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# Unravelling genetic variability and trait association studies in red sorghum (*Sorghum bicolor* L. Moench) genotypes

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**Abstract**
Sorghum (*Sorghum bicolor* L. Moench) is a significant crop known for its resilience, versatility, and nutritional value. The research aimed to enhance yield and nutritional quality through the assessment of genetic variability, heritability, correlations, and causal relationships among traits. Variance component analysis in the $F_2$ population of red sorghum genotypes from the cross between Paiyur 2 and IS 21731 revealed the influence of the environment on trait expression. High variability in flag leaf traits and single plant yield was observed. Traits such as plant height, stem girth, and flag leaf length exhibited high heritability and genetic advancement which indicated that these traits are influenced by additive genetic factors and are suitable for selection processes. Positive correlations were identified between single plant yield and traits like panicle weight and primary branches and hence selection based on these characteristics could directly contribute to improved yield in sorghum. Path analysis highlighted the direct and indirect effects of traits on grain yield with panicle weight emerging as a major driver. This study provided valuable insights into effective breeding strategies emphasizing traits such as panicle weight, primary branches, and seed index for enhancing both yield and nutritional quality in red sorghum genotypes.

**Keywords:** red sorghum, nutritional profiling, genetic variability, correlations

## INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench] popularly called as great millet, Indian millet, milo, durra or shallu holds its importance in the global agriculture scenario in being one of the most resilient, versatile and nutritionally valuable crops contributing to food security and sustainable development. It occupies the fifth position spanning worldwide production mainly after wheat, maize, rice and barley (Cuevas *et al.,*2014) with an area of 40.1 Mha and production of 61.36 MT (FAO, 2021). It is a diploid (2n = 2x = 20), annual cereal crop with high photosynthetic efficiency ($C_4$ plant) and having its roots in Africa (Vinodhini *et al.,* 2022). It is cultivated in an area of 4.38 Mha with a production of about 4.81MT in India and the country is also considered as the secondary centre of origin (Vavilov, 1951). In Tamil Nadu, it spans an area of 0.45 Mha with a production of 0.47 MT (TN Ag Stat, 2021).

Sorghum, being gluten-free is a potential candidate and a healthy alternative for wheat in addressing celiac disease, gluten sensitivity, and wheat allergy (Pezzali *et al.*, 2020). It is often labelled as ‘nutritious grain’ due to its impressive nutritional composition and health benefits (Aruna *et al.,* 2020). Among all the coloured

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sorghum, red sorghum holds significant importance due to its higher levels of antioxidants, diverse food and beverage applications, bioactive compounds, pest resistance, drought tolerance, and potential natural food colouring agent (Aruna and Cheruku, 2019).

Creating populations with diverse traits is crucial for enhancing plant varieties through more effective selection processes. Assessing the extent of genetic variation within segregating generations is essential for improving grain yield and related traits as well as understanding the potential genetic gains achievable through selection. Breeders can choose to select desirable genotypes early on or wait until advanced generations when progenies are nearly homozygous to carry out more intense selection (Savitha and Kumari, 2015). As sorghum grain yield is influenced by multiple genes and is quantitative in nature, selection criteria are based on yield and its related components.

A generation characterized by strong segregation and recombination is considered an ideal generation for implementing selective pressures. The essential prerequisite for enhancing and selecting elite genotypes among the segregating population is contributed by the genetic variability present in breeding material which is studied by the GCV, PCV, heritability and genetic gain for individual quantitative characters. Genetic diversity plays a pivotal role in plant breeding endeavors (Syukur *et al.*, 2010). The success of new variety breeding programs hinges on the presence of extensive genetic variation within the population as it increases the likelihood of attaining desired improvement in traits (Sushma *et al.*, 2020). The efficacy of selection in plant breeding is determined by the availability of abundant genetic diversity and substantial heritability (Sushma *et al.*, 2020). The level of association between characteristics holds significant importance, particularly in intricate and economically valuable attributes like crop yield. The correlation coefficient serves as a statistical metric employed to ascertain the extent of connection among multiple variables. The utilization of path coefficient analysis aids in devising suitable breeding strategies to develop superior-yielding genotypes. The present study was performed to investigate the variability present and association among different characters and their direct and indirect effects on yield in selected red sorghum genotypes.

