Genetic Parameters, Correlation and Stability Analysis of Aromatic Rice Landraces of Nepal

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ABSTRACT

Rice is the major food crop directly related to the livelihood of majority of rural people in Nepal. Aromatic rice is one of the fundamental groups that has great significance from the nutritional and market point of view all over the world. The main objective of this study was to emphasize on the determination of major genetic parameters, genotypic and phenotypic correlations, stability analysis for yield and major quantitative traits of aromatic rice landraces. Altogether 30 aromatic rice landraces were considered in this study and that were evaluated in three locations namely Hardinath, Tarahara and Khajura with three replications. Two years of multilocation data on nine morphological traits were collected and evaluated. The genetic parameters like genetic variance, phenotypic variance, genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance were estimated using the statistical methods. The highest GCV and PCV was exhibited by grain yield (23.67 and 25.7) whereas lowest GCV and PCV was found in panicle length (4.9 and 5.6) respectively. Heritability of various traits was measured from 0.76 to 0.98 where the lowest heritability was observed in panicle length and the highest was observed in both heading and maturity days. The genetic advance as percentage of means value ranging from 8.8 to 45 representing panicle length and grain yield respectively. The genetic correlation of the measured traits showed highly significant positive correlation of heading days with maturity (r=1.0004**) and straw yield (r=0.787**) as well as correlation of maturity days with straw yield (r=0.79**). In case of phenotypic correlation, highly significant positive correlation of heading days with maturity (r=0.99**) and straw yield (r=0.7611**) was obtained however there is negative but significant correlation with tillers per meter square (r=-0.296*), filled grain weight (r=-0.305*), 1000 grain weight (r=0.3115*) and grain yield (r=-0.4*). According to the stability analysis, Gouriya and Karia Kamod (bi=1.1) were found more stable. Based on the value of coefficient of determination (R^2), most of accessions; Lalka Basmati, Sugandhit Dha-1, Suhpat, Gouriya, Bayerni Masino, Kalo Nunia, Balamsari Dhan, Tilki, Tulsiful and Sunaulo Sugandha were obtained stable in all the three locations in both years. Based on the Superiority Measure (Pi), Samba Masuli Sub-1 and Sugandhit Dhan-1 showed lower Pi values of 132556.16 to 377994.35 hence identified as most stable varieties. This study identified the genetic parameters that provides the useful information for breeding of rice varieties, correlation among the major traits and stability of some aromatic landraces Gouriya and Karia Kamod obtained in all the environments. Thus, findings of this study are highly helpful for future studies to identify desirable traits and genotypes in the further varietal development works in coming days.

सारांश

धान नेपालको बहुसंख्यक ग्रामीण जनताको जीविकोपार्जनसँग प्रत्यक्ष रूपमा सम्बन्धित प्रमुख खाद्यान्न बाली हो। धानका मौलिक समूहहरू मध्ये बास्मती धान एक हो, यसको पोषण र बजारको दृष्टिकोणले विश्वभरि ठूलो महत्त्व छ । यस अध्ययनको मुख्य उद्देश्य अध्ययनमा प्रमुख आनुवंशिक मापदण्डहरू, जीनोटाइपिक र फेनोटाइपिक सहसम्बन्धहरू, उपजको लागि स्थिरता विश्लेषण र सुगन्धित चामलको भूमिजातहरूको प्रमुख मात्रात्मक विशेषताहरूको निर्धारणमा जोड दिनु हो । यस अध्ययनमा कुल ३० वटा सुगन्धित धानका ल्याण्डरेसहरू समावेश गरियो र तिनलाई हर्दिनाथ, तरहरा र खजुरा नामक तीन स्थानमा तीन प्रतिकृति सहित मूल्याङ्कन गरियो । नौ बाहिरी स्वरूप मौलिक विशेषताहरूमा दुई वर्षको बहुस्थलीय आंकडा सङ्कलन र मूल्याङ्कन गरिएको थियो । आनुवंशिक मापदण्डहरू जस्तै: आनुवंशिक भिन्नता, फेनोटाइपिक भिन्नता, भिन्नताको जीनोटाइपिक गुणांक, भिन्नताको फेनोटाइपिक गुणांक, आनुवंशिकता र आनुवंशिक अग्रिम मानक विधिहरू प्रयोग गरी अनुमान गरिएको थियो । उच्चतम GCV र PCV अनाज उत्पादन (२३.६७ र २५.७) द्वारा प्रदर्शन गरिएको थियो जबकि सबैभन्दा कम GCV र PCV क्रमशः बालाको लम्बाइ (४.९ र ५.६) मा पाइयो । विभिन्न विशेषताहरूको आनुवंशिकता ०.७६ देखि ०.९८ सम्म मापन गरिएको थियो जहाँ सबै भन्दा कम आनुवंशिकता बालाको लम्बाईमा र उच्चतम हेडिङ र परिपक्वता दिन दुवैमा अवलोकन गरिएको थियो । आनुवंशिक अग्रिम औसतको रूपमा ८.८ प्रतिशत देखि ४५ प्रतिशतसम्मको दायरामा क्रमशः बालाको लम्बाई र अन्न उत्पादनको पाइएको थियो । मापन गरिएका लक्षणहरूको आनुवंशिक सम्बन्धले बाला निस्कने दिनको परिपक्वता (१.००४८८) र परालको उपज (०.७८७८८) सँगसँगै परिपक्वता दिनहरूको परालको उपज (०.७९८८) सँग सकारात्मक सहसम्बन्ध देखाएको छ । फेनोटाइपिक सहसम्बन्धको मामलामा, हेडिङ दिनहरूको परिपक्वता (०.९९८८) र परालको उपज (०.७६११८८) सँग अत्यधिक महत्त्वपूर्ण सकारात्मक सम्बन्ध देखियो । तर बाला निस्कने दिनको प्रति वर्ग मिटर टिलर संख्यासँग (-०.२९६८), भरिएको दाना वजनसंग (-०.३०५८), १००० अनाज वजनसँग (-०.३११५८) र अन्न उपज (-०.४८) संग नकारात्मक तर महत्त्वपूर्ण सम्बन्ध छ। स्थायित्व विश्लेषणका अनुसार, गौरिया र कारिया कमोड (बिआई=१.१) को गुणांकको निर्धारणमान (R^2) को आधारमा जैविक रूपमा स्थिर पाइयो । लल्का बासमती, सुगन्धित धा-१, सुहपाट, गौरिया, बायर्नी मासिनो, कालो नुनिया, बालमसरी धान, तिल्की, तुलसीफुल र सुनौलो सुगन्धा वातावरणमा स्थिर रहेको पाइएको थियो । यस अध्ययनले आनुवंशिक मापदण्डहरू पहिचान गऱ्यो जसले धानका प्रजातिहरूको प्रजनन, प्रमुख विशेषताहरू बीचको सम्बन्ध र सबै वातावरणमा केही सुगन्धित भूमिजातहरूको स्थिरताका लागि उपयोगी जानकारी हासिल गऱ्यो । तसर्थ, यस अध्ययनका निष्कर्षहरू भविष्यका अन्वेषकहरूका लागि आगामी दिनहरूमा थप विविधता विकास कार्यहरूमा वाञ्छनीय विशेषताहरू र जीनोटाइपहरूको पहिचानमा यी भूमिजातहरू धेरै उपयोगी छन् ।

INTRODUCTION

Rice (*Oryza sativa L., 2n=24*) is the principal food crop and has contributed largely to food and nutrition security for majority of people in Nepal and also in many Asian countries. Rice sector supports 5.7% to total GDP and 13.5 % to AGDP as well as accounted 53% to the cereal grain production in the country (MoALD, 2023). It also generates income, employment, and livelihood to more than 70% of households as well as provides 40% of calories requirement to rural people (Gauchan and Pandey, 2011). It is cultivated on a total area of 1,447,789 hectares, with a production of 5,486,472 metric tons and a productivity of 3.78 metric tons per hectare (AITC 2024).

