Bangladesh J. Bot. **45**(3): 707-712, 2016 (September) **- Short communication**

GENETICS OF FLAG SMUT RESISTANCE IN BREAD WHEAT

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Key words: Genetics, Flag smut, Resistance, Bread wheat

Abstract

A field experiment was laid out to investigate genetics of flag smut of wheat under field conditions to know the number of gene governing for resistance/susceptible and find suitability/feasibility for transfer of resistance gene for development and deployment of resistant variety. Six parents i.e. WH283, HD2329, HS277, UP2338, Raj3765 and PBW343 and comprised of 6 generations (P_1, P_2, F_1, F_2, BC_1, BC_2) were studied. Analysis of inheritance of flag smut revealed that F_2 derived from cross WH283 × UP2338 fitted well in monogenic (3 : 1). But, in crosses WH147 × Raj3765 and Raj3765 × PBW343 digenic inheritance (15 : 1) was obtained. In crosses H283 × PBW343, HD2329 × UP2338, HD2329 × Raj3765, HD2329 × PBW343, UP2338 × PBW343 the F_2 generation ratio (63 : 1) indicated trigenic inheritance. In resistant × susceptible crosses, flag smut incidence reduced if the F_1 plants were back crossed to its respective resistant parent, but incidence of flag smut increased when the F_1 plants were backcrossed to their susceptible parent. Therefore, in case of flag smut susceptibility of wheat is particularly dominant and inheritance of resistance against flag smut of wheat is governed by a few genes (one to three), however, role of modifier/ minor gene cannot be ruled out.

Wheat (*Triticum aestivum* L.) is one of the most important staple food crops in the world, but its production is adversely affected by a number of biotic and abiotic stresses from sowing till harvest. The seed and soil-borne fungi like *Urocystis agropyri* (Preuss) Schroet responsible for flag smut causes **c**onsistently significant economic loss on **c**ontinuous cultivation of susceptible variety on same field and leads to inoculum build up in the soil. Flag smut was first time reported in South Australia in 1868 as ‘black rust’ and was subsequently reported from many wheat-growing areas of the world, including Chile, China, Egypt, India, Japan, Mexico, Pakistan, South Africa and the United States of America (Toor *et al.* 2013). It can cause 5 - 20% losses, with occasional total crop failures in very susceptible cultivars (Murray *et al.* 1998). In India, it is estimated that the incidence of disease in some parts of Punjab, Himachal Pradesh and Haryana is up to 75%, highest yield reduction was noted in PBW 343 (Shekhawat and Majumdar 2010). Interestingly, flag smut is not a problem in durum wheat and triticale, which tend to be highly resistant (McIntosh 1968, Goel and Gupta 1990). Flag smut can be controlled by chemical treatment, cultural practices and use of resistant cultivars. The most economical and cost-effective method of controlling flag smut is through deployment of resistant cultivars. Although, flag smut resistant cultivars have been developed and used around the world, very little work has been done on genetics of resistance. *Urocystis agropyri* (Preuss) Schroet is biotrophic fungi where evolution of new races may exist on development of new variety. Among reports on the inheritance of reaction to flag smut in wheat, none identified definitive genomic locations of the genes involved. Present investigation describes results of genetics of flag smut resistance in a population that genotype gene governing is monogenic or polygenic and inheritance of resistance or susceptible gene.

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The present investigation was comprised of three resistant i.e. WH283, HD2329, HS277 and three susceptible cultivars UP2338, Raj3765 and PBW343 having genetic divergence. All the above six parents were crossed in diallel mating lattice design for 15 possible one way during 2012-13 and 2013-2014 at experimental farm of Plant Pathology, Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, India. All possible one way F_1 crosses with six parents were also grown in paired rows of 3 m in RBD in duplicate to develop the F_1, F_2, BC_1 and BC_2 during 2012-14.The generated breeding material constituents of 6 generations (P_1, P_2, F_1, F_2, BC_1, BC_2) was also grown in RBD in duplicate during 2013-14, parents and F_1 crosses in single rows, F_2 generation in six rows and BC_1 and BC_2 in three rows, each of 3 m length in two replications. Statistical analysis was carried out as per Sharma (1998). The seed of each generation was smeared with the dry powder of *Urocystis agropyri* teliospore @ 20 g/kg seed and sown separately in paired rows of 5 m length in an isolated plot in November where flag smut history was not observed. The incidence of flag smut of wheat was recorded on plant at tiller basis end of March of each respective season. The generations were grouped into different categories according to disease reaction scale i.e. 0 to 5% infection = resistant, 5.1 to 20% = intermediate and 20.1 to 100% infection = susceptible (Yu *et al*. 1945). Flag smut incidence for each line was calculated by sum of disease tillers × 100/total number of plants tillers. The F_2 populations of different crosses were tested against different F_2 Mendelian segregation ratio by using Chi square test.

