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Inheritance studies on resistance to botrytis grey mould in chickpea (*Cicer arietinum* L.)

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Abstract

The present investigation was undertaken with the objective to study the inheritance pattern of Botrytis grey mould disease. Field experiments were conducted during the *Rabi* seasons of 2014-15, 2015-16 and 2016-17 at Norman E. Borlaug Crop Research Centre, G. B. Pant University of Agriculture and Technology, Pantnagar. After field screening under artificial inoculation conditions it was found that chickpea line GL10006 was resistant while lines DCP 92-3 & GNG1581 were susceptible to grey mould. Resistant line GL10006 was crossed with two susceptible varieties of chickpea i.e. DCP 92-3 & GNG 1581. GL 10006 × DCP 92-3 and GL10006 × GNG 1581 showed monogenic dominant resistance in ratio of 3R (resistant):1S (susceptible). The results showed the presence of a type of major gene resistance to grey mould in chickpea.

Keywords: Chickpea, botrytis grey mould, inheritance and resistance

Introduction

Chickpea (*Cicer arietinum* L.) is the second largest consumed pulse crop of the world after common bean and it is grown in over 50 countries and traded across 140 countries (FAOSTAT, 2016) [3]. The beneficial effects of chickpea on soil and human health are well recognized. There has been a slow progress in improving the average global productivity of chickpea, which continued to remain below 1.0-ton ha⁻¹. In India, chickpea was planted to 8.25 million hectares during 2016-17 with a production of 7.33 million tons and a productivity of 859 kg/ha. However, the breakthrough in its productivity is still awaited because of the number of biotic and abiotic stresses constrain productivity. Botrytis Gray Mould (BGM) caused by *Botrytis cinerea* is one of the major constraints for low yield of chickpea. This disease leads to subsequent crop loss in certain parts of India (in *Tarai* area of Uttarakhand, *Tal* area of Bihar and in Punjab). Therefore, keeping in view, the above facts and considering the importance of Chickpea, the present investigation was planned and executed by involving the potential parental lines with the objectives to screen the parental, F₁, F₂ and back cross generations for Botrytis Gray Mould in various crosses and to determine the inheritance of Botrytis grey mould.

Material and Methods

Crosses were attempted using hand emasculation followed by immediate pollination between resistant and susceptible parents for Botrytis Grey Mould disease during *Rabi* season of 2014-15. The F₁ seeds of a cross were planted in December, 2015 in between their parental lines to observe Botrytis Grey Mould in comparison to their parents and to attempt backcrosses with both the parents. When, the F₁'s was backcrossed with female parent (P₁), it was designated as BC₁P₁. Similarly, when it was backcrossed to the male parent (P₂), it was designated as BC₁P₂. The F₁'s, F₂'s, BC₁P₁ and BC₁P₂ along with their parents were sown in compact family block design in *Rabi* season of 2016-17. The number of rows of each generation depended on the number of seeds available. The parents, F₁, F₂ and back cross generations were screened under field conditions by spraying the inoculum of BGM and assessed for inheritance of BGM resistance. Disease scale of 1-9 (1-immune, 3-resistant, 5-tolerant, 7-susceptible and 9-highly susceptible) was used for grading the plants 10 days after inoculation. Disease rating up to 3 was considered as resistant and 7, 9 as susceptible. χ^2 test of goodness of fit was applied after recording the observations.

Results and Discussion

The parental line GL 10006 displayed mean disease score of 2.8 to 4.4 on 1-9 disease rating scale. The disease score from 1-5 was taken as resistant for calculating genetic ratio's. Therefore, the parents namely GL 10006 was classified as resistant. The parental lines GNG 1581 and DCP 92-3 displayed mean disease score of 6 and 7.8 on 1-9 disease rating scale. The disease score from 6-9 was taken as susceptible for calculating genetic ratio's. Therefore, the parental lines GNG 1581 and DCP 92-3 were classified as susceptible.

