Website : www.asthafoundation.in
Frontiers in Crop Improvement
Vol 11 (2) : 86-91 (July-2023) Print ISSN : 2393-8234 Online ISSN : 2454-6011
Astha Foundation, Meerut (U.P.) India

Studies on Genetic Diversity Based on Morphological and Quality Characters in Rice (*Oryza sativa* L.)

Santosh Singh Bisht[1], Shiv Kumar[1], A.S. Jeena[2] and M.C. Upreti[2]

[1]*Department of Agricultural Botany, R.M.P. (P.G) College, Gurukul Narsan, Haridwar (Uttarakhand)*

[2]*Department of Genetics and Plant Breeding, G.B. Pant University of Agriculture and Technology, Pantnagar (Uttarakhand)*

Abstract

The present investigation is carried out to study the extant of genetic diversity in Rice germplasm in 31 genotypes of rice. In the present investigation highly significant differences among accession were recorded for all the 24 characters. The results from cluster analysis revealed that the genotypes SKG-2018-07 and SKG-2018-50 (cluster V), SKG-2018-25, SKG-2018-24, SKG-2018-51 (cluster II) and SKG-2018-74 (cluster III) were identified as best suited donors for yield and quality traits in basmati rice. The genotypes SKG-2018-90 and SKG-2018-38 (cluster IV), SKG-2018-25, SKG-2018-24, SKG-2018-51 (cluster II) and SKG-2018-07 and SKG-2018-50 (cluster V) can contribute yield components. These clusters also exhibited the genetic distance of higher order i.e., 9.51 (cluster V and III), 9.43 (cluster IV and V), 7.52 (cluster V and II), 6.95 (cluster II and IV) and 6.68 (cluster II and III) indicating the genetic diversity among them. Hence, selection of these genotypes could bring improvement in yield and yield components.

Key words : *Rice, oryza sativa, genetic diversity, germplasm, yield*

Introduction

Rice (*Oryza sativa* L.) is a self-pollinated crop belongs to the genus *Oryza*, tribe *Oryzeae*, under the sub family *Pooideae* in the grass family *Poaceae*. India is one of the world's largest producers of rice, accounting for 20 percent of all world rice production. India stands first in the area, second in production, followed and preceded by China on these two aspects. Aromatic/basmati quality rice is a nature's gift to Indian sub-continent. Epicureans acclaimed its delightful fragrance, taste and texture which makes it the best among the aromatic rice of the world. The term rice quality encompasses several features like physical appearance, milling, cooking and eating qualities of the grains. *Basmati* distinguishes itself among the slender-grain cultivars by an aggregation of several desirable characters; long and slender grain which elongates further on cooking, integrity of the cooked grain, good fluffy cooked product and finally aroma from grain-filling to post-cooking stages. Grain quality is a very wide area encompassing diverse characters that are directly or indirectly related to exhibit one quality type. Keeping the view of the above-mentioned challenges the only solution is to produce the high yielding rice varieties which can fulfill the demands of the ever-growing population.