The experimental results of flag smut of wheat are presented in Table 1 categories the crosses. The F_1 generation of different crosses indicated the partial dominance of susceptibility in both years. The incidence of flag smut in susceptible parents ranged from 42.28 (Raj 3765) to 63.11% (UP2338). The six possible crosses between resistant × susceptible (R × S) expressed intermediate reaction to flag smut indicating partial dominance of resistance (Table 1). Whereas, crosses included susceptible × susceptible (S × S) parents there was increase of flag smut incidence in the F_1 generation thereby indicate that more than one gene is responsible for enhancing susceptibility to flag smut since gene contribution by susceptible is dominant. In contrast to it, resistant × resistant (R × R) crosses maintained the resistance towards their parents. The average disease incidence in F_1 generation of crosses R × S, S × S, R × R was 32.50, 60.36, 2.48%, respectively. Whereas, in order to have flag smut resistance promising crosses included in Table 1 may be exploited in successive generation for desirable traits. The results presented in Table 1 also revealed that during both crop seasons resistant parents i.e. HS277, HD2329, WH283 were free from flag smut while susceptible parents exhibited high disease incidence thereby indicating flag smut is heritable.

In R × S crosses disease incidence of F_1, F_2, BC_1 and BC_2 generations ranged from 14.57 - 56.42%, 5.11 - 26.66%, 1.66 - 18.66% and 21.83 - 57.83%, respectively. In another R × R crosses, WH283 × HS277 showed very low disease incidence 0.83 - 4.67%. While, in S × S crosses, flag smut incidence exhibited high in F_1 generation, but no definite pattern/ Mendelian ratio for F_2, BC_1 and BC_2 generation, thus indicated that different genes were responsible for this disease which expressed additive effect in progression of flag smut disease. However, Sharma *et al.* (2005) reported both additive and non-additive type of genetic variance for flag smut incidence.

The incidence of flag smut for the parents involved in present study and F_1 generation of different crosses exhibited similar level of disease in both crop seasons thus confirming partial dominance of susceptibility over resistance and also revealing that seed inoculation for each generation was appropriate (Table 2).

It is self evident from Table 2 that backcrosses having HS277 as parent in respective back-crosses lesser disease incidence was noticed which reflects the importance of this parents for incorporating resistance in wheat against flag smut. The back cross having UP2338 as parent showed increase disease incidence. As expected, the disease incidence of flag smut lowered if the F_1 plants were back-crossed to its respective resistant parent whereas, incidence of flag smut got enhance when the F_1 plants were backcrossed to its susceptible parent (Table 2) which also further explains that flag smut is controlled by host resistance.

Table 1. Flag smut incidence in parents and F_1s hybrids during 2012-13.

Genotype	Nature of cross	Parent 1	Parent 2	F_1 hybrid
WH283 × UP2338	R×S	0.00	63.11	41.83
WH283 × Raj3765	R×S	2.83	52.57	48.91
WH283 × PBW343	R×S	2.50	62.50	43.33
HD2329 × UP2338	R×S	3.22	45.00	40.00
HD2329 × Raj3765	R×S	3.11	42.57	22.57
HD2329 × PBW343	R×S	0.00	60.00	36.66
HS277 × UP2338	R×S	0.00	57.42	21.11
HS277 × Raj3765	R×S	0.00	42.28	19.66
HS277 × PBW343	R×S	0.00	53.33	18.50
Mean		1.29	53.18	32.50
SD		1.55	8.28	11.91
UP2338 × Raj3765	S×S	56.66	41.11	66.66
UP2338 × PBW343	S×S	53.33	57.28	53.33
Raj3765 × PBW343	S×S	45.00	52.42	61.11
Mean		51.66	50.27	60.36
SD		6.00	8.29	6.69
WH283 × HD2329	R×R	0.00	3.33	2.50
WH283 × HS277	R×R	2.33	0.00	2.83
HD2329 × HS277	R×R	3.50	0.00	2.11
Mean		1.94	1.11	2.48
SD		1.78	1.92	0.36

In the F_2 generation of different crosses involving either one or both susceptible parents, there was less disease incidence as certain combination of genes governing resistance to flag smut may appear that reduce disease incidence. However, flag smut incidence was higher in crosses termed as R × S (Table 3) thereby indicating dominance of susceptibility. Whereas, in crosses termed as S × S, the disease incidence (24.83%) has been observed higher in F_2 generation of cross Raj3765 × PBW343 and lowest (4.55%) in crosses of UP2338 × Raj3765.

The result on inheritance of flag smut revealed that in cross WH283 × UP2338, the F_2 generation fitted well in monogenic (3 : 1) inheritance of resistance. But, in cross UP2338 × Raj3765 and Raj3765 × PBW343 digenic inheritance (15 : 1) was observed. However, in crosses WH283 × PBW343, HD2329 × Raj3765, HD2329 × PBW343, UP2338 × PBW343 and HS277 × UP2338, the F_2 segregation ratio (63 : 1) indicating trigenic inheritance (Table 3). However, no specific pattern/Mendelian ratio was observed in F_2 segregation ratio in the remaining crosses where still high order of interaction or linked gene for flag smut may be there. The goodness of fit of the observed segregation in an expected ratio revealed the chi square test as significant this indicated that no definite ratio of resistant to susceptible plant showed goodness of fit by chi square test.

