International Journal of Plant & Soil Science

33(17): 183-192, 2021; Article no.IJPSS.70385
ISSN: 2320-7035

Assessment of Genetic Parameter of Variability and Heritability based on Morphological Traits and Disease Parameters for Brown Spot in Rice (*Oryza sativa* L.)

Banshidhar[1], Priyanka Jaiswal[1], Rajesh Kumar[1*] and Bimla Rai[2]

[1]Department of Plant Breeding and Genetics, RPCAU, Pusa, Samastipur, India.
[2]Department of Plant Pathology, RPCAU, Pusa, Samastipur, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/IJPSS/2021/v33i1730563
Editor(s):
(1) Dr. Hon H. Ho, State University of New York, USA.
Reviewers:
(1) Mohd Ikmal Asmuni, Universiti Putra Malaysia Bintulu Campus,Malaysia.
(2) Joanna Kocięcka , Poznań University of Life Sciences, Poland.
Complete Peer review History: https://www.sdiarticle4.com/review-history/70385

Original Research Article

Received 01 May 2021
Accepted 06 July 2021
Published 09 August 2021

ABSTRACT

Cochliobolus miyabeanus is a serious threat to the standing rice crop in context of production and productivity as it results in loss of both grain quality and yield. The pathogen causes brown spot disease in rice which had resulted in two severe famines in past. Hence, in this regard it is imperative to search for new and diverse resistance sources and to evaluate them with respect to genetic variability and inherent genetic potential for various morphological traits including yield and yielding attributing traits and disease estimating parameters for identifying high yielding diverse resistant lines that could be utilized in future breeding programmes aimed at development of superior cultivars against brown spot disease. Keeping this in view this study was conducted at Rice Research Farm, RPCAU, Pusa to evaluate 300 genotypes for rice for various morphological traits and disease estimating parameters along with three checks for disease response in augmented design. All the recommended package of practices was followed along with necessary prophylactic plant protection measures to raise a good crop. Data on different traits and parameters under study were recorded and analysed biometrically to assess the genetic parameter of variability

**Corresponding author: E-mail: rajrau.2007@rediffmail.com;*

and heritability. The ANOVA showed significant difference among the genotypes for most of the traits and parameters under study which reflects ample amount of variability among the genotypes. Further, the smaller difference between GCV and PCV and higher estimates of heritability and genetic advance as percentage of mean revealed higher percentage of inherent genetic potential in overall variability. The higher estimates of heritability and genetic advance as percent of mean for grain yield per plant and AUDPC suggested that the resistant lines identified in this study can be easily advanced through generation following phenotypic selection for derivation of high yielding resistant lines.

Keywords: *Rice; Brown spot; ANOVA; heritability; genetic advance; AUDPC.*

1. INTRODUCTION

Rice (*Oryza sativa L.*) is one of the three most important food crops grown in the world. Being the staple food grain of more than 50% of the world's population it meets 21% of dietary energy and 15% of global protein requirement. More than 3.5 billion people i.e. almost half of the total world's population is dependent on rice to meet their daily requirements. Globally, it is cultivated over an estimated area of 163.51 million hectares producing about 498.70 million tons of grain (USDA, Prel. 2018-19). In India rice is cultivated over an area of 43.19 million hectares producing 115.63 million tons of grains with average productivity of 26.77 Q/ha (3rd Adv. Est. 2018-19, Annual Report, DAC & FW). The average yield of a well-managed crop with adequate irrigation, nutrient and crop health management is 2-3 t/ha. However, it's yield potential is adversely affected by diseases, insect-pest and weeds. Among these, fungal diseases especially brown spot caused by *Cochliobolus miyabeanus* (Ito and Kuribayashi,1972) (Anamorph: *Bipolaris oryzae* (Breda de Haan) Shoemaker [1]*;* Synonyms: *Helminthosporium oryzae*) is a serious threat to the standing crop in context of rice production and productivity as it results in loss of both grain quality and yield. The reduction in yield can be as high as 45% in severe infection and 12% in moderate infection (IRRI, 1983). To cope with this, it is indispensable that the diverse resistant sources should be identified and strategically employed to prevent the speedy spread of the pathogen or to trap it in a limited cropped area. In this regard, breeding programme initially involves screening of available genetic resources for resistance against the pathogen. Subsequently, the identified lines with resistance against the pathogen can be used in a further breeding programme for the development of resistant varieties along with higher yield. The knowledge of the nature and magnitude of genotypic and phenotypic variability present in the crop species plays a vital role in formulating a successful breeding programme aimed at developing a desirable superior cultivar. The development of a high end plant breeding programme is dependent upon the existence of exploitable variability in the population and the extent to which the desirable traits are heritable. Thus, the assessment of existing variability becomes highly essential for a well oriented and high ended resistance breeding programme, hence the study of variability and genetic parameters for yield and yield contributing traits is absolutely essential. For selecting such improved genotypes from diverse genetic stock, a vivid understanding and scientific knowledge on available variability, heritability and the expected genetic advance is necessary. Therefore, the present study was conducted with the aim to estimate variability and genetic parameters of different component traits towards the grain yield and resistance to brown spot disease so that the desired information can be obtained and used in the future rice breeding programmes.

