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Short Communication

Inheritance of resistance to bud fly infestation in linseed (*Linum usitatissimum* L.)

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Abstract

Genetic analysis was carried out to determine the mode of inheritance of resistance to bud fly which is a key pest of linseed during flowering stage. Parents, F_1, F_2, BC_1 and BC_2 populations of three crosses involving two resistant, IC 15888 and JRF4 and two susceptible parents, *viz*., Neelum and GS-41 were the experimental materials. Reaction to bud fly in F_1s of all the three crosses indicated that resistance was dominant over susceptibility. The F_2 and back cross segregants were categorized in to resistant and susceptible classes based on per cent bud infestation. The genetic analysis in F_2 generation revealed that two dominant complementary genes in IC 15888 control the bud fly resistance, while JRF 4 carried a single dominant gene for resistance. The F_2 results were confirmed by genetic analysis of back cross populations. It can be categorically stated that the knowledge of number and nature of resistance genes in IC 15888 and JRF4 will be valuable for development of bud fly resistant varieties in linseed.

Key words : Inheritance, resistance, bud fly, infestation, linseed

Bud fly (*Dasyneura lini* Barnes) is a serious pest of linseed in Asia particularly India, Bangladesh and Pakistan (Pruti and Bhatia 1937; Biswas and Dass 2011) and its incidence on linseed was reported first time in India by Pruthi and Bhatia (c.f.) from Pusa (Bihar). It attacks the crop during flowering stage by infesting flower buds. The maggots of bud fly feed upon the reproductive parts of the flower buds. The infested buds twin hollow due to crumpling of the corolla and their reproductive parts become emaciated at green bud stage. These buds remain unfertilized and no seed formation take place. Yield losses in linseed due to bud fly have been estimated to the tune of 90% in Maharastra followed by 80% in Uttar Pradesh, 75% in Madhya Pradesh, 62% in Odisha, 60% in Bihar, 46% in Rajasthan and 35% in West Bengal. Complete failure of crop due to this pest has also been observed under epidemic conditions (Malik, 1999). Such quantum of yield losses can be kept at bay through the adoption of bud fly resistant linseed varieties which would sustain the crop in the country.

Linseed/flax (*Linum usitatissium* L.) is an oil and fibre producing crop and occupies greater importance among oilseeds owing to its various uses and special qualities *i.e*. flax fibre and omega 3. Important linseed growing countries are India, Canada, China, USA, Ethiopia, Egypt, Argentina and Greece.

Average productivity of this crop in India is 408 kg/ha, which is far below than 575 kg/ha in Asia and 867 kg/ha at global level during 2012-13 (Anonymous 2012). Among the various factors responsible for low productivity, biotic constraints play a significant role. A wide range of chemicals are being used to control the biotic stresses. But the chemicals besides being uneconomical and health hazard, do not provide permanent solution because causal organisms frequently develop resistance to excessively used chemicals. Henceforth, incorporation of genetic resistance is a cheap, viable and eco-friendly alternative to reduce losses from biotic stresses. Though a number of germplasm have been reported

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as resistant to linseed bud fly (Singh and Ramanand 2000; Malik and Srivastava 2011) but the report on its inheritance pattern is lacking till date. Hence, the present investigation was planned in order to understand the mode of inheritance of bud fly resistance in linseed.

In order to determine the nature and number of resistance gene (s), two bud fly resistant genotypes, IC15888 and JRF 4 identified through field screening over the years under late sown conditions were crossed with two susceptible parents *viz*., Neelum and GS 41during *rabi* 2010-2011. Morphological, traits such as flower colour, seed size and other contrasting characters among parents were used as markers to check the trueness of F_1 hybrids (Table 1). Thereon, only true F_1 were used for the backcrossing and advancement of generation. Six basic populations i.e. P_1, P_2, F_1, F_2, BC_1 and BC_2 thus developed were evaluated in compact family block design with three replications under late sown conditions (28.11.12) during 2012-13 at Oilseeds Research Farm, C.S. Azad Univ. of Agric. & Techn., Kanpur. Parents and F1s of each cross were raised in single row of 5 m length whereas, F_2 and backcrosses (BC_1 and BC_2) were grown in four and two rows, respectively. Infector row technique with Neelum was adopted at every 10^{th} row as well as on boarder around the experimental field to maintain the sufficient bud fly populations.

