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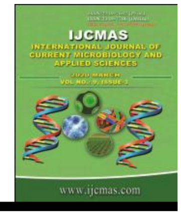

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Assessment of Genetic Variability, Heritability and Genetic Advance for Yield in Advanced Breeding Line (*Oryza sativa* L.) of Low Land Rice in Meghalaya

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The genetic parameters were studied to generate information on genetic variability, heritability and genetic advance among 22 advanced breeding lines including two checks at the experimental Farm of College of post graduate studies, CAU (Imphal), Umiam, Meghalaya during *Kharif* 2017. Analysis of variance indicated the existence of significant differences among the genotypes for most of the characters. High Phenotypic Coefficient of variation (PCV) and Genotypic Coefficient of Variation (GCV) values were recorded for number of grain per panicle and spikelet per plant which suggests the possibility of improving this trait through selection. The low magnitude of difference between phenotypic and genotypic coefficients of variations were recorded for characters such as days to 50 % flowering, leaf length and leaf width indicating limited influence of environment in the expression of this trait. Thus, selection based on phenotypic expression of the trait would be effective for genetic improvement. High heritability in broad sense values indicate that the traits under study are less influenced by environment in their expression. Therefore, the quantitative traits are highly heritable. However, highest heritability was recorded for leaf length and leaf width. Moderate heritability estimates were observed for number of panicles per plant, spikelets per panicle, grains per panicle, and spikelet fertility.

Introduction

The genus *Oryza* consists of two cultivated species *Oryza sativa* (Asian species) and *Oryza glaberrima* (African species). Rice (*Oryza sativa*) is the primary food source for more than a third of the world's population. South Asia is considered to be one of the major centres for rice domestication and is also known as the food bowl of Asia. Asia accounts for over 90% of the world's production of rice, which is mainly contributed by China, India and Indonesia. Among all the Asian countries, India is the prominent rice growing country accounting for about 20% of all world rice production. India is home to wide varieties of rice cultivars, landraces and many lesser known varieties that have been under cultivation since ages by farmers. In India rice is the major crop grown at 43.57 M ha with an average production of 104.32 million tonnes and productivity of 2.39 t/ha. In Meghalaya rice is grown in more than 42% of total arable area, but is having average production of 2.32 lakh tonnes and productivity of 2.12 t/ha. During the post green revolution period due to introduction of improved varieties, rice yield in North Eastern hill region has been enhanced by up to 40 %. Household food security of North-Eastern states of India predominantly depends on rice. Since North Eastern India is home to a wide range of ecological conditions for rice growing in terms of slopes, altitudes, agro climatic conditions, soil types, etc; it has led to immense variability among rice cultivars in the region.

Rice is the staple food of about 3 billion people, nearly half the world's population, depends on rice for survival. In many countries, rice accounts for more than 70% of human caloric intake and main source of protein for poor people in developing countries. It provides 21% of global human per capita energy and 15% of per capita protein (Maclean *et al.,* 2002). Calories from rice are particularly important in Asia, especially among the poor, where it accounts for 50-80% of daily caloric intake. The major part of rice consists of carbohydrate in the form of starch, which is about 72-75 percent of the total grain composition. The protein content of rice is around 7 percent and the protein of rice contains glutelin, which is also known as oryzenin. The nutritive value of rice protein (biological value = 80) is much higher than that of wheat (biological value = 60) and maize (biological value = 50) or other cereals. Rice pericarp and germ contain most of minerals including about 4 percent phosphorus. Rice can also be used in cereals, snack foods, brewed beverages, flour, oil, syrup and religious ceremonies to name a few other uses.

Rice production in North East India can be further increased by effective hybridization of locally superior cultivars and elite germplasm, followed by selection in the segregating generations for development of improved high yielding lines suitable to specific agro climatic zones and agronomic practices. Development of varieties adapted to acidic soils is also an important requirement as more than 70% of the soil in the North East is acidic. As acidic soils suffer from problems of phosphorus deficiency and iron toxicity, it is important to select for improved lines that show tolerance to these stresses. Since low land rice is exposed to many diseases like blast, so breeding of disease resistant varieties, which are the most important part of any Integrated Disease Management (IDM) practice, is required for effective control of disease.

