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Study on morphometric characterization for yield and yield contributing attributes in traditional rice (*Oryza sativa* L.) varieties

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Abstract

The present study was carried out at Agricultural College and Research Institute, Killikulam, Tuticorin district during Rabi 2021-22 to characterize the inherent genetic variability among 105 traditional rice varieties against nine morphometric yield contributing traits in a randomized block design with three replications. Univariate analysis among rice genotypes elucidated significant differences for all the traits studied. Phenotypic coefficient of variation (PCV) was relatively higher than genotypic coefficient of variation (GCV) for all the traits. The traits such as number of productive tillers per plant, number of filled grains per panicle, and thousand-seed weight (g) had exhibited the higher estimates for both PCV and GCV. Heritability and genetic advance were also recorded high for all the yield attributes, indicating the role of additive gene for heritability, suggesting the direct selection for yield contributing trait always will be rewarding.

Keywords: Rice, genetic variability, heritability, genetic advance and yield

Introduction

Rice (*Oryza sativa* L. 2n=2x=24), is an important cereal food crop of the Poaceae family with a haploid chromosome number (n=12), widely portrayed as a “global grain” or “Life of people”. It can be either diploid (or) tetraploid, with the autogenously mode of reproduction Baroudy *et al.*, (2020) [3]. It is a substantial food crop cultivated around the globe, which accounts for 35-80 per cent of total calorific intake Vijay *et al.*, (2019) [30]. Around, 40 per cent of the global and 65 per cent of the Indian population depends on rice as their staple diet, to satisfy their regular dietary intake Singh *et al.*, (2021) [21]. Rice has been domesticated for ages, making it suitable for cultivation in diverse locations around the globe with an extreme environment. Vigueira *et al.*, (2019) [29]. China and India are the two most populous nations and are the largest consumers and producers of rice. FAO (2019) [5]. On a global scale, paddy occupies 75 per cent of cereal grain production followed by wheat, with a cultivable area of 164.0 million hectares and yielding about 516.3 million tonnes with average productivity of 3.15tonnes/ha. FAO/OCED (2022) [16]. India ranked second only to China in terms of total rice production (118.4 million tonnes) and productivity (2.79 t/ha), with a global lead of 43.86 million hectares India stat (2020-21) [10]. Population forecast indicated a rise in the national population may shoot up the production to 130 million tonnes from standard projections, to meet an average of 42 per cent increase in the demand for grain across the nation by 2035 Gaballah *et al.*, (2022) [6].

To meet the reckoning demand for rice shortly, agronomically superior rice varieties with multiple stress resistance must be bred with progressive breeding approaches and biotechnological tools. Several rice varieties have been successfully developed after the green revolution through repeated selection and hybridization programs, eventually, leading to a trivial loss of variations among landraces Nandhini *et al.*, (2017) [15]. Since Traditional rice varieties hold up a high level of heterogeneity, it is crucial to utilize them in present-day breeding programs. To do so it requires an elaborate survey of genetic variability, and a thorough understanding of the genetic makeup of the Traditional rice varieties is essential Govintharaj *et al.*, (2016) [7]. Mostly, any variation in the given population is due to interaction between the genetic and environmental components of the variation, where the genetic one must be heritable Roy and Shil (2020) [18]. Regarding the aforementioned considerations, the current study has been carried out to estimate variability, heritability, genetic advance for yield and yield contributing traits in rice genotypes.

The current investigation was conducted during Rabi 2021 – 2022 at the B block farm of Agricultural College and Research Institute, Killikulam. The experimental material consists of 105 rice genotypes obtained from AC&RI, Killikulam, and sown in a uniform raised bed nursery with the recommended doses of fertilizer of 1.0kg N, 1.0kg P_2O_5, and 0.5kg K_2O per 50 m2 area. Twenty-five days old robust rice seedlings of each genotype were transplanted into the main field with one seedling per hill, by adopting a spacing of 30cm between rows and 20cm between plants within a row in a Randomised Block Design replicated thrice. Required agronomic practices and essential prophylactic remedies were adopted during the entire crop period to raise a good crop. Observations were taken randomly from ten competitive plants of each genotype in every replication for nine yield contributing biometrical traits *viz*, plant height (cm), number of productive tillers, panicle length(cm), number of grains per panicle, single plant yield (g), grain length(mm), and grain breadth(mm) and data for days to 50% flowering was recorded on a plot basis, thousand seed weight(g) was observed for randomly drawn grain samples from each genotype for every replication. The collected data were subjected to standard statistical analysis using WINDOWSTAT software. Univariate analysis of each character (ANOVA) was carried out as suggested by Panse and Sukhatme (1957) [17]. Genetic variability parameters such as GCV and PCV, heritability, and genetic advance as percent of mean were enumerated according to Burton *et al.*, (1953) [4], Lush (1940) [12], and Johnson *et al.*, (1955) [11] respectively.