Bud fly infestation in percent was estimated by counting the number of infested and healthy buds. Plants were classified in to two categories i.e. resistant (up to 15 % bud infestation) and susceptible (above 15 % bud infestation) as classification of plants in several categories may lead to wrong conclusions and a distorted segregation ratio.

Table 1. Details of the parents used in the present study

Parents	Pedigree/source	Pest reaction	Flower colour	Seed colour	Plant height
IC 15888	Indegenous collection	Resistant	Blue	Brown	Medium
Neelum	T1 x NP (RR)-9	Susceptible	Blue	Dark brown	Medium
JRF-4	Exotic	Resistant	White		Tall flax
GS-41	Exotic	Susceptible	Blue	Brown	Dwarf

Table 2. Segregation of field reaction to bud fly infestation in F_1, F_2 and backcross populations of linseed

Cross	No. of observed plants	Observed frequency		Expected frequency		Ratio R : S	χ^2 value	Probability
		R	S	R	S			
IC 15888 (P1) x Neelum (P2)								
F_1	35	35						
F_2	280	149	131	157.50	122.50	9 : 7	1.047	0.30-0.20
BC_1 (F_1 x P_1)	93	93	00	93.00	00	-		
BC_2 (F_1 x P_2)	124	37	87	31.00	93.0	1 : 3	1.548	0.30-0.20
Neelum(P_1) x JRF4 (P_2)								
F_1	32	32						
F_2	269	196	73	201.75	67.25	3 : 1	0.654	0.50-0.30
BC_1 (F_1 x P_1)	114	53	61	57.00	57.00	1 : 1	0.560	0.50-0.30
BC_2 (F_1 x P_2)	91	91	00	91.00	00.00	-		
JRF_4 (P_1) x GS 41 (P_2)								
F_1	30	30						
F_2	286	221	65	214.50	71.50	3 : 1	0.786	0.50-0.30
BC_1 (F_1 x P_1)	89	89	00	89.00	00.00	-		
BC_2 (F_1 x P_2)	118	62	56	59.00	59.00	1 : 1	0.304	0.70-0.50

R = Resistant and S = Susceptible

The chi- square $(\chi)^2$ test was used to study the genetics of bud fly resistance in linseed as suggested by Snedecor and Cochran (Snedecor and Cochran 1989). The significance of chi-square value was tested against table value with (n-1) degrees of freedom, where n is total number of segregating classes

High bud fly infestation was observed in the experimental plot as reflected by more than 60% bud infestation on the susceptible cultivars. The F_1 plants involving resistant x susceptible and/or susceptible x resistant parents were uniformly resistant in all the three crosses studied (Table 2). These observations indicate that resistance to bud fly in linseed was inherited as a dominant trait.

The F_2 populations derived from the cross between IC15888 x Neelum segregated in 149 R : 131S plants. The observed data gave a good fit to the expected segregation ratio of 9R: 7 S with non-significant chi-square value. This finding indicates the involvement and presence of two dominant complementary genes in IC15888 for controlling resistance against linseed bud fly. The backcrosses segregation pattern also confirmed F_2 results as all the plants in BC_1 were observed to be resistant whereas, in BC_2 population all the observed 124 plants segregated in the ratio of 3 susceptible : 1 resistant.

Thus, segregation pattern in backcross progenies further confirms the hypothesis proposed on the basis of F_2 data that two dominant complementary genes are responsible for imparting bud fly resistance in donor parent IC 15888.

F_2 population of the remaining crosses *viz*., Neelum X JRF 4 and JRF 4 x GS 41 showed a good fit to a segregation ratio of 3 R : 1 S with non-significant chi-square values (0.654 and 0.786) indicating that the resistant cultivar JRF 4 carries a single dominant gene for resistance against bud fly. The backcross populations (BC1 and BC2) segregated in 1R : 0S and 1R : 1S ratio, respectively confirming the results observed in F_2 generation of both crosses.

In the light of non-availability of any report on mode of inheritance of bud fly resistance in linseed, the present finding would be very much helpful to linseed breeders in formulating resistance breeding programme worldwide as no differences in insect diversity occur between linseed grown for seed, fibre or both. It can be suggested that simple selection in direct and back cross advanced generations would be effective for introgression of bud fly resistance in linseed.

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