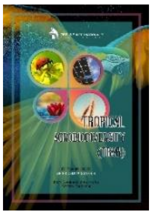
ZIBELINE INTERNATIONAL™ PUBLISHING

ISSN: 2716-7046 (Online)
CODEN: TARGCA

Tropical Agrobiodiversity (TRAB)

DOI: http://doi.org/10.26480/trab.02.2023.36.43



RESEARCH ARTICLE

ASSESSMENT OF GENETIC VARIABILITY, HERITABILITY AND CORRELATION IN SPRING RICE GENOTYPES (*Oryza sativa L.*) AT RATNANAGAR, CHITWAN IN 2022

Susmita Shrestha[a]*, Ram Hari Timilsina[b], Kailash Pandey[c]

[a]*Faculty of Agriculture, Agriculture and Forestry University, Rampur, Chitwan, Nepal*
[b]*Department of Agriculture Extension and Rural Sociology, Agriculture and Forestry University, Chitwan, Nepal*
[c]*Department of Plant Genetics, Breeding and Biotechnology, University of Helsinki, Finland*
**Corresponding Author E-mail: susmitastha250@gmail.com*

ARTICLE DETAILS

Article History:

Received 13 April 2023
Revised 16 May 2023
Accepted 19 June 2023
Available online 26 June 2023

ABSTRACT

The stagnant yield of rice in Nepal can be improved by development of genotypes with improved traits through breeding for which estimates of genetic parameters are essential. Hence, a field experiment was carried out from February to June in the year 2022 with the objectives to evaluate the genetic variability, heritability, genetic advance and character association among yield traits in spring rice genotypes in order to provide valuable insights for rice breeders for the development of high-yielding spring rice varieties. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications comprising 10 genotypes. Various quantitative characters were recorded to estimate variability and correlation coefficient. Analysis of variance indicated significant differences for all traits among the assessed genotypes, indicating the presence of variability among evaluated genotypes. A lower genotypic coefficient of variation than the phenotypic coefficient of variation revealed the presence of environmental influence on the expression of these traits, being higher in fertility percentage and grain yield. High heritability was estimated for all the traits except fertility percentage, harvest index and grain yield. High heritability along with the high genetic advance was reported by the number of filled grains per panicle, thousand grain weight, and straw yield while remaining traits showed moderate to high heritability with low to moderate genetic advance as a percent of the mean. The number of panicles per hill, fertility percentage, biological yield and straw yield exhibited a significant positive association with grain yield indicating the chance of improvement in yield if a selection is applied in favor of those traits among these genotypes. Therefore, the results highlight the potential for selection among these genotypes for traits such as number of filled grains per panicles, number of panicles per hill and straw yield for higher productivity and performance.

KEYWORDS

Rice, variability, heritability, genetic advance, correlation

1. INTRODUCTION

Rice is the important staple crop belonging to Graminae family, genus *Oryza* and has two cultivated species namely, *Oryza sativa* and *Oryza glaberrima*. The most commonly grown rice species, *Oryza sativa* is believed to be originated from the Asia and *Oryza glaberrima* is believed to be originated in the Niger River delta (Khush, 2000). Among these two species of rice, *Oryza sativa* is commercially important cultivated species in the world. Further, *O.sativa species* are divided into *Indica, Japonica* and *Javanica* sub- species. Globally, rice is produced in 164.192 million hectares of land with a total production of 756.744 million tons (FAO, 2020). China (27.99%) and India (23.26%) contributes most to the world rice production and account for more than half of annual global rice production (USDA/ERS, 2022). The global consumption of rice is 521.0 million tons which is expected to be increased by 1.1% per annum (FAO, 2022).

Nepal is one of the centers of rice diversity with about 2000 landraces of rice growing from 60 to 3050 masl. (Mallick, 1981/82; Joshi, 1970). In 1972, National rice improvement program was established at Parwanipur with 48 improved recommended rice cultivars and receive several exotic varieties through IRRI for evaluation every year (Joshi, 2005). It is the first most important cereal crop in Nepal which is cultivated in 1,473,474 hectare of area (8.32% in spring season and 91.68% in main season) with 5,621,710 metric tons of production, of which 10.16% during spring season and 89.84% during main season (MoALD, 2020/21). It contributes almost 7% to GDP and nearly 20% to the agricultural gross domestic product(AGDP) (CDD, 2015) which solely accounts for more than 50% of the total calories of Nepalese people (Kharel et al., 2018). According to MoALD (2020/21), Madhesh Pradesh and Gandaki Province have the highest and lowest share of 25.49% and 7.06% of total rice production in the country respectively with highest productivity in Lumbini Province (3.99Mt/ha) and lowest productivity in Karnali Province (3.51 Mt/ha). Terai region, considered as bread basket of Nepal solely contributes about 70 percent of the total rice output of the country (Gadal et al., 2019). The trend analysis of rice productivity in the past ten years indicates that the yield of rice in Nepal is gradually increasing remaining more or less constant (MoALD, 2020/21).

In the global hunger index, Nepal ranks in 81st position (Grebmer et al., 2022). In order to meet the demand of increasing population, Nepal imported almost 290 thousand tons of husked rice, 2 thousand tons of paddy seed and 410 thousand tons of semi-milled or wholly milled rice in 2076/77 (MoALD, 2020/21). Hence, increase in yield of the rice with selection of suitable traits for the production of the high yielding variety is essential to tackle problem of food insecurity. Furthermore, few research and breeding program for varietal evaluation and selection had led to less development of varieties with high yield potential. Limited choices of

Quick Response Code	Access this article online	
	Website: www.trab.org.my	**DOI:** 10.26480/trab.02.2023.36.43

Cite the Article: Susmita Shrestha, Ram Hari Timilsina, Kailash Pandey (2023). Assessment of Genetic Variability, Heritability and Correlation in Spring Rice Genotypes (*Oryza Sativa L.*) at Ratnanagar, Chitwan In 2022. *Tropical Agrobiodiversity, 4(2): 36-43.*

varieties are available for farmers to cultivate during spring season and need for development of site specific high yielding varieties is essential. Fewer studies have been conducted in assessing the available genetic variability present in yield traits of rice which is essential in breeding program to improve yield.

Hence, the study of genetic variability, heritability and character association between yield traits help in rice breeding through improvement of spring rice genotypes. Heritability coupled with genetic advance provides the precise indication of genetic gain under selection (Adhikari et al., 2018). Correlation analysis further provides information on association between traits which is important in selection of traits contributing to yield (Aditya & Bhartiya, 2013). Further, the information of heritability, genetic advance and correlation helps breeders in planning and execution of breeding program for effective selection of quantitative traits depending on the degree of the variability.

