International Journal of Bio-resource and Stress Management https://ojs.pphouse.org/index.php/IJBSM

IJBSM December 2025, 16(12): 01-15

Article AR6727

Research Article

Natural Resource Management

DOI: HTTPS://DOI.ORG/10.23910/1.2025.6727

Screening and Agronomic Trait Association of Rice Germplasm for False Smut Resistance

Somshetty Ravali[1], S. Ameer Basha[1], Y. Chandra Mohan[2], T. Kiran Babu[1], S. N. C. V. L. Pushpavalli[3], and B. Balaji Naik[4]

[1]Dept. of Plant Pathology, [2]Dept. of Genetics and Plant Breeding, [3]Dept. of Molecular Biology and Biotechnology, [4]Dept. of Agronomy, Professor Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad, Telangana (500 030), India

Corresponding ameerplantpath@gmail.com

0000-0002-3536-5195

ABSTRACT

The experiment was conducted during *kharif*, 2021 and 2022 (June–October) at the College Farm, College of Agriculture, Professor Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad, Telangana, India to study on screening of rice germplasm against false smut disease, caused by *Ustilaginoidea virens*, A total of 60 rice germplasm lines were evaluated for their reaction to false smut. Among these, 16 genotypes, namely Abhaya, Chittimuthyalu, HR 59, IET 23993, JGL 30090, MTU 1153, MTU 3626, MTU 4870, NDLR 7, Swarna, Tellahamsa, WGL 1272, PR 126, PR 127, PR 121, and RNR 11718, exhibited highly resistant reaction, whereas no genotype showed resistant reaction. Four genotypes (PR 124, MTU 1075, NLR 40065, and HR 12) showed moderately resistant reaction, 29 genotypes were moderately susceptible, 10 genotypes were susceptible, while TN 1 recorded a highly susceptible reaction. Genotypes with compact panicles exhibited higher disease incidence. Correlation analysis revealed a significant positive association between false smut incidence and the number of grains per panicle, while a significant negative correlation was observed with panicle length. Grain type also influenced disease incidence, with short slender grains showing the highest susceptibility, followed by medium slender, long bold, long slender, and short bold, while extra-long slender grains showed the least incidence. Cluster analysis based on plant characters and disease response grouped more than 65% of genotypes similarly, indicating a strong relationship between morphological traits and false smut resistance.

KEYWORDS: False smut of rice, *Ustilaginoidea virens*, genotype screening

***Citation* (VANCOUVER):** Ravali et al., Screening and Agronomic Trait Association of Rice Germplasm for False Smut Resistance. *International Journal of Bio-resource and Stress Management,* 2025; 16(12), 01-15. HTTPS://DOI.ORG/10.23910/1.2025.6727.

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The authors have declared that no conflict of interest exists.

RECEIVED on 29th September 2025 RECEIVED in revised form on 06th December 2025 ACCEPTED in final form on 19th December 2025 PUBLISHED on 31st December 2025

1. INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important and widely cultivated staple food crops globally. However, rice production is seriously constrained by several biotic stresses, among which false smut, caused by *Ustilaginoidea virens* (Cooke) Takahashi [teleomorph: *Villosiclava virens* (Tanaka et al., 2008)], has emerged as one of the most devastating diseases (Rush et al., 2000; Singh and Pophaly, 2010; Ladhalakshmi et al., 2012). The disease, first documented in 1878 from Tirunelveli district of Tamil Nadu, India (Cooke, 1878), was earlier considered a minor sporadic occurrence but has now reached epidemic proportions in many rice-growing regions (Singh and Pophaly, 2010; Ladhalakshmi et al., 2012).

The pathogen primarily targets the floral organs of rice, particularly the spikelets, where it replaces individual developing grains with conspicuous smut balls that are often much larger and more rounded than normal grains. These smut balls initially appear whitish or cream-colored and, as the disease progresses, gradually change their coloration to pale yellow, yellow, greenish-yellow, or eventually greenish-black upon full maturity (Fan et al., 2015). In India, the incidence and severity of false smut vary remarkably across regions and cultivars, ranging from as low as 5% to as high as 85%, depending on environmental conditions, cultivar susceptibility, and agronomic practices (Sanghera et al., 2012; Singh et al., 2014; Kumari and Kumar, 2015; Muniraju et al., 2017; Duraisamy et al., 2019; Thapa et al., 2022). Yield losses caused by *Ustilaginoidea virens* have been documented between 0.2% and 49% among different rice varieties, with the extent of damage closely linked to infection intensity and timing (Doden and Singh, 1996; Upadhyay and Singh, 2013; Ladhalakshmi et al., 2012). In addition to direct yield reduction, false smut significantly deteriorates grain quality, milling recovery, seed germination vigor, and overall market acceptability of the produce (Sanghera et al., 2012). A major and alarming consequence of *U. virens* infection is the synthesis of toxic secondary metabolites, primarily ustiloxins and ustilaginoidins. These antimitotic cyclic peptides, formed within the chlamydospores of the fungus, are known to be highly poisonous to humans and animals and have been associated with carcinogenic and neurotoxic effects (Luduena et al., 1994; Koiso et al., 1994; Shan et al., 2013). Their persistence in contaminated grains, husks, and straw not only raises serious food and feed safety concerns but also poses a substantial threat to sustainable rice production and trade.

Several agronomic factors influence disease incidence. Heavy application of nitrogenous fertilizers to responsive cultivars and hybrids tends to increase disease severity, whereas higher phosphorus application has been reported to suppress the disease (Mohiddin et al., 2012; Zhang et al., 2014). Since symptom expression occurs only after flowering, by which time the pathogen has already invaded individual grains of the panicle (Atia, 2004), effective chemical control becomes difficult. Thus, host resistance remains the most economical and sustainable strategy for managing false smut (Cartwright et al., 2000; Wang et al., 2010). Although rice cultivars exhibit significant differences in quantitative resistance, no variety has been identified with complete resistance to *U. virens* (Biswas, 2001; Li et al., 2008; Huang et al., 2015). Given the widespread prevalence of false smut and its multifaceted impact on yield, grain quality, and food safety, systematic screening of rice germplasm for resistance is critical. The objective of this study is to screen rice germplasm for resistance to false smut disease caused by *Ustilaginoidea virens*, identify resistant donor genotypes, and utilize them as potential sources in breeding programs for developing durable resistant varieties to ensure sustainable rice production.

2. MATERIALS AND METHODS

2.1. *Experimental site and plant material*

The experiment was conducted during *kharif*-2021 and *kharif*-2022 at College Farm, College of Agriculture, Rajendranagar, Hyderabad, India, situated at 17.320039°N latitude, 78.409411°E longitude. A total of 60 rice genotypes along with three checks (TN1, NLR 34449 and BPT 5204) were collected from the Institute of Rice Research, Agricultural Research Station, Rajendranagar, Hyderabad used for screening to know resistance against false smut disease (Table 1). The above germplasm was selected based on plant characters like panicle type (compact, intermediate type and loose), grain type (short slender, short bold, medium slender, long slender, long bold and extra-long slender) and days to late booting stage. Germplasm seedlings were raised in an elevated nursery bed, uprooted after 30 days and transplanted into the main field at the rate of two seedlings per hill. An augmented block design with two replications was employed, each germplasm was transplanted into two rows, each 1m in length, with a row-to-row spacing of 20 cm and plant-to-plant spacing of 15 cm. Two rows of susceptible checks (TN1, NLR34449 and BPT5204) were repeated for every five germplasm lines and two rows of TN1 were planted as border rows. Fertilizers like nitrogen (100 kg ha^{-1}), phosphorus (60 kg ha^{-1}), and potash (40 kg ha^{-1}) were applied according to PJTAU recommendations during the *kharif* season.

