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Genetic variability studies for gall midge incidence, yield and its components in rice (*Oryza sativa* L.) genotypes in Northern Telangana

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Abstract

The field experiment was conducted at Agricultural Research Station, Kunaram during the rainy season of 2017 to investigate genetic variability for gall midge incidence, yield and its components among thirty two genotypes. Considerable amount of genetic variability was observed among all the genotypes for all the traits under study. In general, phenotypic coefficients of variation (PCV) estimates were higher than genotypic coefficients of variation (GCV) estimates for all the studied characters. The GCV and PCV were high for gall midge incidence, number of grains per panicle, 1000-grain weight and grain yield. Additive gene action was predominant for gall midge incidence, number of grains per panicle, 1000-grain weight, grain yield, days to 50% flowering and plant height. Hence, combined results of coefficients of variation and heritability studies revealed that gall midge incidence, number of grains per panicle, 1000-grain weight and grain yield could be given due importance among the traits studied for further crop improvement.

Keywords: coefficient of variation, galls, genetic advance, heritability, rice, yield

1. Introduction

Rice (*Oryza sativa* L.) is the world's most important crop and around three billion Asians use rice as an essential staple food that provides 35 to 60% of their daily calories^[12]. Rice has been occupied larger area, accounts for nearly 5 lakh ha among the cereals during every rainy season in Northern region of Telangana State in India. Asian rice gall midge, *Orseolia oryzae* (Wood-Mason) is one of the important insect pests in Northern Telangana. In India, it is rated as third most important pest of rice in terms of spread, severity of damage and yield loss^[7]. More recently, gall midge incidence has been increased in almost all the rice growing states of India which results in considerable yield losses as affected tillers bear no panicles or grains. In contrast, the maggots fail to induce gall formation on the resistance varieties and perish in 2-4 days after hatching. Breeding for gall midge resistant varieties has been important strategy with more yield and acceptable grain quality^[14].

In a breeding programme, refinement of rice varieties with more yields along with gall midge resistance requires information on the nature and magnitude of variation in the available germplasm having wide variability, and degree of environmental influence on the expression of these traits. Knowledge concerning heritability is essential to the plant breeders to provide the information on the nature of progenies in the succeeding generations, to make appropriate selection and to assess the magnitude of genetic improvement. High genetic advance estimates along with high heritability values should be used for the effective selection of superior varieties^[4]. Several workers studied the genetic variability for yield and its components in rice^[11]. Information on the genetic variability of gall midge incidence, grain yield and its components is not available in the experimental material. Present study was hence undertaken to identify the most important traits for breeding programmes by exploring the genetic variation, heritability and genetic advance of yield, its components and gall midge incidence of 32 rice genotypes for development of high yielding, gall midge resistant genotypes for further improvement.

2. Materials and methods

The seed of 32 rice genotypes was raised on nursery beds at Agricultural Research Station, Kunaram during the rainy season of the year, 2017 (Table 1).

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Twenty five days old seedlings of each genotype was transplanted under irrigated system with three replications in a Randomized Block Design (RBD). The farm is located at 18.6°N Latitude, 79°E Longitude and at an elevation of 231m amsl. The soil is silty loam with pH 7.43 and EC 0.26 dS/m. All the recommended package of practices and need based plant protection measures were followed to raise a good crop and to maintain a uniform population per replication. Data was recorded at maturity on 5 random plants for each entry in each replication for plant height (cm), panicle length (cm), number of productive tillers per m² and number of grains per panicle. However, days to 50 % flowering and grain yield (kg/plot) were recorded on whole plot basis, whereas, random sample was used to estimate 1000 grain weight (g) for each

entry in each replication. Number of productive tillers per plant values were converted in to the number of productive tillers per m² and grain yield values recorded from the net plot (kg/plot) were converted in to hectare (kg/ha). The incidence of gall midge was recorded as percent tillers affected with silver shoots (Standard Evaluation System for Rice, IRRI, 2002) on 10 random plants and averaged. The mean data after computing for each trait was subjected to standard methods of analysis of variance as per the formula given by Panse and Sukhatme (1985) [19] described in Table 1. The coefficients of variability were calculated following the methodology given by Burton and De Vane (1953) [9]. Heritability in the broad sense and genetic advance as percentage of mean were calculated by the formula given by Johnson *et al.* (1955) [15].

