092 x ICPR 10934 (222.7). Maximum number of seeds per pod was observed in ICPA 2092 x ICPR 10650 (4.5). Trait 100 seed weight was the highest in ICPA 2092 x ICPR 10650 (14.50 g). Per cent pod setting was maximum in ICPA 2092 x ICPR 10934 (24.1 per cent). The highest seed yield per plant was observed in ICPA 2092 x ICPR 10934 (61.13g). These results were in agreement with Gupta (2005) and Pansare (2008).

### Fertility Restoration Per cent

The study of fertility restoration per cent is essential in hybrid development programme (Table 1). The parent which are able to produce fertile F1 can be used as male parents. The genotype ICPA 2092 x ICPR 10934 (91.66 per cent) showed the highest fertility restoration followed by ICPA 2092 x ICPR 3473 (85.36 per cent) and ICPA 2092 x ICPR 10650 (81.30 per cent). The genotype ICPA 2043 x ICPR 2463 (59.01 per cent) showed the lowest fertility restoration. Similar results were reported earlier by Jogendra Singh and Bajpai (2005).

### Nodulation Characters

The highest numbers of nodules per plant were observed in ICPA 2092 x ICPR 10934 (19.5). Maximum nodules fresh weight was observed in ICPA 2092 x ICPR 10934 (120.65 mg). The nodules dry weight was the highest in ICPA 2092 x ICPR 10934 (20.05 mg). Main root length was highest in ICPA 2092 x ICPR 10934 (44.45 cm). Maximum shoot dry weight was observed in ICPA 2043 x ICPR 3471 (1.35 g). The highest seed protein content was observed in ICPA 2047 x ICPR 3513 (24.56 per cent). Tikle and Gupta (2006) confirmed the above findings.

### Genetic Variability

There can be little doubt that the existence of genetic variability is advantageous to the evolutionary

survival of a species, yield improvement in any crop can be brought out through plant breeding but necessary variability upon which selection is to be practiced must be available in the genetic material. In general, wide range of variability was observed for characters plant height followed by number of pods per plant, yield per plant, number of secondary branches, days to maturity and days to 50 per cent flowering (Pansare, 2008) (Table 2). Among nodulation characters, nodules fresh weight exhibited wide range of variability followed by main root length, number of nodules per plant, nodules dry weight and seed protein content (Namdeo *et al.*, 1988 and Tikle and Gupta, 2006).

In the present study, highest genotypic and phenotypic coefficient of variation were observed for the characters shoot dry weight, number of secondary branches per plant followed by number of primary branches per plant, yield per plant, per cent pod setting, plant height, number of seeds per pod and number of pods per plant (Gupta, 2005). The nodulation characters viz., shoot dry weight followed by nodules dry weight, number of nodules per plant, nodules fresh weight and seed protein content recorded the highest GCV and PCV for the material under study (Karahne *et al.*, 2001). The range of heritability was from 45.14 per cent for number of seeds per pod to 98.00 per cent for seed yield per plant. Heritability estimates were high for days to 50 per cent flowering, days to maturity, plant height, number of secondary branches per plant, number of pods per plant, 100 seed weight, per cent pod setting and seed yield per plant, while number of primary branches per plant and number of seeds per pod recorded moderate heritability estimates. Similar results were obtained by Aher *et al.* (1998) and Patel and Patel (1998). Heritability estimates for nodulation characters were high for all the characters. The range of heritability was from 71.42 per cent for number of nodules per plant to 96.78 per cent for nodules dry weight.

### Correlation

Correlation of characters are of interest for three main reasons, firstly, in connection with genetic cause of correlation through the pleiotropic action of genes, secondly in connection with the change brought about by selection i.e. important to know the improvement of one character will cause simultaneous changes in other characters and thirdly in connection with the natural selection. The characters number of secondary branches per plant, number of pods per plant and per

**Table 1**  
Fertility Restoration in Pigeonpea Hybrids

Sr. No.	Name of genotypes	Total plants	Fertile plants	Sterile plants	Fertility restoration (%)
1	2	3	4	5	6
1	ICPA 2048 x ICPR 10650	118	80	38	67.79
2	ICPA 2092 x ICPR 3473	123	105	18	85.36
3	ICPA 2048 x ICPR 3513	122	79	43	64.75
4	ICPA 2092 x ICPR 10934	120	110	10	91.66
5	ICPA 2048 x ICPR 3514	122	76	46	62.29
6	ICPA 2092 x ICPR 10650	123	100	23	81.30
7	ICPA 2043 x ICPR 2463	122	72	50	59.01
8	ICPA 2043 x ICPR 10650	124	95	29	76.61
9	ICPA 2043 x ICPR 3471	120	87	33	72.50
10	ICPA 2092 x ICPR 87119	119	93	26	78.15
11	GTH 1 (check)	119	83	36	69.74

