

**RESEARCH ARTICLE :**

Genetic divergence in indigenous and exotic rice germplasm

■ **AJAY KUMAR NAIK, S.P. SINGH, DILRUBA A. BANO AND KUDUKA MADHUKAR**

ARTICLE CHRONICLE :

Received :
17.07.2017;

Accepted :
01.08.2017

SUMMARY : Analysis of variance of 222 genotypes suggested that the genotypes differed significantly for all the 11 quantitative traits studied. Seedling height, 100-grain weight, grain yield per plant and number of effective tillers per plant showed higher estimates of genotypic co-efficient of variation. High heritability was recorded for most of the traits. High heritability coupled with high genetic advance was recorded for productive tillers per plant, 100-grain weight, grain yield per plant. Using Tocher's method, all the 222 genotypes were grouped into 15 clusters based on the relative magnitude of the D^2 values. The intra-cluster distance was found minimum for cluster I and maximum for cluster VI while it was zero for VII, VIII, IX, X, XI, XII, XIII, XIV and XV as these clusters consisted of only single genotype. The maximum inter-cluster distance was recorded between cluster II and cluster IX. The cluster V recorded high mean values for plant height, panicle length and 100-seed weight. Cluster XIII recorded highest means for number of effective tillers per plant and yield per plant. Plant height, days to maturity, days to 50% flowering and leaf length contributed relatively maximum to genetic divergence.

KEY WORDS:

Rice, D^2 analysis, Multivariate analysis, GCV, PCV, Heritability, Genetic advance

How to cite this article : Naik, Ajay Kumar, Singh, S.P., Bano, Dilruba A. and Madhukar, Kuduka (2017). Genetic divergence in indigenous and exotic rice germplasm. *Agric. Update*, 12(TECHSEAR-6) : 1633-1640; DOI: 10.15740/HAS/AU/12. TECHSEAR(6)2017/1633-1640.

BACKGROUND AND OBJECTIVES

Rice is the most important food crop of the world and considered as staple food for more than half of the world's population. It is very paramount cereal for the people of South East Asia where about 90 per cent of the population consumes rice. The slogan "Rice is life" is most appropriate for India, as this crop plays a vital role in our national food security and is means of livelihood of millions of household. A large number of cultivated varietal groups are known to exist in India as

identified by their adaptation to different eco-geographical situations. Perhaps there is no other single crop possessing as enormous variation as rice. Varietal and cultural diversity in rice is enormous and its improvement is a challenging task. The most effective way to improve productivity of crops in target environment is to use locally adopted germplasm and selection in the target environment itself (Murphy *et al.*, 2007).

In recent years, rice production has reached a plateau. In general, a narrow

Author for correspondence :

**KUDUKA
MADHUKAR**

Department of Genetics
and Plant Breeding,
Institute of Agricultural
Sciences, Banaras Hindu
University, VARANASI
(U.P.) INDIA
Email:kuduka_madhukar
@yahoo.com

genetic base of semi dwarf varieties is likely to make them vulnerable to different biotic and abiotic stresses. Therefore, to meet the ever-increasing demand of food grains, for higher production emphasis should be given to the genetic improvement of the existing varieties of rice. The major thrust area for such genetic improvement has been known to lay importance on selecting efficient breeding system and identifying desirable parents in hybridization programme. This would depend to large extent on the knowledge of the genetic system controlling the various characters.

Assessment of variability, heritability is prerequisite of the exploitation of genetic potential. Further, D²-analysis given by Mahalanobis is an efficient statistical tool for assessing diversity among genotypes differing for multiple traits. Genetic divergence among the parents is important because a cross involving genetically diverse parents is likely to produce high heterotic effect and also more variability could be expected in segregating generations (Khush, 1997). Therefore, a meaningful classification of genotypes will enable the breeders to identify the best parents with sufficient genetic diversity and to utilize them for hybridization programme. Mahalanobis D²-statistics measures *inter-se* genetic distance amongst the genotype. Their clustering based on the genetic distance finally provides a clear picture about the inter-relationship of the genotypes and helps to pick up appropriate genotype for utilization in the hybridization programme. In the context of above scenario, the present study is aimed to estimate variability, heritability and genetic advance and *inter-se* genetic distance among the genotypes and to group them in different clusters by using D²-statistics.