Table 2. Flag smut incidence in parents, F_1s, F_2s and backcrosses of wheat during 2013-14.

Genotype	Nature of reaction	Disease incidence (%)			
Parents					
HS277	R	0.00			
WH283	R	0.00			
HD2329	R	0.00			
UP2338	S	51.11			
Raj3765	S	45.00			
PBW343	S	38.66			
Cross		F_1	F_2	BC_1	BC_2
WH283× UP2338	R×S	56.42	26.66	11.67	57.83
WH283× Raj3765	R×S	30.00	10.00	18.66	36.66
WH283× PBW343	R×S	28.57	15.67	16.33	48.57
HD2329× UP2338	R×S	26.66	21.11	12.97	39.83
HD2329× Raj3765	R×S	16.66	8.83	11.96	20.00
HD2329× PBW343	R×S	36.83	15.83	3.11	41.11
HS277× UP2338	R×S	21.73	14.57	1.66	24.57
HS277× Raj3765	R×S	14.57	5.11	7.83	21.83
HS277× PBW343	R×S	16.83	5.12	4.57	26.11
Mean		27.58	13.65	9.86	35.16
SD		13.05	7.21	5.93	13.01
WH283× HD2329	R×R	3.33	2.33	2.96	2.67
WH283× HS277	R×R	3.75	0.83	5.11	2.93
HD2329× HS277	R×R	4.67	2.16	4.57	3.71
Mean		3.91	1.77	4.21	3.10
SD		0.68	0.82	1.11	0.54
UP2338× Raj3765	S×S	91.75	5.11	35.46	41.11
UP2338× PBW343	S×S	83.33	18.45	41.28	48.94
Raj3765× PBW343	S×S	63.57	25.00	22.83	31.57
Mean		79.55	16.18	33.19	40.54
SD		14.46	10.13	9.43	8.69

Earlier Sharma *et al*. (2005) has reported single dominant gene with monogenic (3 : 1) inheritance for flag smut resistance and also estimated genetic component for both additive and non-additive type of genetic variance for flag smut incidence that susceptibility is particularly dominant and inheritance of resistance. Resistance has also been reported to be controlled by a single recessive gene (Helm and Allan 1971). Polygenic inheritance of flag smut resistance was suggested by Goel (1991) and McIntosh (1968). Transgressive segregation in reaction to flag smut was noted by different workers (Shen *et al*. 1938, Purdy and Allan 1967, McIntosh 1968) which corroborate present investigation.

Table 3. Flag smut incidence in parents, F_2 and segregation ratio of different crosses of wheat during 2013-14.

Genotype	Nature of Reaction	Disease incidence (%)			
Parents					
HS277	R	0.00			
WH283	R	0.00			
HD2329	R	0.00			
UP2338	S	55.55			
Raj3765	S	44.57			
PBW343	S	35.66			
Cross		F_2	Mendelian ratio		
			3:1	15:1	63:1
WH283× UP2338	R × S	28.12	2. 64	7.75	31.83
WH283× Raj3765	R × S	10.59	62.11	53.33	23.67
WH283× PBW343	R × S	15.78	24.66	18.66	2.75
HD2329× UP2338	R × S	22.22	2.75	2.83	3.53
HD2329× Raj3765	R × S	8.96	70.00	58.53	31.25
HD2329× PBW343	R × S	15.33	25.00	20.25	4.00
HS277× UP2338	R × S	14.67	26.66	20.83	5.24
HS277× PBW343	R × S	5.33	86.47	73.11	46.13
HS277× Raj3765	R × S	5.33	94.33	83.33	53.57
Mean		14.03	277.13	218.24	55.12
SD		7.58			
WH283× HD2329	R × R	2.33	150.11	130.92	96.94
WH283× HS277	R × R	0.83	134.98	118.22	91.00
HD2329× HS277	R × R	2.00	138.42	120.75	90.33
Mean		1.72	424.14	370.59	278.97
SD		0.79			
UP2338× Raj3765	S × S	4.55	1.01	4.73	21.33
UP2338× PBW343	S × S	17.66	10.25	7.72	00.19
Raj3765× PBW343	S × S	24.83	0.03	2.44	12.88
Mean		15.68	1.34	5.14	21.88
SD		10.28			

It may be inferred that in case of flag smut of wheat susceptibility is particularly dominant and inheritance of resistance of flag smut of wheat is governed by a few genes (one to three) i.e. monogenic or oligogenic, more over the role of modifier/minor gene cannot be ruled out.

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(Manuscript received on 24 December, 2014; revised on 21 April, 2015)