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# Genetic Variability and Association Studies in $F_2$ Population of *Indica-Japonica* Crosses of Rice

**Kundan Bedwa, Neelam Bhardwaj * and Surbhi Patyal**

Department of Genetics and Plant Breeding, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176062
*Corresponding author Email: neenabhardwaj@gmail.com

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## Abstract

The present experiment was conducted to evaluate genetic variability among 12 *indica-japonica* crosses and their parents during *kharif*, 2023. Analysis of the variance revealed presence of significant variability among the genotypes for all the characters studied in $F_2$ population. High phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) were observed for spikelets per panicle (19.75%, 17.76%) and grain yield per plant (18.89%, 16.28%) suggesting presence of high variability among the lines that can be exploited for improvement of these traits through selection in advanced generations. High heritability coupled with high genetic advance were observed for spikelets per panicle (80.93%, 32.93%) and 1000 grain weight (80.34%, 21.10%). Based upon the correlation studies grain yield per plant was positively and significantly correlated with effective tillers per plant, panicle length, spikelets per panicle and 1000 grain weight, both at phenotypic and genotypic level. Path coefficient analysis showed that high positive direct effects were exhibited by effective tillers per plant and spikelets per panicle.

**Keywords:** *Indica-japonica* crosses, Heritability, Variability, Correlation

## Introduction

Rice (*Oryza sativa* L.) is a monocotyledonous angiospermic plant of the *Poaceae* family and *Oryzoideae* subfamily and is commonly classified into three subspecies: *indica*, *japonica* and *javanica* (Choi and Jung, 2018). As the staple food for 2.7 billion people, rice's significance led to the declaration of 2004 as the International Year of Rice. India ranks as the world's second-largest producer of rice following China and is also the largest exporter (Khan*,* 2018). The country cultivates rice across 48 million hectares of land achieving an annual production of 134 million metric tons and a productivity of 2.79 tons per hectare (USDA, 2023-24). *Indica* and *japonica* are the two primary subspecies of cultivated Asian rice. *Indica* varieties typically feature taller plants with light green, longer leaves and exhibit tolerance to heat and moisture but are sensitive to low temperatures. They are commonly cultivated in humid regions and lower latitudes. On the other hand, *japonica* varieties are characterized by shorter plant heights and darker green, shorter leaves compared to *indica*. They are known for their tolerance to low temperatures and are suitable for cultivation in both high latitudes and lower latitudes at high altitudes. Genetic variability within and between *indica* and *japonica* rice subspecies has been extensively studied, driven by the quest to enhance grain yield and tolerance to biotic and abiotic stresses including cold stress. The genetic interactions between these two subspecies, particularly in $F_2$ populations resulting from crosses, offers an unique opportunity to explore the genetic basis of complex traits such as grain yield.

The $F_2$ derived lines constitute a segregating population that is far from being homozygous and early generation selection in such populations depends on the assumption that the performance of a line at an early generation of selfing is predicative of its performance at homozygosity (Chahota *et al.,* 2007). Understanding the genetic variability present in the germplasm, the degree to which the desired traits are heritable and associations between traits and both direct and indirect effects on yield and its attributes is crucial for improving the yield through selection. Therefore, the present study was aimed at finding out nature and magnitude of genetic variability present in $F_2$ population of the rice for grain yield and other yield component traits to select the transgressive segregants for further breeding programmes.

## Materials and Methods

The present study was conducted at Rice and Wheat Research Centre, Malan (RWRC) during *kharif*, 2023. The experimental material comprised of 12 *indica-japonica* rice crosses along with eight parents and two checks *viz.,* HPR-2143 and HPR-2880. The detail of parents and checks used in the present study is given in **Table 1**. These crosses and their parents along with two checks were evaluated in Randomized Block design with three replications. Each entry was grown in plots with a spacing of 15 cm between plants and 20 cm between rows (two rows per genotype) across three replications within plot size of 0.81 $m^2$. The observations were recorded for eight yield and its related characters *viz.,* days to 50% flowering, days to 75% maturity, plant height, effective tillers per plant, spikelets per panicle, panicle length, 1000 grain weight and grain yield per plant. 20 plants were randomly selected and tagged for data collection on various traits excluding phenological characteristics such as days to 50% flowering and days to 75% maturity, which were recorded based on the entire plot. The analysis of variance and test of significance was calculated as per the method of Panse and Sukhatme, (1985). The genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability and genetic advance were calculated by the formula given by Burton and De Vane, (1953) and Johnson *et al.,* (1955). Phenotypic and genotypic coefficients of correlation were computed by the formula given by Al-Jibouri *et al.,* (1958). Path coefficient analysis was done by using standard procedure given by Dewey and Lu (1959) in order to estimate the extent of genetic variability present among the parents and crosses.

