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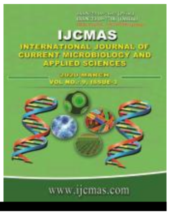

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Assessment of Genetic Variability for Yield and Yield Attributing Traits in F_2 Population of Intervarietal Cross in Rice (*Oryza sativa* L.)

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ABSTRACT

The present investigation was assessed using 100 F_2 individuals, their parents and F_1 for characters days to flowering, plant height, panicle length, productive tillers per plant, number of grains per panicle, grain yield per plant, straw yield per plant and harvest index. These traits are most important for identification of good segregating plants or genotype. Here, in the present study F_2 population was developed from the cross between GAR-13 (improved and high yielding cultivar) and Lalkada (local landrace). Regarding the population distribution analysis, only number of grains per panicle and straw yield per plant was showed normal distribution in segregating population while other characters did not show normal distribution in the population. Productive tillers per plant, grain yield per plant and harvest index considered to be governed by complimentary gene interaction and days to flowering, plant height and panicle length was governed by duplicate gene interaction.

Keywords

Rice, Population distribution, normal distribution, gene interection, skewness and kurtosis

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Introduction

Rice (*Oryza sativa* L., 2n=24) belongs to family *Poaceae*and subfamily *Oryzoidae*. It is believed to be originated in South-East Asia. It is the world's most important cereal crop and is the primary source of food and calories for about half of the mankind (Khush, 2005).Rice is life and princess among the *cereals***,** the staple food of 65 per cent of the total population in India. Asia is considered to be "rice bowl" of the world and it produces and consumes more than 90 per cent of world rice.

India is the largest rice growing country, whereas China is the largest producer of rice. Rice constitutes about 42 per cent of the total food grain production and 45 per cent of total cereal production of our country. In India, rice is cultivated in 43.99 million hectares with production of 109.69 million tones and productivity of 2494 kg per hectare (Anon., 2018a). The cultivated area of rice in Gujarat is 8.05 lakh hectares and production is 17.62 lakh tones with productivity of 2189 kg per hectare (Anon., 2018b).

Mean serves as a basis for eliminating undesirable crosses (Shoba *et al.,* 2012). An insight into the nature and degree of distribution present in population is of utmost importance as it forms the basis for selection in any crop improvement programme (Prabhu *et al.,* 2015).The present study was aimed at studying the genetics of different traits, association with yield and its component traits using first, third and fourth degree statistics in segregating generations of rice.

Materials and Methods

Development of F_2 population

Two cultivated varieties namely GAR-13 and Lalkadaare found diverse as one is improved and well adopted cultivar and latter is local landrace, were selected as parents. The cross was made during *kharif*-2017 to obtain F_1. The F_1 hybrid seeds were sown in the field and subsequently F_2 seeds were harvested from the respective plants during the year summer-2018 and F_2 population was evaluated in *kharif*-2018 at Regional Rice Research Station, NAU, Vyara.

Morphological characters

The observations on morphological characters were taken from ten plants each of GAR-13, Lalkada and F_1, whereas 100 F_2 plants were observed individually for days to flowering, plant height, panicle length, productive tillers per plant, number of grains per panicle, grain yield per plant, straw yield per plant and harvest index.

Statistical analysis

Frequency distribution of the segregating generation was tested for normality by the Shapiro-Wilk, Kormogorov-siminrnov and Anderson Darling tests using R software Ri386 3.6.1. Mean, variance and standard deviation were calculated using Excel Programme.

Skewness (third degree statistics) and kurtosis (fourth degree statistics) were estimated to understand the nature of distribution of different traits (Patel *et al.,* 2018). For the normal distribution skewness is about to zero in the absence of any gene interaction. It is greater and smaller than zero in the presence of average complementary and duplicate interactions, respectively.

Also, gene interactions can be detected by studying the fourth-degree statistics, kurtosis. Which is always negative or zero in the absence of gene interaction and is positive only in the presence of gene interaction.

