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Sreedhar Siddi
Rice Breeding Scheme, Agricultural Research Station, Kunaram, Peddapalli, Professor Jayashankar Telangana State Agricultural University, Telangana, India

Corresponding Author:
Sreedhar Siddi
Rice Breeding Scheme, Agricultural Research Station, Kunaram, Peddapalli, Professor Jayashankar Telangana State Agricultural University, Telangana, India

Genetic variability and trait association studies for gall midge incidence, yield and its traits in rice (*Oryza sativa* L.) genotypes

Sreedhar Siddi

Abstract
Variability and trait association studies were investigated in 18 rice (*Oryza sativa* L.) genotypes with two replications in a RBD design during *kharif*, 2017 at Agricultural Research Station, Kunaram. The traits, plant height, number of productive tillers per m^2 and number of grains per panicle showed high heritability coupled with high genetic advance values indicating these traits were predominantly governed by the additive genes. Grain yield had positively correlated with days to 50% flowering, plant height and number of grains per panicle, and negatively correlated with gall midge incidence at both genotypic and phenotypic levels suggesting that genotypes with longer duration, more plant height and good number of grains panicle with relatively very less silver shoots contribute for more grain yield.

Keywords: variability, trait association, gall midge, rice

1. Introduction
Rice (*Oryza sativa* L.) is an important staple food in India and rice production substantially influences the national food security. Among all the major biotic stresses of rice, gall midge causes significant yield losses that vary from 3 to 70% in almost all the rice growing states of India. In some parts of Telangana state, major problem is high incidence of gall midge in rainy season under early as well as late planting conditions. Recently, the incidence of gall midge has been increased and yield losses have been quite common. Breeding for the refinement of rice varieties with more yields along with gall midge resistance is essential and continuous process due to rapid evolution of new biotypes of gall midge and stagnation in yield levels. In a breeding programme, selection in the available germplasm having wide variability for gall midge resistance and important yield contributing traits would be prospective approach for improving these particular traits. Knowledge on the heritability of genetic trait is essential to the plant breeders in determining the response to selection and to provide the information on the extent of transmissibility of that selected trait of interest to the progenies in the subsequent generations [31]. In addition, high genetic advance estimates in conjunction with high heritability values are more accurate for breeders in calculating the genetic gain under selection and offers the effective conditions for selection for the specific traits. Further, rice grain yield being a complex trait, depends upon the various yield contributing traits like test weight, number of grains per panicle, panicle length and effective bearing tiller number. Hence, the information about the relationship between a trait with gall midge resistance, yield and other yield components would be helpful in selecting proper rice genotypes as parents in breeding programmes.
Keeping in view of the importance, the objectives of the study were to assess the variability, heritability and genetic advance, and to determine the association between yield, its components and gall midge incidence which have not been investigated in a set of genotypes for further improvement to derive high yielding rice genotypes with gall midge resistance and desirable agronomic traits to attain self sufficiency and meet the future demand resulting from population growth.

2. Materials and Methods
The material for the present study consisted of 18 rice genotypes and their seed was raised on nursery beds and 25 days old seedlings of each entry was transplanted under irrigated system with two replications in a RBD design during *kharif*, 2017 at Agricultural Research Station,

Kunaram. The data was recorded at maturity on 5 random plants for plant height (cm), panicle length (cm), number of productive tillers per m^2 and number of grains per panicle. However, days to 50 % flowering and grain yield (kg per plot) were recorded on whole plot basis, whereas, random sample was taken to estimate 1000 grain weight (g) for each entry in each replication. Number of productive tillers per plant values were converted into the number of productive tillers per m^2 and grain yield values recorded from the net plot (kg per plot) were converted in to hectare (kg per ha). The incidence of gall midge was recorded as percent tillers affected with silver shoots (SES, IRRI, 2002) on 10 random plants and averaged. The mean data after computing for each trait was subjected to statistical analysis *viz*., analysis of variance, genotypic coefficient of variation (GCV), phenotypic coefficients of variation (PCV), heritability (h^2) in the broad sense, genetic advance and correlations following standard procedures.