RESOURCES AND METHODS

The present investigation was carried out during *Kharif* 2013 at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi which is situated at 25°18' North latitude and 83°03' East longitude and at altitude of 123.23 meter from sea level. The soil of the experimental plot was fertile, alluvial loam and characterized as the 'Indo-Gangetic Plains' type. The germplasm consisted of two hundred and sixteen genotypes and six check varieties of rice. Seedlings of 222 genotypes were transplanted to main filed at 25 days old from nursery and raised in Augmented Block Design. Observations were recorded on five

randomly selected plants for each genotype for following traits *viz.*, seedling height (cm), leaf length (cm), leaf width (cm), days to 50 per cent flowering, days to maturity, plant height (cm), number of effective tillers per plant, panicle length (cm), yield per plant (g), 100 seed weight (g) and kernel L/B ratio.

Analysis of variance (ANOVA) was done separately for each character for all the treatments. The model of the analysis of variance is given below.

Source of variation	Degrees of freedom (DF)	Sum of squares (SS)	Mean sum of squares (MSS)	F calculated
Blocks (b)	b-1	bSS	bMS	bMS/EMS
Entries (e)	e-1	eSS	eMS	eMS/EMS
Checks (c)	c-1	cSS	cMS	cMS/EMS
Varieties (v)	v-1	vSS	vMS	vMS/EMS
Checks vs varieties	1	cvSS	cvMS	cvMS/EMS
Error	(c-1)(b-1)	ESS	EMS	-----
Total	(bc-1)			

Genotypic, phenotypic and environmental components of variance and their co-efficient of variances (Phenotypic: PCV and Genotypic: GCV) were estimated as methods suggested by Lush (1940) and Burton (1952), respectively. The PCV and GCV values were classified as Low: Less than 10%; Moderate: 10 – 20%; High: More than 20% as suggested by Sivasubramanian and Madhavamenon (1973). Heritability in broad sense [$h^2_{(b)}$] was calculated according to the formulae given by Lush (1940) and categorized as Low: Less than 30%; Medium: 30-60%; High: More than 60% as suggested by Johnson *et al.* (1955).

From the heritability estimates, the genetic advance was estimated by the following formula given by Johnson *et al.* (1955).

$$GA = (K) (\sigma_p) h^2_{(b)}$$

where, GA = Genetic advance under selection (expected); σ_p = Phenotypic standard deviation; $h^2_{(b)}$ = Heritability (broad sense); K = Selection differential at 5% selection intensity (2.06).

Genetic advance as per cent of mean was calculated as per the formula:

$$GA \text{ as per cent of mean} = \frac{GA}{\bar{X}} \times 100$$

where, GA = Genetic advance; \bar{X} = Grand mean of the character.

The range of genetic advance as per cent of mean was classified as Low: Less than 10%; Medium: 10-20%; High: More than 20% as suggested by Johnson *et al.* (1955).

Genetic diversity between genotypes was estimated by using D^2 analysis given by Mahalanobis's (1936).

The D^2 value between i^{th} and j^{th} genotypes for P characters was calculated as:

$$D_{ij}^2 = N P \bar{Y}_{iNI} (\bar{Y}_{it} - \bar{Y}_{jt})$$

where, \bar{Y}_{it} = uncorrected mean value of i^{th} genotype for t character; \bar{Y}_{jt} = Uncorrected mean value of j^{th} genotype for t character; $D_{ij}^2 = D^2$ value between i^{th} and j^{th} genotype.

Grouping of the genotypes into various clusters was done by using Tocher's method as described by Rao (1952).

OBSERVATIONS AND ANALYSIS

The results obtained from the present study as well as discussions have been summarized under following heads:

Analysis of variance :

It is evident from analysis of variance that genotypes differed significantly for all the 11 quantitative trait studied (Table 1). The characters *viz.*, Seedling height, 100-grain weight, grain yield per plant and number of effective tillers per plant showed higher estimates of genotypic coefficient of variation suggesting that these characters are under the influence of genetic control hence, it could be relied upon that these characters may be improved by simple selection. Bhatia *et al.* (2013) and Gyanendrapal *et al.* (2011) had reported similar observation for grain yield per plant and number of effective tillers per plant. Kumar *et al.* (2007) had also reported similar

