ISSN (Online): 2091-2609
DOI Prefix: 10.3126/ijasbt

International Journal of Applied Sciences and Biotechnology (IJASBT)

Research Article

Genetic Variability and Correlation Coefficients of Major Traits in Cold Tolerance Rice (*Oriza sativa* L.) Under Mountain Environment of Nepal

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Article Information

Received: 21 September 2019
Revised version received: 09 November 2019
Accepted: 13 November 2019
Published: 28 December 2019

Cite this article as:
NH Ghimire and PM Mahat (2019) Int. J. Appl. Sci. Biotechnol. Vol 7(4): 445-452.
DOI: 10.3126/ijasbt.v7i3.26922

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Peer reviewed under authority of IJASBT
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Abstract

This study was conducted at Agricultural Research Station (ARS), Vijayanagar, Jumla Nepal comprising fifteen genotypes of cold tolerance rice during regular rice growing season of high hill in 2015 in RCBD (Randomized Complete Block Design) with three replications to observe genetic variability, correlation, heritability, genetic advance and clustering of genotypes in relation to yield and yield associated traits and selection and advancement of early maturing, high yielding, disease resistant, and cold tolerance genotypes for high mountain area. Analysis of variance revealed that all characters except number of panicle per hill were significantly different indicating presence of variation in genetic constituents. Phenotypic coefficient of variance (PCV) was higher than genotypic coefficient of variance (GCV) for all the corresponding traits under study indicating environmental influence for the expression of the traits. Higher PCV and GCV value were obtained in grain yield (Yld), number of grain per panicle (NGPP) and number of panicle per hill (NPPH). Higher heritability coupled with higher genetic advance (GA) was obtained in NGPP, NPPH and Yld, high heritability and medium GA was obtained in thousand grains wt (TGW), plant height (Pht) and panicle length (PL) indicating additive gene action indicating direct selection may be a tool for varietal development. Positive and significant correlation was obtained between all characters except DM and Pht, PL and PHT and TGW and PPH. Total three clusters were obtained in eighty percent euclidean similarity clustering indicating genetic closeness/distances among the genotypes. Culture 1 carries the superior five genotypes including NR-10638-B-B-4 and NR-10695-B-B-B.

Keywords: Clustering; Correlation; Genetic Advance; Heritability; Rice

Introduction

Agriculture is an important sector in the Nepalese economy, contributing to 27.10% (Agriculture and forestry) of its GDP (Gross Domestic Product) and engaging about two-thirds of its population (MoAD, 2018). Rice is the staple food and plays vital role for food security in Nepal. It ranks at top in terms of area, production and livelihood of Nepalese people. Total area of rice cultivation in Nepal is 1,552,469 ha (50.22% of cultivated land) producing 5,230,326 mt with productivity 3.369 mt/ha (MoAD, 2018). Rice is cultivated in diverse agro climatic environment ranging from tropical plain (60 masl) to foot of mountain at highest elevation (3050 masl) that is Chhuma Jyula which lies at Jumla District, Karnali Zone of Nepal (ARS, 2014). Rice is cultivated in 69.92% irrigated land of Nepal and different domain varies for irrigated rice cultivation 51% in mountain, 60% in hill and 75% in terai. Main area and production of rice lies in terai then hill and mountain 70.51, 25.74 and 3.75 percentage of area and 73.01, 24.25 and 2.74 percentage of production respectively. The normal rice (main season) occupies about 92 percent rice cultivated area. According to the statistics (MOAD, 2015) rice supplies about 40% of the food calorie intake and contributes 7% to national GDP and 20% to the agricultural gross domestic product (AGDP). Ninety-one percent of rice production of world contributed by Asia and is stable food of 60% of world's population (Saud, 2010).