**Table 2**  
Parameters of Genetic Variability for Yield and Nodulation Characters in Pigeonpea

Sr. No.	Characters	Range	General mean	Genotypic variance ( $6^2g$ )	Phenotypic variance ( $6^2p$ )	GCV (%)	PCV (%)	Heritability (%)	Genetic advance	EGA (%)
1.	Days to 50% flowering	106.50 - 125.00	118.19	26.33	34.93	4.34	5.00	75.40	9.18	7.77
2.	Days to maturity	169.50 - 188.50	179.38	32.52	37.98	3.18	3.44	85.61	10.87	6.06
3.	Plant height (cm)	177.40 - 236.90	207.83	396.26	408.88	9.58	9.73	96.91	40.37	19.42
4.	Number of primary branches per plant	13.70 - 24.80	17.55	7.73	12.17	15.84	19.87	63.55	4.57	26.02
5.	Number of secondary branches per plant	18.40 - 37.50	26.34	31.34	35.55	21.25	22.63	88.17	10.83	41.10
6.	Number of pods per plant	166.30 - 222.70	197.64	296.44	314.99	8.71	8.97	94.35	34.45	17.43
7.	Number of seeds per pod	3.25 - 4.50	3.72	0.08	0.18	7.71	11.48	45.14	0.39	10.68
8.	100- seed weight (g)	11.75 - 14.50	13.10	0.56	0.74	5.73	6.57	76.09	1.35	10.29
9.	Per cent pod setting	16.00 - 24.10	19.85	6.33	6.62	12.68	12.96	95.65	5.07	25.54
10.	Yield per plant (g)	41.07 - 61.13	49.97	43.17	44.06	13.15	13.28	98.00	13.39	26.81
11.	Number of nodules per plant	10.00 - 19.50	13.91	4.87	6.82	15.86	18.77	71.42	3.84	27.62
12.	Nodules fresh weight (mg)	71.65 - 120.50	93.19	166.34	180.15	13.84	14.40	92.33	25.53	27.39
13.	Nodules dry weight (mg)	11.20 - 20.05	15.04	7.10	7.34	17.72	18.01	96.78	5.40	35.91
14.	Main root length (cm)	33.60 - 44.45	38.18	9.44	11.06	8.05	8.71	85.35	5.85	15.32
15.	Shoot dry weight (g)	0.65 - 1.35	0.95	0.05	0.06	22.25	25.93	73.63	0.37	39.32
16.	Seed protein content (%)	17.09 - 24.56	20.83	5.82	6.79	11.58	12.51	85.78	4.60	22.10
17.	Straw protein content (%)	7.38 - 8.41	7.93	0.07	0.09	3.43	3.78	82.27	0.51	6.40

cent pod setting recorded significant and positive association with yield per plant at both the levels (Table 3). Number of seeds per pod recorded significant and positive correlation with yield per plant at genotypic level indicating that these characters were the prime contributing characters to yield per plant. Among the nodulation characters, number of nodules per plant and shoot dry weight

recorded significant positive association at genotypic level (Table 4). Association at phenotypic level indicating that these characters were the prime contributors for yield per plant. Nodules fresh weight, nodules dry weight and main root length exhibited positive association with yield per plant at both the levels. Namdeo *et al.* (1988) reported the similar findings.

**Table 3**  
**Estimates of Genotypic and Phenotypic Correlation Coefficients between Yield and Yield Contributing Characters in Pigeonpea**

Sr. No.	Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of pods per plant	Number of seeds per pod	100- seed weight (g)	Per cent pod setting	Yield per plant (g)
1	2		3	4	5	6	7	8	9	10	11	12
1.	Days to 50% flowering	G	1.000	0.945**	0.111	-0.524*	0.021	-0.264	0.050	-0.357	-0.120	-0.103
		P	1.000	0.894**	0.108	-0.374	-0.011	-0.231	-0.044	-0.307	-0.111	-0.110
2.	Days to maturity	G		1.000	0.093	-0.316	-0.060	-0.382	-0.227	-0.379	-0.232	-0.268
		P		1.000	0.090	-0.297	-0.045	-0.326	-0.192	-0.361	-0.216	-0.247
3.	Plant height (cm)	G			1.000	0.236	0.513*	0.010	0.102	0.624**	0.183	0.144
		P			1.000	0.183	0.468*	0.014	0.108	0.540*	0.174	0.129
4.	Number of primary branches	G				1.000	0.632**	0.348	-0.127	0.391	0.494*	0.193
		P				1.000	0.385	0.225	-0.109	0.412	0.376	0.161
5.	Number of secondary branches	G					1.000	0.617**	0.405	0.698**	0.789**	0.731**
		P					1.000	0.578*	0.357	0.546*	0.725**	0.696**
6.	Number of pods per plant	G						1.000	0.276	0.323	0.951**	0.921**
		P						1.000	0.214	0.248	0.936**	0.894**
7.	Number of seeds per pod	G							1.000	0.454	0.327	0.652**
		P							1.000	0.102	0.230	0.411
8.	100- seed weight (g)	G								1.000	0.407	0.321
		P								1.000	0.350	0.305
9.	Per cent pod setting	G									1.000	0.907**
		P									1.000	0.892**
10.	Yield per plant (g)	G										1.000
		P										

