**Genetic Analysis of Grain Yield and its Associated traits in Rice (*Oryza sativa* L*.*)**

**ABSTRACT**

In this current study, a comprehensive examination of 72 rice germplasm from the germplasm collection was conducted. Notable checks, Sarjoo-52, NDR-2065, and MTU-7029, exhibited a broad spectrum of variations in multiple traits during the kharif season of 2022. The assessment, conducted at CRS Masodha of Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya, (U.P.). The parameters under scrutiny included days to 50% flowering, days to maturity, plant height, panicle length, number of productive tillers per plant, flag leaf area, fertile spikelets per panicle, spikelet fertility percentage per panicle, biological yield, harvest index, 1000-grain weight, and grain yield. The resulting data were utilized for mean estimation, range determination, least significant differences, correlation analysis, path-coefficients, and genetic divergence exploration. Remarkably, the genotype Lajkulired (53.30), followed closely by Pancham (45.963) and Lakrawa (44.540), demonstrated the highest grain yield per plant. These particular lines showcase promising potential as parental candidates in hybridization programs aiming for the development of high-yielding rice varieties. The close association-ship between grain yield per plant, biological yield per plant, and the number of productive tillers per plant. Path analysis highlighted biological yield per plant and harvest index as major contributors directly influencing grain yield per plant. Additionally, flag leaf area (cm2), panicle length (cm), and the number of productive tillers per plant emerged as crucial indirect yield components associated with biological yield.

**Keywords:** Genetic variability, path analysis, correlation analysis, heritability, rice

**Introduction**

Rice, scientifically known as *Oryza sativa* L., stands as a paramount global sustenance, feeding approximately 40% of the world's population. The pivotal role of rice is especially pronounced in developing countries, where around 90% of its cultivation and consumption occurs (Hashim *et al*., 2024). Archaeological traces of Indian rice cultivation trace back to 1500-1000BC, unveiling its historical significance. Although 42 countries contribute to rice production globally, the primary epicenters are unmistakably China and India. The versatile growth of rice spans varied agro-climatic conditions, from elevated terrains to lowland deltas, covering latitudes from 53°N to 35°S. A staggering 60% of dietary intake in South-East Asia and approximately 35% in East and South Asia is derived from rice. Nations like Bangladesh, Cambodia, Indonesia, Laos, Myanmar, Thailand, and Vietnam exhibit the highest per capita rice consumption, emphasizing its cultural centrality (Kenneth and Kriemhild, 2000). Over the past half-century, the global rice area expanded by 1.37 times, while yield soared threefold and productivity surged 2.3 times. Notably, China stands as the foremost rice producer, generating nearly 125 mt, closely followed by India, contributing a quarter of Asia's total production (Moya *et al*., 2004). The effectiveness of future rice improvement programs hinges on the judicious use of diverse germplasm from across the globe (Gomez-Galera *et al*., 2010). In the context of Indian agriculture, rice plays a pivotal role, serving as the staple food for over 70% of the nation's population and more than half of the global populace. India's notable rice production has propelled it to the status of the fourth-largest rice exporter globally (World meters, 2020). West Bengal, aptly known as the "rice bowl of India," emerges as the leading rice producer in the country, solidifying its position in international trade. As we navigate the intricate web of agriculture and sustenance, rice remains a linchpin in our global food landscape (FAOSTAT, 2020). The present investigation aims to assess to genetic variability present in rice genotypes which can further be used as parents in breeding programs. The degree of genetic diversity among genotypes, which is based on multivariate analysis developed by mahalanobis (Singh *et al.*, 2024). This analysis information about diversity both intra and intercluster level and genotypes drawn from widely divergent clusters.