The rice statistics indicated nearly 90% of both rice production and consumption is accounted from Asian countries and shared 80% rice production and consumption worldwide (Ahmad et al 2015, Ahmed 2024). Currently, rice is cultivated in more than 100 countries and estimated rice cultivated area is approximately 164 million hectares with a production of 510 million metric tons. Rice consumption statistics implies that it is gradually increasing in the all countries during the current few years as global supply of rice was around 502 million metric tons during 2020–21. Per capita annual consumption of rice is 45 kg in the world (Ahmed et al 2024).

Nepal is endowed with enormous genetic diversities in rice comprising 2500 native landraces and 153 modern varieties are cultivated throughout the country starting from altitude range of 60 to 3050 m in Nepal. The national production statistics of Aromatic rice revealed that it is grown in approximately 10% of rice grown area with about 0.15 million ha with total production of 0.375 million ton in Nepal (Joshi et al 2021). The aromatic rice landraces possess low production potential with an average productivity of 2.5 t/ha.

The aromatic rice constitutes of range of varieties that produce aroma when cooked and consists of pleasant eating (softness) qualities, getting lucrative price in both national and international markets (Raymajhi and Malla Thakuri 2023). It is assumed that the Basmati rice of Nepal has characteristics and unique flavored

aromatic fine rice cultivated in lower belts of Churiya hills and Mahabharat range and some plains extending from east to central region and more particularly nearby Koshi river (Joshi et al 2017).

The indigenous rice varieties that have been cultivated by farmers after domestication. Those local rice landraces contain distinguishing characteristics like good aroma, good taste and better cooking and eating quality. Use of rice is directly connected with religious functions and it conserves rich cultural heritage as well as promotes socio-economic values (Islam et al 2016). Aromatic rice makes up special form of rice that are well renowned globally for pleasant aroma and extra fine grain quality.

The morphological and physiological traits is conventional tool to provide the fundamental information and serves as morphological markers. As compared to molecular markers, morphological markers are less expensive and not convincing because they are highly affected by environmental factors. The morphological markers along with molecular markers stands as robust method for investigating genetic variability and yield components which is essential for selection of genotypes for development of new crop varieties (Ahmad et al 2015).

The genetic variability present in germplasm are very essential and are pre-requisite for improvement of any breeding program (Tiwari et al 2019). The quantitative traits are governed by many minor genes and mostly influenced by the environmental factors leading to difficulty in decision making whether the variability is heritable or not (Islam et al 2016). Heritability of a quantitative trait has great significance in genetics and plant breeding that governs affects the effectiveness of selection. It indicates that degree extent of heritable character to the subsequent generation through natural selection or hybridization process (Zhang et al 2010, Sttrek and Beser 2003). Heritability can be utilized to elucidate the population structures to determine the most heritable trait (Ali et al 2000). The yield related traits are responsible for increasing yield only when they are heritable (Sttrek and Beser 2003). Genetic advance is also major concern of plant breeders in selection of yield component factors hence genetic advance play indispensable role for varietal improvement program in crop breeding (Sedeek et al 2009).

The studies reflected that the heading and maturity days, L/B ratio and plant height are found more heritable with heritability more than 90% whereas other traits showed low heritability (Jaiswal et al 2007). All the phenotypic traits that exhibits high heritability coupled with high genetic advance suggesting the presence of additive gene action and selection for such traits would be more reliable (Jaiswal et al 2007).

Breeding programs today have enormous opportunity to move forward that comprises creation of genetic variation, selection and utilization of those variability to develop new breeding materials. Among the various genetic components, genotypic variance, phenotypic variance, heritability, genotypic and phenotypic coefficient of variation, genetic advance for yield attributes is of paramount importance for plant breeders involved in varietal development process (Tiwari et al 2019). The traits showing higher genotypic coefficient of variability (GCV) and heritability accompanied by high genetic advance implies that the character is heritable that can be to subsequent generation hence for such a trait phenotypic selection based on character is more instrumental (Prasad et al 2001).

Very few information is available on the phenotypic diversity and genetic background, stability and correlation coefficient between the different traits among the aromatic rice germplasm present in Nepal. This is because of limited research works undertaken in the various aspects of genotypic and phenotypic diversity, genetic parameters and relationship between the various traits of indigenous aromatic rice landraces. Present study was started with a broad objective to explore the genetic background and inheritance of major agro-morphological traits, correlation between different studied traits of aromatic rice landraces collected from different parts of the country. This study attempts to determine the genetic variance, phenotypic variance, genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), broad sense heritability, genetic advance and genetic advance as percentage of mean,

phenotypic and genotypic correlation and stability parameters of major quantitative traits. The knowledge and information obtained from this study will be useful for the future researchers and plant breeders to know extent of variability exist in the population and assists to select the outstanding genotypes.

MATERIALS AND METHODS

Plant Materials and Experiment Details

Initially 150 fine and aromatic rice landraces were collected from National Agricultural Genetic Resource Center (Gene Bank), Khumaltar and National Rice Research Program, Hardinath and its territory. From the preliminary evaluation of major morphological traits and aroma detection from rice kernels using 1.7 % KOH solution (Tragoonrung et al 1996), twenty-eight aromatic rice landraces were identified and selected for the multi-environment trial. Thirty aromatic rice landraces including two check varieties Samba Masuli Sub-1 as non-aromatic and Kalanamak as aromatic were evaluated in this study. The research trial was conducted during rainy season in two years (2020-2021). This study was conducted basically Terai region of Nepal representing sub-tropical climate zone. Three research stations as experimental sites were selected for multi-environment trial to understand the G x E interaction and stability of rice. The experimental sites were selected representing eastern terai, central terai and western terai region. Directorate of Agricultural Research, Tarahara from eastern terai, National Rice Research Program, Hardinath, Dhanusha represents central terai and Directorate of Agricultural Research, Khajura, Banke falls in western terai. The experimental materials used in this study are presented in **Table** 1.

Table 1. **List of aromatic rice landraces used in multi-environment trial and quality test in 2020/21**

Entry	Genotypes	Local name	Description
1	NGRC 05866	Karia Kamod	Gene-bank accession (landrace)
2	Sunaulo Sugandha	Sunaulo Sugandha	Variety
3	NGRC 03096	Kalo Masino Dhan	Gene-bank accession (landrace)
4	NGRC 01849	Balamsari Dhan	Gene-bank accession (landrace)
5	Karia Kamod 1	Karia Kamod	Local collection (Landrace)
6	NGRC 05813	Tilki	Gene-bank accession (landrace)
7	NGRC 05914	Kalo Nunia	Gene-bank accession (landrace)
8	NGRC 08137	Bayani Masino	Gene-bank accession (landrace)
9	NGRC 05869	Brahmamusi Dhan	Gene-bank accession (landrace)
10	NGRC 05915	Basmati Jhapa	Gene-bank accession (landrace)
11	NGRC 05873	Malbhog	Gene-bank accession (landrace)
12	NGRC 05816	Jhuse Basmati	Gene-bank accession (landrace)
13	NGRC 05827	Gouriya	Gene-bank accession (landrace)
14	NGRC 05018	Hansaraj Dhan	Gene-bank accession (landrace)
15	NGRC 03284	Suhpat Dhan	Gene-bank accession (landrace)
16	NGRC 02113	Damari Dhan	Gene-bank accession (landrace)
17	NGRC 05870	Ujarka Basmati	Gene-bank accession (landrace)
18	Karia Kamod 2	Karia Kamod	Local collection (Landrace)
19	NGRC 03110	Jhinuwa Dhan	Gene-bank accession (landrace)
20	NGRC 05829	Hiupuri	Gene-bank accession (landrace)
21	Sugandhit dhan-1	Sugandhit dhan-1	Variety
22	NGRC 05919	Chananchur	Gene-bank accession (landrace)
23	Lalka Basmati	Lalka Basmati	Variety; landrace selection
24	NGRC 05801	Kalo Jira	Gene-bank accession (landrace)
25	NGRC 05878	Tulsiful	Gene-bank accession (landrace)
26	NGRC 05832	Kalo Basmati	Gene-bank accession (landrace)
27	NGRC 05865	Lalka Basmati Agahani	Gene-bank accession (landrace)
28	NGRC 02137	Gaure Dhan	Gene-bank accession (landrace)
29	Kalanamak	Kalanamak	Variety; used as aromatic check
30	Samba Masuli Sub-1	Samba Masuli Sub-1	Variety; used as non-aromatic check

Remarks: NGRC is an abbreviated form of National Agriculture Genetic Resources Center used in each accession of its collection.