2. MATERIALS AND METHODS

2.1 Experimental Location and material

The present experiment was carried out at Rice Research Farm, Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar on 300 genotypes of rice along with three check varieties (listed in supplementary Table 1) in augmented design. The experimental plot was subdivided into 12 blocks with replicated checks and unreplicated test genotypes to evaluate variability, heritability and genetic advance among the genotypes.

2.2 Inoculum and Method of Inoculation

For disease scoring the field is sprayed with the inoculum for the creation of artificial epiphytotic conditions in both fields as well as in controlled

conditions. The pure culture of *Cochliobolus miyabeanus* was collected from the Department of Plant Pathology, RPCAU, Pusa and plate culturing was done for multiplication of pathogen on agar media. The pathogen cover on agar media was collected and diluted with water. This fungal suspension was used for spraying the crop during morning hours 75 days after sowing using an aerosol sprayer.

2.3 Disease Scoring

In disease scoring, individual scores were provided to the infected leaves based on standard evaluation scale (SES, IRRI, 2013 provide in supplementary Table 2) mean disease score was calculated by multiplying the individual score for each plant within a genotype with the number of plants with that particular score and finally all the scores (individual score × Number of plants) are added and then divided by the total number of plants within a genotype. This gives a mean disease score. Following the mean disease scoring, the disease severity index (DSI) and Area Under Disease Progress Curve (AUDPC) was calculated.

2.4 Data Collection and Biometrical Analysis

Thirty days old seedlings were transplanted 20 cm apart between rows and 15 cm within the row. All the recommended package of practices was followed along with necessary prophylactic plant protection measures to raise a good crop. Data on different traits under study were recorded on ten plants selected for evaluation for all the traits except days to 50% flowering and days to physiological maturity in which plot wise data were recorded and analyzed to calculate genotypic and phenotypic coefficients of Variation (GCV and PCV), heritability (broad sense), genetic advance and expected genetic advance as percent of mean. The analysis of variance for different traits was carried out using mean data in order to assess the genetic variability among the genotypes as given by Cochran and Cox [2]. Phenotypic and genotypic coefficients of variability for all traits were estimated using the formula of Burton and De Vane [3]. The broad sense heritability (h^2bs) was estimated for all traits as suggested by Hanson et al., [4]. Genetic advance for each trait was estimated by using the formula given by Johnson et al. [5].

i. **Mean disease score** =

$$\sum_{i=1}^{n} \frac{\text{Individual score} \times \text{No. of leaves scored}}{\text{Total no. of plants}}$$

where, n: number of plants scored

ii. **Disease incidence** = No. of infected plants / Total no. of plants assessed × 100

$$\text{DSI} = \frac{\text{Sum of all rating}}{\text{Total no.of rating} \times \text{Maximum grade}} \times 100$$

iii. Area under disease progress curve

$$(\text{AUDPC}) = \sum_{i=1}^{K} [(S_i + S_{i+1})/2] \times (t_{i+1} - t_i)$$

where, Si : Disease severity at ith day; t_i : ith day of evaluation of disease; K : No. of dates of evaluations of disease

iv. **Genotypic variance**: $\sigma^2 g = (MSG - MSE)/ r$

where MSE is mean square of error, MSG is mean square of accessions, and r is replications.

v. **Phenotypic variance**: $\sigma^2 p = \sigma^2 g + \sigma^2 e$

where is σ2g genotypic variance and σ2 e is mean squares of error.