Table 1: List of genotypes studied along with the pedigree and status

S. No.	Genotype /Variety	Pedigree	Status
1	JGL 24497	JGL 17004 x NLR 3042	Not released
2	RDR 1162	JGL 11727 x JGL 17004	Not released
3	RNR 15048	MTU 1010 X JGL 3855	Released
4	JGLH 169	IR 62030-54-1-2-2R x IR 42266-29-4-2-2-2-2R	Not released
5	RNR 23595	Yamini x BM 71	Not released
6	RDR 1188	JGL 11118 x RNR 2465	Not released
7	IBT R9	Tellahamsa* 2 x GPP2	Not released
8	MTU 1010	Krishnaveni x IR 64	Released
9	JGL 20776	MTU 1010 x JGL 13595	Not released
10	WGL 1119	WGL 32100 // B95-1 x Abhaya	Not released
11	IET 26241	-	Not released
12	KNM 2305	JGL 11470 x Himalaya 741	Not released
13	IBT R4	Tellahamsa* 2 x GPP2	Not released
14	WGL 962	BPT 5204 x GEB 24 // BPT 5204 x Shatabdi	Not released
15	KMPS 6251	MTU 1001 x NLR 145	Not released
16	KNM 2307	JGL 11727 x JGL 17004	Not released
17	US 314	Private company hybrid	Released
18	IBT R8	Tellahamsa* 2 x GPP2 // Tellahamsa* 2 x NLR 145	Not released
19	KNM 118	MTU 1010 x JGL 13595	Released
20	JGL 23746	JGL 3855 x C 28	Not released
21	WGL 1150	Tellahamsa // B95-1 x Abhaya	Not released
22	RNR 21225	MTU 1075 x Kavva	Not released
23	IET 26224	-	Not released
24	Krishna	Chandan x BPT 5204	Released
25	RNR 17500	Sumathi x Kavva	Not released
26	WGL 1021	WGL 32183 x Sheetal	Not released
27	Pusa 1121	Pusa 614-1-2 x Pusa 614-2-4-3	Released
28	RNR 15435	RNR 17818 x Vasumathi	Not released
29	Sumathi	Chandan x Pak Basmathi	Released
30	MTU 1001	MTU 5249 x MTU 7014	Released
31	JGL 18629	JGL 7046 x Swarna // BPT 5204	Not released
32	JGL 11470	JGL 418 x Gedongibeton	Released

3. Results and discussions

In the present investigation, analysis of variance (Table 2) revealed significant differences among the genotypes for gall midge incidence, yield and its components indicating the presence of considerable amount of variability. Many rice workers, Mohan *et al.* (2015) [18], Ajmera *et al.* (2017) [2],

Behera *et al.* (2018) [6] and Saha *et al.* (2019) [22] recorded high variability for various traits. Thus, it indicated that there was sufficient variability in the material for selecting desirable genotypes by the plant breeder for further improvement.

Table 2: Mean squares corresponding to various sources of variation for eight traits in rice

	Source of Variation		
	Replications	Treatments	Error
Degrees of freedom	2	31	62
Days to 50% flowering	0.07	346.26**	0.29
Plant height (cm)	8.83	641.77**	3.19
Panicle length (cm)	1.33	16.99**	0.69
Number of productive tillers per m ²	339.29	1821.46**	241.79
Number of grains per panicle	275.69	12506.50**	681.64
1000- grain weight (g)	1.79**	65.08**	0.14
Grain yield (kg per ha)	693712.50	2560828.47**	286063.15
Gall midge incidence (%)	88.09	972.83**	36.86

* = Significant at $P < 0.05$, ** = Significant at $P < 0.01$

3.1 Assessment of coefficients of variation for gall midge incidence, yield and its components

The genetic analysis of quantitative traits is a prerequisite for plant breeding programmes which can lead to a systematic method of design and to appropriate planning of plant breeding strategies. The extent of variability was measured in terms of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) and is presented in Table 3.

Interestingly, highest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was exhibited by trait, gall midge incidence, and percentage of galls could be reduced by selecting against this trait which provides ample scope for developing gall midge resistant ones which is in accordance with the findings of Mohan *et al.* (2015) [18] and Thippaswamy *et al.* (2016) [25]. While, yield components both number of grains per panicle and 1000-grain weight exhibited maximum GCV and PCV by which yield could be improved by selecting these traits in positive direction. These results were earlier reported by Sameera *et al.* (2015) [23], Ajmera *et al.* (2017) [2] and Saha *et al.* (2019) [22] for both number of grains per panicle and 1000-grain weight. Rice researchers, Bhati *et al.* (2015) [8], Behera *et al.* (2018) [6] and Saha *et al.* (2019) [22] recorded high PCV and GCV for grain yield indicating the importance of evaluation and selection of high yielding genotypes which are in conformity with the present findings. Low levels of PCV and GCV were observed for panicle length suggesting the less variability among the genotypes for this trait. Similar reports were concluded by Akinwale *et al.* (2011) [3] and Adhikari *et al.* (2018) [1]. In contrary to this, moderate estimates of PCV and GCV were observed for panicle length by Dhanwani *et al.* (2013) [10] and Ajmera *et al.* (2017) [2]. Moderate levels of PCV and GCV for plant height, days to 50% flowering and

number of productive tillers per m² indicated the considerable level of variability in these traits and suggested the possibility of improving these traits through selection. However, Ajmera *et al.* (2017) [2] reported high GCV and PCV values for number of productive tillers per plant and low GCV and PCV for days to 50% flowering and also Dhanwani *et al.* (2013) [10] showed high GCV and PCV for plant height.