Table 1: Analysis of variance (ANOVA) for 11 characters

Source of variation	DF	Seedling Height (cm)	Leaf length (cm)	Leaf width (cm)	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of effective tillers/plant	Panicle length (cm)	Yield/plant (g)	100 seed weight (g)	L/B ratio
Block (eliminating Check+Var.)	3.00	0.22	2.28	0.01	3.43	0.35	58.14	0.09	1.02	0.74	0.00	0.00
Entries (ignoring Blocks)	221.00	15.06**	131.48**	0.04**	421.51**	474.22**	713.93**	1.22**	8.41**	40.05**	0.31**	0.34**
Checks	5.00	19.17**	263.25**	0.09**	1388.50**	1333.54**	662.53**	2.51**	32.70**	121.26**	0.91**	3.60**
Varieties	215.00	11.07**	96.67**	0.04**	344.82**	374.81**	530.34**	1.19**	7.73**	28.82**	0.27**	0.18**
Checks vs. varieties	1.00	853.49**	6957.99**	0.04	12074.75**	17550.30**	40443.26**	1.55**	33.08**	2048.68**	5.42**	19.11**
Error	15.00	0.45	6.78	0.01	5.15	6.21	28.67	1.15	0.50	0.44	0.01	0.00

** indicate significance of value at P=0.01

Table 2 : Variability parameters for 11 quantitative traits in rice

Characters	General mean	Range		Phenotypic variance	Genotypic variance	Error/environmental variance
		Lowest	Highest			
Seedling height (cm)	13.56	6.86	24.48	10.12	9.66	0.46
Leaf length (cm)	54.08	28.89	81.02	88.66	81.88	6.78
Leaf width (cm)	1.00	0.56	1.62	0.04	0.03	0.01
Days to 50% flowering	118.50	69.83	158.83	314.59	309.44	5.15
Days to maturity	150.27	98.20	184.70	342.00	335.79	6.21
Plant height (cm)	138.83	67.08	194.80	485.70	457.02	28.67
No. of effective tillers/plant	7.44	1.62	12.02	4.88	5.07	0.19
Panicle length (cm)	25.34	15.90	31.97	7.08	6.58	0.50
Yield per plant (g)	14.74	2.93	34.41	26.29	25.86	0.44
100-seed weight (g)	2.37	1.03	4.21	0.25	0.23	0.01
Kernel L/B ratio	2.91	2.00	5.48	0.16	0.16	0.01

observations for 100-seed weight and grain yield per plant.

Traits like kernel L/B ratio, leaf width, leaf length, panicle length and plant height recorded moderate to low estimates of genotypic co-efficient of variance indicating little scope for selection (Table 2). Similar findings were reported by Verma *et al.* (2000) in rice for plant height and kernel L/B ratio. Monalisa and Sasmal (2000) reported moderate genotypic and phenotypic co-efficient of variation for panicle length.

Heritability and genetic advance :

In the present investigation, high heritability was recorded for most of the traits *viz.* days to 50 per cent flowering, days to maturity, grain yield per plant, 100-grain weight, seedling height, kernel L/B ratio, leaf length and number of effective tillers per plant (Table 3). These findings were in consonance with the earlier reports made by Dash (1992) for days to 50 per cent flowering and days to maturity; Ali *et al.* (1993) for 100-grain weight, grain yield per plant and number of tillers per plant and Bhatia *et al.* (2013) for productive tillers per plant and yield per plant.

Since heritability estimates are influenced by the environment and experimental material. Thus, heritability values coupled with high genetic advance would be more reliable and useful in formulating selection procedure.

High heritability and genetic advance may be attributed to additive gene action (Khan, 1990) and simple selection could be applied for genetic improvement.

High heritability coupled with high genetic advance was recorded for productive tillers per plant, 100-grain weight, grain yield per plant indicating the additive genes which govern these characters and selection will be rewarding for improvement of such characters. This was in agreement with earlier finding of Gyanendrapal *et al.* (2011) and Bhatia *et al.* (2013).

High genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) with high heritability and high genetic advance as percent of mean indicates the directional selection for concerned characters for improvement at early stages.

Analysis of genetic divergence:

Assessment of genetic diversity was made based on the data recorded for eleven yield and yield contributing characters in 222 rice genotypes using Mahalanobis' D² analysis. Using Tocher's method, all the 216 genotypes and 6 checks were grouped into 15 clusters based on the relative magnitude of the D² values (Table 4).