## MATERIALS AND METHODS

The study was conducted in the summer season of 2023 at the Department of Millets, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu. The experimental materials comprised of $F_2$ population of the cross between red sorghum genotypes *viz.*, Paiyur 2 and IS 21731. The seeds of Paiyur 2 and IS 21731 (Parents) and their $F_1$ hybrid seeds were obtained from the Department of Millets. The $F_2$ population was grown in 11 rows, each of 6 m in length, with a spacing of 45 cm x 15 cm along with their parents. All the recommended crop management practices were followed throughout to maintain a healthy crop stand. The biometrical observations were recorded for 200 individual $F_2$ plants from the cross between Paiyur 2 and IS 21731 on traits *viz.*, plant height (cm), number of leaves, stem girth (cm), days to 50% flowering, days to maturity, flag leaf length (cm), flag leaf width (cm), leaf length (cm), leaf width (cm), panicle length (cm), panicle width (cm), panicle weight (g), number of primary branches, hundred seed weight (g), and grain yield per plant (g). Phenotypic and genotypic coefficients of variation were computed as per the formula given by Burton (1952). Heritability and genetic advance as percent were estimated as per the formulae outlined by Lush (1940) and Johnson *et al.*(1955) respectively. Analysis of the components of variance and heritability was carried out for each biometrical trait in MS Excel. Association study and path analysis were performed by using R software (package – corrplot) and TNAUSTAT respectively.

## RESULTS AND DISCUSSION

Estimation of variance components : Population diversity serves as the primary foundation for enhancing characteristics. Assessing the current range of variations stands as the initial stride in shaping any breeding initiative. Varied components such as Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), heritability ($h^2$), genetic advance, and Genetic Advance as percent of Mean (GAM) were computed for all the 15 quantitative traits and presented in **Table 1**. In the current investigation, the values obtained for phenotypic variances were greater than the corresponding genotypic variances across all the traits. These results suggest a low impact of the environment on the manifestation of the traits. Flag leaf length (27.90, 25.62), flag leaf width (25.83, 22.17) and single plant yield (25.22, 22.73) exhibited high GCV and PCV values (>20 %). This finding was supported by the findings of Subramanian *et al.* (2019). Consequently, a straightforward selection approach could be adopted to enhance these traits. Seed index (14.60, 13.58), number of leaves (12.53, 10.65), and plant height (17.27, 17.27) displayed a moderate level of GCV and PCV (10-20 %), as reported in the studies of Subhashini and Selvi (2019). The selection process for these traits was relatively limited which hindered the efficiency of the selection procedure. High PCV coupled with moderate GCV was observed in the case of leaf length, leaf width, stem girth, panicle length (Subhashini and Selvi*,* 2019), panicle width (Mulualem *et al.,*2018) and number of primary branches per panicle owing to substantial influence of the environmental on the trait was more.

The quantification of the population's responsiveness to selection is assessed through heritability in quantitative genetics. High heritability is evident in phenotypic traits which are more influenced by genetic factors than environmental ones (Hermanto *et al.*, 2017). Broad-sense heritability is characterized as the proportion of phenotypic variance linked to the combined impact of

**Table 1. Estimation of variability parameters for yield and yield components in red sorghum $F_2$ population of Paiyur 2 x IS 21731**

