

Electronic Journal of Plant Breeding



Research Article

Genetic studies on false smut disease resistance and yield components in rice (*Oryza sativa*. L)

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Abstract

The present investigation was performed to explain the genetic variability and association parameters of twenty traits in 30 F_s involving six parents differing in resistance against false smut in rice. Breeding materials were evaluated at hotspot location viz., HREC, Gudalur. The ANOVA revealed significant differences among the studied variables. Higher PCV over other coefficients of variation suggest the role of environment in trait expression. Disease related traits viz., NIP, NIT, NIGPa, PIT, PIGPa and agronomic traits viz., TNFPa, NCGPa, SSP, PH, HGW and SPY showed high magnitude of values for GCV, heritability and GAM indicating the role of additive gene action. Hence, selection of these traits may be effective. Correlation studies indicated that HGW and SPW showed positive significant association with SPY. Path analysis revealed that NIT, NIGPa, NIGP and PIP had negative direct effect and DFF, NPT, TNFPa, SSP, NSRPa and SPW had positive direct effect towards single plant yield.

Keywords: Rice, False smut resistance, Yield, Variability, Association analysis

INTRODUCTION

Rice is the principal food crop of Asian countries and continued breeding efforts are sought for its improvement in terms of production and productivity to feed the escalating population. At all stages of crop growth and development, various biotic and abiotic stresses influence the rice grain production and result in considerable yield losses. False smut is one among the biotic stresses which was sporadic in rice growing areas, but has now increased in the frequency of occurrence due to changing climatic conditions (Wang *et al.*, 2019). The disease can cause 2.8–81% yield losses in different rice-producing areas depending on the rice variety and disease intensity (Andargie *et al.*, 2018). Prophylactic fungicide

spraying can reduce the intensity of the disease since it is difficult to control after the disease after its incidence. This results in huge losses as the grains become unfit for marketing and consumption. Breeding for false smut resistance is the viable option but resistant sources are limited. Many of the high yielding varieties and hybrids in cultivation succumb to this disease. Breeding for resistance in conjunction with high yield depends on the existence of variability in the genetic material handled, heritability, genetic advance, correlation of traits and the nature of gene action governing the traits. Literature on the above aspects is limited with respect to false smut disease. Traits controlled by polygenes like resistance for

false smut disease are difficult to handle (Doddakoppalu Govindaiah *et al.*, 2022). In the present study, hybrids were developed using six rice genotypes with different levels of resistance to false smut and genetic parameters were estimated for further handling of the population for yield and disease resistance.

MATERIALS AND METHODS

The study was conducted at experimental farm of Hybrid Rice Evaluation Centre, Gudalur, Tamil Nadu, India, located at 11.5 °N latitude and 76.5 °E longitude and an altitude of 1072m above mean sea level, during 2021 *Rabi* season under irrigated conditions with conducive weather parameters favouring disease incidence. The experimental material comprised of 36 F₁s generated in a full diallel mating design using six parents *viz.*, resistant genotypes (RG 170, RG 172), moderately resistant genotypes (RG 22, RG 162), susceptible genotypes (RNR 15048, BPT 5204) which were raised in a randomized complete block design (RCBD) with two replications including parents. Each genotype was planted in 2.0m long row with spacing of 30×20 cm. To develop the infection, spreader row CO 43 was planted on all sides of the field in four rows as susceptible check and artificial inoculation of spores was done in the field at boot leaf stage as suggested by Ashizawa *et al.*, (2012). All the agronomic practices were carried out for good crop growth.

Data recorded for days to flowering (DTF) and days to fifty per cent flowering (DFF). At physiological maturity, false smut disease resistance traits *viz.*, number of infected plants (NIP), number of infected tillers (NIT), number of infected grains per panicle (NIGPa), number of infected grains per plant (NIGP), percentage of infected plants (PIP), percentage of infected tillers (PIT) and percentage of infected grains per panicle (PIGPa) were recorded. All the agronomic traits were measured at maturity.

Analysis of variance was performed for the traits under study using mean data. Variability studies were done to analyze the different genetic parameters (Burton and Vane, 1952), for false smut disease resistance and agronomic traits. Association among the traits were studied by correlation and path analysis (Johnson *et al.*, 1955 and Dewey and Lu 1959). All the statistical analyses were carried out using the R software version 0.1.0 (Popat *et al.*, 2020).

RESULTS AND DISCUSSION

Results of ANOVA presented in **Table 1**, indicated highly significant variations for all disease and yield related traits. Such wide range of variations for morphological and disease resistance traits indicated the presence of adequate variation among the genotypes in the population for initiating a successful breeding programme for false smut resistance. Among the traits, PIP, PIT, TNFPa and PH exhibited high variations. Faysal *et al.*, (2022) noticed

high variations for number of filled spikelets per panicle and plant height. Arab *et al.*, (2021) while investigating yellow rust, leaf rust and powdery mildew resistance in wheat obtained high variation for powdery mildew severity.

Statistic and Variability parameters of the studied traits are presented in **Table 2**. Highest standard deviation was observed for percentage of infected plants (PIP), total number of florets per panicle (TNFPa), plant height (PH) and number of chaffy grains per panicle (NCGPa), suggesting that these traits showed high variation in the experimental material. The minimum standard deviation was exhibited by number of infected tillers (NIT) and single panicle weight (SPW). Mahmood *et al.*, (2017) observed high standard deviation for yellow rust infection and lower values for grain yield in wheat for stripe rust resistance. Msundi *et al.*, (2021) also noticed high standard deviation for stem rust area under disease progress and low for matured kernel weight and spike length in bread wheat.