The two pillars of efficient and successful breeding programme are the choice of parental lines and precise selection methodology that can effectively identify transgressive segregants which will lead to increased grain yield per plant and per unit area, eventually leading to development of high yielding varieties. One of the major criteria of parent hybridization programme is the divergence between them with respect to agro-physiological trait.

Researchers have studied complex cause and effect system to determine traits that influence the final grain yield and other important traits during plant ontogeny (Maman *et al.,* 2004, Mohammadi *et al.,* 2003 and Samonte *et al.,* 1998). Yield of paddy is a complex quantitative character controlled by many genes interacting with the environment and is the product of many factors called yield components. Selection of parents based on yield alone is often misleading. Hence, the knowledge about relationship between yield and its contributing characters is needed to form an efficient selection strategy for the plant breeders to evolve an economic variety. Grain quality is an economically important trait in rice, and any information about the genetic mechanisms governing grain quality traits will be useful for the rice breeders.

The presence of genetic variability for morphological and yield related traits is of utmost importance for identification and development of desirable genotypes as improvement in any trait is depends on the amount of genetic variability present in the experimental material of that trait. Besides genetic variability, heritability and genetic advance are useful parameters on which selection efficiency depends upon. Heritability is an index of transmissibility of the characters from the parents to offspring and has a predictive role in plant breeding programme. However estimates of heritability alone fail to indicate the response to selection. Therefore estimates of genetic advance along with heritability estimates takes into account for genetic improvement of the selected genotypes over the parental populations for various traits. Thus, the genetic advance has an advantage over heritability and helps breeders in various selection programmes. The genetic advance for the studied traits is dependent on the extent of heritability, genetic variability and selection intensity.

Relatively high heritability and genetic advance values for the traits under study favour the possibility of selection of desirable genotypes. The present investigation was, therefore, undertaken to estimate of genetic variation, heritability and genetic advance in advanced breeding line of low land rice and to identify best genotypes for cultivation under College of post graduate studies, Umiam, Meghalaya in the *Kharif* season of 2017.

Materials and Methods

The experiment was carried out at the experimental Farm of College of post graduate studies, CAU (Imphal), Umiam, Meghalaya. The experimental area occupied was uniform in respect of topography and fertility. The climate in Barapani is warm and temperate. In winter, there is much less rainfall in Barapani than in summer. The average annual temperature in Barapani is 20.0 °C. Precipitation here averages 4169 mm. July is the warmest month of the year. The temperature in July averages 23.9 °C. January has the lowest average temperature of the year. It is 13.5 °C. The genotypes included in the study are 22 advanced breeding lines (F_7) of rice (*Oryza sativa*) selected based on their yield performance from the previous season. These lines were planted in randomized complete block design with three replications. A detail of genotype are given in Table 1

Experiment consisted of 22 advanced breeding lines and 2 checks lines which were grown in randomized complete block design with three replications. Twenty nine day old seedlings were transplanted in the experimental site with spacing of 20 cm between plant to plant and 20 cm between the rows keeping single seedling per hill. Gap filling was done within a week in order to maintain uniform plant population. The standard agronomic practices were adopted for normal crop growth. Observations were recorded as per the DUS guidelines provided by IIRR (Indian Rice Research Institute) Hyderabad. Observations were recorded on the basis of middle five random competitive plants selected from each line in every replication for the evaluation of yield and yield contributing traits. Mean of main, average and smallest panicle from each of the five randomly selected plants were used to record the observations of panicle traits. Observations on all the morphological characters were recorded on the net plot basis viz., Basal Leaf sheath color, Leaf Auricle, Leaf Ligule, Ligule shape, Leaf collar, Flag Leaf: Attitude of blade, Leaf sheath anthocyanin colouration, Leaf blade: anthocyanin, Panicle secondary branch, Leaf senescence, Spikelet: color of tip of lemma, Panicle: exsertion, Panicle: awns, Lemma:anthocyanin colouration of area below apex and Observations on all the Quantitative characters were Days to 50 per cent flowering, Plant height (cm), Tillers per plant, Panicle per plant, Panicle length (cm), Leaf length (cm), Leaf width(cm), Leaf area index, Canopy temperature (^{0}c), Biological yield per plant (g), Spikelets per plant, Number of grains per plant, Spikelet fertility (%), Harvest Index (%), 1000- grain weight, Grains yield per plant. Data were compiled by taking mean value over randomly selected plants from all the replications and subjected to the statistical analysis for randomized block design as per Panse and Sukhatme 1984. Genetic parameters such as genotypic (GCV) and phenotypic (PCV) coefficients of variation, heritability and genetic advance were computed as per Burton and De Vane, 1953 and Johnson *et al.,* (1955).

