



E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2018; 7(3): 879-881
Received: 04-03-2018
Accepted: 08-04-2018

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Heritability and Genetic advance among yield and related quality traits in rice genotypes (*Oryza sativa* L.)

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Abstract

The present investigation entitled "Heritability and genetic advance among yield and related quality traits in rice genotypes (*Oryza sativa* L.)" was undertaken with twelve parents and their 66 F₁'s crosses for 18 component characters. A two years' study during kharif 2011-12 and 2012-13 with 78 genotypes genotypes were evaluated in a Randomized Complete Block Design with three replications at Crop Research Center of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut. Observations were recorded on ten randomly selected plants in the three replications for eighteen traits viz., days to 50% flowering, days to maturity, plant height, number of productive tillers per plant, panicle length, number of branches per panicle, number of grains per panicle, biological yield per plant, grain yield per plant, harvest index, 1000-grain yield, hulling %, kernel length, kernel breadth, L/B ratio, kernel elongation after cooking, kernel elongation ratio and amylose content. Analysis of variance revealed significant differences for all the traits under study. High heritability coupled with high genetic advance was observed for plant height, number of grains per panicle, biological yield per plant and grain yield per plant.

Keywords: heritability, genetic advance and harvest index

Introduction

Rice (*Oryza sativa* L. 2n: 2x: 24) is the most important cereal crop cultivated widely in many parts of the world. Rice is the world's second most important cereal crop, grain production of rice being exceeded only by that of wheat. Rice is the major caloric source, with nearly 2.5 billion people depending on it as their main food (FAO, 2004). Rice is cultivated in at least 114, mostly developing countries and is the primary source of income and employment for more than 100 million households in Asia and Africa (FAO, 2004). The knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding programme, 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 estimates along.

Materials and Methods

The investigations were conducted at the experimental farm, Crop Research Centre of Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut (U.P.). The experimental material consisted of twelve parents and their 66 F₁'s crosses for 18 component characters. A two years study during kharif 2011-12 and 2012-13 with 78 genotypes genotypes were evaluated in a Randomized Complete Block Design with three replications were obtained from the genetic stock available at Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut. The first nursery was prepared with seed of 78 lines during season 2012. The seedlings of 21 days old were transplanted in field in 2 m long rows with spacing of 25 x 15 cm between and within rows, respectively. The experiment was carried out in randomized block design with three replications. Observations were recorded on ten randomly selected plants in the three replications for eighteen traits viz., days to 50% flowering, days to maturity, plant height, number of productive tillers per plant, panicle length, number of branches per panicle, number of grains per panicle, biological yield per plant, grain yield per plant, harvest index, 1000-grain yield, hulling %, kernel length, kernel breadth, L/B ratio, kernel elongation after cooking, kernel elongation ratio and amylose content. Analysis of variance was carried out as suggested by Panse and Sukhatme (1978), Heritability (BS) and Genetic Advance were estimated by using the formula suggested by Burton and Devane (1953) and Lush (1949).

Result and Discussion

Analysis of variance was carried out of highly significant for all the traits (table 1). Heritability denotes a statistical concept and is an index of transmissibility of attribute from parents to off springs. The concept of heritability is important to determine whether the phenotypic differences observed among various individuals, are due to differences in their genetic makeup or simply as a result of environmental factors. The knowledge of heritability of a character is also important to breeder as it indicates the possibility and extent to which genetic gain is possible through selection (Robinson *et al.*, 1949). Heritability, in broad sense, is the ratio of additive genetic variance to phenotypic variance. Thus, it reflects the comparative value of heredity and environment on character variation. The effective improvement in a particular trait for which the selection is under taken will be based on quantum of genetic advance. In such a case also heritability coefficient will act inside measuring role when expressed in terms of genetic gain. Johnson *et al.*, (1955) [1] pointed out that without genetic advance, the estimates of heritability would not be of practical value for the selection based on phenotypic appearance. According to Hanson (1963), heritability estimates were influenced by the method of estimation, generation of the material under study, experimental sample employed and the environmental conditions under which the material was grown. Hanson (1963) suggested heritability and genetic advance as two complementary concepts.

According to Kung (1977) [2], genetic advance would be overestimated in either one of the following situations:

1. Low selection proportion with high heritability, and
2. High selection proportion with low heritability

Genetic gain would be under estimated when both Selection proportion and heritability are high or, low.