Frequency distribution for each trait was considered significantly deviates from zero at the 0.05 probability level if that value was greater than twice of its standard error. Skewness and kurtosis and its standard error was calculated using R software Ri386 3.6.1.

Results and Discussion

Development of F_2 population

The two parents used in the study were GAR-13 (developed at AAU, Anand) and Lalkada (Local landrace) maintained at RRRS, NAU, Vyara. GAR-13 is an improved and released variety of rice and Lalkada is a local landrace. Grain colour of Lalkada was red due to good iron and zinc content but due to its tall height severe problem of lodging is faced by farmers at maturity. From F_2 seeds, 100 plants were grown along with parents and F_1 during *kharif*-2018. The phenotypic data from 100 plants were used for further analysis.

Phenotyping of F_2 population

The mean, range and variance of F_2 population of GAR-13× Lalkada is given in table 1. To test the goodness of fit for various characters of F_2 segregating population, there were three tests carried out likeShapiro-Wilk, Kormogorov-siminrnovand Anderson Darling tests. Their results are presented in table 2.

Here, three population fitting tests were carried out for all eight characters using R software among them character days to flowering and plant height were found significant to its p value in all three test. While, panicle length, productive tillers per plant, grain yield per plant, straw yield per plant and harvest index were significant to its p value in Shapiro-Wilk and Anderson Darling tests. In Kormogorov-siminrnov test all traits show non-significant p value except days to flowering and plant height. In this experiment, according to population distribution fitting test, this population is normally distributed for number of grains per panicle and straw yield per plant whiledays to flowering, plant height, panicle length, productive tillers per plant, grain yield per plant and harvest indexwere not segregate normally because of their association with other genes. To find out that gene action we were used the third and fourth degree statistics.

Skewness and kurtosis analysis

Quantitative characters show discrete variation in the population. They are also known as the matric characters. Their distribution study gives the idea and nature of gene action and number of genes controlling the traits using skewness and kurtosis, respectively. In the present study, skewness and kurtosis were calculated for days to flowering, plant height, panicle length, productive tillers per plant, grain yield per plant and harvest index.

Skewness for days to flowering was -0.5919 and kurtosis was 2.8317, for plant height skewness was observe as -2.5801 and kurtosis was 15.3118,skewness for panicle length was recorded as -0.1049 and kurtosis was 2.4857 while, skewness for productive tillers per plant, grain yield per plant and harvest index was 0.7120, 2.2682 and 0.4087, respectively. Kurtosis for productive tillers per plant, grain yield per plant and harvest index was 3.6675, 10.7729 and 2.1897, respectively. Days to flowering showed mesokurtic withnegative skewness. plant height and panicle length showed leptokurtic with negative skewness. While, productive tillers per plant and harvest index showed leptokurtic distribution with slightly positive skewness and grain yield per plant showed leptokurtic with positive skewness in the population.

On the basis of above results, productive tillers per plant, grain yield per plant and harvest index considered to be governed by complimentary gene interaction with presence of large number of minor genes with increasing effect. Days to flowering, plant height and panicle length was governed by duplicate gene interaction with increasing gene effect with dominant property. These results were found in accordance with Nachimuthu *et al.*, (2014). They reported that number of productive tillers per plant showed positive skewness and Negative skewness and leptokurtic distribution for plant height and panicle length. According to them, selection was rapid under mild selection from existing variability found among the F_2 population of Rice.