Total area of rice cultivation in mid-west mountain of Nepal is 7764 ha producing 17729 mt with productivity 2.283 mt/ha. Among the mid-west mountain districts Jumla ranks first in terms of area and production of rice. Total cultivated land in Jumla district is 26435 ha out of which rice covered 2950 ha among the rice area: local variety covered 1500 ha producing 2700 mt with productivity 1.8 mt/ha, while improved variety covered 1450 ha with 3190 mt, 2.2 mt/ha production and productivity respectively in 2013 (ADO, 2013). Jumla is high hill and food deficit district of mid-western development region of Nepal. Food habit of Jumli people has been changing; they prefer to consume rice instead of indigenous crops like: millet, buck wheat, barley, foxtail millet, and proso millet. People of Jumla have not completely left the indigenous crop but major consumption is rice because they receive it in subsidized rate through Nepal food Corporation. Recently, due to access of Karnali highway rice is available in local market comparatively affordable price than before. Due to change in the food habit of mid-west mountain's people the demand of rice is increasing. High yielding, cold tolerance, disease resistance varieties are required to meet the increasing demand. Agriculture Research Station (ARS) Vijayanagar, Jumla has been conducting varietal trials on rice since last many years and four varieties released till the date named: Chandannath-1, Chandannath-3, Lekali-1, and Lekali-3 for high hill of Nepal. Present research was also conducted at ARS Jumla located at 2290m amsl of Nepal and a sole research station for cereal, grain legumes and minor crops of the country. So any genotype, variety, and technology developed in this location suits to all mountain environment of the country.

Genetic variability is the formation of individuals differing in genotype, or the presence of genotypically different individuals, in contrast to environmentally induced differences which, as a rule, cause only temporary, nonheritable changes of the phenotype (Rieger *et al.*, 1968). Varietals improvement in crops is slow due to lack of efficiency in utilizing genetic variation for various quantitative traits, which provides genetic basis for choosing parents for the breeding program. Identifying suitable genotypes from existing accessions for biotic and abiotic stress resistance is one of the current thrust areas of plant breeding in Nepal. Genetic variability is the basis for the enhancement of any plant breeding and varietal improvement activities. The breeder should identify the variation of desired character and select with his skill towards desired improvement of the crop. Genetic improvement is a major tool to develop high yielding drought tolerance varieties (Farshadfar *et al.*, 2013).

The process of establishing a relationship or connection between two or more traits is correlation. The knowledge on genetic constituents and correlation between the parameters can be utilized to develop effective breeding methods by breeder. Similarly, heritability is a statistic used in the fields of breeding and genetics that estimates the degree of variation in a phenotypic trait in a population that is due to genetic variation between individuals in that population (Wray and Visscher, 2008).

Genetic variability, heritability, correlation, expected genetic advance and clustering of the genotypes with similarity are key important for crop improvement programs. In general heritability is the ratio of genetic variance to the total phenotypic variance of a trait in the population. It is the good index of transmission of character from parent to their offspring's. Improvement in the mean genetic value of selected plants over the parental population is genetic advance. It is measure of gain under selection. Relationship between yield and yield associated traits are prime important for direct and indirect selection of traits to which contributes to yield. Therefore, this study was carried out to estimate genetic variability, heritability, correlation, genetic advance as percent of mean and clustering of genotypes in relation to yield and yield associated traits and selection and advancement of cold tolerance, early maturing, high yielding, disease resistant, and drought tolerance rice genotypes for high mountain environment of Nepal.

Materials and Methods

Experimental Location, Experimental Design, and Planting Materials

Fifteen advanced breeding lines of rice received from Agricultural Botany Division (ABD) Khumaltar, Nepal Agricultural Research council were evaluated at Agricultural Research Station (ARS), Vijayanagar, Jumla during regular rice growing season of high hill (Last week of March to mid of October 2015). Geographically ARS is situated at an altitude of 2290m amsl and 29°17' north latitude and 28°10' east longitudes of mid-west Nepal (ARS, 2014). This station is located at high hill region and thus is characterized by cool temperate to alpine eco belts with low rainfall. Soil of this station as developed on recent to old river, moderately deep to very deep and moderately to poor drained. The topography is gently sloppy to rolling lying in the high mountain region. Surface soil and sub-surface soils are dominantly coarse textured (Sandy loam) and are acidic to moderately alkaline in reaction. The nitrogen content of the soil is generally very low to medium while available phosphorous is high to very high and available potassium is medium to high. The organic carbon content of farm soil is low to high. The average maximum and minimum temperature is about 25°C in June and 2°C in February. Total rainfall during rice growing period of 2015 was satisfactory 434 mm with an average of 54.28 mm. (Meteology office Jumla, 2016). Detail of weather data is given in Annex 1. List of genotypes and recorded parameters and their abbreviation are given in Table 1.