vi. **Phenotypic coefficient of variance** (PCV):

PCV (%) = $\sigma^2 p/ \sqrt{\bar{X}} \times 100$, where $\sigma^2 p$ is the phenotypic variance and $\bar{X}$ is mean of trait.

vii. **Genotypic coefficient of variance** (GCV):

GCV (%) = $\sigma^2 g/ \sqrt{\bar{X}} \times 100$ where σ^2 g is genotypic variance and $\bar{X}$ is mean of trait.

viii. **Heritability (Broad sense)**:

h^2 B = $\sigma^2 g/ \sigma^2 p$ where σ^2 g is genotypic variance and σ^2 p is phenotypic variance.

ix. **Expected genetic advance** (GA):

GA = $K \times \sqrt{\sigma^2 p} \times h^2 B \times 100$

GA as a % of the mean for selection of the superior 5% of genotypes: GA (%) = $K \times \sqrt{\sigma^2 p} \times h^2 B \times 100/\bar{X}$

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance (ANOVA)

The ANOVA for the morphological traits and disease estimating parameters under study was performed and the results are presented in Table 1 and Table 2 respectively. The ANOVA for morphological traits revealed significant differences among genotypes for all the traits under study at 0.1% level of significance for treatments (eliminating blocks), checks and varieties while for checks vs. varieties it was significant for all the traits under study at 0.1% level of significance except plant height and test weight. Further for blocks (eliminating checks and varieties) the mean sum of square was significant at 0.1% level of significance for days to 50% flowering, plant height and grain per panicle and at 5% level of significance for days to physiological maturity while for other traits it was non-significant. The error mean sum of square for all these traits were insignificant. These results inferred that there was ample genetic variability among the genotypes for all the traits under study and these traits were least affected by environmental variation. Similar results were reported by Madhukar et al., [6]; Dariush et al., [7]. Also the error variance for these traits was low and non-significant that reinforced the findings of presence of inherent genetic variability among the genotypes. The significant differences among the blocks for days to flowering, days to maturity, plant height and number of grains per panicle may be attributable to the planting pattern of genotypes in which the early maturing and semi-dwarf genotypes were transplanted in first 6 blocks while the late maturing and tall genotypes were transplanted in next 6 blocks for effective crop management. Similar results were reported by Paswan et al*.,* [8]; Madhukar et al., [6]; Saba et al., [9]; Longjam and Singh [10] for significant differences among block for some of the trait and non-significant error variance. The ample amount of inherent genetic variability in the studied genotypes could be exploited for effective selection of desirable traits in further breeding programmes.

The ANOVA for disease estimating parameters revealed significant differences among genotypes for all the parameters used for disease estimation in this study at 0.1% level of significance for treatments (eliminating blocks), checks, varieties and checks vs. varieties while the error mean sum of square was insignificant for all the disease estimating parameters. The significant mean sum of square for genotypes and insignificant error variance inferred that the genotypes were widely different among themselves in relation to response of disease and their response towards the disease was greatly due to their inherent genetic potential. Thus, the genotypes selected as resistant sources based on their AUDPC values were diverse from each other and could be effectively used in maintenance of resistance gene.

3.2 Estimation of Mean Performance and Variance

The mean, range and variance for various morphological traits and disease estimating parameters is presented in table 3. Mean performance of genotypes in concern of a particular trait reflect the central value of measurement for that trait i.e. half of the genotypes have trait value higher than the mean while other half of the genotypes have trait value lower than the mean. However, this not holds true in all situations as it is highly sensitive to extreme values in a data set [11]. Nevertheless, mean values for a trait under study forms the basis of analysis and interpretation of all other complex statistics viz. standard deviation, coefficient of variation, genetic advance as percentage of mean, etc. Standard deviation is often used as an estimator of variance and provides insight about the dispersion of a data set with respect to its mean while range provide a crude estimate of data dispersion. The estimates of genotypic, phenotypic and environmental variance along with their coefficient is presented in table 3. The genotypic, phenotypic and environmental variance were calculated according to Burton and De Vane [3] for each studied character and results were compared to assess variability. The maximum variance (all three genotypic, phenotypic and environmental) among the morphological traits was reported for number of grains per panicle, plant height, grain yield per plant, days to physiological maturity, days to 50% flowering, panicle length and test weight while minimum variance was reported for number of effective tillers per plant.

