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Genetic Variation, Correlation and Metroglyph Analysis in Rice (*Oryza sativa* L.) for Grain Yield Characters

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

Rice is the only cereal crop cooked and consumed mainly as whole grains, and quality considerations are more important. Rice has been reported to possess diverse therapeutic properties capable of treating diabetics to neurotic ailments as evidenced by ancient literatures apart from its nutritional importance as a major source of calories for a majority of the world population. The present investigation was taken up to study the total of 20 lines of rice including a check variety were evaluated in randomized block design for genetic variability, heritability and genetic advance by using 13 quantitative traits by metroglyph and index score method. Analysis of variance for various quantitative characters revealed that the mean sum of squares due to genotypes showed high significant difference for all characters under study at 1% level and 5% level of significance. Scattered diagram revealed that 20 genotypes were grouped in to 5 complexes and maximum number of genotypes 11 was found in complex-1. High index score observed was 33 for a genotype SHIVA-555.

Keywords: Genetic variability; GCV; PCV; metroglyph; index score; rice (Oryza sativa L.).

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1. INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important staple cereal food crop in the world and belongs to the genus *Oryza* of family Graminae (Poaceae). The genus Oryza has 24 species, 22 of which are wild and two of which are cultivated, especially *Oryza sativa* and Oryza glaberimma. The basic chromosomes (n) number of the genus *Oryza sativa* is 12 (2n=24). The cultivated varieties of *Oryza sativa* grouped in to three sub species, Indica, Japonica, and Javanica. Indica rice varieties are grown throughout the tropical and subtropical regions. Japonica varieties are grown throughout the temperate zone, and Javanica varieties are grown mainly in parts of Indonesia [1-10].

Globally, rice is cultivated now in 162.41 million hectares with annual production of around 728 million tones and average productivity of 4.65 tons/ha (USDA-2018). Asia is considered to be 'rice bowl' of the world, and it produces and consumes more than 90% of world rice. In World, China, India, Indonesia, Bangladesh, Vietnam and Thailand are the major rice producing countries. China is the largest rice producing country of the world. It has 33% share in the rice production of the world. Thailand is the largest rice exporting country of the world. It has 8% share in the rice export of the world [11-20].

In India, rice is staple food of 65% of the total population. It constitutes about 42% of the total food grain production and 45% of total cereal production. In India, rice is grown in 44.78 million ha, the production level is 115.65 million tons and the productivity is about 2.7 tons/ha during 2018-19 (NRRI-2019).

Genetic variability is the foremost important breeding tool in order to break yield stagnation and developing high yielding varieties. The quantity of genetic diversity among genotypes determines the range of genetic variability in segregating populations, which provides more selection opportunities. The degree of heritable variation in the variables evaluated is extremely important for determining the genotype's breeding potential [21-30].

For a successful breeding effort, a full understanding of the nature and extent of genetic diversity as well as the relationship of traits in a crop species is required. The ability to see the direct and indirect effects that each character has on yield will be a huge help in the choosing process. The measure of the mutual relationship between two variables is correlation. The study of correlations may aid plant breeders in understanding how improving one feature leads to improvements in other characters. A path coefficient analysis is a standardized regression coefficient that assesses the direct impact of one variable on another.

As a result, it's critical to determine the component qualities that might help boost yield. Selection would be more successful for a characteristic with a high genetic progress and a strong link to grain output. The correlation coefficient is used to determine the degree of link between yield and yield components, as well as other characteristics that have a significant impact on yield (Singh, 2009).

Metroglyph and Index score analysis is the technique was developed by Anderson (1957) to investigate the pattern of morphological variation in chickpea genotypes.

The main features of Metroglyph analysis are given below:

- Analysis is based on first order statistics and therefore, results are statistically more reliable and robust.
- Analysis is possible from both replicated as well as non-replicated data. The analysis is simple.
- The pattern of variability is depicted by glyph on the graph.

1.1 Objectives

1. To assess the genetic variability parameters for yield and its contributing factors in rice genotypes.
2. To investigate the relationship between grain yield characteristics of rice. 3.To assess genetic diversity among rice germplasm.

2. MATERIALS AND METHODS

The present investigation was carried out in the Field Experimentation Centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad, U.P during *Kharif*-2021. A randomized block design was adopted with three replications and row to row spacing is 20cm and plant to plant spacing is 15cm with plot size of 5mx2m.