Table 1: List of genotypes and quantitative traits of rice used in the study

En	Genotypes	En	Genotypes	Traits	Abbreviation
1	NR-10638-B-B-4	9	NR-10562-8-7-5	Days to 50% heading	DH
2	NR-10914-1-4-3-2	10	K-39-96-1-1-1-2	Days to 90% maturity	DM
3	NR-10906-B-B-2-3	11	YUNLEN-6	Number of grains per spike	NGPP
4	NR-10682-B-B-B-3	12	NR-10481-B-11-1-1-1	Plant height (CM)	PHT
5	NR-10695-B-B-B-5	13	NR-10695-B-B-B	Panicle length (CM)	PL
6	NR-10682-B-B-B-2	14	Lekali-1(Std. Che.)	Number of panicle per hill	NPPH
7	NR-10689-B-B-B	15	Jumlai Marshi(Loc. Che.)	Thousands grain weight (g)	TGW
8	NR-10695-B-B-B-5-1			Grain yield kg per hac	YLD

Seed Bed Preparation and Cultural Practices

Jumla has a different historical perspective on rice seedling development; cleaning of stored rice seed on 12th of March each year, deeping the seed in clean water and draining of excess water on 29th of march each year. The moistened seed are then kept inside warm room or nearby burning wooden fire to increase the temperature for 72 hours. The germinated seeds are broadcasted on puddled flatbed on 2th of April. Precautions are taken to protect from birds. All steps mentioned above were followed in this experiment.

Experiment was laid out in RCBD (Randomized Complete Block Design) in three replications in 4.8 m^2 plot size for each entry and net harvested area 3.6 m^2. The spacing for row to row and plant to plant was maintained as 20 x 15 cm. Fertilizer was applied at the rate of 80:30:30; $N:P_2O_5:K_2O$ kg./ha and FYM 6 mt/ha. Half dose of nitrogen and full dose of phosphorus and potassium and FYM was applied at final field preparation and remaining half dose of nitrogen top dressed. Irrigation, intercultural operation like weeding and day to day monitoring were followed as required and recommended for the crop. Transplanting was done on 30th May 2015 and harvesting on 20th October 2015.

Data Collection

Morphological data were collected at appropriate growth stage by adopting the standard evaluation method given by IRRI (2002). Two boarder rows were excluded while recoding parameters days to heading, days to maturity, grain yield on plot basis, while plant height and number of grain per panicle, panicle length was recorded from randomly selected ten plants from inner lines of the plot. Similarly, number of plants per hill was also counted from selecting five hills from inner lines. Thousands grain weight and grain yield was adjusted in 14% moisture content.

Statistical Analysis

Analysis of variance done by using Genstat 18th edition, correlation was computed by using statistical software SPSS at significance level of (0.05), mean separation among the lines was done with statistical software ADEL-R and clustering of the genotypes was done with statistical software MINITAB. The phenotypic and genotypic variances were derived according to Falconer (1964) and broad sense heritability was calculated according to Allard (1960). Broad sense heritability values are characterized as low <30%, moderate 30-60% and high >60% Johnson *et al*. (1955). Estimation and categorization of genetic advance was done according to Johnson *et al*. (1955). Methods proposed by Sivasubramanian and Madhavamenon (1973) were used to categorize genotypic coefficient variation (GCV) and phenotypic coefficient variation (PCV).

Results and Discussion

Analysis of Variance

Analysis of variance among 15 genotypes of rice for eight ancillary characters revealed highly significance differences (<0.001) for the traits days to heading, days to maturity, number of grains per panicle, plant height, thousand grains weight and grain yield indicating presence of inherent genetic variation among the genotypes for the concerned traits. Number of panicles per hill was found nonsignificant (Table 2). The result showed presence of variation in genetic constituent Breeder can utilize the variability for selection and may use in hybridization for trait improvement, gene transfer to the other genotypes. Our finding supported by Tiwari *et al*. (2019), Ogunbayo *et al*. (2014), Akinwale *et al*. (2011) also reported similar findings for all traits but he also reported significance difference for plant per hill this differ from our finding. Similarly, result obtained by Selvaraj *et al*. (2011) is very similar with our findings. Seyoum *et al*. (2012) supported out result that significant difference for all trait but not panicle per hill. Yadav *et al*. (2010) also reported similar findings.