Description of Experimental Sites

Directorate of Agricultural Research, Khajura is situated in Banke district of Lumbini province and it falls between $81^037^`E$ longitude and $28^006^`N$ latitude and an altitude of this research station is 181 m asl. An average rainfall of station is 1000-1500mm in a year. The highest and the lowest temperature regime remains at 46^0C and 5.4^0C respectively, relative humidity was 27-94% in a year. The distinguishing characteristics of soil in the station is sandy to silty loam with poor organic carbon content and available nitrogen. However, phosphorus and potassium contents were moderatel. The pH of soil in the station varies from 7.2-7.5 (RARS Khajura 2012). Similarly, National Rice Research Program, Hardinath is situated at Dhanusha district in Madhesh Province. Geographically the station falls in the latitude of 26^0 49' E and 86^0, 01' N with an altitude of 93 meters above sea level. The dominant soil type is silty clay to sandy loam and slightly neutral pH value around 6.3. An annual rainfall of the station is approximately 1281 mm. The relative humidity is found in between 55 to 90% throughout the year (NRRP 2016). DoAR Tarahara is located at 26°42'16.85" N latitude and 87°16'38.43" E longitude, at an elevation of 136 meters above sea level. The soil pH ranges from 6.5 to 7.0, indicating slightly acidic to neutral status (DoAR Tarahara 2020). The detailed monthly record of weather parameters during the crop season is presented in **Table 2**.

Table 2. Monthly weather data of different locations during crop growing period of 2020 and 2021.

Location	Months	Max. Temp. (0C)		Min. Temp. (0C)		RH (%)		Rainfall (mm)	
		2020	**2021**	**2020**	**2021**	**2020**	**2021**	**2020**	**2021**
Hardinath	June	33	32.5	26.2	26	83.6	82.2	383.6	160.4
	July	32.2	32.4	26.6	26.4	87.1	82.9	591.9	517.9
	August	33.3	31.8	27.3	25.7	86.3	86.6	183.5	387.1
	September	32.2	32.5	25.9	25.5	85.5	82.9	206.5	100
	October	33.9	31.1	23.3	23.4	81.7	86.4	0	241.9
	November	30.2	28.6	14.4	15.5	80.8	82.6	0	0
Tarahara	June	32	32.8	24.9	23.2	80.9	83	466.5	354
	July	31.5	32	25.3	25.4	86.8	83.2	437.7	643
	August	32.7	32.7	25.9	25.3	82.7	87.4	209	442.1
	September	31.7	31.7	24.5	24.8	88.8	82.9	621.1	229.2
	October	32.2	33.1	22.1	21.8	81	84.8	29	495.2
	November	31.1	30.1	13.5	14.3	80.3	80.3	0	0
Khajura	June	34.4	35	22.8	23	78	70	165.6	0
	July	33.8	34.1	26.4	29.9	86	79	366.9	220.5
	August	34.2	33.4	26.7	27.2	84	79	258.7	507.6
	September	33.9	33.9	25.7	26.5	85	86	118.8	175.5
	October	34.2	32.4	19.5	23.6	78	85	0	41.6
	November	28.5	27.5	11.9	16.1	82	83	0	0

Note*: Max. Temp. indicates to maximum temperature; Min. Temp. indicates minimum temperature, RH; relative humidity*

Field experiment

Thirty aromatic rice landraces, including checks; Samba Masuli Sub-1 (non-aromatic) and Kalanamak were tested in a Randomized Complete Block Design (RCBD) with three replications across all the three locations (Hardinath, Tarahara, and Khajura). The experimental design and works were carried out following the uniform standards in all the locations. The plot size of experimental unit was 6 m² (2m x 3m) which accommodates ten rows of 3m long was designed with plant-to-plant spacing of 20 cm × 20 cm. Seed sowing was performed during the second week of June, and 22-day-old seedlings were transplanted

into the main field. The recommended cultural practices were followed for all intercultural operations throughout the cropping period as guided by experimental protocol designed by NRRP, Hardinath (Tiwari et al 2019).

Data Collection
Eleven quantitative traits measured in each location were heading and maturity days, plant height, panicle length, filled grains per panicle, tillers per square meter, 1000 grain weight, filled grain weight, straw as well as grain yield. The days to heading and maturity was taken from date of seeding and 50% heading was recorded when half plots showing fully emerged panicles. Similarly, days to maturity was taken when more than 85% of panicles achieved maturity stage. The plant height was mainly measured from base of plant near soil surface to top of the panicle. Similarly, panicle length was measured from the base of the first spikelet branch to top of panicle. The filled grains and unfilled grains were counted from the five selected panicles. Tillers was counted from one square meter of area in the middle of the plot. Grain and straw yield were taken from the entire plot and later converted into ton per hectare.

Statistical data analysis
Analysis of variance (ANOVA) was carried out to derive the effects of genotype, environment and their interaction and means were compared among different treatments according to the least significant difference (LSD) test at 5% levels of significance. The ANOVA was performed applying incomplete randomized complete block design following the treatment structure Rep + Trt +Loc +Yr +Trt *Loc*Yr to derive variance components. The experimental results statistically analyzed using the software packages GenStat 15th Edition for multivariate analysis. The mean sum of square and error variance is used to calculate the different genetic parameters. Genetic parameters; genetic and phenotypic variance, genotypic and phenotypic coefficient of variation, (GCV, PCV), heritability (H^2), genetic advance (GA) and genetic advance as % of mean were estimated as per the methods as described for genetic analysis later. The Phenotypic and genotypic correlation coefficient values were calculated and computed as suggested by Pearson's Correlation Coefficient method (Hossain et al 2015).

Genetic parameters
G x E variance component was estimated according to DeLacy et al (1996). We used the standard procedure of Johnson et al. (1955), Miller et al. (1958), Hanson et al. (1956) and Singh and Chaudhary (1985) for phenotypic and genotypic correlation analysis. Similarly, genotypic variance, phenotypic variance, Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated according to Burton (1951,1952), Burton and Devane (1953), Miller et al (1958) and Johnson et al (1955). It was categorized according to Sivasubramanian and Madhava Menon (1973) as low when value was below 10, medium for value between 10 to below 20 and high for 20 or more. Similarly, broad sense heritability (H^2) was calculated following DeLacy et al (1996), Allard (1999), Miller et al (1958), Lush (1940) and categorized by Robinson (1966) as low (H^2= <30), medium (30 or more to less than 60), and high ($\geq$ 60). Genetic advance (GA) and genetic advance as a percentage of mean were calculated and categorized according to Johnson et al. (1955), Allard (1999. Low GAM for less than 10 value, medium for values between 10 and below 20, and high for 20 or above.

Stability analysis
The stability analysis was performed following the method developed by Eberhart and Russell (1966) introducing the concept of regression model that helps in selecting genotype based on their relative performance in various environments. Two stability parameters were computed basically regression coefficient (bi) and deviation from linear regression (S2di) were used for characterizing the genotype and environment as proposed by Eberhart and Russell (1966) by using GEA-R software.