Replication wise data on the basis of five randomly taken competitive plants from each replication were recorded on following fourteen quantitative traits : 1) Days to 50% flowering, 2) Days to maturity, 3) Flag leaf length, 4) Flag leaf width, 5) Plant height, 6) Number of total tillers per hill, 7) Panicle length, 8) Number of spikelets per panicle, 9) Number of filled grains per panicle, 10) Number of unfilled grains per panicle, 11) Test weight, 12) Harvest index, 13)Biological yield, 14) Grain yield per plant.

The recorded for all the considered characters were subjected to analysis of variance with the formula suggested by Panse and Sukhatme [1]. Further, different components of variance i.e., phenotypic, genotypic and environmental variance were estimated and genetic parameters like genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability in broad sense, genetic advance as percent of mean and correlation analysis were conducted by following appropriate statistical procedure.

Crop: Rice
Season: *kharif*, 2021
Experimental desi: Randomized Block Design
No. of Replications: 3
No. of Genotype: 20
Gross Area: 128 sq. m
Net cultivated area: 120 sq.m
Row to Row distance: 20 cm
Plant to Plant distance: 15 cm
Date of Sowing: 20/06/2021
Date of Transplanting: 21/07/2021
Fertilizer dose: N:P:K @ 120:60:60 kg/ha

3. RESULT AND DISCUSSION

3.1 Analysis of Variance for Quantitative Characters in rice (*Oryza sativa* L.)

The abundant scope for improving these characters including grain yield per plant provided the material is subjected to judicious selection programme. Due to diverse source of material taken as well as environmental influence affecting the phenotypes the presence of variability might be large.

ANOVA for different characters is present in Table 1. The mean squares due to genotypes showed highly significant differences (α=0.01) for all characters indicating the presence of substantial amount of genetic variability among the rice genotypes. In Table 2. which revealed a wide range of variation for all traits studies the mean values, the coefficient of variation (C.V.), standard error of the mean (SEm+), the critical difference (C.D.) at 5% and 1%, range of 20 genotypes for 13 quantitative characters are presented.

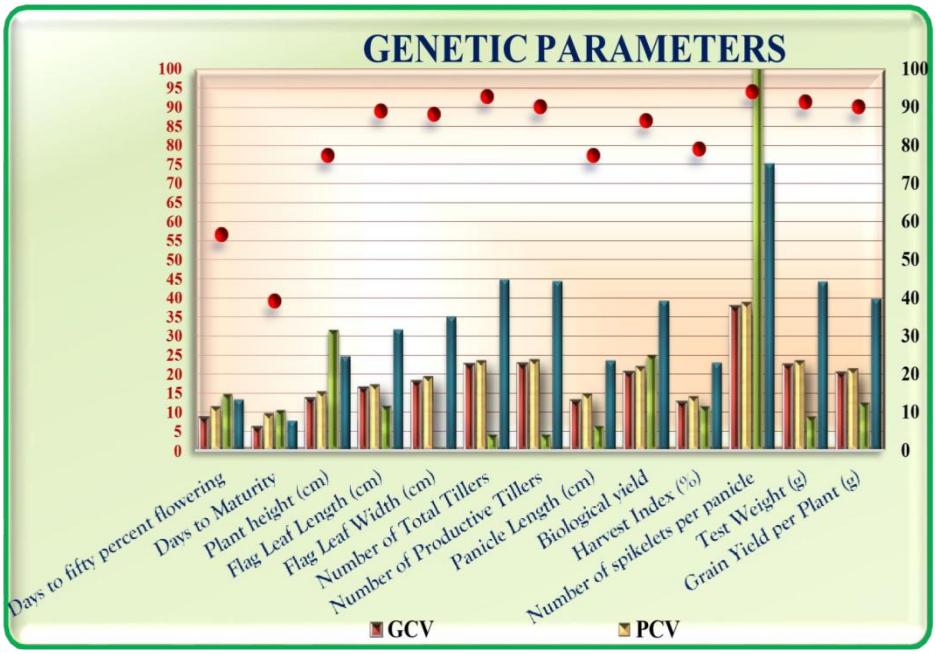

Fig 1. Histogram depicting GCV, PCV, Genetic advance and h^2 for 13 quantitative characters of rice genotypes