Grain yield resembled highest variability (13.6) followed by number plants per hill (11.30) and followed by number of grains per spike (6.7). Lowest variability was observed by days to maturity, then days to heading and thousands grain weight, plant height and panicle length (Table 3). Similar result was obtained by Adhikari *et al*. (2018).

Table 2: Analysis of variance for the eight ancillary characters of rice genotypes

SN	Traits	Rep	Treat	Error	Fcal	CV	P value
1	DH	49.28	61.07	2.61	18.85	1.1	**
2	DM	41.38	47.40	2.57	16.12	0.8	**
3	NGPP	185.40	1503.61	46.78	32.14	6.7	**
4	Pht	115.27	165.51	7.77	21.31	2.6	**
5	PL	3.41	6.34	0.76	4.49	4.3	**
6	NPPH	2.16	7.50	1.24	1.75	11.30	ns
7	TGW	2.08	13.07	0.14	93.33	1.6	**
8	Yld	3412717	2746622	450223	6.1	13.6	**

Note; DH: Days to heading, DM: Days to maturity, NGPP: Number of grains per panicle, Pht: Plant height (cm), PL: Panicle length (cm), NPPH: Number of panicle per hill, TGW: Thousand grain wt (gm) and Yld: Grain yield (kg/ha)

Table 3: Mean performance and LSD value of the quantitative traits of rice at high hill of Nepal in 2015

EN	Genotypes	DH	DM	NGPP	PHT	PL	PPH	TGW	Yld
1	NR-10638-B-B-4	152.3 ^{ab}	201.7 ^{c}	104.3 ^{bcd}	110.3 ^{bc}	20 ^{abc}	11	27.5 ^{a}	6253 ^{a}
2	NR-10914-1-4-3-2	147.7 ^{bc}	203.3 ^{bc}	96 ^{cd}	99.7 ^{e}	20.33 ^{abc}	9.333	22.53 ^{def}	4435 ^{abc}
3	NR-10906-B-B-2-3	152.7 ^{ab}	206.7 ^{abc}	104.7 ^{bcd}	108.7 ^{bcd}	21.38 ^{ab}	10.267	23.2 ^{cdef}	4384 ^{abc}
4	NR-10682-B-B-B-3	152.7 ^{ab}	204 ^{bc}	112.7 ^{abc}	101 ^{de}	22.4 ^{a}	9.833	23.75 ^{bc}	5720 ^{a}
5	NR-10695-B-B-B-5	148.7 ^{bc}	203.7 ^{bc}	110 ^{abcd}	120.3 ^{a}	21 ^{ab}	10.333	23.78 ^{bc}	4903 ^{abc}
6	NR-10682-B-B-B-2	155 ^{a}	206 ^{abc}	110.7 ^{abcd}	108 ^{bcde}	19.56 ^{bc}	9.333	24.92 ^{b}	5063 ^{abc}
7	NR-10689-B-B-B	148.3 ^{bc}	203.3 ^{bc}	113 ^{abc}	106.7 ^{bcde}	20.77 ^{ab}	10	23.33 ^{cde}	5233 ^{ab}
8	NR-10695-B-B-B-5-1	142.3 ^{d}	203.3 ^{bc}	60 ^{e}	90.3 ^{f}	20 ^{abc}	10	22.03 ^{f}	3196
9	NR-10562-8-7-5	152.7 ^{ab}	208 ^{ab}	90 ^{d}	114.3 ^{abc}	19.17 ^{bc}	8.333	20 ^{g}	4511 ^{abc}
10	K-39-96-1-1-1-2	152.7 ^{ab}	202 ^{c}	112 ^{abcd}	114.3 ^{abc}	21 ^{ab}	10	20 ^{g}	5074 ^{abc}
11	YUNLEN-6	157 ^{a}	209.7 ^{a}	125 ^{ab}	105.7 ^{cde}	20 ^{abc}	10	22.17 ^{ef}	5920 ^{a}
12	NR-10481-B-11-1-1-1	155.3 ^{a}	203.3 ^{bc}	102.7 ^{cd}	114.7 ^{ab}	20 ^{abc}	11	23.03 ^{cdef}	5509 ^{a}
13	NR-10695-B-B-B	148 ^{bc}	202.3 ^{c}	130.3 ^{a}	110.7 ^{bc}	20.67 ^{ab}	10.667	22.93 ^{cdef}	6038 ^{a}
14	Lekali-1(Std. Che.)	152.7 ^{ab}	204.7 ^{abc}	111 ^{abcd}	115 ^{ab}	20.5 ^{abc}	10	23.73 ^{bcd}	4701 ^{c}
15	Jumlai Marshi(Loc. Che.)	145 ^{cd}	193 ^{d}	45.7 ^{e}	108.3 ^{bcde}	17.7 ^{c}	8	19 ^{g}	2932 ^{c}
	Grand mean	150.87	203.6667	101.87	108.53	20.299	9.8733	22.793	4924.8
	SEM	1.61	1.6	6.84	2.78	0.87	1.11	0.37	671
	LSD (0.05%)	2.704	2.68	11.44	4.66	1.45	1.86	0.62	1122.2