Higher PCV than GCV for all studied traits indicated the role of environmental factors influencing their expression. All the disease related traits expressed high PCV, GCV and ECV compared to agronomic traits. Among them, number of infected grains per plant ranked the top for highest PCV and ECV. Similar results of high variations were noticed by Malizu *et al.*, (2021) for downy mildew severity and incidence in pearl millet. The trait, number of infected plants, had the highest GCV. This was accordance with the result of Begum *et al.*, (2018) in number of spots per plant for blast disease in rice.

High values of all three coefficients of variation were observed for agronomic traits *viz.*, spikelet sterility percentage (SSP) and number of chaffy grains per panicle (NCGPa). The next highest value of PCV and ECV was observed for single plant yield (SPY). High PCV and GCV were noticed for grain yield per plant by Immanuel *et al.*, (2011) in rice genotypes screened for blast resistance and for panicle weight and grain weight in pearl millet in screening against downy mildew by Malizu *et al.*, (2021). Flowering traits and panicle length had exhibited low PCV, GCV and ECV, hence lower scope for their improvement under selection. Arab *et al.*, (2021) also observed lower coefficient of variations for days to maturity in wheat genotypes under rust and powdery mildew infestation.

For disease resistance traits, the broad sense heritability was found to be high (above 60%) for five out of seven traits namely NIP, NIT, NIGPa, PIT, PIGPa, low for NIGP (<30%) and moderate for PIP (**Table 2**). Traits with high heritability have the tendency to be inherited to next generation. High broad sense heritability was also observed by Msundi *et al.*, (2021) for AUDPC of yellow rust and stem rust in bread wheat under rust epiphytotic conditions. Five resistance related traits namely NIP, NIT, NIGPa, PIT, PIGPa had high heritability, genetic

Table 1. Analysis of variance for false smut (FS) disease resistance and agronomic traits in rice

Traits	Mean Sum of Squares			
	Replication	Genotypes	Error	CV (%)
NIP	6.72	21.95***	2.43	16.24
NIT	0.36	1.10***	0.21	13.87
NIGPa	2.54*	8.52***	0.61	14.50
NIGP	1.44	7.17*	4.06	19.18
PIP	1535.81	1399.89**	593.78	17.80
PIT	5.143	34.77***	6.29	20.22
PIGPa	1.48*	2.81***	0.28	17.91
DTF	24.50	75.53***	16.90	5.25
DFF	11.68	91.37***	11.96	4.96
PH	158.12	635.05***	42.94	13.19
PL	0.66	6.85***	2.31	8.18
NPT	29.26	22.25*	11.98	19.65
TNFPa	54.60	2099.48***	227.72	20.51
NCGPa	0.756	226.59***	36.55	18.92
SSP	5.44	141.52***	23.10	16.63
NPRPa	0.52	3.11***	0.95	15.06
NSRPa	3.42	35.38***	7.95	17.19
HGW	3.55	19.57***	1.59	14.39
SPW	0.00	0.36***	0.09	20.60
SPY	0.834	69.48**	24.02	17.20

DTF- days to flowering, DFF- days to fifty per cent flowering, PH-plant height, PL-panicle length, NPT-number of productive tillers, TNFPa -total number of florets per panicle, NCGPa- number of chaffy grains per panicle, SSP -spikelet sterility percentage, NPRPa- number of primary rachis per panicle, NSRPa -number of secondary rachis per panicle, HGW- Hundred grain weight, SPW- single panicle weight, SPY- single plant yield, NIP- number of infected plants, NIT-number of infected tillers, NIGPa-number of infected grains per panicle, NIGP- number of infected grains per plant, PIP-per centage of infected plants, PIT- per centage of infected tillers, IGPa- per centage of infected grains per panicle

*-Significant at 5% level, **-Significant at 1% level, ***-Significant at 0.1% level

advance as percentage mean and genotypic coefficient of variation indicating the preponderance of additive gene action. Even the traits with low and moderate heritability have high GAM and hence selection may be effective. Singh *et al.*, (2015) obtained high heritability for disease severity in bacterial leaf blight disease but genetic advance as percentage of mean was low which implies that high heritability does not always indicate high genetic gain.

For agronomic traits, high heritability was observed for eight traits namely plant height, HGW, TNFPa, DFF, NCGPa, SSP, DTF and NSRPa, while others exhibited moderate values. Among them, PH, TNFPa, NCGPa, SSP, NSRPa and HGW exhibited both high heritability and high genetic advance as percent of mean. Singh *et al.*, (2015) observed high heritability coupled with genetic advance for plant height and panicle weight and Immanuel *et al.*, (2011) observed similar trend for plant height and total number of florets per panicle for improving the grain yield in blast resistant genotypes in rice. Among the traits with moderate heritability, single panicle weight and single plant yield had high GAM.

Since many of the false smut related traits and agronomic traits in the present study showed moderate to high heritability coupled with high GAM, development of resistant lines with good plant type is possible by effective selection of heritable traits namely NIP, NIT, NIGPa, PIT, IGPa, PH, TNFPa, NCGPa, SSP, NSRPa and HGW with additive gene action.

