

## Inheritance of arthritic mutation in pea

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### ABSTRACT

The inheritance of arthritic mutation in pea was studied using 10 crosses involving 11 parents of diverse origin. The inheritance pattern was studied with the  $\chi^2$  test for goodness of fit for segregation in individual crosses as well as on pooled data basis. The total number of plants in  $F_2$  generation ranged from 133 (P 1746-1 X P 1760) to 830 (P 1743 X P 1746-4-1) in different crosses (total 3134 plants). The study confirmed that arthritic mutation is controlled by a single recessive gene designated as *art 1*. This character has potential application in pea breeding for restructuring plant type for higher productivity.

Key words: Arthritic, Inheritance, Pea, *Pisum sativum*

Pea (*Pisum sativum* L.) has been one of the most classical plants for genetic studies for over a century. Mendel (3) laid the foundation of genetics by discovering the laws of seven qualitative characters using pea as an object of study. Since then, nearly 500 genes have been discovered in pea having simple monogenic inheritance obtained through spontaneous or induced mutations. About 200 genes have been mapped and have been assigned to different linkage groups (2, 5). Restructuring the plant type for higher productivity is an important option. The arthritic mutation (1), characterized by swelling of nodes and availability of several nodes (very short internodes) in dwarf genetic background has definite scope in pea breeding. In view of this, the present study was undertaken to understand the inheritance of arthritic mutation in pea.

### MATERIALS AND METHODS

The present study was undertaken with 10 crosses derived from eleven parental lines of diverse origin where three lines (P 1746-4-1, P 1746-23-2, P 1746-1) possess the arthritic nature and remaining lines (P 1760, P 1757, P 1746-21-2, P 1743, P 1745, P 1879, P 1883-2, P 1749) have normal plant type. The crosses were attempted during *rabi* 2001-02 at the Research Farm of the Division of Genetics, IARI, New Delhi (Table 1). The part of  $F_1$  seeds were grown for generation advancement at Off-season Wheat Summer Nursery, Dalang Maidan, Lahaul Valley, H.P. The  $F_2$  populations along with parents and  $F_1$ s were raised during *rabi* 2002-03 at IARI, New Delhi. All the  $F_2$  plants were tagged in each population and data on presence or absence of arthritic mutation were recorded at podding stage. The plants were classified either arthritic or normal as there was conspicuous difference between the two phenotypes. The observations were also recorded in parents and all the  $F_1$ s. The  $\chi^2$  test was applied to test the goodness of fit for 3:1 segregation ratio as per method of Panse and Sukhatme (4). Pooled analysis over all the 10 crosses was also done to interpret the results. The selected  $F_3$  progenies were also grown to confirm the  $F_2$  segregation ratio.

### RESULTS AND DISCUSSION

The  $F_1$ s of all the ten crosses were found to be having normal phenotype indicating recessive nature of arthritic mutation. For testing of the goodness of fit of the observed segregation pattern with that of expected ratio, the  $F_2$  data

Table 1.  $F_2$  segregation for arthritic character in different crosses of pea

Cross	$F_1$ phenotype	$F_2$ segregation			$\chi^2$ (3:1)	P value
		Normal	Arthritic	Total		
P1879 X P 1746-4-1	Normal	185	62	247	0.001	0.97
P 1746-21-2 X P 1746-23-2	Normal	122	45	167	0.337	0.59
P 1749 X P 1746-1	Normal	280	96	376	0.056	0.81
P 1883-2 X P 1746-4-1	Normal	322	97	419	0.764	0.45
P 1746-1 X P 1757	Normal	160	55	210	0.158	0.69
P 1743 X P 1746-4-1	Normal	630	200	830	0.361	0.68
P 1745 X P 1746-1	Normal	225	76	301	0.010	0.92
P 1746-1 X P 1743	Normal	172	55	227	0.072	0.79
P 1746-1 X P 1760	Normal	101	32	133	0.062	0.80
P 1746-23-2 X P 1745	Normal	165	59	224	0.214	0.68
Pooled analysis over 10 crosses	Normal	2362	772	3134	0.225	0.65
Heterogeneity $\chi^2$ at 9 d.f.	Normal				1.81	>0.90

were considered for  $\chi^2$  test for 3:1 ratio. The number of plants in different categories regarding all the 10 crosses and their respective calculated  $\chi^2$  values are given in Table 1. The  $\chi^2$  value based on pooled data over all the crosses has also been given in Table 1 along with P value at 9 d.f. The ratio of normal and arthritic plants in each  $F_2$  population of each of the 10 crosses was tested for goodness of fit to the expected segregation of 3 normal : 1 arthritic as the number of normal plants were far exceeding than the arthritic plants in each crosses.

The calculated  $\chi^2$  values of all the crosses were found to be non-significant at 5% level of significance. This indicated that the segregation pattern in all the crosses under study were in close agreement with the segregation pattern of 3 normal : 1 arthritic plants at 95% level of confidence. Additionally, higher P-values ranging from 0.45 (P 1883-2 X P 1746-4-1) to 0.97 (P 1879 X P 1746-4-1) in different crosses also supported the acceptability of 3 normal : 1 arthritic phenotypes. The non-significant heterogeneity  $\chi^2$  ( $P > 0.90$ ) for 3:1 segregation ratio allowed the pooling of data of all the crosses. The pooled analysis of data over 10 crosses (3134 plants) also segregated in the ratio of 3 normal : 1 arthritic plants with non-significant  $\chi^2$  value at 5% level of significance. Thus, it can be concluded that the arthritic phenotype in pea

is controlled by a single recessive gene, designated as *art 1*. The homozygous dominant (*Art 1 Art 1*) and heterozygous (*Art 1 art 1*) plants will produce normal phenotype whereas the arthritic plants will be produced under homozygous recessive (*art 1 art 1*) condition. The segregation behaviour of selected  $F_2$  progenies (data not presented) also confirmed the monogenic recessive nature of *art 1* gene.

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