Results and Discussion

Analysis of Variance (ANOVA)

Results of Univariate analysis (ANOVA) for all nine yield contributing traits were enumerated in Table 1. It revealed that the mean sum of squares due to treatment is significant for all the traits studied, indicating that genotypes included in the study have diverse genetic roots and hold up adequate variation among them. Therefore, this germplasm can be employed for an effective selection process of genetic advancement of yield attributes. Similar findings were reported by Girma *et al.*, (2018) [8], Sujitha *et al.*, (2020) [26], and Sowjanya *et al.*, (2021) [22].

Peres performance

Mean values of all nine yield contributing traits of each genotype were given in brief (Table 2). Variation for the trait days to fifty per cent flowering ranged from 119 days to 42 days with a *per se* value of 90.5 days, implying that the genotype with a lower estimate for days to fifty percent flowering can be used as a donor parent to develop short duration variety. The variation for plant height ranged from 167.0cm to 71.7cm with an average value of 115.4cm. The number of productive tillers fluctuated between 29.0 to 10.70 with an average value of 18.9. The length of the panicle varied from 36.2cm to 15.0cm with a median value of 24.6cm. Trait number of grains per panicle differed between 340.7 to 86.7 per se value of 159.7. Thousand seed weight could be varied between 36.7g to 13.7g with a mean value of 25.4g. Grain length may differed between 10.5cm to 5.7cm with a mean of 7.7cm. The highest grain width was 4.9cm and the lowest was 2.0cm with an average of 2.9cm. The variation for single plant yield ranges from 77.9g to 34.9g with an average of about 55.5g. Hence, the *per se* performance of the given genotypes entails that no specific genotypes were significant for all the yield contributing traits, indicating that sufficient variation was present in the genotypes that can be exploited in the crop improvement schemes.

Range and variability parameters

The range and variability parameters of all the genotypes were depicted in detail (Table 2). In accordance with the results, the number of grains per panicle showed a high range of variability (86.7-340.7), whereas the least range of variability was observed for grain breadth (2.0-4.9) Madhubabu *et al.*, (2020) [13] and Sharma *et al.*, (2021) [20]. Reports from journals quenched that the success of any selection process in a crop improvement scheme always rests on the presence of relative divergence among traits, calibrated using the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV).

The PCV estimates were kind of greater than the GCV estimates (Table 2 and Figure 1) for all traits evaluated, although the variation seemed extremely small, emphasizing that divergence may arise not only by genotype but also by an environmental effect on trait expression, which is invariably similar to the findings of Tiwari *et al.*, (2019) [27], Sabri *et al.*, (2020) [19], Sudeepthi *et al.*, (2020) [25] and Sowjanya *et al.*, (2021) [22].

PCV and GCV are higher for the trait number of grains per panicle (32.24 and 32.13) followed by thousand seed weight (23.56 and 23.42) and the number of productive tillers (21.77 and 21.61) respectively. Traits such as plant height (20.12 and 19.97), single plant yield (16.81 and 16.62), grain breadth (16.39 and 16.17), days to fifty per cent flowering (14.40 and 14.16), panicle length (13.49 and 13.22) and grain length (11.78 and 11.41) have moderate estimates for both PCV and GCV. These results were comparable with Srilakshmi *et al.*, (2018) [24], Tiwari *et al.*, (2019) [27] and Sabari *et al.*, (2020) [19]. Traits that possessed moderate PCV and GCV are likely to be included in crop advancement plans. Similarly, yield attributes that have high PCV and GCV are predominantly influenced by genetic factors rather than the environment, suggesting that these traits are genetically divergent and hence there is an ample scope for selection.