2.2. *Inoculum application*

The native isolate of Rajendranagar, *Uv15* (Accession no. OR461676) was used for inoculum preparation. Freshly prepared 2 ml of conidial suspension (2x10^{5} conidia ml^{-1})

Table 1: Plant characters of different rice germplasm

Sl. No.	Genotype name	Panicle length (cm)	Panicle type	Grain length (L) (mm)	Grain breadth (B) (mm)	L/B ratio	Grain type	Days to late booting (DAP)
1.	Abhaya	21.23	LP	6.59	2.63	2.51	Long Bold	65
2.	AD16037	21.74	LP	6.00	2.15	2.79	Long Bold	73
3.	Bhadrakali	24.37	IP	6.95	1.97	3.53	Long Slender	80
4.	Chittimuthyalu	22.58	LP	3.87	1.83	2.11	Short Bold	87
5.	HMT Sona	17.55	IP	5.80	1.70	3.41	Short Slender	80
6.	HR 59	30.05	LP	5.19	2.27	2.29	Short Bold	80
7.	IET23993	26.03	LP	5.83	2.68	2.17	Short Bold	73
8.	Improved Pusa Basumati	30.05	LP	7.79	1.61	4.83	Extra long Slender	73
9.	Jaisriram	17.03	IP	5.31	1.51	3.52	Short Slender	75
10.	JGL13595	24.01	CP	5.30	1.89	2.80	Medium Slender	73
11.	JGL1798	24.33	CP	5.37	2.01	2.67	Medium Slender	73
12.	JGL30090	24.16	IP	6.95	2.31	3.01	Long Slender	80
13.	JGL3828	21.11	CP	5.46	1.96	2.79	Medium Slender	80
14.	JGL3844	24.42	IP	5.71	1.94	2.94	Medium Slender	80
15.	JGL3855	23.20	CP	5.32	1.85	2.87	Medium Slender	80
16.	MTU1010	21.12	LP	6.78	2.10	3.24	Long Slender	65
17.	MTU1064	25.24	LP	5.73	2.18	2.63	Medium Slender	65
18.	MTU1075	24.29	LP	6.26	2.02	3.10	Long Slender	73
19.	MTU1121	25.64	IP	5.93	2.08	2.86	Medium Slender	73
20.	MTU1153	23.87	LP	6.53	1.97	3.32	Long Slender	65
21.	MTU3626	23.55	LP	6.51	2.56	2.54	Long Bold	70
22.	MTU4870	23.59	LP	5.59	2.21	2.53	Medium Slender	70
23.	NDLR7	22.57	LP	5.54	1.93	2.87	Medium Slender	73
24.	NLR3041	22.41	CP	5.09	2.01	2.53	Medium Slender	65
25.	NLR3513	24.97	IP	5.96	2.34	2.54	Medium Slender	65
26.	NLR40065	23.89	LP	6.46	1.94	3.34	Long Slender	73
27.	Rasi	20.86	LP	5.69	2.26	2.52	Medium Slender	65
28.	RNR2358	23.49	IP	5.08	1.82	2.79	Medium Slender	70
29.	RNR2458	23.84	IP	5.66	1.91	2.96	Medium Slender	70
30.	RNR M7	24.35	CP	5.85	1.81	3.23	Short Slender	65
31.	Swarna	24.31	IP	5.55	2.19	2.53	Medium Slender	80
32.	Tellahamsa	22.70	LP	6.64	2.11	3.15	Long Slender	65
33.	WGL 44	23.21	CP	5.39	1.84	2.93	Medium Slender	70
34.	WGL 915	23.71	IP	5.43	1.92	2.83	Medium Slender	70
35.	WGL 1272	25.79	IP	4.99	1.68	2.96	Medium Slender	70
36.	WGL 347	24.82	CP	5.34	1.72	3.11	Short Slender	70
37.	RNR 35194	28.11	IP	7.26	1.82	4.00	Long Slender	75
38.	RNR 35989	24.08	LP	6.89	1.92	3.59	Long Slender	75

Table 1: Continue...

Sl. No.	Genotype name	Panicle length (cm)	Panicle type	Grain length (L) (mm)	Grain breadth (B) (mm)	L/B ratio	Grain type	Days to late booting (DAP)
39.	RNR 35999	29.54	LP	7.02	2.31	3.04	Long Slender	75
40.	IET 28529	26.87	CP	6.19	2.16	2.87	Long Bold	73
41.	WGL 1377	22.73	CP	5.29	1.93	2.74	Medium Slender	73
42.	IET 29265	23.73	CP	6.39	2.09	3.05	Long Slender	75
43.	IET 29270	23.16	CP	5.43	2.29	2.37	Short Bold	75
44.	IET 29289	19.84	CP	5.39	2.14	2.52	Medium Slender	75
45.	Akshayadhan	23.52	LP	6.16	2.13	2.90	Long Bold	73
46.	JGL 33164	21.51	CP	5.32	1.71	3.11	Short Slender	75
47.	IET 29291	23.71	LP	5.18	2.35	2.20	Short Bold	75
48.	IET 29506	23.68	CP	6.11	1.90	3.21	Long Slender	75
49.	HR 12	31.82	LP	5.27	2.09	2.52	Medium Slender	73
50.	PR 114	26.89	LP	7.52	1.90	3.96	Extra long Slender	55
51.	PR 124	23.35	LP	7.51	2.15	3.49	Extra long Slender	65
52.	PR 126	24.52	IP	6.65	2.03	3.27	Long Slender	73
53.	PR 127	23.84	LP	6.48	2.25	2.88	Long Bold	55
54.	PR 128	25.23	LP	5.32	1.96	2.71	Medium Slender	64
55.	PR 121	21.14	LP	7.09	2.25	3.15	Long Slender	64
56.	PR 129	22.68	LP	7.06	2.3	3.07	Long Slender	65
57.	RNR 11718	23.67	IP	5.60	2.17	2.58	Medium Slender	65
58.	TN 1 (C1)	25.56	CP	6.88	2.62	2.63	Long Bold	60
59.	BPT 5204 (C2)	23.12	CP	5.25	1.79	2.93	Medium Slender	75
60.	NLR 34449 (C3)	22.76	CP	5.26	1.83	2.87	Medium Slender	70

CP: compact panicle; LP: loose panicle; IP: intermediate type panicle; C: checks; DAP: days after planting

was injected in the leaf sheaths of each germplasm during their late booting stages (3–5 days before heading) using sterilized dermal syringe (Ladhalakshmi et al., 2012; Ashizawa et al., 2011).

2.3. Disease observations

Disease variables like the number of infected tillers and the number of smut balls per panicle were recorded at the maturity stage of the germplasm. % disease incidence, % infected grains and % disease severity were calculated as per the formulae given by Singh and Dube (1978).

$$\% \text{ disease incidence (PDI)}=\frac{\text{No. of infected tillers/m}^2}{\text{Total no. of tillers/m}^2}\times 100$$

$$\% \text{ infected grains} = \frac{\text{No. of diseased grains/panicle}}{\text{Total no. of grains/panicle}}\times 100$$

% disease severity (PDS) = % disease incidence×% infected grains

Rice germplasm were screened for false smut disease resistance using the disease score (0-9 scale) given by Anonymous (2002) (Table 2) (Rashmi et al., 2016; Lore et al., 2021).

2.4. Categorization of paddy grains

Initially, dehulled grains of germplasm were imaged under a zoom stereo microscope, later grain length, breadth, perimeter and area were measured using T-capture software. Subsequently, the grains were categorized using the scale provided by Ramaiah (1969) (Table 3).

Table 2: Disease scale for false smut of rice given by Anonymous (2002)

Scale	% disease incidence	Host response
0	0 (No disease)	Highly Resistant
1	<1%	Resistant
3	1.1–5%	Moderately Resistant
5	5.1–25%	Moderately Susceptible
7	25.1–50%	Susceptible
9	>50%	Highly Susceptible

Table 3: Classification of rice grains (Ramaiah, 1969)

Grain type	L (mm)	L/B ratio
Short slender	<6.0	>3
Short bold	<6.0	<2.5
Medium slender	<6.0	2.5–3.0
Long slender	>6.0	>3.0
Long bold	>6.0	<3.0
Extra-long slender	>7.5	>3.0

L: length; B: breadth

2.5. *Cluster analysis of germplasm lines*

Cluster analysis was done using the plant characters of germplasm lines to determine the effect of different characters on false smut disease incidence. Parameters like panicle type (loose, intermediate type, compact), grain type (short slender, short bold, medium slender, long slender, long bold and extra-long slender) and days to late booting stage were recorded for each germplasm line (Table 1). A binary matrix was constructed with the presence or absence of plant characters scored as 1 and 0 respectively and analyzed using NTSYSPC (version 2.02) software, following the methodology outlined by Jamshidi and Jamshidi (2011). Jaccard similarity coefficient was utilized to cluster the matrices, generating a dendrogram through the SHAN clustering program, which employed the UPGMA (unweighted pair group method with arithmetic averages) method, aimed to group similar germplasm based on shared characteristics. Similar cluster analysis was conducted for germplasm based on false smut disease parameters (% disease incidence, number of smut balls panicle^{-1}, % infected grains and % disease severity).

3. RESULTS AND DISCUSSION

3.1. *Genotype's reaction to false smut disease*

The data presented in Table 4 indicated that, the disease severity varied from genotype to genotype. The maximum mean % disease incidence was recorded in TN 1 (C_1) with 51.40% followed by IET 29289 (44.65%), Jaisriam (39.28%), IET 29270 (37.25%), NLR 3041 (32.15%), IET 29265 (31.64%), RNR M7 (30.19%), BPT 5204 (C_2) (29.15%), WGL 44 (29.08%), NLR 34449 (C_3) (27.96%), IET 29506 (26.71%), MTU1121 (24.42%), RNR 35999 (24.21%), IET 28529 (23.90%), JGL 1798 (23.55%), JGL 3828 (21.57%), WGL 347 (19.54%), JGL 33164 (18.02%), RNR 35194 (17.14%), WGL 915 (16.85%), WGL 1377 (13.71%), PR 129 (12.39%), RNR 2358 (11.72%), JGL 3855 (10.89%), PR 114 (10.88%), PR 128 (10.34%), Akshayadhan (10.17%), HMT Sona (10.11%), Bhadrakali (10.10%), JGL13595 (10.07%), IET 29291 (9.97%), JGL3844 (9.07%), MTU1064 (7.90%), AD16037 (7.56%), RASI (6.25%), RNR 35989 (6.09%), RNR 2458 (6.00%), Improved Pusa Basumati (5.97%), MTU 1010 (5.59%), NLR 3513 (5.59%), HR 12 (4.21%), NLR 40065 (3.61%), MTU 1075 (2.66%) and PR 124 (2.50%). Among 60 germplasm lines screened against U. virens 16 genotypes (Abhaya, Chittimuthyalu, HR 59, IET 23993, JGL 30090, MTU 1153, MTU 3626, MTU 4870, NDLR7, Swarna, Tellahamsa, WGL 1272, PR 126, PR 127, PR 121 and RNR 11718) were found to be completely free from the disease.

