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Research Paper

Diversity analysis of rice (*Oryza sativa*) genotype for improving the productivity for mid-hills of the eastern Himalayas

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ABSTRACT

In the present study, 12 high-yielding varieties (HYVs) and 13 traditional landraces collected from the various places of north-east India were evaluated during 2014 and 2015 for genetic improvement of yield potential of rice (*Oryza sativa* L.) for diversity analysis for its wider adoption in mid-hills of Nagaland. Among the evaluated 25 varieties, 'RCPL 412' (2.88 t/ha), 'IURON 514' (2.61 t/ha), 'VL Dhan 209' (2.53 t/ha), and 'Rukhathang' (2.52 t/ha) performed better in respect of yield potential than 'Bhalum 3' (2.42 t/ha). Magnitude of the difference between phenotypic and genotypic coefficient variation for the characters analyzed was relatively low, indicating less influence of environmental factors. High heritability with high genetic advance was recorded for yields, spikelet fertility, seeds/panicle, days to 50% flowering, panicle weight and panicle length. The principal component analysis (PCA) also identified that, yields, panicle weight, percentage of filled grain and seeds/panicle are the most important traits for classifying the variation among the genotypes. The PCA and cluster analysis revealed that, the presence of sufficient diversity among the genotypes and indicate hybridization of 'RCPL1 412' with 'VL Dhan 221' will be highly useful for development of short-stature early, high-yielding varieties of 'Shengyayouh' with 'RCPL1 412' may produce the transgressive segregants for development of medium-duration and medium-tall, high-yielding pureline for mid-as well as hill altitudes of eastern Himalayas.

Key words: Yield potential, heritability, hybridization, transgenic segregants, rice landraces

Rice is a principle staple food crop of more than half of the world population. The world's population is expected to grow to 10 billion by 2050 and, thus, demand for cereals, for both food and animal feed uses are projected to reach ~2.1 billion tonnes by 2050 (Kumar *et al.,* 2018a). Rice production has to be increased to 122.4 million tonnes by 2030 in India to meet the future rice demand (Kumar *et al*., 2018b). Thus, there is a need to increase the rice productivity. Rice is the most important staple cereal food crop for nutritional security in North East (NE) India. It occupies ~75% of the total cultivated area of region (4.58 million ha) (Kumar *et al*., 2016a). North-East (NE) India is secondary source of origin of rice and the region is also highly rich in its bio-diversity. Farming community of the region has been cultivating rice under diverse agro-ecological condition from rainfed to irrigated, valley land to upland, deep-water system on steep terrace and *jhum* lands (Verma *et al*., 2019). The average productivity of rainfed rice in NE India is 0.8 to 3.0 t/ha under diverse agro-ecosystem, which is much lower than a irrigated ecosystem. As farmers in region cultivating local landraces have lower yield potentials in comparison to high-yielding varieties (HYVs). This imposes varying levels of socio-economic problem and causing food shortage in the regions. Thus, in the present study, we had evaluated all together 25 rice genotypes including 12 high-yielding varieties with the main objective to identify the most promising HYVs suitable for mid-as well as high-hills of Nagaland, find out the suitable parental lines used in hybridization programme to develop the varieties suitable for mid-and high hill of eastern Himalayas.

MATERIALS AND METHODS

A field experiment was conducted at the farmer's field of Krishi Vigyan Kendra, Longleng, Nagaland (260 26' 0''

