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Inheritance of yellow rust resistance in barley (*Hordeum vulgare* L.)

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Abstract

The study was undertaken to determine the mode of inheritance of resistance to yellow rust (*Puccinia striiformis* f.sp. *hordei*) in identified barley lines, which are to be utilized in crossing programme for development of resistant varieties. Four resistant lines namely, RD 2552, RD 2503, RD 2508 and RD 2634 were crossed with susceptible line RD 103 to know the inheritance pattern of yellow rust resistance. The parents, F_1, F_2 and back cross generations of each cross were screened under artificially created epiphytic conditions for yellow rusts using a mixture of five barley pathotypes. The genetic analysis of different generations indicated that resistance to yellow rust of barley in the lines studied was governed by single dominant gene as the observed data segregated in 3:1 ratio. The dominance of resistance over susceptibility was confirmed by F_2 and back cross generations of different cross combinations.

Key words: Barley, *Puccinia striiformis*, inferitance, genetic analysis

Introduction

Yellow rust caused by (*Puccinia striiformis hordei*) is one of the disastrous disease of barley (*Hordeum vulgare* L.) in the world. In India it is very important in the north western plains and adjoining Himalayan hills region, where its annual recurrence is ensured by the summer crop and volunteer plants in the higher hills. The disease starts appearing in the plains during mid December to beginning of January and thrives well under the cold conditions. It reaches the peak infection level during the month of February and persists till March (in plains) to April/ May (in lower hills). In case of the early incidence, it can cause very heavy losses in the crop and can sometimes prevent the ear head emergence or the grain formation/ development. Losses to the tune of 38% have been reported under severe incidence [1].

Since the chemical control is not a vaible proposition, being the multiple cycle disease with 12-15 days incubation period for fresh infection, resistance breeding has been preferred under the all India coordinated programme. The successful breeding programmes designed to produce disease resistant barley varieties starts with identifying sources and nature of resistance conferring genes [2, 3]. By knowing whether the resistance being handled, is controlled by either one, a few or many genes and also whether it is dominant or recessive to susceptibility, a breeding programme can be designed for the development of yellow rust resistant barley varieties. In India, the information on the inheritance pattern of the resistance to yellow rust is very limited [4-6]. An attempt was also made to develop the isogenic lines by transferring the known resistance genes in the background of Fongtein barley at IARI, Shimla [7], however that material is no more available for studies. Identification of new sources from different accessions [8-10] have also been taken up, but the inheritance studies have not been taken up on these sources in recent past. In the present study an attempt has been made to know the inheritance of the resistance in three newly developed cultivars and one advanced line to enable the breeders to plan their yellow rust breeding programme in the country.

Materials and methods

The genetic material was developed by using five barley varieties including resistant (RD 2552, RD2503, RD2508 and RD 2634) and susceptible (RD103) parents for barley yellow rust (Table 1). Crosses were made between susceptible variety RD 103 (as female) with all the resistant parents. The F_1 was used for back crossing with both the parents to raise the back cross generations BC_1 and BC_2 as well as selfed to raise F_2 generation. The parents, F_1, BC_1, BC_2 and F_2 generations of each cross were screened under artificially created epiphytic conditions for yellow rusts using a mixture of five barley pathotypes (0S0-1, 1S0, 5S0, 0S0 and 4S0)

received from DWR RS, Flowerdale, Shimla. The seeds were sown with 23cm row to row and 10 cm plant to plant distances, and experimental lines were surrounded with the infector line (RD103) for development of proper epiphytic condition. The infector was first inoculated at 21 day seedling stage with the mixed inoculum of yellow rust races followed by repeated sprays of inoculum collected from infector on the test lines. The field was given extra irrigation for better development of disease and the inoculum load was so heavy that there were no chances of escape from disease.

Observations were taken at the late flowering stage when the maximum epiphytotic condition was obtained and when the susceptible (infector) rows showed 100% disease development. The plants were classified as resistant (no apparent symptoms or flecking on the leaf or with very small resistant types pustules) or susceptible (showing well developed susceptible type of pustules of yellow rust with no yellowing of tissue around). The goodness of fit to Mendelian segregation of resistant and susceptible plants in the segregating population was tested by Chi-Square test. The significance of Chi-Square (χ^2) value was tested with (n-1) degrees of freedom, where n is the total number of segregating classes [11].

