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Morphological variation in aromatic rice lines

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Abstract
Crop improvement relies on understanding the morphological variation and population structure of germplasm collections. Because of the importance of rice (*Oryza sativa* L.) as a major world crop, the origin and diversity of this plant have piqued the curiosity of many people. In this study, A total of 107 aromatic rice lines were classified using five quantitative traits. The rice germplasm contains adequate genetic variation for most of the quantitative traits. Yield per plant had significant association with total tiller number and other traits had positive association with each other except with panicle length. Cluster analysis produces three groups. PCA also show considerable diversity among the genotypes. The characterization of landraces of aromatic rice would provide significant benefits to breeders in their efforts to design and implement further rice improvement programmes.

Keywords: Rice, PCA, cluster analysis

1. Introduction

Rice (*Oryza sativa* L.), one of the most significant food crop, belonging to the family Poaceae. It is cultivated in more than 100 nations throughout the world and provides food for around half of the world's population. India has largest area under rice cultivation worldwide, next just to China (Singh *et al*., 2001; Azharudheen *et al.,* 2018) [12, 2]. The production of grain from rice and export has to be increased with the growing population and to add foreign earning from rice grain. India is one of the largest producers and exporters of rice in the world. In 2020-21, India's rice exports (Basmati and Non-Basmati) rose by a huge 87 per cent to 17.72 million Tonne (Mt) from 9.49 MT achieved in 2019-2021. In terms of value realization, India's rice exports rose by 38 per cent to USD 8815 million in 2020-21 from USD 6397 million reported in 2019-2021 (Anonymous 2021) [1].

Since ancient times, aromatic rice has been treasured in Indian culture for both its superior quality and its auspiciousness. Due to the chemical 2-acetyl-1-pyrroline, aromatic rice is distinguished by its flavour and aroma (Ghareyazie *et al.*, 1997) [4]. In the Indian subcontinent, there are many different fragrant rice kinds that have been grown. In recent years, there has been a significant rise in India's foreign exchange revenue generated through the exportation of Basmati rice. Similarly, the aromatic rice line gaining importance in the market. Therefore, it is imperative to have a larger genetic variation and diversity in the rice gene pool to effectively use it in breeding programmes. The existence of genetic diversity plays a crucial role in facilitating adaptation under different environmental conditions (Sah *et al.,* 2020; Azharudheen *et al.,* 2022) [9, 3, 8]. Increased deviation within a population enhances the probability of certain individuals possessing alleles that are better adapted to the prevailing environmental conditions (Sah *et al.,* 2022) [8].

The agro-morphological characterization should eventually result in a system for logging and archiving relevant information that can be readily utilized for breeding programmes and improving the cultivars. Estimating relationship between the variable helps in the selection of the traits and utilization of the traits in the breeding programme (Sanghamitra *et al.,* 2018; Sah *et al.,* 2022) [11, 8]. Increased variation within a population increases the likelihood that some individuals will have alleles that are better suited to the current environmental conditions (Sah *et al.,* 2022) [8]. The presence of variability within a population has been noted by Nachimuthu *et al.* (2014) [6], and one of the methods employed to address this is multivariate analysis. Principal component analysis has been identified as a viable method for identifying patterns and reducing redundancy in data sets, particularly in the context of crop species where variations in yield and grain quality are common (Maji *et al.,* 2012) [5].

The present study used a correlation matrix to extract the principal components. Principal Component Analysis (PCA) provides a means to assess the importance of each dimension in explaining the variability of a given dataset. Therefore, the current study was conducted on aromatic rice germplasm with the aim of analysing traits related to yield and quality.

2. Materials and Methods
2.1 Plant material and experimental design
The experimental materials comprise of 107 aromatic rice genotypes collected from various parts of Chhattisgarh. All the lines were sown in *kharif* 2020 at Indira Gandhi Agricultural University, Raipur, Chhattisgarh and kharif 2021 at the ICAR-National Rice Research Institute (NRRI), Cuttack, Odisha. The material was grown in Replicated block design (RBD) at both locations with 2 replications.

2.2 Data collection
Data for the following five morphological traits were recorded from all genotypes at each of the replication: 50% flowering (DF, day), number of tillers (NT, no), plant height (PHT, cm), Heading date (HD, day), yield (YLD, g).