Results and Discussion

Analysis of variance

Analysis of variance indicated the existence of significant differences among the genotypes for most of the characters viz., days to 50% flowering, plant height, Tillers per plant, Panicle per plant, Plant length, Leaf length, Leaf area index, Canopy temperature, Biological yield, Spikelet per plant, No. Of grains per plant, Spikelet fertility, 1000 grain weight and grain yield per plant studied except Leaf width, and Harvest index. The results of analysis of variance are presented in Table 2.

Analysis of variance indicated that mean sum of squares due to genotypes were significant for all the quality traits. This indicates the presence of considerable variability among the breeding lines. Number of grains per plant, spikelet per plant, yield per hectare, leaf area index, days to 50% flowering, biological yield and plant height he showed maximum variation among breeding lines whereas qualitative traits showed relatively less variation. Padmaja *et al.,* (2008), Khan *et al.,* (2012) and Sahidullah *et al.,* (2009) have also reported highly significant differences for all the characters except flag leaf width and 1000 seed weight among the genotypes. In a similar study, Laxuman *et al.,* (2010) have reported that estimates of genotypic and phenotypic coefficients of variation were high for all the characters except days to fifty per cent flowering and panicle length.

Mean, Genetic variability, heritability

The genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV), heritability were estimated on the basis of data recorded on twenty four breeding lines including two standard checks. The results obtained for various morphological traits are furnished in Table 3 and mean performance of rice genotypes for various quantitative characters in Table 4.

The characters studied in the present investigation exhibited low, moderate and high PCV and GCV values. Among the metric characters, number of grains per plant recorded highest PCV (28.04) followed by spikelet per plant (24.23) and the lowest PCV (7.16) was recorded for plant height.

Highest GCV values were recorded for the number of grain per panicle (19.48) followed by spikelet per plant (16.38) whereas lowest GCV value (3.75) was recorded for plant height.

Heritability is classified as low (below 0.30), medium (0.30-0.60) and high (above 0.61). Three characters studied in the present investigation expressed high heritability estimates ranging from 0.62 to 0.99. Among the metric characters, highest heritability was obtained for leaf length (0.88), followed by leaf width (0.79) and days to 50% flowering (0.66). Number pf panicles per plant, canopy temperature, number of spikelets per plant and grains per plant showed medium heritability estimates.

A high coefficient of variability indicates that there is a scope of selection and improvement of these traits. High PCV and GCV values were recorded for number of grain per panicle and spikelet per plant which suggests the possibility of improving this trait through selection. The low magnitude of difference between phenotypic and genotypic coefficients of variations were recorded for characters such as days to 50 % flowering, leaf length and leaf width indicating limited influence of environment in the expression of this trait. Thus, selection based on phenotypic expression of the trait would be effective for genetic improvement.

High heritability in broad sense values indicate that the traits under study are less influenced by environment in their expression. Therefore, the quantitative traits are highly heritable. However, highest heritability was recorded for leaf length and leaf width. Moderate heritability estimates were observed for number of panicles per plant, spikelets per panicle, grains per panicle, and spikelet fertility. Unlike our study, high heritability for grain yield plant-1 has been reported by Reddy and De (1996), Reddy *et al.*, (1997), Ashvani *et al.*, (1997), Murthy *et al.*, (1999), Tripathi *et al.*, (1999), Durai *et al.*, (2001), Mishra and Verma (2002), Elayaraja *et al.*, (2004), Hasib *et al.*, (2004), Madhavilatha *et al.*, (2005), Panwar (2005), Girish *et al.*, (2006), Muthuswamy and Ananda Kumar (2006), Narinder (2006), Kole *et al.*, (2008) and Selvaraj *et al.*, (2011). Under low input acidic soil conditions, this was not found to be the case in our study.