High estimates of PCV were observed than GCV for all the traits in the rice researcher's findings of Mohan *et al.* (2015) [18], Bagati *et al.* (2016) [5], Hefena *et al.* (2016) [13], Rusdiansyah *et al.* (2017) [21] and Gyawali *et al.* (2018) [11] which are in agreement with the present study and also they reported that the environmental effect on any trait is indicated by the magnitude of difference between the genotypic and phenotypic coefficients of variation; large differences reflect a large environmental effect, where as small differences reveal a high genetic influence. It is interesting to note that small differences between the corresponding values of PCV and GCV were observed for days to 50% flowering, plant height, panicle length and 1000-grain weight representing less environmental interference on the expression of these traits which are in agreement with the results explained by Karim *et al.* (2007) [17] and Saha *et al.* (2019) [22] for plant height, panicle length and 1000 grain weight. It also suggests that selection based on these traits would be effective for future crossing programme. However, values of PCV were considerably higher than GCV for number of productive tillers per m², number of grains per panicle, grain yield and gall midge incidence indicated the sensitive nature of these traits to environmental fluctuations. Similar findings are in conformity with the earlier reports of Thippaswamy *et al.* (2016) [25], Tripathi *et al.* (2017) [27] and Adhikari *et al.* (2018) [1] for effective bearing tillers, number of grains per panicle and grain yield.

Table 3: Genetic parameters for various traits in rice

Character	GCV (%)	PCV (%)	Heritability (%)	Genetic advance % of mean
Days to 50% flowering	11.8	11.8	99.8	24.3
Plant height (cm)	12.5	12.6	98.5	25.5
Panicle length (cm)	8.9	9.4	88.7	17.2
Number of productive tillers per m ²	9.4	11.3	68.5	16.0
Number of grains per panicle	33.2	36.0	85.3	63.2
1000 grain weight (g)	23.1	23.2	99.3	47.4
Grain yield (kg/ha)	19.7	23.1	72.6	34.6
Gall midge incidence (%)	37.2	39.3	89.4	72.4

GCV = Genotypic coefficients of variation, PCV = Phenotypic coefficients of variation

3.2 Estimation of heritability and genetic advance for gall midge incidence, yield and its components

In the present investigation, heritability in the broad sense was found to be high for the traits, namely days to 50% flowering,

plant height, panicle length, number of grains per panicle, 1000-grain weight, grain yield and gall midge incidence indicated that selection based these traits would be more effective and efficient in the segregating generations due to

accumulation of additive genes which can exploit good amount of variation for the future breeding programmes. In contrary to this, moderate heritable values were reported by Seyoum *et al.* (2012) ^[24] for days to maturity, Thomas and Gabriel (2012) ^[26] for test weight, Ramanjaneyulu *et al.* (2014) ^[20] for days to flowering and panicle length. Percentage of galls, number of grains per panicle, 1000-grain weight, grain yield, days to 50% flowering and plant height recorded high heritability coupled with high genetic advance which can be easily scored by their phenotypic performance. This study also implies preponderance of additive gene affect, which will help to make selection in early segregating generations and there is a scope for developing widely adopted genotypes if these traits are subjected to any selection scheme for exploiting fixable genetic variance. Ajmera *et al.* (2017) ^[2] estimated the heritability and genetic advance to be very high for number of grains per panicle, 1000-grain weight and grain yield and also Karende *et al.* (2015) ^[16] recorded high heritability and high genetic advance values for number of grains per panicle and grain yield. High heritability and high genetic advance values for gall midge incidence were recorded by Mohan *et al.* (2015) ^[18] and Thippaswamy *et al.* (2016) ^[25] which are in accordance with present findings. High heritability coupled with moderate genetic advance estimates were recorded by the researchers, Ajmera *et al.* (2017) ^[2] and Behera *et al.* (2018) ^[6] for panicle length which are in agreement with the present findings suggested the role of both additive and non-additive gene effects in their inheritance, therefore, selection could be practiced in the later generations by hybridization programme for exploiting hybridity (Table 3). In contrary to this, Sameera *et al.* (2015) ^[23] reported high heritability coupled with high genetic advance for panicle length. Moderate heritability with low genetic advance values were recorded for number of productive tillers per m² reveals that character is governed by non additive gene effects and moderate heritability is exhibited due to considerably high environmental effects.

4. Conclusion

A proper follow up of this study would be justifiable by practicing selection for the number of grains per panicle, 1000-grain weight and grain yield, and also by practicing selection against percentage of galls in the experimental material which would be useful for further breeding schemes for the development of gall midge resistant or tolerant high yielding rice genotypes.

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