Table.1 Mean, range, variance skewness and kurtosis of F_2 population of GAR-13 × Lalkada

Mean±Standard Error					Range	Variance	Skewness	Kurtosis
Trait	GAR 13	Lalkada	F_1	F_2	F_2	F_2	F_2	**F_2**
DF	100.3±0.33	89±0.28	98.1±0.34	86.36±0.33	78-93	10.68	-0.5919	**2.8317**
PH	112.6±0.52	149.5±0.58	147.96±0.7	137.81±1.6	99-165	255.89	-2.5801	**15.3118**
PL	22.44 ±0.23	21.75±0.51	19.5±0.53	21.54±0.38	12-30	14.80	-0.1049	**2.4857**
PTP	8.2±0.29	11.1±0.42	8.4±0.28	8.31±0.29	3-17	8.42	0.7120	**3.6675**
NGP	164.8±0.33	107.3±0.32	177.3±0.46	113.15±1.13	86-142	128.45	0.1710	**2.7489**
GYP	17.63±0.64	17.19±0.44	15.45±0.95	14.95±0.62	7.7-47.3	38.71	2.2682	**10.7729**
SYP	19.84±0.50	28.73±0.85	17.7±1.00	30.34±1.02	9-60	104.75	0.3497	**2.7232**
HI	**147.05±0.41**	**37.53±0.75**	**46.5±0.53**	**33.35±0.81**	**20-51.94**	**65.87**	**0.4087**	**2.1897**

DF= Days to flowering, PH= Plant height (cm), PL= Panicle length (cm), NGP= No. of grains per panicle, GYP= Grain yield per plant (g), SYP=Straw yield per plant (g), HI=Harvest index (%)

Table.2 Shapiro-Wilk, Kormogorov-siminrnov Z-statistics, Cramer-Von Mises and Anderson Darling tests and their statistical values

Trait	**Shapiro-Wilk**		**Kormogorov-siminrnov**		**Anderson Darling**	
	Statistics	**p value**	**Statistics**	**p value**	**Statistics**	**p value**
Days to flowering	0.9533*	0.0014	0.1476*	0.0256	1.5098*	**0.0004**
Plant height (cm)	0.8032*	0.0001	0.1681*	0.0070	3.3820*	**0.0001**
Panicle length (cm)	0.9841*	0.2717	0.0791^{ns}	0.5584	0.5405*	**0.1616**
Productive tillers per plant	0.9555*	0.0019	0.1222^{ns}	0.1008	1.1900*	**0.0040**
No. of grains per panicle	0.9890^{ns}	0.5879	0.0628^{ns}	0.8253	0.3898^{ns}	**0.3769**
Grain yield per plant (g)	0.8125*	0.0001	0.1273^{ns}	0.0782	3.6754*	**0.0001**
Straw yield per plant (g)	0.9848*	0.3093	0.0637^{ns}	0.8112	0.4201^{ns}	**0.3195**
Harvest index (%)	**0.9573***	**0.0026**	**0.0914^{ns}**	**0.3731**	**1.1687***	**0.0045**

DF= Days to flowering, PH= Plant height (cm), PL= Panicle length (cm), NGP= No. of grains per panicle, GYP= Grain yield per plant (g), SYP=Straw yield per plant (g), HI=Harvest index (%),*: significant, ns: nonsignificant