Heritability and genetic advance as percent of mean

Measures of heritability and genetic advance as per cent of the mean are of great importance for selection. High heritability coupled with high genetic advance suggests a more precise prediction of genetic gain under selection Arora (1991) [2]. Estimates of heritability (Table 2 and Figure 2) ranged from 99.30 per cent for number of filled grains per panicle to 93.30 per cent for grain length. Values of heritability for all the yield contributing traits were high. Similar kinds of reports were given by Srilakshmi *et al.*, (2018) [24], Sujitha *et al.*, (2020) [26] and Sowjanya *et al.*, (2021) [22]. (Table 2 and Figure 2) The results for genetic advance as a percentage of mean found high values for all the traits included in the study, which range between 65.97 per cent for the number of filled grains per panicle to 22.78 per cent for grain length. These results were in consonance with the earlier reports of Umarani *et al.*, (2017) [28], Sreedhar and Reddy (2019) [23], and Sujitha *et al.*, (2020) [26].

Yield attributes with high heritability coupled with high genetic advance per cent of mean are controlled by additive gene action and substantial enhancement of these traits can be achieved through the direct selection which include mass selection, progeny selection, and pure line selection. Johnson *et al*., (1955) [4]. In the current study, high GCV and PCV coupled with high heritability and genetic advance were observed for traits that include the number of filled grains per panicle, thousand seed weight, and the number of productive tillers per plant, implying the predominance of additive gene action and hence the traits are potential for improvement by selection. Similar findings of the study were consistent with reports of Maurya *et al*., (2021) [14], Hake and Bhoite (2021) [9] and Akshay *et al*., (2022) [1].

Table 1: ANOVA for nine yield attributes

Source of variation	**Mean Sum squares**		**CV**	**S.E.D**	**CD (5%)**
	Replication	**Genotypes**			
	DF = 2	**DF = 104**			
Days to fifty per cent flowering	5.668	498.510**	2.59	1.92	3.78
Plant height (cm)	7.884	1600.345**	2.52	2.37	4.68
Number of productive tillers per plant	0.163	50.064**	2.57	0.40	0.78
Panicle length (cm)	0.079	32.071**	2.65	0.53	1.05
Number of filled grains per panicle	7.151	7919.646**	2.61	3.40	6.70
Thousand seed weight (g)	0.424	106.346**	2.59	0.54	1.06
Grain length (mm)	0.029	2.378**	2.91	0.18	0.36
Grain breadth (mm)	0.004	0.647**	2.67	0.06	0.12
Single plant yield (g)	0.029	257.144**	2.52	1.14	2.26

*Significant at 5% level **Significant at 1% level

Table 2: Summary statistics of genetic variability parameters for nine yield attributes

Traits	**Range**	**Mean**	**PCV (%)**	**GCV (%)**	**H (%)**	**GAM (%)**
DFF	42.00 – 119.00	90.54	14.40	14.16	96.8	28.69
PH	71.70 – 167.00	115.38	20.12	19.97	98.4	40.81
NoPT	10.70 – 28.97	18.86	21.77	21.61	98.6	44.21
PL	15.00 – 36.20	24.56	13.49	13.22	96.1	26.71
GPP	86.70 – 340.70	159.73	32.24	32.13	99.3	65.97
TSW	13.67 – 36.67	25.37	23.56	23.42	98.8	47.95
GL	5.70 – 10.50	7.72	11.78	11.41	93.9	22.78
GB	1.97 – 4.87	2.86	16.39	16.17	97.3	32.87
SPY	34.90 – 77.90	55.49	16.81	16.62	97.7	33.85

DFF - Days to fifty percent flowering, PH - Plant height, NoPT- Number of productive tillers per plant, PL - Panicle length, GPP - Number of grains per panicle, TSW - Thousand-seed weight, GL - Grain length, GB - Grain breadth, SPY - Single plant yield, PCV - Phenotypic coefficient of variation, GCV - Genotypic coefficient of variation, H - Heritability, GAM – Genetic Advance as per cent of mean.