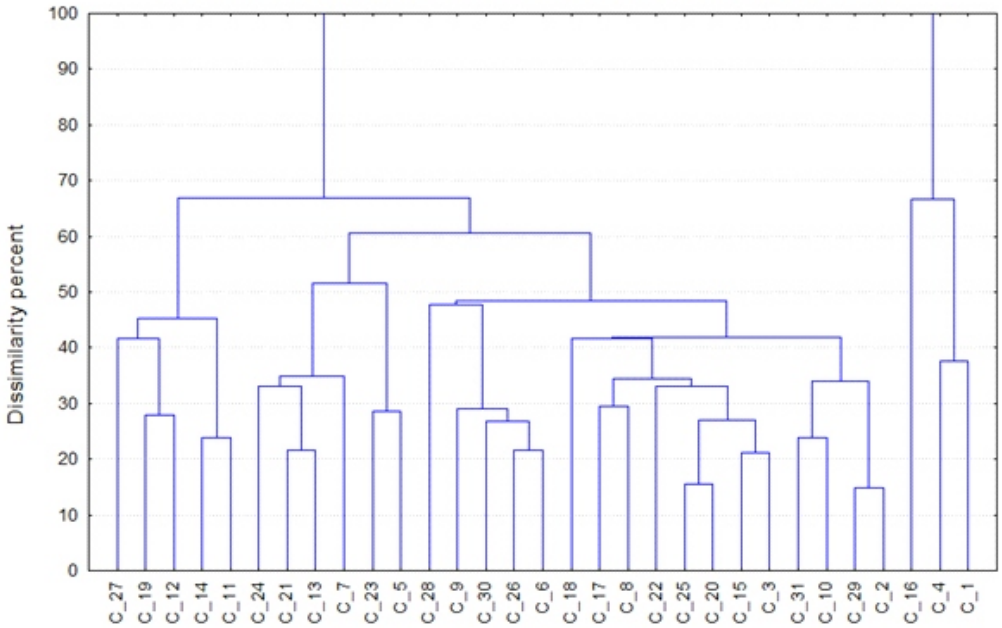
Genetic diversity is prerequisite for any crop improvement program as it helps breeders in the development of superior recombinants. Genetic diversity gives species the ability to adapt to changing environments, including new pests and diseases and new climatic conditions. Plant genetic resources, that component of genetic diversity is of actual or potential use to humanity, provides the raw material for breeding new varieties of crops. These, in turn, provide a basis for more productive and resilient production systems that are better able to cope with biotic and abiotic stresses. Knowledge about genetic diversity is a prerequisite of any breeding programme. Realization of germplasm diversity and genetic relationships among breeding materials could be crucial step in crop improvement strategies. Inclusion of diverse parents in hybridization programmes serves the purpose of combining desirable genes in new recombinations. Several studies on degree of divergence based on phenotypic observations in different crops shown that accessions from the same geographical region may differ genetically as well as phenotypically and also in adaptability. There are several method of studying genetic diversity which includes morphometric, biochemical and molecular methods. Hirarchical cluster analysis is a morphometric method and a powerful tool in quantifying the divergence at genotypic level. In view of the above facts present investigation was carried out with the objective to estimate the extant of genetic diversity in rice germplasm.

Materials and Methods

The present study was conducted during *kharif* season of 2019 at Research farm of R.M.P. P.G. College, Gurukul Narsan, Haridwar (Uttarakhand). The Gurukul Narsan is situated in the foothills of Shivalik range of Himalaya at 29.7oN latitude, 77.85oE longitude and at an elevation of

Received : May-2023; Revised : June-2023; Accepted : July-2023

Fig.1 Dendrogram of 31 rice genotypes through Hirarchical cluster analysis using Euclidean distances calculated based on morphological and quality characters



261 m amsl, which falls in the humid sub-tropical climate Zone. The soil texture of experimental plot was sandy loom. In present Investigation, 30 improved genotype of basmati rice alongwith a check SKG-2018-93 were evaluated for different yield components and quality parameters. The Material was planted in a randomized complete block design (RBD), with three replications in 2 m^2 plot keeping 20x15 cm spacing at field research farm of R.M.P. P.G. College, Gurukul Narsan, Haridwar. Standard agronomic practices compatible to this agro-ecological zone were adopted to ensure good crop growth.

The observations were recorded for Days to 50% flowering, Days to maturity, plant height at maturity (cm), Number of tillers per plant , Panicle length (cm), Length of leaf sheath (cm), Length of leaf blade (cm), Peduncle length (cm), Secondary branches per panicle, Grain weight per panicle, number of grains per panicle, Grain yield per plant, 100 grain weight (g), 100 Kernel weight (g), Hulling (%), Kernel length before cooking (mm), Kernel breadth before cooking (mm), Kernel length after cooking (mm), Kernel breadth after cooking (mm), 100 Kernel weight after cooking (g), Length/Breadth ratio before cooking, Kernel Elongation ratio, Kernel Breadth Increase ratio, Water Absorb by 10g Kernel (ml). The mean performance of individual genotype employed for statistical analysis as per methodology advocated by (1). The use of MahalanobisD2 statistic becomes limited in application when a large number of entries are to be objectively evaluated in breeding programme. Under these conditions the Hierarchical Cluster analysis (2), a method for numerical taxonomy has been found successful as a tool for estimation of genetic divergence. Therefore, in the present study hierarchical cluster analysis based on Euclidean distance was employed for genetic divergence among rice germplasm. Hierarchical cluster analysis was performed on the basis of Euclidean distance between the genotypes for unveiling the genetic diversity as outlined by (3).