Note; DH: Days to heading, DM: Days to maturity, NGPP: Number of grains per panicle, Pht: Plant height (cm), PL: Panicle length (cm), NPPH: Number of panicle per hill, TGW: Thousand grain wt (gm) and Yld: Grain yield (kg/ha)

Mean Separation and Range

Mean separation and range of 15 rice genotypes for eight yield and yield attributing character is presented in Table 3 and Table 4. Rice genotypes exhibited considerable variation for all the traits except number of plants per hill. The mean value of days to heading is 150.87 and it ranges from 142.3 to 157. Genotype NR-10695-B-B-B-5-1 was earlier for days to heading while genotype YUNLEN-6 was late for days to heading but it is statistically at par with genotypes NR-10481-B-11-1-1-1 and NR-10682-B-B-B-2. Earlier maturing genotypes was jumlai marshi (193 days) while late maturing genotype was Yunlen-6 (209.7 days) and mean was 203.66 days. Maximum NGPP was produced by NR-10695-B-B-B (130.3) and this is statistically at par with Yunlen-6 (125) and minimum was recorded in jumlai marshi (45.7) and mean was 101.87. Genotype NR-10695-B-B-B-5 was tallest (120.3 cm) and NR-10695-B-B-B-5-1 was dwarfest (90.3 cm) and mean was 108.53 cm. The obtained range for panicle length was (17.7 to 22.4 cm) minimum recorded in jumlai marshi and highest in NR-10682-B-B-B-3 with mean value 20.29 cm. Lowest number of panicles obtained in jumlai marshi (8) and highest NR-10638-B-B-4 and NR-10481-B-11-1-1-1 (11) and mean 9.87. Highest TGW (27.5 gm) recorded in NR-10638-B-B-4 and lowest was obtained by jumli marshi (19 gm) and mean was 22.7 gm. The grain yield varied from highest 6253 kg/ha (NR-10638-B-B-4) and lowest 2932 kg/ha (jumli marshi) and mean 4924 kg/ha. From the variation breeder can select genotypes having high number of grain per panicle, more panicle length, high number of panicle per hill, high thousand grains weight and having high yield for further improvement, hybridization gene transfer for betterment of breeding program.

Table 4: Range, standard deviation, variance, broad sense heritability, PCV, GCV and percent mean genetic advance for quantitative traits of rice genotypes

SN	Traits	Range	Std	Vg	Vp	H	PCV	GCV	% mean GA
1	DH	142.3-157	4.49	19.48	22.10	0.88	3.12	2.93	5.66
2	DM	193-209.7	4.12	14.94	17.51	0.85	2.05	1.90	3.61
3	NGPP	45.7-130.3	7.93	485.61	517.75	0.94	22.34	21.63	43.16
4	Pht	90.3-120.3	1.36	52.58	60.35	0.87	7.16	6.68	12.85
5	PL	17.7-22.4	1.35	1.86	2.62	0.71	7.98	6.72	11.66
6	NPPH	8.0-11.0	22.73	2.09	3.33	0.63	18.47	14.64	23.90
7	TGW	19-27.5	2.08	4.31	4.45	0.97	9.26	9.11	18.47
8	Yld	2932-6253	1146.98	765466	1215689	0.63	22.39	17.77	29.04