In the present investigation, the high heritability estimates were recorded for plant height, number of grains per panicle, biological yield per plant, kernel elongation after cooking,

grain yield per plant, harvest index, days to 50% flowering, number of productive tillers per plant, 1000-grain weight, panicle length, kernel length, days to maturity, L/B ratio, hulling%, amylose content, kernel elongation ratio, kernel breadth and number of branches per panicle (table no.2). Similar results were also observed by Girish *et al.*, (2006), Karim *et al.*, (2007), Khan *et al.*, (2007) [3], Nandan and Sweta Singh (2010), Ullah *et al.*, (2011), Akter *et al.*, (2011) [10], Asfaliza *et al.*, (2012), Osman *et al.*, (2012) [9], Hossein Sabouri *et al.*, (2013) [4], Pallabi *et al.*, (2013), Rafii *et al.*, (2014), Ghara *et al.*, (2014) [7] and Sawarkar and Senapati (2014) [5]. These could be owing to greater contribution of additive genetic component in the inheritance of these attributes suggesting that, if these traits may be subjected to mass or progeny or family selection or any selection scheme, aimed at exploiting additive (fixable) genetic variance, a widely adapted genotype could be developed.

The genetic advance of a trait is a product of the heritability and selection differential expressed in terms of phenotypic standard deviation of the trait concerned. For comparison of the different attributes, it is better to express it as a percentage of mean. Heritability values in conjunction with selection differential are more effective as they indicate the expected genetic gain resulting from selection. Hanson (1963) reported that heritability and genetic advance are two complementary concepts.

High genetic advance was recorded for number of grains per panicle, plant height, and biological yield per plant. While it was low for grain yield per plant, harvest index, days to 50% flowering, number of productive tillers per plant, 1000-grain weight, panicle length, days to maturity, kernel elongation after cooking, amylose content, hulling, kernel length, L/B ratio, number of branches per panicle, kernel breadth and kernel elongation ratio. Present findings are in agreement with earlier workers Sreeparvathy *et al.*, (2010), Chakraborty and Chakraborty (2010) [8], Selvaraj *et al.*, (2011), Osman *et al.*, (2012) [9], Pallabi *et al.*, (2013) and Ghara *et al.*, (2014) [7].

Table 1: Analysis of variance for yield and yield components in rice (*Oryza sativa* L.)

Source	d.f.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of productive tillers/plant	Panicle length (cm)	No. of branches/panicle	No. of grains/panicle	Biological yield per plant (g)	Grain yield per plant (g)
Replication	2	0.75	0.26	0.02	0.26	0.18	0.03	1.63	1.19	0.34
Treatments	77	90.75**	7.48**	1118.27**	20.57**	11.06**	0.89**	2443.19**	786.12**	114.00**
Error	154	0.44	0.36	0.35	0.24	0.30	0.34	0.72	0.49	0.40
Total	233	30.29	2.71	369.79	6.96	3.86	0.52	807.90	260.13	37.95

Source	d.f.	Harvest index (%)	1000-grain weight (g)	Hulling (%)	Kernel length (mm)	Kernel breadth (mm)	L/B ratio	Kernel elongation after cooking (mm)	Kernel elongation ratio	Amylose content (%)
Replication	2	0.012	0.024	0.125	0.038	0.003	0.006	0.016	0.001	0.568
Treatments	77	100.72**	14.09**	2.84**	2.14**	0.02**	1.24**	4.97**	0.008**	3.65**
Error	154	0.45	0.19	0.18	0.06	0.005	0.07	0.006	0.002	0.34
Total	233	33.58	4.78	1.06	0.75	0.009	0.45	1.64	0.004	1.44

**significance level at 1%

Table 2: Mean, Range, Heritability Genetic advance and Genetic advance as % of mean

Parents Characters	Mean	Range	Heritability (h ²)	Genetic advance	Genetic advance as per cent of mean
Days to 50% flowering	109.42	99.33-120.67	98.56	11.22	10.25
Days to maturity	150.18	147.33-153.33	86.96	2.96	1.97
Plant height (cm)	117.50	74.39-166.16	99.91	39.75	33.83
No. of productive tillers per plant	14.47	8.40-25.77	96.55	5.27	36.42
Panicle length (cm)	28.67	21.77-32.09	92.18	3.74	13.06
No. of branches per panicle	11.53	9.40-12.87	34.79	0.52	4.51
No. of grains per panicle	161.50	91.67-207.87	99.91	58.75	36.38
Biological yield per plant (g)	101.70	59.66-138.92	99.81	33.31	32.75
Grain yield per plant (g)	26.04	9.42-44.85	98.94	12.61	48.42
Harvest index (%)	25.88	12.02-38.28	98.67	11.83	45.71
1000-grain weight (g)	23.73	20.21-30.83	96.15	4.35	18.33

Hulling (%)	79.36	75.73-80.83	83.31	1.77	2.23
Kernel length (mm)	7.83	5.53-9.31	92.01	1.65	21.03
Kernel breadth (mm)	1.63	1.49-1.83	45.63	0.09	5.58
L/B ratio	4.84	3.10-5.82	85.13	1.18	24.50
Kernel elongation after cooking (mm)	10.82	7.43-12.62	99.63	2.64	24.43
Kernel elongation ratio	1.38	1.29-1.56	50.71	0.06	4.63
Amylose content (%)	21.00	18.33-23.33	76.25	1.89	8.99

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