Among the disease estimating parameters maximum variance was observed for AUDPC followed by disease severity index and mean disease score. The variance of a data series indicates how widely individual data in a group vary. However, comparison of degree of variability between two or more data series, even

Table 1. ANOVA for various morphological traits under study

Sources of error	df	DFL	DPM	PH	PL	ETP	GPP	TW	GY
		Mean sum of squares							
Block (eliminating Check+Var.)	11	3.97 **	5.31 *	440.62 **	0.170	0.097	44.284 **	0.172	1.361
Treatment (eliminating Blocks)	302	200.09 **	239.58 **	825.81 **	14.48 **	14.15 **	1511.46 **	15.06 **	254.0 **
Checks	2	429.70 **	406.86 **	310.37 **	12.56 **	485.71 **	30225.46 **	13.92 **	6905.02 **
Varieties	299	293.60 **	335.46 **	1209.18 **	20.47 **	13.64 **	2576.52 **	19.010 **	414.64 **
Checks vs. Varieties	1	35.96 **	179.36 **	2.53	254.74 **	907.16 **	19239.54 **	0.75	11651.34 **
Error	22	1.18	2.16	13.35	0.31	0.08	6.81	0.20	1.75

*, **: Significant at $\infty = 0.05$ and $\infty = 0.01$ respectively

DFL: Days to 50% flowering; DPM : Days to physiological maturity; PH: Plant height; PL: Panicle length; ETP: Number of effective tillers per plant; GPP: Number of grains per panicle; TW: Test weight; GY: Grain yield per plant

Table 2. ANOVA for various disease estimating parameters under study

Sources of error	df	MDS CC	MDS FIELD	DSI CC	DSI FIELD	AUDPC CC	AUDPC FIELD
		Mean sum of squares					
Block (eliminating Check+Var.)	11	0.175 **	0.030	22.469 **	3.892	11130.640 **	1533.888
Treatment (eliminating Blocks)	302	0.243 **	0.335 **	29.878 **	41.390 **	13710.630 **	19535.400 **
Checks	2	9.319 **	19.613 **	1145.471 **	2423.451 **	529827.700 **	1165603.000 **
Varieties	299	0.244 **	0.244 **	30.110 **	30.127 **	14136.040 **	13725.870 **
Checks vs. Varieties	1	1.474 **	2.626 **	171.003 **	332.895 **	88853.520 **	209278.800 **
Error	22	0.013	0.046	1.835	5.580	966.178	2591.333

**: Significant at $\infty = 0.01$

MDS CC: Mean Disease Score in controlled conditions; DSI CC: Disease severity index in controlled conditions; AUDPC CC : Area under disease progress curve in controlled conditions

Table 3. Estimates of genetic parameters of variability and heritability for various morphological traits and disease parameters under study

