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Estimate of heritability and co-heritability for yield and quality traits in segregating rice populations

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Abstract

An investigation was conducted in kharif 2016 with 225 F3 segregating rice lines to estimate heritability along with genetic advance and co-heritability for yield and quality characters. Considerable amount of genetic variability was present among the lines for the traits under study which revealed that exploitable level of variability exist in the population. High heritability with high genetic advance was observed for traits *viz*. grain length, decorticated grain length, amylose content, plant height, stem length, length breadth ratio of decorticated grain, decorticated grain breadth, grain breadth, fertile spikelets/panicle, number of spikelets/panicle, 1000-grain weight, spikelet density, panicle length, biological yield/plant, panicle weight/plant and grain yield/plant. The positive and substantial co-heritability estimates were recorded by stem length and length breadth ratio of decorticated grain with grain yield/plant. This finding indicated that there is preponderance of additive gene action in the inheritance of these traits. This indicates the traits showing high heritability combined with high genetic advance should be more preferred during selection of potential rice lines.

Keywords: Heritability, genetic advance, co-heritability and segregating populations

Introduction

Rice (*Oryza sativa* L.) is one of the most important food crop in the world, considered a model cereal crop due to its relatively small genome size. Possibly the oldest domesticated grains, rice is the staple food for 2.5 billion people and growing rice is the largest single use of land for producing food, covering 9% of the earth's arable land. In India, rice is staple food for two thirds population of this country. It contributes 43 per cent of caloric requirement and 20-25% of agricultural income. China and India alone account for more than 50% of the rice grown and consumed. Among the different options available to increase yield, hybrid rice technology has been found to be the most feasible. Hybridization for incorporation of desired gene in rice is one of the most important techniques to broaden the genetic base of crop (Duan, 2016) [3]. Segregating populations are more important for improving plant types by operating further selection improvement. Systematic screening of segregating lines may provide desired plant types with acceptable genes. Screening of segregating lines for different genetic architecture and their characterization may reward for the future rice breeding use. To achieve this goal, the breeder has the option of selecting desirable genotypes in early generations to reduce plant height, number of filled grains per panicle and to identify useful segregates with high yield coupled with earliness. Correlation studies provide better understanding of yield components. Yield component breeding to increase grain yield would be most effective, if the components involved were highly heritable and genetically independent or positively correlated.The present investigation was designed primarily to study the segregating populations (F_3's) of fifteen crosses to identify useful segregates with high yield and quality coupled with earliness.

Materials and Method

The present investigation was carried out at Seed Breeding Farm under Rice Improvement Project, Department of Plant Breeding and Genetics, College of Agriculture, J.N.K.V.V., Jabalpur (M.P.). The experimental area occupied was quite uniform in respect of topography and fertility. The experimental material consisted 15 cross combinations of F_3 generation segregating lines (Kranti × Madhuri, Kranti × P1401, WGL32100 × Kodokapoor, NPT 13-01× Sugandhamati, NPT 27-01 × Dubraj, NPT 27-01 × Kalanamak, NPT 27-01 × badshahbhog, NPT 25 × ANP 497, JR 201 × Danteshwari, IR 64 × PS5, IR 64 × P1121, Kavya × NPT 37, IR 64 × kavya, IR 64 × PS3, MTU1010 × PS5).In each cross combinations, a total of 15 lines were selected for the data recording and other scientific observations regarding present investigation.

A total of 225 lines derived from *indica* x *indica* and *indica* × *japonica* subspecies developed by Rice Improvement Project, JNKVV, Jabalpur were utilized in this study. These lines were planted in Randomized Complete Block Design with three replications. Twenty one days old seedlings were transplanted in the experimental plot with spacing of 15 cm between plant to plant and 20 cm between the rows, keeping single seedling/hill. Gap filling was done within a week in order to maintain uniform plant population. Fertilizer dose of 100 kg N, 60 kg P_2O_5, and 40 kg K_2O was applied. Entire dose of P_2O_5 and K_2O along with half dose of N was applied as basal dose at the time of final field preparation, remaining amount of nitrogen was splatted in two equal splits and were applied at the time of active growth and grain filling stages.

The standard agronomic practices were adopted for normal crop growth. Observations were recorded on the basis of five random competitive plants, selected from each line in every replication for the evaluation of yield and yield contributing traits. Observations regarding morphological characteristics were recorded on individual plant as well as net plot basis. For quantitative observations, mean of large, medium and smallest value of each traits like plant height, no. of productive tillers, panicle length etc. from each of the five randomly selected plants were used to record the observations of proposed segregating lines in this investigation. The mean data for each character individually was subjected to statistical analysis. Standard statistical procedures were used for the computation of mean variance, genotypic and phenotypic coefficients of variation, heritability (Hanson *et al.*, 1956) [4], genetic advance and Co-heritability (Janssen's, 1979) [5].