The phenotypic (rp) correlation of all traits in thirty F₁s and six parents with single plant yield is represented in **Fig.1** and genotypic correlation (rg) in **Table 3**. Genotypic correlation showed higher coefficient values over phenotypic coefficients for most of the traits which signifies that, trait association is not influenced by the external environment in this breeding population. With regard to false smut resistance traits, the disease scoring trait NIGPa showed strong positive significant association with all other disease resistance related traits *viz.*, NIGP, PIP, PIT, IGPa, NIP and NIT at both phenotypic and genotypic levels of their expression (**Fig. 2**). Hence, negative selection of one of these traits could alleviate the severity of disease incidence. In addition to this, NIGPa

Table 2. Variability parameters for false smut disease resistance and agronomic traits in rice

Traits	Mean	Range	PCV (%)	GCV (%)	ECV (%)	H ²	GA	GAM	CD (5%)	SEm	SD
NIP	2.22	0.00-18.00	157.15	140.5	70.24	0.80	5.75	259.06	3.16	1.10	6.6
NIT	0.64	0.00-4.00	125.32	103.27	71.00	0.67	1.13	175.31	0.93	0.32	1.92
NIGPa	1.66	0.00-11.00	128.05	119.10	47.04	0.86	3.80	228.19	1.59	0.55	3.3
NIGP	1.45	0.00-11.30	163.19	85.78	138.83	0.27	1.34	92.89	4.09	1.42	8.52
PIP%	32.14	0.00-100.00	98.21	62.45	75.80	0.40	26.29	81.80	49.46	17.23	103.38
PIT%	3.53	0.00-21.80	128.27	106.80	71.04	0.69	6.47	183.20	5.09	1.77	10.62
PIGPa	1.16	0.00-6.47	107.35	97.01	45.96	0.81	2.09	180.59	1.08	0.37	2.22
DTF	101.44	83.00 -120.00	6.70	5.33	4.05	0.63	8.88	8.75	8.34	2.90	17.4
DFF	105.93	86.00-124.00	6.78	5.94	3.26	0.76	11.37	10.74	7.02	2.44	14.64
PH (cm)	91.01	39.10-152.00	20.22	18.90	7.19	0.87	33.12	36.39	13.30	4.63	27.78
PL (cm)	22.52	19.40-29.60	9.50	6.69	6.75	0.49	2.18	9.70	3.08	1.07	6.42
NPT	8.00	8.00-30.40	22.84	12.51	19.11	0.30	2.55	14.11	7.02	2.44	14.64
TNFPa	138.82	82.00-262.60	24.57	22.03	10.87	0.80	56.51	40.71	30.63	10.67	64.02
NCGPa	15.89	4.70-83.00	72.16	61.32	38.04	0.72	17.06	107.36	12.27	4.27	25.62
SSP%	11.83	3.00-68.00	76.66	65.02	40.61	0.71	13.44	113.61	9.75	3.39	20.34
NPRPa	7.80	5.00-14.00	18.28	13.31	12.53	0.53	1.55	19.97	1.98	0.69	4.14
NSRPa	23.77	12.00-34.00	19.58	15.57	11.86	0.63	6.06	25.52	5.72	1.99	11.94
HGW (g)	16.93	11.10-25.70	19.21	17.70	7.46	0.84	5.69	33.60	2.56	0.89	5.34
SPW (g)	2.27	1.40-3.70	21.22	16.13	13.78	0.57	0.57	25.27	0.63	0.22	1.32
SPY (g)	22.61	10.50-46.10	30.23	21.07	21.67	0.48	6.84	30.27	9.95	3.46	20.76