Results and Discussion

The present investigation was conducted with the aim of assessing the genetic diversity among 31 genotypes of basmati rice through hierarchical cluster analysis based on yield contributing traits and quality parameters. The performance of 31 genotypes were evaluated for grain yield and its component and quality parameters of basmati rice. In the present investigation highly significant differences among accession were recorded for all the 24 characters. Earlier workers also found highly significant variations amongst the rice genotypes with regard to all the characters studied except for kernel elongation ratio (4). The ultimate aim of breeding programme is to evolve superior accession which can be exploited as cultivars. The success of any crop improvement programme is depended on the magnitude of variability present in the crop. For this reason, there is renewed interest in germplasm as a source of genetic variation. The knowledge of generic divergence has been successfully utilized in different crop species for the selection of suitable parents for varying conditions as the concept of

Table-1 : Grouping of the basmati rice genotypes through hierarchical cluster analysis.

Clusters	Genotypes
I	SKG – 2018 – 01, SKG – 2018 – 79, SKG – 2018 – 60, SKG – 2018 – 84, SKG – 2018 – 06, SKG – 2018 – 36, SKG – 2018 – 43, SKG – 2018 – 63, SKG – 2018 – 78, SKG – 2018 – 44, SKG – 2018 – 88, SKG – 2018 – 72, SKG – 2018 – 55, SKG – 2018 – 69, SKG – 2018 – 89, SKG – 2018 – 57, SKG – 2018 - 93 -CHECK
II	SKG – 2018 – 25, SKG – 2018 – 62, SKG – 2018 – 23, SKG – 2018 – 24, SKG – 2018 – 51
III	SKG – 2018 – 54, SKG – 2018 – 74, SKG – 2018 – 37, SKG – 2018 – 83
IV	SKG – 2018 – 90, SKG – 2018 – 38
V	SKG – 2018 – 07, SKG – 2018 – 50
VI	SKG – 2018 – 92

Table-2 : Intra (diagonal) and Inter cluster distance (Euclidian distance) between different clusters through hierarchical cluster analysis.

Clusters	I	II	III	IV	V	VI
I	5.59	7.17	6.83	6.48	9.28	7.57
II		5.50	6.68	6.95	7.52	7.19
III			4.89	6.20	9.51	8.68
IV				4.61	9.43	8.69
V					5.29	7.04
VI						0.00

“genetic divergence” has been vital utility in differentiating well defined populations. The adjusted mean of genotypes was subject to hierarchical cluster analysis (HCA) and the genotype were grouped in different clusters based on 40% dissimilarity level in the dendrogram (Fig.-1) prepared after the HCA. All the 31 genotypes were grouped into 6 clusters based on hierarchical cluster analysis and the distribution of a genotype in each cluster is presented in Table-1. Cluster I had the highest number of genotype (17) followed by cluster II (5) and cluster III (4) whereas cluster IV and V accommodated two genotypes each. Cluster VI were observed as mono-genotypic having only one genotype. (5) grouped 62 rice genotypes into eight clusters where, cluster I was largest genotypes, while (6, 7) also reported that maximum numbers of genotypes were included in cluster I.

The number of clusters represents the number of groups in which a population can be classified. The distance between two clusters is the measure of the degree of diversification. The greater the distance between two cluster the greater the divergence and vice versa. The genotypes falling in the same cluster are more likely to be related than those belonging to another cluster. The intra and inter cluster distance for different clusters have been presented in Table-2.