**Table 1: List of cross combinations, parents and checks used in this study**

| Sl. No. | Cross Combinations |
|---|---|
| 1 | HPR 2143 × Naggardhan |
| 2 | HPR 2143 × Giza 14 |
| 3 | HPR 2143 × Koshihikari |
| 4 | HPR 3106 × Hinohikari |
| 5 | Giza 14 × HPR 2143 |
| 6 | Giza 14 × HPR 3106 |
| 7 | Pusa Basmati 1509 × Hinohikari |
| 8 | Hinohikari × HPR 2143 |
| 9 | Bhrigudhan× HPR 2143 |
| 10 | Koshihikari× HPR 2143 |
| 11 | HPR 3106 × Koshihikari |
| 12 | HPR 2143 × Hinohikari |

| Sl. No. | Parents and Checks |
|---|---|
| 1 | Pusa Basmati 1509 (*indica*) |
| 2 | HPR 3106 (*indica*) |
| 3 | Hinohikari (*japonica*) |
| 4 | Bhrigudhan (*japonica*) |
| 5 | Naggardhan (*japonica*) |
| 6 | Giza14 (*japonica*) |
| 7 | Koshihikari (*japonica*) |
| 8 | HPR 2143 (*indica*) (Check) |
| 9 | HPR 2880(*indica*) (Check) |

## Results and Discussion

### Variability Parameters

Assessing variability parameters is essential for any breeding programme to assess the nature and magnitude of existing variability (Begna and Teressa, 2024). Estimated values phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ($h^2_{bs}$) and expected genetic advance as a percentage of the mean for various traits are presented in **Table 2**. In the present study, results showed significant genetic variation for all traits studied in the $F_2$ population. All the characters studied exhibited low, moderate and high PCV and GCV values. PCV estimates were higher than the corresponding GCV for all the traits studied, indicating that the apparent variation is not only due to genotypes but also due to the influence of the environment (Gupta *et al.,* 2022). Highest PCV (>15%) was obtained for spikelets per panicle (19.75%) followed by grain yield per plant ((18.89%) and effective tillers per plant (15.88%). Moderate PCV (10-15%) was obtained for 1000-grain weight (12.75%), panicle length (11.74%) and plant height (11.17%). On the other hand, low PCV (<10%) was obtained for days to 50% flowering (5.26%) and days to 75% maturity (4.15). High GCV (>15%) was obtained for spikelets per panicle (17.76%) and grain yield per plant (16.28%) followed by moderate GCV obtained for effective tillers per plant (13.54%), 1000-grain weight (11.43%) and low GCV (<10%) for plant height (9.94%), panicle length (7.27%), days to 50% flowering (5.13%) and days to 75% maturity (4.01%). El-malky and Al-Dahej, (2023), Surjaye *et al.,* (2022), Kurmanchali *et al.,* (2019) and Rachappanavar, (2017) also reported similar results, with higher phenotypic coefficient of variation (PCV) compared to genotypic coefficient of variation (GCV) in their studies.

**Table 2: Estimated parameters of variability for yield and its related traits in *indica-japonica* crosses and the parents**