RESULTS

Analysis of Variance

The analysis of variance (ANOVA) revealed significant differences among the genotypes (G), environments (E), and their interactions (G x E) for several key agronomic traits of aromatic rice landraces. Genotypes showed highly significant variation for heading days (HD) with a mean square value of 3895.6 (p < 0.01). The environment also had a highly significant effect in heading days (2830.97**, p < 0.01), and significant G x E interaction (54.4**, p < 0.01) was obtained (**Table** 3). Likewise, highly significant difference was obtained between the landraces (3599.36**, p < 0.01) and environments (2481.67**, p < 0.01) for maturity days (MD). Genotypes and environments had a highly significant effect on panicle length (43.89** and 75.02** respectively, p < 0.01). Significant differences were found among genotypes (4299.4**, p < 0.01) and environments (12513.1**, p < 0.01) for plant height. However, non-significant difference observed for G x E interaction. Both genotypes and environments significantly influenced the number of filled grains (79403** and 281786** respectively, p < 0.01). Genotypes (141.16**, p < 0.01) and environments (18.8*, p < 0.05) significantly affected thousand-grain weight, whereas the G x E interaction was not significant (**Table 3**). Similarly, Genotypes (9514**, p < 0.01) and environments (269572**, p < 0.01) significantly influenced the number of panicles per square meter. Grain yield exhibited significant differences among genotypes (3995897**, p < 0.01), environments (18663020**, p < 0.01), and their interactions (573039**, p < 0.01).

Table 3. **Mean sum of square of Genotype (G), Environment (E) and G x E interaction for quantitative traits of 30 aromatic landraces**

Source of variation	DF	HD	MD	PL	PH	FG	TGW	TPSM	GY
Replication	2	12.95	15.54	27.46	186.8	30440	1.86	6100	819532
Genotype (G)	29	3895.6**	3599.36**	43.89**	4299.4**	79403**	141.16**	9514**	3995897**
Environment (E)	2	2830.97**	2481.67**	75.02**	12513.1**	281786**	18.8*	269572**	18663020**
G x E	58	54.4**	74.64**	8.96*	190.1	13723	1.1	1327	573039**
Error	352	26.7	31.26	5.52	160.8	13646	4.1	2654	262551

Note: *GY-grain yield, HD-heading days, MD-maturity days, PL-panicle length, PH-plant height, FG-filled grains, FGW-filled grains weight, TGW-thousand grain weight, GY-grain yield, SY-straw yield, TPMS-tillers per square meter*

Agro-Morphological Variation

The analysis of variance (ANOVA) for the 2-year means revealed significant effects of genotype, location, year, and their interactions on various agronomic traits (**Table 4**). Highly significant differences (p<0.001) were found among genotypes, locations and years for heading and maturity days. The interaction between genotype and environment (G × E) was also highly significant (p < 0.001). The mean heading across genotypes was 109 days, with 'Hansaraj Dhan' showing the earliest heading (78 days) and 'Karia Kamod' the most delayed in heading (128 days). The mean maturity days was 138 days, ranging from 108 days for 'Hiupuri' to 156 days for 'Kalo Nunia. For panicle length, significant differences were found among genotypes (p < 0.001) but not among locations (p = 0.9) or years (p = 0.36). The G × E interaction was significant at the 5% level (p = 0.005). The average panicle length was 26.26 cm, with 'Kalo Masino Dhan' having the longest panicles (30.1 cm) and 'Damari Dhan' the shortest (23.7 cm) (**Table** 4). Genotype, location, and year all significantly influenced plant height (p < 0.001), but the G × E interaction was not significant (p = 0.18). The average plant height was 145 cm, with 'Tilki' being the tallest (169 cm) and 'Samba Masuli Sub-1' the shortest (100 cm). In case of thousand grain weight, significant differences were found among genotypes (p < 0.001) and years (p < 0.001), but not among locations (p = 0.1) or for the G × E interaction (p = 1). The mean TGW was 17.04 g, ranging from 13.1 g for 'Hiupuri' to 23.1 g for Sugandhit dhan-1 (**Table** 4). Tillers per square meter (TPSM) was significant (p<0.001) among genotypes, locations and years, however study revealed non-significant G × E interaction (p = 0.9). The mean TPSM was 243.5,

with 'Hiupuri' having the highest number of panicles (288) and 'Karia Kamod' the lowest (209). Genotype, location, and year all significantly influenced the number of filled grains ($p < 0.001$), but the G × E interaction was not significant ($p = 0.4$). The average number of filled grains was 510, with 'Chananchur' showing the highest count (656) and 'Kalo Jira' the lowest (390). The economically important trait, grain yield was highly significant ($p<0.001$) in case of all genotypes, locations and years, as well as for the G × E interaction ($p = 0.002$). The mean yield performance was 1.76 t/ha, where Samba Masuli Sub-1 producing the highest yield (3.35 t/ha) and Kalanamak the lowest (1.26 t/ha) (**Table 4**).

Table 4. Mean performance of 30 aromatic rice landraces across three locations in year 2020 and 2021

Genotype	HD	MD	PL (cm)	PH (cm)	TGW (g)	TPSM	FG	GY (t/ha)
Karia Kamod	125	152	26.2	155	16.5	209	566	1.36
Sunaulo Sugandha	111	141	27.5	115	20.5	256	511	2.47
Kalo Masino Dhan	102	131	30.1	158	17.8	213	445	1.44
Balamsari Dhan	81	109	24.6	131	19.1	267	579	2.42
Karia Kamod	123	150	26.9	140	14.2	242	580	1.32
Tilki	105	135	24.8	169	14.9	213	628	2.15
Kalo Nunia	128	156	25.7	144	15.1	265	537	1.40
Bayani Masino	112	143	25.9	167	16.6	224	439	1.49
Brahmamusi Dhan	113	142	25.4	155	13.5	216	618	1.73
Basmati Jhapa	126	154	25.9	146	17.3	267	413	1.29
Malbhog	122	151	26.3	149	16.7	269	499	1.56
Jhuse Basmati	95	124	29.7	155	19.5	222	456	1.82
Gouriya	103	132	25.9	145	19.3	233	495	1.80
Hansaraj Dhan	89	119	28.5	152	22.5	273	514	1.69
Suhpat Dhan	111	140	26.1	147	20.9	205	501	1.91
Damari Dhan	82	112	23.7	126	15.9	257	549	2.21
Ujarka Basmati	122	152	27.7	158	19.9	236	444	1.67
Karia Kamod	122	152	26.6	141	14.0	247	575	1.33
Jhinuwa Dhan	90	121	25.7	152	17.5	229	464	1.31
Hiupuri	78	108	25.4	114	13.1	288	487	1.98
Sugandhit dhan-1	105	135	25.5	122	23.1	287	490	3.10
Chananchur	123	153	25.7	148	13.1	239	656	1.35
Lalka Basmati	123	152	25.2	143	18.6	248	452	1.78
Kalo Jira	105	135	28.5	162	16.3	223	390	1.33
Tulsiful	126	155	26.4	147	13.1	243	586	1.34
Kalo Basmati	103	132	26.5	148	18.6	228	462	2.11
Lalka Basmati Agahani	121	150	26.9	147	19.5	263	420	1.60
Gaure Dhan	108	138	25.7	164	15.7	228	538	1.53
Kalanamak	125	151	26.1	141	14.9	228	436	1.26
Samba Masuli Sub-1	109	138	21.9	100	13.3	277	562	3.35
Mean	109	138	26.26	145	17.04	243.5	510	1.76
Genotype (G)	<.001	<.001	<.001	<.001	<.001	<.001	<.001	<.001
Location (L)	<.001	<.001	0.9	<.001	0.1	<.001	<.001	0.002
Year (Y)	<.001	<.001	0.36	<.001	<.001	<.001	0.2	<.001
Environment (E)	<0.001	<0.001	<0.001	<0.001	0.01	<0.001	<0.001	<0.001
G × E	<.001	<.001	0.005	0.18	1	0.9	0.4	0.002
LSD	8.37	9.05	3.81	20.55	3.28	83.5	195.7	0.93
CV%	4.7	4.04	8.95	8.7	11.9	21.16	22.8	28.3