2. MATERIALS AND METHODS

2.1 Description of Research Site

The site of study was Jayamanagala, Ratnanagar Municipality-13, Chitwan, Nepal at farmer field located at latitude 27˚ 39’ 1.34” N and longitude 84˚ 30’ 36.58” E which is shown in Figure 1. The texture of soil in experimental field was sandy loam with the pH 6.3. The organic matter content was found to be 3.4%, nitrogen level 0.06, phosphorus 28 kg/ha and potassium 107 kg/ha. The climate is tropical type with the total rainfall during the crop period was 136.49 mm, average relative humidity of 37.91% during the crop period and monthly average maximum temperature ranged from 25.04^0C (February) to 39.60^0C (June) and the monthly average minimum temperature ranged from 12.66^0C (February) to 27.45^0C (June) which is shown in Figure 2.

2.2 Experimental Materials And Design

The experimental material consisted of 10 rice genotypes which consisted two cultivated, one recently released, four pipeline and three hybrid collected from PMAMP, Chitwan and kindly provided by National Rice Research Program, Hardinath, Dhanusa, Kisan Agro-center and Muktinath krishi Company Limited, Basundhara, Kathmandu which is presented in Table 1. The research was conducted from February to June in year 2022. In randomized complete block design with 3 replications. The size of the plot was 2m*3m with spacing of 50 cm within the replication and 1 m between the replication. Plants were maintained at the distance of 20 cm*20 cm inside the plot.

FYM was applied @ 15 ton/ha during land preparation and chemical fertilizers were applied at dose of 100:60:40 Kg NPK/ha as per NRRP (2020) in the form of urea, DAP and Muriate of Potash (MOP). Full dose of DAP and potassium were applied as basal dose in all plots. Urea was applied at three split doses at 20, 35 and 50 days after transplanting. Pre-emergence herbicide Petrilachlor was applied at the rate of 2.5 ml per liter, a day after transplanting followed by one hand weeding at 30 DAT. Irrigation was given regularly soon after transplantation in order to ensure good crop establishment followed by supplementary irrigations at three to four days interval in such a way that soil was kept moist throughout the cropping period.

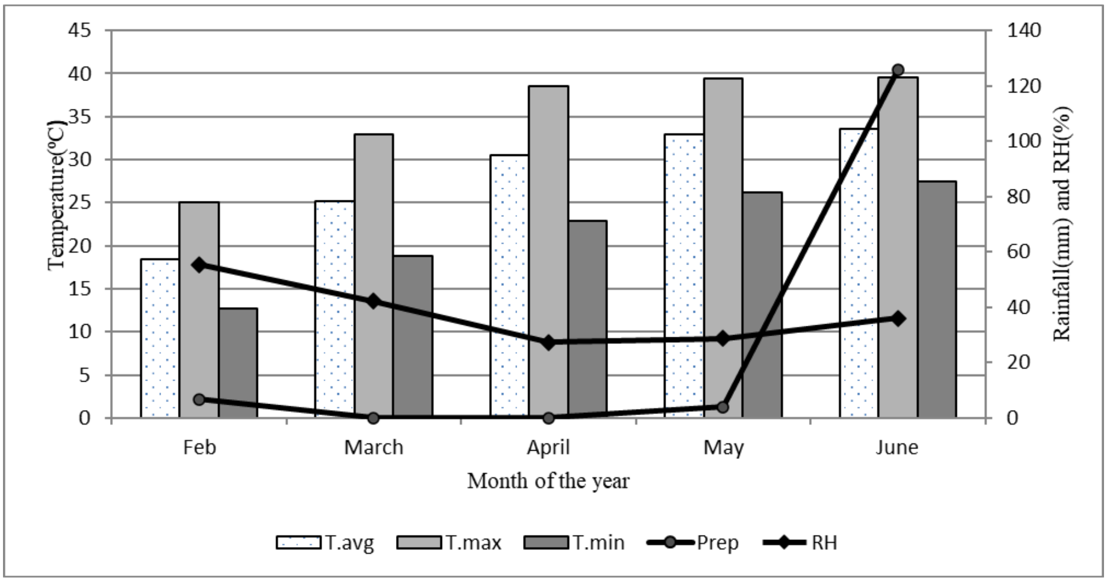


Figure 1: Climatic condition during experimentation at Ratnanagar, Chitwan in 2022
Source: www.power.larc.nasa.gov/data-access-viewer

Table 1: The Detailed of Genotypes Used in Genetic Variability Estimation in Spring Rice in Ratnanagar, Chitwan In 2022

Name	Type	Source
Hardinath-1	Cultivated	Kisan Agro Center
IR16L1831	Pipeline	NRRP, Dhanusa
IR 17A1731	Pipeline	NRRP, Dhanusa
Chaite-5	Cultivated	NRRP, Dhanusa
IR 17A 1730	Pipeline	NRRP, Dhanusa
HARDINATH-4	Recently released	NRRP, Dhanusa
IR 16L1636	Pipeline	NRRP, Dhanusa
PAC 807 Plus	Hybrid	Mukti krishi Company Ltd
ADV 8100	Hybrid	Mukti Krishi Company Ltd
ADV 8082	Hybrid	Mukti Krishi Company Ltd

2.3 Data Recorded

Data of different quantitative traits of rice were recorded according (Center, 2007).

Days to 50% heading
Days to 50% heading was recorded when 50% of the plants in the plots had a visible head.

Days to maturity
Days to maturity was recorded when 80% of the grains in the panicle had turned golden yellow and covered 80% of the plot area.

Plant height
Five hills were selected randomly from the each plot excluding the border for measuring the plant height from ground level to the tip of the panicle at maturity.

Flag leaf length
The length from the collar region to the tip of the leaf blade was taken as flag leaf length from the five randomly selected hills.

Number of panicle per hill
The panicles were counted from the five randomly selected hills and averaged to get number of panicles per plant.

Cite the Article: Susmita Shrestha, Ram Hari Timilsina, Kailash Pandey (2023). Assessment of Genetic Variability, Heritability and Correlation in Spring Rice Genotypes (*Oryza Sativa L.*) at Ratnanagar, Chitwan In 2022. *Tropical Agrobiodiversity, 4(2): 36-43.*

Panicle length

Measurement of length was taken from the base to the tip of panicles from ten different tillers of different hills from the net plot area of each plot.

Filled and unfilled grains per panicle

Ten panicles were randomly selected from each plot, filled and unfilled grains were counted, and the values obtained were averaged to determine to calculate the filled and unfilled grains per panicle, respectively.

Fertility percentage

Fertility percentage was calculated using formula.

$$\text{Fertility percentage}=\frac{Filled\ grains}{Filled\ grains+Unfilled\ grains}\times 100$$

Thousand grain weight

One thousand filled grains from the grain yield of net plot were counted and weighed in a digital weighing balance to record the thousand grain weight at 12% moisture. The process was repeated five times for each plot and averaged to obtain thousand grain weight of each plot.