Table 1. Analysis of variance for 13 quantitative traits of rice genotypes

	Source	**Replication**	**Treatment**	**Error**
S. No.	**Degrees of freedom**	**2**	**19**	**38**
1	Days to fifty percent flowering	87.2950	338.802**	69.058
2	Days to Maturity	97.4720	303.584**	103.534
3	Plant height	71.2050	1003.51**	89.606
4	Flag Leaf Length	8.4830	113.87**	4.52
5	Flag Leaf Width	0.0010	0.144**	0.006
6	Number of Total Tillers	0.3380	13.352**	0.341
7	Number of Productive Tillers	0.1010	13.609**	0.48
8	Panicle Length	0.4120	39.979**	3.57
9	Biological yield	8.3980	539.328**	26.951
10	Harvest Index	15.1250	130.589**	10.638
11	Number of spikelets per panicle	103.2220	15345.37**	321.431
12	Test Weight	2.5860	62.238**	1.906
13	Grain Yield per Plant	0.1730	128.102**	4.56

Table 2. Genetic parameters for 13 quantitative characters in rice genotypes

S. No	**Genetic parameters**	**GCV**	**PCV**	**H2**	**GAM%**
1	Days to fifty percent flowering	8.637	11.484	56.56	13.381
2	Days to Maturity	6.029	9.633	39.18	7.774
3	Plant height	13.635	15.512	77.271	24.691
4	Flag Leaf Length	16.365	17.35	88.966	31.797
5	Flag Leaf Width	18.126	19.308	88.125	35.052
6	Number of Total Tillers	22.661	23.534	92.719	44.951
7	Number of Productive Tillers	22.731	23.944	90.123	44.453
8	Panicle Length	13.055	14.852	77.271	23.641
9	Biological yield	20.543	22.104	86.371	39.329
10	Harvest Index	12.57	14.143	78.985	23.012
11	Number of spikelets per panicle	37.734	38.926	93.97	75.351
12	Test Weight	22.509	23.552	91.344	44.317
13	Grain Yield per Plant	20.396	21.496	90.03	39.867

Table 3. Phenotypic correlation coefficient between yield and its component traits in rice:

Phenotypical Correlation Matrix													
TRAITS	**DFF**	**DM**	**PH**	**FLL**	**FLW**	**NTT**	**NPT**	**PL**	**BY**	**HI**	**NSP**	**TW**	**GYP**
DFF	1.0000	0.618**	-0.1655	-0.0911	0.1471	-0.2299	-0.2267	-0.523**	-0.0632	-0.343*	0.2300	-0.541**	-0.296*
DM		1.0000	-0.1825	-0.1608	0.1734	-0.1792	-0.1788	-0.485**	0.0249	-0.2449	0.282*	-0.406*	-0.1401
PH			1.0000	0.545**	0.0454	-0.275*	-0.318*	0.442**	-0.0032	-0.1670	-0.438**	0.411*	-0.1192
FLL				1.0000	-0.1257	-0.2267	-0.256*	0.2506	-0.1574	-0.1018	-0.319*	0.357*	-0.2263
FLW					1.0000	0.477**	0.313*	-0.2098	0.0088	-0.301*	0.511**	-0.2031	-0.1281
NTT						1.0000	0.918**	-0.1391	0.2115	-0.1496	0.334*	0.1029	0.1984
NPT							1.0000	-0.1454	0.320*	-0.0945	0.325*	0.0621	0.332*
PL								1.0000	0.0177	0.1272	-0.512**	0.667**	0.1281
BY									1.0000	-0.311*	0.371*	0.1388	0.694**
HI										1.0000	-0.0603	0.0125	0.276*
NSP											1.0000	-0.419**	0.364*
TW												1.0000	0.1995
GYP													1.0000

Table 4. Genotypic correlation coefficient between yield and its component traits in rice