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N, 940 52' 0'' E, 1,366 m above mean sea-level) during 2014 and 2015 to compare the yield potential of high-yielding varieties (HYVs) with the local check and replicated thrice. Experimental materials for the present study comprised 12 HYVs and 13 traditional landraces of collected from different places of Nagaland. Among the evaluated genotypes, (HYVs, 'RCPL1 412', 'IURON 514', 'Bhalum 3', 'Bhalum 4' from the ICAR-Research Complex for North-East Hill Region, Umiam (Meghalaya), and the remaining 8 from ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan (VPKAS), Almora, Uttarakhand. The experiment was laid out in a complete-randomized block design. The soil of the experimental field was sandy loam (Inceptisols, sand of 58.3%, silt of 11.7% and clay of 30%) and acidic in reaction (*p*H 5.3), high in organic carbon (0.93%), medium in available N (294 kg/ha), P (13.6 kg/ha) and K (183.2 kg/ha). The monthly mean temperatures varies from 18.3°C to 24.9°C in 2014 and 20.0°C to 26.4°C in 2015. Total rainfall received during the cropping was 1,442 and 1,160 mm in 2014 and 2015, respectively. Monthly rainfall was recorded maximum in June 2014 and July 2015. Rice was sown across the slope with a row spacing of 20 cm. Recommended dose of N, P and K @ 80 : 60 : 40 kg/ha was applied. Half dose of N, full dose of P and K were applied basal through urea, diammonium phosphate and muriate of potash, respectively. Remaining half doses of N was applied as top-dressing 45 days after sowing (DAS). Ten plants were selected randomly from each plot to record the observation on growth and yield attributes. Seed yield was recorded on 14% moisture content. The collected data were subjected to the analysis of variance (ANOVA) using F-test. Different characters were further statistically analyzed to study the genetic variability i.e. genotypic and phenotypic variance, heritability, genetic advance, genotypic and phenotypic correlation coefficient of the different pairs of characters. The cluster analysis on algorithm of unweighted pair group method with arithmetic mean (UPGMA) and principal component analysis (PCA) was done using R package.

RESULT AND DISCUSSION

Mean performance of yield and yield attributes

Analysis of the variance revealed that presence of significant difference among genotypes for yield attributing characters except for length of flag leaf. It indicated abundant genetic variation among the genotypes. Majority of the genotypes showed medium plant stature (111–113 cm). 'VL Dhan 154' and 'VL Dhan 85' have the shortest plant. 'Shengya Youh', 'SARS 5' and 'IURON 514' had the longest panicles. Ongsho youh had the highest number of grains/panicle. The highest grain filling was recorded in 'RCPL 412' (86.93%) followed by 'Chakko Youh' (86.9%), 'Bhalum 3' (86.6%), 'SARS 5' (86%) and 'IURON 514' (84.3%). The maximum 1,000-grain weight was recorded with 'VL Dhan 62' (31.6 g). Days to 50% flowering of all the local cultivars ranged from 110 to 125 days, and HYVs from 79 to 112 days. Variations in growth and yield attributes of rice varieties might be due to having different genetic characters (Kumar *et al.,* 2016a). Higher grain yield was recorded in 'RCPL 412' (2.88 t/ha), 'IURON 514' (2.61 t/ha), 'VL Dhan 209' (2.53 t/ha) and 'Rukhatang' (2.52 t/ha) than the check 'Bhalum 3' (2.42 t/ha) (Table 1). The variation in yield attributes might be due to genetic yield potential of different rice cultivars (Kumar *et al*., 2016b).

Genetic variation

Mean values and heritability range, an estimate of genotypic and phenotypic coefficient of variation (GCV and PCV) were studied in a broad sense and expected genetic advance as a percentage mean at 5% for grain quality traits for genotypes were estimated (Tables 2, 3). Magnitude of the difference between PCV and GCV was lower for all attributes analyzed and indicating less influence of environmental factors. The close correspondence between GCV/PCV was observed for yield and yield-attributing traits, as reported by Girma *et al.* (2018). Higher gcv was recorded for yield and spikelet fertility, which indicated that the sufficient presence of variability that indicates scope for selection of genotypes based on yield and spikelet fertility. Generally, yield is considered a highly complex trait and associated with low heritability, but in the present study high heritability noted for yields because of homogeneity maintained in experimentation (Saha *et al.,* 2019).

Moderate estimates of PCV and GCV were recorded seeds/panicle, panicle weight, panicle length, day to 50% flowering and plant height. However, 1,000-grain weight and secondary leaf length showed lower GCV, which indicated limited scope for selection within experimental materials. High heritability values were recorded for most of the attributes except for secondary leaf length, plant height and 1,000-grain weight indicating less influence of environment on expression of traits. Higher heritability along with genetic advance recorded for yield, spikelet fertility, seeds/panicle, days to 50% flowering, panicle weight and panicle length. High heritability along with moderate genetic advance as per cent of mean was recorded for plant height. This indicated that the presence of additive gene effect in genetic control of these traits and suggested scope for improvement based on phenotypic performance in the present breeding material. Saha *et al.* (2019) also reported that, higher heritability coupled with high genetic advance for seeds/panicle, panicle weight, filled grains/panicle, days to 50% flowering and grain yield. Kumar *et al.* (2016a) also reported higher heritability with more genetic advance for grain yield and plant height. Grain yield, panicle weight, and seeds/panicle traits are the best attributes to be used in breeding programmes considering gcv, heritability and genetic advance.