| Traits | Mean ±SE(m) | Range | PCV (%) | GCV (%) | Heritability ($h^2_{bs}$) (%) | Genetic advance (as % of mean) |
|---|---|---|---|---|---|---|
| Days to 50% flowering | 85.48 ±0.81 | 80.00-98.00 | 5.26 | 5.13 | 95.14 | 10.31 |
| Days to 75% maturity | 112.49 ±1 | 107.00-126.00 | 4.15 | 4.01 | 93.12 | 7.96 |
| Plant height | 129.45 ±5.39 | 101.13-146.47 | 11.17 | 9.94 | 79.15 | 18.22 |
| Effective tillers per plant | 9.71 ±0.66 | 7.47-11.87 | 15.88 | 13.54 | 72.68 | 23.78 |
| Panicle length | 23.53 ±1.77 | 20.05-27.32 | 11.74 | 7.27 | 38.33 | 9.27 |
| Spikelets per panicle | 144.19 ±10.15 | 103.27-192.97 | 19.75 | 17.76 | 80.93 | 32.93 |
| 1000-grain weight | 20.77 ±0.96 | 16.17-26.46 | 12.75 | 11.43 | 80.34 | 21.10 |
| Grain yield per plant | 17.13 ±1.11 | 9.13-26.19 | 18.89 | 16.28 | 74.21 | 28.82 |

Heritability estimates serve as an anticipating tool to quantify the accuracy of phenotypic values. For a given character, greater heritability thus aids in efficient selection. High heritability was observed for the traits *viz;* days to 50% flowering (95.14%), days to 75% maturity (93.12%), spikelets per panicle (80.93%) and 1000-grain weight (80.34%). High heritability suggests that these traits are minimally affected by environmental factors, making selection for their improvement potentially more effective based only on the phenotypic expression of these traits. Low heritability was shown by only one trait *i.e*., panicle length (38.33%) suggesting significant environmental influence on the expression of this particular trait. Research findings of Tuwar *et al.*, (2013), Srivastava *et al.,* (2017), Srujana *et al.,* (2017) and Tiwari *et al.,* (2019) provides additional support to the findings of the present investigation.

Genetic advance in conjunction with heritability would give a more reliable index of selection value (Johnson *et al.,* 1955). Genetic advance was highest for spikelets per panicle (32.93%) followed by grain yield per plant (28.82%), effective tillers per plant (23.78%) and 1000-grain weight (21.10%). The high value of genetic advance indicated that the inheritance of these traits is under the influence of additive genes, suggesting selection would be effective and beneficial for improving these traits. The knowledge of genetic variability, heritability and genetic advance aids in anticipating the potential genetic gain in subsequent generations when selection methods are used to improve the specific traits (Saha *et al.,* 2019). High heritability coupled with high genetic advance was observed for spikelets per panicle and 1000-grain weight indicating that the heritability was due to additive gene effects making selection potentially effective for given traits.

**Correlation analysis**

Correlation analysis revealed significant associations among yield along with its component traits at both the genotypic and phenotypic levels (**Table 3**) offering insights into associations among yield and component traits that may guide effective selection. Grain yield showed correlations that were strongly positive for effective tillers for each plant (r = 0.992 genotypic; 0.950 phenotypic), for panicle length (r = 0.989; 0.854), for spikelets per panicle (r = 0.988; 0.956), and for 1000-grain weight (r = 0.757; 0.652) suggesting that these traits contribute to total grain yield and can function as reliable indices for selection. Grain yield exhibited negative correlation to plant height (r = –0.795 genotypic; –0.670 phenotypic), this suggests that taller genotypes are potentially less efficient for yield performance and for yield-related traits, shorter plants are more favourable. Effective tillers per plant correlated positively to panicle length (r = 0.987; 0.895), spikelets per panicle (r = 0.980; 0.938) and 1000-grain weight (r = 0.743; 0.581) emphasizing role of tillering in improving grain productivity. Association studies indicated that simultaneous selection will be useful for these traits with respect to yield improvement. Similar kind of association was revealed by Bose *et al.,* (2024), Billa *et al*., (2024), Prajapati *et al.,* (2022) and Dinesh *et al.,* (2023).

