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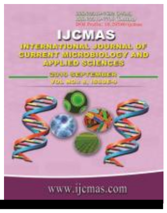

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Estimation of Genetic Parameters for Yield and Related Traits in Advanced Recombinant Lines of Kalanamak Rice (*Oryza sativa* L.)

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ABSTRACT

Keywords

Kalanamakrice, Variability, Heritability, Genetic Advance, GAM, RCBD

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The present investigation was undertaken with the objectives to assess variability, heritability, genetic advance and genetic advance as percentage of mean (GAM)in 11 advanced recombinant lines of *Kalanamak* rice for fifteen quantitative traits. Trials were conducted for two seasons during wet season of 2016 and 2017 at Norman E. Borlaug Crop Research Centre (NEBCRC), G. B. Pant University of Agriculture and Technology (GBPUAT), Pantnagar, Uttarakhand in a Randomized Complete Block Design (RCBD) with three replications with the spacing of 20 cm × 15 cm and the recommended cultural practices were followed. The data were analyzed for using OPSTAT statistical software. Over the year high GCV and PCV was observed fortest weight (23.36 g and23.82 g) and grain yield (21.28 g and 21.88 g). Highest heritability was observed for weight of 1000 grains (96.02%) while lowest heritability was observed for days to maturity (27. 34%). Genetic advance as percentage of mean was observed highest for test weight(47.20 %) and lowest for days to maturity (1.01%). High heritability coupled with high genetic advance as percentage of mean was observed for test weight(96.20%& 47.21%) followed by stem thickness (95.36%& 24.60%) and yield (94.55%& 42.62%) indicating their usefulness in indirect selection to improve yield.

Introduction

Rice *(Oryza sativa* L.*)*caters to the dietary need ofalmost half of the global population (CGIAR, 2012).It is the staple food in Asiaticregion whereabout 90% of global rice is produced and about 75% thereof is consumed. Globally, it is cultivated over an estimated area of 160.10 million hectares producing about 483.80 million tons of grains(USDA,2017). In India, rice is cultivated over an area of 43.38 million hectares producing 104.32 million tons of grains with an average productivity of 2404 kg/ha (DAC&FWAnnual report,2015-2016).Basmati and Non- Basmati aromatic rice has played a significant role in boosting rice economy through earning foreign exchange. Among the aromatic varieties *Kalanamak* is one of the finest quality rice cultivated in India.It derives its name from black husk of kernel (*Kala*) and its ability to successfully adapt in*usar* soils characterized by high salt concentration and high pH and/or having a distinctive salty taste (*Namak*). Except for grain length, *Kalanamak* rice outshines even the most demanded Basmati rice in rest of the quality parameters. But, the *Kalanamak* rice succumbs to various biotic and abiotic stresses. Hence, there is an imperative need to develop improved genotypes that can withstand these stresses. Towards this end it is desirable to study genetic variability, heritability and genetic advance for seed yield and yield contributing traits that will further assist in breeding improved rice genotypes with high yield potential coupled with multiple resistances biotic and abiotic stresses.

For selecting such improved genotypes from diverse genetic stock a clear understanding and scientific knowledge on existing variability, heritability and the expected genetic advance is necessary. Therefore, the present study was conducted with the aim to estimate variability and other relevant genetic parameters for yield and yield contributing traits so that the information gained can further be applied in genetic improvement of *Kalanamak* rice.

Materials and Methods

The present investigation was conducted on eleven *Kalanamak* Advanced Recombinant Lines of rice along with the reference variety Pant Sugandh Dhan 17.

The entries were evaluated in Randomized Complete Block Design (RCBD) with three replications at NEBCRC, GBPUAT, Pantnagar, Uttarakhand, during wet season of 2016 and 2017. The recommended packages of agronomic practices were followed throughout the crop growth period.

Sampling and observed traits

Data were scored for measureable traits following DUS guidelines. Flag leaf length and flag leaf width from penultimate row was measured on 10 plants at booting stage. Stem thickness was measured on same 10 plants at milk development stage. Data for stem length and panicle length of main axis was recorded at milk development stage. Panicles per plant were counted on 10 plants at dough development stage. 1000 fully developed and matured grains from composite sample of each entry were weighed using electronic balance at hard caryopsis stage to record weight of 1000 grains. Grain length and kernel length were recorded by placing 10 grains length wise and width wise just adjacent to one another, respectively, on graph paper and measuring the distance between first and last grain and kernel. The procedure defined by (Juliano, 1971) was used to determine the content of amylose in endosperm. The mean values computed from the observations for each replication were used for statistical analysis.