Grain yield

After harvesting, they were sun-dried, threshed and grain yield was recorded from the net plot area in kilograms by using a digital weighing balance along with the measurement of the moisture content in the grain. The grain yield per hectare was computed and standardize at 12% moisture content using the formula suggested by (Shrestha, et al., 2021).

$$\text{Grain yield (kg/ha)} = \frac{(100 - \text{MC}) \times \text{plot yield(kg)} \times 10000}{(100 - 12) \times \text{net plot area } (\text{m}^2)}$$

Where MC=Moisture Content of Grains in Percentage

Straw yield

At the time of harvesting, fresh weight of threshed portion of the paddy obtained from the net plot area was weighed and recorded in kilograms by using a digital weighing balance. About 200 gm of threshed portion of paddy was weighted and oven dried for 48 hrs at 80 ^{0}C to obtain dry weight. The straw yield was then calculated from net plot area using the dry weight of the sample.

Biological yield

Straw yield and grain yield obtained from the net plot area was added to determine the biological yield for each genotype.

Harvest index

Harvest index was calculated by dividing the economic yield by the biological yield. It is the ratio of grain yield to the biological yield of rice crop.

$$\text{HI } (\%) = \frac{\text{Grain yield}}{\text{Biological yield}}$$

2.4 Statistical Analysis

The data recorded on different parameters from field and laboratory were entered and arranged systematically in MS-Excel. R Studio software was used to analyze the data. The significance was determined computing Analysis of Variance (ANOVA) and Duncan's Multiple Range Test (DMRT) was employed to find out the significant differences between mean values at 5% level of significance. The phenotypic and genotypic correlation coefficient was carried out in R-studio using variability package. Genetic parameters were calculated using formula from different source as indicated in Table 2. Genotypic and phenotypic coefficient of variation were categorized as low (0–10%), moderate (10–20%) and high (>20%) as per Sivasubramanian & Madhavamenon (1973).Broad sense heritability were categorized as low (0-30%), moderate (30% - 60%) and high (>60%) and genetic advance as percent of mean were classified as low (<10%), moderate (10%-20%) and high (>20%) as per (Johnson, Robinson, and Comstock, 1955).

Table 2: Formula for Estimation of Genetic Parameters

Genetic Parameters	Symbol	Formula	Source
1.Variance			
1.1 Genotypic variance	σ^2g	$\sigma^2 g=\frac{MSG-MSE}{r}$	(Johnson et al., 1955)
1.2 Phenotypic variance	σ^2p	$\sigma^2\text{p} = \sigma^2\text{ g} + \sigma^2\text{ e}$	(Johnson et al., 1955)
2. Coefficient of variation (CV)			
2.1. Genotypic coefficient of variation	GCV	GCV(%)=$\frac{\sqrt{\sigma^2 g}}{m}\times 100$	(Singh and Chaudhary, 1985)
2.2.Phenotypic coefficient of variation	PCV	PCV (%)=$\frac{\sqrt{\sigma^2 p}}{m}\times 100$	(Singh and Chaudhary, 1985)
3.Genetic Advance	GA	GA =$\frac{\sigma^2 g}{\sigma^2 p}\times K \times \sigma p$	(Allard, 1960)
4.Genetic advance as per mean	GAM	GAM (%)= $\frac{GA}{X}\times 100$	(Allard, 1960)
5.Broad sense heritability	h^2_{bs}	h^2_{bs} (%) =$\frac{\sigma^2 g}{\sigma^2 p}\times 100$	(Lush, 1940)

Where, MSG=Mean Sum of genotypes, MSE= mean sum of error, r=No. of replication, σ^2 e= environmental variance, σp =Phenotypic standard deviation, σg = Genotypic standard deviation, m= Population mean, K=selection differential at 5% selection intensity = 2.06

3. RESULTS AND DISCUSSION

3.1 Assessment of Rice Genotype's Performance

3.1.1 Analysis of Variance (ANOVA)

The analysis of variance (Table 3) revealed highly significant differences at p <0.001 for days to heading, days to maturity, plant height, flag leaf length, panicle length, number of panicles per hill, filled per panicles, thousand grain weight, straw yield and biological yield while significant difference at P<0.01 was found in harvest index and significant differences at p <0.05 was observed for fertility percentage and grain yield which indicated the presence of variability among evaluated genotypes for all the studied traits. Others also reported significant differences among the evaluated genotypes of rice. The findings highlight the potential for selection and breeding improved varieties with desirable traits for higher productivity and performance (Adhikari, et al., 2018; Shrestha, et al., 2021).

3.1.2 Mean Performance of Ten Spring Rice Genotypes for Yield and Yield Attributing Traits

Table 4 presents the significant differences in grain yield among ten evaluated rice genotypes. The grain yield was found maximum in PAC 807 Plus (7874.32 kg/ha) followed by ADV 8082 (7666.26 kg/ha), Hardinath-1 (7249.65kg/ha) and ADV 8100 (7071.84 kg/ha) which were found statistically similar. Hardinath-4 manifested lowest grain yield (6162.78 kg/ha) which was statistically at par with IR 16L 1831 (6187.64 kg/ha), Chaite-5 (6200.52 kg/ha), IR 16L 1636 (6401.63 kg/ha), IR 17 A 1730 (6494.95 kg/ha) and IR 17A 1731 (6716.66 kg/ha).

The high yield of PAC 807 Plus could be attributed due to number of panicles per hill, filled grain and fertility percentage. Similarly, comparatively lower yield of IR 16L 1636 could be due to lower number of filled grain per panicle. The yield of Hardinath-4, IR 16L 1831 and IR 16L 1636 were found similar to the findings of (Yadaw, 2021). The identified high-yielding genotypes could serve as valuable genetic resources for developing new cultivars with improved productivity. All the genotypes except IR 16L 1831, Chaite-5 and Hardinath-4 were found earlier to maturity than Hardinath-1 which could be exploited for the early maturing trait. These results were in accordance with (NRRP, 2020; Yadaw, 2021).

3.2 Estimate of Genetic Parameters

3.2.1 Phenotypic and Genotypic Coefficient of Variation

Genetic variance and GCV were lower than phenotypic variance and PCV respectively for all traits under studied which is presented in Table 5, unveiling the influence of the surrounding environments on the traits. However, days to heading, days to maturity, plant height and thousand grain weight showed minimum influences of environment as represented

Cite the Article: Susmita Shrestha, Ram Hari Timilsina, Kailash Pandey (2023). Assessment of Genetic Variability, Heritability and Correlation in Spring Rice Genotypes (*Oryza Sativa L.*) at Ratnanagar, Chitwan In 2022. *Tropical Agrobiodiversity, 4(2): 36-43.*

by smaller differences between phenotypic and genotypic variance similar to findings of Adhikari et al. (2018) except for thousand grain weight. The impact of environment on the phenotypic variance was higher for fertility percentage and grain yield over the other traits as indicated by the larger difference between the genotypic and phenotypic variance (Adhikari et al., 2018).