Genotypical Correlation Matrix													
Traits	**DFF**	**DM**	**PH**	**FLL**	**FLW**	**NTT**	**NPT**	**PL**	**BY**	**HI**	**NSP**	**TW**	**GYP**
DFF	1.0000	0.521**	-0.2042	-0.1409	0.2459	-0.2391	-0.283*	-0.897**	-0.0693	-0.406*	0.318*	-0.747**	-0.429**
DM		1.0000	-0.295*	-0.318*	0.289*	-0.2198	-0.271*	-0.956**	0.0002	-0.392*	0.431**	-0.780**	-0.327*
PH			1.0000	0.665**	0.0261	-0.325*	-0.369*	0.537**	-0.0434	-0.266*	-0.506**	0.447**	-0.1786
FLL				1.0000	-0.1450	-0.2453	-0.269*	0.287*	-0.1849	-0.1492	-0.336*	0.377*	-0.2244
FLW					1.0000	0.503**	0.362*	-0.2463	0.0428	-0.355*	0.571**	-0.2116	-0.1651
NTT						1.0000	0.996**	-0.1515	0.264*	-0.1796	0.355*	0.1173	0.2055
NPT							1.0000	-0.2289	0.348*	-0.0927	0.382*	0.0729	0.350*
PL								1.0000	0.0152	0.2049	-0.588**	0.724**	0.1445
BY									1.0000	-0.356*	0.403*	0.1313	0.809**
HI										1.0000	-0.0485	0.0369	0.353*
NSP											1.0000	-0.447**	0.384*
TW												1.0000	0.2170
GYP													1.0000

DFF: Days to 50% flowering, DM: Days to maturity, FLL: Flag leaf length (cm), FLW: Flag leaf width (cm), PH: Plant height (cm), NTT: Number of total tillers per plant, NPT: Number of Productive tillers per plant, PL: Panicle length (cm), NSP: Number of Spikelets per panicle, BY: Biological yield (g), HI: Harvest Index TW: Test weight (g), HI: Harvest index (%), GYP: Grain yield per plant (g)

*** 1% Level of Significance *5% Level of Significance*

Table 5. Index scores and signs used for characters for metroglyph analysis of 20 genotypes of rice

Character	Range of Mean	Score 1	Sign	Score 2	Sign	Score 3	Sign
		Value <		Value from - to		Value >	
DFF	81-121.73	99.16	○	99.16-120.42		120.42	
DM	104.47-147.73	125.38	○	125.38-145.5		145.50	
PH	104.64-162.07	109.72	○	109.72-146.29		146.29	
FLL	28.72-51.99	30.73	○	30.73-43.05		43.05	
FLW	0.86-1.8	0.96	○	0.96-1.4		1.40	
NTT	7.33-15.6	7.08	○	7.08-11.3		11.30	
NPT	7.33-15.73	7.07	○	7.07-11.33		11.33	
PL	22.09-34.89	23.03	○	23.03-30.33		30.33	
BY	47.67-95.4	50.21	○	50.21-77.03		77.03	
HI	40.46-59.69	43.71	○	43.71-56.9		56.90	
NSP	63.13-309.33	116.02	○	116.02-259.06		259.06	
TW	14-30	15.37	○	15.37-24.48		24.48	
GYP	22.67-47.44	24.93	○	24.93-38	○	38.00	○

Table 6. Genotypes in different complex in metroglyph analysis

Complex	Name of complex	No. of lines	Name of lines	Range and average score
I	High number of spikelets per plant with moderate plant height	11	BPT -1768, BPT-204, BPT -74, MTU-7029, NP9558, BPT -01, BPT-02, KNM -118, MTU-1271, NLR and NDR-359 (Check)	24.00-29.00 (26.36)
II	Low number of spikelets per plant with higher plant height	5	Dhan sharabathi, Dhan Pusa, Dhan-1718, Dhan1121 and Basmathi CSR 30	23.00-28.00 (26.20)
III	Moderate number of spikelets per plant with moderate plant height	2	Dhan Moti and RGL -2332	24.00-28.00 (26.00)
IV	High number of spikelets per plant with moderate plant height	1	Dhan-1509	25
V	Low number of spikelets per plant with shorter plant height	1	SHIVA-555	30