Note: GY-grain yield, HD-heading days, MD-maturity days, PL-panicle length, PH-plant height, FG-filled grains, FGW-filled grains weight, TGW-thousand grain weight, GY-grain yield, SY-straw yield, TPMS-tillers per square meter, LSD- least significant difference, CV- coefficient of variation

Genetic analysis of phenotypic traits

The genetic parameters of major morphological traits were performed combined over the years across the three locations. The different genetic parameters considered for measuring variability has been presented in **Table** 5. The result indicated that the traits exhibited wide range of variability in this population. The result demonstrated high variability in GCV (4.9 to 23.67) and PCV (5.6 to 25.7) in the studied traits. The highest GCV and PCV was exhibited by grain yield (23.67 and 25.7) whereas the lowest GCV and PCV was found in panicle length (4.9 and 5.6) respectively. Heritability of various traits was measured from 0.76 to 0.98 where the lowest heritability was obtained in panicle length and the highest was obtained in both heading and maturity days. Similarly, genetic advance ranged from 2.3 to 797.4 in which panicle length showed the least GA and grain yield showed the highest GA. The GAM also varied from 8.8 to 45 in case of the panicle length and grain yield respectively (**Table** 5).

Table 5. **Genetic parameters of different traits evaluated across the three locations over the years 2020-2021.**

Traits	Range	Mean	Sem	σ2G	σ2P	GCV	PCV	h2B	GA	GAM
HD	77-135	109	2.1	211.91	214.93	13.35	13.45	0.98	29.6	27.15
DM	107-163	138	2.2	194.1	198.25	10.1	10.2	0.98	28.42	20.6
PH	98.8-177.3	145	4.3	219.36	229.92	10.2	10.5	0.95	29.67	20.46
PL	21.3-30	26	0.4	1.63	2.13	4.91	5.61	0.76	2.3	8.8
TPSM	198.7-312.2	244	9.2	307.4	381.17	7.2	8	0.8	32.2	13.2
FG	356.6-721.3	512	39.4	2890.78	3653.2	10.5	11.8	0.79	98.3	19.2
TGW	11.9-23.2	17	0.8	7.4	8.7	15.9	17.3	0.8	5.57	32.77
GY	1135.2-3786.6	1769.9	273.4	175572.6	207408.1	23.67	25.73	0.85	797.4	45

note: GY-genotype, HD-heading days, MD-maturity days, PL-panicle length, PH-plant height, FG-filled grains, FGW-filled grains weight, TGW-thousand grain weight, GY-grain yield, SY-straw yield, TPMS-tillers per square meter, SEm-standard error of mean, σ^2_G - genotypic variation, σ^2_P - phenotypic variation, GCV and PCV refers to genotypic and phenotypic coefficients of variation, h^2_B- implies broad sense heritability, GA- genetic advance, GAM- genetic advance as a percentage of mean.

Genetic and Phenotypic Correlation

The genotypic and phenotypic correlation of associated traits of aromatic rice accessions was derived to unveil the association between the traits. In case of genetic correlation coefficient, there exists significant (p<0.001) and positive correlation between some traits as well as significant (p<0.001) and negative correlation (**Table** **6**). The genetic correlation of the measured traits showed highly significant positive correlation of heading days with maturity (r=1.0**) and straw yield (r=0.787**) as well as correlation of maturity days with straw yield (r=0.79**). The result revealed highly significant and positive correlation between plant height with panicle length (r=0.5087**), however, highly significant and negative correlation among tillers per meter square (r=-0.74**) and grain yield (r=-0.78**). The result also revealed that there is highly significant and negative correlation between panicle length and filled grain (r=-0.62**), 1000 grain weight (r=-0.475**) and grain yield (r=-0.58**). In a similar way, tillers per meter square have also exhibited negative and highly significant correlation with heading and maturity days (r=-0.3625**, -0.3635**), plant height (r=-0.7401**) but positive and significant correlation with grain yield (r=0.62**). The filled grain trait has negative correlation (r=-0.054**) with 1000 grain weight, however, highly significant and positive correlation between filled grain weight and 1000 grain weight (r=0.80**) and grain yield (r=0.57**). The result also reflected that 1000 grain weight and grain yield are highly correlated (r=0.38**).

In case of the phenotypic correlation, result showed highly significant positive correlation of heading days with maturity (r=0.99**) and straw yield (r=0.7611**), however, there is negative but significant correlation with tillers per meter square (-0.296*), filled grain weight (r=-0.305*), 1000 grain weight (r=-0.3115*) and grain yield (r=-0.4*). In the similar manner, authors observed significant and positive correlation of maturity

days with straw yield (r=0.7632**) and relationship with other traits such as tillers (r=-0.29*), filled grain weight (r=-0.3*), 1000 grain weight (r=-0.2935*) and grain yield (r=-0.427**) was found strongly significant but negative (**Table** **6**). The correlation of plant height was found positive and highly significant with panicle length (r=0.4337**), however, two other negative and highly significant correlation was found with tillers per meter square (r=-0.62**) and grain yield (r=-0.664**). The result further revealed that there was negative and highly significant correlation of panicle length with filled grain (r=-0.3447**) and grain yield (r=-0.664**) but positive and significant correlation with thousand grain weight (r=0.344**). Additionally, significant and positively correlation (r=0.4577**) between tillers and grain yield. Furthermore, relationship between filled grain and filled grain weight (r=0.367**) was highly significant and positive, however, its correlation with 1000 grain weight was negatively correlated (r=-0.452**). Furthermore, filled grain weight was positively and significantly correlated with 1000 grain weight (r=0.65**) and grain yield (r=0.45**). The result also reflected that grain yield and straw yield were negatively correlated (r=-429**) with each other.

Yield Stability

Stability parameters such as regression coefficient (bi), and deviation from regression (S^2d_i) of the tested genotypes were derived following simple linear regression method (Finlay & Wilkinson, 1963; Eberhart & Russell, 1966) (**Table** **7**). According to the Model, the accessions showing bi-value close to unity are assumed to be adapted to all environments, while those showing bi-value greater than or less than unity would show specific adaptation to rich or poor environment reflecting high yield in rich environment and low yield in poor environment, respectively. Likewise, the accessions depicting low and non-significant S^2di values are representing stability of performance over the range of environments. According to Eberhart and Russell (1966), a stable genotype is one with a high mean, a regression coefficient of unity (bi=1), and a minimum deviation from the regression coefficient (S^2di) = 0 or close to these values of non-significant deviation. It allows the identification of stable accession that are explained as most responsive to favorable or unfavorable environment. The result demonstrated that aromatic rice landraces; Gouriya and Karia Kamod (bi=1.1) were found more stable and well adapted to the all environments (**Table** 7). Eberhart and Russel mentioned that mean square deviation (S^2di) of stability coefficient (-189717 to -8880.5) indicated that majority of aromatic rice accessions except Jhuse Basmati, Jhinuwa Dhan, Gaure Dhan and Samba Masuli Sub-1 were found stable. Based on coefficient of determination (R^2), most of accessions; Lalka Basmati, Sugandhit Dha-1, Suhpat, Gouriya, Bayerni Masino, Kalo Nunia, Balamsari Dhan, Tilki, Tulsiful and Sunaulo Sugandha identified as stable in all environments in both years. According to the Superiority Measure (Pi), Samba Masuli Sub-1 and Sugandhit Dhan-1 possessed small values as 132556.16 to 377994.35 reflecting that both varieties found stable and well adapted.