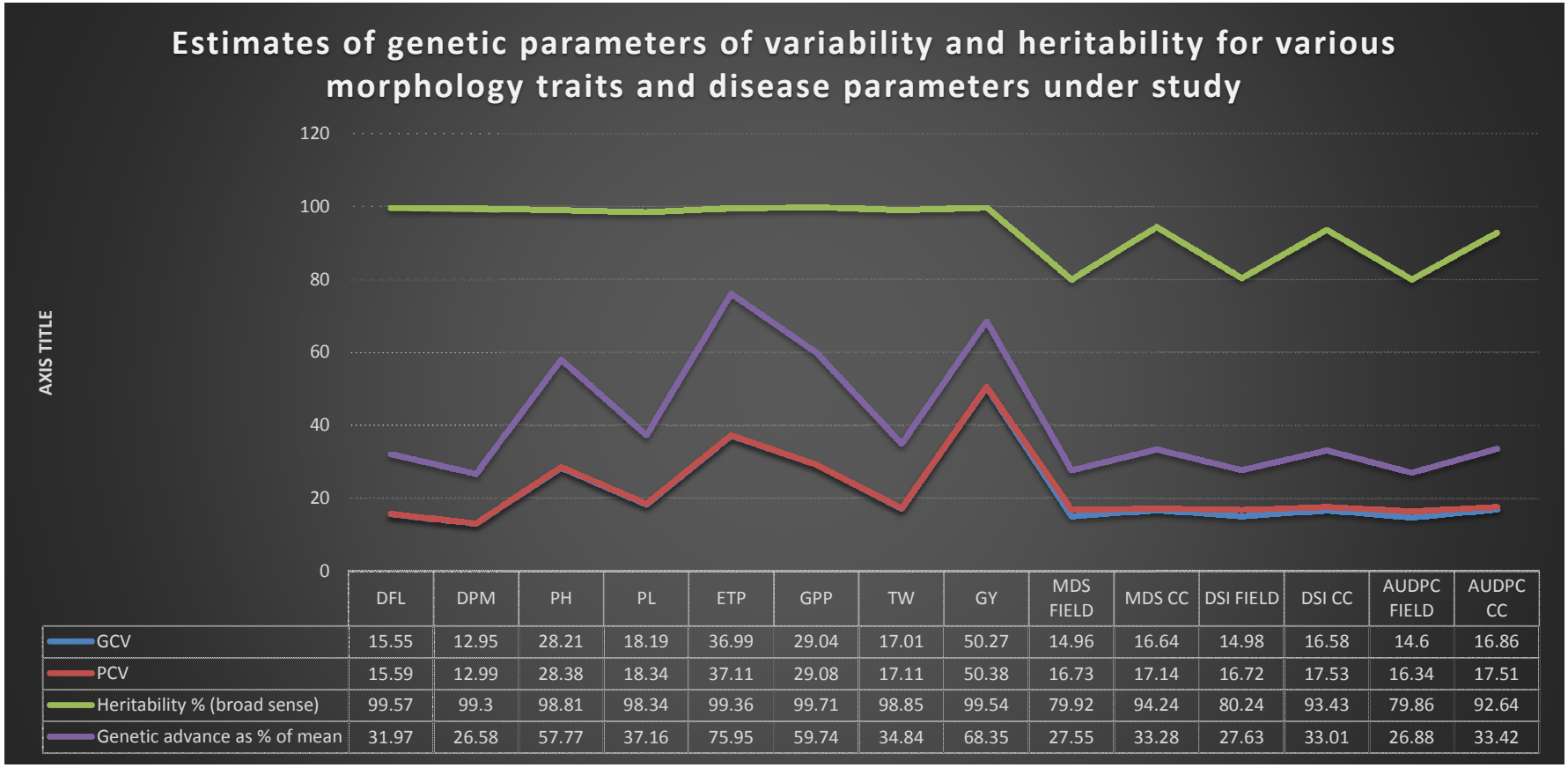
Traits	Mean	Range (minimum - maximum)	Phenotypic variance	Genotypic variance	Environmental variance
Morphological traits					
DFL	105.50	75-151	271.03	269.86	1.17
DPM	135.80	109-179.50	309.74	307.58	2.16
PH	118.15	70.10-282.30	1116.91	1103.57	13.34
PL	23.83	10.10-33.30	18.92	18.60	0.31
ETP	9.48	4.10-17.70	12.59	12.51	0.08
GPP	166.48	95.00-289.00	2378.24	2371.43	6.81
TW	24.48	15.48-38.49	17.56	17.36	0.20
GY	58.69	28.67-115.43	382.78	381.03	1.74
Disease Parameters					
MDS FIELD	2.86	1.80-3.90	0.23	0.18	0.05
MDS CC	2.77	1.75-3.95	0.23	0.21	0.01
DSI FIELD	31.77	20.00-43.38	28.23	22.65	5.58
DSI CC	30.79	19.44-43.89	27.93	26.09	1.83
AUDPC FIELD	693.91	420.00-939.81	12866.67	10275.40	2591.26
AUDPC CC	653.54	412.22-933.33	13119.84	12153.66	966.18

DFL: Days to 50% flowering; DPM : Days to physiological maturity; PH: Plant height; PL: Panicle length; ETP: Number of effective tillers per plant; GPP: Number of grains per panicle; TW: Test weight; GY: Grain yield per plant; MDS CC: Mean Disease Score in controlled conditions; DSI CC: Disease severity indexin controlled conditions; AUDPC CC : Area under disease progress curve in controlled conditions