Table.1 List of advanced breeding lines and checks used in the study

Advanced breeding lines		**Checks**
CAUS101	CAUS112	**CAU R1 Shasharang**
CAUS102	CAUS113	
CAUS103	CAUS114	
CAUS104	CAUS115	
CAUS105	CAUS116	
CAUS106	CAUS117	
CAUS107	CAUS118	
CAUS108	CAUS119	
CAUS109	CAUS120	
CAUS110	CAUS121	
CAUS111	CAUS122	

Table.2 ANOVA for important morphological characters and yield in different rice genotypes

Sl.no.	Traits	MEAN Square				Range		
		Genotype (df=23)	Error (df=46)	Total SS (df=71)	mean value	Maximum	Minimum	CV
1	DTF	199.15**	29.40	94.90	125.56	140.00	102.00	4.31
2	PH	71.94**	33.68	50.02	95.13	105.27	85.40	6.12
3	TPP	3.16**	1.52	2.01	11.43	14.00	9.40	10.87
4	PPP	6.51**	2.00	3.43	9.65	12.93	6.53	14.70
5	PL	6.20**	2.96	4.06	24.77	27.67	22.67	6.97
6	LL	48.04**	2.12	17.18	34.51	41.87	28.73	4.23
7	LW	0.15	0.01	0.07	1.80	2.27	1.53	6.09
8	LAI	21350.95**	10333.65	14177.65	537.51	742.96	380.59	18.79
9	CT	4.22**	1.34	2.36	19.86	23.64	18.19	5.80
10	BY	125.86**	61.82	84.42	51.33	64.53	38.60	15.24
11	SPP	138257.54**	39227.57	77044.17	1109.02	1585.93	757.26	18.03
12	NGPP	115378.78**	30394.70	62793.84	864.22	1250.13	510.47	20.62
13	SF	92.87**	23.39	45.33	77.92	86.09	64.12	6.21
14	HI	0.06	0.02	0.04	0.71	0.93	0.41	21.94
15	1000 GW	25.22**	11.40	16.48	24.96	32.44	19.21	13.42
16	GYPP	38.13**	17.87	29.81	21.20	29.02	15.69	20.17
17	YPH	1165583.46**	409627.08	671908.30	3699.23	4936.00	2341.84	17.20

DTF=Days to 50% flowering; PH=Plant height (cm); TPP=Tillers per plant; PPP=Panicle per plant; PL=Panicle length (cm); LL=Leaf length (cm); LW= Leaf width (cm); LAI= Leaf area index; CT= Canopy temperature (^{0}c); BY= Biological yield (g); SPP=Spikelet per plant; NGPP=No. Of grains per plant; SF=Spikelet fertility (%); HI=Harvest index; 1000GW=1000 grain weight (g); GYPP=grain yield per plant (g); YPH=Yield per hectare (kg).
*significant at 5% level of significance, * *significant at 1% level of significance