The phenotypic coefficient of variation was high for number of unfilled grains per panicle (44.52%), number of filled grains per panicle (22.68%). The low PCV was observed for days to maturity (5.93%), panicle length (6.47%), harvest index (6.64%), days to heading (8.04%) and plant height (8.40%). Moderate PCV were found in straw yield (16.72%), number of panicles per hill (15.00%), thousand grain weight (14.63%), biological yield (12.81%), grain yield (11.76%), fertility percentage (10.83%) and flag leaf length (10.10%).

The genotypic coefficient of variation was highest in number of unfilled grains per panicle (36.55%) followed by number of filled grains per panicle (18.89%) while moderate GCV was found in straw yield (14.78%), thousand grain weight (14.48%), number of panicles per hill (12.06%) and biological yield (10.54%). The low GCV was observed for harvest index (5.07%), days to maturity (5.92%), panicle length (5.84%), fertility percentage (6.48%), plant height (7.99%), days to heading (8.00%), grain yield (7.73%) and flag leaf length (8.33%).

Table 3: Analysis of Variance Results of Observed Traits Derived from 10 Rice Genotypes Grown at Ratnanagar, Chitwan, 2022

Traits	Mean sum of square of source of variation		
	Replication (df=2)	Genotypes (df=10)	Residuals (df=18)
DH	0.433	127.12***	0.47
MD	0.033	137.21***	0.107
PH	21.242	193.488***	6.546
FLL	0.54	13.39***	2.62
PL	0.1526	7.0346***	0.5010
PN	1.4093	6.7354***	1.039
FG	39.08	2573.14***	329.34
UFG	115.46	1242.55***	172.54
FP	8.571	110.78*	41.517
TGW	0.002	35.855***	0.234
GY	226319	1193236*	362855
SY	823877	2377753***	312874
BY	1057213	5072523***	696962
HI	14.04646	26.2101**	5.0637

* = significant at 5%, ** = significant at 1%, *** =significant at 0.1%; df = degree of freedom, DH=Days to heading, MD= Days to maturity, PH= Plant height, FLL= Flag Leaf Length, PL = panicle length, PN=Number of panicles per hill, FG = filled grains per panicle, FP = fertility percentage, TGW = thousand grain weight, GY= grain yield, SY= straw yield, BY= Biological yield and HI= Harvest Index.

Table 4: Mean Performance of Spring Rice Genotypes for Yield and Yield Attributing Traits at Ratnanagar, Chitwan, 2022

Genotypes	DH	MD	PH	FLL	PN	PL	FG	UnFG	FP	TGW	GY	SY	BY	HI
Hardinath-1	83^{d}	117^{d}	99.23^{cd}	28.73^{b}	12.13^{ab}	23.97^{de}	142.4^{bcd}	43.13^{bc}	76.78^{a}	21.94^{f}	7249.65^{abc}	5398.33^{bcd}	11778.02^{c}	54.17^{ab}
IR 16L 1831	87.67^{b}	117.67^{c}	101.83^{c}	32.30^{a}	9.87^{cd}	27.01^{a}	110.33^{d}	36.43^{bc}	74.58^{a}	30.74^{a}	6187.64^{c}	5296.17^{cde}	10741.29^{cde}	50.41^{bc}
IR 17A 1731	76.67^{f}	107^{g}	92.61^{ef}	26.90^{b}	10.4^{bc}	23.70^{de}	148.93^{bc}	44.03^{bc}	77.02^{a}	24.74^{c}	6716.66^{bc}	4979.80^{de}	10890.46^{cde}	54.23^{ab}
Chaite-5	87.67^{b}	120^{b}	108.65^{b}	29.61^{ab}	8.33^{d}	27.00^{a}	216.67^{a}	85.83^{a}	71.52^{a}	18.51^{h}	6200.52^{c}	5563.62^{cd}	11020.07^{cde}	49.50^{c}
IR 17A 1730	76^{f}	106.67^{g}	89.65^{f}	23.36^{c}	11.73^{abc}	23.01^{e}	135.77^{bcd}	46.63^{bc}	74.42^{a}	23.05^{de}	6494.95^{c}	4287.50^{e}	10003.05^{de}	57.21^{a}
Hardinath-4	91^{a}	121^{a}	92.97^{ef}	27.51^{b}	11.73^{abc}	24.58^{cd}	128.03^{bcd}	88.93^{a}	59.38^{b}	20.39^{g}	6162.78^{c}	4244.32^{e}	9667.55^{e}	56.33^{a}
IR 16L 1636	84.67^{c}	114^{e}	94.15^{ef}	28.09^{b}	13.47^{a}	25.36^{bc}	120.5^{cd}	25.87^{c}	82.19^{a}	27.37^{b}	6401.63^{c}	5877.87^{bc}	11511.30^{cd}	48.94^{c}
PAC 807 Plus	72^{h}	103^{i}	94.97^{de}	28.27^{b}	12.13^{ab}	26.49^{ab}	157.77^{b}	41.87^{bc}	79.23^{a}	23.67^{d}	7874.32^{a}	6442.81^{ab}	13372.21^{ab}	51.86^{bc}
ADV 8100	74^{g}	105^{h}	98.76^{cd}	27.23^{b}	11.73^{abc}	24.62^{cd}	153.97^{bc}	55.23^{b}	73.63^{a}	22.73^{ef}	7071.84^{abc}	5769.13^{bcd}	11992.34^{bc}	51.84^{bc}
ADV8082	79.67^{e}	109.33^{f}	115.58^{a}	31.78^{a}	12.73^{a}	27.11^{a}	133.03^{bcd}	48.73^{bc}	73.14^{a}	24.82^{c}	7666.26^{ab}	6905.48^{a}	13651.79^{a}	49.48^{c}
F-test	***	***	***	***	***	***	***	***	*	***	*	***	***	**
LSD(0.05)	1.18	0.94	4.39	2.78	1.75	1.21	31.13	22.53	11.05	0.83	1033.31	732.83	1432.09	3.86
$SE_m(\pm)$	0.40	0.19	1.48	0.93	1.06	0.41	10.48	7.58	3.72	0.28	347.79	246.65	482.00	4.29
CV, %	0.84	0.49	2.59	5.70	8.92	2.80	12.54	25.42	8.69	2.03	8.86	7.80	7.28	5.64
Grand mean	81.23	112.30	98.84	28.38	11.43	25.28	144.74	51.67	74.19	23.80	6802.62	5476.50	11462.81	52.40

DH=Days to Heading, MD= Days to Maturity, PH= Plant height, FLL= Flag leaf length, PN= Number of panicles per hill, PL= Panicle length, FG= Number of filled grains, UnFG= Number of unfilled grains, Fertility percentage, TGW= Thousand grain weight, GY= Grain Yield (Kg/ha), SY= Straw Yield (Kg/ha), Biological Yield (Kg/ha), HI=Harvest index (%). Means followed by the same letter(s) in a column are not significantly different by DMRT at 5% level of significance. ns= Non-significant, *=significant at 5% probability level, **= significant at 1% probability level, ***=significant at 0.1% probability level