**Materials and Methods**

In this experiment 72 rice germplasm, along three checks - Sarjoo-52, MTU-7029, and NDR-2065 - within an Augmented Block Design at Crop Research Station Masodha, Ayodhya. This diverse set of genotypes exhibited a rich tapestry of variations in various agronomical and morphological traits. The experimental field was divided into 8 blocks, each housing 12 plots. Within each block, 9 genotypes and 3 checks are plotted. Each genotype, organized into three rows of 3-meter length, maintained a spacing of 10 cm between plant to plant and 20 cm between row to row. Data collection encompassed key parameters such as days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, panicle length (cm), flag leaf area (cm­­2), number of fertile spikelets per panicle, spikelet fertility (%), biological yield per plant (g), harvest index (%), 1000-grain weight (g), and grain yield per plant (g). The analysis of variance, following Federer (1956), scrutinized diverse traits in the augmented design. Variability estimation for different characters aligned with Burton *et al.*, (1953). Broad-sense heritability (h2) employed Hanson *et al*. (1956), while the expected genetic advance (GA) relied on Johnson *et al*. (1955). Correlations between characters were assessed in line with Searle's (1961) methodology. Path coefficient analysis following Dewey and Lu's (1959) approach unveiled insights into the intricate relationships.

“hidden hunger” is caused by the

**Results and Discussion**

Analysis of variance (Table 2) described the distinctive outcomes derived from the scrutiny of augmented design, encompassing all 12 traits. Significance echoes through the variation attributed to blocks, with marked or highly significant implications for all the characters examined-except for 1000- grain weight. Notably, the check varieties reveal a tapestry of significance, pronounced or highly significant disparities across all scrutinized characters -except in the realm of Spikelet fertility (%). This exploration sheds light on the intricate interplay of variables, unveiling a nuanced spectrum of statistical significance. Also, the similar finding, Analysis of variance revealed that wide range of variability was observed among 36 genotypes of rice for all the traits except number of productive tillers per m2 under study (Sreedhar et al. 2017). In the present investigation we found that similar results for twelve traits. Analysis of variance (ANOVA) revealed significant differences among the genotypes for all the studied characteristics (Dey et al. 2019).

Estimation of Genetic variability, heritability and genetic advance exploring the heritability and genetic advancements in the realm of twelve distinct characters, a captivating landscape of genetic dynamics emerges. Noteworthy instances of broad-sense heritability exceeding 70% were witnessed in fertile spikelets per panicle (97.57), biological yield per plant (94.97), and 1000-grain weight (92.29). Characters such as Panicle length (25.55) and Number of productive tillers/plant (02.28) displayed a comparatively lower heritability, lingering below the 50% mark. Venturing into the realm of genetic advancement, striking instances of significant progress exceeding 15% unfolded in Biological yield per plant (g). On the flip side modest strides, falling below the 15% benchmark characterized Harvest index % (11.98) and Days to 50% flowering (10.82). This nuanced exploration delves into the genetic intricacies shaping these traits, underscoring the varying degrees of their responsiveness to selective pressures. In a broader context, the phenotypic coefficient of variation showcased a tendency to outpace its genotypic counterpart for all characters, with conspicuous disparities surpassing 20%. Notable instances include Biological yield per plant (29.32g) for GCV and (30.08g) for PCV, as well as Grain yield per plant (28.60) for GCV and (31.29) for PCV. In the middle ground, characters like 1000-grain weight (g) exhibited a moderate estimate (10-20%) for both GCV (12.42) and PCV (12.93). This intricate dance of genetic and phenotypic variations adds depth to our understanding of the diverse traits under scrutiny. The same results found that, high to moderate phenotypic and genotypic coefficient of variation were observed for number of panicles per plant and number of tillers per plant, grain yield per plant, test weight and flag leaf length, indicating that these traits are most probably under the control of additive gene action and hence these traits can be fixed by proper selection (Rajasekhar et al.). Eleven rice hybrids including two check varieties were evaluated to approximate their genetic variability, heritability and genetic advance for ten quantitative traits. The genotypes G3 and G6 were selected as high response superior promising rice hybrids for achievable yield advantage 49% and 23%, respectively over best check varieties (Lipi et al. 2020).