2.3 Statistical analysis
The statistical analysis was done by using the software MS-Excel for descriptive statistics, Past 4.3 for correlogram, PCA and Darwin for dendogram. In this study, descriptive statistics are employed to describe the basic characteristics of the data. It divides the data into central tendency measurements. The PCA was done by using software past. Cluster analysis was done by the software Darwin.

3. Result
3.1 Phenotypic variations
The 107 aromatic rice line were grown and five morphological traits were measured to estimate the variation available in the genetic materials. The metrics of central tendency for morphological traits like mean, standard deviation, median, mean absolute deviation, range, skew, kurtosis and standard error are presented in table 1.
The 50% flowering of varieties ranged from 62 days (IG 40) to 120 days (IG 76) with overall mean of 95. The plant height of varieties ranged from 89.39cm (IG 78) to 310.90 cm (IG 86) with overall mean of 136.45 cm. The panicle length of varieties ranged from 21.34 cm (IG 101) to 33.39 cm (IG 21) with overall mean of 26.58 cm. The total tiller of varieties ranged from 6 (IG 64, IG 86) to 10 (IG 1, IG 3, IG 4) with overall mean of 8. The yield of varieties ranged from 8.29 g/plant (IG 13) to 31.80 g/plant (IG 53) with overall mean of 17.15 g/plant. The distribution of phenotypes in the population was analyzed using third-degree statistics (Skewness) and fourth-degree statistics (kurtosis). kurtosis for DF, PH, TT showed positive and for PL, YLD showed negative. Except DF the skewness of the population for all

traits was showed positive.

3.2 Correlation analysis
A correlation study was performed by using PAST software to better understand the linear relationship between all the morphological traits, as shown in figure 1. Pearson's correlation coefficients between morphological traits were calculated and presented in figure 1. Among the morphological traits, days to 50% grain was positively and significantly correlated with plant height, grain yield per plant at $p \leq 0.05$. Similarly, the panicle length positively significantly correlated with plant height. The grain yield was positively significantly correlated with total tiller number. All traits were identified as positively correlated among each other, except for PL with TT and YLD.
The phenotypic data of 107 genotypes were clustered using Darwin based on Unweighted Neighbor Joining method, as shown in figure 2. The unrooted tree classified 107 rice genotypes into three distinct groups. Cluster one has 62 lines, Cluster two has 43 lines and Cluster three has only two lines (IG 92 and IG 108). Cluster-1 was further subdivided into two sub-clusters: sub-cluster-a (61 lines) and sub-cluster-b (1 line) (IG 34). Cluster-2 is also divided into two sub-clusters: sub-cluster-a (42 lines) and sub-cluster-b (1 line) (IG 104).