In general, the inter-cluster distance was higher than the intra-cluster distance suggesting wider diversity among the genotypes (8, 9). The highest intra cluster distance was estimated for cluster I (5.59) followed by cluster II (5.50), cluster V (5.29), cluster III (4.89) and cluster IV (4.61). The lowest intra cluster distance was observed for cluster VI (0.00) because of presence of only one genotype in the cluster. More distance among the members of a cluster means there is wide range of variability still present for the concerned character. If we lower down the dissimilarity level these clusters will be further breakdown exhibiting new clusters. On the other hand, clusters with less intra-cluster distance imply that these genotypes are closely related and less variable with respect to this mean values. These genotypes had mean value close to the cluster mean so the extraction of donors from these cluster will be easier. (10) also had the view that high intra-cluster distance indicates the existence of variability within the cluster. The inter cluster distance was highest between cluster III and cluster V (9.51) followed by cluster IV and cluster V (9.43), cluster I and cluster V (9.28), cluster IV and cluster VI (8.69), cluster III and cluster VI (8.68) and cluster I and cluster VI (7.57). On the other hand, narrow distance was estimated between cluster III and cluster IV (6.20) thereafter between cluster I and cluster IV (6.48). The greater the distance between the two clusters indicates wider the genetic diversity between genotypes (11, 12). Highest inter cluster distance between cluster III and cluster V revealed that these two clusters and members of these clusters are distinctly related to each other. More the inter cluster distance more be the diversity between the genotypes which provide opportunity to select a number of donors to carry out hybridization programmes for the improvement of desirable trait in the rice. We can proceed with the hybridization program by making cross between the two distinctly related genotype with desired traits in order to get a greater number of transgressive sergeants, out of which may undergo selection for desirable ones.

Table-3 : Cluster Means for yield, different yield components and quality parameters for different clusters of the basmati rice genotypes.

Character / Cluster	I	II	III	IV	V	VI
Days to 50% flowering	98.88	105.00	113.25	91.50	106.00	106.00
Days to Maturity	124.41	129.13	136.25	120.50	126.50	137.00
Plant height (cm)	121.86	143.00	156.00	145.67	119.00	97.00
Number of tillers per plant	13.47	14.04	14.90	11.93	15.70	13.00
Panicle length (cm)	27.18	30.80	30.67	27.67	30.33	24.67
Length of leaf sheath (cm)	31.33	35.67	36.75	47.17	35.00	25.67
Length of leaf blade (cm)	36.82	40.40	38.33	45.67	42.00	34.33
Peduncle length (cm)	3.97	5.27	6.17	19.67	5.00	1.00
Secondary branches per panicle	11.65	12.47	11.75	9.67	14.08	14.00
Grain weight per panicle (g)	2.33	2.81	2.29	2.72	4.09	2.06
tNo. of grains per panicle	100.80	137.73	103.92	103.67	183.17	145.00
Yield per plant (g)	3.30	3.65	3.73	2.91	2.96	2.25
100 grain weight (g)	2.22	2.19	2.23	2.25	2.03	1.87
100 kernel weight (g)	1.89	1.92	1.81	1.83	1.60	1.67
Hulling (%)	85.14	87.84	82.45	81.50	78.37	89.28
Kernel length before cooking (mm)	7.84	8.06	7.74	7.40	6.65	6.70
Kernel breadth before cooking (mm)	1.87	1.88	1.81	1.83	1.82	1.80
Kernel length after cooking (mm)	8.86	9.15	8.80	8.75	8.00	7.70
Kernel breadth after cooking (mm)	2.22	2.26	2.23	2.35	2.55	2.40
100 kernel weight after cooking (g)	3.31	3.30	3.13	3.40	3.30	2.87
L.B. ratio before cooking	4.24	4.33	4.25	4.04	3.67	3.73
Kernel elongation rations	1.13	1.14	1.14	1.18	1.21	1.15
Kernel Breath increase ratio after cooking	1.19	1.20	1.24	1.29	1.40	1.33
Water absorb by 10 gm kernel (ml)	17.42	17.18	17.32	18.59	21.04	17.21

Table-4 : List of donors identified for different traits among rice genotypes.