Table.3 Components of Variance

sl.no	character	Vp	Vg	PCV (%)	GCV (%)	ECV (%)	h^2	GA	GG (%)	GG/Y (%)
1	DTF	85.99	56.58	7.39	5.99	4.32	0.66	15.52	13.08	1.87
2	PH	46.43	12.75	7.16	3.75	6.10	0.27	7.37	7.78	1.11
3	TPP	2.07	0.55	12.59	6.46	10.80	0.26	1.52	13.25	1.89
4	PPP	3.50	1.50	19.38	12.70	14.64	0.43	2.53	25.06	3.58
5	PL	4.04	1.08	8.12	4.19	6.95	0.27	2.14	8.46	1.21
6	LL	17.43	15.31	12.10	11.34	4.22	0.88	8.07	23.81	3.40
7	LW	0.06	0.04	13.19	11.70	6.09	0.79	0.44	24.70	3.53
8	LAI	14006.09	3672.43	22.02	11.27	18.91	0.26	125.02	25.03	3.58
9	CT	2.30	0.96	7.63	4.93	5.83	0.42	2.02	9.41	1.34
10	BY	83.16	21.35	17.77	9.00	15.32	0.26	9.53	17.57	2.51
11	SPP	72237.56	33009.99	24.23	16.38	17.86	0.46	374.82	29.53	4.22
12	NGPP	58722.73	28328.02	28.04	19.48	20.17	0.48	347.22	35.08	5.01
13	SF	46.55	23.16	8.76	6.18	6.21	0.50	9.93	12.65	1.81
14	HI	0.01	0.00	19.01	9.57	16.43	0.25	0.08	12.52	1.79
15	1000 GW	16.01	4.61	16.04	8.61	13.54	0.29	4.43	17.41	2.49
16	GYPP	24.62	6.75	23.41	12.26	19.95	0.27	5.36	21.81	3.12
17	YPH	661612.54	251985.46	21.99	13.57	17.30	0.38	1035.59	29.92	4.27

Vp: Phenotypic variance, Vg: Genotypic variance, PCV: Phenotypic coefficient of variance(%), GCV: Genotypic coefficient of variance(%), ECV: Environmental coefficient of variance(%), GA: Genetic advance, GG: Genetic gain(%), GG/Y: Genetic gain per year(%). *significant at 5% level of significance, **significant at 1% level of significance

Table.4 Mean performance of rice genotypes for various quantitative characters

Genotype	DTF	PH	TPP	PPP	PL	LL	LW	LAI	CT	BY	SPP	NGPP	SF	HI	1000-GW	GYPP	YPH
CAUS101	128.00	89.40	14.00	12.93	24.13	41.87	1.58	454.85	18.70	52.53	1414.00	1205.80	84.54	0.91	20.90	25.08	3826.20
CAUS102	117.67	105.27	9.40	6.53	27.67	34.30	2.14	505.60	19.75	46.40	918.80	775.27	84.43	0.69	26.19	20.28	2865.28
CAUS103	126.67	98.53	12.33	10.40	24.00	29.47	1.66	581.43	18.87	49.93	1213.00	1002.60	79.36	0.82	23.03	23.08	3943.82
CAUS104	125.67	94.67	12.53	8.07	26.07	33.00	2.09	566.17	19.60	49.53	1050.67	626.00	84.35	0.66	30.77	19.27	4520.01
CAUS105	130.67	94.40	10.73	8.96	25.07	36.47	1.93	455.72	20.51	54.13	1258.27	1035.27	79.04	0.86	25.72	26.49	4710.40
CAUS106	127.67	93.40	10.60	8.33	24.80	35.87	1.85	626.21	18.19	48.40	1097.73	847.40	77.31	0.82	26.33	22.17	3827.63
CAUS107	118.33	97.33	11.47	9.53	23.93	28.73	1.82	573.86	19.61	47.27	940.80	728.47	71.05	0.66	25.66	19.23	4170.24
CAUS108	116.00	95.07	11.07	10.73	22.53	39.07	1.45	742.96	21.83	51.80	1118.13	873.73	75.83	0.69	25.21	22.05	3044.86
CAUS109	128.67	93.80	12.00	10.43	25.47	32.20	1.92	607.28	19.71	46.20	1094.08	824.18	75.25	0.61	21.85	18.09	3721.37
CAUS110	135.33	99.93	13.13	12.13	23.73	36.67	1.67	465.78	19.09	64.53	1247.80	956.33	76.55	0.93	27.54	26.33	4936.19
CAUS111	140.00	95.47	12.13	11.80	23.40	37.73	1.55	506.07	18.75	50.47	899.40	687.67	76.32	0.58	23.36	16.08	3816.80
CAUS112	123.00	98.67	12.60	10.73	23.67	31.00	1.85	439.48	20.51	60.40	898.80	690.00	76.76	0.60	26.66	18.39	3699.27
CAUS113	128.00	94.20	11.53	9.80	25.87	33.80	1.82	533.27	19.37	58.67	1382.87	1099.27	78.12	0.83	22.11	24.29	2714.28
CAUS114	123.00	90.27	11.00	7.67	24.60	32.13	1.78	519.06	20.41	41.20	883.13	652.53	73.87	0.52	24.02	15.69	3282.04
CAUS115	133.67	98.33	11.20	9.07	27.19	30.40	1.91	629.01	19.05	52.67	1058.33	659.07	64.12	0.57	24.28	15.99	3544.02
CAUS116	125.33	91.80	10.27	9.13	24.09	34.27	1.90	555.41	19.59	54.73	1490.27	1192.33	79.86	0.79	19.20	22.87	3510.89
CAUS117	121.67	101.80	11.13	9.27	26.13	35.13	1.91	473.19	19.67	49.13	1026.73	868.53	84.03	0.73	24.29	21.14	3692.93
CAUS118	131.33	88.80	10.67	8.73	22.67	29.07	1.39	541.82	20.83	38.60	887.33	765.20	86.09	0.61	24.66	18.85	3621.39
CAUS119	129.33	93.47	11.13	9.47	23.07	43.73	2.27	666.85	20.13	57.80	1318.77	964.73	73.48	0.75	23.22	22.38	3538.31
CAUS120	132.00	100.07	10.00	8.33	25.73	36.50	2.08	531.23	18.57	46.27	1105.87	892.27	80.83	0.81	24.73	22.05	3815.93
CAUS121	132.00	93.73	11.07	9.07	25.27	38.33	1.68	430.50	19.71	50.00	1016.07	904.67	84.58	0.79	25.52	23.19	4715.05
CAUS122	102.00	85.40	11.27	10.38	24.67	30.80	1.53	495.31	21.23	40.63	757.26	510.47	67.23	0.41	32.43	16.54	2341.84
CAU R1	112.00	87.47	11.00	9.16	23.40	30.53	1.82	380.59	23.64	45.83	952.53	729.36	75.86	0.45	27.69	20.15	3563.17
Shasharang	125.33	101.87	12.00	11.03	27.27	37.27	1.71	618.50	19.29	62.67	1585.93	1250.13	81.15	0.86	23.16	29.02	3359.51
SEM	3.36	3.37	0.61	0.70	0.85	0.76	0.10	26.75	0.53	4.02	102.50	93.34	2.00	0.14	1.04	2.55	376.85

