



GENETIC VARIABILITY AND DIVERSITY IN RICE (*Oryza sativa* L.) UNDER RAINFED UPLAND SITUATION OF ASSAM

Nimisha Parasar, Priyanka Bairagi, M. K. Sarma¹, Rupam Bora and Sangeeta Baruah

BN College of Agriculture, Biswanath Chariali, Biswanath, Assam

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Abstract: An investigation was carried out to study genetic variation and diversity pattern in a set of 70 upland rice genotypes under rainfed direct seeded condition of Assam. Amongst the 11 traits under study, highest genotypic coefficient of variation was exhibited by panicle weight, followed by number of primary branches per plant, number of secondary branches per plant and grain yield. Heritability in broad sense was highest for grain weight followed by days to flowering and plant height. More than 80 % heritability in broad sense was, however, observed for all other traits under study. Genetic advance as per cent of mean was observed highest for panicle weight followed by number of primary branches per plant and by number of secondary branches per plant. Selection for these traits, therefore, will be most effective for further genetic improvement. At the intermediate linkage distance, we obtained nine diverse clusters out of the 70 entries following Euclidean cluster analysis. The cluster I was the largest consisting of 45 genotypes followed by cluster II with 16 and cluster III, and IV with two genotypes each. All other clusters consisted of single genotype. Estimates of coefficient of variation indicated that panicle weight followed by number of primary and secondary branches per panicle and grain yield contributed mostly to the total diversity. Considering the mean performance of genotypes, and their distribution in diverse clusters a group of genotypes were identified as parents for hybridization programme to incorporate desirable values of the traits under investigation. The above findings, thus, would be useful for planning a comprehensive hybridization programme for obtaining desirable segregants for selection of improved genotypes under rainfed upland direct seeded situation of Assam.

Key Words: Genetic variation, genetic divergence, Rainfed upland Rice.

Rice is the most important cereal crop in the country and is the only crop providing staple food to the people of the State of Assam. Except for the coastal saline environment, rice is grown in all other ecosystems in the state throughout the year. Of these, the productivity of the rainfed direct seeded is the least i.e. only 1.2 t/ha (Bhattacharyya et al., 2015). In comparison to the other groups, rainfed upland rices have got very less scientific attention for improvement. Increasing productivity of upland rice is also important in view of large water demand of transplanted rice. It is estimated that 5000 liters of water is needed to produce 1 Kg of rice (Sarma et al, 2015). In view of the dwindling water resources day by day this figure alarms the need to think over the reduction in the water demand of rice cultivation. Rice is a crop that possesses enormous varietal diversity ranging from its adaptation under deep

water condition to the hill top and on the other hand from the tropical to temperate climate of the world. Large number of rice varieties is known worldwide for their adaptation under upland environment with various degrees of moisture stress tolerance. The state of Assam and adjoining parts of North East India is the traditional home for a large array of rice germplasm. Altogether, 13 categories of rices are known to exist in the state (Sarma et al., 2015), of which the productivity of rainfed direct seeded *Ahu* group is the least. A total of 1003 upland adapted rice germplasm are known to exist and are being conserved in the state of Assam (Das and Ahmed, 1995). However, in view of their low yield potentiality it is necessary to exploit the variability in rice germplasm available elsewhere as well. This investigation was, therefore, planned to study the genetic variability and genetic diversity in a set of 70

upland rice genotypes procured from the All India Coordinated Research Project, BHU centre, Varanasi, India.

Material and Methods

The experiment was carried out during Kharif season of 2016 with 70 upland rice genotypes under rainfed upland direct seeded situation in the experimental field of Biswanath College of Agriculture, AAU, Biswanath Chariali, Assam. The experiment was laid out in a randomized block design with three replications. Each plot consisted of three rows of three meter length. Seeds were direct sown in line with 20 cm inter row spacing maintaining 5 cm seedling to seedling distance for assessment of individual plant performance and the crop was raised following the recommended package of practices under rainfed upland condition of Assam.

Ten plants were randomly selected from each plot to record the yield attributes viz. Plant height, Effective tillers per plant, Panicle length, Number of primary branches per plant, Number of secondary branches per plant, Panicle weight and Filled Spikelets per panicle. Grain weight was taken for 100 random filled grains. The days to 50% flowering and maturity was recorded on plot basis. Seed yield was recorded on randomly taken one meter length of crop row. The data were subjected to the analysis of variance of RBD design with three replications following Panse and Sukhatme (1967). The mean sum of squares obtained from the analysis of variance were subjected to estimation of genetic parameters of variation as per Singh & Choudhury (1988). Estimates of variability parameters, heritability and genetic advance were calculated using standard methods of Burton and Devane (1953) and Johnson *et al.* (1955). The mean data set for all the variables under study were subjected to Diversity analysis using Euclidian Cluster Analysis following single linkage rule (Sneath and Socal, 1973) and using the software STATISTICA.