The maximum mean number of smut balls per panicle (NSBPP) of 10.81 was recorded in TN 1 (C_1) with 9.01% of infected grains followed by IET 29270 (9.61, 3.18%) IET 29265 (8.42, 4.09%), WGL 44 (7.68, 3.14%), Jaisriram (7.68, 2.40%), IET 29289 (7.29, 2.80%), BPT 5204 (C_2) (6.81, 3.10%), NLR 34449 (C_3) (6.70, 3.35%), IET 28529 (6.31, 1.43%), NLR 3041 (6.24, 2.56%), JGL1798 (6.13, 1.74%), RNR M7 (5.85, 2.20%), MTU 1121 (5.83, 1.76%), JGL 3828 (5.59, 1.91%), RNR 35999 (4.86, 2.75%) IET 29506 (4.70, 1.65%) RNR 35194 (3.55, 1.07%) JGL 33164 (3.37, 1.65%), WGL 1377 (3.35, 0.95%) JGL 3844 (3.26, 1.14%), RNR 2358 (3.26, 1.10%), WGL 915 (3.12, 0.95%), JGL 3855 (2.90, 0.67%), PR 114 (2.57, 1.26%), PR 129 (2.52, 1.32%), WGL 347 (2.38, 0.58%), JGL13595 (2.30, 0.51%), Bhadrakali (2.26, 0.94%), RNR 35989 (2.04, 1.04%), IET 29291 (2.02, 1.75%), AD16037 (1.97, 0.98%), PR 128 (1.94, 0.98%), Rasi (1.91, 1.64%), HMT Sona (1.90, 1.84%), NLR 3513 (1.79, 0.89%), Akshayadhan (1.78, 1.19%), MTU 1075 (1.77, 0.73%), RNR 2458 (1.67, 0.58%), MTU 1010 (1.55, 1.46%), NLR 40065 (1.48, 0.73%), PR 124 (1.18, 0.59%), MTU 1064 (1.14, 0.99%), Improved Pusa Basumati (0.80, 0.47%) and HR 12 (0.75, 0.37%).

The maximum mean % disease severity (PDS) was recorded in TN 1 (C_1) (467.95%) followed by IET 29265 (129.96%), IET 29289 (124.55%), IET 29270 (119.01%), Jaisriram (95.93%), BPT 5204 (C_2) (92.86%), NLR 34449 (C_3) (92.84%), WGL 44 (91.78%), NLR 3041 (83.29%), RNR 35999 (67.05%), RNR M7 (66.22%), IET 29506 (44.65%), MTU 1121 (43.10%), JGL 3828 (41.39%), JGL 1798 (41.17%), IET 28529 (34.11%), JGL 33164 (29.96%), HMT Sona (18.90%), RNR 35194 (18.30%), IET 29291 (17.29%), PR 129 (16.53%), WGL 915 (16.39%), PR 114 (13.77%), WGL 1377 (12.93%), RNR 2358 (12.85%), Akshayadhan (12.15%), WGL 347 (11.38%), JGL 3844 (10.40%), RASI (10.14%), PR 128 (10.05%), Bhadrakali (9.33%), MTU 1010 (8.06%), MTU 1064 (7.80%), JGL 3855 (7.39%), AD 16037 (7.16%), RNR 35989 (6.13%), JGL 13595 (5.32%), NLR 3513 (5.00%), RNR 2458 (3.47%), Improved Pusa Basumati (3.08%), NLR 40065 (2.59%), MTU 1075 (1.99%), HR 12 (1.82%) and PR 124 (1.48%).

Table 4: Screening of rice genotypes against false smut during *kharif*-2021 and 2022

Sl. No.	Genotype	*Kharif*-2021				*Kharif*-2022				Mean				Disease	
		PDI	NS BPP	PIG	PDS	PDI	NS BPP	PIG	PDS	PDI	NS BPP	PIG	PDS	(0-9)	Reation
1.	Abhaya	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	HR
2.	AD16037	8.79	1.63	0.81	7.09	6.32	2.31	1.15	7.24	7.56	1.97	0.98	7.16	5	MS
3.	Bhadrakali	9.64	2.88	1.19	11.48	10.56	1.64	0.68	7.17	10.10	2.26	0.94	9.33	5	MS
4.	Chittimuthyalu	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	HR
5.	HMT sona	10.87	2.27	2.20	23.90	9.35	1.53	1.49	13.90	10.11	1.90	1.84	18.90	5	MS
6.	HR 59	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	HR
7.	IET 23993	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	HR
8.	Improved Pusa Basumati	6.58	1.60	0.94	6.15	5.37	0.00	0.00	0.00	5.97	0.80	0.47	3.08	5	MS
9.	Jaisriram	44.88	8.53	2.67	119.80	33.68	6.83	2.14	72.05	39.28	7.68	2.40	95.93	7	S
10.	JGL 13595	11.21	2.92	0.65	7.31	8.94	1.67	0.37	3.33	10.07	2.30	0.51	5.32	5	MS
11.	JGL 1798	24.53	6.77	1.92	47.12	22.57	5.50	1.56	35.23	23.55	6.13	1.74	41.17	5	MS
12.	JGL 30090	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	HR
13.	JGL 3828	20.56	5.05	1.72	35.41	22.58	6.14	2.10	47.36	21.57	5.59	1.91	41.39	5	MS
14.	JGL 3844	9.68	3.78	1.32	12.73	8.46	2.74	0.95	8.07	9.07	3.26	1.14	10.40	5	MS
15.	JGL 3855	11.50	3.46	0.80	9.23	10.28	2.33	0.54	5.56	10.89	2.90	0.67	7.39	5	MS
16.	MTU 1010	5.06	1.75	1.65	8.37	6.12	1.34	1.27	7.75	5.59	1.55	1.46	8.06	5	MS
17.	MTU 1064	7.48	1.25	1.09	8.17	8.32	1.02	0.89	7.42	7.90	1.14	0.99	7.80	5	MS
18.	MTU 1075	2.20	1.50	0.62	1.36	3.12	2.03	0.84	2.62	2.66	1.77	0.73	1.99	3	MR
19.	MTU 1121	25.26	6.33	1.91	48.28	23.57	5.33	1.61	37.93	24.42	5.83	1.76	43.10	5	MS
20.	MTU 1153	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	HR
21.	MTU 3626	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	HR
22.	MTU 4870	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	HR
23.	NDLR 7	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	HR
24.	NLR 3041	34.85	7.15	2.93	102.17	29.46	5.33	2.19	64.41	32.15	6.24	2.56	83.29	7	S
25.	NLR 3513	6.06	1.83	0.91	5.53	5.12	1.75	0.87	4.46	5.59	1.79	0.89	5.00	5	MS
26.	NLR 40065	4.59	1.40	0.69	3.16	2.64	1.56	0.77	2.02	3.61	1.48	0.73	2.59	3	MR
27.	Rasi	7.14	1.80	1.55	11.04	5.35	2.01	1.73	9.24	6.25	1.91	1.64	10.14	5	MS
28.	RNR 2358	12.62	3.23	1.09	13.74	10.82	3.28	1.11	11.96	11.72	3.26	1.10	12.85	5	MS
29.	RNR 2458	6.17	1.20	0.42	2.60	5.82	2.13	0.75	4.35	6.00	1.67	0.58	3.47	5	MS
30.	RNR M7	31.73	5.70	2.14	67.90	28.64	6.00	2.25	64.54	30.19	5.85	2.20	66.22	7	S
31.	Swarna	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	HR
32.	Tellahamsa	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	HR
33.	WGL 44	28.00	6.61	2.70	75.61	30.15	8.76	3.58	107.95	29.08	7.68	3.14	91.78	7	S
34.	WGL 915	18.37	3.89	1.19	21.78	15.34	2.35	0.72	10.99	16.85	3.12	0.95	16.39	5	MS
35.	WGL 1272	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	HR
36.	WGL 347	18.90	2.25	0.55	10.41	20.18	2.50	0.61	12.35	19.54	2.38	0.58	11.38	5	MS

Table 4: Continue...

