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Evaluation of Rice Genotypes for Resistance against False Smut of Rice (*Oryza sativa* L.) under Middle IGP of Bihar

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A B S T R A C T

The present study was conducted at the experimental farm of ICAR Research Complex for Eastern Region, Patna, India in *Kharif* season 2016 with an objective to identify false smut resistance rice genotypes. False smut (*Ustilaginoidea virens* (Cooke) Takahashi) is of serious concern to the rice growers as it affects rice quality and significantly reduces the yield particularly in irrigated ecosystem. Twenty one genotypes were evaluated for their resistance and susceptibility to the disease under *in-situ* conditions. Significant differences were observed for resistance to false smut disease among genotypes. Four rice genotypes Swarna Shreya, IR96321-1447-521-B-2-1-2, IR96321-1447-651-B-1-1-2, and IR 83294-66-2-2-3-2 were immune or highly resistant against false smut. Maximum per cent infected panicles and the number of smut balls per panicle were observed in genotype Sabbhagi Dhan (65.00%) followed by IR96321-1099-227-B-3-1-3 (55.00%). The resistance genotypes may be further utilized as the genetic sources in disease resistance rice breeding programme.

Introduction

Rice (*Oryza sativa* L.) is a vital world commodity as it is the staple food of about half of the world population. It is the primary source of energy and protein for 4.5 billion peoples in the most populous nations of Asia. Rice is cultivated under diverse ecologies, ranging from irrigated to rain-fed and upland to lowland and deep water system (Kumar *et al.,* 2014). False smut (green smut or pseudo smut) of rice caused by *Ustilaginoidea virens* (Cooke) Takahashi has long been considered as minor disease. However, more recently epidemics have been reported with increasing frequency in different parts of world because of the large scale expansion of high yielding cultivars, the use of chemical fertilizers, irrigation at high levels and climate change. The disease causes reduction not only in quality and quantity of the produce, but also reduces the germination vigour of the infected seedlings (Sanghera *et al.*, 2012). The damage by disease includes the contamination of grains and straw with ustiloxins, the mycotoxins produced by *U. virens* on diseased tissues and the antimitotic cyclic peptides from its chlamydospores, which are poisonous to both humans and animals (Nakamura *et al.*, 1994). The symptoms of the

disease become visible after flowering only as a few spikelets in a panicle transform into globose, yellowish green and velvety spore balls that are 2 to 5 cm in diameter Reddy and Reddy (1992) also described that the pathogen grows in the ovary and transforms it into large, yellowish and velvety green balls, which become greatly enlarged at later stage. They found that the spore balls were covered by a membrane in the early stages, which bursts with further growth and the loose velvety pseudomorphs become visible. The surface of the ball was found to crack at this stage. Although the disease can be managed by using various chemical (Hegde *et al.*, 2000) and cultural management strategies (Brooks *et al.*, 2009), but identification of resistant lines from diverse sources is more desirable. Keeping this in view, the present study was undertaken to evaluate of 21 rice genotypes for resistance and susceptibility against false smut.

Materials and Methods

The field experiments were carried out at ICAR Research Complex for Eastern Region, Patna, (latitude 25.30^0N, longitude 85.15^0E), Bihar, India during *Kharif* season 2016. Twenty one rice genotypes (Table 1) were evaluated in a randomized complete block design (RCBD) with three replicates. The experimental site having clay loam soil with pH 7.5, organic carbon 0.65 %, bulk density 1.47 g/cm^3, electrical conductivity 0.26 dS/m, available nitrogen 227 kg/ha, available phosphorous 28.4 kg/ha, and exchangeable potassium 218 kg /ha. The total rainfall was 921 mm during crop growth periods (June-November) in 2016.