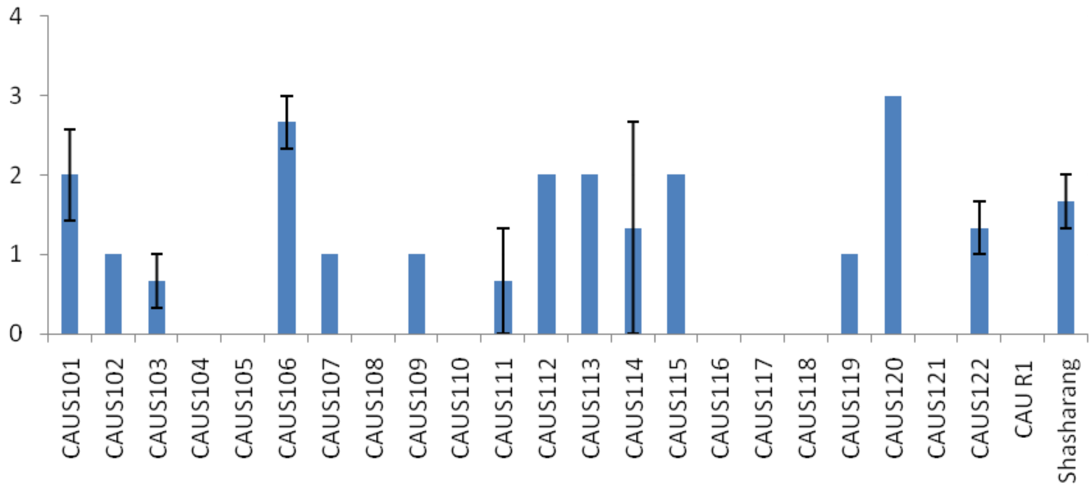
Table.5 Characterization of rice genotypes with respect to discreet characters