Sl. No.	Genotype	*Kharif*-2021				*Kharif*-2022				Mean				Disease	
		PDI	NS BPP	PIG	PDS	PDI	NS BPP	PIG	PDS	PDI	NS BPP	PIG	PDS	(0-9)	Reation
37.	RNR 35194	16.67	3.81	1.15	19.17	17.61	3.28	0.99	17.43	17.14	3.55	1.07	18.30	5	MS
38.	RNR 35989	6.86	1.57	0.80	5.49	5.32	2.50	1.27	6.77	6.09	2.04	1.04	6.13	5	MS
39.	RNR 35999	23.08	4.22	2.39	55.17	25.34	5.50	3.11	78.92	24.21	4.86	2.75	67.05	5	MS
40.	IET 28529	23.47	5.96	1.35	31.58	24.34	6.67	1.51	36.65	23.90	6.31	1.43	34.11	5	MS
41.	WGL 1377	14.85	3.20	0.90	13.43	12.57	3.50	0.99	12.43	13.71	3.35	0.95	12.93	5	MS
42.	IET 29265	30.00	7.91	3.84	115.33	33.28	8.94	4.34	144.59	31.64	8.42	4.09	129.96	7	S
43.	IET 29270	38.89	10.55	3.49	135.82	35.61	8.67	2.87	102.19	37.25	9.61	3.18	119.01	7	S
44.	IET 29289	46.67	6.96	2.67	124.54	42.63	7.63	2.92	124.56	44.65	7.29	2.80	124.55	7	S
45.	Akshayadhan	9.86	1.43	0.95	9.38	10.48	2.14	1.42	14.93	10.17	1.78	1.19	12.15	5	MS
46.	JGL 33164	19.32	3.59	1.76	34.08	16.72	3.14	1.55	25.84	18.02	3.37	1.65	29.96	5	MS
47.	IET 29291	11.69	1.89	1.64	19.13	8.25	2.16	1.87	15.44	9.97	2.02	1.75	17.29	5	MS
48.	IET 29506	28.24	5.54	1.95	55.13	25.18	3.85	1.36	34.16	26.71	4.70	1.65	44.65	7	S
49.	HR 12	4.88	1.50	0.75	3.64	3.54	0.00	0.00	0.00	4.21	0.75	0.37	1.82	3	MR
50.	PR 114	10.53	2.50	1.23	12.95	11.23	2.64	1.30	14.59	10.88	2.57	1.26	13.77	5	MS
51.	PR 124	2.56	1.00	0.51	1.30	2.43	1.35	0.68	1.66	2.50	1.18	0.59	1.48	3	MR
52.	PR 126	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	HR
53.	PR 127	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	HR
54.	PR 128	9.88	2.38	1.20	11.89	10.80	1.50	0.76	8.21	10.34	1.94	0.98	10.05	5	MS
55.	PR 121	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	HR
56.	PR 129	12.79	3.55	1.85	23.68	11.98	1.50	0.78	9.38	12.39	2.52	1.32	16.53	5	MS
57.	RNR 11718	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	HR
58.	TN 1 (C_1)	55.56	12.24	10.20	566.71	47.23	9.38	7.82	369.18	51.40	10.81	9.01	467.95	9	HS
59.	BPT 5204 (C_2)	32.84	8.39	3.81	125.12	25.46	5.23	2.38	60.59	29.15	6.81	3.10	92.86	7	S
60.	NLR 34449 (C_3)	28.37	8.46	4.23	120.00	26.59	4.94	2.47	65.68	27.96	6.70	3.35	92.84	7	S

HR: Highly resistant; R: Resistant; MR: Moderately resistant; MS: Moderately susceptible; S: Susceptible; HS: Highly susceptible; C: Check

Germplasm response to false smut disease was calculated based on % disease incidence (PDI) and grouped into six disease scoring scale (0-9) (Table 5). Among 60 genotypes, 16 genotypes viz., Abhaya, Chittimuthyalu, HR 59, IET 23993, JGL 30090, MTU 1153, MTU 3626, MTU 4870, NDLR7, Swarna, Tellahamsa, WGL 1272, PR 126, PR 127, PR 121 and RNR 11718 were showed highly resistant reaction (0 score), no genotype was showed resistant reaction (<1% score) to false smut disease and only four genotypes (PR 124, MTU1075, NLR40065 and HR 12) showed moderately resistant reaction (1.1-5% score) and 29 genotypes (AD16037, Bhadrakali, HMT Sona, Improved Pusa Basumati, JGL 13595, JGL 1798, JGL 3828, JGL 3844, JGL 3855, MTU 1010, MTU 1064, MTU 1121, NLR 3513, Rasi, RNR 2358, RNR 2458, WGL 915, WGL 347, RNR 35194, RNR 35989, RNR 35999, IET 28529, WGL 1377, Akshayadhan, JGL 33164, IET 29291, PR 114, PR 128 and PR 129) were found moderately susceptible (5.1-25% score) and 10 genotypes (IET 29506, WGL 44, RNR M7, IET 29265, NLR3041, IET 29270, Jaisriram, IET 29289, BPT 5204 (C_2) and NLR 34449 (C_3)) were showed susceptible reaction and TN 1 (C_1) found highly susceptible reaction to false smut disease.

The studies conducted by Rani et al. (2016) revealed that among 31 elite germplasm lines, noting three lines (PAU-3965-11-4-1-4-2, PAU-3965-11-4-1-1-2 and PR118)

Table 5: Grouping of rice genotypes based on their reaction to false smut disease

Scale	% infected panicles (Host response)	Genotypes	No. of genotypes
0	0 (No disease) (Highly resistant)	Abhaya, Chittimuthyalu, HR 59, IET 23993, JGL 30090, MTU 1153, MTU 3626, MTU 4870, NDLR7, Swarna, Tellahamsa, WGL 1272, PR 126, PR 127, PR 121 and RNR 11718	
1	<1% (Resistant)	-	-
3	1.1-5% (Moderately resistant)	PR 124, MTU1075, NLR40065 and HR 12	4
5	5.1-25% (Moderately susceptible)	AD16037, Bhadrakali, HMT Sona, Improved Pusa Basumati, JGL 13595, JGL 1798, JGL 3828, JGL 3844, JGL 3855, MTU 1010, MTU 1064, MTU 1121, NLR 3513, Rasi, RNR 2358, RNR 2458, WGL 915, WGL 347, RNR 35194, RNR 35989, RNR 35999, IET 28529, WGL 1377, Akshayadhan, JGL 33164, IET 29291, PR 114, PR 128 and PR 129	29
7	25.1-50% (Susceptible)	IET 29506, WGL 44, RNR M7, IET 29265, NLR3041, IET 29270, Jaisriram, IET 29289, BPT 5204 (C_2) and NLR 34449 (C_3)	10
9	>50% (Highly susceptible)	TN 1 (C_1)	1

with high resistance and two varieties (PR122 and PR114) showing resistance against false smut. Lore et al. (2013) reported that two cultivars, PR113 and PR114, displaying the least intensity of false smut disease. Raji et al. (2016) reported that out of twenty genotypes, seven (Ptb 7, Ptb 23, Ptb 24, Ptb 32, Ptb 36, Ptb 42 and Ptb 46) were disease-free. Four genotypes showed 0.80 to 0.97% infected grains and 0.5 to 7.17% disease incidence. Eight genotypes (Ptb 1, Ptb 2, Ptb 28, Ptb 34, Ptb 35, Ptb 39, Ptb 49 and Ptb 51) had 1.23 to 5.10% infected grains and 0.43 to15.95% disease incidence. One genotype (Ptb 52) had 7.20% infected grains and 31.43% disease incidence. Similarly, Hiremath et al. (2021) found that, out of 125 diverse lines, 21 lines consistently displayed high resistance, while 31 lines showed moderate resistance.

3.2. *Effect of different characters of rice genotypes on false smut*

3.2.1. *Panicle type*

Among 60 germplasm, 18 genotypes (JGL 13595, JGL 1798, JGL 3828, JGL 3844, NLR 3041, RNR M7, WGL 44, WGL 347, WGL 1377, IET 29265, IET 28529, IET 29270, IET 29289, IET 29506, JGL 33164, TN 1 (C_1), BPT 5204 (C_2) and NLR 34449 (C_3)) showed compact type panicle, 15 genotypes (Bhadrakali, HMT Sona, Jaisriram, JGL 30090, JGL 3855, MTU 1121, NLR 3513, RNR 2358, RNR 2458, Swarna, WGL 915, WGL 1272, RNR 35194, PR 126 and RNR 11718) showed intermediate type panicle and 27 germplasm (Abhaya, AD16037, Chittimuthyalu, HR 59, IET 23993, Improved Pusa Basumati, MTU 1010, MTU 1064, MTU 1075, MTU 1153, MTU 3626, MTU 4870, NDLR7, NLR 40065, Rasi, Tellahamsa, RNR 35989, RNR 35999, Akshayadhan, IET 29291, HR 12, PR 114, PR 124, PR 127, PR 128, PR 121, PR 129) showed loose panicle type (Table 6).