The correlation coefficient reveals a captivating narrative within the realm of rice plant dynamics. The spotlight shines brightly on grain yield per plant, intricately linked with biological yield per plant (0.678), Number of productive tillers per plant (0.299), Flag leaf area (0.271), 1000-grain weight (0.265), Panicle length (0.252), and Number of fertile spikelets per panicle (0.216). However, a non-significant positive correlation weaves through Spikelet fertility % (0.104) and Harvest index (0.042). On the flip side, a compelling negative correlation takes center stage with Days to maturity (-0.265), while non-significant threads intertwine with Days to 50% flowering (-0.037) and Plant height cm (0.121). Days to maturity, a pivotal character in this botanical tale, engages in a highly significant and positive dance with Days to 50% flowering (0.651). Biological yield per plant finds harmony with Flag leaf area (0.386), panicle length (0.354), Number of productive tillers per plant (0.289), Plant height (0.237), and 1000-grain weight, forming a symphony with biological yield per plant (0.347), Days to 50% flowering (0.253), and Spikelet fertility %. This intricate dance of correlations further unfolds with Number of fertile spikelets per panicle (0.305), panicle length (0.261), and Harvest index (0.278). Panicle length and Flag leaf area engage in a dynamic interplay with plant height (0.227) and the number of productive tillers per panicle.

Path coefficient analysis, utilizing the simple correlations among the twelve’s traits, was conducted to analyze the direct and indirect effects on grain yield per plant as presented in table 4. The direct and indirect effects elegantly revealed in Table 4, where biological yield per plant takes the lead with a formidable direct effect of 0.7665. Harvest index follows suit with a noteworthy direct effect of 0.3246, accompanied by the impactful contributions of days to 50% flowering (0.2413), number of productive tillers per plant (0.1219), and panicle length (0.1210), all exerting a highly positive and significant influence on grain yield per plant. Indirect effects, Flag leaf area (0.2959 cm­­2), panicle length (0.2714), 1000-grain weight (0.2660), and number of productive tillers per plant (0.2215) weave a symphony of positive influences on grain yield per plant. However, days to maturity (-0.3037) and plant height (-0.1661) showed considerable negative direct effects on the grain yield per plant. Days to 50% flowering (-0.1357) and days to maturity (-0.1211) follow suit, exhibiting considerable negative indirect effects. The path analysis studies revealed that kernel length was the major contributor for grain yield plant-1 followed by plant height, spikelet fertility, number of grains per panicle, 1000 grain weight. These characters showed direct positive effects for grain yield plant. From the study it can be concluded that the above characters can be used directly as the selection criteria in any rice yield improvement breeding programs (Vennela *et al*. 2021).

**Conclusion:**

The high broad-sense heritability (˃70%) identified in crucial traits, such as fertile spikelets per panicle, biological yield per plant, and 1000-grain weight, the underscores the potential for diverse breeding programs. The significant variation observed in genotypes of most traits highlights the abundant genetic diversity available in future breeding programs. Analysis of correlation and pathway coefficients showed that biological yield per plant, and weight of 1000 grains not only had a positive association with grain yield, but also had a strong direct effect on yield improvement strategies. Conversely, characteristics such as the day to maturation showed a negative link to grain yield. This illustrates a compromise that must be taken into consideration in the development of early high-wave varieties.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **D.F.** | **Days to 50% flowering** | **Days to maturity** | **Plant height (cm)** | **No. of productive tillers/plant** | **Panicle length (cm)** | **Leaf area index (cm2)** | **Fertile Spikelets/ panicle** | **Spikelets fertility %** | **Biological yield / plant (g)** | **Harvest index %** | **1000- grain weight (g)** | **Grain yield /plant** |
| **Block (ignoring Treatments)** | 7 | 192.208  \*\* | 97.423\*\* | 217.047\* | 36.718 | 12.565\* | 41.035\*\* | 858.363\*\* | 70.374\* | 339.624\*\* | 82.555\* | 5.365\*\* | 149.159\*\* |
| **Treatment (eliminating Blocks)** | 74 | 41.065\*\* | 49.440\*\* | 258.721\*\* | 21.017 | 9.390\* | 53.371\*\* | 731.927\*\* | 128.317\*\* | 334.691\*\* | 68.808\* | 11.604\*\* | 71.904\*\* |
| **Varieties** | 71 | 53.252  \*\* | 56.590  \*\* | 258.731  \*\* | 18.482 | 5.258 | 36.920  \*\* | 840.456  \*\* | 101.321  \*\* | 226.025  \*\* | 48.482 | 11.325\*\* | 75.467\*\* |
| **Checks** | 2 | 165.167  \*\* | 124.625  \*\* | 201.988 | 57.093 | 133.856  \*\* | 525.409  \*\* | 226.255  \*\* | 1182.671  \*\* | 189.742  \*\* | 209.688  \*\* | 40.526\*\*\* | 134.697\*\* |
| **Checks vs. Varieties** | 1 | 253.125  \*\* | 28.125 | 1429.342  \*\* | 223.979  \*\* | 123.114\*\* | 531.326  \*\* | 27.720 | 266.843  \*\* | 10601.260  \*\* | 1732.103  \*\* | 6.805\*\* | 673.047\*\* |
| **ERROR** | 14 | 11.119 | 7.577 | 65.832 | 17.963 | 3.689 | 5.511 | 16.536 | 22.507 | 9.258 | 22.242 | 0.715 | 10.339 |