3. Results and Discussions

Table 1: Genetic parameters for gall midge incidence, yield and yield contributing traits in rice

Character	GCV	PCV	h^2 (Broad Sense)	GA in % over mean
Days to 50% flowering	9.12	9.23	97.7	18.57
Plant height (cm)	15.48	15.79	96.1	31.25
Panicle length (cm)	9.54	10.98	75.5	17.08
Number of productive tillers per m^2	21.91	25.89	71.6	38.20
Number of grains per panicle	17.09	19.19	79.3	31.35
1000- grain weight (g)	5.42	7.02	59.6	8.63
Gall midge incidence (%)	13.55	19.35	49.1	19.56
Grain yield (kg per ha)	13.43	21.11	40.5	17.61

GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation

The perusal of the variability estimates (Table 1) for yield and its contributing traits exhibited that estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for number of productive tillers per m^2 suggesting that trait is under genetic control, and simple selection can be practiced for further improvement. These results are in agreement with the findings obtained by Mohan *et al*. (2015) [24], Sameera *et al*. (2015) [33], Srinivas *et al*. (2016) [37], Ajmera *et al*. (2017) [3] and Saha *et al*. (2019) [32] for number of grains per panicle; Ahmed *et al*. (2010) [2], Sameera *et al*. (2015) [33], Ajmera *et al*. (2017) [3] and Saha *et al*. (2019) [32] for 1000-grain weight; Ajmera *et al*. (2017) [3] and Saha *et al*. (2019) [32] for productive tillers per plant; Mohan *et al*. (2015) [24] and Thippaswamy *et al*. (2016) [38] for gall midge incidence; Allam *et al*. (2015) [5], Bhati *et al*. (2015) [8], Ajmera *et al*. (2017) [3], Behera *et al*. (2018) [7] and Saha *et al*. (2019) [32] for grain yield. Rice workers, Akinwale *et al*. (2011) [4] and Ramanjaneyulu *et al*. (2014) [27] reported moderate GCV and high PCV values for grain yield which are in accordance with present findings. Medium estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for gall midge incidence in the present study. However, highest GCV and PCV values were observed for gall midge incidence among all the traits which is supported by Mohan *et al*. (2015) [24] and Thippaswamy *et al*. (2016) [38]. Low estimates of PCV and GCV were observed for 1000-grain weight, days to 50% flowering and panicle length indicated that these traits are under high influence of environment suggesting need for creation of variability with hybridization followed by selection. Similar reports have been obtained for panicle length by Adhikari *et al*. (2018) [1]. In contrary to this, Dhanwani *et al*. (2013) [13] and Ajmera *et al*. (2017) [3] reported moderate estimates for panicle length, and also Dhanwani *et al*. (2013) [13] showed high GCV and PCV for plant height.

High estimates of PCV than GCV were observed for all the traits studied which may be due to the high degree of interaction of genotypes with environments. A similar finding has been noted by Vanisree *et al*. (2013) [41], Ketan and Sarkar (2014) [21], Mohan *et al*. (2015) [24], Srinivas *et al*. (2016) [37], Ajmera *et al*. (2017) [3] and Gyawali *et al*. (2018) [15]. It was observed that PCV was slightly higher than GCV for days to 50% flowering, plant height and panicle length reflecting less influence of environment in the expression of traits and greater role of genetic control governing the characters is in agreement with the results explained by Karim *et al*. (2007) [20], Sravan *et al*. (2012) [36], Mohan *et al*. (2015) [24], Ajmera *et al*. (2017) [3], Behera *et al*. (2018) [7] and Saha *et al*. (2019) [32] for plant height, panicle length and 1000 grain weight. However, estimates of PCV were considerably higher than GCV for number of productive tillers per m^2, number of grains per panicle, 1000-grain weight, gall midge incidence and grain yield indicating the sensitive nature of these traits to environmental fluctuations and predominance of non-additive gene effects. Similar findings are in accordance with the earlier reports of Mohan *et al*. (2015) [24], Thippaswamy *et al*. (2016) [38] and Adhikari *et al*. (2018) [1] for effective bearing tillers, number of grains per panicle and grain yield.