Among different panicle types compact panicle type germplasm showed the highest average % disease incidence (25.25) with 5.70 smut balls per panicle, 1.98% of infected grains and 59.12% of disease severity. Followed by germplasm with intermediate type panicle showed 15.18% disease incidence, 3.34 smut balls per panicle, 1.57% of infected grains and 48.10% disease severity. The least disease incidence of 4.83% was shown in loose panicle type germplasm with 1.12 smut balls per panicle, 0.68% infected grains and 6.93% disease severity (Table 6).

3.2.2. *Panicle length*

The correlation matrix provided in Table 7 shows the Pearson correlation coefficients between disease parameters (% disease incidence, number of smut balls per panicle, % infected grains and % disease severity) and panicle length,

Table 6: False smut disease reaction among different panicle types of rice genotypes

Panicle type	PDI	NSBPP	PIG	PDS
Compact panicle (18)	25.25	5.70	1.98	59.12
Intermediate type panicle (15)	15.18	3.34	1.57	48.10
Loose panicle (27)	4.83	1.12	0.68	6.93
CD (p<0.05)	2.21	2.63	1.76	1.51
SEm±	0.74	0.89	0.63	0.52

PDI: % disease incidence; NSBPP: no. of smut balls per panicle; PIG: % infected grains; PDS: % disease severity along with their corresponding R-squared values. In this correlation matrix % disease incidence, number of smut balls per panicle, % infected grains and % disease severity showed negative correlation with panicle length at 5% level of significance with the correlation coefficients of -0.287*, -0.268*, -0.297* and -0.304* respectively. The results suggest that an increase in panicle length leads to a decrease in false smut disease in rice. These results were on par with the results obtained for survey observations during *kharif,* 2021 and 2022 (Table 7).

Table 7: Pearson correlation matrix between false smut and panicle length of rice genotypes

Disease parameters	Panicle length	R^2
% disease incidence	-0.287*	0.082
Number of smut balls panicle^{-1}	-0.268*	0.072
% infected grains	-0.297*	0.088
% disease severity	-0.304*	0.092

Pearson's correlation co-efficient at 5%: ≥ 0.273 to ≤ 0.324 "*"; Pearson's correlation co-efficient at 1%: ≥ 0.325 "**"

3.2.3. Number of grains panicle^{-1}

Correlation coefficients presented in the Table 8 revealed that, % disease incidence and number of smut balls per panicle showed positive correlation with number of rice grains per panicle observed among the germplasm at five % level of significance, with coefficients of 0.262* and 0.283*, respectively. This indicates that an increase in the number of grains panicle^{-1} tends to result in an increase in the % disease incidence and number of smut balls per panicle among the germplasm. Meanwhile, % infected grains and % disease severity showed non-significant negative correlations with the number of grains per panicle, with coefficients of -0.073 and -0.063, respectively.

3.2.4. Grain type

The grain type of genotypes was categorized based on the scale provided by Ramaiah (1969) (Table 3). Among the 60 genotypes, three genotypes (Improved Pusa Basumati, PR 114 and PR 124) was categorized as extra-long slender grain type. Seven genotypes (Abhaya, AD16037, MTU3626, IET 28529, Akshayadhan, TN 1 (C_1) and PR 127) were classified as long bold grain type. Fifteen genotypes (Bhadrakali, JGL30090, MTU 1010, MTU 1153, NLR4 0065, Tellahamsa, RNR 35194, MTU1075, RNR 35989, RNR 35999, IET 29265, IET 29506, PR 126, PR 121 and PR 129) were categorized as long slender grain type. Twenty-five genotypes (JGL 13595, JGL 1798, JGL 3828, JGL 3844, JGL 3855, MTU 1064, MTU 1121, MTU 4870, NLR 3041, NLR 3513, Rasi, RNR 2358, RNR 2458, NDLR7, Swarna, WGL 44, WGL 915, WGL 1272, WGL 1377, IET 29289, HR 12, PR 128, BPT 5204 (C_2), NLR 34449 (C_3) and RNR 11718) were classified as medium slender grain type. Five genotypes (Chittimuthyalu, HR 59, IET23993, IET 29270 and IET 29291) were categorized as short bold grain type. Five genotypes (HMT Sona, Jaisriram, RNR M7, WGL 347 and JGL 33164) were classified as short slender grain type (Table 9).

Table 8: Correlation between false smut and number of grains per panicle in rice genotypes

Disease parameters	No. of grains per panicle	R^2
% disease incidence	0.262*	0.069
Number of smut balls panicle^{-1}	0.283*	0.080
% infected grains	-0.073	0.005
% disease severity	-0.063	0.004

Pearson's correlation co-efficient at 5%: ≥ 0.273 to ≤ 0.324 "*"; Pearson's correlation co-efficient at 1%: ≥ 0.325 "**"

As showed in the Table 9, among the all grain types, genotypes having short slender grains showed the highest average disease incidence (17.39%) with 3.07 smut balls per panicle, followed by medium slender (15.01% and 3.42), long bold (13.29% and 2.98), long slender (9.34% and 2.21) and short bold (9.44% and 2.33). The least disease incidence (6.45%) was recorded in extra-long slender grain type with 1.52 smut balls per panicle. The maximum average % infected grains was observed in long bold grain type (1.80%) with 74.48% disease severity, followed by medium slender (1.33% and 31.23%), short slender (1.29% and 31.23%), long slender (1.05% and 20.31%), short bold (0.99% and 27.26%) and extra-long slender (0.77% and 6.11%).

The literature on the detailed study of the effect of grain type of rice genotypes on false smut is relatively limited. Nevertheless, Sanghera et al. (2012) screened ten rice genotypes (eight long slender and two medium bold grain types) against false smut disease in 2010 and 2011. Among the eight long slender grain types, Pusa Sungadh-3 exhibited the highest mean disease incidence at 34.11% with 14.47% disease severity, followed by Pusa Sungadh-5 with a 26.94% incidence and 13.18% disease severity. In contrast, SKUA-417 showed the least incidence at 2.10% with 0.55% disease severity. Notably, the medium bold grain genotypes Jhelum and Shalimar Rice-I showed no disease incidence in both years.

3.3. Cluster analysis of rice genotypes against false smut incidence

Sixty rice genotypes were clustered based on false smut disease incidence and plant characters as described in the

Table 9: False smut disease in different grain types of rice genotypes

Grain type	PDI	NSBPP	PIG	PDS	Number of genotypes
Short slender	17.39	3.07	1.29	31.23	(5): HMT Sona, Jaisriram, RNR M7, WGL 347 and JGL 33164
Short bold	9.44	2.33	0.99	27.26	(5): Chittimuthyalu, HR 59, IET23993, IET 29270 and IET 29291
Medium slender	15.01	3.42	1.33	31.23	(25): JGL 13595, JGL 1798, JGL 3828, JGL 3844, JGL 3855, MTU 1064, MTU 1121, MTU 4870, NDLR7, NLR 3041, NLR 3513, Rasi, RNR 2358, RNR 2458, Swarna, WGL 44, WGL 915, WGL 1272, WGL 1377, IET 29289, HR 12, PR 128, BPT 5204 (C_2), NLR 34449 (C_3) and RNR 11718
Long slender	9.34	2.21	1.05	20.31	(15): Bhadrakali, JGL30090, MTU 1010, MTU1075, MTU 1153, NLR4 0065, Tellahamsa, RNR 35194, RNR 35989, RNR 35999, IET 29265, IET 29506, PR 126, PR 121 and PR 129
Long bold	13.29	2.98	1.80	74.48	(7): Abhaya, AD16037, MTU3626, IET 28529, Akshayadhan, TN 1 (C_1) and PR 127
Extra long slender	6.45	1.52	0.77	6.11	(3): Improved Pusa Basumati, PR 114 and PR 124
CD (p<0.05)	2.83	1.09	0.63	3.38	-
SEm±	0.91	0.35	0.20	1.09	-

PDI: % disease incidence; NSBPP: no. of smut balls per panicle; PIG: % infected grains; PDS: % disease severity

Table 10. Cluster analysis based on disease parameters, all genotypes were classified into four clusters (Cluster I, Cluster II, Cluster III and Cluster IV) at Jaccard similarity coefficient of 0.73 (Figure 1). Out of sixty, 16 genotypes (Abhaya, Chittimuthyalu, HR 59, IET 23993, JGL 30090, MTU 1153, PR 127, PR 126, MTU 3626, MTU 4870, NDLR 7, RNR 11718, PR 121, Swarna, Tellahamsa and WGL 1272) showed no false smut disease were grouped into Cluster I. A total of 33 genotypes were categorized under Cluster II, further divided into two subclusters: Subcluster II (a) comprising 28 genotypes (AD16037, Bhadrakali, HMT sona, JGL 13595, MTU 1010, PR 128, MTU 1064,