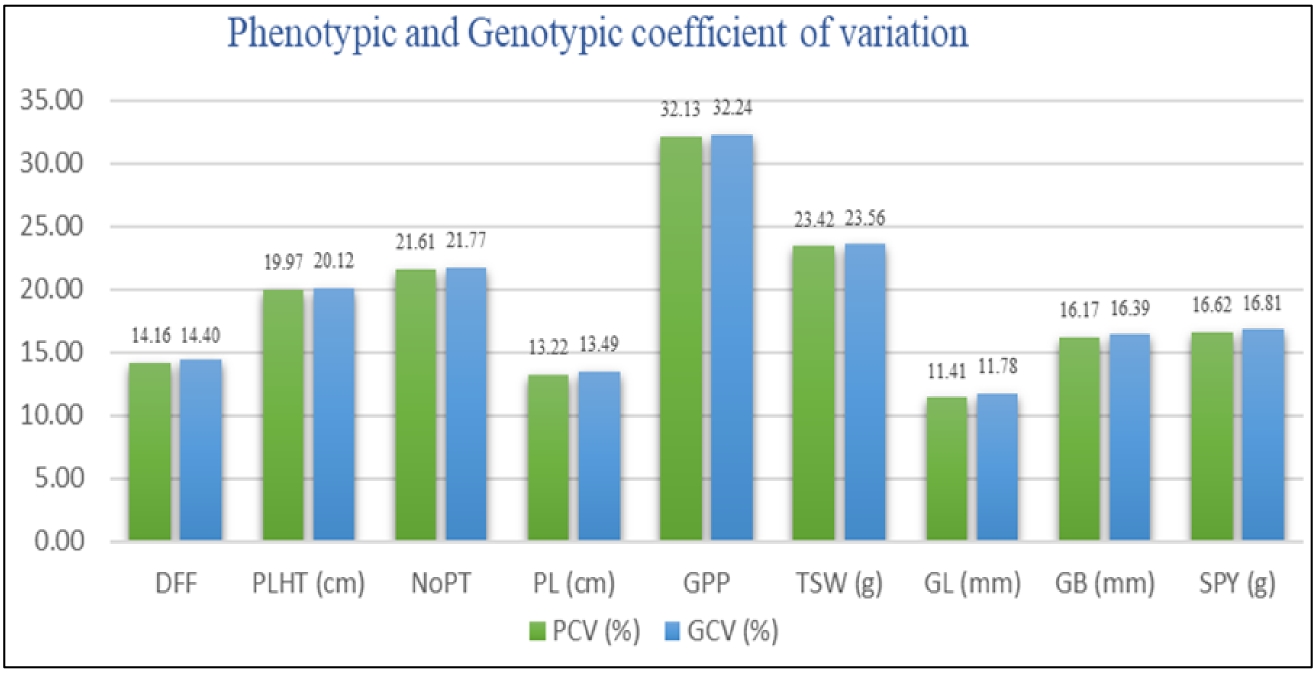

Fig 1: Phenotypic and Genotypic coefficient of variation for nine yield attributing attributes