**Table 1:** Analysis of variance of augmented design for 12 characters in rice germplasm

\*, and \*\* Significant at 5% and 1% level, respectively

**Table 2:** Estimation of Mean, Range, Heritability, genetic advance and coefficient of variability analysis in Rice

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Characters** | **Mean** | **Min** | **Max** | **GCV (%)** | **PCV (%)** | **Heritability (%)** | **GA % Mean** |
| **Days to 50% flowering** | 96.14 | 78.20 | 111.20 | 6.05 | 6.97 | 75.35 | 10.82 |
| **Days to maturity** | 119.07 | 101.21 | 136.88 | 5.27 | 5.76 | 83.92 | 9.96 |
| **Plant height (cm)** | 116.91 | 85.47 | 170.47 | 10.70 | 12.76 | 70.27 | 18.48 |
| **No. of productive tillers/plant** | 11.93 | 04.55 | 25.20 | 5.49 | 36.36 | 02.28 | 1.70 |
| **Panicle length (cm)** | 24.36 | 19.40 | 31.04 | 04.83 | 09.17 | 25.55 | 04.82 |
| **Leaf area index (cm2)** | 25.24 | 12.48 | 39.09 | 20.13 | 22.19 | 82.14 | 37.55 |
| **Fertile Spikelets/ panicle** | 90.34 | 29.21 | 183.96 | 28.55 | 28.90 | 97.57 | 58.10 |
| **Spikelets fertility %** | 79.10 | 57.68 | 100.33 | 10.06 | 11.70 | 73.86 | 17.81 |
| **Biological yield / plant (g)** | 46.07 | 19.83 | 90.15 | 29.32 | 30.08 | 94.97 | 58.86 |
| **Harvest index %** | 54.83 | 38.99 | 70.60 | 08.33 | 11.93 | 48.77 | 11.98 |
| **1000- grain weight (g)** | 23.56 | 16.87 | 32.22 | 12.42 | 12.93 | 92.29 | 24.59 |
| **Grain yield /plant** | 25.58 | 12.15 | 53.30 | 28.60 | 31.29 | 83.56 | 53.86 |

**Table 3:** Simple correlation coefficients among different characters in rice germplasm

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Traits | Days to maturity | Plant height(cm) | No. of Productive Tillers/plant | Panicle length (cm) | Flag leaf area(cm2) | No. of fertile spikelets / panicle | Spikelets fertility (%) | Biological yield /plant(g) | Harvest Index(%) | 1000-grain weight(g) | Grain yield/plant(g) |
| Days to 50% flowering | 0.651\*\* | -0.101 | -0.010 | -0.383\*\* | -0.134 | -0.050 | -0.036 | -0.177 | 0.278\*\* | 0.253\* | -0.037 |
| Days to maturity |  | -0.075 | -0.068 | -0.184 | -0.173 | -0.047 | -0.014 | -0.158 | 0.081 | -0.018 | -0.265\*\* |
| Plant height(cm) |  |  | -0.070 | 0.227\* | 0.170 | -0.006 | -0.022 | 0.237\* | -0.480\*\* | 0.115 | -0.121 |
| No.of Productive Tillers/plant |  |  |  | 0.030 | 0.213\* | 0.003 | -0.140 | 0.289\*\* | -0.241\* | 0.082 | 0.299\*\* |
| Panicle length (cm) |  |  |  |  | 0.073 | 0.088 | 0.261\* | 0.354\*\* | -0.249\* | -0.182 | 0.252\* |
| Flag leaf area(cm2) |  |  |  |  |  | 0.149 | -0.232\* | 0.386\*\* | -0.214\* | 0.188 | 0.271\*\* |
| No.of fertile spikelets / panicle |  |  |  |  |  |  | 0.305\*\* | 0.141 | 0.083 | -0.216\* | 0.216\* |
| Spikelets fertility (%) |  |  |  |  |  |  |  | 0.022 | 0.115 | -0.171 | 0.104 |
| Biological yield /plant(g) |  |  |  |  |  |  |  |  | -0.456\*\* | 0.347\*\* | 0.678\*\* |
| Harvest index (%) |  |  |  |  |  |  |  |  |  | -0.083 | 0.042 |
| 1000-grain weight(g) |  |  |  |  |  |  |  |  |  |  | 0.265\*\* |

