

Genetic Parameters for Yield and Quality Traits in New Plant Type Lines of Rice

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Abstract

The present investigation was undertaken to study the variability and genetic parameters in NPT lines derived from indica X japonica Sub species of rice for yield and quality traits. Analysis of variance indicated variation is present in the observed characters of NPT lines as the mean sum of squares due to genotype was significant for all the characters. High PCV and GCV were found for characters viz., number of productive tillers, harvest index, spikelet density, filled spikelet, panicle weight, and biological yield per plant. High heritability coupled with high GA as percent of mean was observed for characters viz., Biological yield per plant, filled spikelet, spikelet fertility, panicle index, panicle weight, grain yield, total spikelet, harvest index, and spikelet density which indicates that the additive gene has the major role in the expression of these characters and can be further used for the crop improvement by selecting such characters

Key Words: GA; GCV; Heritability; NPT lines; PCV and Variability

Introduction

Rice is the staple food for more than 50% world population and 85% Indian population. In India it is cultivated in an area of 45.54 million hectares with a production of 99.18 million tones and productivity of 2177kg ha⁻¹ (Singh et al., 2014).

In India it is a staple food and it becomes necessary to improve its yield so that it can be fed

to the increasing population. The top most priority of any breeding program is to enhance the yield. Results have indicated that an effective way to develop super rice lines first is developing the new plant type and strong vigor by crossing *indica* with *japonica* subspecies, and then consolidating the advantages by optimizing the combination of desirable traits via multiple crossing and backcrossing (Chang et al. 2001).

In rice first generation New Plant Type (NPT) was having low tillering capacity with few unproductive tillers, sturdy stems, erect leaves, a vigorous root system and increased harvest index (Peng et al. 1994). Breeders at IRRRI had adopted a different ideotype, known as new plant type (NPT), which has increased the yield potential of direct-seeded, irrigated crop. The chief characteristics of this new ideotype which have been derived from a number of physiological considerations (Vergara, 1988) are that plants should produce 3-4 tillers, all of which produce panicles containing 200-250 grains on a very sturdy stems, should bear dark green and erect leaves. It should be 90cm in height and of 100-130 days growth duration; and should have multiple disease and insect resistance, with harvest index of 0.6. The favorable alleles for yield and yield contributing traits are distributed among two subspecies i.e., *indica* and *japonica* of cultivated rice.

Thus, when we can go and use inter sub-specific *indica* x *japonica* diversity for the architecture of New Plant Type and utilize

pedigree breeding, for breaking genetic ceiling to yield in rice.

Materials Required

The experimental material under the investigation consisted of 65 NPT lines grown in randomized complete block design in three replication during kharif 2013 at Seed Breeding Farm, JNKVV, Jabalpur. Twenty one day old seedlings were transplanted in the experimental site with the spacing 20 cm between plant to plant and 15 cm between rows to rows. The fertilizer dose used were 120 kg N, 60 kg P₂O₅, and 60 kg K₂O were applied. Entire dose of P₂O₅ and K₂O along with half dose of N was applied as basal dose at the time of field preparation, remaining amount of nitrogen was split in two equal splits and were applied at the time of active filling stage. The standard agronomic practices were adopted for normal growth. Randomly ten plants were selected for taking the observation and statistical procedures were applied to find out the genetic parameters.

Results and Discussions

Analysis of variance indicated variation is present in the observed characters of NPT lines as the mean sum of squares due to genotype was significant for all the characters {Table 1(1.1-1.4)}. High PCV and GCV were found for characters viz., number of productive tillers, harvest index, unfilled spikelet, spikelet density, seed yield, total spikelet, number of tillers, filled spikelet, panicle weight, and biological yield per plant (Table 2).

This was in conformity with Nayak et al. (2002), Tiwari et al. (2011), Selvaraj et al. (2011) for grain yield per plant, number of productive tillers and number of tillers. Biological yield per plant, total spikelet, filled spikelet, spikelet density and grain yield recorded a high PCV and GCV and it was in agreement with the findings of Sharma (2013). Moderate GCV and PCV were observed for characters viz., panicle index, seed length, flag

leaf length, seed width, L/B ratio, decorticated seed breadth, flag leaf width, spikelet fertility, 1000 grain weight, plant height, culm length, panicle length. Plant height recorded a moderate value of genotypic and phenotypic coefficient of variation. This result was not in agreement with the findings reported by Tiwari et al. (2011) and Khan (2012). Low GCV and PCV were found for characters like decorticated seed length, hulling %, milling % and days to 50% flowering. All quality related traits in present investigation recorded low value of GCV and PCV. The result was in confirmation with Bhaskar (2006), whereas not in confirmation for grain length and grain breadth with the findings of Chand et al. (2004) and Saxena et al. (2005) for L/B ratio.