Cite the Article: Susmita Shrestha, Ram Hari Timilsina, Kailash Pandey (2023). Assessment of Genetic Variability, Heritability and Correlation in Spring Rice Genotypes (*Oryza Sativa L.*) at Ratnanagar, Chitwan In 2022. *Tropical Agrobiodiversity, 4(2): 36-43.*

Table 5: Phenotypic (σ^2p), Genotypic (σ^2g) Variances, Phenotypic (PCV) and Genotypic (GCV) Coefficient of Variation for Different Traits Studied in Spring Rice Genotypes Evaluated at Ratnanagar In 2022

Traits	σ^2g	σ^2p	GCV	PCV
DH	42.22	42.69	8.00	8.04
MD	44.03	44.14	5.92	5.93
PH	62.31	68.86	7.99	8.40
FLL	5.59	8.21	8.33	10.10
PN	1.89	2.94	12.06	15.00
PL	2.18	2.68	5.84	6.47
FG	747.93	1077.27	18.89	22.68
UnFG	356.67	529.21	36.55	44.52
FP	23.09	64.60	6.48	10.83
TGW	11.87	12.11	14.48	14.63
SY	655540.73	838044.92	14.78	16.72
BY	1458520.18	2155482.29	10.54	12.81
HI	7.05	12.11	5.07	6.64
GY	276793.60	639648.37	7.73	11.76

DH= Days to heading, MD=Days to maturity, PH=Plant height, FLL=Flag Leaf Length, PN=Number of Panicles per hill, PL=Panicle length, FG = Number of filled grains per panicle, UnFG=Number of unfilled grains per panicle, FP=Fertility percentage, TGW Thousand grain weight, SY= Straw yield (Kg/ha), GY=Grain yield (Kg/ha), BY=Biological Yield (kg/ha) and HI= Harvest index (%)

The traits with low GCV such as harvest index, days to maturity, panicle length, fertility percentage, plant height, days to heading, grain yield and flag leaf length indicates the presence of low genetic variability. Direct selection on the basis of phenotypic observation for these traits would be unrewarding, thus, requiring targeted breeding strategies to increase genetic diversity for scope of selection to be effective. However, selection for the traits showing moderate to high GCV such as thousand grain weight, straw yield, flag leaf, length numbers of filled grains per panicle and number of unfilled grains per panicle through phenotypic observation maybe effective. Therefore, the traits such as number of filled grains per panicles, number of unfilled grains per panicle could be prioritized for further improvement and selection. Similar results were reported for plant height, panicle length, number of grains per panicle, grain yield while for panicle length, days to heading, days to maturity and number of panicles per hill, then for plant height, days to maturity, biological yield and harvest index and for thousand grain weight, straw yield and grain yield (Venkanna et al., 2022; Shrestha et al., 2021; Lamichhane et al., 2021; Singh et al., 2020; Adhikari et al., 2018; Sumanth et al., 2017; Acharya et al., 2019).

3.2.2 Estimate of Heritability and Genetic Advance as Percentage of Mean

The estimation of broad sense heritability provides insights into how much genetic factors contribute to the observed variation in a trait within a population. Among the studied traits, broad sense heritability ranged from 35.74% (fertility percentage) to 99.90% (days to heading). The study revealed that highest heritability was shown by days heading (99.90%) followed by days to maturity (99.75%), thousand grain weight (98.02%), plant height (90.49%), panicle length (81.34%), straw yield (78.22%), number of filled grains per panicle (69.43%), flag leaf length (68.09%), biological yield (67.67%), number of panicles per hill (64.29%), harvest index (58.19%), grain yield (43.27%), and fertility percentage (35.74%).

Higher broad sense of heritability of traits such as days to maturity, days to heading, thousand grain weight, plant height, panicle length, straw yield, number of filled grains per panicle, flag leaf length, biological yield and number of panicles per hill which are supported by researchers suggests that variation observed in these traits are primarily influenced by genetic factors, with minimal contribution from environmental factors (Singh et al., 2020; Rashid et al., 2017; Lingaiah et al., 2020; Sandeep et al., 2018; Subedi et al., 2018; Sumanth et al., 2017). Moderate heritability of grain yield in unison with previous finding and harvest index indicates the presence of environmental influence on the variation observed in these traits while low heritability of fertility percentage indicate variation is predominantly influenced by environmental factor over genetic factor (Venkanna et al., 2022).

Genetic advance as percentage of mean provides valuable insights into the potential for improvement in different traits through selective breeding. Genetic advance as percentage of mean (GAM) was found high in number of filled grains per panicle (32.43%), thousand grain weight (29.54%), straw yield (26.94%) while moderate in number of panicles per hill (19.97%), biological yield (17.85%), days to heading (16.39%), plant height (15.65%), flag leaf length (14.16%), days to maturity (12.18%), panicle length (10.84%), grain yield (10.48%) and low in fertility percentage (7.97%) and harvest index (7.96%).

The high GAM of number of filled grains per panicle and thousand grain weight exhibits higher scope of improvement through selection, consequently, contributing to crop productivity. Although the potential for improvement in number of panicles per hill, biological yield, days to heading, plant height, flag leaf length, days to maturity, panicle length and grain yield is not as high as in the traits with high GAM value; they still offer room for progress through selective breeding. On the other hand, traits such as fertility percentage and harvest index displaying low GAM values suggests that improvement in these traits through selective breeding is challenging. Even though the potential for improvement is relatively lower, efforts can still be made to enhance these traits through careful selection and breeding strategies. The findings were aligned with previous research of fertility percentage, number of panicles per hill, a plant height, panicle length and thousand grain weight, flag leaf length and for grain yield. (Lamichhane et al., 2021; Singh, Singh and Lal, 2011; Lingaiah et al., 2020; Subedi et al., 2018; Chakrobarty and Chakborty, 2010; Venkanna et al.,2022; Adhikari et al., 2018)

Table 6: Heritability (H^2_{bs}), Genetic Advance (GA) and Genetic Advance as Percentage of the Mean (GAM) for Different Traits Studied in Spring Rice Genotypes Evaluated at Ratnanagar In 2022

Traits	h^2_{bs}	GA	GAM
DH	98.90	13.31	16.39
MD	99.75	13.65	12.18
PH	90.49	15.47	15.65
FLL	68.09	4.01	14.16
PN	64.29	2.28	19.97
PL	81.34	2.74	10.84
FG	69.43	46.94	32.43
UnFG	67.40	31.94	61.81
FP	35.74	5.92	7.97
TGW	98.02	7.03	29.54
SY	78.22	1475.14	26.94
BY	67.67	2046.48	17.85
HI	58.19	4.17	7.96
GY	43.27	712.94	10.48

DH=Days to heading, MD=Days to maturity, PH=Plant height, FLL=Flag Leaf Length, PN= Number of Panicles per hill, PL=Panicle length, FG=Number of filled grains per panicle, UnFG= Number of unfilled grains, FP=Fertility percentage, TGW=Thousand grain weight, SY=Straw yield, GY=Grain yield, BY=Biological Yield and HI=Harvest index.