if the means of these data series varied drastically from one another can be done using the estimates of coefficient of variability. In present investigation the maximum coefficient of variation (all three genotypic, phenotypic and environmental) was observed for grain yield per plant followed by number of effective tillers per plant, number of grains per panicle, plant height, panicle length, test weight and days to 50% flowering while the minimum coefficient of variability was reported for days to physiological maturity. Among the disease estimating parameters maximum GCV was observed for AUDPC in controlled condition followed by mean disease score in controlled condition, DSI in controlled condition, DSI in field, mean disease score in field and AUDPC in field while maximum PCV was observed for DSI in controlled condition followed by AUDPC in controlled condition, mean disease score in controlled condition, mean disease score in field, DSI in field and AUDPC in field. In this study the difference between Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) is small for all traits under study which reveals lower influence of environment in inherent potential of a trait and higher genetic inherent potential which is a prerequisite in any crop improvement programme. Similar results were also reported by Ramanjaneyulu et al., [12]; Khatun et al., [13]; Kumar et al., [14].

3.4 Estimation of Heritability and Genetic Advance

Heritability defines the proportion of observed variation in a particular trait that can be attributed to an inherited genetic factor in contrast to environmental factors. In present investigation high value of heritability was observed for each trait under study (listed in table of chart 1). The maximum heritability among the morphological traits included in present investigation was recorded for number of grains per panicle (99.71) followed by days to 50% flowering (99.57), grain yield per plant (99.54), number of effective tillers per plant (99.36), days to physiological maturity (99.30), test weight (98.85), plant height (98.81) and panicle length(98.34). Among the disease estimating parameters mean disease score in controlled condition scored maximum for heritability (94.24) followed by DSI in controlled condition (93.43), AUDPC in controlled condition (92.64), DSI in field (80.24), MDS in field (79.92) and AUDPC in field (79.86). In present study high estimates of heritability in broad sense (h^2_b) was observed for each trait under study. This may be attributable to highly diverse genotypic constitution of these genotypes constituting a



	DFL	DPM	PH	PL	ETP	GPP	TW	GY	MDS FIELD	MDS CC	DSI FIELD	DSI CC	AUDPC FIELD	AUDPC CC
GCV	15.55	12.95	28.21	18.19	36.99	29.04	17.01	50.27	14.96	16.64	14.98	16.58	14.6	16.86
PCV	15.59	12.99	28.38	18.34	37.11	29.08	17.11	50.38	16.73	17.14	16.72	17.53	16.34	17.51
Heritability % (broad sense)	99.57	99.3	98.81	98.34	99.36	99.71	98.85	99.54	79.92	94.24	80.24	93.43	79.86	92.64
Genetic advance as % of mean	31.97	26.58	57.77	37.16	75.95	59.74	34.84	68.35	27.55	33.28	27.63	33.01	26.88	33.42

Chart 1. Estimates of genetic parameters of variability and heritability for various morphology traits and disease parameters under study

DFL: Days to 50% flowering; DPM : Days to physiological maturity; PH: Plant height; PL: Panicle length; ETP: Number of effective tillers per plant; GPP: Number of grains per panicle; TW: Test weight; GY: Grain yield per plant; MDS CC: Mean Disease Score in controlled conditions; DSI CC: Disease severity index in controlled conditions; AUDPC CC : Area under disease progress curve in controlled condition

number of obsolete varieties, advanced breeding lines and modern cultivars. Further, these genotypes were tested in single location with lesser variation in edaphic and environmental variation. Hence, most of the phenotypic variation observed was due to variation in genotypic constitution that leads to higher estimates of h^2_b. High heritability for these traits demonstrated that these traits could be successfully transferred to offspring, and selection for such trait is easy and quick. These traits can also be used for indirect selection of some other correlated characters that have low heritability and complex inheritance. Further, higher estimates of heritability among the disease estimating parameters in controlled conditions as against of that in field condition revealed these parameters are more affected by environment which is a major factor in disease quadrant. Similar results were also reported by Kumar *et al*., [14] for all characters viz. days to 50% flowering (99.00), days to maturity (99.00), spikelets per panicle (99.00, 1000-grain weight (98.00), plant height (97.00), grain yield per plant (97.00), panicle bearing tillers per plant (95.00), panicle length (91.00). Rashid *et al.,* [15] also reported higher estimates of h^2_b for plant height (98.79), days to 50 % flowering (98.75) and days to maturity (98.36). Nihad *et al.,* [16] also reported higher estimates of h^2_b for days to 50 % flowering (98.36) and days to maturity (98.60). Similar reports of high estimates of h^2_b was reported by Yadav *et al.,* [17]; Longjam and Singh, [10]; Roy and Shil, [18].