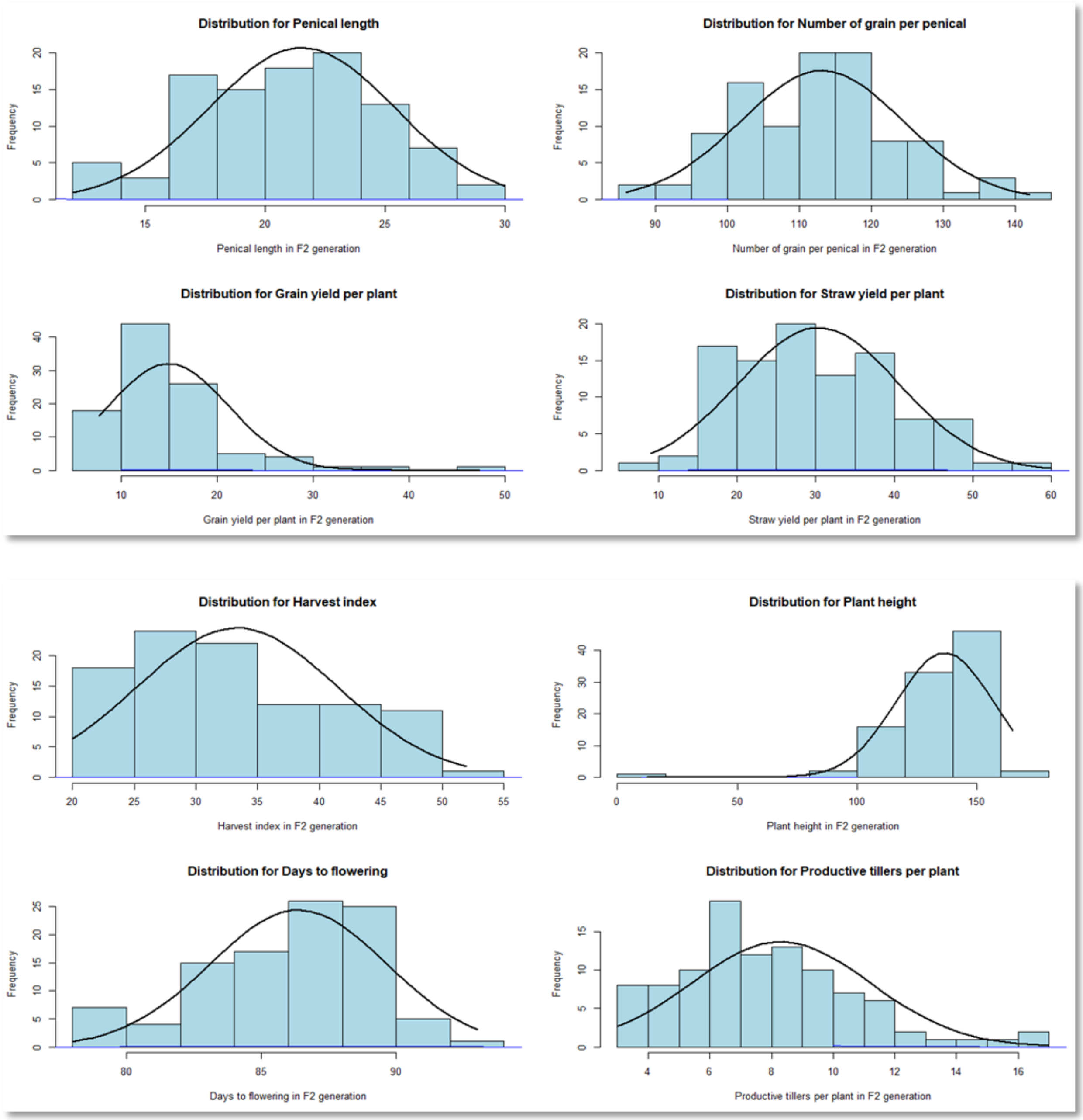

Fig.1 Distribution pattern of various characters in F_2 segregating generation of rice

In conclusion distribution study of matric characters in segregating generation gave the idea and nature of gene action and number of genes controlling the traits using skewness and kurtosis, respectively. Skewness for days to flowering was -0.5919 and kurtosis was 2.8317, for plant height skewness was observe as -2.5801 and kurtosis was 15.3118, skewness for panicle length was recorded as -0.1049 and kurtosis was 2.4857 while, skewness for productive tillers per plant, grain yield per plant and harvest index was 0.7120, 2.2682 and 0.4087, respectively. Kurtosis for productive tillers per plant, grain yield per plant and harvest index was 3.6675, 10.7729 and 2.1897, respectively. Days to flowering showed mesokurtic with negative skewness. plant height and panicle length showed leptokurtic with negative skewness. While, productive tillers per plant and harvest index showed leptokurtic distribution with slightly positive skewness and grain yield per plant showed leptokurtic with positive skewness in the population. Productive tillers per plant, grain yield per plant and harvest index considered to be governed by complimentary gene interaction and days to flowering, plant height and panicle length was governed by duplicate gene interaction.

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