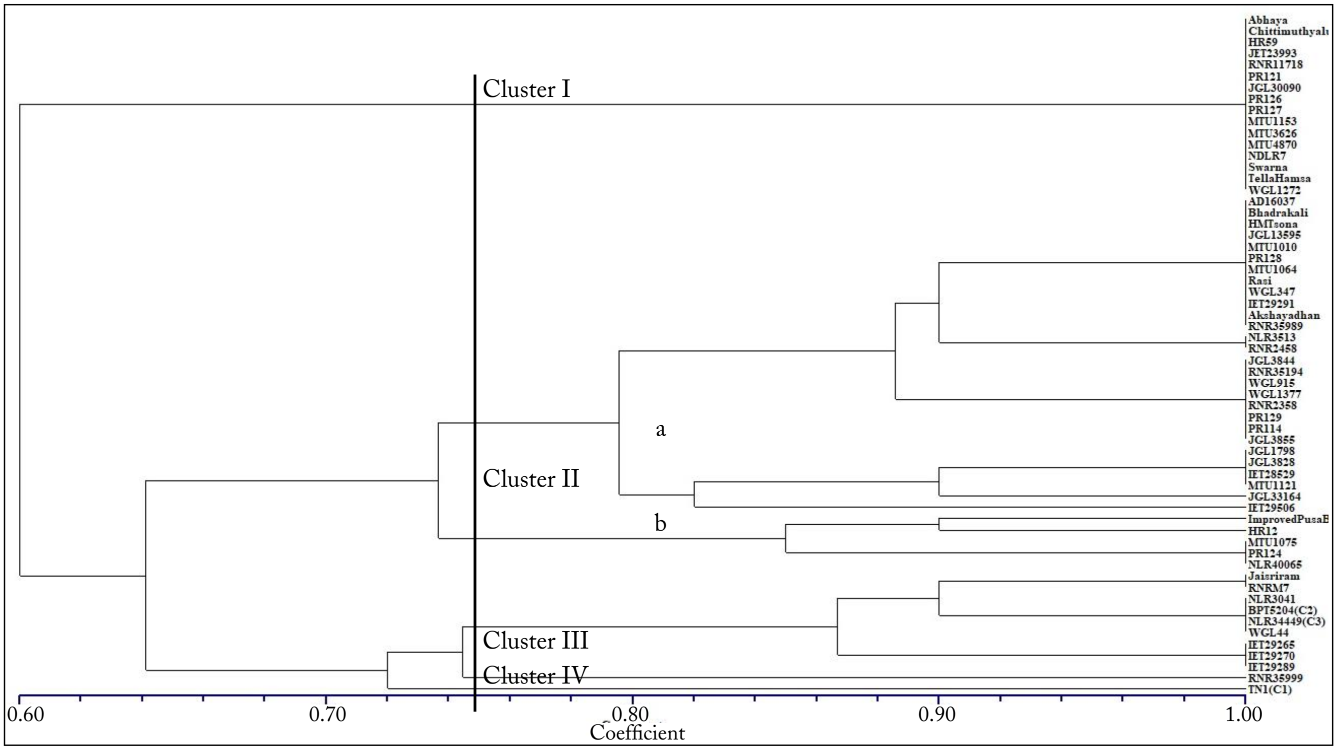

Figure 1: Cluster analysis of rice genotypes based on false smut disease observed during *kharif*-2021 and 2022

Table 10: Scoring of false smut disease parameters and genotype characters used for cluster analysis

Sl. No.	Disease parameters	Scale	Scoring
1.	% disease incidence	0, <1, 1.1-5%, 5.1-25%, 25.1-50%, >50%	Presence- 1
			Absence- 0
2.	Number of smut balls per panicle	0, <0.1, 0.51-2.5, 2.51-5.0, >5.0	Presence- 1
			Absence- 0
3.	% infected grains	0, <0.1%, 0.51-2.5%, 2.51-5.0%, >5.0%	Presence- 1
			Absence- 0
4.	% disease severity	0, <1, 1.1-5%, 5.1-25%, 25.1-50%, 50.1-100%, >100%	Presence- 1
			Absence- 0
Sl. No.	**Plant characters**	**Scale**	**Scoring**
1.	Panicle type	Compact, intermediate type, loose	Presence- 1
			Absence- 0
2.	Grain type	Short slender, short bold, medium slender, long slender, long bold, extra long slender	Presence- 1
			Absence- 0
3.	Days to late booting (DAP*)	≤70, >70-80, >80	Presence- 1
			Absence- 0

*DAP: Days after planting

Rasi, WGL 347, IET 29291, Akshayadhan, RNR 35989, NLR 3513, RNR 2458, JGL 3844, RNR 35194, WGL 915, WGL 1377, RNR 2358, PR 129, PR 114, JGL 3855, JGL 1798, JGL 3828, IET 28529, MTU 1121, JGL 33164 and IET 29506) showed 5.1 to 25% of disease incidence and Subcluster II (b) consisting of five genotypes (Improved Pusa Basumati, HR 12, MTU 1075, PR 124 and NLR 40065), most of them showed 1.1 to 5% disease incidence. Ten genotypes were allocated to Cluster III (Jaisriram, RNR M7, NLR 3041, BPT 5204 (C_2), NLR 34449 (C_3), WGL 44, IET 29265, IET 29270, IET 29289 and RNR 35999) showed 25.1 to 50% disease incidence. While, Cluster IV consisting of only one genotype (TN 1 (C_1) with more than 50% false smut disease incidence.

Cluster analysis of genotypes based on plant characters revealed that, sixty genotypes were classified into five clusters (Cluster I, Cluster II, Cluster III, Cluster IV and Cluster V) at Jaccard similarity coefficient of 0.71 (Figure 2). Cluster I comprised 17 genotypes (Abhaya, PR 127, AD16037, MTU 3626, Akshayadhan, Improved Pusa Basumati, MTU 4870, HR 12, NDLR 7, MTU 1075, NLR 40065, RNR 35989, RNR 35999, Chittimuthyalu, HR 59, IET 23993 and IET 29291). Cluster II consisted of 13 genotypes (MTU 1010, PR 129, MTU 1153, Tellahamsa, PR 121, PR 114, PR 124, MTU 1064, PR 128, Rasi, NLR 3513, RNR 11718 and Swarna). Cluster III included 24 genotypes (Jaisriram, WGL 347, JGL 33164, JGL 13595, JGL 1798, BPT 5204 (C_2), NLR 34449 (C_3), WGL 44, WGL 1377, IET 29289, NLR 3041, JGL 3828, JGL 3855, IET 28529, IET 29270, IET 29265, IET 29506, MTU 1121, RNR 2358, RNR 2458, WGL 915, WGL 1272, RNR 35194 and PR 126). Cluster IV had two genotypes (RNR M7 and TN 1 (C_1)) and Cluster V included 4 genotypes (Bhadrakali, JGL 30090, HMT sona and JGL 3844).

3.4. Comparison of germplasm clustering based on plant characters and false smut disease observations

As mentioned above, genotypes were grouped into five clusters based on plant characters and four clusters based on false smut disease observations. More than 65% of the genotypes were grouped similarly in each clustering (Table 11). For instance, in Cluster I of genotype clustering based on plant characters, shared eight genotypes (Abhaya, PR 127, MTU 3626, MTU 4870, NDLR 7, Chittimuthyalu, HR 59 and IET 23993) from Cluster I, eight genotypes (AD16037, Akshayadhan, Improved Pusa Basumati, HR 12, MTU 1075, NLR 40065, RNR 35989 and IET 29291) from Cluster II and one genotype (RNR 35999) from Cluster III of genotype clustering based on disease observations. Cluster II of genotype clustering based on plant characters included five genotypes (MTU 1153, Tellahamsa, PR 121, RNR 11718 and Swarna) from Cluster I and eight genotypes (MTU 1010, PR 129, PR 114, PR 124, MTU 1064, PR 128, Rasi and NLR 3513) from Cluster II of genotype clustering based on disease observations. Cluster III of genotype clustering based on plant characters shared two genotypes (WGL 1272 and PR