Heritability expresses the reliability of phenotype as a guide for selection and there is a direct relationship between heritability and response to selection, which is referred to as genetic advance. Heritability coupled with genetic advance is a more reliable parameter of selection for improvement of a trait. The estimates of genetic advance as percentage of mean is presented in table of chart 1. In this investigation highest genetic advance as percentage of mean was observed for number of effective tillers per plant followed by grain yield per plant, number of grains per panicle, plant height, panicle length, test weight, days to 50% flowering and days to physiological maturity. Among the disease estimating parameters highest genetic advance as percentage of mean was observed for AUDPC in controlled condition followed by mean disease score in controlled condition, DSI in controlled condition, DSI in field, mean disease score in field and AUDPC in field. Heritability of a trait expresses the reliability of phenotype as a guide for selection. However, heritability alone does not truly predict the transmission of a trait if there is a prevalence of non-additive gene action. Thus, estimates of heritability along with the genetic advance is preferred in predicting the gain under selection than the heritability alone [19]. Genetic advance provides an insight on expected genetic progress that could be realised for a particular trait under suitable selection procedure. The estimates of genetic advance as percentage of mean is a relative parameter of comparing transmissibility of a trait with respect to other variables. Expected genetic advance for each character was calculated by using the formula suggested by Johnson et al., [5]. They categorized genetic advance as percentage of mean into low (0–10%), medium (10.1–20%) and high (>20.1%). In this research investigation panicle length, number of effective tillers per plant and test weight showed lower estimates of genetic advance however higher estimates of genetic advance as percentage of mean and heritability. All other traits showed higher estimates of heritability in broad sense, genetic advance and genetic advance as percentage of mean. Thus, it can be inferred that there is predominance of additive gene action and the expression of these traits are less influences by environment. High heritability coupled with high genetic advance suggested that the trait under consideration can be easily improved through phenotypic selection. The higher estimates of heritability and genetic advance as percentage of mean for grain yield per plant and AUDPC suggested that the resistant lines identified in this study can be easily advanced through generation following phenotypic selection for derivation of high yielding resistant lines. The results obtained in this study in respect to heritability and genetic advance are in agreement with earlier reports on rice by Rai et al*.,* [20]; Nandan et al*.,* [21]; Nuruzzaman et al., [22] and Barik et al., [23].

4. CONCLUSION

The ANOVA for morphological traits and disease estimating parameters revealed significant differences among genotypes for most of the morphological traits and disease estimating parameters under study at 0.1% level of significance that inferred that there was ample genetic variability among the genotypes for all the traits and disease estimating parameters under study and these traits and parameters were least affected by environmental variation. Further, difference between Phenotypic Coefficient of Variation (PCV) and Genotypic

Coefficient of Variation (GCV) is small for all traits under study which reveals lower influence of environment in inherent potential of a trait and higher genetic inherent potential which is a prerequisite in any crop improvement programme. These findings were further supported by higher estimates of heritability and genetic advance as percentage of mean for all the traits and parameters. The presence of inherent genetic variability among the genotypes with respect to their response towards the disease reflects that these genotypes were widely different among themselves and could be effectively used in maintenance of resistance gene. The higher estimates of heritability and genetic advance as percent of mean for grain yield per plant and AUDPC suggested that the resistant lines identified in this study can be easily advanced through generation following phenotypic selection for derivation of high yielding resistant lines.

SUPPLEMENTARY MATERIALS

Supplementary material is available in this following link: https://www.journalijpss.com/index.php/IJPSS/libraryFiles/downloadPublic/15

