Genetic Variability in Yield and its Components in Upland Rice Grown in Acid Soils of North East India

Khriedinuo P. Fukrei[1], Amit Kumar[2], Wricha Tyagi[1] , Myank Rai[1], A. Pattanayak[2]*

[1]School of Crop Improvement, College of Post Graduate Studies, Central Agricultural University Umiam - 793103, Meghalaya

[2] Division of Plant Breeding, ICAR Research Complex for NEH Region, Umiam - 793103, Meghalaya

Abstract

Upland rice grown in hills suffers serious yield loss due to soil acidity. A core set of germplasm was used for genetic analysis of yield and nineteen other component traits. Analysis of variance revealed presence of high variability among the genotypes for all the traits. Heritability (h2) estimates were generally high except for flag leaf angle. GCV was high for flag leaf area, plant height, no. of tillers per plant, no. of ear bearing tillers, no. of filled grains/panicle, panicle weight, root length and area, straw weight and grain yield. The results indicted the core set of germplasm contained high genetic variability. The broad sense heritability and genetic advance as percentage of mean indicated that panicle weight and grain yield/plant are the two most important yield components and selection based on these traits would be very effective in upland rice grown under acid soil conditions.

Upland rice, the staple food of a hundred million people including some of the poorest in the world, suffers serious yield reductions due to soil acidity. Amending soil to suit rice cultivars is not the choice that upland farmers would find practically feasible, hence the need to exploit the genetic tolerance to develop cultivars adapted to specific upland environments.

Aluminum (Al) toxicity is the major problem in acid soils. Natural variation for Al tolerance has been identified in many crop species, and in some crops, tolerance to Al has been introduced into productive, well-adapted varieties. Rice is considered to be the most Al-tolerant species among small grain crop.

*Corresponding author: apat.icarneh@gmail.com

Supplementary Tables only in online edition

Experiments with upland rice have shown that roots of tolerant genotypes accumulate less Al particularly at the root apex, which is the primary site of action for Al. The present study was undertaken to estimate genetic variability of yield and its components in upland rice grown under acid soil condition in mid-altitude hills.

Materials and Methods

The experimental material consisted of a core set of 21 rice germplasm with varying degree of tolerance to acid soil. These were selected from the set of 183 germplasm collection from North East (NE) India and some international collection. The trial was conducted at the research farm of ICAR Research Complex for NEH Region, Umiam (980 m above sea level) in a Randomized Block Design with 3 replications and with a spacing of 20 x 15 cm. Average pH of the plot was 5.2 (range 5.03 – 5.29, depending on moisture). No fertilizer was applied but need-based plant protection measures were taken. The trial was conducted during 2009 and 2010. In 2009, observations were taken for sixteen traits which were then used for construction of the core set. In 2010, twenty agronomic traits, as listed in Table 1, related to growth and yield were recorded from the core set. Chlorophyll index was recorded using a SPAD meter (Minolta Corporation). Root length and root area were measured using a root scanner (Delta T Corporation, England). Analyses of variance (ANOVA - Panse and Sukhatme, 1967); genetic parameters such as GCV and PCV (Burton, 1952), broad sense heritability (h^2 -Burton and De Vane, 1953) and genetic advance as percentage of mean (Johnson *et.al.*, 1955) were calculated. For calculation of genotypic variance (Vg), phenotypic variance (Vp), heritability, genetic advance (GA) and genetic advance as percentage of mean (GA%) a software TNAUSTAT (http://sites.google.com/ site/tnaustat) was

used. ANOVA, GCV and PCV were calculated using Microsoft Excel.

Results and Discussion

Analysis of variance revealed significant differences among the genotypes for all traits, indicating presence of high variability. Some of the traits which have high possibility of being influenced by soil acidity *viz.* chlorophyll index, number of ear bearing tillers, root length and root area showed highly significant differences among the genotypes. Thus, there is ample scope of selection for different agronomic and soil acidity tolerance related traits for rice improvement.

Phenotypic and genotypic variances for the different traits are presented in Table 1. Genotypic and phenotypic variances were highest for grain yield/plant and lowest for 100 grain weight. Both the variances were high for no. of filled grains/panicle, plant height, days to 50% flowering, days to maturity, flag leaf area and straw weight. Environmental variance (Ve) was low for several traits like 100 grain weight, chlorophyll index, panicle node number and no. of ear bearing tillers indicating least influence of environment on these traits. Values of phenotypic and genotypic variance were close for majority of the traits indicating their stable nature. Similar findings were reported by Rao *et al.* (1996). Close values of genotypic and phenotypic variances may be due to the use of traditional germplasm which, because of their selection over long period of time, remain more or less stable across locations.