Results and discussion

Promising and stable resistance is being sought for development of rust resistant high yielding variety in the barley improvement programme. Inheritance of yellow rust reaction was studied in the parents and their F_1, F_2, BC_1 and BC_2 generations involving four crosses of barley. Results of field study are presented in Table 2. As expected all plants of resistant parents, namely RD 2552, RD 2503, RD 2508 and RD 2634 were free from yellow rust, while all plants of RD 103 were highly susceptible to it. The F_1 plants of all the four crosses were also resistant. It indicated that resistance is dominant over susceptibility in all the cases. The F_2 populations of all the crosses segregated in a phenotypic ratio of 3:1 (resistant: susceptible) indicating that resistance in all the four crosses was governed by single dominant gene (Table 2).

When each of the F_1 was back crossed to susceptible parent RD 103, the BC_1 population segregated into 1 resistant: 1 susceptible phenotypic ratio in all the four crosses supporting the F_2 data observations of single dominant gene for resistance. In

Table 1. Parentage of the resistant and susceptible genotypes used in the study

Genotype	Parentage	Reaction to yellow rust
RD 103	RDB 1 / K18	Susceptible
RD 2503	RD 103/ BH153 // RD2046	Resistant
RD 2508	RD 2035 / P490	Resistant
RD 2552	RD 2035 / DL 472	Resistant
RD 2634	RD2035 / RD2535	Resistant

Table 2. Yellow rust observations in different generations of resistant x susceptible crosses

Genotype/ Generation	Disease reaction ratio (Observed)		Disease reaction ratio (Expected)		χ^2(C)
Cross I	R	S	R	S	
RD 103	0	All			
RD 2552	All	0			
F_1	All	0			
BC1(F_1x RD103)	15	13	14	14	0.035
BC2(F_1x 2552)	29	0			
** F_2	57	16	54.75	18.25	0.222
Cross II					
RD103	0	All			
RD2503	All	0			
F_1	All	0			
BC1(F_1x RD103)	27	28	27.5	27.5	0.001
BC2(F_1x RD2503)	35	0			
** F_2	60	18	58.5	19.5	0.068
Cross III					
RD 103	0	All			
RD2508	All	0			
F_1	All	0			
BC1(F_1x RD103)*	24	25	24.5	24.5	0.001
BC2(F_1x RD2508)	37	0			
** F_2	58	21	59.25	19.75	0.037
Cross IV					
RD 103	0	All			
RD2634	All	0			
F_1	All	0			
BC1(F_1x RD103)*	24	26	25	25	0.020
BC2(F_1x RD2634)	29	0			
** F_2	63	20	62.25	20.75	0.004

*,**Expected ratios are 1:1 & 3:1 respectively in BC_1 & F_2.
χ^2 (T)= 3.84 (at 1 d.f. & 5 % L.S); R = resistant; S = Susceptible and C = Calculated value

the BC_2 (F_1 backcrossed to resistant parents), there was no segregation for resistance and as expected all the plants were resistant like the resistant parent (Table 2). These observations again proved the assumption of the F_2 generation pattern, indicating that the resistance was governed by dominant single gene in all the four crosses.

The results of this study agree largely with some of the reported findings, indicating that resistance is dominant to susceptibility as reported [4,5] in few genotypes for selective pathotypes of barley yellow rust. However, dominance of susceptibility over resistance have also been reported against individual pathotypes in other genotypes [4-6]. The dominant nature of this resistance is especially encouraging, since its incorporation and selection may be easier than the one with recessive nature. The penetrance of the resistance genes was of very high level and no intermediate/ moderate types were observed in the different generations in any of the four crosses.

However, the test of allelism for the resistance genes observed in the four different sources (as evident from the parentage of the parental lines in Table 1) needs to be taken up by studying the R x R types of crosses or by a kind of matching technique for gene postulation, shall be highly desirable to know the diversity amongst the four resistance sources studied. If found diverse, these can be utilised for gene pyramiding for better resistance against a number of pathotypes of yellow rust in India as well as to give the long lasting protection as compared to single source of resistance.

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