DISCLAIMER

The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Shoemaker RA. Nomenclature of Drechslera and Bipolaris, grass parasites segregated from *'Helminosporium*'. Canadian Journal of Botany. 1959;37(5):879-887.
2. Cochran WG, Cox GM. Experimental design. 2nd edition, John Wiley and Sons, New York. 1957;615.
3. Burton GW, De Vane EW. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 1953;45:478-481.
4. Hanson CH, Robinson HF, Comstock RE. Biometrical studies on yield in segregating population of Korean lespedesa. Agron. J. 1956;48:268-272.
5. Johnson, HW, Robinson HF, Comstock R. Estimates of genetic and environmental variability in soybeans. Agron. J. 1955;47:314–318.
6. Madhukar P, Raju CS, Senguttuvel P, Vanisree S. Evaluation and selection of promising rice (Oryza sativa L.) genotypes under augmented block design in aerobic system. Int. J. Pure App. Biosci. 2017;5(4):1358-1367.
7. Dariush S, Darvishnia M, Ebadi AA, Padasht-Dehkaei F, Bazgir E. Screening rice genotypes for brown spot resistance along with yield attributing characters and its association with morphological traits. Journal of Crop Protection. 2020;9(3):381-393.
8. Paswan SK, Sharma V, Singh VK, Ahmad A, Deepak. Genetic variability studies for yield and related attributes in rice genotypes (*Oryza sativa* L.). Research Journal of Agricultural Sciences. 2014;5(4):750-752.
9. Saba I, Sofi PA, Zeerak N, Mir R, Gull M. Using augmented design for evaluation of common bean (Phaseolus vulgaris L.) germplasm. International Journal of Current Microbiology and Applied Science. 2017;6(7):246-254.
10. Longjam S, Singh NB. Assessment of heritability and genetic advance for yield contributing characters in hill rice (*Oryza sativa* L.) genotypes of Manipur. The Pharma Innovation Journal. 2019;8(4):07-11.
11. Rumsey DJ. Statistics for dummies. John Wiley and Sons; 2016.
12. Ramanjaneyulu AV, Shankar VG, Neelima TL, Shashibhusahn D. Genetic analysis of rice (*Oryza sativa* L.) genotypes under aerobic conditions on Alfisols. Sabrao Journal of Breeding and Genetics. 2014;46(1).
13. Khatun T, Hanafi M, Rafii Yusop MM, Wong M, Salleh MY, FM, Ferdous J.

Genetic variation, heritability, and diversity analysis of upland rice (*Oryza sativa* L.) genotypes based on quantitative traits. Bio Med Research International; 2015.

14. Kumar S, Chauhan MP, Tomar A, Kasana RK, Kumar N. Correlation and path coefficient analysis in rice (*Oryza sativa* L.). The Pharma Innovation Journal. 2018;7(6):20-26.
15. Rashid MM, Nuruzzaman M, Hassan L, Begum SN. Genetic variability analysis for various yield attributing traits in rice genotypes. Journal of the Bangladesh Agricultural University. 2017;15(1):15-19.
16. Nihad SAI, Manidas AC, Hasan K, Hasan MAI, Honey O, Latif MA. Genetic variability, heritability, genetic advance and phylogenetic relationship between rice tungro virus resistant and susceptible genotypes revealed by morphological traits and SSR markers. Current Plant Biology. 2021;25:100194.
17. Yadav R, Rajpoot P, Verma OP, Singh PK, Pathak V. Genetic variability, heritability and genetic advance in Rice (*Oryza sativa* L.) for grain yield and it's contributing attributes under sodic soil. J Pharmacogn Phytochem. 2017;6(5):1294-1296.
18. Roy SC, Shil P. Assessment of genetic heritability in rice breeding lines based on morphological traits and caryopsis ultrastructure. Scientific Reports. 2020;10(1):1-17.
19. Kumari N, Parmar MB. Heritability and genetic advance analysis in rice (*Oryza sativa* L.) genotypes under aerobic condition. Int. J. Curr. Microbiol. App. Sci. 2020;9(03):1196-1204.
20. Rai SK, Chandra R, Suresh BG, Kumar R, Sandhya R. Genetic diversity analysis of rice germplasm lines for yield attributing traits. Int. J. Life Sci. Res. 2014;4:225–228
21. Nandan R, Shravan KS. Character association and path analysis in rice (*Oryza sativa* L.) genotypes. Agricultural Science Digest. 2018;37(3):1012-1017.
22. Nuruzzaman M, Hasan L, Shamsun NB, Huda MH. Correlation and path coefficient analysis of yield components in NERICA mutant rice lines under rained conditions. Journal of Experimental Agriculture International. 2017;16(1):18.
23. Barik Jijnasa, Kumar Vajinder, Pande Debarata. Assessment of variation in morpho-physiological traits and genetic diversity in relation to submergence tolerance of five indigenous lowland rice landraces. Rice Science. 2020;27(1):32-43.

Peer-review history:
The peer review history for this paper can be accessed here:
https://www.sdiarticle4.com/review-history/70385