Inheritance of Resistance to BGM

1. GL 10006 × GNG1581

The data regarding the disease response to different generations of this cross is given in Table 1. The mean disease score of parent GL10006 was 2.8 and of GNG1581 was 6.0, showing resistant and susceptible reaction, respectively. The reaction pattern in F₁ plants, showed the disease score of 3.5, showing resistant reaction. This indicated that resistance is dominant over susceptibility. The disease reaction pattern in F₂ generation showed the disease score from 1 to 9 with a mean of 4.8, showing segregation for resistance. The segregation of F₂ population from the cross GL10006 ×

GNG1581 showed a wide range of response to BGM (Table 1). The F₂ plants were divided into two large groups i.e. resistant and susceptible. The F₂ plants which were having the disease score from 1-5 were called resistant and F₂ plants which were having disease score between 6-9 were marked susceptible. In this particular cross out of 150 F₂ plants 109 were resistant and 41 were susceptible. These numbers fit to the ratio of 3 (resistant): 1 (susceptible) with chi - square value 0.436 which is less than 3.841 i.e. chi square tabulated value at 5% level of significance [$\chi^2_{cal} < 3.841(\chi^2_{0.05,1df})$]. The segregation pattern of 3:1 in F₂ generation showed that inheritance of resistance to BGM is controlled by single dominant gene. The backcross generations were also tested for the disease reaction. In the backcross of F₁ with resistant parent i.e., BC₁P₁ (GL 10006×GNG1581) ×GL10006, with the mean disease score of 4.0 all plants showed resistant response. On the other hand, cross between F₁ and susceptible parent i.e. BC₁P₂ (GL10006×GNG1581)×GNG1581, total 13 plants segregate into resistant (9) and susceptible (4) with the mean disease score of 5.2. The segregation pattern in BC₁P₂ showed a good fit in ratio 1:1 with chi square value of 1.923. The results obtained from these backcrosses showed that resistance in this cross is controlled by single dominant gene and this also confirms the result obtained from F₂ generation.

Table 1: Inheritance pattern of Botrytis Grey Mould in chickpea using cross GL10006×GNG1581

Parent/Cross	Generation	BGM score					Total no. of plants	Mean disease score	Observed frequency		Expected frequency		Expected Ratio	χ^2_{cal}	χ^2_{tab} (0.05,1df)
		1	3	5	7	9			R	S	R	S			
GL 10006	P ₁	3	5	2			10	2.8							
GNG1581	P ₂			5	5		10	6.0							
GL 10006 × GNG581	F ₁	1	6	5			12	3.5							
(GL 10006 × GNG1581) × GL 10006	BC ₁ P ₁		7	7			14	4.0	14	0	14	0	1:0		3.841
(GL 10006 × GNG1581) × GNG1581	BC ₁ P ₂		3	6	4		13	5.2	9	4	6.5	6.5	1:1	1.923	3.841
GL 10006 × GNG1581	F ₂	4	42	63	41		150	4.8	109	41	112.5	37.5	3:1	0.436	3.841

2. GL 10006 × DCP92-3

The data regarding the disease response to different generations of this cross are given in Table 2. The mean disease score of parent GL10006 was 2.8 and of DCP92-3 was 7.8, showing resistant and susceptible reaction, respectively. The reaction pattern in F₁ plants, showed the disease score of 3.9, showing resistant reaction. This indicated that resistance is dominant over susceptibility. The disease reaction pattern in F₂ generation showed the disease score from 3 to 9 with a mean of 5.2, showing segregation for resistance. The segregation of F₂ population from the cross GL10006×H208 showed a wide range of response to BGM. The F₂ plants were divided into two large groups i.e. resistant and susceptible. The F₂ plants which were having the disease score from 1-5 were called resistant and F₂ plants which were having disease score between 6-9 were marked susceptible. In this particular cross out of 128 F₂ plants 90 were resistant and 38 were susceptible. These numbers fit to the ratio of 3 (resistant): 1 (susceptible) with chi - square value 1.500 which is less than 3.841 i.e. chi square tabulated value at 5% level of significance [$\chi^2_{cal} < 3.841(\chi^2_{0.05,1df})$]. The segregation pattern of 3:1 in F₂ generation showed that inheritance of resistance to BGM is controlled by single dominant gene. The backcross generations were also tested for the disease reaction. In the backcross of F₁ with resistant parent i.e., BC₁P₁ (GL10006 × DCP92-3) ×GL10006, the mean disease score of BC₁P₁ is 4.7.