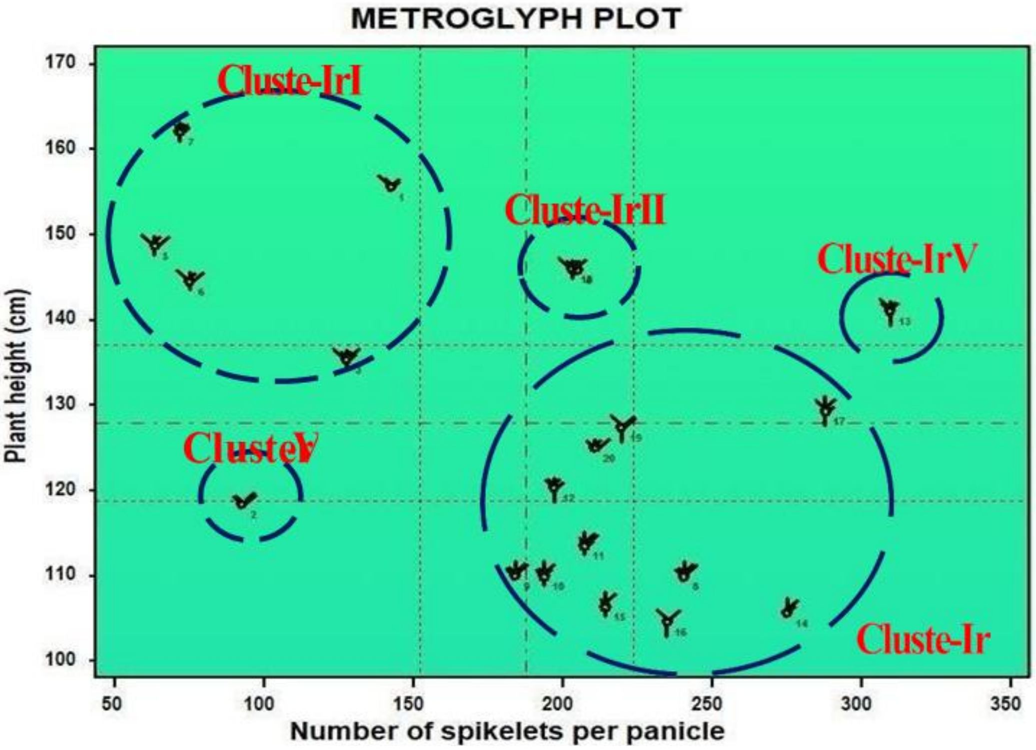

Fig. 2. Scattered diagram of Metroglyph analysis showing 20 genotypes of rice

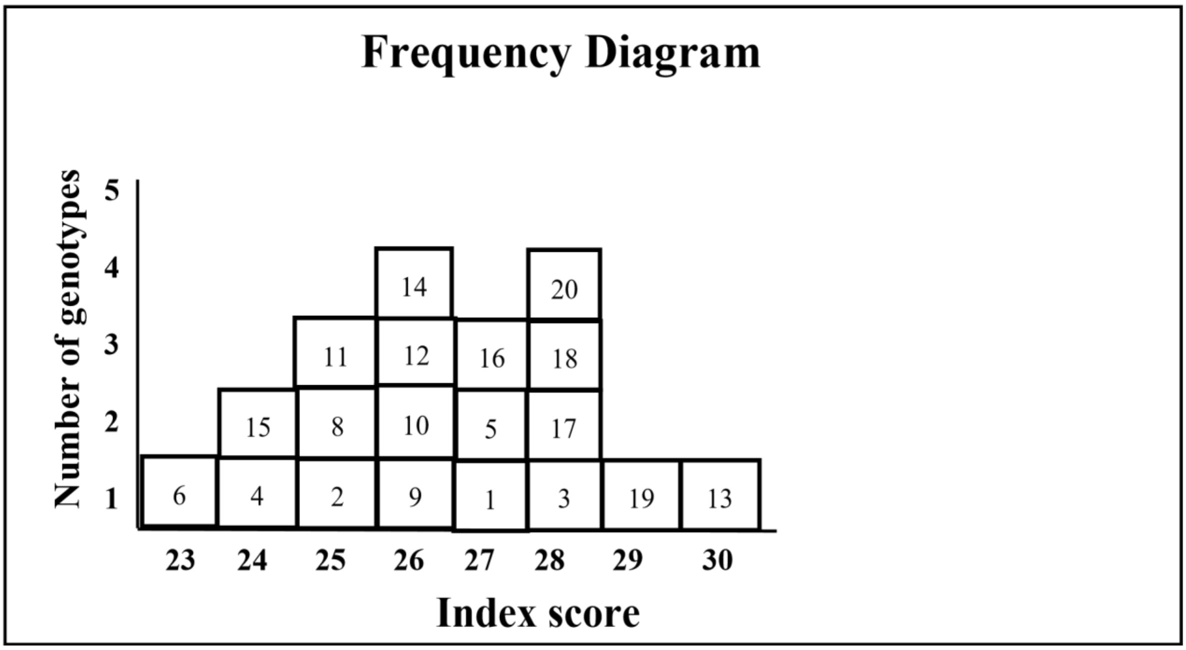

Fig. 3. Metroglyph frequency diagram showing 20 genotypes of rice

- Among 20 genotypes, genotype NLR(47.44gm), KNM-118(43.67gm), SHIVA-555 (39.74gm), MTU-1271 (38.42gm), UNNAO DHAN PUSA(34.56gm) were found to be superior in grain yield.
- In the present study Phenotypic Coefficient of Variation (PCV) were higher

than Genotypic Coefficient Variation (GCV) indicating that these characters are influenced by the environment for all the characters.