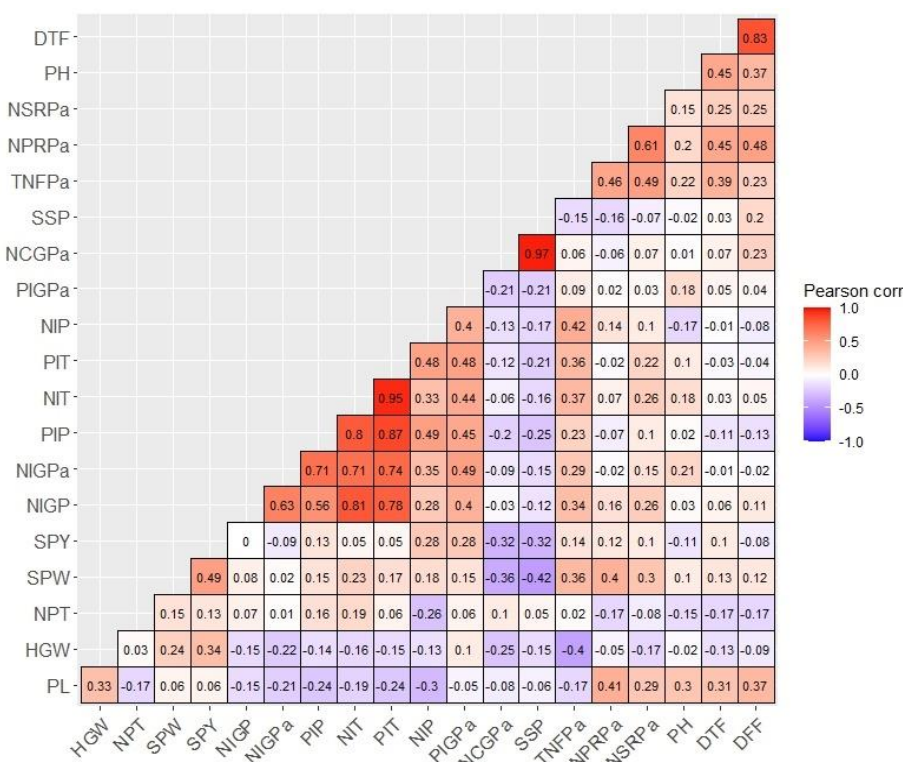


Fig. 1. Phenotypic correlation of false smut disease resistance and agronomic traits with single plant yield in rice

Table 3. Genotypic (rg) correlation between false smut resistance and yield components in rice

Traits	NIP	NIT	NIGPa	NIGP	PIP	PIT	PIGPa	DTF	DFF	PH	PL	NPT	TNFPa	NCGPa	SSP	NPRPa	NSRPa	HGW	SPW	SPY
NIP	1**	0.27	0.80**	0.34*	0.55**	0.41*	0.98**	0.00	-0.08	-0.23	-0.53**	-0.61**	0.48**	-0.21	-0.25	0.18	0.09	-0.13	0.26	0.38*
NIT		1**	0.59**	1.14**	0.98**	1.00**	0.56**	0.16	0.13	0.21	0.46**	0.02	0.38*	-0.15	-0.24	0.08	0.36*	-0.14	0.30	-0.21
NIGPa			1**	0.72**	0.86**	0.71**	0.93**	0.11	0.04	0.06	-0.41*	-0.44**	0.50**	-0.21	-0.28	0.17	0.23	-0.30	0.15	0.13
NIGP				1**	1.30**	1.10**	0.73**	0.04	0.03	-0.04	-0.51**	-0.10	0.31	-0.24	-0.32	0.03	0.48**	-0.24	0.43**	-0.18
PIP					1**	-0.08	0.82**	0.04	-0.03	-0.04	-0.78**	-0.21	0.44**	-0.38*	-0.47**	0.05	0.36*	-0.19	0.43**	-0.08
PIT						1**	0.68**	0.12	0.11	0.17	-0.48**	0.00	0.41*	-0.16	-0.25	0.14	0.40*	-0.21	0.33*	-0.13
PIGPa							1**	-0.11	-0.16	0.02	-0.40*	-0.45**	0.22	-0.28	0.30	-0.03	0.10	-0.23	-0.02	0.09
DTF								1**	0.99**	0.57**	0.49**	-0.27	0.47**	0.05	0.00	0.68**	0.32	-0.20	0.37*	0.20
DFF									1**	0.39*	0.54**	-0.35*	0.28	0.17	0.13	0.67**	0.38*	-0.16	0.26	0.02
PH										1**	0.30	-0.28	0.22	0.01	-0.01	0.25	0.12	-0.04	0.18	-0.12
PL											1**	0.76**	-0.36*	-0.05	0.05	0.48**	0.26	0.36*	0.03	0.10
NPT												1**	0.02	0.01	-0.06	-0.77**	-0.32*	0.15	-0.12	-0.31
TNFPa													1**	0.00	-0.19	0.58**	0.50**	-0.45**	0.49**	0.17
NCGPa														1**	0.97**	-0.09	0.16	-0.31	-0.55**	-0.57**
SSP															1**	-0.19	0.03	-0.18	-0.61**	-0.54**
NPRPa																1**	0.69**	-0.06	0.65**	0.39*
NSRPa																	1**	-0.15	0.27	0.03
HGW																		1**	0.39*	0.66**
SPW																			1**	0.58**
SPY																				1**