Biometrical analysis

The pooled data over two years for various traits were analyzed. The partitioning of the total variance assignable to different sources viz.Genotypic coefficients of variation (GCV) and Phenotypiccoefficients of variation (PCV) (Burton, 1952), heritability (broad sense), genetic advance and expected genetic advance as percent of mean(Allard,1960). The GCV and PCV values were ranked as low, medium and high (Sivasubramanian and Menon, 1973). Heritability in broad sense was categorized as low, moderate and high (Robinson *et al.*, 1949). Genetic advance as percentage of mean was categorized as low moderate and high as given by (Johnson *et al.*,1955).

Results and Discussion

Analysis of Variance (ANOVA)

The analysis of variance (ANOVA) showed that sufficient genetic variability exists for all the studied traits (Table 1) providing opportunity to alter the trait in desirable direction through selection. Phenotypic Coefficient of Variations (PCV) was slightly higher than Genotypic Coefficient of Variation (GCV) for all the studied traits, indicating that the traits were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits. Over the year 2016 and 2017high GCV and PCV was observed for weight of 1000 grains (23.36&23.82) and grain yield (21.28&21.88). medium GCV and PCV was observed for length of leaf blade (14.32 &15.38), width of leaf blade (19.42&20.49), stem thickness (12.23 &12.53) and number of panicle per plant (11.14 &12.25) and low GCV and PCV was observed for time of heading (2.24 &3.25), stem length (6.83 &7.02), panicle length (9.26 &9.50), days to maturity (0.94 &1.80), grain length (4.52 &5.65), grain width (5.38 &6.71), decorticated grain length (8.11 & 8.95), decorticated grain width (8.76 &9.55) and amylase content (3.08 &3.29). Genotypic coefficient of variation provides information on the extent of genetic variability present in any quantitative trait but it, solely, can not predict the heritability of trait. Heritability measures the fraction of phenotype variability that can be attributed to genetic variation. Therefore, high heritability helps in effective selection for a particular character. Heritability in broad sense [$h^2_{(bs)}$]calculated for various traits are presented in Table 2.Highest heritability was observed for weight of 1000 fully developed kernel (96.02%) followed by stem thickness (95.37%), panicle length (95.16%), stem length (94.63%), grain yield (94.55), width of leaf blade (89.82%), amylose content (87.93%),length of leaf blade (86.71%), decorticated grain width (84.10%), panicle number plant^{-1} (82.75 %), decorticated grain length (81.99%), grain width (64.42%) and grain length (63.89%). 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. Based upon variability and heritability estimates, it could be concluded that improvement by direct selection in rice is possible for traits like weight of 1000 fully developed kernel, stem thickness, panicle length, stem length, grain yield, width of leaf blade, amylose content, length of leaf blade, decorticated grain width, panicle number per plant, decorticated grain length, grain width and grain length. Moderate heritability was observed for time of heading (47.31%) while the low heritability was observed for time of maturity (27. 34%).Selection for low heritable traits is not effective.

Genetic advance is the mean genotypic improvement of selected individuals over the parental population. The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population (Vanniarajan *et al.*, 1996). High heritability with high genetic advance considered together should be used in predicting the ultimate effect of selecting superior varieties (Ali *et al.*, 2002).Highest genetic advance as percentage of mean was observed for weight of 1000 fully developed kernels (47.20 %) followed by yield (42.61%), width of leaf blade (37.90%), length of leaf blade (27.46%), stem thickness (24.50%) and panicle number plant^{-1} (20.88%).Moderate genetic advance as percentage of mean was observed for panicle length (18.61), decorticated grain width (16.54%), decorticated grain length (15.11%) and stem length (13.68%).Low genetic advance as percentage of mean was observed for grain width (8.90%), grain length (7.44%), amylose content (5.95%), and time of heading (3.16%) and lowest genetic advance as percentage of mean was observed for days to maturity (1.01%).