Results and Discussion

Heritability measures the contribution of genetic variability to the phenotypic variability observed for quantitative traits and it is good index for the transmission of characters from parents to their offspring. Heritability estimates along with genetic advance are normally more helpful in predicting the genetic gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance. Result of heritability along with genetic advance given in table 1. Parameters of genetic variability for yield, yield attributing and quality traits are summarized in table 2.

The estimates of heritability in broad sense were found high for grain length (99.80%) followed by decorticated grain length (99.80%), amylose content (99.80%), plant height (99.70), stem length (99.50%), length breadth ratio of decorticated grain (99.30%), decorticated grain breadth (98.90%), days to 50% flowering (98.80%), days to maturity (98.80%), grain breadth (98.80%), fertile spikelets/panicle (93.60%), number of spikelets/panicle (92.80%), 1000-grain weight (92.60%), spikelet density (90.50%), panicle length (89.60%), biological yield/plant (83.90%), panicle weight/plant (81.40%), grain yield/plant (79.90%) and spikelet fertility (73.80%). The estimates of heritability in broad sense were found moderate for stem thickness (67.90%) followed by harvest index (67.80%), panicle index (66.00%), number of panicle/plant (56.00%), number of productive tillers/plant (55.40%), number of tillers/plant (54.60%) and flag leaf length (50.80%). The estimates of heritability in broad sense were found low for flag leaf width (47.60%).

Table 1: Estimate of heritability along with genetic advance for different traits

Characteristics	Traits
High Heritability with High Genetic Advance	Grain length, decorticated grain length, amylose content, plant height, stem length, length breadth ratio of decorticated grain, decorticated grain breadth, grain breadth, fertile spikelets/panicle, number of spikelets/panicle, 1000-grain weight, spikelet density, panicle length, biological yield/plant, panicle weight/plant, grain yield/plant.
High Heritability with Moderate Genetic Advance	Days to 50% flowering, days to maturity, spikelet fertility.
Moderate Heritability with Moderate Genetic Advance	Flag leaf length.
Moderate Heritability with high Genetic Advance	Stem thickness, harvest index, panicle index, number of tillers/plant, number of productive tillers/plant, number of panicles/plant.
Low Heritability with high Genetic Advance	Flag leaf width.

Plant height, fertile spikelets/panicle, 1000- grain weight, grain yield/plant, fertile spikelets/panicle, panicle weight/plant, length breadth ratio of decorticated grain was recorded as high heritability with high genetic advance. This result was in agreement with the findings of Chandra *et al.* (2017) [2] for plant height, filled grains per panicle, test weight, yield per plant, and length/breadth ratio. This find was also in agreement with Sala *et al.* (2016) [9] for thousand grain weight, number of fertile spikelet per panicle and single plant yield. Biological yield/plant was recorded as high heritability coupled with high genetic advance. This result was in confirmation of Soni *et al.* (2013) [10] and Rajput *et al.* (2014) [8]. High heritability with high genetic advance was recorded for number of spikelets/panicle. This result was in the favour of the findings of Patil and Sarawgi (2005) [7].

The high heritability coupled with moderate genetic advance observed for Days to 50% flowering, days to maturity and spikelet fertility. Days to 50% flowering recorded as high heritability coupled with moderate genetic advance. This result was in agreement with Ketan and Sarkar (2014) [6] for high heritability only. In the present investigation majority of the traits recorded high heritability accompanied with high genetic advance, it indicates that most likely the heritability is due to additive gene effects and may be effective.

Co-heritability: Estimates of co-heritability for different character pairs were worked out which are mentioned character-wise in table 3. The positive and substantial co-heritability estimates (>1) were recorded by Days to 50% flowering with number of productive tillers/plant, number of panicles/plant, flag leaf length, 1000-grain weight, flag leaf width, grain breadth, decorticated grain breadth and harvest index. Plant height with flag leaf length, flag leaf width, panicle index, stem thickness and1000-grain weight. Stem length with flag leaf length, flag leaf width, panicle length, panicle index and harvest index. Panicle length with number of tillers/plant, number of panicles/plant, number of productive tillers/plant, grain yield/plant, spikelet fertility and panicle weight/plant. Number of tillers/plant with number of spikelets/panicle, spikelet fertility, fertile spikelets/panicle and length breadth ratio of decorticated grain. Number of productive tillers/plant with days to maturity, 1000-grain weight, number of spikelets/panicle, grain length, spikelet fertility and decorticated grain length. Number of panicles/plant with days to maturity, fertile spikelets/panicle, spikelet fertile, number of spikelets/panicle and length breadth ratio of decorticated grain. Flag leaf length with number of spikelets/panicle, harvest index, days to maturity, spikelet fertility and biological yield/plant. Flag leaf width with number of spikelets/panicle and spikelet density. Days to maturity with 1000-grain weight, grain breadth and decorticated grain breadth. Stem thickness with spikelet fertility, spikelet density, amylose content, biological yield/plant and harvest index. Panicle weight/plant with spikelet fertility and amylose content. Number of spikelets/panicle with spikelet fertility, 1000-grain weight and length breadth ratio of decorticated grain. Fertile spikelets/panicle with 1000-grain weight and length breadth ratio of decorticated grain. Spikelet fertility with harvest index, spikelet density, amylose content and 1000-grain weight. 1000-grain weight with spikelet density and length breadth ratio of decorticated grain. Spikelet density with length breadth ratio of decorticated grain and grain length. Biological yield/plant with amylose content only. Grain yield/plant with length breadth ratio of decorticated grain. Harvest Index with grain breadth, decorticated grain breadth, length breadth ratio of decorticated grain, amylose content and grain length. Panicle index with grain length and decorticated grain length. Grain breadth with amylose content. Decorticated grain breadth with amylose content. Length breadth ratio of decorticated grain with amylose content.