The intra-cluster distance was found minimum for cluster I and maximum for cluster VI while it was zero for VII, VIII, IX, X, XI, XII, XIII, XIV and XV as these clusters

Table 3 : Estimates of PCV, GCV and GCV %, heritability, genetic advance and genetic advance as per cent of mean

Characters	PCV%	GCV%	ECV%	Heritability %	Genetic advance		GA as % of mean	
					(at 5%)	(at 1%)	(at 5%)	(at 1%)
Seedling height (cm)	23.75	23.21	5.03	95	6.26	8.02	46.74	59.90
Leaf length (cm)	17.25	16.58	4.77	92	17.91	22.95	32.83	42.07
Leaf width (cm)	20.16	17.30	10.35	73	0.30	0.39	30.58	39.19
Days to 50% flowering	14.88	14.76	1.90	98	35.94	46.05	30.16	28.65
Days to maturity	12.24	12.13	1.65	90	37.40	47.93	24.76	31.73
Plant height (cm)	15.74	15.27	3.82	94	42.71	54.74	30.51	39.10
No. of effective tillers/plant	25.23	24.47	4.93	96	4.46	5.72	49.99	64.07
Panicle length (cm)	10.51	10.14	2.78	93	5.09	6.53	20.14	25.82
Yield per plant (g)	35.42	35.12	4.56	98	10.38	13.31	71.76	91.96
100-seed weight (g)	21.20	20.60	5.00	94	0.97	1.24	41.25	52.86
Kernel L/B ratio	14.07	14.06	0.68	99	0.83	1.07	28.93	37.08
Characterization of values								
PCV and GCV	h ²					GA		
L : Low (< 10 %)	L : Low (< 30 %)					L : Low (< 10 %)		
M : Moderate (10-20 %)	M : Moderate (30-60 %)					M : Moderate (10-20 %)		
H : High (> 20 %)	H : High (> 60 %)					H : High (> 20 %)		

consisted of only single genotype (Table 5). The inter-cluster distance was minimum between cluster VII and cluster IX indicating close relationship and similarity for most of the characters of rice genotypes falling in these clusters. The maximum inter-cluster distance was recorded between cluster II and cluster IX suggesting highest genetic divergence existing between the genotypes of these clusters. The inter-cluster distances

were higher than the intra-cluster distances which indicate the existence of substantial diversity among the parents. Similar results of inter and intra cluster distances in rice were reported by Sarkar *et al.* (2005); Singh *et al.* (2006) and Kuchanur *et al.* (2009).

The cluster means for different characters indicated differences between the clusters for all the characters (Table 6). The cluster V recorded high mean values for

Table 4 : Clustering pattern of 222 genotypes for eleven quantitative traits in rice (Tocher's method)