\* and \*\* indicates significance at 5 and 1 per cent level respectively.

**Table 4**  
**Estimates of Genotypic and Phenotypic Correlation Coefficients between Yield and Nodulation Characters in Pigeonpea**

Sr. No.	Characters		Number of nodules per plant	Nodules fresh weight (mg)	Nodules dry weight (mg)	Main root length (cm)	Shoot dry weight (g)	Seed protein content (%)	Straw protein content (%)	Yield per plant (g)
1	2		3	4	5	6	7	8	9	10
1.	Number of nodules per plant	G	1.000	0.982**	0.918**	0.845**	0.704**	-0.173	-0.599**	0.544*
		P	1.000	0.923**	0.817**	0.697**	0.656**	-0.177	-0.441	0.460
2.	Nodules fresh weight (mg)	G		1.000	0.928**	0.791**	0.663**	-0.185	-0.583*	0.373
		P		1.000	0.914**	0.714**	0.635**	-0.199	-0.512*	0.364
3.	Nodules dry weight (mg)	G			1.000	0.593**	0.492*	0.019	-0.425	0.162
		P			1.000	0.548*	0.450	0.015	-0.352	0.169
4.	Main root length (cm)	G				1.000	0.638**	-0.322	-0.790**	0.357
		P				1.000	0.569*	-0.249	-0.614**	0.322
5.	Shoot dry weight (g)	G					1.000	-0.429	-0.821**	0.483*
		P					1.000	-0.391	-0.595**	0.422
6.	Seed protein content (%)	G						1.000	0.399	-0.574*
		P						1.000	0.404	-0.512*
7.	Straw protein content (%)	G							1.000	-0.214
		P							1.000	-0.166
8.	Yield per plant (g)	G								1.000
		P								

\* and \*\* indicates significance at 5 and 1 per cent level respectively.

**Table 5**  
**Genetics of Fertility Restoration in Pigeonpea**

Cross	Total plants	$\chi^2$ cal	Cross	Total plants	$\chi^2$ cal
F <sub>2</sub> ratio			BC <sub>1</sub> F <sub>1</sub> ratio		
3:1 ratio			1:1 ratio		
ICPA 2092 x ICPR 2766	428	0.20**	(ICPA 2092 x ICPR 2766) x ICPR 2766	110	3.5**
ICPA 2048 x ICPR 3477	430	4.42*	(ICPA 2048 x ICPR 3477) x ICPR 3477	115	3.83**
15:1 ratio			3:1 ratio		
ICPA 2047 x ICPR 3513	376	0.01**	(ICPA 2047 x ICPR 3513) x ICPR 3513	376	21.57
ICPA 2043 x ICPR 2766	179	0.31**	(ICPA 2043 x ICPR 2766) x ICPR 2766	108	0.44**

### Genetics of Fertility Restoration

The genetics of fertility restoration has importance for the transfer of restorer gene from one parent to another parent having other desirable characters. Similarly, as it is controlled by few genes, identification of restorer parents is also easy. The data collected on segregation of F<sub>2</sub> and BC<sub>1</sub>F<sub>1</sub> population for fertility restorations is given in (Table 5). Out of four cross combinations, two crosses exhibited 3 fertile : 1 sterile ratio in F<sub>2</sub> and 1 fertile : 1 sterile in backcross generations. This reveals the monogenic control for fertility restoration. The genetics of fertility restoration has importance for transfer of restorer genes from one parent to another having other desirable characters. Verulkar and Singh (1997) observed 3 fertile : 1 sterile ratio in F<sub>2</sub> and 1:1 ratio in backcross generation in pigeonpea. Desirable genotypes having positive correlation, high direct effects and high indirect effects via other characters if coupled with high heritability can be advanced for further improvement.

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