Results and Discussion

Analysis of variance indicated significant mean sum of squares for all the 11 traits under study

indicating wide variability in the set of rice genotypes under study. The estimates of genetic parameters of variation are presented in Table 1. Highest Genotypic variance was observed for the attribute number of filled spikelet per panicle followed by days to maturity and plant height. The same pattern was also observed for variance due to phenotype which indicated good agreement between the phenotypic observations with the genotypic values. Similar observations were also made by Manikya and Reddy (2011) and Sarma *et al* (2015). Mere studying the magnitude of variance does not justify the comparison of variability exhibited by different traits. Estimation of coefficient of variation which takes into account the mean of each characters, gives the real basis for comparison. In this investigation, highest genotypic coefficient of variation was exhibited by panicle weight, followed by number of primary branches per plant, number of secondary branches per plant and grain yield. There was good agreement between the genotypic coefficient of variation and phenotypic coefficient of variation indicating less influence of environmental variance. Mere presence of high magnitude of variation also does not indicate the effectiveness of selection (Burton, 1952). Here lies the essence of estimation of heritability and genetic advance (Sarma and Richharia, 1995). Heritability in broad sense was highest for grain weight followed by days to flowering and plant height. More than 80 % heritability in broad sense was, however, observed for all other traits under study. Genetic advance as per cent of mean was observed highest for panicle weight followed by number of primary branches per plant and by number of secondary branches per plant. High heritability coupled with high genetic advance indicates effectiveness of selection (Johnson *et al.*, 1959, and Gandhi *et al.*, 1964). Based on the above observation it may be inferred that selection for the traits, panicle weight, primary branches per panicle and secondary branches per panicle should be considered for further genetic improvement in the set of germplasm under study.

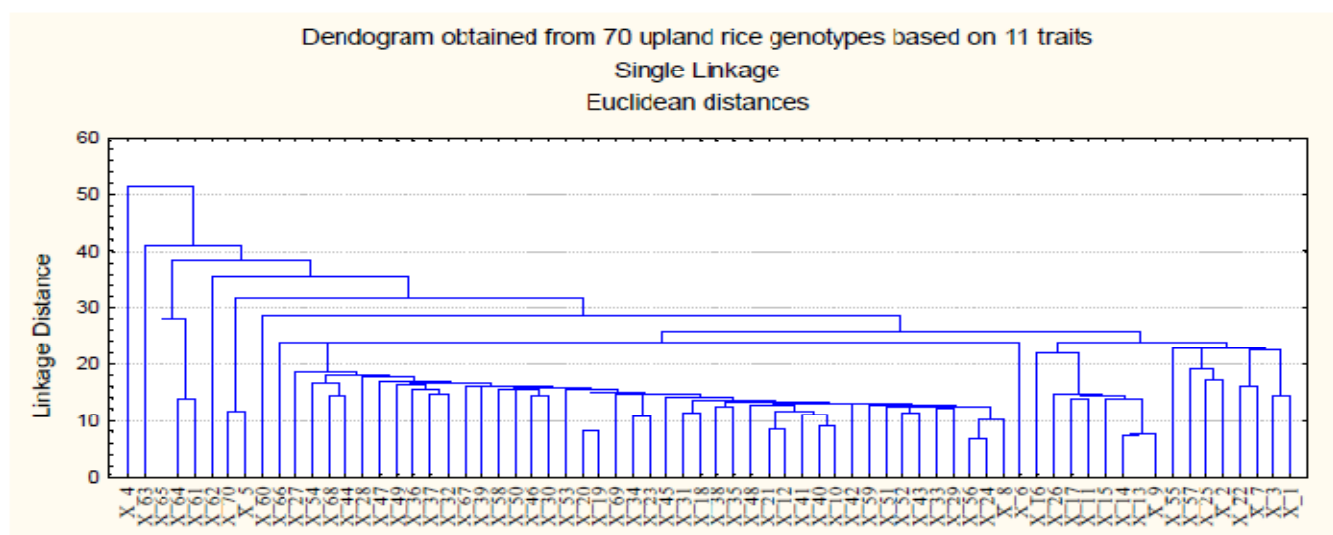
Selection of parent is the important step for initiating hybridization programme. The variability spectrum generated in the segregating generation depends on the genetic distance between the parents. The wider the genetic distance between the parents, wider is the variability generated in the segregating generation (Sarma *et.al*, 2015). With a view to select parent for hybridization programme the set of rice genotypes under study was subjected to genetic diversity analysis following Euclidean cluster analyses based on single linkage rule. The diversity pattern obtained from the analysis is presented in the form of dendrogram (Fig 1). At the intermediate linkage distance, we obtained nine diverse clusters out of the 70 entries. In the present investigation, the cluster I was the largest consisting of 45 genotypes followed by cluster II with 16 and cluster III, and IV with two genotypes each. All other clusters were monogenotypic. Based on the coefficient of variation it may be assumed that panicle weight followed by number of primary and secondary branches per panicle and grain yield contributed mostly to the total diversity. Cluster mean values for all the 11 traits are presented in Table 2. The diversity pattern and the *per se* performances of the genotypes indicated that there exist scope for further improving grain yield by accumulating more useful traits into the high yielding background. Undertaking crossing programme between superior genotypes of above diverse cluster pairs may yield desirable transgressive segregants for developing high yielding varieties under rainfed upland situation. However, while selecting diverse genotypes for hybridization programme their yield potential should not be overlooked (Sharma and Bhuyan, 2004). Thus, considering the mean performance of genotypes, and their distribution in diverse clusters, entries viz., IC 578621, IC 578414,,IC 580434,IC 578303, and IC 580440 all belonging to cluster II, could be considered as desirable parent for earliness. Many