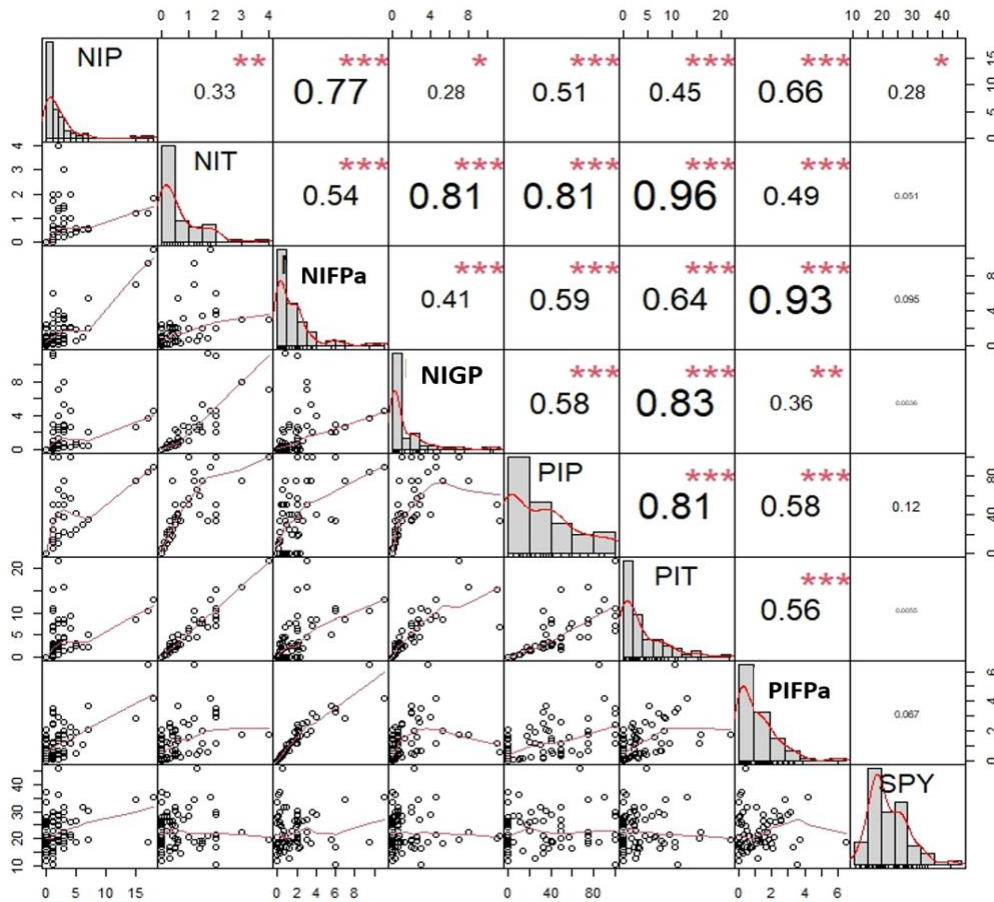


Fig. 2. Genotypic Inter-correlation of false smut disease resistance traits with single plant yield in rice

had significantly negative phenotypic and genotypic association with panicle length and number of productive tillers. At phenotypic level, NIGPa showed negative significant association with SSP and 1000 grain weight. Singh and Sunder (2015) reported that, increase in false smut disease severity is attributed to reduced 1000 grain weight. Das *et al.*, (2012) observed that *Fusarium* infected rotted seeds had negative relationship with seed weight of sorghum. False smut related traits NIT, NIGP, PIP and PIT showed negative but, non-significant genotypic association with grain yield in this study. Focusing on one disease resistance trait in plant selection will be helpful to improve the false smut resistance since all false smut resistance traits are associated among themselves.

Panicle length (PL) exhibited significantly negative phenotypic and genotypic correlations with false smut resistance traits *viz.*, NIP, PIP and PIGPa. Arab *et al.*, (202) recorded negative association of spike length with yellow rust incidence in wheat. The trait total number of florets per panicle (TNFPa) exhibited positively significant relation with NPRPa, NSRPa, SPW at phenotypic and genotypic levels. These findings are supported by the results of Chethana *et al.*, (2018) who observed that number of grains per panicle had strong

positive association with number of spikelets per spike under spot blotch disease. Number of infected grains per plant (NIGP) had significantly negative phenotypic and genotypic association with HGW. Number of chaffy grains per panicle (NCGPa) had significant negative phenotypic association with PIP and HGW. The trait SSP showed significant genotypic negative association with SPW and PIP. The result is in concordance with Lilian *et al.*, (2016) who noted significant negative correlation of disease incidence and severity of head smut with 1000 seed weight of pearl millet. The trait number of secondary rachis per panicle (NSRPa) exhibited significant positive phenotypic and genotypic correlations with resistance traits *viz.*, NIT, NIGP, PIT and genotypic correlation alone with PIP, while phenotypic correlation alone with the agronomic trait *viz.*, SPW. The trait single panicle weight (SPW) exhibited significantly positive genotypic association with NIGP, PIP, PIT, HGW and phenotypic association alone with NIT. Islam *et al.*, (2020) reported significant positive correlation of thousand grain weight with total grain weight per panicle in rice.

For genetic improvement of the crop, grain yield is an utmost trait of importance, which is to be focused. Yield is a complex trait for which direct selection is ineffective.

Table 4. Direct and Indirect effects for false smut resistance and agronomic traits in rice based on phenotypic correlation coefficients