| S.No | Characters | Range | | Mean | Variance | | PCV (%) | GCV (%) | $h^2$ bs (%) | Genetic advance | GAM |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Minimum | Maximum | | Phenotypic | Genotypic | | | | | |
| 1 | Number of leaves | 6.00 | 13.00 | 8.70 | 1.19 | 0.86 | 12.53 | 10.65 | 72.27 | 1.62 | 18.66 |
| 2 | Plant height (cm) | 106.68 | 237.74 | 173.21 | 895.16 | 894.97 | 17.27 | 17.27 | 99.98 | 61.62 | 35.58 |
| 3 | Stem girth (cm) | 0.80 | 2.30 | 1.52 | 0.13 | 0.10 | 23.87 | 19.37 | 73.47 | 0.55 | 36.12 |
| 4 | Days to flowering (days) | 56.00 | 73.00 | 65.21 | 8.74 | 7.75 | 4.53 | 4.27 | 88.68 | 5.40 | 8.28 |
| 5 | Days to maturity (days) | 90.00 | 112.00 | 98.30 | 34.69 | 32.80 | 5.99 | 5.83 | 94.54 | 11.47 | 11.67 |
| 6 | Flag leaf length (cm) | 17.80 | 57.20 | 35.47 | 97.92 | 82.57 | 27.90 | 25.62 | 84.32 | 17.19 | 48.46 |
| 7 | Flag leaf width (cm) | 2.10 | 9.20 | 5.23 | 1.82 | 1.34 | 25.83 | 22.17 | 73.65 | 2.05 | 39.19 |
| 8 | Leaf length (cm) | 25.70 | 86.70 | 61.12 | 170.80 | 138.63 | 21.38 | 19.26 | 81.16 | 21.85 | 35.75 |
| 9 | Leaf width (cm) | 3.60 | 11.30 | 7.26 | 2.70 | 1.85 | 22.62 | 18.72 | 68.51 | 2.32 | 31.93 |
| 10 | Panicle length (cm) | 10.50 | 33.20 | 20.80 | 20.96 | 16.71 | 22.01 | 19.65 | 79.72 | 7.52 | 36.15 |
| 11 | Panicle width (cm) | 2.90 | 9.20 | 4.82 | 1.09 | 0.83 | 21.68 | 18.97 | 76.52 | 1.65 | 34.18 |
| 12 | Panicle weight (g) | 39.90 | 89.90 | 50.83 | 137.69 | 114.75 | 23.08 | 21.07 | 83.34 | 20.14 | 39.63 |
| 13 | Number of primary branches per panicle | 14.00 | 54.00 | 35.13 | 66.67 | 42.70 | 23.24 | 18.60 | 64.04 | 10.77 | 30.66 |
| 14 | Seed index (g) | 1.20 | 3.70 | 2.49 | 0.13 | 0.11 | 14.60 | 13.58 | 86.47 | 0.65 | 26.00 |
| 15 | Single plant yield (g) | 23.80 | 79.40 | 35.67 | 80.91 | 65.71 | 25.22 | 22.73 | 81.21 | 15.05 | 42.19 |

additive, dominance, and epistasis effects within the entire genotype (Falconer, 1960). A combination of notable heritability and considerable genetic advancement suggests a strong likelihood of the heritability being attributed to additive genetic effects. Broad-sense heritability spanned from 64.04% for number of primary branches per panicle to 99.98% for plant height, while the genetic advance, presented as a percentage of the mean, ranged from 8.28% for days to flowering to 48.46% for flag leaf length. In the study, heightened heritability and genetic advancement as a percentage of mean were detected among the majority of the assessed attributes, namely, plant height, stem girth, flag leaf length, flag leaf width, leaf length, leaf width, panicle length, panicle width, panicle weight, number of primary branches per panicle, seed index, and single plant yield. This underscores the promising viability of employing these traits for effective selection purposes. Traits demonstrating high GCV, heritability and GAM are primarily driven by additive factors. These traits serve as valuable selection criteria for enhancing yield. Heritability estimates offer a clear projection of the potential improvement achievable through selection.

Association study: Yield, a trait influenced by the interplay of multiple component traits, necessitates understanding their relationships and associations. This knowledge is vital for effective breeding programs aiming to enhance grain yield while improving related traits by improving multiple traits simultaneously. Associations can stem from pleiotropic gene effects, linkage, or a combination of both. Correlation studies uncover the connections between yield and contributing traits, aiding breeders in selecting and improving multiple characteristics simultaneously. Positive genetic correlation between desirable traits enables plant breeders to enhance both traits concurrently. However, a negative correlation between desirable traits hinders or prevents significant improvements in both traits. Thus, the correlation coefficient helps distinguish favourable associations for breeding from unfavourable ones (Falconer, 1981).In the studied $F_2$ population; correlation coefficients were computed for single plant yield and its component traits (**Table 2**).It could be clearly observed from the corrplot that, single plant yield exhibited a highly significant and positive correlation with panicle weight (0.81), number of primary branches (0.60), seed index (0.44), panicle length (0.43) leaf width (0.37), panicle width (0.32), flag leaf width (0.26), stem girth (0.39) and plant height. Also, a significant and positive correlation was observed for days to flowering (0.28) and flag leaf width (0.26) in relation to single plant yield. These findings were similar to those obtained by Birhan *et al.* (2020) and Nirosh *et al.* (2021) for plant height; Rini *et al.* (2022) for all the panicle-related traits (panicle weight, panicle length, panicle width) and stem girth. Chittapur and Biradar, (2015) for primary branches per panicle;