The climate of the experimental site is humid sub-tropical in nature characterized by the monsoon season from late June to late September and chilly winter nights and foggy or sunny days from November to February. The genotypes screened in this study included advanced breeding lines as well as high yielding varieties of eastern India. The advanced breeding rice genotypes used under present study were collected from ICAR-IRRI collaboration programme. Rice nursery was seeded on 15 June 2016. Twenty five days old seedlings were uprooted from the seedbed very carefully and then transplanted in the main field with row to row spacing of 20 cm and plant to plant spacing of 15 cm. In each plot a uniform plant stand was maintained and standard agronomic practices were followed for raising and maintenance of plants. The crop was irrigated as per need on regular basis and fertilizers were applied @ 120, 60 and 40 kg ha^{-1} N, P_2O_5 and K_2O, respectively. Nitrogen was applied on three occasions (1/3each at basal, maximum tillering and panicle initiation stage), while the $P_2O_5$and K_2O were applied as a basal application.

Assessment of the disease incidence

Each plot was visited on regular basis for recording observations. The disease incidence was recorded at maturity stages of the plant. Data were recorded visually by observing the symptoms (Fig. 1). Twenty plants were randomly selected from each unit plot and the following parameters were considered for data collection.

Number of panicle/plants
Number diseased panicle/plants
Disease incidence was calculated by the following formula (Rajput and Bartaria, 1995):

Disease incidence =
Number of diseased panicles /Total number of inspected panicles x 100

For grading the disease incidence was recorded as per following IRRI recommended grading scale (Standard Evaluation System

for Rice, 2002). The disease incidence was recorded at maturity stages of the crop.

Isolation and identification of causal organism

The pathogen *U. virens* was isolated from the false smut-infected spikelets were collected from the field and cut into small pieces along with healthy portion. Cut pieces were sterilized by the surface disinfectants e.g. 0.1% mercuric chloride for 30 seconds. After sterilization the cut pieces were washed three times with sterile water. The cut pieces were then placed on sterile blotter paper to remove excess water. The cut pieces were then placed on the Potato Dextrose Agar plate. The plate were labelled and placed in the incubation chamber for 7 days at 25 ± 2^{o} C. After 7 days of incubation, the fungi grown on culture media. A portion of culture was taken on slide and observed under microscope and identified the pathogenic fungi *i.e. U. virens*, with the help of relevant literature (Mew and Gonzales, 2002; Barnet and Hunter, 1972).

Data analysis

The data on different characters were subjected to estimates of ANOVA (analysis of variance) by using statistical software OPSTAT.

Results and Discussion

Evaluation of rice genotypes against disease incidence

The evaluation of twenty one rice genotypes against false smut (*U. Virens)* disease revealed that four genotypes *viz.* IR96321-1447-521-B-2-1-2, IR96321-1447-651-B-1-1-2, Swarna Shreya and IR 83294-66-2-2-3-2 were found to be completely free from the disease incidence (Table 2). Significant differences were observed for resistance to false smut disease among genotypes. The disease scoring against bacterial leaf blight was varied from 0 to 65 %. Maximum per cent infected panicles and the number of smut balls per panicle were observed in Sabbhagi Dhan (65.00%) followed by IR96321-1099-227-B-3-1-3 (55.00%) and IR96321-558-209-B-6-1-1(54.3%).

Disease reaction data inferred that germplasm lines *viz.* Swarna Shreya, IR96321-1447-521-B-2-1-2, IR96321-1447-651-B-1-1-2 and IR83294-66-2-2-3-2 were highly resistant (HR). Eleven rice genotypes *viz.* IR96321-558-257-B-4-1-2, IR96322-34-127-B-2-1-3, IR 96321-315-323-B-3-1-3, IR 96321-558-563-B-2-1-1, IR 96321-558-563-B-2-1-3, Swarna sub 1, Swarna, R-RHZ-7, CGZR-1, IR 83668-35-2-2-2 and MTU 1010 were found to be moderately susceptible (MS) against false smut disease. Three genotypes *viz.* IR96321-315-323-B-3-1-1, IR83383-B-B-129-4 and Rajendra sweta were found to be susceptible (S) and three genotypes *viz.* IR96321-558-209-B-6-1-1, IR96321-1099-227-B-3-1-3 and Sabbhagi Dhan were highly susceptible (Table 3).