Table.1 ANOVA, Genotypic and Phenotypic variance for different traits in Kalanamak Rice

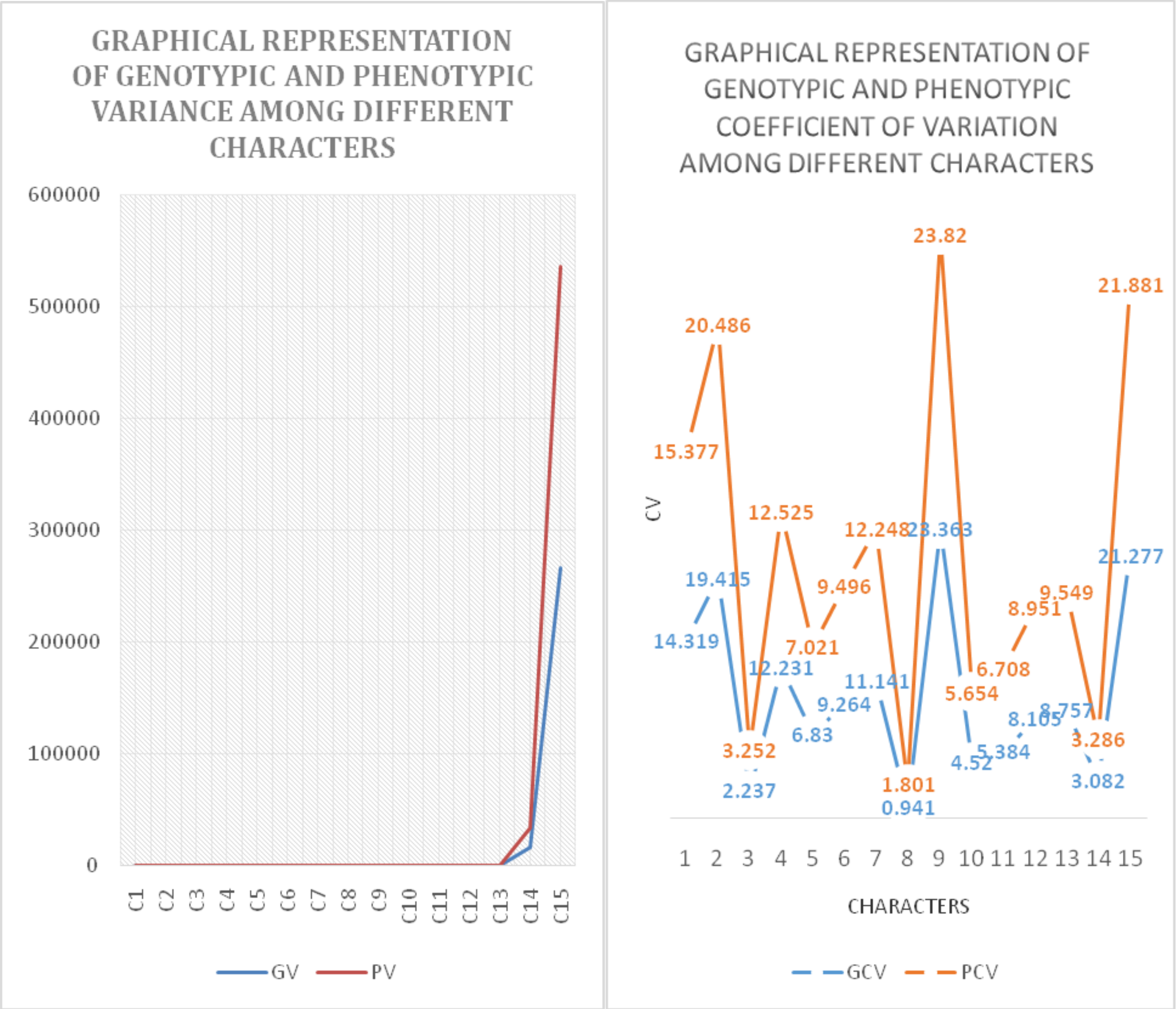
S.No.		**Mean sum of squares**			**Genotypic variance**	**Phenotypic variance**
		Replication	Treatment	Error		
	Character df	2	11	22		
1	Leaf: Length of blade (cm)	1.44	63.36**	3.08	20.09	23.17
2	Leaf: Width of blade(cm)	0.00	0.14**	0.01	0.05	0.05
3	Time of 50 % heading (days)	14.78	42.71**	11.57	10.38	21.95
4	Stem thickness (cm)	0.01	0.26**	0.00	0.09	0.09
5	Stem length of main stem (cm)	6.86	235.86**	4.38	77.16	81.54
6	Panicle: Length of main axis (cm)	1.00*	16.36**	0.27	5.36	5.64
7	Panicle: Number per plant	1.36*	4.62**	0.30	1.44	1.74
8	Time of maturity (days)	18.08	15.40	7.24	2.72	9.96
9	Test weight(g)	1.14	31.24**	0.41	10.28	10.68
10	Grain: Length (mm)	0.00	0.00**	0.00	0.00	0.00
11	Grain: Width (mm)	0.00	0.00	0.00	0.00	0.00
12	Decorticated grain: Length (mm)	0.00	0.01**	0.00	0.00	0.00
13	Decorticated grain: Width (mm)	0.00	0.00	0.00	0.00	0.00
14	Endosperm: amylose content	7974.52**	50584.57**	953.07	16543.83	17496.91
15	Yield (g/6m^2)	1.44	63.36**	3.08	266549.40	269325.50