3.3 Principal component analysis
PCA was used to analyse phenotypic data from 107 genotypes as shown in figure 3, revealing that all 107 rice genotypes were distributed throughout four quadrants, The result of PCA analysis showed three principal component with eigen value greater than 1.00 (Table 2) *i.e.* PC 1 (788.53), PC 2 (65.81) and PC 3 (20.50) which together explained 99.44 per cent of total phenotypic variation. The eigen value of all the five principal components ranged from 0.605 to 788.53. The principal component 1 accounted for (PC1) 89.6% of total phenotypic variability with major contribution from plant height (factor loading 0.99). the principal component 2 (PC 2) accounted for 7.4% of total phenotypic variability and major contributors were days to 50% flowering (factor loading 0.96) followed by yield per plant (factor loading 0.22). Similarly, the principal component 3 (PC 3) explained only 2.3% total phenotypic variation with major contribution from yield per plant (factor loading 0.97) and followed by days to 50% flowering (-0.22). Further, the results of PCA depicted the presence of morphological differences among genotypes were dispersed in all the four quadrants on the contrary, neighbour joining tree form 3 groups. Principal component analysis confirmed the presence of morphological differences among genotypes spread over the four quadrants. In the figure 3, the colour combination denotes the distribution of genotypes based on neighbour joining tree with in the PCA. There was a specific observation neighbour joining tree showed two genotypes IG 92 and IG 108 are in same group, but PCA shows these two genotypes are highly diverse.
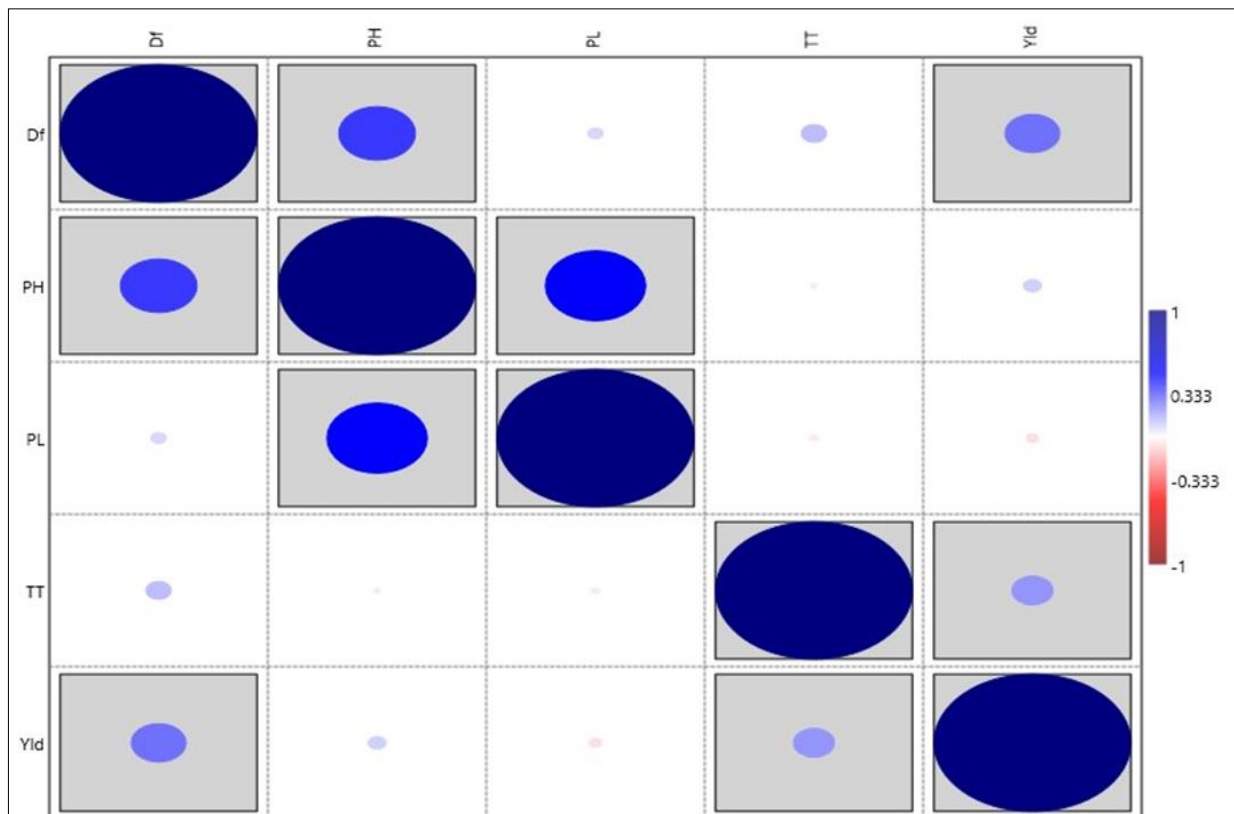
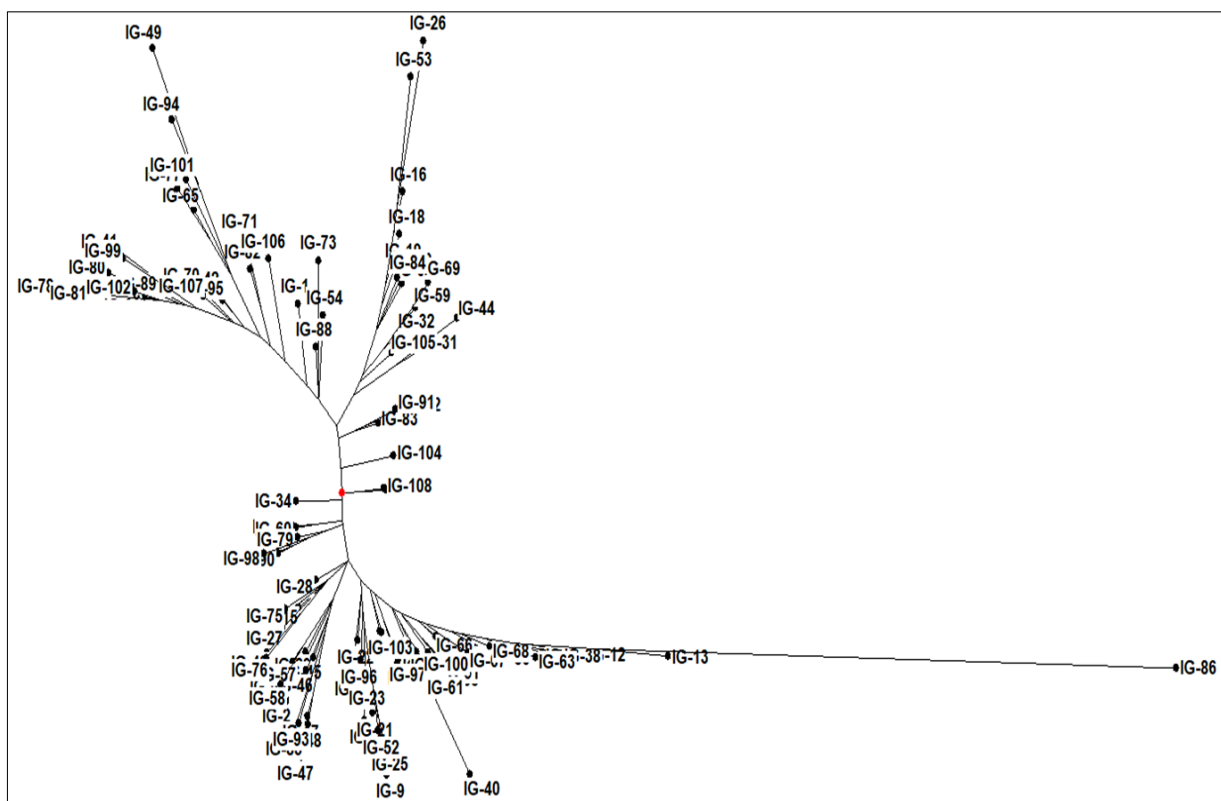**Fig 1:** Correlation coefficients and trend of distribution among Agro-morphological characters