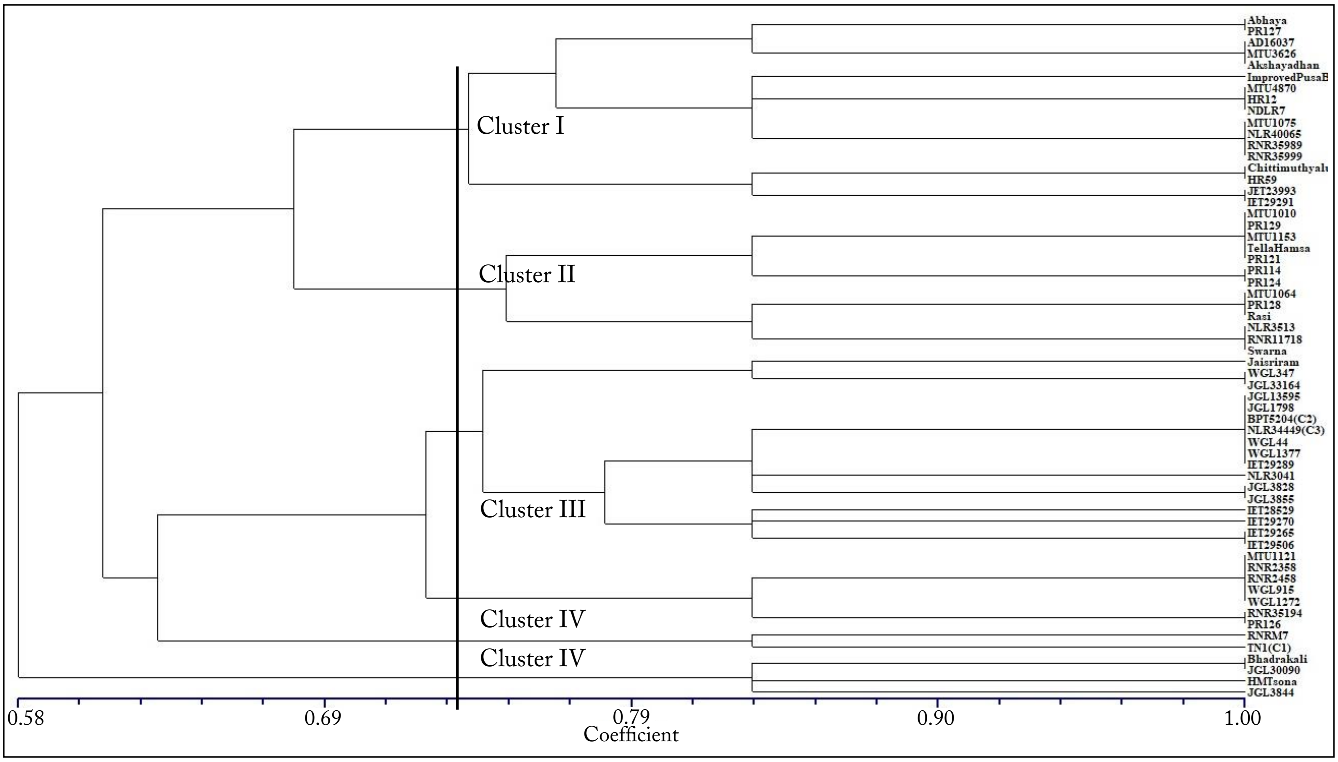

Figure 2: Cluster analysis of rice genotypes based on plant characters

126) from Cluster I, 14 genotypes (WGL 347, JGL 33164, JGL 13595, JGL 1798, WGL 1377, JGL 3828, JGL 3855, IET 28529, IET 29506, MTU 1121, RNR 2358, RNR 2458, WGL 915 and RNR 35194) from Cluster II and

Table 11: Comparison of germplasm clustering based on plant characters and false smut disease observations

Clusters based on germplasm characters		Germplasm shared from false smut disease clustering	
I(17)	Abhaya, PR 127, AD16037, MTU 3626, Akshayadhan, Improved Pusa Basumati, MTU 4870, HR 12, NDLR 7, MTU 1075, NLR 40065, RNR 35989, RNR 35999, Chittimuthyalu, HR 59, IET 23993 and IET 29291	I(8)	Abhaya, PR 127, MTU 3626, MTU 4870, NDLR 7, Chittimuthyalu, HR 59 and IET 23993
		II(8)	AD16037, Akshayadhan, Improved Pusa Basumati, HR 12, MTU 1075, NLR 40065, RNR 35989 and IET 29291
		III(1)	RNR 35999
II(13)	MTU 1010, PR 129, MTU 1153, Tellahamsa, PR 121, PR 114, PR 124, MTU 1064, PR 128, Rasi, NLR 3513, RNR 11718 and Swarna	I(5)	MTU 1153, Tellahamsa, PR 121, RNR 11718 and Swarna
		II(8)	MTU 1010, PR 129, PR 114, PR 124, MTU 1064, PR 128, Rasi and NLR 3513
III(24)	Jaisriram, WGL 347, JGL 33164, JGL 13595, JGL 1798, BPT 5204 (C_2), NLR 34449 (C_3), WGL 44, WGL 1377, IET 29289, NLR 3041, JGL 3828, JGL 3855, IET 28529, IET 29270, IET 29265, IET 29506, MTU 1121, RNR 2358, RNR 2458, WGL 915, WGL 1272, RNR 35194 and PR 126	I(2)	WGL 1272 and PR 126
		II(14)	WGL 347, JGL 33164, JGL 13595, JGL 1798, WGL 1377, JGL 3828, JGL 3855, IET 28529, IET 29506, MTU 1121, RNR 2358, RNR 2458, WGL 915 and RNR 35194
		III(8)	Jaisriram, BPT 5204 (C_2), NLR 34449 (C_3), WGL 44, IET 29289, NLR 3041, IET 29270 and IET 29265
IV(2)	RNR M7 and TN 1 (C_1)	III(1)	IET 29506
		IV(1)	TN 1 (C_1)
V(4)	Bhadrakali, JGL 30090, HMT sona and JGL 3844	I(1)	JGL 30090
		II(3)	Bhadrakali, HMT Sona and JGL 3844

eight genotypes (Jaisriram, BPT 5204 (C2), NLR 34449 (C3), WGL 44, IET 29289, NLR 3041, IET 29270 and IET 29265) from Cluster III of genotype clustering based on disease parameters. Similarly, Cluster IV of geotype clustering based on plant characters having two genotypes, one (IET 29506) from Cluster III another (TN 1 (C1)) from Cluster IV of genotype clustering based on disease parameters. Cluster V of genotype clustering based on plant characters shared one genotype (JGL 30090) from Cluster I, three genotypes (Bhadrakali, HMT sona and JGL 3844) from Cluster II of genotype clustering based on disease parameters.

The results revealed that, the clustering of genotypes based on plant characters and false smut disease observations revealed a significant overlap, with more than 65% of the genotypes grouped similarly in both clusterings. This high degree of similarity suggests a strong correlation between plant characteristics and disease response.

4. CONCLUSION

The evaluation of 60 rice germplasm lines against false smut revealed significant variation in disease response. Sixteen genotypes were highly resistant, while TN 1 was highly susceptible. Compact panicles and higher grain number showed a positive correlation with disease incidence, whereas panicle length showed a negative correlation. Grain type influenced susceptibility, with short slender types being most affected. Cluster analysis indicated that morphological traits are closely associated with false smut resistance, aiding future resistant variety development.

5. REFERENCES

Ashizawa, T., Takahashi, M., Moriwaki, J., Hirayae, K., 2011. A refined inoculation method to evaluate false smut resistance in rice. Journal of General Plant Pathology 77, 10–16. https://doi.org/10.1007/s10327-010-0279-5.

Anonymous, 2002. IRRI, I., 2002. Standard Evaluation System for Rice. International Rice Research Institute, Philippines 1–45. Available at: http://www.knowledgebank.irri.org/images/docs/rice-standard-evaluation-system.pdf. Accessed Date: 24.01.2024.

Atia, M.M.M., 2004. Rice false smut (*Ustilaginoidea virens*) in Egypt. Journal of Plant Diseases and Protection 111, 71-82. https://doi.org/10.1007/BF03356134.

Biswas, A., 2001. Field reaction of hybrid rice varieties to False Smut (FSm) and Kernel Smut (KSm) diseases in West Bengal, India. Environment and Ecology 19(1), 229–230. Available at: https://www.cabidigitallibrary.org/doi/full/10.5555/20013049902.

Cartwright, R.D., Lee, F.N., Beaty, T., Sutton, E.A., Parsons, C.E., 2000. Reaction of rice cultivars/lines to false smut, stem rot and black sheath rot disease. Research Series-Arkansas Agricultural Experiment Station 476, 158–168. Available at: https://api.semanticscholar.org/CorpusID:82895175.

Cooke, M.C., 1878. Some extra-European fungi. Grevillea 7, 13–15. Available at: https://www.scirp.org/reference/referencespapers?referenceid=1317353.

Doden, D.S., Singh, R., 1996. False smut of rice: Present status. Agricultural Review 17(4), 227–240. Available at: https://www.researchgate.net/publication/296003020_False_smut_of_rice_Present_Status.

Duraisamy, L., Madamsetty, S.P., Vellaichamy, P., Donempudi, K., Banda, S., Singh, R., Laha, G.S., 2019. Geographic distribution of false smut disease of rice in India and efficacy of selected fungicides for its management. International Journal of Pest Management 65(2), 177–185. Available at: https://doi.org/10.1080/09670874.2018.1494865?urlappend=%3Futm_source%3Dresearchgate.

Fan, J., Guo, X.Y., Li, L., Huang, F., Sun, W.X., Li, Y., Huang, Y.Y., Xu, Y.J., Shi, J., Lei, Y., Zheng, A.P., 2015. Infection of *Ustilaginoidea virens* intercepts rice seed formation but activates grain-filling-related genes. Journal of Integrative Plant Biology 57(6), 577–590. https://doi.org/10.1111/jipb.12299.