Traits	NIP	NIT	NIGPa	NIGP	PIP	PIT	PIGPa	DTF	DFP	PH	PL	NPT	TNFPa	NCGPa	SSP	NPRPa	NSRPa	HGW	SPW	SPY
NIP	0.505	0.319	1.047	0.051	0.033	-0.624	0.787	-0.008	0.005	0.038	-0.040	-0.007	0.348	0.206	-0.271	-0.054	0.027	-0.040	0.053	0.28 *
NIT	0.162	0.994	0.727	0.150	0.052	-1.348	0.585	0.009	-0.002	-0.036	-0.026	0.004	0.310	0.097	-0.243	-0.026	0.072	-0.049	0.070	0.04
NIGPa	0.389	0.531	1.359	0.075	0.037	-0.888	1.116	0.004	0.001	-0.008	-0.038	-0.006	0.355	0.274	-0.360	-0.050	0.052	-0.074	0.039	0.09
NIGP	0.140	0.805	0.556	0.185	0.037	-1.155	0.425	0.019	-0.006	-0.004	-0.020	0.001	0.279	0.055	-0.189	-0.063	0.072	-0.047	0.023	0.00
PIP	0.256	0.801	0.792	0.106	0.065	-1.132	0.686	-0.040	0.006	0.001	-0.033	0.003	0.215	0.280	-0.354	0.025	0.034	-0.055	0.043	0.11
PIT	0.225	0.956	0.862	0.152	0.052	-1.400	0.678	0.019	-0.004	-0.034	-0.030	-0.000	0.355	0.124	-0.274	-0.020	0.075	-0.059	0.051	0.00
PIGPa	0.330	0.483	-1.260	0.065	0.037	-0.788	1.204	-0.068	0.014	-0.001	-0.037	-0.005	0.119	0.374	-0.373	0.015	0.011	-0.053	-0.000	0.06
DTF	-0.011	0.024	0.016	0.009	-0.006	-0.072	-0.218	0.379	-0.054	-0.095	0.040	-0.004	0.326	-0.120	0.035	0.183	0.068	-0.040	0.039	0.09
DFP	-0.042	0.044	0.037	0.019	-0.006	-0.092	-0.263	0.315	-0.066	-0.078	0.049	-0.004	0.190	-0.372	0.310	-0.194	0.068	-0.028	0.035	-0.08
PH	-0.091	0.168	0.052	0.004	-0.000	-0.224	0.010	0.168	-0.024	-0.214	0.040	-0.004	0.180	-0.017	-0.037	-0.079	0.041	-0.007	0.028	-0.11
PL	-0.011	-0.198	0.386	-0.028	-0.016	0.317	-0.334	0.115	-0.024	-0.063	0.134	-0.004	-0.141	0.139	-0.093	-0.166	0.080	0.097	0.016	0.06
NPT	-0.140	0.177	0.323	0.011	0.007	0.000	-0.266	-0.072	0.012	0.035	-0.024	0.026	0.018	-0.15	0.071	0.074	-0.019	0.006	0.045	0.12
TNFPa	0.214	0.376	0.588	0.063	0.017	-0.605	0.174	0.150	-0.015	-0.047	-0.023	0.000	0.821	-0.101	-0.231	-0.189	0.133	-0.117	0.108	0.14
NCGPa	-0.063	-0.059	0.228	-0.006	-0.011	0.106	-0.276	0.028	-0.015	-0.002	-0.011	0.002	0.051	-1.634	1.447	0.025	0.019	-0.075	-0.108	-0.32**
SSP	-0.090	-0.158	0.321	-0.023	-0.015	0.252	0.294	0.008	-0.013	0.005	-0.008	0.001	-0.124	-1.583	1.525	0.066	-0.018	-0.044	-0.126	-0.32**
NPRPa	0.067	0.065	0.170	0.029	-0.004	-0.071	-0.046	0.171	-0.031	-0.041	0.055	-0.004	0.382	0.102	-0.250	-0.406	0.166	-0.016	0.121	0.11
NSRPa	0.051	0.266	0.262	0.049	0.008	-0.388	0.049	0.095	-0.016	-0.032	0.039	-0.001	0.403	-0.119	-0.104	-0.249	0.272	-0.048	0.092	0.10
HGW	-0.069	-0.163	0.340	-0.029	-0.012	0.278	-0.214	-0.051	0.006	0.005	0.044	0.000	-0.325	0.412	-0.226	0.022	-0.044	0.297	0.073	0.34**
SPW	0.089	0.232	0.178	0.014	0.009	-0.237	-0.003	0.049	-0.007	-0.020	0.007	0.003	0.295	0.586	-0.640	-0.164	0.083	0.072	0.301	0.49**

Residual effect for path analysis = 0.388

Table 5. Direct and Indirect effects for false smut resistance and yield related traits in rice based on genotypic correlation coefficients