Table 6. Genotypic and phenotypic correlation coefficients of 10 quantitative traits of aromatic rice landraces determined from mean data of two years across four locations.

	HD	MD	PH	PL	TPSM	FG	FGW	TGW	GY	SY
HD	-	1.00**	0.27	0.15	-0.36*	0.12	-0.37*	-0.34	-0.56**	0.79**
MD	0.99**	-	0.29	0.16	-0.36*	0.14	-0.36*	-0.34	-0.56**	0.79**
PH	0.22	0.24	-	0.51**	-0.74**	-0.24	-0.26	-0.02	-0.78**	0.27
PL	0.1	0.12	0.43**	-	-0.3	-0.61**	0.09	0.47**	-0.58**	0.29
TPSM	-0.29*	-0.29*	-0.62**	-0.18	-	0.05	0.27	0.19	0.62**	-0.1
FG	0.06	0.05	-0.11	-0.34**	-0.05	-	0.07	-0.54**	0.11	-0.23
FGW	-0.30*	-0.30*	-0.1	0.06	0.14	0.37**	-	0.80**	0.57**	-0.32
TGW	-0.31*	-0.29*	0.02	0.34**	0.16	-0.45**	0.65**	-	0.38*	-0.08
GY	-0.42**	-0.43**	-0.66**	-0.44**	0.46**	0.2	0.45**	0.24	-	-0.61**
SY	0.76**	0.76**	0.19	0.24	0	-0.17	-0.27*	-0.1	-0.43**	-

*Note: *, ** indicates significant at 5% (<0.05) and 1% (<0.05) respectively, the upper and lower diagonal of table represents genotypic and phenotypic correlation coefficients respectively. GY-genotype, HD-heading days, MD-maturity days, PL-panicle length, PH-plant height, FG-filled grains, FGW-filled grains weight, TGW-thousand grain weight, GY-grain yield, SY-straw yield, TPMS- tillers per square meter*

Table 7. Stability analyses on grain yield (kg/ha) of 30 aromatic landraces evaluated at three environments.

Genotype	Francis			Eberhart & Russell			Superiority Measure
	Mean	Sd	CV (%)	Bi	S2di	R2	Pi
Karia Kamod	1394.8	245.9	17.6	1.4	-114899	0.4	3191762.3
Sunaulo Sugandha	2527.1	958.5	37.9	9	-179493	1	1223861.2
Kalo Masino Dhan	1415.9	231.4	16.3	-0.8	-96331.9	0.1	3163038.7
Balamsari Dhan	2453	854.7	34.8	-7.5	-16588.4	0.9	1233453.1
Karia Kamod	1305.8	363.1	27.8	2.7	-94826.9	0.6	3438461.5
Tilki	2088.7	114.5	5.5	-1	-185892	0.8	1641836.6
Kalo Nunia	1305.6	347.3	26.6	3.1	-161227	0.9	3382221.3
Bayani Masino	1311.5	236.1	18	-2.2	-187399	1	3331696.6
Brahmamusi Dhan	1724.3	58.6	3.4	0.4	-187391	0.6	2322689.2
Basmati Jhapa	1310.4	454.4	34.7	3.2	-8880.51	0.6	3492303.8
Malbhog	1470.9	246	16.7	1.6	-128252	0.5	3001880.4
Jhuse Basmati	1879.5	581.1	30.9	4	129079.3	0.5	2332436.5
Gouriya	1946.8	120.4	6.2	1.1	-189717	1	1913296.9
Hansaraj Dhan	1638	348.6	21.3	2.3	-63063.2	0.5	2684097.8
Suhpat Dhan	1885.5	469.6	24.9	4.4	-186023	1	2048465.6
Damari Dhan	2245.1	333.6	14.9	-2.4	-100458	0.6	1341973.9
Ujarka Basmati	1617.9	198.2	12.2	-0.4	-115188	0	2483384.4
Karia Kamod	1269.2	154.7	12.2	1.1	-169778	0.6	3442072.7
Jhinuwa Dhan	1302.6	390.8	30	-0.3	112999.7	0	3558995.5
Hiupuri	1975.8	286.8	14.5	-2.1	-127642	0.6	1801844.9
Sugandhit dhan-1	3222.3	166	5.2	1.5	-189284	1	377994.35
Chananchur	1330.2	239.1	18	-1.9	-154395	0.7	3334440.8
Lalka Basmati	1849.3	423.7	22.9	3.9	-179427	1	2092581.8
Kalo Jira	1358.7	193.6	14.2	-1.5	-166403	0.7	3130288.4
Tulsiful	1334.8	187.9	14.1	-1.6	-176069	0.8	3201427.8
Kalo Basmati	2047	251.2	12.3	1.9	-145313	0.6	1660524.9
Lalka Basmati Agahani	1505.2	324.2	21.5	2.5	-124000	0.7	2935677.8
Gaure Dhan	1591.7	364.7	22.9	0.7	64318.1	0	2481053.7
Kalanamak	1294	368.3	28.5	2.7	-80908.5	0.6	3477455.6
Samba Masuli Sub-1	3495.1	1222.5	35	4.2	2398534	0.1	132556.16

Note: Sd- standard deviation, CV- coefficient of variation, Bi- regression coefficient, S^2Di- mean square deviation, R^2- determination coefficient, Pi- superiority measure

DISCUSSIONS

Analysis of variance (ANOVA) indicated the significant variation among genotypes for most traits, which indicates the presence of substantial genetic diversity in the studied fine and aromatic rice landraces. The highly significant effects of environments on all traits suggested experimental site and soil conditions as major environmental variables play a crucial role in the expression of these traits. The significant G x E interactions for traits like heading date, maturity date, panicle length, and grain yield indicated that the performance of genotypes is not consistent across different environments. This suggests the need for location-specific selection to identify the best-performing genotypes under specific environmental conditions. In particular, the significant G x E interaction for grain yield highlighted the complexity of yield performance, which is influenced by both genetic and environmental factors. The identification of stable genotypes with consistent performance across environments would be critical for breeding programs targeting wide adaptability. The non-significant G x E interactions for plant height, filled grains, thousand-grain weight, and total panicles per square meter suggested that these traits are relatively stable across different environments, making them reliable selection criteria in breeding programs. In conclusion, the results underscore the importance of considering both genetic and environmental factors in rice breeding programs.

The significant variation obtained among genotypes for all agro-morphological traits suggested the presence of substantial genetic diversity in the rice germplasm under study. The significant effects of location and year indicated the influence of environmental factors on the performance of these traits. This aligns with previous studies that emphasize the importance of G X E effects in determining the stability in performance and adaptability among crop varieties (Kang 2002; Yan and Tinker 2006). The highly significant genotype and environment interactions for heading and maturity days suggested that these traits are sensitive to environmental conditions. This finding is consistent with reports by Dingkuhn et al (1995), who noted that temperature and photoperiod significantly affect the phenological development of rice. The wide range of heading and maturity dates among genotypes indicated the potential for selecting early- or late-maturing varieties based on specific agro-ecological needs. The non-significant G × E interaction for plant height suggested that this trait is relatively stable across environments, making it a reliable criterion for selection. In contrast, the significant interaction for panicle length indicates that this trait is more sensitive to environmental variation, which may necessitate environment-specific breeding strategies (Annicchiarico 2002). The non-significant G × E interaction for Thousand Grain Weight-TGW suggested that this trait is less influenced by environmental factors, supporting its use as a stable selection criterion. However, the significant G × E interaction for grain yield underscores the complexity of yield performance, which is influenced by both genetic and environmental factors (Blum 2011). The significant effects of genotype and environment on TPSM and FG reflect the importance of both genetic potential and environmental conditions in determining yield components. The stability of TPSM across environments suggests that this trait could be a reliable indicator of yield potential, while the variability in FG emphasizes the need for careful selection to enhance grain filling under different environmental conditions. In conclusion, the significant G × E interactions for key traits such as grain yield, heading date, and maturity date emphasize the importance of environment-specific breeding programs. The identification of stable genotypes with consistent performance across diverse environments, or those with specific adaptation, will be crucial for improving rice productivity in varying agro-ecological zones.