Genotypic correlation coefficient between all the pairs of combination were studied for yield-attributing traits. Secondary leaf length and panicle weight had positive correlation with seeds/panicle, spikelet fertility, plant height and grain yield. Such association indicates that focus should be given on panicle weight, spikelet fertility and seeds/panicle for improvement in rice yield. In upland rice ecosystem, tall and vigorous plants can compete with weed for sunlight and nutrients, thus, selection for taller plants may help in improving the yield in an upland agro-ecosystem. Bhadru *et al.* (2012) also reported a similar association between grain yield, plant height, filled grain/panicle, panicle length and flag-leaf length of rice in their field investigations. Improvement in grain yields can be achieved by improving seeds/panicle, panicle weight, and secondary leaf length of rice.

Principle component analysis

Principal components, eigen value, per cent of total variation, cumulative per cent variability and component loading of different quantitative characters were studied and presented in Table 4 and Fig. 1. The PCA had shown genetic diversity of population panel. First three axes explained the 83.74% of cumulative variance with eigen value of 0.89 among the rice genotypes for yield-attributing traits, which indicated that identified traits within the axes exhibited great inuence on phenotype of population panel. Tiruneh *et al.* (2019) reported that, first 6 PC ex-

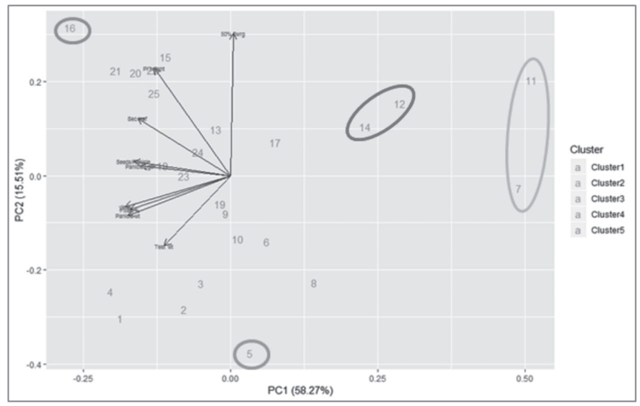

Fig. 1. Relative position of rice genotypes based on PCA scores of yield attributing traits. Note: Numbering correspondence with the serial number of mean Table.

Table 1. Growth and yield attributes of rice genotypes under mid-hills of Nagaland (mean data of 2 years)

Rice varieties	Plant height (cm)	Secondary leaf length (cm)	Panicle length (cm)	Panicle weight (g)	Seeds/ panicle (no.)	Grain filling (%)	1,000-grain weight (g)	Days to 50% flowering	Grain yield (t/ha)
‘RCPL1 412’	111.1	45.55	23.50	3.80	127.5	89.20	30.20	94.0	2.88
‘Bhalum 3’	106.2	44.20	22.47	3.60	109.5	86.60	29.50	95.0	2.42
‘Bhalum 4’	102.2	51.17	23.03	3.60	97.13	78.83	28.20	99.0	2.17
‘IURON 514’	112.6	50.62	25.50	3.80	123.1	84.30	29.60	91.0	2.61
‘VL DHAN 62’	91.9	38.80	22.33	3.60	92.8	70.50	31.60	101.0	1.90
‘VL DHAN 65’	98.0	42.37	22.03	3.50	98.3	71.50	28.40	105.0	1.63
‘VL DHAN 85’	85.8	38.87	21.17	2.13	56.5	19.46	25.37	97.0	2.17
‘VL DHAN 154’	89.0	42.15	21.77	3.20	80.3	66.03	28.13	100.0	1.66
‘VL DHAN 208’	104.0	47.25	21.17	3.60	86.0	74.50	29.10	110.0	2.37
‘VL DHAN 209’	93.8	42.43	22.08	3.52	91.2	78.20	28.60	112.5	2.53
‘VL DHAN 221’	99.9	30.45	16.52	1.98	82.1	35.41	23.40	79.2	0.62
‘Azoitomok’	104.5	41.82	19.90	3.18	41.2	34.73	29.93	125.0	0.73
‘SARS 1’	110.6	47.98	19.78	3.63	103.6	85.30	27.70	118.0	2.14
‘SARS 2’	97.1	44.62	18.22	2.75	84.0	60.08	26.63	115.0	1.45
‘SARS 5’	120.6	48.70	25.10	3.50	118.1	86.08	26.80	120.0	2.11
‘Shengya Youh’	138.6	56.23	29.48	3.80	126.8	70.21	28.60	115.5	2.31
‘Taiyo’	96.2	48.78	21.12	2.83	104.1	68.20	30.20	120.0	1.44
‘Ongsho youh’	104.1	52.45	23.43	3.60	132.3	75.20	28.30	110.0	2.26
‘Toiya youh’	94.2	47.68	21.46	3.60	108.7	82.24	29.20	115.0	2.02
‘Chakko youh’	122.6	55.48	23.47	3.52	114.8	86.93	28.50	118.0	2.33
‘Rukhatang’	133.2	53.78	23.44	3.60	117.9	81.20	29.60	117.5	2.52
‘Manna’	133.6	50.23	23.53	3.40	115.4	76.20	29.20	116.0	2.27
‘Motiro’	103.8	50.68	23.22	3.50	114.4	74.20	29.60	113.0	2.16
‘Malenken’	113.9	43.25	23.59	3.60	101.2	74.21	29.20	117.5	2.33
‘Mesa’	124.9	53.85	23.17	3.60	119.2	71.51	27.52	110.0	2.44
CD (P=0.05)	22.9	12.48	1.77	0.47	20.4	11.11	2.12	4.32	0.41