Hiremath, S.S., Bhatia, D., Jain, J., Hunjan, M.S., Kaur, R., Zaidi, N.W., Singh, U.S., Zhou, B., Lore, J.S., 2021. Identification of potential donors and QTLs for resistance to false smut in a subset of rice diversity panel. European Journal of Plant Pathology 159, 461–470. https://doi.org/10.1007/s10658-020-02172-w.

Huang, F., Li, Y., Shi, J., Fan, J., Xu, Y.J., Wang, W.M., 2015. Screening and polymorphism analysis of rice germplasms for resistance to false smut disease in Sichuan Province. Acta Phytopathology Sin 46(2), 247–257. https://doi.org/10.13926/j.cnki.apps.2016.02.013.

Jamshidi, S., Jamshidi, S., 2011. NTSYSpc 2.02 e implementation in molecular biodata analysis (clustering, screening and individual selection). In Proceedings of 4th International Conference on Environmental and Computer Science (11), 165–169. Accessed Date: 24.01.2024. Available at: https://www.researchgate.net/publication/268270321_NTSYSpc_202e_Implementation_in_Molecular_Biodata_Analysis_Clustering_Screening_and_Individual_Selection.

Koiso, Y., Li, Y., Iwasaki, S., Hanaoka, K., Kobayashi, T., Sonoda, R., Fujita,Y., Yaegashi, H., Sato, Z., 1994. Ustiloxins, antimitotic cyclic peptides from false smut balls on rice panicles caused by *Ustilaginoidea* *virens*. Journal of Antibiotics 47, 765–772. https://doi.org/10.7164/antibiotics.47.765.

Kumari, S., Kumar, J., 2015. Evaluation of yield losses and management practices of false smut in rice (*Oryza sativa*). Indian Phytopath 68(1), 45–49. Available at: https://epubs.icar.org.in/index.php/IPPJ/article/view/46971.

Ladhalakshmi, D., Laha, G.S., Singh, R., Karthikeyan, A., Mangrauthia, S.K., Sundaram, R.M., Thukkaiyannan, P., Viraktamath, B.C., 2012. Isolation and characterization of *Ustilaginoidea virens* and survey of false smut disease of rice in India. Phytoparasitica 40, 171–176. https://doi.org/10.1007/s12600-011-0214-0.

Li, Y.S., Zhang, Y.D., Zhu, Z., Zhao, L., Wang, C.L., 2008. QTL analysis for resistance to rice false smut by using recombinant inbred lines in rice. Chinese Journal of Rice Science 22, 472–476. http://www.ricesci.cn/EN/.

Lore, J.S., Jain, J., Kumar, S., Kamboj, I., Khanna, R., Dhillon, B.S., Zaidi, N.W., Singh, U.S., 2021. Prevention of false smut (*Ustilaginoidea virens*) on rice hybrids and pure-line cultivars by manipulating planting date. Journal of Phytopathology 169(10), 597–606. https://doi.org/10.1111/jph.13030.

Lore, J.S., Pannu, P.P.S., Jain, J., Hunjan, M.S., Kaur, R., Mangat, G.S., 2013. Susceptibility of rice hybrids and inbred cultivars to false smut under field conditions. Indian Phytopathology 66(4), 397–399. Available at: https://epubs.icar.org.in/index.php/IPPJ/article/view/36018.

Luduena, R.F., Roach, M.C., Prasad, V., Banerjee, M., Koiso, Y., Li, Y., Iwasaki, S., 1994. Interaction of ustiloxin A with bovine brain tubulin. Biochemical Pharmacology 47(9), 1593–1599. https://doi.org/10.1016/0006-2952(94)90537-1.

Mohiddin, F. A., Bhat, F. A., Gupta, V., Gupta, D., Kalha, C.S., 2012. Integrated disease management of false smut of rice caused by *Ustilaginoidea virens*. Trends in Biosciences 5(4), 301–302. https://www.semanticscholar.org/paper/Integrated-Disease-Management-of-False-Smut-of-Rice-Mohiddin-Bhat/13bb268338f7c0d91063e8949f2eb112a5ba56b1?utm_source=direct_link.

Muniraju, K.M., Pramesh, D., Mallesh, S.B., Mallikarjun, K., Guruprasad G.S., 2017. Disease severity and yield losses caused by false smut disease of rice in different rice ecosystems of Karnataka. International Journal of Microbiology Research 9(10), 963–966. Available at: https://api.semanticscholar.org/CorpusID:86292365.

Raji, P., Sumiya, K.V., Dhanya, S., Remya, K., Narayanankutty, M.C., 2016. Screening of rice varieties and in vitro evaluation of botanicals against false smut pathogen, *Ustilaginoidea virens*. International Journal of Agricultural Science and Research 6(2), 79–86.

Ramaiah, K., 1969. Grain type classification. Rice Research in India. Indian Council of Agricultural Research, New Delhi, 628-629.

Rani, R., Sharma, V.K., Lore, J.S., Pannu, P.P.S., Kaur, Y., 2016. Screening of rice germplasm against *Ustilaginoidea virens*, the incitant of false smut. Agricultural Research Journal 53, 134–137. https://doi.org/10.5958/2395-146X.2016.00026.0.

Rashmi, C.R., Gokulapalan, C., Raji, P., Surendran, M., 2016. Screening of varieties for resistance to false smut (*Ustilaginoidea virens* (Cook) Tak.) disease of rice. ORYZA-An International Journal on Rice 53(1), 102–105. Available at: https://www.researchgate.net/publication/337160569.

Rush, M.C., Shahjahan, A.K.M., Jones, J.P., Groth, D.E., 2000. Outbreak of false smut of rice in Louisiana. Plant disease 84(1), 100–100. https://doi.org/10.1094/PDIS.2000.84.1.100D.

Sanghera, G.S., Ahanger, M.A., Kashyap, S.C., Bhat, Z.A., Rather, A.G., Parray, G.A., 2012. False smut of rice (*Ustilaginoidea virens*) under temperate agro-climatic conditions of Kashmir, India. Elixir Bio Tech 49, 9827-9830. Available at: https://www.scirp.org/reference/referencespapers?referenceid=1317338.

Shan, T., Sun, W., Wang, X., Fu, X., Sun, W., Zhou, L., 2013. Purification of ustiloxins A and B from rice false smut balls by macroporous resins. Molecules 18(7), 8181–8199. https://doi.org/10.3390/molecules18078181.

Singh, A.K., Pophaly, D.J., 2010. An unusual rice false smut epidemic reported in Raigarh District, Chhattisgarh. International Rice Research Notes 35, 1–3. Available at: https://www.scribd.com/doc/101893582/An-unusual-rice-false-smut-epidemic-reported-in-Raigarh-District-Chhattisgarh-India.

Singh, R.A., Dube, K.S., 1978. Assessment of loss in seven rice cultivars due to false smut. Indian Phytopathology 31, 186–188. Available at: https://api.semanticscholar.org/CorpusID:84091614.

Singh, S., Lal, A.A., Simon, S., Singh, A., Taduman, R., Kamaluddeen, D.A., David, A.A., 2014. Survey of false smut (*Ustilaginoidea virens*) of rice (*Oryza sativa* L.) in selected districts of Utter Pradesh, India. The Bioscan 9, 389–392. Available at: https://thebioscan.com/index.php/pub/article/view/1931.

Tanaka, E., Ashizawa, T., Sonoda, R., Tanaka, C., 2008. *Villosiclava virens* gen. nov., comb. nov., the teleomorph of *Ustilaginoidea virens*, the causal agent of rice false smut. Mycotaxon 106(1), 491–501. Available at: https://www.researchgate.net/publication/234130822.

Thapa, S., Mahapatra, S., Baral, D., Lama, A., Shivakoty, P., Das, S., 2022. Status of false smut of rice in different districts of West Bengal. Oryza 59(2), 167–171. https://doi.org/10.35709/ory.2022.59.2.5.

Upadhyay, A.L., Singh, R.V., 2013. Yield loss assessment in rice due to false smut. Annals of Plant and Soil Research 15(2), 173–174. Available at: https://www.gkvsociety.com/control/uploads/Yield-loss-assessment-in-rice-due-to-false-smut.pdf.

Wang, Y., Fan, R., Yang, B., Liu, B., Zhang, J., Hu, D., 2010. Comparison of isolation methods for *Ustilaginoidea virens*, the pathogen of rice false smut. Mycosystema 29(1), 59–63. https://www.cabidigitallibrary.org/doi/full/10.5555/20103155635.

Zhang, Y., Zhang, K., Fang, A., Han, Y., Yang, J., Xue, M., Bao, J., Hu, D., Zhou, B., Sun, X., Li, S., 2014. Specific adaptation of *Ustilaginoidea virens* in occupying host florets revealed by comparative and functional genomics. Nature Communications 5(1), 3849. https://doi.org/10.1038/ncomms4849.