Cluster	Number of genotypes	Genotypes
I	45	IC 114295, IC 381827, IC 449821, IC 460007, IC 459772, IC 459408, IC 450369, IC 449848, IC 457884, IC 370806, IC 449805, IC 449745, IC 459931, IC 449585, IC 459649, IC 450473, IC 450268, IC 334202, IC 372828, IC 381804, IC 450592, IC 449831, IC 114186, IC 332672, IC 310033, IC 381905, IC 111884, IC 450586, IC 450006, IC 17024, IC 449759, IC 449853, IC 17084, IC 450624, IC 449994, IC 459351, IC 449886, IC 332639, IC 17060, IC 459932, IC 449780, IC 450305, IC 461261, IC 449750, IC 461206
II	3	IC 145386, IC 145388, NDR-97
III	22	IR-64, Annada, EC 545408, IC 371895, ICs 400080, IC 145419, EC 496943, EC 496994, EC 497006, IC 337529, EC 496995, EC 49697, IC 416700, IC 370818, IC 337218, EC 497018, IC 145416, IC 145440, IC 331645, EC 497012, EC 497021, EC 497015.
IV	82	IC 450082, IC 459958, IC 459963, IC 459747, IC 460016, IC 450349, IC 450250, IC 350270, IC 394994, IC 330849, IC 381981, IC 461265, IC 337148, IC 458397, IC 85817, IC 116100, IC 332052, IC 450325, IC 371898, IC 115169, IC 115875, IC 17118, IC 332998, IC 461224, IC 450153, IC 450251, IC 449761, IC 337601, IC 343058, IC 450262, IC 450481, IC 460064, IC 461254, IC 319488, IC 449693, IC 17023, IC 449789, IC 121873, IC 85997, IC 450033, IC 333018, IC 459902, IC 450239, IC 343075, IC 449963, IC 461048, EC 545515, IC 450116, IC 449961, EC 545464, IC 349678, IC 125024, IC 459959, IC 17029, EC 545476, IC 461256, IC 459894, IC 459889, EC 545404, IC 450092, IC 450067, IC 381834, IC 115608, IC 340548, EC 545460, EC 545456, EC 545457, EC 545458, IC 461202, IC 352794, IC 459362, IC 145420, IC 145439, EC 545461, IC 461289, IC 461253, IC 459984, IC 450639, IC 459645, IC 330793, IC 115845, IC 371899
V	25	IC 413638, IC 413643, IC 413645, IC 413639, IC 449682, IC 415633, IC 459712, IC 459733, IC 334104, IC 381759, IC 459794, IC 450292, IC 450443, IC 450041, IC 145357, IC 449744, IC 450530, IC 459775, IC 450466, IC 450451, EC 545522, IC 381906, IC 450430, IC 381818, IC 459725
VI	36	IC 145421, IC 316279, IC 350796, IC 325163, IC 145429, IC 330705, IC 316276, IC 145441, EC 545419, IC 324315, IC 145447, EC 496957, EC 545400, EC 54540, IC 114652, IC 382613, IC 418664, IC 319524, IC 334113, IC 334080, IC 321300, EC 496997, Pusa Basmati 1, Jaya, IC 332045, IC 115617, IC 86495, IC 332026, IC 449942, IC 145363, IC 334234, IC 330135, IC 336384, IC 336076, IC 334323, IC 145409
VII	1	IC 450426
VIII	1	IC 449679
IX	1	EC 545530
X	1	IC 114286
XI	1	IC 449673
XII	1	IC 145351
XIII	1	Swarna
XIV	1	IC 310017
XV	1	IC 459981

plant height, panicle length and 100-seed weight. Cluster VIII recorded high value for leaf length. Cluster IX recorded high values for seedling height and leaf width. Cluster XI recorded high values for days to 50% flowering and days to maturity. Cluster XIII recorded high values for number of effective tillers per plant and yield per plant. The genotypes belonging to clusters V,

VIII, IX, XI and XIII could be used in hybridization programme to obtain better recombinants.

The relative contribution of different plant characters to the total genetic divergence estimated by D^2 analysis indicated that plant height, days to maturity, days to 50% flowering and leaf length contributed relatively maximum to genetic divergence (Table 7). Similar results in rice

Table 5: Average intra (bold) and inter cluster D^2 values for 15 clusters (Tocher's method)

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I	221.77	14371.41	6997.13	733.84	939.70	3706.34	848.51	1067.50	732.92	4099.02	1938.48	10589.48	4659.02	3174.43	765.81
II		306.99	1738.20	12775.19	17182.59	5438.51	19692.54	20525.20	18891.71	4901.17	21811.30	584.50	5655.93	8664.58	13213.40
III			474.67	6118.45	9075.84	1914.84	10930.36	11516.90	10342.84	1832.99	12781.57	857.92	2591.47	4206.13	6466.90
IV				590.99	2041.48	3636.36	1186.98	1461.44	1181.30	2714.22	1828.63	8916.39	3115.39	1800.31	1136.13
V					931.12	4950.14	1814.36	1575.71	1711.85	6542.64	3193.83	13527.01	7611.14	5869.45	1749.77
VI						1496.33	6844.35	7160.58	6340.89	2323.92	8736.46	3788.70	3222.60	3840.79	3698.69
VII							0.00	339.41	151.13	6024.24	347.91	14748.87	6197.58	3735.51	1356.88
VIII								0.00	680.35	6532.82	524.15	15657.82	7332.72	4631.24	1775.78
IX									0.00	5863.53	715.44	14159.28	5834.23	3629.57	1119.05
X										0.00	6687.12	2424.65	358.16	739.29	3788.09
XI											0.00	16339.41	6814.67	3889.00	2263.24
XII												0.00	2877.78	5105.19	9640.78
XIII													0.00	474.49	4218.29
XIV														0.00	2735.62
XV															0.00