Traits	NIP	NIT	NIGPa	NIGP	PIP	PIT	PIGPa	DTF	DFP	PH	PL	NPT	TNFPa	NCGPa	SSP	NPRPa	NSRPa	HGW	SPW	SPY
NIP	2.527	-1.473	-8.422	-0.162	-0.245	2.199	5.948	0.020	-0.035	0.047	0.095	-0.933	0.837	1.539	-1.814	-0.174	0.197	0.001	0.232	0.38 *
NIT	0.688	-5.412	-6.250	-0.541	-0.434	5.315	4.904	0.341	0.054	-0.044	0.083	0.035	0.668	1.114	-1.708	-0.079	0.780	0.001	0.266	-0.21
NIGPa	2.034	-3.233	-10.46	-0.342	-0.384	3.817	8.135	0.237	0.019	-0.012	0.073	-0.679	0.882	1.561	-2.050	-0.165	0.564	0.004	0.135	0.13
NIGP	0.863	-6.175	-7.543	-0.474	-0.557	5.869	6.369	0.102	0.014	0.009	0.091	-0.152	0.555	1.755	-2.278	-0.028	1.024	0.003	0.386	-0.18
PIP	1.401	-5.317	-9.086	-0.619	-0.442	5.607	7.219	0.083	-0.013	0.008	0.142	-0.325	0.780	2.746	-3.377	-0.047	0.770	0.002	0.384	-0.08
PIT	1.048	-5.422	-7.529	-0.525	-0.467	5.305	5.952	0.263	0.045	-0.334	0.087	0.012	0.725	1.184	-1.786	-0.137	0.848	0.002	0.296	-0.13
PIGPa	1.725	-3.047	-9.771	-0.346	-0.366	3.625	8.710	-0.239	-0.068	-0.005	0.073	-0.685	0.397	2.017	-2.157	0.031	0.222	0.003	-0.023	0.09
DTF	0.025	-0.889	-1.196	-0.023	-0.017	0.672	-1.005	2.078	0.404	-0.116	-0.088	-0.414	0.817	-0.420	0.007	-0.647	0.691	0.002	0.329	0.20
DFP	-0.221	-0.719	-0.496	-0.017	0.015	0.589	-1.470	2.063	0.407	-0.080	-0.098	-0.539	0.493	-1.242	0.924	-0.637	0.820	0.002	0.230	0.02
PH	-0.586	-1.174	-0.630	0.023	0.017	0.907	0.233	1.196	0.161	-0.203	-0.054	-0.429	0.398	-0.099	-0.079	-0.238	0.272	0.000	0.160	-0.12
PL	-1.345	2.502	4.292	0.242	0.349	-2.568	-3.533	1.026	0.224	-0.060	-0.180	-1.152	0.642	0.405	0.408	-0.459	0.570	-0.005	0.034	0.10
NPT	-1.557	-0.126	4.691	0.047	0.095	0.044	-3.942	-0.568	-0.145	0.057	0.136	1.515	0.047	-0.089	-0.437	0.724	-0.698	-0.002	-0.114	-0.31
TNFPa	1.217	-2.081	-5.311	-0.151	-0.198	2.214	1.990	0.978	0.115	-0.046	0.066	0.041	1.738	-0.012	-1.344	-0.552	1.065	0.006	0.439	0.17
NCGPa	-0.541	0.838	2.271	0.115	0.168	-0.874	-2.444	0.121	0.070	-0.002	0.010	0.018	0.003	-7.189	6.910	0.085	0.342	0.004	-0.487	-0.57**
SSP	-0.648	1.307	3.033	0.152	0.211	-1.340	-2.657	0.002	0.053	0.002	-0.010	-0.093	0.330	-7.024	7.072	0.186	0.076	0.002	-0.538	-0.54**
NPRPa	0.468	-0.458	-1.844	-0.014	-0.022	0.777	-0.296	1.432	0.276	-0.051	-0.088	-1.168	1.023	0.651	-1.402	-0.939	1.476	0.000	0.577	0.39*
NSRPa	0.236	-1.995	-2.791	-0.229	-0.160	2.127	0.917	0.679	0.158	-0.026	-0.048	-0.499	0.875	-1.162	0.254	-0.655	2.115	0.002	0.242	0.03
HGW	-0.352	0.784	3.241	0.114	0.085	-1.151	-2.009	-0.435	-0.065	0.008	-0.066	0.242	0.786	2.278	-1.297	0.062	-0.328	-0.013	0.350	0.66**
SPW	0.667	-1.632	-1.610	-0.207	-0.192	1.784	-0.233	0.776	0.106	-0.037	-0.006	-0.196	0.865	3.975	-4.316	-0.614	0.5808	-0.005	0.881	0.58**