The positive and substantial co-heritability estimates (>1) were recorded by stem length and length breadth ratio of decorticated grain with grain yield/plant. This result was not in confirmation with Chakraborty (2010) [1], who observed high positive and substantial co-heritability with harvest index, effective grains/panicle and panicle length. In general, as the sign and magnitude of co-heritability estimates obtained were satisfactory, selection pressure mounted on co-heritable pair of traits may lead to simultaneous improvement of physiological and economic traits.

Table 2: Parameters of genetic variability for yield, yield attributing and quality traits in segregating rice genotypes

S. No.	Traits	Mean	Range		Coefficient of variation		h^2(b) (%)	Genetic Advance at 5%	Genetic Advance as 5% of Mean
			Min.	Max.	GCV (%)	PCV (%)			
1	DFF	103.20	84.33	116.00	7.57	7.62	98.80	16.01	15.51
2	PH	113.56	74.66	177.00	20.38	20.40	99.70	47.61	41.92
3	SL	88.05	51.00	153.33	25.21	25.28	99.50	45.62	51.81
4	PL	25.54	20.66	33.00	12.03	12.70	89.60	5.99	23.45
5	TNT	5.75	3.33	10.00	17.16	23.23	54.60	1.50	26.11
6	NPT	5.42	3.00	9.66	16.08	21.60	55.40	1.33	24.66
7	NPP	5.44	3.00	9.66	16.34	21.84	56.00	1.37	25.18
8	FLL	30.09	15.00	39.15	12.14	17.04	50.80	5.36	17.82
9	FLW	1.51	1.00	2.43	14.83	21.49	47.60	0.31	21.08
10	DM	133.20	114.33	146.00	5.87	5.90	98.80	16.01	12.01
11	ST	0.67	0.41	1.30	20.83	25.27	67.90	0.23	35.36
12	PW	21.56	9.66	44.66	25.18	27.90	81.40	10.09	46.80
13	SPP	163.01	74.00	265.66	21.41	22.23	92.80	69.26	42.48
14	FSPP	136.50	54.00	249.00	25.08	25.92	93.60	68.25	49.99
15	SF	83.37	51.52	96.04	7.01	8.61	73.80	10.34	12.40
16	TGW	20.65	14.06	25.56	10.46	10.87	92.60	4.28	20.74
17	SD	6.44	2.95	9.58	21.97	23.08	90.50	2.77	43.06
18	BYPP	39.17	15.00	81.66	28.05	30.63	83.90	20.74	52.94
19	GYPP	40.17	16.70	70.30	30.00	33.57	79.90	8.49	55.23
20	HI	45.43	21.12	69.75	19.23	23.35	67.80	13.11	32.63
21	PI	65.43	31.12	99.75	14.58	17.95	66.00	17.42	24.41
22	GL	8.95	5.91	10.32	10.76	10.77	99.80	1.90	22.15
23	GW	2.94	2.13	4.01	14.17	14.26	98.80	0.85	29.02
24	DGL	6.7	3.81	9.59	17.26	17.28	99.80	2.31	35.52
25	DGW	2.36	1.53	3.71	18.37	18.47	98.90	0.88	37.63
26	LBR	3.78	1.83	5.74	23.54	23.63	99.30	1.37	48.33
27	AC	21.98	12.33	26.64	10.09	10.11	99.80	4.57	20.78

Table 3: Co-heritability for yield, yield components and quality traits in segregating rice genotypes