Table 6: Mean values of clusters for eleven quantitative traits (Tocher's method)

Clusters	Seedling height (cm)	Leaf length (cm)	Leaf width (cm)	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of effective tillers/ plant	Panicle length (cm)	Yield/ plant (g)	100 seed weight (g)	L/B ratio
I	12.14	56.35	1.05	126.97	159.56	156.13	7.46	26.65	15.14	2.20	2.90
II	16.04	30.25	0.66	74.03	99.31	72.41	5.96	22.21	14.56	2.59	2.95
III	15.12	39.42	0.90	88.47	118.12	100.00	6.60	22.67	14.56	2.48	3.08
IV	12.98	57.11	1.00	130.27	163.18	138.73	7.62	24.40	14.56	2.31	2.87
V	13.63	66.35	1.23	122.89	154.75	171.51	7.76	28.34	13.48	2.74	2.86
VI	15.41	47.71	0.88	96.45	128.08	126.79	7.36	25.58	16.13	2.47	2.93
VII	9.53	56.93	1.18	147.00	177.21	158.46	7.70	27.03	11.37	2.46	2.89
VIII	12.75	73.61	0.74	144.83	174.71	160.34	7.89	25.97	5.46	1.88	3.01
IX	17.31	50.30	1.28	146.00	172.88	160.53	8.62	26.56	15.98	1.91	2.69
X	15.18	50.80	1.05	116.17	144.21	96.21	5.99	25.41	17.17	2.68	2.80
XI	11.85	62.49	1.04	158.83	184.71	150.26	8.09	24.73	4.86	1.86	2.79
XII	14.28	31.54	0.59	87.17	116.21	76.35	6.59	21.37	13.22	2.15	3.64
XIII	16.81	36.13	1.02	122.00	151.00	93.31	8.77	26.18	23.73	2.29	2.98
XIV	15.02	42.62	1.19	135.17	160.21	103.23	7.59	24.95	15.39	2.60	3.14
XV	11.27	48.04	1.16	142.00	142.88	150.95	8.02	28.10	7.82	1.76	3.37

Table 7: Per cent contribution of different quantitative characters towards diversity

Sr. No.	Source	Times ranked 1 st	Contribution %
1.	Seedling height (cm)	225	0.92
2.	Leaf length (cm)	1704	6.95
3.	Leaf width (cm)	0	0.00
4.	Days to 50% flowering	4527	18.45
5.	Days to maturity	4910	20.02
6.	Plant height (cm)	11893	49.83
7.	No. of effective tillers/plant	332	1.01
8.	Panicle length (cm)	62	0.25
9.	Yield/plant (g)	878	3.58
10.	100 seed weight (g)	0	0.00
11.	Kernel L/B ratio	0	0.00

were also reported by Kuchanur *et al.* (2009) and Sravanan *et al.* (2013) for days to 50% flowering and leaf width, Vennila *et al.* (2011) and Saravanan and Pachiyappan (2013) for plant height.

Conclusion:

It may be concluded that characters like number of effective tillers per plant, 100- grain weight and grain yield per plant had substantial genetic variability and were controlled by additive gene effect. Hence, selection for these traits would be proved effective in improving the grain yield. Hybridization among the genotypes drawn from widely divergent clusters with high yield potential is likely to produce more heterotic effects. Apart from the divergence, the performance of genotypes and the characters with maximum contribution towards divergence should also be given due consideration which appears to be desirable for improvement of rice.

Acknowledgement:

Authors are grateful to the Department of Plant Breeding and Genetics, Instt. of Agril. Scis., BHU, Varanasi for extending co-operation and lending help during the course of work. Also, we would like to extend our whole hearted obligations by bowing to “Mahamana” Pandit Madan Modan Mohan Malviya, founder of BHU.