Fig 2: Neighbour joining tree illustrating the genetic relationships of the 107 rice varieties
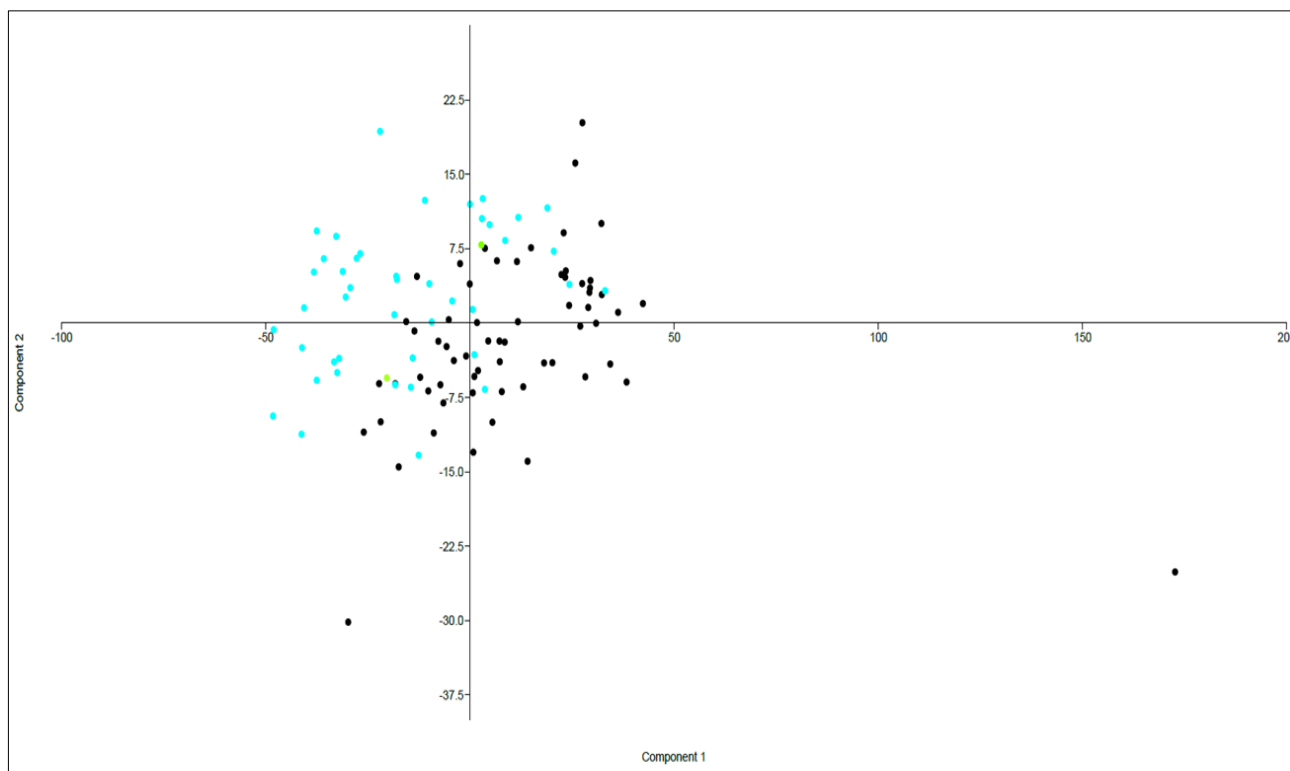
Fig 3: PCA of 107 accessions of aromatic rice collection using 5 qualitative morphological traits