Genetic Variability, Heritability and Genetic Advance

Heritability, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) and genetic advance at 5% selection intensity as percent of mean for quantitative traits of rice genotypes is presented in Table 4. The success of genetic advance under selection depends upon three factors (Allard, 1960). Genetic variability: greater the amount of genetic variability in base populations higher the genetic advance, Heritability: the G.A. is high with characters having high heritability and Selection intensity : the proportion of individuals selected for the study is called selection intensity high selection intensity gives better results. Our result showed PCV is higher than GCV for all traits. Higher the difference between PCV and GCV indicates higher influence of environment for the expression of traits. Smaller the difference little effect of environment and selection will be effective in this condition. High broad sense heritability obtained for the trait TGW (0.97), followed by number of grains per panicle (0.94), DH (0.88), plant height (0.87), DM (0.85), PL (0.71) and grain yield (0.63). Yadav *et al.* (2010), Patel *et al.* (2014) reported similar high heritability for such parameters. Selvaraj *et al.* (2011) reported very similar result as our findings. Akinwale *et al.* (2011) reported high heritability for Yld, DH, DM, Pht, NGPP similar to our finding but low for TGW and NPPH in contradiction. Similarly, Ogunbayo *et al.* (2014) reported similar result for all traits but medium heritability for grain yield (44.6). Higher the broad sense heritability character are least influenced by environment and selection for improvement of such characters may be useful. Lower the broad sense heritability genetic improvement through selection will be difficult.

Our result showed higher GA as percent of mean (≥20%) by traits number of grains per panicle (43.16%), grain yield (29.04%), and number of panicle per hill (23.90%), medium (10-20%) by traits TGW (18.47%), PHT (12.85%) and PL (11.66%) and low (<10%) by traits DM (5.66%) and DH (3.61%). If the value of genetic advance is high the character is governed by additive genes and selection will be beneficial for such traits. If genetic advance is low the character is governed by non additive genes and heterosis breeding may be useful. Genetic advance as percent mean ranged from 3.61% for days to heading to 43.16% for number of grains per panicle indicating that selecting the top 5% of the genotypes could result in an improvement range of 3.61% for days to heading to 43.16% for number of grains per panicle and 29.04% for grain yield. Ogunbayo *et al*. (2014) reported high GA for yield, medium for pht and low for DH and DM support our findings. Tiwari *et al.* (2019) also reported high GA and high heritability for yield and low GA and high heritability for DH and DM this is similar to our findings. Akinwale *et al.* (2011) reported similar findings high heritability coupled with high GA for NGPP, Yld and NPPH. Selvaraj *et al.* (2011) reported similar result as our findings for Yld, NGPP, NPPH but in contradiction he reported high GA for DH and DM at 1% level of selection intensity.

High heritability coupled with high genetic advance was recorded for grain yield, number of grains per panicle and number of panicle per hill. High heritability with medium genetic advance traits TGW, PHT and PL are governed by additive gene effects and direct selection for these traits would be more effective for desired genetic improvement.

Clustering

Cluster analysis or clustering is the task of grouping a set of objects in such a way that objects in the same group (called a cluster) are more similar (in some sense) to each other than to those in other groups (clusters). It is a main task of exploratory data mining, and a common technique for statistical data analysis, used in many fields, including machine learning, pattern recognition, image analysis, information retrieval, bioinformatics, data compression, and computer graphics. Dendrogram generated based on UPGMA clustering method and Euclidean similarity coefficient among fifteen rice genotypes is given in Table 5 and Figure 1. Clustering was done with UPGMA clustering method with 80% Euclidean similarity coefficient and four cluster were generated. Cluster 1 contains 5 genotypes (33.3%) out of total 15 genotypes named (NR-10638-B-B-4, NR-10682-B-B-B-3, NR-10481-B-11-1-1-1, YUNLEN-6, NR-10695-B-B-B). This cluster carries higher value for grain yield, thousand grains weight, number of panicle per hill, panicle length and number of grains per panicle than total average. All genotypes in the cluster are superior and can be selected for further breeding. Similarly, cluster 2 carries eight genotypes 53% of total. This cluster is inferior than cluster one values of quantitative traits Yld, TGW are below the total average but DH and DM is higher than grand centroid. Cluster 3 contains two genotype NR-10695-B-B-B-5-1 and Jumli marshi lowest yielder and lower other values than grand centroid.