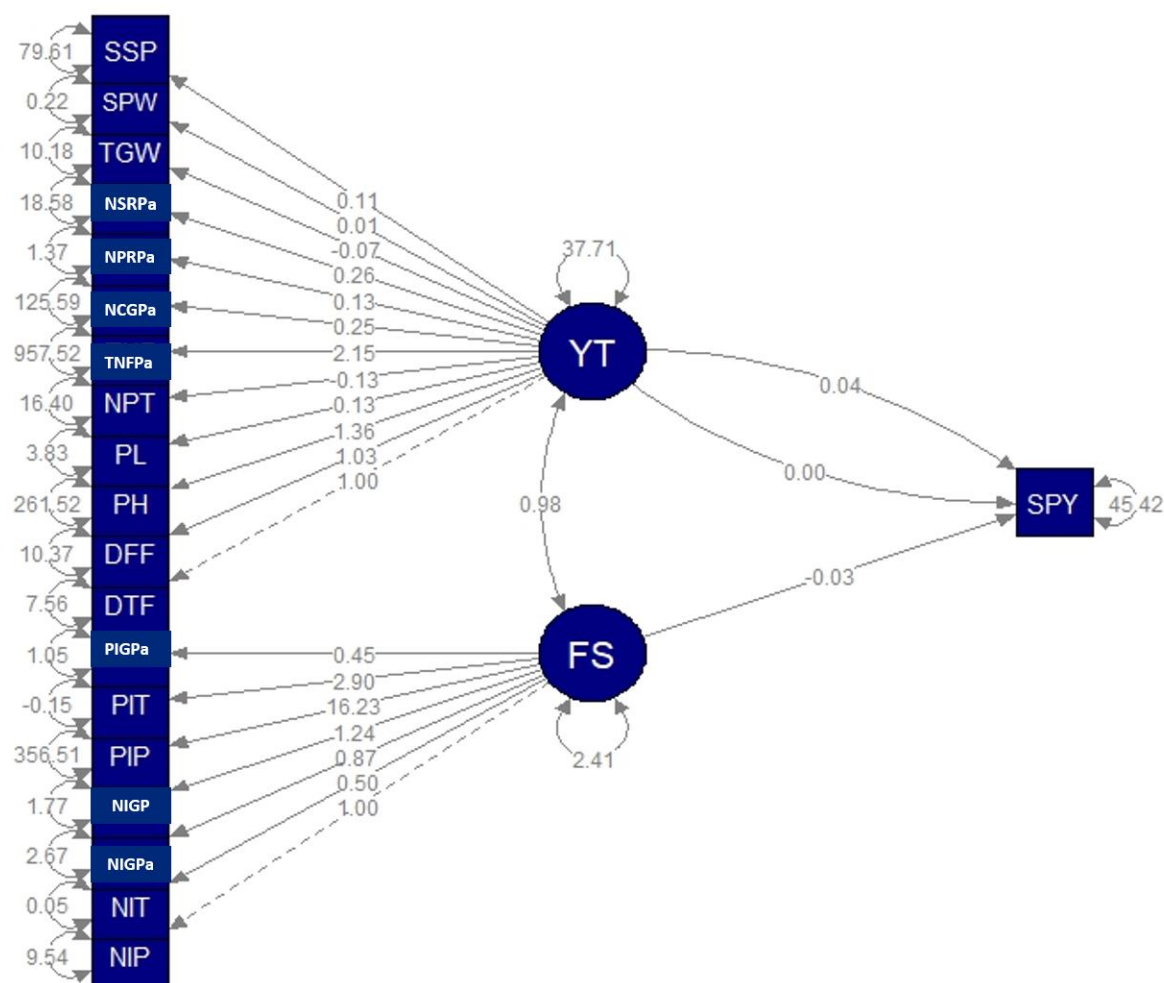


Fig. 3. Direct and indirect effects of agronomic and false smut resistance traits on grain yield in rice

Hence, yield associated traits are taken into consideration for advancement of plants. Highly significant positive correlation of single plant yield with NIP, HGW and SPW at both phenotypic and genotypic level (**Fig. 1, Table 3**). NPRPa showed significant positive correlation with SPY at genotypic level. Immanuel *et al.*, (2011) observed significant positive association of grain yield per plant with test weight under blast incidence in rice. As presumed, the traits NCGPa and SSP showed highly significant negative correlation with SPY at both phenotypic and genotypic levels. The results of Zarbafi *et al.*, (2019) about the negative correlation of grain yield with number of unfilled grains per panicle upon neck blast infestation in rice further gives a strong evidence.

Path analysis was done to study the direct and indirect effects of the false smut disease resistance traits and agronomic traits influencing the single plant yield in rice.

The responses of different variables are presented in **Table 4, Table 5 and Fig.3**. Two disease resistance traits viz., NIP and PIGPa and six agronomic traits viz., DTF, NPT, TNFPa, SSP, NSRPa and SPW showed positive direct effect on single plant yield (SPY) at both phenotypic and genotypic levels. Therefore, direct selection of these traits is advised for combining grain yield with resistance. Begum *et al.*, (2018) obtained higher positive direct effect of percent leaf blast severity, number of tillers, spikelets per panicle and 1000 grain weight on grain yield in rice.

Indirect effects of characters on single plant yield play a crucial role in plant selection by the breeders. One disease resistance trait viz., NIP and two agronomic traits viz., HGW and SPW expressed high positive indirect effect on SPY. The trait NIP expressed high phenotypic indirect effect on SPY through NIGPa and TNFPa whereas, high genotypic indirect effect was observed through PIGPa and

NCGPa. Das *et al.*, (2012) observed high indirect effect of grain mould incidence through panicle grade score and seed weight on seed germination and yield in sorghum. The high phenotypic and genotypic indirect effect of HGW on single plant yield was observed through NIGPa and NCGPa. Begum *et al.*, (2018) observed the high indirect effect of thousand grain weight through length of largest spot of blast disease and six agronomic traits in rice. The high phenotypic indirect effect of SPW on SPY was observed through NIT, NCGPa and TNFPa whereas, high genotypic indirect effect was noticed through PIT, NCGPa and TNFPa. Singh *et al.*, (2015) observed high phenotypic indirect effect of test weight *via* plant height and panicle length on grain yield in bacterial leaf blight resistance study in rice.

The low residual effect of 0.388 explained that the estimated 19 variables account for 62.0% variability in single plant yield of rice in the present study. On the contrary, Rodríguez-Herrera *et al.*, (2009) obtained high residual effects in four different environments which could explain only 1-36% variation between grain mould incidence and kernel traits in sorghum.

Adequate genetic variability is prevalent in the investigated breeding population for all the 20 traits to exercise selection. The role of environmental factors influencing trait expression was witnessed in computation of variances which was of higher magnitude particularly, for all false smut disease resistance related traits and two agronomic traits namely number of chaffy grains per panicle and spikelet sterility percentage. Comprehensive analysis of agronomic traits on the basis of high genotypic co-efficients of variation, high heritability, high genetic advance, significant phenotypic and genotypic correlations with single plant yield and path computation revealed five traits to be worthy of exploitation. Spikelet sterility percentage is the key character showing strong expression in negative direction for all parameters. Total number of florets per panicle had positive expression for all parameters except non-significant correlation with single plant yield. Single panicle weight conforms all parameters except moderate GCV, while hundred grain weight has both moderate GCV and significant direct effect at phenotypic level only on single plant yield. The trait number of secondary rachis per panicle fulfils all parameters except moderate GCV and non-significant correlation with single plant yield. Grain yield improvement along with false smut resistance in rice can be accomplished by forwarding the present breeding material based on these five traits along with screening for disease resistance

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