The genetic parameters analyzed indicate significant variability and potential for selection in the rice genotypes evaluated across three locations over the years 2020-2021. Traits such as heading days, maturity days, plant height, and grain yield showed high broad-sense heritability (h²B > 0.85), coupled with substantial genetic advance (GAM > 20%). This suggests that these traits are predominantly controlled by additive gene action, making them reliable targets for selection in breeding programs. It was evident that high heritability along with by high genetic advance suggested that selection based on such traits results in

significant improvement in the next generation (Islam et al 2016, Johnson et al 1955; Falconer and Mackay 1996, Prasad et al 2001, Jaiswal et al 2007, Tiwari et al., 2019). Traits like panicle length and total panicles per square meter exhibited moderate GCV and PCV values, indicating that these traits are influenced by both genetic and environmental factors. The relatively lower GCV compared to PCV for these traits suggested the presence of environmental influence, as PCV includes both genetic and environmental variances. Selection for these traits might require more extensive testing across different environments to accurately assess their genetic potential (Burton and Devane 1953). Grain yield demonstrated the highest GCV (23.67%) and PCV (25.73%) among the traits, with a high heritability of 0.85 and a GAM of 45%. These values indicated considerable genetic variability for grain yield, offering substantial scope for selection. The high GCV suggested that the observed phenotypic variation is largely genetic, making grain yield a key trait for improvement in these genotypes. Similar findings were reported by Singh et al (2011), where grain yield was found to have high heritability and genetic advance, indicating its potential for improvement through selection. TGW had a high GCV (15.9%) and PCV (17.3%), with a heritability of 0.8 and a GAM of 32.77%. The substantial genetic advance for TGW indicates that selection for this trait can lead to significant improvement. This trait is often considered critical for yield improvement, as it is less influenced by environmental factors compared to other yield components (Kumar et al 2017).

The correlation analysis revealed significant relationships between key agronomic traits in aromatic rice landraces, providing valuable insights for rice breeding programs. The strong positive correlation between heading and maturity days and their negative correlation with grain yield suggested that selecting for early maturity might reduce grain yield. This trade-off is crucial for breeding programs targeting environments with shorter growing seasons, where early maturity is essential (Cai et al 2002). The highly significant and negative correlation between plant height and grain yield suggested that selecting for taller plants might not be advantageous for yield improvement. Similarly, the negative correlation between panicle length and grain yield indicated that longer panicles may not contribute positively to yield. These findings suggest that shorter plants with optimal panicle lengths may be more desirable in breeding for higher yields (Peng et al 1999). The positive correlation between tillers per square meter and grain yield highlights the importance of tiller number in yield improvement. This suggests that increasing the number of tillers per plant could directly enhance grain yield, making it a valuable trait for selection (Yoshida 1981). The negative correlation between filled grains and thousand grain weight suggested a trade-off between the number of filled grains and their weight. Breeding programs must consider this trade-off to optimize grain yield and quality, as selecting for more filled grains could reduce grain size and vice versa (Yuan et al 1993). From the study, result revealed that straw yield and grain yield are negatively correlated suggesting a potential trade-off between straw and grain yield which means increase in one trait decreases the potential of another trait. This is particularly relevant in regions where straw is a valuable byproduct. Breeders may need to prioritize one over the other based on specific needs (Sharma and Das 2013).

The stability analysis provides valuable insights into the adaptability and performance of different rice genotypes across multiple environments, which is crucial for identifying stable genotypes for breeding programs. According to the Eberhart and Russell model, genotypes like Brahmamusi Dhan, with bi values close to 1 and low S^2di, demonstrated average responsiveness and high stability across environments. Conversely, Sunaulo Sugandha, with a high bi value and significant deviation from regression, shows specific adaptability, likely performing well in certain environments but poorly in others. Such genotypes might be better suited for specific regions rather than wide adaptation (Eberhart and Russell, 1966). The Superiority Measure (Pi) identifies genotypes like Samba Masuli Sub-1 and Sugandhit Dhan-1 as superior in terms of stability and adaptability across environments. Lower Pi values suggest that these genotypes consistently outperform others, making them ideal candidates for large-scale cultivation across diverse agro-climatic zones (Lin and Binns, 1988). The combination of these models provides a comprehensive understanding of genotype stability and adaptability. For instance, Samba Masuli Sub-1, with a low Pi value and moderate CV%, emerges as a top-performing genotype with broad adaptability. This genotype could be prioritized in breeding programs aimed at developing widely adapted rice varieties. On the other hand,

genotypes with high *bi* values and significant deviations from regression may require further evaluation under specific conditions to maximize their potential.

CONCLUSION

The agro-morphological study revealed that the yield performance of aromatic rice landraces Balamsari Dhan (2.24 t/ha), Damari Dhan (2.21 t/ha) and Tilki (2.15 t/ha) was at par with yield of released varieties Samba Masuli Sub-1 (Check), Sugandhit Dhan-1 and Sunaulo Sugandha considered in this study. The study reflected the significant variation among genotypes explaining the presence of enormous genetic diversity in aromatic rice landraces. The significant G x E interactions for major yield attributing traits including grain yield indicated that the performance of genotypes is not consistent across different environments. It highlights the need for location-specific selection to identify the best-performing genotypes. The major traits heading and maturity days, plant height and grain yield showed heritability above 85% accompanied by GAM>20%. It is stated that high heritability coupled with genetic advance indicates effective selection these traits are predominantly governed by additive gene action. There is positive correlation between heading and maturity days and both showed negative correlation with grain yield indicated that selection for early maturity could be detrimental to increased yield and vice versa. Authors observed positive correlation between tillers per square meter and grain yield suggesting significance of increased number of tiller number in yield enhancement. According to the Eberhart and Russell model, genotypes like Brahmamusi Dhan, Balamsari Dhan, Tilki, Gouriya, Damari Dhan, Hiupuri and Kalo Basmati with bi values close to 1 and low S^2di, demonstrated average responsiveness and high stability across environments. The findings of present study will provide in-depth understanding and information on the genetic basis of aromatic rice landraces available in Nepal. It would offer great opportunity to the future researchers using the knowledge received from this study and help prepare research strategy and emphasize their efforts to molecular level studies to understand the population structure of aromatic rice germplasm and genetic architecture of aroma gene present.

ACKNOWLDEGEMENT

EFERENCES
Ahmed F., MM, Hanafi, MA, Hakim, MY, Rafii, IW Arolu and SN Akmar Abdullah. 2015. Genetic divergence and heritability of 42 coloured upland rice genotypes (*Oryza sativa*) as revealed by microsatellites marker and agro-morphological traits. 10, e0138246.

Ahmed MS, A Majeed, KA Attia, RA Javaid, F Siddique, MS Farooq, M Uzair, SH Yang and AMJSR Abudhadi. 2024. Country-wide, multi-location trials of Green Super Rice lines for yield performance and stability analysis using genetic and stability parameters. **14**:9416.

Ali SS, S Jafri, ZK Tasleem-Uz, M Aamir and M Butt. 2000. Heritability of yield and yield components of rice. Pak J Agricultural Research **16**: 89-91.

Allard RW. 1999. Principles of plant breeding, John Wiley & Sons.

Annicchiarico P. 2002. Genotype × environment interactions: challenges and opportunities for plant breeding and cultivar recommendations. FAO Plant Production and Protection Paper No. 174. Food and Agriculture Organization of the United Nations, Rome.