High estimates of heritability was recorded for days to 50% flowering, plant height, number of grains per panicle, panicle length and number of productive tillers per m^2. Whereas, 1000-grain weight, grain yield and gall midge incidence had relatively moderate estimates; hence, improvement through selection could be low due to masking effect of environment on the expression of these traits (Table 1). Similarly, moderate heritable values were reported by Sangram kumar *et al*. (2011) [34], Thomas and Gabriel (2012) [39] for test weight, Seyoum *et al*. (2012) [35] for days to maturity, Ramanjaneyulu *et al*. (2014) [27] for days to flowering and panicle length. In the present investigation, plant height, number of productive tillers per m^2 and number of grains per panicle showed high heritability combined with high genetic advance values reflecting the existence of additive gene action in the expression of these traits and hence selection would be effective as investigated by Karande *et al*. (2015) [19], Ajmera *et al*. (2017) [3] and Saha *et al*. (2019) [32] for number of grains per panicle; Toshimenla and Changkija (2013) [40], Chandramohan *et al*. (2016) [11], Islam *et al*. (2016) [17], Srinivas *et al*. (2016) [37] and Ajmera *et al*. (2017) [3] for 1000-grain weight; Mohan *et al*. (2015) [24] for gall midge incidence; Rahman *et al*. (2014) [26], Karande *et al*. (2015) [19]

and Ajmera *et al*. (2017) [3] for grain yield. Similarly, high heritability coupled with moderate genetic advance estimates were recorded for days to 50% flowering and panicle length. Ketan and Sarkar (2014) [21], Chandramohan *et al*. (2016) [11] and Behera *et al*. (2018) [7] also found the same result for panicle length suggesting the role of both additive and non-additive gene effects in their inheritance, therefore, adoption of breeding procedures which could exploit both the gene actions would be a effective approach. In contrary to this, high heritability coupled with high genetic advance was reported for panicle length by Sameera *et al*. (2015) [33].

Table 2: Phenotypic (P) and genotypic (G) correlation coefficients among gall midge incidence, yield and its components in rice

Character		Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Number of productive tillers per m^2	Number of grains per panicle	1000 grain weight (g)	Gallmidge incidence (%)	Grain yield (kg/ ha)
Days to 50% flowering	P	1.0000	0.1689	0.3759*	-0.7159**	0.3358*	-0.2283	0.2688	0.4456**
	G	1.0000	0.1592	0.4435**	-0.8533**	0.3553*	-0.2617	0.3393*	0.6652**
Plant height (cm)	P		1.0000	0.5106**	0.0073	0.3241	0.1521	-0.2068	0.3833*
	G		1.0000	0.5793**	-0.0272	0.3323*	0.2368	-0.3343*	0.5323**
Panicle length (cm)	P			1.0000	-0.1600	0.1172	0.1403	0.2194	0.2889
	G			1.0000	-0.2355	0.1125	0.1795	0.2021	0.5521**
Number of productive tillers per m^2	P				1.0000	-0.2896	0.3338*	-0.3577*	-0.2328
	G				1.0000	-0.3594*	0.4161*	-0.4842**	-0.5191**
Number of grains per panicle	P					1.0000	-0.2404	-0.3274	0.4276**
	G					1.0000	-0.2678	-0.5881**	0.5694**
1000 grain weight (g)	P						1.0000	-0.1420	-0.0304
	G						1.0000	-0.3928*	0.1141
Gall midge incidence (%)	P							1.0000	-0.1930
	G							1.0000	-0.8473**

P: Phenotypic correlation coefficients, G: Genotypic correlation coefficients;
*=significant at P< 0.05, **=significant at P<0.01
Gen: R^2= 2.1337; Residual effect = SQRT (1- 2.1337)
Phe: R^2= 0.3811; Residual effect =0.7867