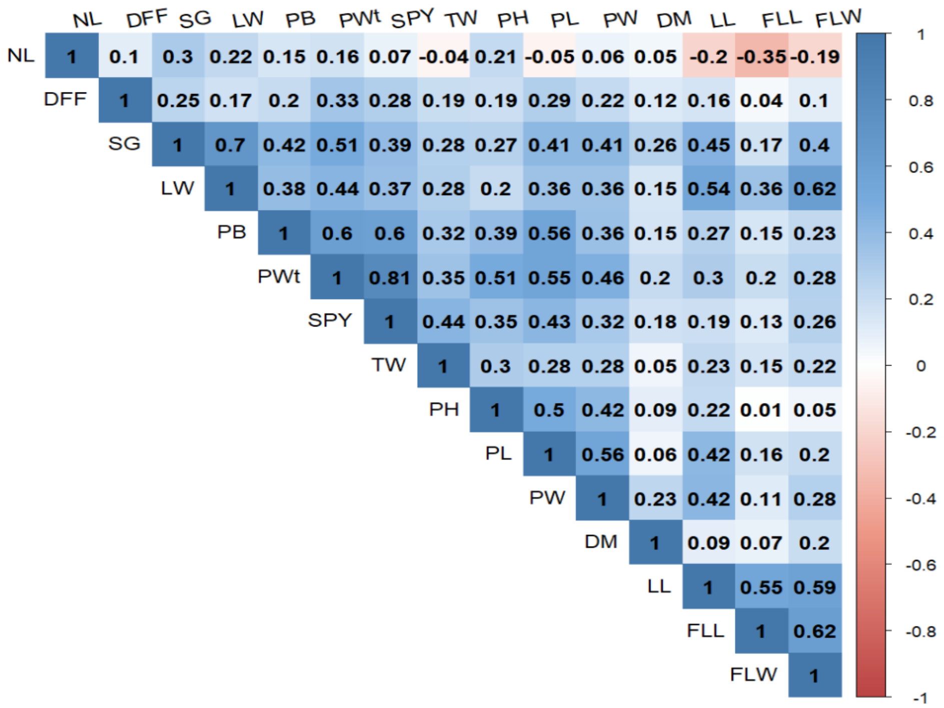
**Table 2. Correlation between variables in the red sorghum $F_2$ population of Paiyur2 x IS 21731**