Blum A. 2011. Plant breeding for water-limited environments. Springer Science & Business Media.

Burton GW and E DEVANE. 1953. Estimating Heritability in Tall Fescue (Festuca Arundinacea) from Replicated Clonal Material . Agronomy Journal, **45:** 478-481.

Cai W, Y Gao, Z Zhang and G Li. 2002. Breeding for Early Maturity in Rice. *Field Crops Research*, **78**(2-3): 95-102.

Choudhary M, B Mishra and JP Lal. 2020. Genetic variability and interrelationship of traits for grain yield improvement in rice (Oryza sativa L.). Journal of Genetics and Plant Breeding, **74**(4):619-624.

DeLacy, IH, KE Basford, M Cooper, JK Bull, and CG McLaren. 1996. Analysis of multi-environment trials–an historical perspective. *Plant adaptation and crop improvement*, **pp.** 39-124.

Dingkuhn M, F Asch, KM Miezan and A Sow. 1995. Climatic determinants of irrigated rice performance in the Sahel—III. Characterizing environments by simulating the yield of a rice ideotype. Agricultural Systems, **48**(4)**:** 435-456.

Eberhart SA and WA Russell. 1966. Stability Parameters for Comparing Varieties. Crop Science, **6**(1): 36-40.

Falconer DS and TFC Mackay. 1996. Introduction to Quantitative Genetics (4th ed.). Longman Group Ltd.

Fitzgerald MA, SR McCouch and RD Hall 2009. Not just a grain of rice: The quest for quality. Trends in Plant Science, **14**(3): 133-139.

Francis TR and LW Kannenberg. 1978. Yield Stability Studies in Short-Season Maize. I. A Descriptive Method for Grouping Genotypes. Canadian Journal of Plant Science, **58**(4): 1029-1034.

Gauchan D., & Pandey, S. 2011. Is investment in rice research in Nepal adequate and balanced across production environments? Some empirical evidence. *Quarterly Journal of International Agriculture*, *50*(4), 305-324.

Hanson CH, HF Robinson and RE Comstock. 1956. Biometrical studies of yield in segregating populations of Korean Lespedza. Agron. J. **48**: 268-272.

Islam MZ, M Khalequzzaman, MK Bashar, NA Ivy, MM Haque and MAK Mian. 2016. Variability assessment of aromatic and fine rice germplasm in Bangladesh based on quantitative traits. The Scientific World Journal.

Jaiswal H, A Srivastava and A Dey. 2007. Variability and association studies in indigenous aromatic rice (Oryza sativa L.). ORYZA-An International Journal on Rice, **44**: 351-353.

Johnson HW, HF Robinson and RE Comstock. 1955. Estimates of genetic and environmental variability in soybeans. Agronomy Journal, **47**: 314-318.

Joshi BK, KH Ghimire, PR Bista, RB Yadaw, RK Shrestha, GK Kharel, P Paneru, RB KC and D Bhandari. 2021. Intellectual property right on Basmati rice: Current scenario and evidences of origin, diversity, cultivation and use values of Basmati rice in Nepal. Nepal Journal of Biotechnology, **9**(1): 93-108.

Karim D, MNA Siddique, U Sarkar, Z Hasnat and J Sultana. 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.

Kang MS. 2002. Quantitative genetics, genomics, and plant breeding. CABI.

Kumar R, Y Singh and SP Singh. 2017. Genetic variability, heritability and genetic advance studies in rice (Oryza sativa L.) under sodic soil. Journal of Pharmacognosy and Phytochemistry, **6**(4): 1903-1906.

Lin CS and MR Binns. 1988. A Superiority Measure of Cultivar Performance for Cultivar x Location Data. Canadian Journal of Plant Science, **68**(1): 193-198.

Miller PA, Jr JC Williams, HF Robinson and RE Comstock. 1958. Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection 1. Agronomy journal, **50**(3): 126-131.

MOALD 2023. Statistical Information on Nepaleses Agriculture. In: Planning and Development Cooperation Coordination Division, S. A. A. S. (ed). Singhdurbar, Kathmandu, Nepal: Government of Nepal.

Peng S, GS Khush, and KG Cassman. 1999. Yield Potential Trends of Tropical Rice since the Release of IR8 and the Challenge of Increasing Rice Yield Potential. *Crop Science*, **39**(6): 1552-1559.

Prasad B, AK Patwary and PS Biswas. (2001). Genetic variability and selection criteria in fine rice (Oryza sativa L.). Pakistan Journal of Biological Science, *4*(10): 1188-1190.

Raymajhi K and B Malla Thakuri. 2023. Nepalese Fine and Aromatic Rice Landraces: A Review. The Journal of Agriculture and Environment, **24:** 197-204.

Robinson, HF, RE Comstock and PH Harvey. 1949. Estimates of heritability and the degree of dominance in corn. Agronomy Journal. **pp.** 353-359.

Sah RP, M Chakraborty, K Prasad, M Pandit, VK Tudu, MK Chakravarty, ... and S Narayan. 2014. Impact of water deficit stress in rice: A review. Agronomy, **4**(4): 285-311.

Sarker MAH. 2002. Indigenous Fine Aromatic Rice Production: Bangladesh Perspective. 12-15 November, 2002. Development of Basic Standard for Organic Rice Cultivation. 1st DA/ARNOA International Conference. RDA and Dankook Univ., Korea.

Sedeek SEM., SAA Hammoud, MH Ammar and TF Metwally. 2009. Genetic variability, heritability, genetic advance and cluster analysis for some physiological traits and grain yield and its components in rice (Oryza sativa L.). J. Agric. Res. Kafer El-Sheikh Univ, *35*(3): 858-878.

Sharma RK, and A Das. 2013. Performance of Rice (Oryza sativa L.) Varieties in Relation to Their Straw Yield. Indian Journal of Agricultural Sciences, **83**(10): 1057-1061.

Singh RK and BD Chaudhary. 1981. Biometrical methods in quantitative genetic analysis.

Singh SP, RC Bharati, NC Manibhushan and A Pedapati. 2011. An assessment of faba bean (Vicia faba L.) current status and future prospect. African Journal of Agricultural Research, **6**(22)**:** 4981-4992.

Sttrek H and N Beser. 2003. Selection for grain yield and yield components in early generations for temperate rice. J Philippine Journal of Crop Science, **28:** 3-15.

Tiwari DN, SR Tripathi, MP Tripathi, N Khatri and BR Bastola. 2019. Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. *Advances in Agriculture*, *2019*(**1**): 5975901.

Tragoonrung S, JQ Sheng, and A Vanavichit. 1996. Tagging an aromatic gene in lowland rice using bulk segregant analysis. In *Rice Genetics III: (In 2 Parts)* (**pp.** 613-618).

Varatharajan N, DC Sekaran, K Murugan and V Chockalingam. 2021. Rice aroma: Biochemical, genetics and molecular aspects and its extraction and quantification methods. Integrative Advances in Rice Research, **33**: 1-25

Yan W, and NA Tinker. 2006. Biplot analysis of multi-environment trial data: Principles and applications. Canadian Journal of Plant Science, **86**(3): 623-645.

Yan W, and MS Kang. 2003. GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists. CRC Press

Yoshida S. 1981. Fundamentals of Rice Crop Science. *International Rice Research Institute*.

Yuan, LP, SB Peng and WD Cheng. 1993. Breeding of Super Rice Varieties. *China Rice*, **3**(4): 23-27.

Zhang T, XL NI, KF Jiang, HF Deng, H Qing, QH Yang, Y Li, W Xian-QI, YJ Cao, and JK Zheng. 2010. Relationship between heterosis and parental genetic distance based on molecular markers for functional genes related to yield traits in rice. Rice Science, **17:** 288-295.

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