**Table 3: Estimates of genotypic (G) and phenotypic (P) correlation coefficients among yield and its related traits**

| Traits | Correlation coefficient | Days to 75% maturity | Plant height | Effective tillers per plant | Panicle length | Spikelets per panicle | 1000-grain weight | Grain yield per plant |
|---|---|---|---|---|---|---|---|---|
| Days to 50% flowering | **G** | 0.987* | -0.137 | -0.183 | -0.118 | -0.117 | -0.006 | -0.090 |
| | **P** | 0.979* | -0.091 | -0.138 | -0.043 | -0.095 | 0.020 | -0.081 |
| Days to 75% maturity | **G** | | -0.149 | -0.166 | -0.110 | -0.115 | 0.004 | -0.087 |
| | **P** | | -0.088 | -0.114 | -0.038 | -0.092 | 0.054 | -0.077 |
| Plant height | **G** | | | -0.833* | -0.979* | -0.844* | -0.763* | -0.795* |
| | **P** | | | -0.623* | -0.534* | -0.658* | -0.565* | -0.670* |
| Effective tillers per plant | **G** | | | | 0.987* | 0.980* | 0.743* | 0.992* |
| | **P** | | | | 0.895* | 0.938* | 0.581* | 0.950* |
| Panicle length | **G** | | | | | 0.972* | 0.912* | 0.989* |
| | **P** | | | | | 0.862* | 0.528* | 0.854* |
| Spikelets per panicle | **G** | | | | | | 0.739* | 0.988* |
| | **P** | | | | | | 0.585* | 0.956* |
| 1000-grain weight | **G** | | | | | | | 0.757* |
| | **P** | | | | | | | 0.652* |

### Path coefficient analysis

Path coefficient analysis revealed the magnitude and direction of both direct and indirect effects of yield-related traits on grain yield per plant at genotypic and phenotypic levels. The association among phenotypic characters and their effect on yield is highly beneficial for selecting desired lines that can integrated in breeding programme in later generations. Perusal of the data revealed that at genotypic level, spikelets per panicle (1.194) exhibited the highest positive direct effect on grain yield, followed by plant height (0.208), 1000-grain weight (0.180), effective tillers per plant (0.172), days to 75% maturity (0.056), and days to 50% flowering (0.020), whereas panicle length showed a negative direct effect (–0.303). Various traits also contributed indirectly to grain yield, with effective tillers per plant showing high positive indirect effects via spikelets per panicle (1.171) and 1000-grain weight (0.134), and panicle length contributing indirectly through spikelets per panicle (1.169), effective tillers (0.170), and 1000-grain weight (0.164) suggesting that the direct selection for these traits will lead to overall improvement in grain yield per plant (**Table 4**). The significant negative correlation of plant height with grain yield per plant was due to high negative indirect effect *via* spikelets per panicle at genotypic level and high negative indirect effect *via* effective tillers per plant at phenotypic level. At genotypic level, positive correlation of panicle length with grain yield per plant was due to high indirect effect of spikelets per panicle and at phenotypic level, *via* high indirect effect of effective tillers per plant. Positive direct effects of selected traits on grain yield observed in the present experiment are in accordance with Priya *et al.,* (2017), Francis *et al.,* (2018), Nithya *et al.,* (2021), Chavan *et al.,* (2022) and Goud *et al.,* (2022).

**Table 4: Estimates of genotypic and phenotypic path coefficients among yield and its related traits**

| Traits | Correlation coefficient | Days to 50% flowering | Days to 75% maturity | Plant height | Effective tillers per plant | Panicle length | Spikelets per panicle | 1000-grain weight | Grain yield per plant |
|---|---|---|---|---|---|---|---|---|---|
| Days to 50% flowering | **G** | **0.020** | 0.055 | -0.028 | -0.032 | 0.036 | -0.140 | -0.001 | -0.090 |
| | **P** | **0.330** | -0.305 | 0.001 | -0.071 | 0.003 | -0.042 | 0.003 | -0.081 |
| Days to 75 % maturity | **G** | 0.020 | **0.056** | -0.031 | -0.029 | 0.033 | -0.137 | 0.001 | -0.087 |
| | **P** | 0.323 | **-0.311** | 0.001 | -0.059 | 0.002 | -0.041 | 0.007 | -0.077 |
| Plant height | **G** | -0.003 | -0.008 | **0.208** | -0.144 | 0.296 | -1.007 | -0.137 | -0.795* |
| | **P** | -0.030 | 0.027 | **-0.015** | -0.321 | 0.035 | -0.294 | -0.072 | -0.670* |
| Effective tillers per plant | **G** | -0.004 | -0.009 | -0.173 | **0.172** | -0.299 | 1.171 | 0.134 | 0.992* |
| | **P** | -0.046 | 0.035 | 0.009 | **0.515** | -0.058 | 0.420 | 0.074 | 0.950* |
| Panicle length | **G** | -0.002 | -0.006 | -0.203 | 0.170 | **-0.303** | 1.169 | 0.164 | 0.989* |
| | **P** | -0.014 | 0.012 | 0.008 | 0.461 | **-0.065** | 0.385 | 0.067 | 0.854* |
| Spikelets per panicle | **G** | -0.002 | -0.006 | -0.175 | 0.169 | -0.324 | **1.194** | 0.133 | 0.988* |
| | **P** | -0.031 | 0.029 | 0.010 | 0.484 | -0.056 | **0.447** | 0.074 | 0.956* |
| 1000-grain weight | **G** | 0.000 | 0.000 | -0.158 | 0.128 | -0.276 | 0.883 | **0.180** | 0.757* |
| | **P** | 0.007 | -0.017 | 0.008 | 0.299 | -0.034 | 0.261 | **0.127** | 0.652* |