Similar studies were also conducted by earlier by various workers and wide variation in response of genotypes against false smut disease (Singh *et al.,* 1987; Sugha *et al.,* 1992; Kurauchi *et al.,* 2006). Lore *et al.,* (2013) reported that two cultivars *viz.* PR113 and PR114 were having the lowest level of disease intensity and two hybrids *viz.* NPH 369 and NPH 909, consistently had the highest level of disease intensity. Based on the reaction of 41 rice hybrids to false smut, Biswas (2001) reported that eight hybrids were free from the disease. Singh and Singh (2005) also screened 98 genotypes against false smut and reported that 27 were highly resistant and 45 were resistant while remaining 26 had infection from 5 to 70%.

Table.1 Detailed information of the rice genotypes used in the experiment

Sl. No.	Name of Rice genotypes	Plant height (cm)	DFF
1	IR 96321-558-257-B-4-1-2	105.0	103
2	IR 96322-34-127-B-2-1-3	111.9	104
3	IR 96321-1447-521-B-2-1-2	112.6	98
4	IR 96321-1447-651-B-1-1-2	112.0	101
5	IR 96321-558-209-B-6-1-1	109.4	111
6	IR 96321-315-323-B-3-1-1	110.5	108
7	IR 96321-315-323-B-3-1-3	108.2	107
8	IR 96321-558-563-B-2-1-1	103.0	113
9	IR 96321-558-563-B-2-1-3	109.6	116
10	IR 96321-1099-227-B-3-1-3	114.5	120
11	IR83383-B-B-129-4	112.5	107
12	R-RHZ-7	103.2	97
13	CGZR-1	118.7	85
14	IR 83294-66-2-2-3-2	96.8	84
15	IR 83668-35-2-2-2	103.4	87
16	Sabbhagi Dhan	109.5	85
17	Rajendra Sweta	110	112
18	Swarna Sub 1	108.3	109
19	Swarna	103.9	111
20	Swarna Shreya	109.8	89
21	MTU 1010	113.6	86

DFF: Days to 50% flowering

Table.2 Disease incidence of false smut of paddy in different rice genotypes

Sl. No.	Name of varieties	Disease incidence (%)
1	IR 96321-558-257-B-4-1-2	6.33
2	IR 96322-34-127-B-2-1-3	13.00
3	IR 96321-1447-521-B-2-1-2	0.00
4	IR 96321-1447-651-B-1-1-2	0.00
5	IR 96321-558-209-B-6-1-1	54.33
6	IR 96321-315-323-B-3-1-1	46.00
7	IR 96321-315-323-B-3-1-3	5.67
8	IR 96321-558-563-B-2-1-1	17.00
9	IR 96321-558-563-B-2-1-3	8.00
10	IR 96321-1099-227-B-3-1-3	55.00
11	IR83383-B-B-129-4	32.67
12	R-RHZ-7	13.00
13	CGZR-1	17.00
14	IR 83294-66-2-2-3-2	0.00
15	IR 83668-35-2-2-2	17.67
16	Sabbhagi Dhan	65.00
17	Rajendra Sweta	35.00
18	Swarna sub 1	6.67
19	Swarna	20.00
20	Swarna shreya	0.00
21	MTU 1010	15.33
	SE (m)	***2.74***
	LSD $_{(0.05)}$	***7.86***

Table.3 Disease reaction of rice genotypes under field conditions

Scale	Infected florets	Resistance level	Name of germplasm
0	No incidence	Highly resistant (HR)	IR96321-1447-521-B-2-1-2, IR96321-1447-651-B-1-1-2, Swarna Shreya and IR 83294-66-2-2-3-2
1	Less than 1%	Resistant (R)	0
3	1-5 %	Moderately resistant (MR)	0
5	6-25%	Moderately susceptible (MS)	IR96321-558-257-B-4-1-2,IR 96322-34-127-B-2-1-3, IR 96321-315-323-B-3-1-3, IR 96321-558-563-B-2-1-1, IR 96321-558-563-B-2-1-3, Swarna Sub 1, Swarna, R-RHZ-7, CGZR-1, IR 83668-35-2-2-2 and MTU 1010.
7	26-50%	Susceptible (S)	IR96321-315-323-B-3-1-1, IR83383-B-B-129-4 and Rajendra Sweta
9	51-100%	Highly susceptible	IR96321-558-209-B-6-1-1,IR96321-1099-227-B-3-1-3 and Sahbhagi Dhan