	BLSC	LA	LL	LS	LC	FLAB	LSAC	LBA	PSB	LS	SCTL	PE	PA	LABA
CAUS101	Green	Present	Present	Cleft type	Absent	Semi-erect	Green	Absent	Present	Late	White	Well exserted	Absent	Absent
CAUS102	Green	Present	Present	Cleft type	Absent	Erect	Green	Absent	Present	Early	Purple	Partly	Absent	Present
CAUS103	Green	Present	Present	Cleft type	Absent	Erect	Green	Absent	Present	Medium	Brown	Partly	Absent	Absent
CAUS104	Green	Present	Present	Cleft type	Present	Erect	Green	Absent	Present	Medium	Purple	Well exserted	Absent	Present
CAUS105	Green	Present	Present	Cleft type	Absent	Erect	Green	Absent	Present	Late	Yellow	Partly	Absent	Absent
CAUS106	Green	Present	Present	Cleft type	Absent	Erect	Green	Absent	Present	Late	Brown	Well exserted	Absent	Absent
CAUS107	Green	Present	Present	Cleft type	Absent	Erect	Green	Absent	Present	Early	Yellow	Partly	Absent	Absent
CAUS108	Green	Present	Present	Cleft type	Absent	Erect	Green	Absent	Present	Early	White	Partly	Absent	Absent
CAUS109	Green	Present	Present	Cleft type	Absent	Erect	Green	Absent	Present	Medium	Yellow	Well exserted	Absent	Absent
CAUS110	Green	Present	Present	Cleft type	Absent	Erect	Green	Absent	Present	Late	Brown	Partly	Absent	Absent
CAUS111	Green	Present	Present	Cleft type	Absent	Horizontal	Green	Absent	Present	Late	Brown	Partly	Absent	Absent
CAUS112	purple	Present	Present	Cleft type	Absent	Erect	purple	Absent	Present	Early	Purple	Partly	Absent	Present
CAUS113	Green	Present	Present	Cleft type	Absent	Erect	Green	Absent	Present	Medium	White	Well exserted	Absent	Absent
CAUS114	Green	Present	Present	Cleft type	Absent	Erect	Green	Absent	Present	Medium	Purple	Partly	Absent	Present
CAUS115	purple	Present	Present	Cleft type	Present	Semi-erect	purple	Absent	Present	Late	Purple	Partly	Absent	Present
CAUS116	Green	Present	Present	Cleft type	Absent	Semi-erect	Green	Absent	Present	Medium	White	Partly	Absent	Absent
CAUS117	Green	Present	Present	Cleft type	Absent	Erect	Green	Absent	Present	Medium	White	Partly	Absent	Absent
CAUS118	purple	Present	Present	Cleft type	Present	Erect	purple	Absent	Present	Medium	Purple	Partly	Absent	Present
CAUS119	purple	Present	Present	Cleft type	Present	Erect	purple	Absent	Present	Early	White	Partly	Absent	Absent
CAUS120	purple	Present	Present	Cleft type	Present	Semi-erect	purple	Present	Present	Medium	Purple	Partly	Absent	Present
CAUS121	Green	Present	Present	Cleft type	Absent	Erect	Green	Absent	Present	Medium	Yellow	Well exsertion	Absent	Absent
CAUS122	Green	Present	Present	Cleft type	Absent	Erect	Green	Absent	Present	Early	White	Partly	Absent	Absent
CAU R1	Green	Present	Present	Cleft type	Absent	Erect	Green	Absent	Present	Early	White	Partly	Absent	Absent
Shasharang	Green	Present	Present	Cleft type	Absent	Erect	Green	Absent	Present	Early	White	Partly	Absent	Absent