The GCV and PCV provide a measure to compare the variability present in the traits. The GCV especially helps to compare the genetic variability in the traits. GCV and PCV were classified as suggested by Sivasubramanian and Madhavamenon (1973). GCV was high (more than 20%) for flag leaf area, plant height, no. of tillers per plant, no. of ear bearing tillers, no. of filled grains/panicle, panicle weight, root length and area, straw weight and grain yield (Table 1). It was low (less than 10%) for days to maturity and chlorophyll index at heading. GCV was moderate for rest of the traits. High GCV for the traits is indicative of the high genetic variability within the test genotypes. This also indicated that the construction of core set was successful. Low GCV in the chlorophyll index may be due to the continuous low light conditions during the crop growing period. In general PCV was higher than GCV. Two traits, root length and no. of filled grains/panicle showed appreciable difference between GCV and PCV when compared with other traits. High influence of environment on root length may be due to variations in pH with changing soil moisture content. The high influence of environment on filled grains/panicle may be due to the combined effect of soil acidity and low temperature (at the site) at grain filling stage. The small difference observed between GCV and PCV indicate the presence of high genetic variability for the traits which may facilitate selection (Yadav, 2000).

The broad sense heritability can be used as a predictor in the selection procedure (Allard, 1960). This gives an idea about the exploitable portion of variation. Heritability (h^2) estimates were high for most of the traits although it was moderate for flag leaf angle, no. of filled grains/panicle, root length and root area. Similar results for yield related traits of upland rice were reported in earlier studies (Sharma and Choubey, 1985; Pattanayak *et al*., 2000).

High heritability does not always indicate high genetic gain. Therefore, heritability and genetic advance should be considered together. High genetic advance occurs due to additive gene action (Panse, 1957). High heritability with high genetic advance was recorded for grain yield/plant and plant height. Similar result for these traits was reported by Yadav *et al.* (2010). When genetic advance as percent of mean was considered; flag leaf area, no. of tillers/plant, no. of ear bearing tillers, panicle weight, straw weight and grain yield showed high heritability with high genetic advance. Among these, the role of panicle weight has been pointed out in several previous studies (for a brief review see Samonte *et al*., 1998).

The overall results indicted the core set of germplasm contained high genetic variability. The broad sense heritability and genetic advance as percentage of mean indicated that panicle weight and grain yield/plant are the two most important yield components and selection based on these traits would be very effective in upland rice grown under acid soil conditions.

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Table 1: Phenotypic and genotypic variation for different plant growth parameters

	Traits	Variance			GCV	PCV	h^2 (%)	GA	GA as % of mean
		Vg	Vp	Ve					
1	Days to 50% flowering	134.50	154.58	20.78	10.66	11.43	87.01	22.29	20.49
2	Days to maturity	125.00	133.56	8.56	7.85	8.12	93.59	22.28	15.65
3	Chlorophyll index at heading	8.35	10.42	2.06	7.63	8.52	80.19	5.33	14.07
4	Chlorophyll index at flowering	25.66	31.35	5.68	11.78	13.02	81.86	9.44	21.96
5	Chlorophyll index at milking	22.28	25.27	2.99	11.03	11.75	88.17	9.13	21.34
6	Flag leaf area	128.99	142.88	13.89	34.46	36.27	90.28	22.23	67.46
7	Flag leaf angle	46.09	63.73	17.65	9.98	11.74	72.31	11.89	17.48
8	Plant height	696.96	838.72	141.76	23.75	21.65	83.10	49.56	40.66
9	Number of tillers per plant	15.08	17.60	2.52	37.43	15.29	85.70	7.40	71.39
10	Panicle length	7.58	8.75	1.17	10.30	11.07	86.59	5.28	19.74
11	Panicle node number	1.86	2.16	0.30	13.83	14.91	85.98	2.60	26.41
12	No. of primary branches / panicle	3.69	4.42	0.73	14.57	15.95	83.39	3.61	27.40
13	No. of filled grains / panicle	2640.727	4309.18	1668.45	25.20	32.19	61.28	82.87	40.64
14	No. of ear bearing tillers / plant	9.02	11.15	2.13	32.00	35.58	80.89	5.56	59.29
15	Single panicle weight	71.33	84.95	13.61	40.97	44.71	83.97	15.94	77.35
16	Straw weight	113.34	142.22	28.88	32.95	36.91	79.69	19.58	60.60
17	Root length	63.54	101.19	37.64	33.49	42.26	62.80	13.01	54.67
18	Root area	22.74	30.84	8.10	24.97	29.08	73.74	8.43	44.17
19	Grain yield	82386.16	95394.36	13008.2	45.37	48.82	86.36	549.49	86.85
20	Weight of 100 grain	0.25	0.29	0.04	18.98	20.44	86.17	0.95	36.29

Vg = genotypic variance, Vp = phenotypic variance, Ve = environmental variance, GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, h^2 = heritability, GA = genetic advance