- The variability is classified as low if coefficient of variation (<10%), moderate (10-20%) and high (>20%) by Siva Subramanian and Menon (1973).
- GCV (%) values ranged between least of 6.029 (Days to maturity) to a highest value of 37.734 (Number of spikelet's per panicle) PCV (%) followed a similar pattern had a range of 9.633 (Days to maturity) to a highest value of 38.926 (Number of spikelet's per panicle).

Heritability: The present investigation, all traits showed the high heritability ranging from 39.174% to 93.969%. No of spikelet's per plant(93.969%) showed the highest heritability among all the characters followed by No of total tillers (92.719%), Test weight (91.344) and No of productive tillers (90.123%). Moderate range heritability showed by Days to maturity (39.175%) and low range heritability has not observed among these characters.

The high heritability values of the considered traits in the present study indicated that those were less influenced by the environment and thus help in effective selection of the traits based on the phenotypic expression by adopting simple selection method and suggested the scope of genetic improvement.

Genetic advance as a percentage mean: The estimation of genetic advance as percent mean is classified as low (<10%), moderate (10 to 20%) and high (>20%) proposed by Johnson *et* al., (1955).

In the present investigation all the characters showed highest genetic advance as a percentage of mean present in No of Spikelet per Panicle (75.31), No of Total Tillers (44.951), No of Productive Tillers (44.45), Test Weight (44.317), Grain Yield per Plant(39.867), Biological Yield (39.329), Flag Leaf Width(35.052), Flag Leaf Length(31.797), Plant Height (24.691), Panicle Length (23.641), Harvest Index (23.012).

Moderate genetic advance as a percent of mean was observed in Days to Fifty percent Flowering (13.381).

Low genetic advance as a percent of mean was observed in Days To Maturity (7.774).

Correlation analysis: Correlation analysis among the yield and its contributing characters revealed that the genotypic correlation coefficients in most cases were higher than their phenotypic correlation coefficients indicating the association was largely due to genetic reason. At both genotypic and phenotypic levels, significant positive correlations were observed for Number of spikelet's per panicle, Test Weight ,Grain Yield per Plant, Number of Total Tillers, Number of Productive Tillers, Panicle Length, Days to Maturity.

Metroglphy analysis: The scatter diagram revealed that five complexes could be distinguished on the basis of morphological variation. Complex-I was represented by 11 genotypes with High number of spikelet's per plant with moderate plant height.

Complex-II was represented by 5 genotypes with Low number of spikelet's per plant with higher plant height.

Complex-III was represented by 2 genotypes Moderate number of spikelet's per plant with moderate plant height.

Complex-IV was represented by 1 genotype with High number of spikelet's per plant with moderate plant height.

Complex-V was represented by 1 genotype with Low number of spikelet's per plant with shorter plant height.

The index scores and signs used for 13 characters for metroglyph analysis were presented in Table 5. It was observed that maximum variability was in number of spikelet's per plant (63.13309.33) followed by plant height (104.64-162.07).

The mean performance and total index score of 20 genotypes are presented in Table 6. The total index score was varied from 23 (UNNAO DHAN-1121) to 30 (SHIVA-555).

The frequency diagram revealed that the index scores ranged from 23-30. maximum frequency of genotypes 4 occurred for index score of 26and 28 followed by minimum frequency of genotypes 1 occurred for index score of 23, 29 and 30. Highest index score of 30 recorded by only one line (SHIVA-555) followed by index score of 29, 28 and 27 by 1, 4, and 3 lines.

4. CONCLUSION

This study evaluated the genetic variability parameters for yield and its contributing factors in rice genotypes. Genetic variability is the foremost important breeding tool in order to break yield stagnation and developing high yielding varieties. The study of correlations may aid plant breeders in understanding how improving one feature leads to improvements in other characters.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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