Fig.1 Infected rice genotypes: Spore balls are initially orange and turn greenish black when mature

In conclusion based on above findings it was observed that four rice genotypes *viz.* IR96321-1447-521-B-2-1-2, IR96321-1447-651-B-1-1-2, Swarna shreya and IR 83294-66-2-2-3-2 were found to be immune or highly resistant against false smut disease. Maximum per cent infected panicles and the number of smut balls per panicle were observed in genotype Sabbhagi Dhan (65.00%) followed by IR96321-1099-227-B-3-1-3 (55.00%). In the present study, the promising resistance genotypes may be further utilized as the genetic sources in disease resistance rice breeding programme.

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References

Barnett, H.L., Hunter, B.B. 1972. Illustrated genera of imperfect fungi, Burgess Publishing Company, pp: 241.

Biswas, A. 2001. False smut disease of rice- a review. *Environ. Ecol.*, 19: 67-83.

Brooks, S.A., Anders, M.M. and Yeater, K.M. 2009. Effect of cultural management practices on the severity of false smut and kernel smut of rice, *Pl. Dis.*, 93: 1202-08.

Hegde, Y., Anahosur, K.H. and Kulkarni, S. 2000. Chemical control of false smut of rice caused by *Claviceps oryzae sativae* Hashioka. *Karnataka J. Agric. Sci.*, 13: 623-27.

Kumar, S., Dwivedi, S.K., Singh, S.S., Elanchezhian, R., Mehta, P., Singh, B. P., Singh, O.N., and Bhatt, B.P. 2014. Morpho-physiological traits associated with reproductive stage drought tolerance of rice (*Oryza sativa* L.) genotypes under rain-fed condition of eastern Indo-Gangetic plain. *Indian J. Plant Physiol.*, 19(2): 87-93.

Kurauchi, K., Kudo, Y., Kimura, T. and Uemura, T. 2006. Difference in resistance to false smut disease between rice cultivars in Aomori prefecture. *A Rep. Pl. Prot Nth Jpn.*, 57: 17-21.

Lore, J.S., Pannu, P.P.S., Jain, J., Hunjan, M.S., Kaur, R. and Mangat, G.S. 2013. Susceptibility of rice hybrids and inbred cultivars to false smut under field conditions. *Indian Phytopath.*, 66: 397-99.

Mew, T.W., Gonazales, P. 2002. A handbook of rice seed bore fungi, International Rice Research Institute, Los Banos, Philippines. pp: 20.

Nakamura, K., Izumiyama, N., Ohtsubo, K., Koiso, Y. and Iwasaki, S. 1994. "Lupinosis"- like lesions in mice caused by ustiloxin produced by *Ustilaginoidea virens*: A morphological study. *Nat. Toxins*, 2: 22-28.

Rajput, R.L. and Bartaria, A.M. 1995. Reaction of rice cultivars to brown spot. *Agric. Sci. Dig. J.*, 15: 205-206.

Reddy, C.S. and Reddy, S.M. 1992. Smuts of Rice. *Indian J. Mycol. Pl. Pathol.*, 22(2): 125-138.

Sanghera, G.S., Ahanger, M.A., Kashyap, S.C., Bhat, Z.A., Rather, A.G. and Parray, G.A. 2012. False smut of rice (*Ustilaginoidea virens*) under temperate agro-climatic conditions of Kashmir, India. *Elixir. Bio. Tech.*, 49: 9827- 9831.

Singh G.P., Singh, R.N. and Singh, A. 1987. Status of false smut (FS) of rice in eastern Uttar Pradesh, India. *IRRI-Newslett.*, 12: 28.

Singh, A.K. and Singh, R.N. 2005. Screening for resistance to false smut (*Ustilaginoidea virens* Takahashi) of rice (*Oryza sativa* L.) *Indian J. Genet.*, 65: 49-50.

Standard Evaluation System for Rice. 2002. International rice research institute manila Philippines pp. 14.

Sugha, S.K., Sharma, O.P. and Kaushik, R.P. 1992. Performance of rice genotypes against false smut pathogen under rainfed conditions. *Pl. Dis. Res.*, 8: 76-77.

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