## Conclusion

In summary, the results of this investigation indicated that effective tillers per plant, panicle length, spikelets per panicle and 1000-grain weight could be considered as critical criteria for yield improvement in segregating generations of rice. The study exhibited high genetic variation in the $F_2$ population from *indica* × *japonica* crosses for grain yield and its component traits, suggesting a broad range of opportunity for selection and genetic enhancement. High heritability in association with high genetic advance for characters like spikelets per panicle and 1000-grain weight supports the dominance of additive gene action, which renders them suitable candidates for early generation selection. Correlation and path coefficient analyses indicated that effective tillers per plant, spikelets per panicle, panicle length, and 1000-grain weight had significant positive association and direct or indirect effects on grain yield, making them important yield-contributing traits. The results suggest that selection on these identified traits in segregating populations can be extremely effective in separating transgressive segregants with superior yield potential. The outcome of this research offers a useful basis for future breeding programs to develop high-yielding, climate-resistant rice varieties through strategic hybridization and selection.

## References

Al-Jibouri HA, Miller PA and Robinson HF. 1958. Genotypic and environment variances and covariances in upland cotton cross of interspecific origin. *Agronomy Journal*, 50(10): 633-636.

Begna T and Teressa T. 2024. Genetic variability and its benefits in crop improvement: A review. *Middle East Journal of Agriculture Research*, 13(01): 128-136.

Billa SC, Haritha T, Krishna VB, Swapna M and Tushara M. 2024. Character association studies for yield, nutritional and cooking quality characters in coloured rice (*Oryza sativa* L.). *Journal of Rice Research,* 17(1): 65-71.

Bose CGS, Krishna Veni B, Rani Ch, Tushara M and Ramesh D. 2024. Genetic parameters and association studies for yield and grain quality traits in rice genotypes derived from distant crosses. *Journal of Rice Research,* 17(1): 57-64.

Burton GW and De Vane EH. 1953. Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicated colonal material. *Agronomy Journal*, 45(10): 478-481.

Chahota RK, Kishore N, Dhiman KC, Sharma TR, Sharma SK. 2007. Predicting transgressive segregants in early generation using single seed descent method derived micro-macrosperma gene pool of lentil. *Euphytica,* 156: 305-310.

Chavan BR, Dalvi VV, Kunkerkar RL, Mane AV and Gokhale NB. 2022. Study of correlation and path analysis in aromatic rice genotypes (*Oryza sativa* L.). *The Pharma Innovation Journal*, 11(2): 1704-1707.

Choi HS and Jung SK. 2018. Review of various issues and productivity of organic rice paddy in South Korea. *Research on Crops*, 19(1): 28-33.

Dewey DR and Lu KH. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal,* 51(9): 515-518.

Dinesh K, Devi MS, Sreelakshmi C and Paramasiva I. 2023. Exploring the genetic diversity for yield and quality traits in indigenous landraces of rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding,* 14(2): 502-510.

El-Malky MM and Al-Dahej MI. 2023. Assessment of inbreeding depression genetic variability and genetic diversity in rice (*Oryza sativa* L.) based on agro-morphological traits. *Fresenius Environmental Bulletin,* 32(4): 2067-2077.