Table 7: Pearson Correlation Coefficient Among Yield and Yield Contributing Traits in Ten Spring Rice Genotypes Evaluated at Ratnanagar in 2022

Traits	*DH*	*MD*	*PH*	*FLL*	*PL*	*PN*	*FG*	*UnFG*	*FP*	*TGW*	*SY*	*BY*	*HI*
MD	0.975***												
PH	0.194	0.209											
FLL	0.370*	0.349	0.626***										
PL	0.244	0.199	0.675***	0.726***									
PN	-0.271	-0.311	-0.20	-0.153	-0.162								
FG	-0.074	0.016	0.288	-0.026	0.256	-0.363*							
UnFG	0.382*	0.413*	0.128	0.082	0.083	-0.415*	0.333						
FP	-0.390*	-0.379*	0.004	-0.121	0.061	0.274	0.193	-0.852***					
TGW	-0.035	-0.150	-0.033	0.310	0.229	0.197	-0.618***	-0.690***	0.383*				
SY	-0.298	-0.304	0.613***	0.474**	0.603***	0.309	0.167	-0.275	0.382*	0.205			
BY	-0.452*	-0.439*	0.523**	0.305	0.463*	0.400*	0.189	-0.340	0.452*	0.139	0.928***		
HI	-0.106	-0.077	-0.507*	-0.584***	-0.598**	0.017	-0.065	0.073	-0.130	-0.268	-0.711***	-0.402*	
GY	-0.554**	-0.519**	0.288	0.014	0.175	0.431*	0.177	-0.348	0.442*	0.035	0.625***	0.871***	0.095

DH= Days to heading, MD= Days to maturity, PH=Plant height, FLL= Flag leaf length, PL= Panicle length, PN= Number of panicles per hill, FG= Number of filled grains per panicle, FP= Fertility percentage, TGW= Thousand grain weight, SY= Straw Yield, BY= Biological Yield, HI= Harvest Index, GY= Grain Yield, *=significant at 5% probability level, **= significant at 1% probability level, ***=significant at 0.1% probability level

Table 8: Estimation of the Phenotypic Correlation for Yield and Yield Contributing Traits of Ten Spring Rice Genotypes Evaluated at Ratnanagar in 2022

Traits	*DH*	*MD*	*PH*	*FLL*	*PL*	*PN*	*FG*	*UnFG*	*FP*	*TGW*	*SY*	*BY*	*HI*
MD	0.976**												
PH	0.194	0.211											
FLL	0.369*	0.348	0.634**										
PL	0.243	0.199	0.684**	0.725**									
PN	-0.277	-0.317	-0.189	-0.166	-0.175								
FG	-0.074	0.016	0.297	-0.028	0.255	-0.379**							
UnFG	0.382*	0.415*	0.189	0.074	0.075	-0.444*	0.332						
FP	-0.389*	-0.380*	0.012	-0.116	0.067	0.287	-0.194	-0.852**					
TGW	-0.035	-0.149	-0.034	0.311	0.229	0.201	-0.618**	-0.696**	0.386*				
SY	-0.313	-0.314	0.621**	0.473**	0.607**	0.302	0.168	-0.314	0.419*	0.211			
BY	-0.466*	-0.447*	0.516**	0.301	0.464*	0.411*	0.195	-0.355*	0.480**	0.141	0.929**		
HI	-0.104	-0.078	-0.534**	-0.590**	-0.606**	0.064	-0.058	0.114	-0.160	-0.279	-0.699**	-0.391*	
GY	-0.564**	-0.526**	0.271	0.016	0.179	0.464**	0.187	-0.355	0.457*	0.020	0.638**	0.877**	0.093

DH= Days to heading, MD= Days to maturity, PH=Plant height, FLL= Flag leaf length, PL= Panicle length, PN= Number of panicles per hill, FG= Number of filled grains per panicle, FP= Fertility percentage, TGW= Thousand grain weight, SY= Straw Yield, BY= Biological Yield, HI= Harvest Index, GY= Grain Yield, *=significant at 5% probability level, **= significant at 1% probability level, ***=significant at 0.1% probability level

Table 9: Estimation of the Genotypic Correlation for Yield and Yield Contributing Traits of Ten Spring Rice Genotypes Evaluated at Ratnanagar in 2022

Traits	*DH*	*MD*	*PH*	*FLL*	*PL*	*PN*	*FG*	*UnFG*	*FP*	*TGW*	*SY*	*BY*	*HI*
MD	0.979**												
PH	0.210	0.227											
FLL	0.4440	-0.433	0.876**										
PL	0.268	0.227	0.777**	0.929**									
PN	-0.318	-0.381	-0.235	-0.209	-0.291								
FG	-0.096	0.033	0.293	-0.078	0.157	-0.758**							
UnFG	0.462	0.497	0.220	-0.137	0.065	-0.512	0.712*						
FP	-0.646*	-0.609	-0.149	0.131	0.015	0.216	-0.290	-0.875**					
TGW	-0.033	-0.147	-0.044	0.403	0.219	0.231	-0.787**	-0.849**	0.604				
SY	-0.335	-0.341	0.669*	0.674*	0.724*	0.263	0.116	-0.359	0.567	0.208			
BY	-0.543	-0.522	0.546	0.542	0.532	0.368	0.039	-0.362	0.482	0.113	0.971**		
HI	-0.141	-0.094	-0.769**	-0.841**	-0.976**	-0.070	-0.234	0.327	-0.705*	-0.393	-0.859**	-0.715*	
GY	-0.829**	-0.764*	0.254	0.236	0.121	0.501	-0.101	-0.316	0.265	-0.067	0.821**	0.909**	-0.362

DH= days to heading, MD= Days to maturity, PH=Plant height, FLL= Flag leaf length, PL= Panicle length, PN= Number of panicles per hill, FG= Number of filled grains per panicle, UnFG=Number of unfilled grains per panicle, FP= Fertility percentage, TGW= Thousand grain weight, SY= Straw Yield, BY= Biological Yield, HI= Harvest Index, GY= Grain Yield, *=significant at 5% probability level, **= significant at 1% probability level, ***=significant at 0.1% probability level

3.2.3 Correlation Study

Pearson correlation was computed among yield and yield contributing traits which is presented in Table 7 which was further separated into phenotypic level (Table 8) and genotypic level (Table 9) for clear understanding of correlation coefficients. Higher genotypic correlation coefficients than phenotypic correlation coefficients were reported in most traits, manifesting the association to have genetic cause. In some cases, phenotypic correlation coefficient was higher than genotypic correlation indicating suppressing effect of the environment which modified the expression of the traits at phenotypic level.