Trait association studies between yield and other traits and among the traits were studied for 18 genotypes revealed high magnitude of genotypic correlation coefficients in most of the cases as compared with the corresponding phenotypic correlation coefficients indicating the negligible influence of environmental factors. Similar results were reported by Bhattacharya *et al*. (2007) [9] Ravindra Babu *et al*. (2012) [29], Hossain *et al*. (2015) [16], Mohan *et al*. (2015) [24], Ratna *et al*. (2015) [28] and Kalyan *et al*. (2017) [18]. In some cases, phenotypic correlation coefficients were higher than their genotypic correlation coefficients, which indicate the suppressing effect of the environment that can alter the expression of the characters at the phenotypic level. Rice yield recorded significantly positive correlation with days to 50% flowering, plant height and number of grains per panicle at both genotypic and phenotypic levels suggested that genotypes with long duration, more plant height and good number of grains per panicle contribute for more grain yield. The results are in agreement with Saha *et al*. (2019) [32] for days to 50% flowering and number of grains per panicle. Similarly, positive correlation of panicle length, 1000-grain weight and straw yield on grain yield was also reported by Kumar *et al*. (2018) [22]. However, negative relationship between days to 50% flowering and grain yield was reported by Babu *et al*. (2006) [6] and Chandan Kumar and Nilanjaya (2014) [10]. The gall midge incidence expressed negative association with grain yield at both phenotypic and genotypic levels indicated the genotypes with less silver shoots were high yielders.

Inter correlation studies may facilitate breeder to decide upon the intensity and direction of selection pressure to be given on related traits for simultaneous improvement of these traits. Gall midge incidence exhibited significant negative correlation with number of productive tillers per m^2 at both genotypic and phenotypic levels, while plant height, number of grains per panicle and 1000-grain weight exhibited significant negative correlation with gall midge incidence at genotypic level indicating high yielding short stature with medium slender grains and good number of productive tillers genotypes were relatively tolerant to gall midge incidence. Hence, selection of genotypes in this direction might help for gall midge resistance. These results are contrary to Ogunbayo *et al*. (2010) [25], Mohan *et al*. (2015) [24] and Tippaswamy *et al*. (2016) [38] as test weight and effective bearing tillers were positively associated with gall midge incidence in their findings.

Significant positive association for days to 50% flowering with panicle length and number of grains per panicle was noticed at both genotypic and phenotypic levels. Similar results were supported for days to 50% flowering with number of grains per panicle by Saha *et al*. (2019) [32] and positive correlation between panicle length and days to 50% flowering was also reported by Ravindra Babu *et al*. (2012) [29] and Mohan *et al*. (2015) [24]. This might be due to higher accumulation of assimilates as growth duration becomes longer. Plant height had significant positive correlation with panicle length at both phenotypic and genotypic levels. However, negative association for the plant height with tillers per plant and grains per panicle was obtained by Chandan Kumar and Nilanjaya (2014) [10]. Number of grains per panicle showed significant positive correlation with grain yield and negative correlation with 1000-grain weight indicating the practice of selecting medium slender grain genotypes would enhance the yield levels. The positive association of grain yield with filled grains per panicle was observed by Akinwale *et al*. (2011) [4], Ruth Elizabeth Ekka *et al*. (2011) [30], Ravindra Babu *et al*. (2012) [29], Gopikannan and Ganesh (2013) [14], Ratna *et al*. (2015) [28] and Kumar *et al*. (2017) [23]. Similarly, positive and significant association of grains per panicle with 1000 grain weight was earlier reported which

was contradictory with the studies of Deepa sankar *et al*. (2006) [12] and Chandan Kumar and Nilanjaya (2014) [10]. These above correlations also indicated that by selecting any one the above traits might be useful to improve the grain yield along with gall midge resistance.

4. Conclusion

On the basis of results as summarized above, it is concluded that varying genetic variability exists in the germplasm provides opportunities for this collection to be useful for genetic improvement. Traits with high heritability coupled with high genetic advance are attributable to additive gen action which could be improved through simple selection procedures. Days to 50% flowering, plant height and number of grains per panicle showed positive contribution, and gall midge incidence recorded negative contribution towards grain yield. Thus, these plant traits deserve greater attention in further breeding programmes for developing high yielding gall midge resistant rice varieties.

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