Table 5: The average of traits for each cluster obtained from UPGMA cluster analysis

Variable	**Cluster1**	**Cluster2**	**Cluster3**	**Grand centroid**
DH	153.06	151.31	143.65	150.87
DM	204.2	204.71	198.15	203.67
NGPP	115	105.93	52.85	101.87
PHT	108.48	110.88	99.3	108.53
PL	20.61	20.46	18.85	20.3
PPH	10.5	9.7	9	9.87
TGW	23.88	22.69	20.52	22.79
Yld	5888	4788	3064	4924.8

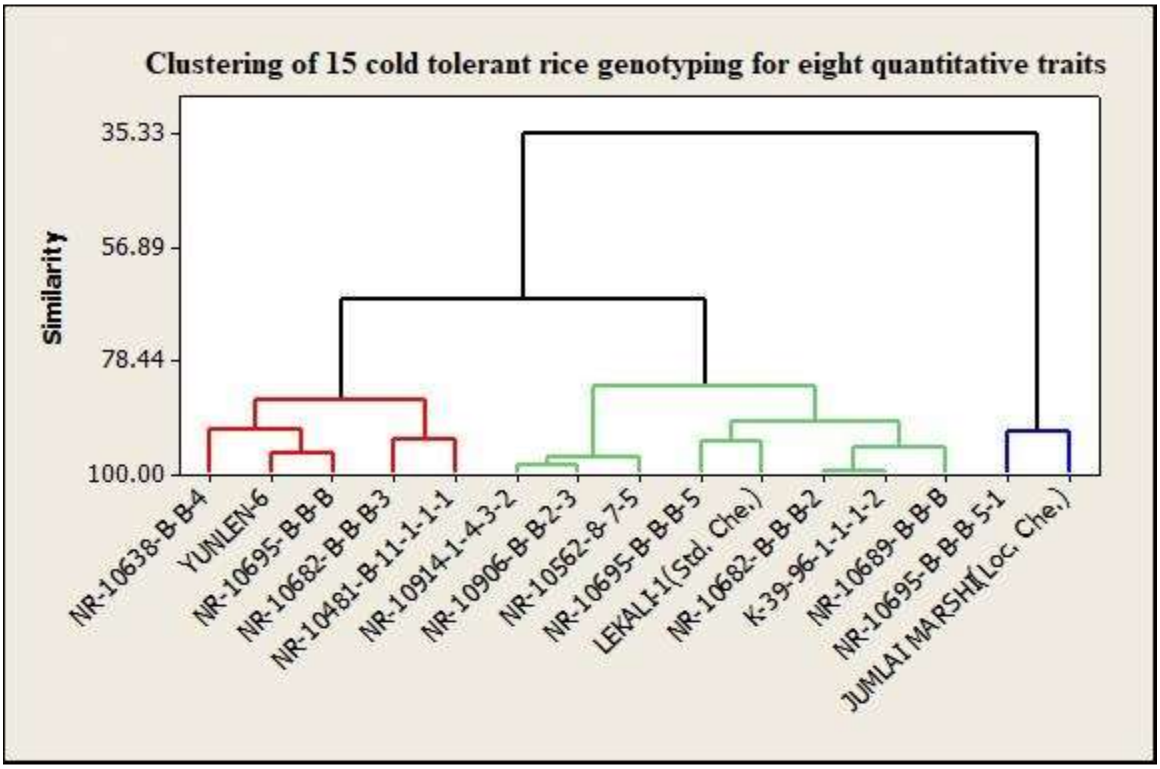

Fig 1: Unwaited pair group method with arithmetic mean (UPGMA) clustering of cold tolerance rice genotypes