| | NL | PH | SG | DF | DM | FLL | FLW | LL | LW | PL | PW | PWt | PB | SI | Correlations SPY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NL | **-0.0936** | -0.0154 | -0.0151 | 0.0017 | 0.0009 | 0.0389 | -0.0156 | 0.0169 | 0.0138 | 0.0022 | -0.0050 | **0.1216** | 0.0281 | -0.0069 | **0.0727** |
| PH | -0.0198 | **-0.0726** | -0.0135 | 0.0032 | 0.0016 | -0.0008 | 0.0043 | -0.0184 | 0.0126 | -0.0209 | -0.0324 | **0.3853** | 0.0762 | 0.0500 | **0.3547** |
| SG | -0.0282 | -0.0195 | **-0.0500** | 0.0042 | 0.0047 | -0.0189 | 0.0322 | -0.0375 | 0.0434 | -0.0173 | -0.0321 | **0.3835** | 0.0810 | 0.0465 | **0.3921** |
| DFF | -0.0098 | -0.0137 | -0.0125 | **0.0167** | 0.0022 | -0.0043 | 0.0082 | -0.0133 | 0.0106 | -0.0121 | -0.0171 | **0.2542** | 0.0388 | 0.0326 | **0.2805** |
| DM | -0.0047 | -0.0065 | -0.0132 | 0.0021 | **0.0178** | -0.0079 | 0.0158 | -0.0077 | 0.0091 | -0.0024 | -0.0181 | **0.1542** | 0.0298 | 0.0085 | **0.1768** |
| FLL | 0.0327 | -0.0005 | -0.0085 | 0.0006 | 0.0013 | **-0.1115** | 0.0498 | -0.0459 | 0.0222 | -0.0069 | -0.0086 | **0.1495** | 0.0286 | 0.0259 | **0.1287** |
| FLW | 0.0181 | -0.0039 | -0.0200 | 0.0017 | 0.0035 | -0.0690 | **0.0806** | -0.0495 | 0.0384 | -0.0085 | -0.0215 | **0.2107** | 0.0438 | 0.0364 | **0.2608** |
| LL | 0.0188 | -0.0158 | -0.0223 | 0.0026 | 0.0016 | -0.0608 | 0.0474 | **-0.0842** | 0.0337 | -0.0174 | -0.0329 | **0.2252** | 0.0522 | 0.0381 | **0.1863** |
| LW | -0.0208 | -0.0147 | -0.0349 | 0.0028 | 0.0026 | -0.0398 | 0.0497 | -0.0456 | **0.0622** | -0.0149 | -0.0277 | **0.3306** | 0.0741 | 0.0474 | **0.3710** |
| PL | 0.0048 | -0.0363 | -0.0207 | 0.0048 | 0.0010 | -0.0183 | 0.0164 | -0.0350 | 0.0222 | **-0.0419** | -0.0433 | **0.4178** | 0.1085 | 0.0466 | **0.4267** |
| PW | -0.0060 | -0.0302 | -0.0206 | 0.0037 | 0.0041 | -0.0123 | 0.0222 | -0.0356 | 0.0222 | -0.0233 | **-0.0779** | **0.3529** | 0.0705 | 0.0469 | **0.3167** |
| PWt | -0.0150 | -0.0368 | -0.0253 | 0.0056 | 0.0036 | -0.0220 | 0.0224 | -0.0250 | 0.0271 | -0.0230 | -0.0362 | **0.7590** | 0.1164 | 0.0595 | **0.8102** |
| PB | -0.0136 | -0.0285 | -0.0209 | 0.0033 | 0.0027 | -0.0164 | 0.0182 | -0.0227 | 0.0238 | -0.0234 | -0.0283 | **0.4559** | **0.1938** | 0.0530 | **0.5968** |
| SI | 0.0039 | -0.0216 | -0.0139 | 0.0032 | 0.0009 | -0.0172 | 0.0175 | -0.0191 | 0.0176 | -0.0116 | -0.0218 | **0.2692** | 0.0612 | **0.1677** | **0.4360** |

Kavipriya *et al.* (2020) and Kumar *et al.* (2021) for 100 seed weight (seed index); Patil *et al.* (2022) for days to flowering all in case of sorghum. In the present study, panicle weight showed significant and positive correlation with all other important yield-contributing traits. Similar kind of positive association of panicle weight with other traits *viz.* plant height, number of leaves per plant, flag leaf length, and flag leaf width was also observed as reported by Shamini and Selvi (2022). Plant height exhibited a significant and positive correlation with the number of leaves, stem girth, leaf length, leaf width, panicle length, panicle width, panicle weight, number of primary branches, and hundred seed weight. The majority of traits exhibited strong and desirable positive correlations with grain yield. Improving these specific characters can lead to significant enhancements in grain yield. Opting for selection based on strongly correlated traits, particularly single plant yield and panicle weight (with a correlation coefficient of 0.81; p <0.001), would result in the enhancement of both characteristics within the examined sorghum population.

Path analysis: Even though correlation studies reveal associations among these components, but relying solely on correlation estimates can sometimes lead to misleading results due to the mutual cancellation of component characters. Hence the simple correlation coefficient was subjected to path analysis as per the method suggested by Dewey and Lu (1959). Using grain yield as the dependent variable, the study was conducted partitioning genotypic correlations into direct and indirect effects. The direct and indirect effects were categorized following the recommendations provided by Lenka and Misra (1973). They were classified as very high (more than 1.00), high (0.30 to 0.99), moderate (0.20 to 0.29), low (0.10 to 0.19), and negligible (0.0 to 0.09). Panicle weight, in particular, exhibited a high and positive direct effect on grain yield. The path coefficient analysis results showed positive correlations and significant direct effects of panicle weight, number of primary branches and 100-seed weight (seed index) on single plant yield. Similar results were reported by Deshmukh *et al.* (2018) for 100 seed weight.