On the other hand, cross between F₁ and susceptible parent i.e. BC₁P₂ (GL10006 × DCP92-3) ×DCP92-3, total 15 plants segregate into resistant (8) and susceptible (7) with the mean disease score of 5.9. The segregation pattern in BC₁P₂ showed a good fit in ratio 1:1 with chi square value of 0.125 which is much lesser than chi square tabulated value at 5% level of significance. The results obtained from these backcrosses showed that resistance in this cross is controlled by single dominant gene and this also confirms the result obtained from F₂ generation. The limited reports available on genetics of BGM resistance suggests that the resistance is controlled by few genes. A single dominant gene 'Bor1' for resistance was identified by Tiwari *et al.* (1985) ^[1], while two genes with dominant and recessive epistasis (13:3 ratio) were reported by Rewal and Grewal (1989) ^[2] and duplicate dominant epistasis (15:1 ratio) by Chaturvedi *et al.* (1995) ^[4]. Some of the resistant chickpea lines such as ICC1069, P349-2 and NEC2451 have been widely used in breeding (Haware *et al.*, 1993) ^[5] but higher levels of host resistance still need to be identified. Furthermore, these resistances are unlikely to hold in the longer term as pathogen diversity indicates likely breakdown of host resistance. The findings of Tewari *et al.* (1985) ^[1] were in similar direction to the present research findings that resistance was dominant over susceptibility and had monogenic controlled.

Table 2: Inheritance pattern of Botrytis Grey Mould in chickpea using cross GL10006×DCP92-3

Parent/Cross	Generation	BGM score					Total no. of plants	Mean disease score	Observed frequency		Expected frequency		Expected Ratio	χ^2_{cal}	χ^2_{tab} (0.05,1df)
		1	3	5	7	9			R	S	R	S			
GL 10006	P ₁	1	5	4			10	2.8							
DCP 92-3	P ₂				6	4	10	7.8							
GL 10006 X DCP 92-3	F ₁		5	5			10	3.9							
(GL 10006 X DCP 92-3) X GL 10006	BC ₁ P ₁		3	10	1		14	4.6	13	1	14	0	1:0	0.071	3.841
(GL 10006 X DCP 92-3) X DCP 92-3	BC ₁ P ₂		3	5	4	3	15	5.9	8	7	7.5	7.5	1:1	0.067	3.841
GL 10006 X DCP 92-3	F ₂		37	53	25	13	128	5.2	90	38	96	32	3:1	1.500	3.841

Conclusion

The parental materials used for study of genetics of resistance to botrytis grey mould disease in chickpea (*Cicer arietinum* L.) were having different reaction for the botrytis grey mould disease viz. resistant reaction (GL 10006) and susceptible reaction (GNG1581 and DCP 92-3). Resistant was found dominant over susceptibility in F₁ generation of resistant × susceptible crosses (GL10006 × GNG1581 and GL10006 × DCP92-3). In the F₂ generation a ratio of 3 (resistant): 1 (susceptible) was observed for both crosses. This suggested that resistance to BGM was governed by single dominant gene and resistance is dominant over susceptibility. Backcross of F₁ with resistant parents gave all resistant plants and backcross with susceptible parent gave segregants into 1(resistant):1(susceptible) ratio. The backcrosses also confirmed the results obtained in F₂ generation that resistance is governing by single dominant gene. The result indicated that resistance to BGM is under control of major gene(s), which can be incorporated in elite lines of chickpea from identified donors through backcross breeding methods.

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