\*, and \*\* Significant at 5% and 1% level, respectively.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Traits | Days to 50% flowering | Days to maturity | Plant height(cm) | No. of Productive Tillers/plant | Panicle length (cm) | Flag leaf area(cm2) | No. of fertile spikelets / panicle | Spikelets fertility (%) | Biological yield /plant(g) | Harvest Index (%) | 1000-grain weight(g) | Grain yield/plant(g) |
| Days to 50% flowering | **0.2413** | -0.1977 | 0.0168 | -0.0012 | -0.0464 | -0.0018 | -0.0030 | -0.0008 | -0.1357 | 0.0902 | 0.0012 | -0.037 |
| Days to maturity | 0.1571 | **-0.3037** | 0.0125 | -0.0083 | -0.0223 | -0.0023 | -0.0028 | -0.0003 | -0.1211 | 0.0263 | -0.0001 | -0.265\*\* |
| Plant height(cm) | -0.0244 | 0.0228 | **-0.1661** | -0.0085 | 0.0275 | 0.0022 | -0.0004 | -0.0005 | 0.1817 | -0.1558 | 0.0005 | -0.121 |
| No. of Productive Tillers/plant | -0.0024 | 0.0207 | 0.0116 | **0.1219** | 0.0036 | 0.0028 | 0.0002 | -0.0031 | 0.2215 | -0.0782 | 0.0004 | 0.299\*\* |
| Panicle length (cm) | -0.0924 | 0.0559 | -0.0377 | 0.0037 | **0.1210** | 0.0010 | 0.0052 | 0.0057 | 0.2714 | -0.0808 | -0.0008 | 0.252\* |
| Flag leaf area(cm2) | -0.0323 | 0.0525 | -0.0282 | 0.0260 | 0.0088 | **0.0132** | 0.0088 | -0.0051 | 0.2959 | -0.0695 | 0.0009 | 0.271\*\* |
| No. of fertile spikelets / panicle | -0.0121 | 0.0143 | 0.0010 | 0.0004 | 0.0106 | 0.0020 | **0.0591** | 0.0067 | 0.1081 | 0.0269 | -0.0010 | 0.216\* |
| Spikelets fertility (%) | -0.0087 | 0.0043 | 0.0037 | -0.0171 | 0.0316 | -0.0031 | 0.0180 | **0.0219** | 0.0169 | 0.0373 | -0.0008 | 0.104 |
| Biological yield /plant(g) | -0.0427 | 0.0480 | -0.0394 | 0.0352 | 0.0428 | 0.0051 | 0.0083 | 0.0005 | **0.7665** | -0.1480 | 0.0016 | 0.678\*\* |
| Harvest Index (%) | 0.0671 | -0.0246 | 0.0797 | -0.0294 | -0.0301 | -0.0028 | 0.0049 | 0.0025 | -0.3495 | **0.3246** | -0.0004 | 0.042 |
| 1000-grain weight(g) | 0.0610 | 0.0055 | -0.0191 | 0.0100 | -0.0220 | 0.0025 | -0.0128 | -0.0037 | 0.2660 | -0.0269 | **0.0046** | 0.265\*\* |

**Table 4:** Path analysis for different characters on grain yield per plant in Rice germplasm

Residual effects = 0.5368

\*, and \*\* Significant at 5% and 1% level, respectively

Disclaimer (Artificial intelligence)

Option 1:

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

Option 2:

Author(s) hereby declare that generative AI technologies such as Large Language Models, etc. have been used during the writing or editing of manuscripts. This explanation will include the name, version, model, and source of the generative AI technology and as well as all input prompts provided to the generative AI technology

Details of the AI usage are given below:

1.