Additionally, the study observed positive correlations and negligible direct effects of flag leaf width, leaf width, days to flowering and days to maturity on single plant yield. Panicle weight exhibited a significant and highly positive correlation (0.8102) with single plant yield and exerted a considerable and strong positive direct effect (0.7590). The correlation coefficient (0.8102) for this trait is nearly equivalent to its direct effect, suggesting that the relationship between this trait and grain yield is primarily attributed to its direct influence. Hence, a direct selection based on this trait would be effective in improving grain yield. Number of leaves (-0.0936), plant height (-0.0726), stem girth (-0.0500), flag leaf length (-0.1115), leaf length (-0.0842), panicle length (-0.0419), panicle width (-0.0779) showed negative direct effects, but had considerable indirect effects of 0.1216, 0.3853, 0.3835, 0.1495, 0.2252, 0.4178, and 0.3529 respectively, on seed yield through panicle weight. Khandelwal *et al.* (2015) documented similar findings concerning



| | NL | DFF | SG | LW | PB | PWt | SPY | TW | PH | PL | PW | DM | LL | FLL | FLW |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NL | 1 | 0.1 | 0.3 | 0.22 | 0.15 | 0.16 | 0.07 | -0.04 | 0.21 | -0.05 | 0.06 | 0.05 | -0.2 | -0.35 | -0.19 |
| DFF | | 1 | 0.25 | 0.17 | 0.2 | 0.33 | 0.28 | 0.19 | 0.19 | 0.29 | 0.22 | 0.12 | 0.16 | 0.04 | 0.1 |
| SG | | | 1 | 0.7 | 0.42 | 0.51 | 0.39 | 0.28 | 0.27 | 0.41 | 0.41 | 0.26 | 0.45 | 0.17 | 0.4 |
| LW | | | | 1 | 0.38 | 0.44 | 0.37 | 0.28 | 0.2 | 0.36 | 0.36 | 0.15 | 0.54 | 0.36 | 0.62 |
| PB | | | | | 1 | 0.6 | 0.6 | 0.32 | 0.39 | 0.56 | 0.36 | 0.15 | 0.27 | 0.15 | 0.23 |
| PWt | | | | | | 1 | 0.81 | 0.35 | 0.51 | 0.55 | 0.46 | 0.2 | 0.3 | 0.2 | 0.28 |
| SPY | | | | | | | 1 | 0.44 | 0.35 | 0.43 | 0.32 | 0.18 | 0.19 | 0.13 | 0.26 |
| TW | | | | | | | | 1 | 0.3 | 0.28 | 0.28 | 0.05 | 0.23 | 0.15 | 0.22 |
| PH | | | | | | | | | 1 | 0.5 | 0.42 | 0.09 | 0.22 | 0.01 | 0.05 |
| PL | | | | | | | | | | 1 | 0.56 | 0.06 | 0.42 | 0.16 | 0.2 |
| PW | | | | | | | | | | | 1 | 0.23 | 0.42 | 0.11 | 0.28 |
| DM | | | | | | | | | | | | 1 | 0.09 | 0.07 | 0.2 |
| LL | | | | | | | | | | | | | 1 | 0.55 | 0.59 |
| FLL | | | | | | | | | | | | | | 1 | 0.62 |
| FLW | | | | | | | | | | | | | | | 1 |

**Fig. 1. Direct (diagonal) and indirect effects of yield components with single plant yield of red sorghum $F_2$ population of Paiyur2 x IS 21731**

RESIDUE = 0.5188

Note: NL = Number of leaves; PH = Plant height; SG= Stem girth, DF = Days to flowering; DM = Days to maturity; FLL = Flag leaf length; FLW = Flag leaf width; LL = Leaf length; LW = Leaf width; PL = Panicle length; PW = Panicle width; PW = Panicle weight; PB = Number of primary branches per panicle; SI = Seed index (100- seed weight); SPY = Single plant yield

parameters like number of leaves and plant height. Also, the result was in consistent with the conclusion reached by Silva da *et al*. (2017) for stem girth. Despite the significantly high positive correlation with single plant yield, when comparing the high positive correlation with the negative direct effects, it becomes evident that the indirect effect of these traits might be the cause of the correlation.

Certain traits such as days to flowering (0.0167), days to maturity (0.0178), flag leaf width (0.0806), and leaf width (0.0622), on the other hand, were observed to exhibit positive direct effects that were relatively low in magnitude compared to their correlation coefficients. However, these traits contributed significant positive indirect effects to single plant yield through panicle weight. Singh *et al*. (2018) observed similar kind indirect effect of leaf width on single plant yield via stem girth in multicut fodder sorghum. Therefore, choosing panicle weight as the basis for selection would be the most effective approach to increase single plant yield. This character has demonstrated a strong positive direct effect and a considerable indirect effect on single plant yield, making it a highly influential factor in enhancing overall productivity. In the current study, the residual effect observed was 0.5188, indicating that there is still a need of including other characters for study.