entries exhibited short plant stature belonging to different clusters : IC 337593, IC 336983, IC 334080, IC 580627, IC 950085, IC 580626, IC 578937, 369301, 384292 and IC 578035 in cluster I, IC 578681, IC 311862, IC 578124, IC 578944, and IC 337588 in cluster II, IC 580439 and IC 384190 in cluster IV, IC 565343 in cluster VI and IC 282418 belonging to cluster VIII. Two entries viz. IC 580434 and IC 337569 in cluster I and IC 387146, in cluster II may be considered as parents for higher number of effective tiller. Genotypes IC 565389 in cluster I, IC 580228 and IC 260917 in cluster II and IC 463356 in cluster V were identified as parents for higher panicle length. For primary branches per panicle genotypes viz. IC 256749, IC 578949 and IC 578945 in cluster I, IC 334113 in cluster II and IC 463356 in cluster 5 may be considered, Likewise, entries viz., IC 578949, IC 336983, IC 578945, IC 426256, IC 950085, IC 578272 and IC 565343 in cluster I, and 11 in cluster II may be selected for secondary branches per panicle. Five entries viz., IC 578949, IC 565343, IC 578734, IC 580726 in cluster I, and IC 580228 in cluster II were identified best for panicle weight. Entries viz., IC 580439, IC 466460, IC 282418, IC 565343 and IC 577109 belonging to different clusters were identified as parents with respect to spikelets per panicle. Genotypes IC 337569 and IC 282418 were considered for lower grain weight, which may be desirable for breeding fine grained rice. Entries, IC 578953, IC 467044, IC 578937, IC 466905 in cluster I and IC 337588 in cluster II were identified for higher grain weight. Genotypes identified best for yield *per se* were IC 580438, IC 578465, IC 282418 and IC 554824 belonging to clusters I, VII, VIII and IX, respectively. The above findings, thus, would be useful for planning a comprehensive hybridization programme for obtaining desirable segregants for development of improved genotypes under rainfed upland situation of Assam.

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Genotypes with against numbers in X axis:

1. IC 578681
2. IC 580228
3. IC 311862
4. IC 463356
5. IC 580 439,
6. IC 578441,
7. IC 578 124,
8. IC 256749,
9. IC 578414,
10. IC 578030,
11. IC 260917,
12. IC 580434,
13. IC 334113,
14. IC 578303,
15. IC 580440,
16. IC 384176,
17. IC 580753,
18. IC 578949,
19. IC 565389,
20. IC 578956,
21. IC 319524,
22. IC 578944,
23. IC 580416,
24. IC 578927,
25. IC580752,
26. IC 578537,
27. IC 337593,
28. IC 336983,
29. IC 578945,
30. IC 580241,
31. IC 578133,
32. IC 334080,
33. IC 426256,
34. IC 337569,
35. IC 463725,
36. IC 580627,
37. IC950085,
38. IC 580272,
39. IC 580626,
40. IC 578953,
41. IC 467044,
42. IC 559053,
43. IC 424569,
44. IC 466497,
45. IC 578937,
46. IC 578947,
47. IC 578272,
48. IC 578935,
49. IC 369301,
50. IC 384292,
51. IC 298552,
52. IC 256736,
53. IC 580597,
54. IC 559056,
55. IC 310012,
56. IC 466905,
57. IC 337588,
58. IC 578035,
59. IC 467368,
60. IC 554824,
61. IC 466460,
62. IC 282418,
63. IC 565343,
64. IC 577109,
65. IC 578465,
66. IC 580438,
67. IC 578734,
68. IC 577919,
69. IC 580726,
70. IC 384190