Strong signification positive correlation was found between days to headings and maturity at both phenotypic and genotypic level which suggests that genotypes with earlier heading tend to have a shorter time to reach maturity, thereby avoiding adverse climatic conditions or pests during later stages of growth (Subedi et al., 2018). Similarly, positive significant correlation between plant height and flag leaf length as well as plant height and panicle length at phenotypic and genotypic level which was similar with the findings of indicates that genotypes with taller height tend to have longer flag leaves and longer panicles (Hasan et al., 2013; Hefena et al., 2016). Straw yield exhibited significant positive correlation with panicle length which was in agreement with (Lohiteswararao et al., 2021). This finding directs that the genotypes with taller height accumulate more biomass in non-reproductive part of rice.

The negative correlation observed between number of panicles per hill and number of filled grains per panicles and thousand grain weight in unison with the study of Karim et al. (2014) could be due to resource allocation within the plant, where genotypes with more panicles per hill may allocate fewer resources per panicle, resulting in reduced number of filled grains per panicle (Karim et al., 2014). The significant negative correlations between fertility percentage and days to maturity and significant positive correlation between fertility percentage and traits such as thousand grain weight, straw yield, biological yield and grain yield signifies that the genotypes with a higher fertility percentage may allocate more resources to grain production, leading to faster maturity.

Harvest index represents the proportion of total biomass allocated to grain production. The significant negative correlations between harvest index and plant height, flag leaf length, panicle length which was in uniformity with finding of Reddy et al. (2013) suggest that genotypes with taller plants, longer flag leaves, and longer panicles may allocate a relatively larger proportion of biomass to non-grain components, resulting in a lower harvest index. This finding highlights the importance of selecting genotypes that balance vegetative growth and grain production to achieve higher harvest index and overall yield potential (Reddy et al., 2013).

Grain yield was positively correlated with number of panicles per hill, fertility percentage, biological yield and straw yield while negatively correlated with days to heading and days to maturity which indicates genotypes with early maturity tend to produce more yields due to lesser exposure of crop in the adverse climatic condition with lower maturity days, prioritizing resource allocation to grain production. However, other traits including plant height, flag leaf length, panicle length and thousand grain weight showed positive but non-significant phenotypic and genotypic correlation. The findings were similar to the study conducted by (Chakrobarty and Chakborty, 2010; Hasan et al., 2013; Karim et al., 2014; Subedi et al., 2018; Adhikari et al., 2018). There was non-significant positive phenotypic correlation and negative genotypic correlation of harvest index with grain yield which could be due to the use of diverse genotypes for evaluation.

4. CONCLUSION

The significant difference among genotypes for all the studied traits reveals the existence of the genetic variability for studied traits among the evaluated genotypes of spring rice. The existence of sufficient amount of genetic variability in these genotypes facilitates genotypes as breeding materials in selective breeding. However, the moderate genotypic coefficient of variation with high to moderate broad sense heritability and low to moderate genetic advance as percent of mean of most of the studied traits exhibits the influence of both genetic and environmental factor on the variation of these traits among genotypes. High estimates of heritability along with high genetic advance as percentage of mean in traits such as number of filled grains, thousand grain weight and straw yield shows scope of improvement and more likely response to selection while grain yield and fertility percentage may require additional strategies such as consideration of correlated traits or environment manipulation to achieve improvement through selection. In addition, selection based on number of panicles per hill, straw yield and fertility percentage may result in chance improvement of grain yield as they are significantly positively correlated with grain yield. Further research and selection can be focused on these traits to develop improved spring rice genotypes and optimize the resource allocation to achieve higher grain yield.

ACKNOWLEDGEMENTS

Authors would like to express profound gratitude to Agriculture and Forestry University, Rampur, Nepal, Ratnanagar municipality, Chitwan and PMAMP, Chitwan for funding the research. In addition, authors are thankful to farmer Mr. Ram Lal Shrestha for helping to complete the research.

REFERENCES

Acharya, N., Acharya, S. S., Poudel, A., & Neupane, N. 2019. Genetic Variability, Correlation and Path Analysis of Different Hill-Rice (Oryza Sativa) Genotypes. Global Journal of Science Frontier Research: D Agriculture and Veterinary, 19(4), 37-41.

Adhikari, B. N., Joshi, B. P., Shrestha, J., & Bhatta, N. R. 2018. Genetic variability, heritability, genetic advance and correlation among yield and yield components of rice (Oryza sativa L.). Journal of Agriculture and Natural Resources, 1(1), 149-160. doi:10.3126/janr.v1i1.22230

Aditya, J., & Bhartiya, A. 2013. Genetic variability, correlation and path analysis for quantitative characters in rainfed upland rice of Uttarakhand hills. Journal of Rice Research., 6(2), 24-34.

Allard, R. 1960. Principles of Plant Breeding. New York, USA, : John Willey and Sons, Inc.

CDD. 2015. Rice varietal mapping in Nepal: implication for development and adoption. Hariharbhawan, lalitpur: Crop Development Directorate, DOA. Retrieved from http://doacrop.gov.np/

Center, A. R. 2007. Descriptors for wild and cultivated rice (Oryza spp.).

Chakrobarty, R., & Chakborty, s. 2010. Genetic variability and correlation of some morphometric traits with grain yield in bold grained rice (Oryza sativa L.) gene pool of Barak valley. American-Eurasian Journal of Sustainable Agriculture , 4(1), 26-29.

FAO. 2020. FAOSTAT. Retrieved from Food and Agriculture Organization of the United Nations: http://www.fao.org/faostat/.

FAO. 2022. Food Outlook – Biannual Report on Global Food Markets. Rome: Food and Agriculture Organization of the United Nations.

Gadal, N., Shrestha, J., Poudel, M. N., & Pokharel, B. 2019. A review on production status and growing environments of rice in Nepal and in the. Archives of Agriculture and Environmental Science, 4(1), 83-87.

Grebmer, K., Bernstein, J., Wiemers, M., Reiner, L., Bachmeier, M., Hanano, A., Fritschel , H. 2022. 2022 Global Hunger Index: Food Systems Transformation And Local Governance. International Food Policy Research Institute.

Hasan, M., Kulsum, M., Akter, A., Masuduzzaman, A., & Ramesha, M. 2013. Genetic Variability And Character Association For Agronomic Traits In Hybrid Rice (Oryza Sativa L.). Bangladesh Journal of Plant Breeding and Genetics, 45-51.

Hefena, A., Sultan, M., Abdel-Moneam, M., Hammoud, S., Barutçular, C., & EL-Sabagh, A. 2016. Assessment of Genetic Variability and Correlation Coefficient to Improve Some Agronomic Traits in Rice. Journal of Experimental Agriculture International, 14(5), 1-8.