plained 75.2% of total variation for yield-attributing traits in upland rice. Khare *et al.* (2014) reported that, PCA first 4 components explained 77.1% of the total variation for yield traits for upland rice. First principal component (PC1) with an eigen value of 5.24 accounted 58.27% of contribution to total variation in population. The PC 2, PC3 with an eigen value of 1.4 and 0.89, explained 15.5 and 9.96% of the contribution to the total variability, respectively. In PC1, grain yield, panicle weight, filled grains (%) and seeds/ panicle trait contributed towards 58% of total variability present among the genotypes. In PC2, day to 50% flowering (DFF) and plant height accounted 16% of total variability among the genotypes. The PCA analysis indicates that hybridization of genotype 'RCPL1 412' with 'Shengya Youh', 'RCPL1 412' with 'VL Dhan 221' will be complementary for producing transgressive segregants in segregating generation for development of HYVs.

Cluster analysis

Cluster analysis using UPGMA method revealed that 5 clusters in 25 genotypes of the present study material (Fig. 2). Among the clusters, cluster V was the largest group, comprising 19 genotypes, followed by clusters I and II, each comprising 2 genotypes. Cluster I genotypes 'Azoitomok' and 'ARS 2', have fewer seeds/panicle, short panicle length and finally lower grain yields. Cluster II consisted 'VL Dhan 85' and 'VL Dhan 221', and this cluster was characterized by early maturity, short panicle length and low panicle weight. Cluster III composed of Shengya youh, which is tall (138 cm) with long panicle length (29.5 cm) and higher panicle weight (3.8 g). Cluster IV consists of 'Vivek Dhan 62', and this particular variety has high 1,000-grain weight and low secondary leaf length. Cluster V was largest one comprising 19 genotypes. Genotypes of cluster V showed that the high yield, panicle weight, numbers of seeds/plant and percentage of filled grains. In this group, 'RCPL1 412' was best the genotypes for grain yield of 2.88 t/ha.

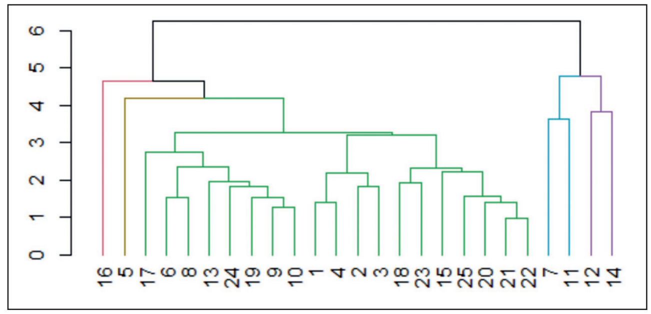

Fig. 2. UPGMA clustering of 25 genotypes based on yield and yield attributes

Table 2. Genetic variability of yield attributes of rice genotypes under mid-hills of Nagaland