Table1: Genetic parameters of variation for 11 quantitative traits in rice under rainfed upland situation

Genetic parameters	Days to 50% flowering	Days to maturity	Plant Height (cm)	Effective tillers per plant	Panicle length (cm)	Number of primary branches per plant	Number of secondary branches per plant	Panicle weight (g)	Filled spikelets per panicle	100-grain weight (g)	Grain yield per meter row length (g)
Range: Max	116	156	142.6	8.0	27.9	13.4	37.6	4.67	167.7	3.57	112.01
Range: Min	64	93	63.9	4.0	14.8	5.6	6.5	1.03	42	1.07	12.71
Mean	98.55	138.27	108.89	6.05	19.87	9.5	21.4	2.56	98.84	1.87	49.69
Phenotypic variance	259.69	345.67	265.25	1.21	4.56	14.8	59.7	8.5	459.00	0.200	275.67
Genotypic variance	256.97	334.87	260.24	0.97	4.26	14.2	54.5	7.9	439.00	0.199	236.55
PCV	16.35	13.45	14.96	18.18	10.75	40.50	36.11	113.89	21.68	23.92	33.41
GCV	16.27	13.23	14.81	16.28	10.39	39.67	34.50	109.79	21.20	23.86	30.95
Heritability (bs) %	98.95	96.88	98.11	80.17	93.42	95.95	91.29	92.94	95.64	99.50	85.81
Genetic advance	32.85	37.10	32.92	1.82	4.11	7.60	14.53	5.58	42.21	0.92	29.35
Genetic advance (% of mean)	33.33	26.83	30.23	30.03	20.68	80.04	67.90	218.04	42.71	49.02	59.06
CV	1.67	2.38	2.06	8.10	2.76	8.15	10.66	30.26	4.52	1.69	12.59
SEm	0.98	1.20	1.34	0.56	0.78	0.87	1.32	0.94	8.56	0.08	5.85

Table 2: Mean values for 11 quantitative traits in nine clusters obtained from 70 rice genotypes

Clusters	Genotypes as in X axis of Fig 1	DF*	DM	PH	ETN	PL	PB	SB	PW	SN	GW	RY
I	66, 27, 54, 68, 44, 28, 47, 49, 36, 37, 32, 67, 39, 58, 40, 46, 30, 53, 20, 19, 69, 34, 23, 45, 31, 18, 38, 35, 48, 21, 12, 41, 40, 10, 42, 59, 51, 52, 43, 33, 29, 56, 24, 8, 6	106.93	147.37	111.09	6.25	19.6 4	7.88	22.97	2.77	96.26	1.91	48.09
II	16,26,17,11,15,14,13,9,55,57,25,2,22, 7,3,1	71.04	<u>107.60</u>	105.41	6.10	20.3 3	8.06	20.89	<u>2.30</u>	87.93	1.81	44.48
III	61,64	109.33	153.50	126.87	5.17	18.8 8	7.65	26.04	3.04	159.03	2.04	62.20
IV	5,70	95.00	137.00	83.32	5.33	22.1 3	6.95	<u>18.31</u>	2.20	128.73	1.73	66.91
V	4	103.00	138.67	<u>66.37</u>	<u>4.33</u>	26.4 3	12.60	22.51	2.58	<u>45.03</u>	1.36	<u>16.05</u>
VI	63	110.33	147.67	91.47	5.67	<u>17.6</u> 3	<u>6.20</u>	27.62	4.67	161.23	1.53	43.89
VII	65	109.67	153.33	140.27	5.00	18.7 3	6.80	27.15	3.41	162.53	1.79	85.83
VIII	62	105.67	145.67	90.67	4.67	19.1 3	6.40	21.51	3.41	149.13	<u>1.12</u>	94.13
IX	60	109.33	151.67	122.27	5.33	18.7 3	6.50	26.30	2.90	91.03	2.37	108.55

*NB. DF= Days to 50% flowering, DM= Days to maturity, PH= Plant height, ETN= Effective tiller number, PL= Panicle length, PB= Primary branches per panicle, SB= Secondary branches per panicle, PW= Panicle weight, SN= Filled spikelets per panicle, GW= 100-grain weight, RY= grain yield of one meter row length
 Bold figures indicate highest cluster mean values and underlined figures indicate lowest cluster mean values.