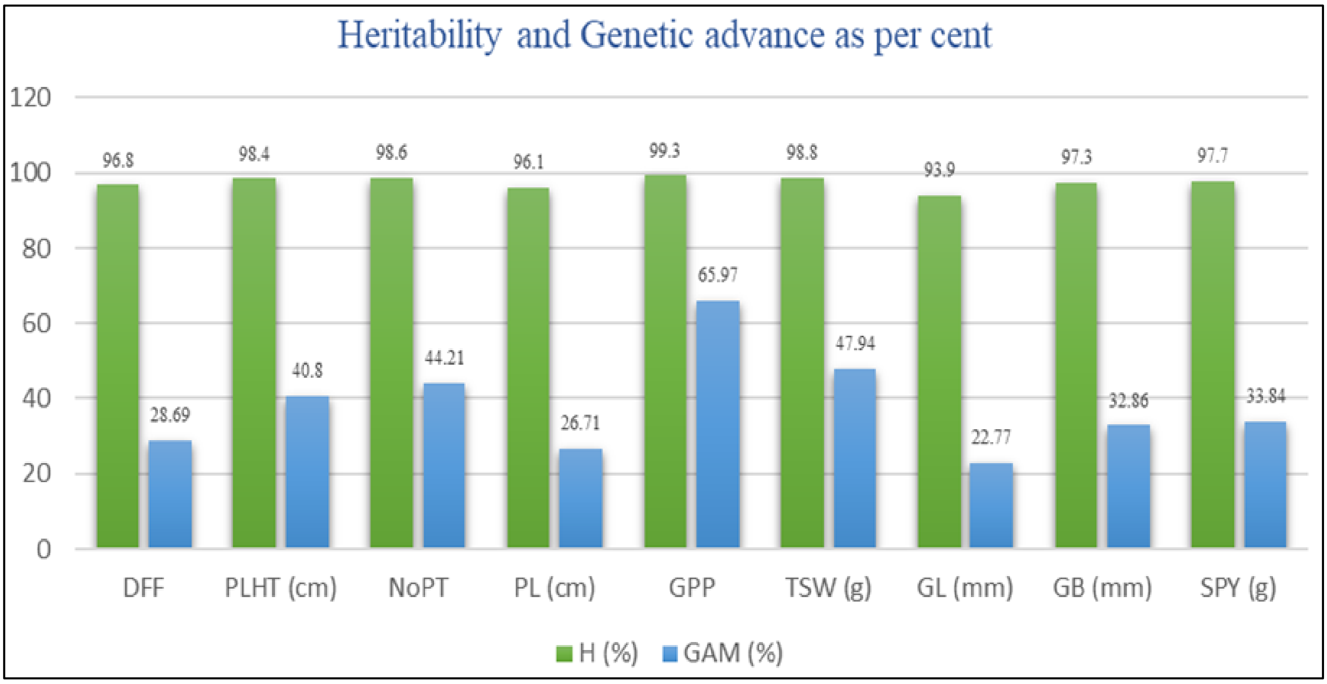

Fig 2: Heritability and Genetic advance as percentage of the mean for nine yield attributing attributes

Conclusion

The results of the analysis of variance suggest that the material under the present study have a significant level of variability. High magnitude of PCV and GCV were observed for the traits such as number of filled grains per panicle, thousand seed weight, and number of productive tillers per plant revealing that a substantial degree of variation present in the traits can be exploited in trait-based crop improvement schemes through efficient selection. Higher estimates of heritability in a broad sense and high genetic advance as per cent of mean were observed for all the traits under study, indicating that these traits were under the influence of additive gene action and hence direct selection of these traits is beneficial for improving yield in any future breeding programs.

References

1. Akshay M, Chandra SB, Devi RK, Hari Y. Genetic variability studies for yield and its attributes, quality and nutritional traits in rice (*Oryza sativa* L.). The Pharma Innovation Journal. 2022;11(5):167-172.
2. Arora PP. Agricultural statistics of Pakistan. Planning unit, Ministry of Food. Agriculture and Cooperation, 1991, 134.
3. Baroudy AAE, Ali AM, Mohamed ES, Moghanm FS, Shokr MS, Savin I, *et al.* Modelling land suitability for rice crop using remote sensing and soil quality indicators: the case study of the Nile delta. Sustainability. 2020;12(22):9653.
4. Burton GW, Devane DE. Estimating heritability in tall fescue (*Festuca arundiaceae*) from replicated clonal material 1. Agronomy Journal. 1953;45(10):478-481.
5. FAO. The State of Food and Agriculture 2019. Moving forward on food loss and waste reduction. Rome, 2019. www.fao.org.
6. Gaballah MM, Attia KA, Ghoneim AM, Khan N, El-Ezz AF, Yang B, *et al.* Assessment of Genetic Parameters and Gene Action Associated with Heterosis for Enhancing Yield Characters in Novel Hybrid Rice Parental Lines. Plants. 2022;11(3):266.
7. Govintharaj P, Shalini T, Manonmani S, Robin S. Estimates of genetic variability, heritability and genetic advance for blast resistance gene introgressed segregating population in rice. Int. J. Curr. Microbiol. App. Science. 2016;5(12):672-677.
8. Girma BT, Kitil MA, Banje DG, Biru HM, Serbessa TB. Genetic variability study of yield and yield related traits in rice (Oryza sativa L.) genotypes. Adv Crop Sci Tech. 2018;6(4):381.
9. Hake PA, Bhoite KD. Genetic variability studies in rice (*Oryza sativa* L.). The Pharma Innovation Journal. 2021;10(12):432-434.
10. Indiastat. Agriculture Production Statistical Database. 2019-20. http://www.indiastat.com
11. Johnson H, Robinson H, Comstock R. Estimate of genetic and environment studies in soybean. Agron. J. 1995;47:314-18.
12. Lush JL. Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. Journal of Animal Science. 1940(1):293-301.
13. Madhubabu P, Surendra R, Suman K, Chiranjeevi M, Fiyaz RA, Rao DS, *et al.* Assessment of genetic variability for micronutrient content and agro-morphological traits in rice (*Oryza sativa* L.). Indian Journal of genetics and plant breeding. 2020;80(02):130-139.
14. Maurya RK, Dwivedi DK, Khan NA, Giri SP, Dixit S. Genetic variability studies for qualitative and quantitative traits in rice (*Oryza sativa L.*). The Pharma Innovation Journal. 2022;11(5):1140-1143.
15. Nandini B, Gangappa E, Rajanna MP, Mahadevu P, Ramesh S, Hittalmani PS. Genetic variability analysis for grain yield and its components traits in traditional rice varieties (TRVs). Int. J. Curr. Microbiol. App. Sci. 2017;6(8):494-502.
16. OECD-FAO. Agricultural Outlook 2022-2031 – © OECD/FAO, 2022.