Authors' affiliations :

AJAY KUMAR NAIK, S.P. SINGH AND DILRUBA A. BANO,
Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, VARANASI (U.P.) INDIA

REFERENCES

- Ali, S.S.,** Jafri, S.J.H., Khan, M.G. and Butt, M.A. (1993). Heritability and genetic advance estimates for agronomic traits in rice. *J. Agric. Engg. & Veterinary Sci.*, **9**(1-2): 34-40.
- Bhatia, Pankaj,** Jain, R.K. and Chowdhury, V.K. (2013) Genetic variability, correlation and path co-efficient analysis for grain yield and its components in rice (*Oryza sativa* L.) genotypes. *Ann. Biology*, **29** (3): 282-287.
- Burton, G.W.** (1952). Quantitative inheritance in grasses. *Proc. 6th Int. Grasslands Cong. J.*, **1**:227-283.
- Dash, S.K.** (1992). Variability, association and genetic divergence in rice (*Oryza sativa* L.) Ph. D. Thesis, in Genetics and Plant Breeding, Banaras Hindu University, pp. 1-151.
- Gyanendrapal,** Verma, O.P., Pratap, N., Kumar, M., Chaudhary, R.K. and Singh, K. (2011). Genetic variability, heritability and divergence studies in rice (*Oryza sativa* L.) under sodic soil. *Environ. & Ecology*, **29**: 1597-1600.
- Johnson, H.W.,** Robinson, H.F. and Comstock, R.E. (1955). Estimation of genetic variability and environmental variability in soybean. *Agron. J.*, **47**: 314-318.
- Kuchanur, P.H.,** Dronavalli, N. and Vijaykumar, A.G. (2009). Genetic variability and divergence in ‘New Plant Type’ genotypes. *Crop Improvement*, **36** (1): 20-24.
- Khan, N.I.** (1990). Variability and character association in wheat. *J. Agric. Res.*, **28**(3): 193-200.
- Khush, G. S.** (1997). Origin, dispersal, cultivation and variation of rice. *Pl. Mol. Biol.*, **35** : 25-34.
- Kumar, S.T.,** Narasimman, R., Eswaran, R., Kumar, C.P.S. and Anandan, A. (2007). Studies on genetic variability, heritability and genetic advance in segregating generations of rice (*Oryza sativa* L.). *Int. J. Pl. Sci.*, Muzaffarnagar, **2** (1): 48-51.

- Lush, J.L.** (1940). Intra-sire correlation and regression of offspring on dams as a method of estimating heritability of characters. In: *Proc. of "American Society of Animal Production"*, **33**: 293-301.
- Mahalanobis, P.C.** (1936). On the generalized distance in statistics. *Proc. Natl. Inst. Sci. India*, **2**: 49-55.
- Monalisa, M.** and Sasmal, B.G. (2000). Genetic variability and character association of grain size in semi-deep rice. *Environ & Ecol.*, **18**: 714-717.
- Murphy, K.M.**, Campbell, K.G., Lyon, S.R. and Jones, S.S. (2007). Evidence of varietal adaptation to organic farming systems. *Field Crops Res.*, **102**: 172-177.
- Rao, C.R.** (1952). *Advanced statistical methods in biometrical research*. John Willey and Sons Inc., NEW YORK, U.S.A.
- Saravanan, K.** and Pachiyappan, R. (2013). Genetic divergence analysis in rice. *Internat. J. Agric. Sci.*, **9**(1):197-200.
- Sarkar, K.K.**, Bhutia, K.S., Senapati, B.K., Roy, S.K., Panda, S. and Mondal, A.B. (2005). Genetic variability and relationships between grain yield and its component traits in rice (*Oryza sativa* L.). *Environ. Ecol.*, **23**: 702-706.
- Singh, P.K.**, Mishra, M.N., Hore, D.K. and Verma, M.R. (2006). Genetic divergence in lowland rice of north eastern region of India. *Communications Biometry & Crop Sci.*, **1**(1): 35-40.
- Sivasubramanian, J.** and Madhavamenon, P. (1973). Genotypic and phenotypic variability in rice. *Madras Agric. J.*, **12**: 15-16.
- Sravan, T.**, Rangare, N.R., Suresh, B.G., Reddy, G.E. and Reddy, P.A. (2013). Genetic divergence in upland rice germplasm (*Oryza sativa* L.). *Trends Biosciences*. **6**(5): 583-585.
- Vennila, S.**, Anbuselvam, Y. and Palaniraja, K. (2011). D² analysis of rice germplasm for some quantitative and quality traits. *Electronic J. Plant Breed.*, **2**: 392-396.
- Verma O.P.**, Santhoshi, U.S., Dwivedi, J.L. and Singh, P.P. (2000). Genetic variability, heritability and genetic advance for quantitative traits in rice. *Oryza*, **37**: 38-40.

12th
Year
of Excellence
 ★★★★★