*, **: Significant at 5% and 1% probability levels, respectively

Table.2 Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), Heritability (h^2),genetic advance (GA) and Genetic Advance as (%) of means (GAM)for different traits in Kalanamak Rice.

Characters	Genotypic Coefficient of Variation (GCV)	Phenotypic Coefficient of Variation (PCV)	Heritability (%)	Genetic Advance (GA)	Genetic Advance as (%) of Means
Leaf: Length of blade (cm)	14.32	15.38	86.71	8.60	27.47
Leaf: Width of blade(cm)	19.42	20.49	89.82	0.42	37.90
Time of 50 % heading (days)	2.24	3.25	47.31	4.57	3.17
Stem thickness (cm)	12.23	12.53	95.37	0.60	24.61
Stem length of main stem (cm)	6.83	7.02	94.63	17.60	13.69
Panicle: Length of main axis (cm)	9.26	9.50	95.16	4.65	18.62
Panicle: Number per plant	11.14	12.25	82.75	2.25	20.88
Time of maturity (days)	0.94	1.80	27.34	1.78	1.01
Test weight (g)	23.36	23.82	96.20	6.48	47.21
Grain: Length (mm)	4.52	5.65	63.90	0.06	7.44
Grain: Width (mm)	5.38	6.71	64.42	0.02	8.90
Decorticated grain: Length (mm)	8.11	8.95	82.00	0.07	15.12
Decorticated grain: Width (mm)	8.76	9.55	84.10	0.03	16.54
Endosperm: Content of amylose	3.08	3.29	87.93	1.25	5.95
Yield (g/6m^2)	21.28	21.88	94.55	257.65	42.62

Fig.1



High heritability coupled with high genetic advance as percentage of mean was observed for weight of 1000 grains(96.20 & 47.21),stem thickness (95.36 & 24.60), yield (94.55 & 42.62),flag leaf width (89.81 & 37.40), flag leaf length (85.70 & 27.46) and panicles per plant (82.75 & 20.87).This suggests for rapid improvement in the character due to selection and these characters can be further improved by following simple selection procedure. This also suggests that these traits were controlled by additive type of gene action in the inheritance of these characters, the low estimates of genetic advance as percent of mean for time of heading with 50% panicles (3.16) and days to maturity (1.01) indicated the presence of non-additive gene effects, in addition to influence of environment to some extent. Similar result was reported by (Prasad *et al.*,2017). These traits can be improved by intermating superior genotypes from segregating population developed from combination breeding.

The salient findings of the present study

Pooled analysis of variance for measurable characters showed significant variation among genotypes for all the traits under study. Grains per panicle and plant height exhibited highest genotypic and phenotypic variances, followed by spikelet fertility and days to 50% flowering.

The insignificant difference between PCV and GCV indicate that the environment has very less role in inheritance of these characters.

Highest heritability was exhibited for all the traits except time to maturity and time to 50 % heading.

Highest genetic advance as percentage of mean was observed for weight of 1000 fully developed kernels followed by yield, width of leaf blade, length of leaf blade, stem thickness and panicle number per plant.

High heritability coupled with high genetic advance as percentage of mean was observed for 1000 fully developed kernels, yield, width of leaf blade, length of leaf blade, stem thickness and panicle number per plant.

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