S.N.	Character	Donors
1.	Days to 50% flowering	SKG-2018-90 (IV), SKG-2018-38(IV), SKG-2018-89 (I)
2.	Days to Maturity	SKG-2018-90 (IV), SKG-2018-38(IV), SKG-2018-89 (I)
3.	Plant height	SKG-2018-92 (VI)
4.	Number of tillers per plant	SKG-2018-07 (V), SKG-2018-50 (V)
5.	Panicle length	SKG-2018-62 (II), SKG-2018-51(II)
6.	Length of leaf sheath	SKG-2018-90 (IV), SKG-2018-38(IV),
7.	Length of leaf blade	SKG-2018-90 (IV), SKG-2018-38(IV),
8.	Peduncle length	SKG-2018-90 (IV), SKG-2018-38(IV),
9.	Secondary branches per panicle	SKG-2018-07 (V), SKG-2018-50 (V), SKG-2018-92 (VI)
10.	Grain weight per panicle	SKG-2018-07 (V), SKG-2018-50 (V), SKG-2018-25 (II)
11.	No. of grains per panicle	SKG-2018-07 (V), SKG-2018-50 (V), SKG-2018-92 (VI)
12.	Yield per plant	SKG-2018-37 (III), SKG-2018-6 (I), SKG-2018-57 (I), SKG-2018-51(II)
13.	100 grain weight	SKG-2018-90 (IV), SKG-2018-38(IV),
14.	100 kernel weight	SKG-2018-25 (II), SKG-2018-51 (II), SKG-2018-69 (I), SKG-2018-55 (I)
15.	Hulling (%)	SKG-2018-92 (VI), SKG-2018-25 (II), SKG-2018-62 (II)
16.	Kernel length before cooking	SKG-2018-25 (II), SKG-2018-24 (II), SKG-2018-69 (I), SKG-2018-57 (I)
17.	Kernel breadth before cooking	SKG-2018-92 (VI), SKG-2018-74 (III)
18.	Kernel length after cooking	SKG-2018-25 (II), SKG-2018-57 (I), SKG 2018-43 (I)
19.	Kernel breadth after cooking	SKG-2018-07 (V), SKG-2018-50 (V)
20.	100 kernel weight after cooking	SKG-2018-90 (IV), SKG-2018-38(IV),
21.	L.B. ratio before cooking	SKG-2018-24 (II), SKG-2018-25 (II)
22.	Kernel elongation rations	SKG-2018-07 (V), SKG-2018-50 (V)
23.	Kernel Breath increase ratio after cooking	SKG-2018-07 (V), SKG-2018-50 (V)
24.	Water absorb by 10 gm kernel	SKG-2018-07 (V), SKG-2018-50 (V)

The cluster mean of different character under study was computed and presented in Table 3. The perusal of the table revealed that the clusters are exhibiting differences for yield and its components and quality parameters. Majority of the characters exhibited wide differences among the cluster means except for the traits viz., 100 grain weight, 100 kernel weight, hulling %, kernel breadth before cooking, kernel breadth after cooking, 100

kernel weight after cooking, kernel elongation ratio and kernel breadth increase ratio after cooking for whom less differences among the cluster means were observed. Based on cluster means, we can identify donors for different traits to be proposed for inclusion in hybridization programme.

Cluster IV revealed to have the genotype with earliness in flowering so genotypes from this cluster can be included in breading program as donors for earliness. Cluster IV and V exhibited highest mean value for majority of traits including earliness, early maturity, number of tillers per plant, length of leaf sheath and blade, secondary branches per panicle, grain weight per panicle, number of grains per panicle, 100 kernel weight after cooking, kernel elongation ratio, kernel breadth increase ratio after cooking and water absorb by 10 g kernel. Therefore, genotypes of these clusters can throw donors for rice quality traits. The genotype of cluster III could be the best donor for high yield per plant. The cluster means indicated that none of the clusters contained genotypes with all the desirable characters which could be directly selected and utilized. Hence recombination breeding between genotypes of different clusters may be followed. The selection of most divergent clusters would produce broad spectrum of variability for yield and other attributing traits, which may enable furthers selection and genetic improvement (13).

Yield is the multiplicative product of several yield component characters. The improved genetic donors may be employed for combining additional desirable characters in an otherwise good variety. Germplasm may serve as a valuable genetic donor for which a careful screening and evaluation is a must. The critical analysis of means, variability and genetic diversity in the present investigation revealed that some of the genotype of rice could be utilized as donors for different yield components in order to bred for high yielding varieties. Characters wise donors' identification for yield and its components along with quality parameters are presented in Table-4. Perusal of the results from cluster analysis revealed that the genotypes SKG-2018-07 and SKG-2018-50 (cluster V), SKG-2018-25, SKG-2018-24, SKG-2018-51 (cluster II) and SKG-2018-74 (cluster III) were identified as best suited donors for yield and quality traits in basmati rice. The genotypes of cluster IV (SKG-2018-90 and SKG-2018-38), SKG-2018-25, SKG-2018-24, SKG-2018-51 (cluster II) and SKG-2018-07 and SKG-2018-50 (cluster V) can contribute yield components such as panicle length, length of leaf sheath, secondary branches per panicle, grain weight per panicle, number of grains per panicle and yield per se as well as transfer genes for basmati quality viz., 100 grain weight,100 kennel weight, kernel length before cooking, kernel breadth before cooking, kernel length after cooking, 100 kernel weight after cooking, L:B ratio before cooking, kernel elongation ratio, kernel breadth increase ratio after cooking.