2.

3.

**References:**

Burton, J. A., Prim, R. C., & Slichter, W. P. (1953). The distribution of solute in crystals grown from the melt. Part I. Theoretical. *The journal of chemical physics*, 21(11), 1987-1991.

Dewey, D. R., and Lu, K. H. (1959). A Correlation and path co-efficient analysis of components of crested wheat grass seed production. *Agro. J*., 51:515-518.

Dey, P., Sahu, S., & Kar, R. K. (2019). Estimation of Phenotypic Coefficients of Variation (PCV), Genotypic Coefficients of Variation (GCV), Heritability and Genetic Gain for Yield and its Components in Rice Landraces of Odisha. *International Journal of Agriculture, Environment and Biotechnology*, 12(3), 181-185.

FAOSTAT (2020). <https://www.fao.org>

Federer, W. T. (1956). Augmented designs with one-way elimination of heterogeneity. *Biometrics*, 17(3), 447-473.

Gómez-Galera, S., Rojas, E., Sudhakar, D., Zhu, C., Pelacho, A. M., Capell, T., & Christou, P. (2010). Critical evaluation of strategies for mineral fortification of staple food crops. *Transgenic research*, *19*, 165-180.

Hansen, C., & Shrestha, J. N. B. (1997). Heritability and repeatability estimates for ewe productivity traits of three breeds under 8-month breeding cycles and artificial rearing of lambs. *Small Ruminant Research*, 24(3), 185-194.

Hashim, N., Ali, M. M., Mahadi, M. R., Abdullah, A. F., Wayayok, A., Kassim, M. S. M., & Jamaluddin, A. (2024). Smart farming for sustainable rice production: an insight into application, challenge, and future prospect. *Rice science*, 31(1), 47-61.

Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy journal*, 47(7):314-318.

Kenneth, F., & Kriemhild, C. O. (2000). The Cambridge world history of food.

Lipi, L. F., Hasan, M. J., Akter, A., Quddus, M. R., Biswas, P. L., Ansari, A., & Akter, S. (2020). Genetic variation, heritability and genetic advance in some promising rice hybrids.

Moya, P. F., Dawe, D., Pabale, D., Tiongco, M., Chien, N. V., Devarajan, S., ... & Wardana, P. (2004). The economics of intensively irrigated rice in Asia. *Increasing productivity of intensive rice systems through site-specific nutrient management*, *586*(100), 29.

Rajasekhar, J., Lavanya, G. R., Purushotham, G., & Kumar, D. P. Character Association and Path Coefficient Analysis in Upland Rice (Oryza sativa L.) for Grain Yield and Quality Characters.

Searle, S. R. (1961). Phenotypic, genotypic and environmental correlations. *Biometrics*, 17: 474- 480.

Singh, T., Singh, P. K., Yadav, R. K., Saxena, P., & Singh, S. (2024). Assessment of genetic variability, character association of yield related traits and genetic divergence study in rice (Oryza sativa L.). *International Journal of Plant & Soil Science*, *36*(9), 545-555.

Sreedhar, S. (2017). Studies on Variability, Heritability, Genetic Advance and Divergence for Yield and Yield Components in Various Maturity and Grain Type Groups of Rice (Oryza Sativa L.) Genotypes. *Bull. Env. Pharmacol. Life Sci*, 6(1), 467-474.

Vennela, M., Srinivas, B., Reddy, V. R., & Balram, N. (2021). Studies on correlation and path coefficient analysis in hybrid rice (Oryza sativa L.) for yield and quality traits. *International Journal of Bio-resource and Stress Management*, 12(5), 496-505.

Worldmeters (2020). Current world population, July 2020.info/worldometers population/ Accessed 11th July