The study explored the genetic potential of red sorghum genotypes for quantitative traits. Variance component analysis revealed environmental impact on trait manifestation. High variability in flag leaf traits and single plant yield was noted through PCV and GCV. Traits like plant height, stem girth and flag leaf length showed notable heritability and genetic advancement. Positive correlations were found between yield and traits such as panicle weight and primary branches. Path analysis highlighted the direct and indirect effects of traits on grain yield, with panicle weight as a major driver. This research offered insights for effective breeding strategies, focusing on traits like panicle weight, primary branches, and seed index to enhance the yield and nutritional quality of red sorghum genotypes.

## REFERENCES

Aruna, C. and Cheruku, D. 2019. Genetic improvement of grain sorghum, in Breeding sorghum for diverse end uses., 1st Edn. Eds. C. Aruna, K. B. R. S. Visarada, B. V. Bhat and V. A. Tonapi (Sawston, UK: Woodhead Publishing), 157–173. [Cross Ref]

Aruna, C.R., Ratnavathi, C.V., Suguna, M. Ranga, B., Praveen Kumar, P., Annapurna, A., Bahadure, D.M. and Toapi, V.A. 2020. Genetic variability and G x E interactions for total polyphenol content and antioxidant activity in white and red sorghums (*Sorghum bicolor*). *Plant Breeding*., **139**(1): 119-130. [Cross Ref]

Birhan, T., Bantte, K., Paterson, A., Getenet, M. and Gabizew, A. 2020. Evaluation and genetic analysis of a segregating sorghum population under moisture stress conditions. *Journal of Crop Science and Biotechnology*, **23**: 29-38. [Cross Ref]

Burton, G.W. 1952. Quantitative inheritance in grasses. Pro VI Int Grassl Cong,**1952**:277-283.

Chittapur, R. and Biradar, B. D. 2015. Association studies between quantitative and qualitative traits in *rabi* sorghum. *Indian Journal of Agricultural Research*, **49**(5): 468-471. [Cross Ref]

Cuevas, H.E., Prom, L.K., Erpelding, J.E. and Brotons, V. 2014. Assessments of genetic diversity and anthracnose disease response among Zimbabwe sorghum germplasm. *Plant Breeding*, **133**:234–242. [Cross Ref]

da Silva, K. J., Teodoro, P. E., de Menezes, C. B., Júlio, M. P. M., de Souza, V. F., da Silva, M. J., Pimentel, L. D. and Borém, A. 2017. Contribution of morphoagronomic traits to grain yield and earliness in grain sorghum. *Genetics and molecular research: GMR*, **16**(2): https://doi.org/10.4238/gmr16029649 [Cross Ref]

Deshmukh, S. B., Bagade, A. B. and Choudhari, A. K. 2018. Correlation and path analysis studies among *rabi* sorghum (*Sorghum bicolor* L. Moench) mutants. *International Journal of Current Microbiology and Applied Science*, **6**: 1014-1020.

Dewey, D.R. and Lu, K.H. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*, **51**: 515-518. [Cross Ref]

Falconer, D. S. 1960. Introduction to quantitative Genetics. Oliver & Boyd, Edinburgh and London

Falconer, D.S. 1981. Introduction to Quantitative Genetics. Second edition. Longman, New york.

Hermanto, R., Syukur, M. and Widodo. 2017. Estimation of genetic variance and heritability of yield characters and yield components of tomato (*Lycopersicum Esculentum* Mill.) at two locations. *Hortikultura Indonesia Journal*, **8**(1): 31-37. [Cross Ref]

Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Estimates of genetic and environmental variability in soybeans 1. *Agronomy journal*, **47**(7): 314-318. [Cross Ref]

Kavipriya, C., Yuvaraja, A., Vanniarajan, C., Senthil, K. and Ramalingam, J. 2020. Genetic variability and multivariate analyses in coloured sorghum landraces (*Sorghum bicolor* (L.) Moench) of Tamil Nadu. *Electronic Journal of Plant Breeding*, **11**(02): 538- 542. [Cross Ref]

Khandelwal, V., Shukla, M., Nathawat, V.S. and Jodha, B.S. 2015. Correlation and path coefficient analysis for agronomical traits in sorghum [*Sorghum bicolor* (L.) Moench] under shallow saline soil condition in arid region. *Electronic Journal of Plant Breeding*, **6** (4): 1143-1149.