Table 1(1.1): Analysis of variance for quantitative traits of rice (NPT) lines

S. No.	Source of variation	d.f.	Mean sum of squares								
			TS	FS	US	SL	SW	NOT	NOPT	PH	CH
1.	Replication	2	128.84	1.300	3.42	0.01	.002	4.94	9.60	1.03	1.02
2.	Genotypes	64	12552.94**	10990.35**	1839.67**	0.31**	.0029**	6.03**	6.95**	645.72**	588.61**
3.	Error	128	205.96	2.260	3.04	0.004	.0002	2.09	1.43	2.29	3.08

Table 1(1.2)

S. No.	Source of variation	d.f.	Mean sum of squares									
			FLL	FLW	PL	PW	TWG	SF	BYP	PI	HI	SD
1.	Replication	2	0.91	0.09	4.08	2.81	0.01	11.16	1.87	4.11	1.28	0.34
2.	Genotypes	64	163.23**	22.18**	25.79**	220.51**	49.96**	222.05**	1073.43**	385.76**	143.64**	16.81**
3.	Error	128	2.51	6.42	1.83	2.65	12.05	1.45	1.86	1.43	3.43	0.96

Table 1(1.3)

S. No.	Source of variation	d.f.	Mean sum of squares		
			DFF	MATURITY	GY
1.	Replication	2	11.60	7.54	27.18
2.	Genotypes	64	149.18**	50.51**	93.86**
3.	Error	128	2.277	1.38	1.44

Table 1(1.4)

Source of variation	d.f	Mean Sum of Square				
		DSL	DSW	L/BR	H%	M%
Replication	2	0.001	0.001	0.006	0.37	6.90
Genotypes	64	0.01**	0.0011**	0.58**	75.71**	70.21**
Error	128	0.0002	0.0005	0.02	1.86	1.04

Table 2. Genetic parameters of yield attributing traits of NPT lines

S.No.	Characters	Mean	Range		Coefficient of variation		Heritability	Genetic Advance	Genetic Advance as % of Mean
			Max.	Min.	GCV	PCV			
1	SL	0.92	1.06	0.74	10.14	12.67	0.64	0.15	16.73
2	SW	0.26	0.32	0.21	11.20	12.46	0.80	0.05	20.73
3	PH	131.69	156.81	104.27	11.12	11.18	0.98	30.00	22.78
4	Pl.W	31.92	47.66	19.66	26.68	27.17	0.96	17.24	54.00
5	FLL	44.62	58.89	31.00	16.40	16.78	0.95	14.73	33.01
6	FLW	2.41	3.12	1.60	12.99	15.95	0.66	0.52	21.79
7	CL	103.87	128.66	81.77	13.44	13.55	0.98	28.55	27.48
8	DTF	103.38	121.00	90.00	6.76	6.92	0.95	14.09	13.62

9	DTM	148.20	155.33	141.00	2.73	2.84	0.92	8.00	5.400
10	GY	20.35	40.44	13.33	27.27	27.90	0.95	11.17	54.90
11	BYP	71.82	156.55	51.00	26.31	26.38	0.99	38.83	54.06
12	1000GW	28.01	35.70	20.61	14.55	14.59	0.99	8.37	29.37
13	HI	28.32	56.13	16.35	24.13	25.00	0.93	13.59	47.98
14	PL	28.05	32.55	21.22	10.07	11.17	0.81	5.24	18.70
15	US	74.06	134	22	33.40	33.49	0.99	50.84	68.65
16	NOT	7.17	11.00	4.22	15.96	25.74	0.38	1.46	20.38
17	NOPT	6.53	10.33	4.00	20.78	27.71	0.56	2.09	32.10
18	FS	238.67	357	112	25.35	25.36	0.99	124.63	52.21
19	TS	310.37	458	202	20.66	21.18	0.96	128.96	41.55
20	SF	77.05	94.35	57.84	11.12	11.23	0.98	17.49	22.70
21	SD	11.16	17.21	6.70	20.58	22.37	0.84	4.35	38.99
22	PI	65.24	91.74	48.54	17.34	17.44	0.98	23.18	35.53
23	DSL	0.59	0.76	0.44	9.90	10.24	0.11	0.11	19.711
24	DSW	0.22	0.28	0.18	6.32	11.93	0.28	0.01	6.91
25	L/BR	2.77	3.93	1.67	15.67	16.49	0.90	0.85	30.68
26	H%	59.74	67.37	47.06	8.30	8.61	0.92	9.85	16.49
27	M%	53.18	61.21	40.30	9.02	9.23	0.95	9.67	18.18

High heritability in broad sense coupled with high genetic advance as percent of mean was observed for characters viz., Biological yield per plant, culm length, plant height, 1000 grain weight, unfilled spikelet, filled spikelet, spikelet fertility, panicle index, panicle weight, flag leaf length, grain yield, total spikelet, L/B ratio, harvest index, and spikelet density. Grain yield per plant was in agreement with the findings reported by Sharma (2013) and Selvaraj et al. (2011). However, the same for biological yield per plant was in agreement with the result Abdul Fiyaz et al. (2011).

High heritability and high GA for number of filled spikelet's per panicle was in agreement with results of Narinder (2006). Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability alone. It indicates that the heritability is most likely due to additive gene effect and selection may be effective.

Conclusion

From the investigation we can conclude that high estimates of phenotypic and genotypic coefficient of variation were recorded for total spikelet, filled spikelet, number of tillers, number of productive tillers, panicle weight, biological yield per plant, harvest index, spikelet density, unfilled spikelet and grain yield which indicates that selection for such characters will be rewarding.

High heritability with high GA was observed for traits viz, Biological yield per plant, panicle weight, filled spikelet, harvest index, total spikelet, spikelet density, panicle index, flag leaf length, 1000 grain weight, plant height, spikelet fertility. It indicates that heritability is most likely due to additive gene effect and selection may be effective. Thus when we will go for selection we can take the above characters under consideration for the crop improvement.

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