Parameter	Range		Mean (SEm±)	Genetic coefficient variations	Phenotypic coefficient variation	h² (Broad Sense)	Genetic advance as % of mean 5%
	Minimum	Maximum					
Plant height	85.82	138.63	107.70 ± 8.05	11.09	17.05	42.28	14.86
Secondary leaf	30.45	56.23	46.77 ± 4.38	8.81	18.48	22.73	8.65
Panicle length	16.51	29.48	22.41 ± 0.621	10.69	11.72	83.21	20.1
Panicle weight	19.00	3.8	3.37 ± 0.164	13.14	15.61	70.91	22.8
Seeds/panicle	41.2	132.33	101.83 ± 7.16	20.3	23.68	73.53	35.87
Filling (%)	19.45	89.2	71.23 ± 3.90	23.77	25.6	86.23	45.47
1,000-grain weight	23.40	31.6	28.52 ± 0.74	5.29	6.46	57.73	8.28
50% flowering	79.16	125	108.56 ± 1.51	10.26	10.54	94.72	20.57
Grain yield	2.16	28.76	19.79 ± 1.43	32.63	34.63	86.79	61.92

Table 3. Genotypic and phenotypic correlation coefficient between yields attributes of rice genotypes

Parameter	Plant height	Secondary leaf	Panicle length	Panicle weight	Seeds/ panicle	Filled % weight	Test	Days to 50% flowering	Grain yield
Plant height	1	0.934	0.748	0.658	0.714	0.486	0.204	0.446	0.671
Secondary leaf	0.514	1	0.91	0.923	0.968	0.856	0.615	0.752	0.95
Panicle length	0.47	0.542	1	0.706	0.686	0.508	0.475	0.179	0.652
Panicle weight	0.33	0.449	0.612	1	0.702	0.885	0.804	0.319	0.975
Seeds/panicle	0.466	0.5	0.572	0.506	1	0.849	0.347	0.057	0.864
Filling (%)	0.308		0.463	0.756	0.688	1	0.568	0.202	0.97
1,000-grain weight	0.366	0.173	0.313	0.555	0.159	0.434	1	0.359	0.579
50% flowering	0.231	0.338	0.201	0.268	0.048	0.195	0.273	1	0.155
Grain yield	0.351	0.35	0.532	0.732	0.68	0.836	0.459	0.134	1

Table 4. Eigen value and percent of total variation and component matrix for principal component axes

Principal component	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8	PC 9
Eigen value	5.24	1.40	0.89	0.64	0.29	0.22	0.19	0.06	0.05
% age of variance	58.2	15.5	9.96	7.12	3.30	2.45	2.13	0.69	0.57
Cumulative proportion	58.2	73.7	83.7	90.8	94.1	96.6	98.7	98.4	100
Component matrix									
Plant height	–0.29	0.51	0.16	0.16	–0.56	0.21	–0.46	0.05	0.16
Secondary leaf length	–0.36	0.27	0.04	0.16	0.77	0.39	–0.17	0.02	–0.04
Panicle length	–0.34	0.05	0.25	0.62	–0.06	–0.31	0.51	0.28	–0.06
Panicle weight	–0.39	–0.19	–0.22	0.04	–0.17	0.34	0.38	–0.61	0.31
Seeds/panicle	–0.37	0.07	0.32	–0.31	0.16	–0.65	–0.19	–0.41	0.07
% age of filled grains	–0.38	–0.16	–0.06	–0.48	0.01	0.03	0.11	0.61	0.45
1,000-grain weight	–0.25	–0.34	–0.64	0.34	0.01	–0.28	–0.45	0.07	–0.02
Days to 50% flowering	0.01	0.68	–0.58	–0.20	0.02	–0.23	0.32	0.00	–0.10
Grain yield	–0.41	–0.15	0.01	–0.29	–0.20	0.18	0.05	0.06	–0.81

The PCA and UPGMA cluster analysis revealed that the presence of sufficient variability and diversity among the present materials. Rice cv. 'RCPL 412', 'IURON 514', 'VL Dhan 209' and 'Rukhatang' are the most promising ones, suggesting for the development of early maturity, short stature HYVs, hybridization of 'RCPL1 412' with 'VL Dhan 221' will be highly useful. For the development of medium-duration and medium-tall HYVs, hybridization of 'Shengya Youh' with 'RCPL1 412', parent may produce transgressive segregants, which can be utilized for development of a pureline variety for mid-and high hill of Nagaland under eastern Himalayas.

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