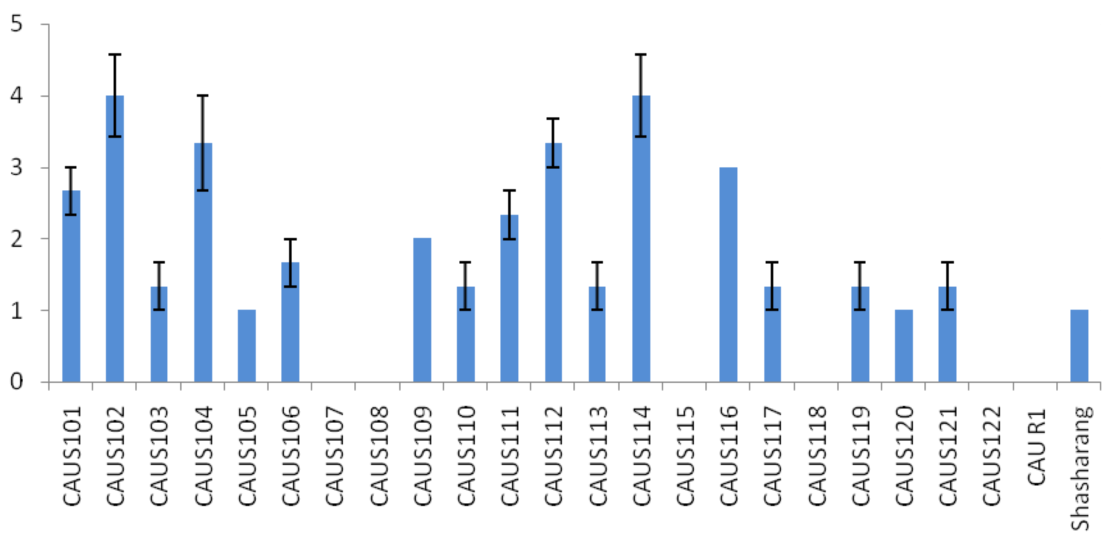
BLSC=Basal Leaf sheath colour ; LA=Leaf Auricle; LL=Leaf Ligule ; LS=Ligule shape; LC=Leaf collar ; FLAB=Flag Leaf: Attitude of blade ; LSAC=Leaf sheath anthocyanin colouration ;LBA=Leaf blade: anthocyanin ; PSB=Panicle secondary branch; LS= Leaf senescence ;SCTL Spikelet: color of tip of lemma ; PE=Panicle: exserted ; PA=Panicle: awns ; LABA=Lemma:anthocyanin colouration of area below apex

Fig.(A) Blast Disease Scoring; **(B)** Bronzing Scoring

(A)



(B)



DUS characterization

Twenty four genotypes were characterized using seventeen morphological characters as per standard evaluation system (IRRI, 1996) (Table 5). These descriptors are highly heritable, unambiguous and easily identifiable. The study of morphological traits was carried to describe each genotype and establish their diagnostic characteristics. The experimental material showed great variability for the sixteen morphological traits (Table 5). All the traits viz. basal leaf sheath colour, Leaf Auricle, Leaf Ligule, Ligule shape, Leaf collar, Flag Leaf: Attitude of blade, Leaf sheath anthocyanin colouration, leaf blade: anthocyanin, Panicle secondary branch, Stem thickness, Leaf senescence, Spikelet: color of tip of lemma, Panicle: exsertion, Panicle: awns, Lemma: anthocyanin colouration of area below apex, Resistance to blast Disease Scoring 0 to 5. (Fig.A), Bronzing Scoring 0 to 5. (Fig.B) exhibited wide variation among the genotypes under study.

In conclusion, analysis of variance indicated that mean sum of squares due to genotypes were significant for all the quality traits. This indicates the presence of considerable variability among the breeding lines. Number of grains per plant, spikelet per plant, yield per hectare, leaf area index, days to 50% flowering, biological yield and plant height showed maximum variation among breeding lines whereas qualitative traits showed relatively less variation. A high coefficient of variability indicates that there is a scope of selection and improvement of these traits. High PCV and GCV values were recorded for number of grain per panicle and spikelet per plant which suggests the possibility of improving this trait through selection. The low magnitude of difference between phenotypic and genotypic coefficients of variations were recorded for characters such as days to 50% flowering, leaf length and leaf width indicating limited influence of environment in the expression of this trait. Thus, selection based on phenotypic expression of the trait would be effective for genetic improvement. High heritability in broad sense values indicate that the traits under study are less influenced by environment in their expression. Therefore, the quantitative traits are highly heritable. However, highest heritability was recorded for leaf length and leaf width.

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