Francis N, Packiaraj D, Geethanjali S and Hemaprabha K. 2018. Correlation and path coefficient analysis for yield contributing characters in rice (*Oryza sativa* L.) cultivars. *International Journal of Current Microbiology and Applied Science,* 7(06): 2292-2296.

Goud GB, Naik DS, Fiyaz RA, Azam MM, Reddy SN and Naik BB. 2022. Phenotypic correlation between morphological and yield related traits of rice (*Oryza sativa* L.). *International Journal of Agriculture, Environment and Biotechnology,* 15(Special Issue): 515-520.

Gupta H, Purushottam GY, Yadav SK, Singh S and Kumar S. 2022. Genetic variability, heritability and genetic advance for yield and its related traits in rainfed upland rice (*Oryza sativa* L.) genotypes. *The Pharma Innovation Journal*, 11(2): 2520-2524.

Johnson HW, Robinson HF and Comstock RE. 1955. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal,* 47(7): 314-318.

Khan M. 2018. Evaluation of various rice (*Oryza sativa* L.) genotypes for yield and yield characters under agro ecological conditions of Peshawar. *Advances in Plants and Agriculture Research*, 8(6): 491-494.

Kurmanchali M, Kurmanchali N, Kukreti A, Sihag N, Chaudhary H and Karnwal MK. 2019. Study of genetic variability, heritability and genetic advance for various yield attributing and quality traits in basmati rice (*Oryza sativa* L.). *International Journal of Chemical Sciences,* 7(1): 2486-2489.

Nithya N, Beena R, Abida PS, Sreekumar J, Stephen R, Jayalekshmi VG, Manju RV and Viji MM. 2021. Genetic diversity and population structure analysis of bold type rice collection from Southern India. *Cereal Research Communications,* 49: 311-328.

Panse VG and Sukhatme PV. 1985. Statistical Methods for Agricultural Workers. ICAR, New Delhi.

Prajapati MR, Bala M, Patel VP, Patel RK, Sushmitha US, Kyada AD, Patel DP, Pranati J and Kumar SB. 2022. Analysis of genetic variability and correlation for yield and its attributing traits in $F_2$ population of rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding,* 13(3): 983-990.

Priya CHS, Suneetha Y, Babu DR and Rao VS. 2017. Inter-relationship and path analysis for yield and quality characters in rice (*Oryza sativa* L.). *International Journal of Science, Environment and Technology,* 6(1): 381-390.

Rachappanavar V. 2017. Morphological and molecular characterization of traditional and improved germplasm of paddy cultivated in Himachal Pradesh. M.Sc. Thesis, p 172. Department of Genetics and Plant Breeding, CSK Himachal Pradesh KrishiVishvavidyalaya, Palampur, India

Saha SR, Hassan L, Haque MA, Islam MM and Rasel M. 2019. Genetic variability, heritability, correlation and path analyses of yield components in traditional rice (*Oryza sativa* L.) landraces: Variability and traits association in rice. *Journal of the Bangladesh Agricultural University*, 17(1): 26-32.

Srivastava N, Babu GS, Singh ON, Verma R, Pathak SK, Behra M, Jena D and Chanda M. 2017. Genetic variation, heritability and diversity analysis of exotic upland rice (*Oryza sativa* L.) germplasms based on quantitative traits. *The Pharma Innovation Journal,* 6(12): 316-320.

Srujana G, Suresh BG, Lavanya GR, Ram BJ and Sumanth V. 2017. Studies on genetic variability, heritability and genetic advance for yield and quality components in rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry,* 6(4): 564-566.

Surjaye N, Singh Y, Singh SK, Rahangdale S and Mehta AK. 2022. Genetic variability, correlation and path coefficient study for various yield and quality traits in NPT lines of rice (*Oryza sativa* L.). *Environment and Ecology,* 40(1): 115-122.

Tiwari DN, Tripathi SR, Tripathi MP, Khatri N and Bastola BR. 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. https://doi.org/10.1155/2019/5975901.

Tuwar AK, Singh SK, Sharma A and Bhati PK. 2013. Appraisal of genetic variability for yield and its component characters in rice (*Oryza sativa* L.). *Biolife,* 1(3): 84-89.

United States Department of Agriculture (USDA). 2023. Commodity Intelligence Report, United States Development Agriculture, Foreign Agriculture Service. http://www.fas.usda.gov.