Table 1: Descriptive statistics for 5 agro-morphological trait

Traits	Mean	Standard Error	Median	Mode	Standard Deviation	Sample Variance	Kurtosis	Skewness	Range	Minimum	Maximum
DF	95	0.84	95.63	100.25	8.70	75.62	1.49	-0.38	58.50	62	120.00
PH	136.45	2.68	137.03	137.81	27.83	774.40	13.09	2.19	221.51	89.39	310.90
PL	26.58	0.23	26.38	26.18	2.43	5.92	-0.08	0.17	12.05	21.34	33.39
TT	8	0.08	7.75	8.00	0.79	0.62	1.01	0.71	4.38	6.00	10
YLd	17.15	0.46	16.61	#N/A	4.74	22.45	-0.03	0.60	23.50	8.29	31.80

DF-Days of 50% flowering, PH-Plant height, PL-Panicle length, TT-Total no of tiller, YLD-Yield per plant

Table 2: Eigenvalue and % variance of the principal components.

PC	Eigenvalue	% variance
1	789.145	89.627
2	65.7896	7.472
3	20.5113	2.3296
4	4.42946	0.50307
5	0.604716	0.06868

4. Discussion

Genetic diversity and heritable variation are the key to crop improvement (Sanghamitra *et al.,* 2018) [11]. The genetic diversity of aromatic rice cultivars that could be differentiated morphologically was assessed using morphological traits. Basmati's long grains have dominated fragrant rice markets worldwide. Indian farmers still grow native, non-Basmati landraces with medium and short grains that are aromatic, tasty and healthy. Culturally, these aromatic landraces are superior for amylose content, grain length, grain elongation after cooking and rice texture. Selective breeding for fragrant rice requires assessing germplasm variation.

The variation in aromatic rice with respect to range, mean for morphological traits was higher in genotypes. This variation was an ideal to initiate the breeding programme. Such variation in rice were also observed by other researcher (Nayak *et al*., 2022; Azharudheen *et al,*. 2022) [7, 3, 8]. In order to select the traits efficiently knowledge of correlations

among the characters was useful. In this study, grain yield per plant were positively correlated to total tiller. Tiller number was also important parameter for increasing the grain yield (Sanghamitra *et al.,* 2018) [11]

The dendrogram classified rice genotypes into three primary groupings, this implied a considerable level of morphological variability among rice genotypes. The grouping of genotypes very clearly indicated the diverse nature of the lines. Only two lines IG-108 and IG-92 fall in a single group and much diverse from the other genotypes. However, this relationship was not in line with the findings of PCA and both genotypes fall in separate groups. Principal Component Analysis (PCA) is a method for reducing the dimensions of a dataset by condensing a number of variables into a smaller subset that preserves most of the information present in the original set (Sah *et al.,* 2022) [8]. Facilitate ease of analysis and improve the quality of discussion, only two principal component that exhibited eigen values greater than one were selected for study. Nevertheless, the initial two principal components under consideration were found to account 97% of the overall variation. This observation implies that the aromatic lines that were examined and the molecular markers that were used have contributed to a multidimensional genetic diversity. The PCA usefulness in measuring of diversity in genotypes also reported by Sah *et al.,* 2022 [8]; Azharudheen *et al.,* 2022 [3, 8] (Overall the genotypes were diverse in nature in relation to traits of study.