Traits	PH	SL	PL	TNT	NPT	NPP	FLL	FLW	DM	ST	PW	SPP	FSPP
DFF	0.9975	0.9967	0.9645	0.5294	2.9638	2.2550	1.1713	1.0152	0.9873	0.7695	0.7283	0.9974	0.9904
PH		0.9984	0.9945	0.9960	0.9669	0.9701	1.0862	1.0817	0.9970	1.0120	0.9896	0.9977	1.0000
SL			1.0242	0.9882	0.8876	0.9028	1.1666	1.0357	0.9964	1.0045	0.9718	1.0007	1.0005
PL				3.0086	2.4149	2.6146	0.8538	0.6029	0.9494	1.0033	1.1028	0.9732	0.9728
TNT					-0.5810	0.5817	0.9271	0.4483	0.5749	0.8142	0.7050	1.1655	1.0770
NPT						0.5536	0.9800	0.4095	2.7341	0.9289	0.6811	1.0834	1.0140
NPP							1.0081	0.3933	2.1205	0.8985	0.6817	1.0362	1.1545
FLL								-0.9872	1.1093	0.9134	0.9784	1.9266	0.5908
FLW									0.9164	-0.5390	0.7344	1.1733	0.9967
DM										0.7005	0.7325	0.9968	0.9889
ST											0.9392	0.7520	0.6337
PW												0.9329	0.9140

SPP												0.9489
Traits	SF	TGW	SD	BYPP	HI	PI	GL	GB	DGL	DGB	LBR	AC	GYPP
DFF	0.9724	1.0321	0.9997	0.8532	1.0117	0.9609	0.9984	1.0127	0.9983	1.0126	0.9615	0.9935	0.8735
PH	1.0092	1.0100	1.0008	0.9929	0.9680	1.0287	0.9990	1.0003	0.9980	1.0000	0.9973	0.9978	0.9969
SL	1.0012	1.0082	0.9664	0.9944	1.0147	1.0225	0.9984	1.0002	0.9974	1.0000	0.9967	0.9999	0.9813
PL	1.1190	0.9064	0.8456	0.9975	0.6439	0.9218	0.9880	0.9362	0.9870	0.9346	0.9866	0.9878	1.1423
TNT	1.0833	0.9069	0.9143	0.6313	0.5578	-0.2135	0.8368	1.0201	0.8354	1.0181	1.0301	0.9849	0.6288
NPT	1.0405	1.3853	0.6893	0.6338	0.4644	-0.0831	1.0507	1.0077	1.0304	1.0061	1.0180	1.0004	0.5975
NPP	1.0550	-4.9092	0.7433	0.6432	0.4415	-0.0221	0.9244	1.0080	0.9142	1.0061	1.0187	1.0013	0.6013
FLL	1.1033	0.8057	0.4620	1.0389	1.4370	0.8953	-2.0891	0.9965	-1.0981	0.8945	0.9753	0.9301	0.9674
FLW	0.7405	0.7056	1.0497	-2.0213	0.6358	-0.7536	1.0098	1.0079	1.0038	1.0019	0.7566	0.9928	0.4445
DM	0.9709	1.0312	0.9991	0.8534	1.0078	0.9641	0.9983	1.0121	0.9882	1.0112	0.9615	0.9945	0.8759
ST	4.7938	0.6107	1.2149	1.0871	1.0116	0.7820	1.0080	0.9750	1.0040	0.9351	0.9868	1.1757	0.9724
PW	1.1548	0.9202	0.8993	0.8765	0.5676	-4.1169	0.9691	0.9922	0.9496	0.9823	1.0002	1.0139	0.8203
SPP	1.1674	1.0372	0.9218	0.9654	0.7531	0.9368	1.0070	0.7720	1.0040	0.7420	1.0218	0.9792	0.9375
FSPP	0.8039	1.0405	0.9457	0.9633	0.6750	0.9330	0.9995	0.8963	0.9675	0.8763	1.0104	0.9739	0.9306
SF		1.0426	1.1827	0.9759	1.8011	0.8873	0.9854	0.9695	0.9654	0.9285	0.9966	1.0483	0.6827
TGW			1.1152	-1.4764	0.9146	0.9168	0.9981	0.9608	0.9821	0.9428	1.0033	0.9803	0.9300
SD				0.9605	0.7251	0.9309	1.0142	0.9190	1.0042	0.9291	1.0198	0.9820	0.9171
BYPP					0.7981	0.6495	0.9988	0.9873	0.9882	0.9671	0.9609	1.0195	0.8425
HI						0.6995	1.0025	1.3630	1.0003	1.0620	1.0183	1.0144	0.6768
PI							1.0101	0.9993	1.0001	0.9843	1.0902	0.9811	0.7304
GL								0.9981	0.9970	0.9786	0.9963	0.9926	0.9962
GB									0.9981	0.9873	0.9875	1.0105	0.9953
DGL										0.9981	0.9963	0.9926	0.9962
DGB											0.9875	1.0105	0.9953
LBR												1.0435	1.0027
AC													0.9594

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