17. Panse VG, Sukhatme PV. Genetics of quantitative characters in relation to plant breeding. Indian J. Genet. 1957;17(2):318-328.
18. Roy SC, Shil P. Assessment of genetic heritability in rice breeding lines based on morphological traits and caryopsis ultrastructure. Scientific Reports. 2020;10(1):1-17.
19. Sabri RS, Rafii MY, Ismail MR, Yusuff O, Chukwu SC, Hasan NA. Assessment of agro-morphologic performance, genetic parameters and clustering pattern of newly developed blast-resistant rice lines tested in four environments. Agronomy. 2020;10(8):1098.
20. Sharma M, Abdullah GM, Salgotra RK, Hangloo S, Singh AK, Sharma V, Singh A. Genetic diversity analysis in rice (*Oryza sativa* L.) germplasm of Jammu region of Jammu and Kashmir. Indian Journal of Genetics and Plant Breeding. 2021;81(04):35-43.
21. Singh KM, Ahmad N, Pandey VV, Kumari T, Singh R. Growth performance and profitability of rice production in India: An Assertive Analysis, 2021, 481-486.
22. Sowjanya MS, HV Vijayakumar Swamy, HE Shashidhar, Prakash Patil, Vimarsh HS. Genetic Variability Study of Rice Germplasm Accessions under Aerobic Condition. International J. of Current Microbiology and Applied Sci. 2021;10(1):452.
23. Sreedhar S, Reddy UR. Association studies for yield and its traits in rice (*Oryza sativa* L.) genotypes. International J of Current Microbiology and Applied Sci. 2019;8(1):2337-2342.
24. Srilakshmi P, Chamundeswari N, Ahamed LM, Rao SV. Assessment of genetic variability studies in wet direct sown rice. The Andhra Agri. J. 2018;65(3):555-560.
25. Sudeepthi K, Srinivas TVSR, Kumar BR, Jyothula DPB, Umar SN. Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding. 2020;11(01):144-148.
26. Sujitha R, Pillai MA, Kannan R, Shoba D. Genetic diversity and association studies in Rice (Oryza sativa L.). Journal of Pharmacognosy and Phytochemistry. 2020;9(6):487-492.
27. Tiwari DN, Tripathi SR, Tripathi MP, Khatri N, Bastola BR. Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. Advances in Agriculture, 2019.
28. Umarani E, Radhika K, Padma V, Subbarao LV. Variability, heritability and genetic advance for agro morphological and grain quality parameters in landraces of rice (*Oryza sativa* L.). Environment and Ecology. 2017;35(3):1682-1687.
29. Vigueira CC, Qi X, Song BK, Li LF, Caicedo AL, Jia Y, *et al.* Call of the wild rice: *Oryza rufipogon* shapes weedy rice evolution in Southeast Asia. Evolutionary applications. 2019;12(1):93-104.
30. Vijay P, Choudhary AK, Bana RS, Pankaj P. Zinc bio-fortification and kernel quality enhancement in elite basmati rice (*Oryza sativa*) cultivars of south Asia through legume residue-recycling and zinc fertilization. Indian Journal of Agricultural Sciences. 2019;89(2):279-287.