Lenka, D. and Misra, B. 1973. Path co-efficient analysis of yield in rice varieties. *Indian Journal of Agricultural Science*, **43**: 376-379

Lush, J. L. 1940. 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.

Mulualem, T., Alamrew, S., Tadesse, T. and Wegary, D. 2018. Genetic variability, heritability and genetic advance for agronomical traits of Ethiopian sorghum [*Sorghum bicolor* (L.) Moench] Genotypes. *Academic Research Journal of Agricultural Science and Research*, **6**(4): 251-259.

Nagesh Kumar, M.V., Ramya, V., Govindaraj, M., Sameer Kumar, C.V., Maheshwaramma, S., Gokenpally, S., Prabhakar, M., Krishna, H., Sridhar, M., Venkata Ramana, M., Avil Kumar, K. and Jagadeeshwar, R. 2021. Harnessing sorghum landraces to breed high-yielding, grain mold-tolerant cultivars with high protein for drought prone environments. *Front. Plant Sc*., **12**: 659874. [Cross Ref]

Nirosh, P. V., Yuvaraja, A., Thangaraj, K. and Menaka, C. 2021. Genetic variability and association studies in segregating generation of red sorghum (*Sorghum bicolor* (L.) Moench) population. *Electronic Journal of Plant Breeding*, **12**(2): 521-524. [Cross Ref]

Pezzali, J. G., Rodriguez, Cerezo, E. and Chiesa, S. 2020. Sorghum, an ancient and safe grain with high potential for the transition to organic and gluten free agriculture. *Journal of the Science of Food and Agriculture*, **100**(2): 585-590.

Rini, E. P., Marwiyah, S. and Wirnas, D. 2022. Genetic Analysis in an $F_2$ Population Derived from Indonesian Local Sorghum with New Superior Variety. *Jurnal Agronomi Indonesia (Indonesian Journal of Agronomy)*, **50**(3): 275-282. [Cross Ref]

R Studio Team. RStudio: Integrated Development for R; RStudio, PBC: Boston, MA, USA, 2002. http://www.rstudio.com / https://cran.r-project.org (accessed on 20/07/23)

Savitha, P. and Kumari, R. U. 2015. Genetic variability studies in f2 and f3 segregating generations for yield and its components in rice (*Oryza sativa* L.). *Indian Journal of Science and Technology,* **8**(17): 748-754. [Cross Ref]

Subhashini, S. and Selvi, B. 2019. Association and variability studies in F2 population of sorghum (*Sorghum bicolor* (L.) Moench). *Electronic Journal of Plant Breeding*, **10**(2): 483-489. [Cross Ref]

Shamini, K. and Selvi, B. 2022. Association studies in sorghum for stay green and yield associated traits. *Madras Agricultural Journal*, **109** (September (7-9)), 1. [Cross Ref]

Subramanian, A.. Raj, R.N. and Elangovan,M. 2019. Genetic variability and multivariate analysis in sorghum (*Sorghum bicolour*) under sodic soil conditions. *Electronic Journal of Plant Breeding*, **10**(4): 1405-1414. [Cross Ref]

Sushma, K., Reddy, K. R. and Saidaiah, P. 2020: Studies on genetic variability, heritability and genetic advance in tomato (*Solanum lycopersicum* L.) genotypes. – International *Journal of Chemical Studies,* **8**(6): 2672-75. [Cross Ref]

Syukur, M., Sujiprihati, S., Yunianti, R. and Kusumah, D. A. 2010: Evaluation of hybrid chili yields and their adaptability in four locations in two years. *Indonesian Journal of Agronomy*, **38**(1): 43-51.

Manivannan, N. 2014. TNAUSTAT-Statistical package. Retrived from https://sites.google.com/site/tnaustat

Vavilov, N.I. 1951. The origin, variation, immunity and breeding of cultivated plants. *Chronica Botanica*, **13**: 1-366.

Vinodhini, K., Kalaimagal, T., Kavithamani, D. and Senthil, A. 2022. Genetic variability and character association studies among grain yield and yield component traits in red sorghum [*Sorghum bicolor* (L.) Moench]. *The Pharma Innovation Journal*, **11**(8): 1327-1331.