5. Conclusions

The result of the present study indicates that ample amount of variation present in the rice germplasm studied gesturing towards the usefulness of selection in the improvement of yield and yield attributing traits. The promising lines exhibiting desirable magnitude of specific traits studied can be used as donor in rice breeding program. The study also emphasizes the need for balanced selection in light of negative association among panicle length, total tillers per plant and yield. The genotypes were successfully classified into three distinct clusters with different mean value. The genotypes belonging to distinct cluster were genetically more diverse compared to genotype belonging to same cluster. Hence, by making crosses between genotypes from different clusters. The PCA aided in identification of traits which were most important in determining variation amongst different genotypes. Therefore, such germplasm lines can play significant role in rice improvement programme.

6. Reference

1. Annonymous; c2021, https://pib.gov.in/PressReleasePage.aspx?PRID=1782368
2. Azharudheen TPM, Molla KA, Lenka S, Bose LK, Kar MK, Singh ON, *et al*. Marker-assisted screening of *Oryza rufipogon* accessions for sheath blight tolerance. Int. J. Pharmacogn. Phytochem. Res. 2018;SP1:701-707.
3. Muhammed Azharudheen TP, Nayak AK, Behera S, Anilkumar C, Marndi BC, Moharana D, Singh LK, *et al*., Genome-wide association analysis for plant type characters and yield using cgSSR markers in rice (*Oryza sativa* L.). Euphytica. 2022;218(6):69.
4. Ghareyazie B, Alinia F, Menguito CA, Rubia LG, de Palma JM, Liwanag EA, *et al*., Enhanced resistance to two stem borers in an aromatic rice containing a synthetic cryIA (b) gene. Mol. Breed. 1997;3:401-414.
5. Maji AT, Shaibu AA. Application of principal component analysis for rice germplasm characterization and evaluation. j. plant breed. crop sci. 2012;4(6):87-93.
6. Nachimuthu VV, Robin S, Sudhakar D, Raveendran M, Rajeswari S, Manonmani S. Evaluation of rice genetic diversity and variability in a population panel by principal component analysis. Indian J Sci. Technol. 2014;7(10):1555-1562.
7. Nayak AK, Anilkumar C, Behera S, Sah RP, Lavanya GR, Kumar A, *et al*., Genetic dissection of grain size traits through genome-wide association study based on genic markers in rice. Rice Sci. 2022;29(5):462-472.
8. Sah RP, Behera S, Dash SK, Azharudheen TM, Meher J, Kumar A, *et al*. Unravelling genetic architecture and development of core set from elite rice lines using yield-related candidate gene markers. Physiol. Mol. Biol. Plants. 2022;28(6):1217-1232.
9. Sah RP, Chakraborty M, Prasad K, Pandit M, Tudu VK, Chakravarty MK, *et al*. Impact of water deficit stress in maize: Phenology and yield components. Sci. Rep. 2020;10(1):2944.
10. Sah RP, Nayak AK, Chandrappa A, Behera S, Azharudheen TPM, Lavanya GR. cgSSR marker-based genome-wide association study identified genomic regions for panicle characters and yield in rice (*Oryza sativa* L.). J. Sci. Food Agric. 2023;103(2):720-728.
11. Sanghamitra P, Sah RP, Bagchi TB, Sharma SG, Kumar A, Munda S, *et al*. Evaluation of variability and environmental stability of grain quality and agronomic parameters of pigmented rice (*O. sativa* L.). J. Food Sci. Technol. 2018;55(3):879-890.
12. Singh BN, Dhua SR, Sahu RK, Patra BC, Marndi BC. Status of rice germplasm-Its collection and conservation in India. Indian Journal of Plant Genetic Resources. 2001;14(2):105-106.
13. Tp MA, Kumar A, Anilkumar C, Sah RP, Behera S, Marndi BC. Understanding natural genetic variation for grain phytic acid content and functional marker development for phytic acid-related genes in rice. BMC Plant Biol. 2022;22(1):1-14.