These clusters also exhibited the genetic distance of higher order i.e., 9.51 (cluster V and III), 9.43 (cluster IV and V), 7.52 (cluster V and II), 6.95 (cluster II and IV) and 6.68 (cluster II and III) indicating the genetic diversity among them. It is therefore concluded that hybridization among these genotypes will certainly throw transgressive segregants combining yield as well as quality characters for selection of improved basmati rice genotypes for developing high yielding basmati varieties. (14, 15) also opined that hybridization among the genotypes from the clusters which had maximum inter-cluster distances and desirable values for yield components is likely to produce heterotic combinations and wide variability in segregating generations. (16) also suggested a good scope to bring about improvement through hybridization and selection by crossing accessions from different clusters.

References

1. Panse V.G. and Sukhatme P.V. (1967). Statistical methods of agricultural workers.2nd edition, pp:381, *I.C.A.R. Publ*. New Delhi.
2. Ward J.H. (1963). Hierarchical Grouping to Optimize an Objective Function. *Journal of the American Statistical Association,* 58: 236–244.
3. Adenberg M.R. (1973). Cluster analysis for applications. Academic Press. New York.
4. Jha, V.B., Sharma, A.K. and Singh, B. 2014.Genetic divergence in early rice genotypes. *Annals of Biology*. 30(1): 68-70.
5. Dutta A., Ghosh P.D., Hossain F. and Sadhukhan R. (2011). Genetic divergence of local germplasms of rice (*Oryza sativa* L.) in red and laterite tracts of West Bengal, India. *Journal of Crop and Weed*; 7(1): 26-29.
6. Patra B.C., Das S., Mohapatra S. and Bose L.K. (2017). Genetic divergence in rice germplasm collected from north east India. *Advance Research Journal of Crop Improvement*; 8(2): 117-122.
7. Irappa B.M., Lakshmana D. and Chandana B.C. (2018). Genetic divergence study for yield and its components traits in rice. *Green Farming*; 2018. 9(1): 18-20.
8. Qamar Z.U., Akhtar J., Ashraf M., Akram M. and Hameed A. (2012). A multivariate analysis of rice genetic resources. *Pakistan Journal of Botany*. 44(4): 1335-1340.
9. Bhati P.K., Singh S.K., Dhurai S.Y. and Sharma A. (2015). Genetic divergence for quantitative traits in rice germplasm. *Electronic Journal of Plant Breeding*; 6(2): 528-534.
10. Prasad K.R.K., Suneetha Y. and Srinivas T. (2018). Genetic diversity studies in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*; 9(4): 1335-1341.
11. 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 in Biosciences*; 6(5): 583-585.

12. Sarwar G., Rashid M.H., Parveen S. and Hossain M.S. (2015). Evaluation of genetic diversity in agromorphological traits of forty-two Aman rice genotypes (*Oryza sativa* L.) using D^2 analysis. *American Journal of Experimental Agriculture*; 8(5): 280-288.
13. Behera B. Sahu S., Kar R.K. and Pandey R.K. (2017). Studies on nature of genetic diversity in slender grain rice genotypes. *Environment and Ecology*. 35(4E): 3791-3794.
14. Kumar P. and Singh G. (2017). Genetic diversity within commercialized paddy (*Oryza sativa* L.) cultivars. *Indian Journal of Ecology*; 44(1): 81-84.
15. Akter N., Islam M.Z., Chakrabarty T. and Khalequzzaman M. (2018). Variability, heritability and diversity analysis for some morphological traits in Basmati rice (*Oryza sativa* L.) genotypes. *The Agriculturists,* 16(2): 1-14.
16. Biswash M.R., Sharmin M., Rahman N.M.F., Farhat T. and Siddique M.A. (2016). Genetic diversity in modern T. Aman rice varieties of Bangladesh (*Oryza sativa* L.). *Sains Malaysiana*. 45(5): 709-716.