Table 6: Phenotypic correlation coefficient between eight parameters of rice

	DH	**DM**	**Pht**	**PL**	**PPh**	**NGPP**	**TGW**
DM	0.668**						
Pht	0.533**	0.162					
PL	0.41**	0.54**	0.179				
PPh	0.669**	0.558**	0.455**	0.721**			
NGPP	0.639**	0.6**	0.405**	0.631**	0.655**		
TGW	0.307*	0.47**	0.029	0.541**	0.258	0.472**	
GY	0.717**	0.63**	0.384**	0.785**	0.817**	0.839**	0.509**

** Correlation is significant at the 0.01 level. * Correlation is significant at the 0.05 level.

Correlation

Correlation coefficient is a measure of the degree of association and relationship between two variables. In a distribution if the change in one variable effects a change in the other variable, the variable are said to be correlated. Correlation is very important tool in plant breeding because we can use indirect selection to improve another targeted parameter. There is positive and negative effect in correlation which results in simultaneous changes in related character. Phenotypic correlation between eight parameters of 15 genotypes of rice is illustrated in Table 6. Result showed all parameters significantly correlated each other except days to maturity and plant height, plant height and panicle length, plant height and thousand grains weight, thousand grains weight and number of panicle per hill. All parameters TGW (0.509**), NGPP (0.839**), NPPH (0.817**), PL (0.785**) and DM, DH, PHT contribute for higher grain yield. We can select plants having high number of panicles per hill, more thousand grain weight, more number of grains per panicle, longer panicle etc for higher grain yield. Similar result was obtained by Selvaraj *et al*. (2011) positive correlation of thousand grain weight, panicle per hill, panicle length and number of grains/panicle to the rice yield. Tiwari *et al*. (2019) reported sigficant correlation of DH and DM to grain yield. Patel *et al*. (2014), Yadav *et al*. (2010) and Akinwale *et al*. (2011) reported partial support to our findings.

Conclusion

Obtained results indicate presence of sufficient genetic variability for the studied traits and genotypes are suitable for breeding purpose. Result resembled high heritability coupled with high genetic advance were recorded for grain yield, number of grains per panicle and number of panicle per hill and high heritability with medium genetic advance was obtained thousand grain weight, panicle length and plant height shows these traits are governed by additive gene effects and selection of these traits would be more effective for genetic improvement. Mean separation and clustering showed genotypes NR-10638-B-B-4, NR-10682-B-B-B-3, NR-10481-B-11-1-1-1, YUNLEN-6, NR-10695-B-B-B are better than check lekali-1 and can be selected for further evaluation in advance trial. All parameters TGW, NGPP, NPPH, PL, DH and PHT contribute for higher grain yield. We can select plants having high number of panicle per hill, more thousand grain weight, more number of grains per panicle and longer panicle for higher grain yield.

Acknowledgements

The authors would like to thank Agricultural Botany Division Khumaltar, Lalitpur for providing genetic materials. We would like to thank technical assistant staffs of Agricultural Research Station Vijayanagar, Jumla for their support on conducting experiment on the field.

Author's contribution

N.H. Ghimire designed and performed experiment, analyzed data and wrote the manuscript. P. M. Mahat performed experiment and data recorded. Final form of manuscript was approved by both authors.

Conflict of Interest

The authors declare that there is no conflict of interest regarding publication of this manuscript.

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Appendix

Annex 1: Weather data of research place Jumla 2015.

Year	Month	Average Temperature		Relative Humidity %	Total Rainfall (mm)
		Maximum (^{0}C)	Minimum (^{0}C)		
2015	January	14.8	-4.4	NA	42
	February	15.1	-2.5	NA	13.2
	March	18.7	0.2	NA	57.6
	April	22.6	0.4	NA	15.9
	May	25.1	7.1	NA	43.7
	June	28.2	13.1	NA	24.5
	July	24.01	15.08	75.29	111
	August	24.67	15.56	78.32	117.7
	September	27.18	11.98	67.59	29.6
	October	23.07	4.64	62.95	34.3
	November	20.18	-0.2	55.91	6.8
	December	16.25	-4.23	-4.23	0

Source: Meterological Field Office, Jumla