Islam, M. Z., Khalequzzaman, M., Bashar, M. K., Haque, M. M., Ivy, N. Y., & Mian, M. K. 2016. Variability Assessment of Aromatic and Fine Rice Germplasm in Bangladesh Based on Quantitative Traits. Scientific World Journal.

Johnson, H., Robinson, H., & Comstock, R. 1955. Estimates of genetic and environmental variability in soybeans (Vol. 47).

Joshi, B. K. 1970. Rice Gene Pool for Tarai and Inner Tarai Areas of Nepal. Nepal Agricultural research journal, 24-27.

Karim, D., Siddique, M. N.-E.-A., Sarkar, U., Hasnat, M. Z., & Sultana, J. 2014. Phenotypic and genotypic correlation co-efficient of quantitative characters and character association of aromatic rice. Journal of Bioscience and Agriculture Research, 1(1), 34-46.

Kharel, L., Ghimire, S. K., Shrestha, J., Kunwar, C. B., & Sharma, S. 2018. Evaluation of rice genotypes for its response to added fertility levels and induced drought tolerance during reproductive phase. Journal of Agrisearch, 5(1), 13-18.

Khush, G. 2000. Taxonomy and origin of rice. In R. Singh, U. Singh, & G. Khush, Aromatic rices (pp. 5-13). New delhi, Culcutta: Oxford and IBH Publishing Co. Pvt. Ltd.

Lamichhane, S., Adhikari, N. R., K.C, B., & Thapa, S. 2021. Estimating Variability, Heritability, and Genetic Advance of Rice Genotypes in Mid-Hills of Nepal. Indonesian Journal of Agricultural Science, 22(2), Indonesian Journal of Agricultural Science. doi:10.21082/IJAS.V22N2.2021.P92-101

Lingaiah, N., Chandra, B. S., Venkanna, V., Devi, K. R., & Hari, Y. 2020. Genetic Variability and Correlation Studies in Yield Traits of Elite Rice (Oryza sativa L.) Genotypes. Ind. J. Pure App. Biosci , 8(6), 359-363. Retrieved from http://dx.doi.org/10.18782/2582-2845.8428

Lohiteswararao, R., Kumar, P., Sravani, P., Raju , K. K., & Gogada, R. 2021. Correlation and path analysis of grain yield and its attributes of traditional rice (Oryza sativa L.) genotypes. The Pharma Innovation Journal , 10(12), 1055-1058.

Lush, J. 1940. Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristice. Proceedings of the American Society of Animal Nutrition, (pp. 293-301).

Mallick, R. 1981/82. Rice in Nepal. Kala Prakanshan, Kathmandu.

MoALD. 2020/21. Statistical Information On Nepalese Agriculture 2077/78 (2020/21). Kathmandu: Ministry of Agriculture and Livestock Department of Agriculture, Government of Nepal.

NASA POWER. (n.d.). Retrived from https://power.larc.nasa.gov/data-access-viewer/.

NRRP. 2020. Annual report. National Rice Research Program.

Rashid, M. M., Nuruzzaman, M., Hassan, L., & Begum, S. N. 2017. Genetic variability analysis for various yield attributing traits in rice genotypes. Journal of the Bangladesh Agricultural University, 15(1), 15-19.

Reddy , G. E., B.G., S., Sravant, T., & Ashok, P. 2013. Interrelationship And Cause-Effect Analysis Of Rice Genotypes In North East Plain Zone. The bioscan, 8(4), pp. 1141-1144.

Sandeep, S., Sujatha, M., Subbarao, L. V., & Neeraja, C. N. 2018. Genetic Variability, Heritability and Genetic Advance Studies in Rice (Oryza sativa L.). International Journal of Current Microbiology and Applied Sciences, 7(12), 3719-3727. Retrieved from https://doi.org/10.20546/ijcmas.2018.712.424

Shrestha, J., Subedi, S., Subedi, N. R., Subedi, S., Singh, U. K., Maharjan, B., & Subedi, M. 2021. Assessment of Variability, heritability and correlation in Rice Genotype. Natural Resources and Sustainable Development, 181-192.

Singh, A., Ekka, R. E., Sinha, S., & Tiwari, J. 2020. Genetic variability, heritability and genetic advance for yield contributing traits in aromatic and pigmented rice (Oryza sativa L.). Journal of Pharmacognosy and Phytochemistry 2020; SP6: 05-08, 5-8.

Singh, R., & Chaudhary, B. 1985. Biometrical Methods in Quantitative Analysis. New Delhi: Kalayani Publishers.

Singh, S. K., Singh, C. M., & Lal, G. 2011. Assessment of genetic variability for yield and its component characters in rice (Oryza sativa L.). Research in Plant Biology, 1(4), 73-76.

Sivasubramanian, S., & Madhavamenon, P. 1973. Genotypic and phenotypic variability in rice. Madras Agriculture Journal. Madras Agriculture Journal, 1093-1096.

Subedi, S., Sharma, S., Poudel, A. P., Iqbal, M., Umer, S., & Jabeen, S. 2018. and path coefficient analysis of pipeline sprinHeritability , correlation , genotypic and phenotypic coefficient of variance , and path coefficient analysis of pipeline spring rice genotypes in western hills of Nepal. International Journal of Agronomy and Agricultural Research (IJAAR), 13, 128-135.

Sumanth, V., BG, S., Ram , B. J., & Srujana, G. 2017. Estimation of genetic variability, heritability and genetic advance for grain yield components in rice (Oryza sativa L.). Journal of Pharmacognosy and Phytochemistry, 6(4), 1437-1439.

USDA/ERS. 2022. Rice Outlook- 2016 by Nathan Childs and Bonnie LeBeau. Retrieved from https://www.ers.usda.gov/webdocs/outlooks/103052/rcs-22a.pdf

Venkanna, V., Devi, K., Hari, Y., Chandra, B. S., Lingaiah, N., & Prasad, K. 2022. Variability studies in promising elite rice (Oryza sativa L.) genotypes. The Pharma Innovation Journal, 11(1), 1987-1989.

Yadaw, R., Subedi, S. R., Tiwari, D. N., Bastola, B. R., Yadaw, B., Tripathi, S. P., . . . Sharma, P. 2021. Varietal Improvement on Short Duration Rice Varieties for Spring Season. Proceedings of 30th National Summer Crops Workshop (pp. 199-210). Nepal Agriculture Research Council: Government of Nepal.

Cite the Article: Susmita Shrestha, Ram Hari Timilsina, Kailash Pandey (2023). Assessment of Genetic Variability, Heritability and Correlation in Spring Rice Genotypes (*Oryza Sativa L.*) at Ratnanagar, Chitwan In 2022. *Tropical Agrobiodiversity, 4(2): 36-43.*