



# Correlation and Path Coefficient Analysis for Yield and Contributing Traits in Yellow Sorghum (*Sorghum bicolor* (L.) Moench)

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## ABSTRACT

The present study was conducted during *rabi*, 2024–25 at Agricultural Research Station, Tandur to assess the nature of the association between grain yield and its component traits and monitor the direct and indirect effects of each of the component traits on grain yield of yellow sorghum. Fifty-two genotypes were evaluated for twelve yield contributing traits under residual soil moisture conditions in black soil. Correlation analysis indicated that fodder yield, number of grains panicle<sup>-1</sup>, number of leaves plant<sup>-1</sup>, leaf width, test weight, and panicle width had significant positive association with grain yield at both genotypic and phenotypic levels. Poor and insignificant correlation of grain yield was observed with plant height, leaf length, and panicle length. Path analysis partitioned the correlations into direct and indirect effects, providing a deep insight into trait–yield relationship. Significant positive direct effects of number of grains panicle<sup>-1</sup>, test weight, days to maturity and fodder yield and significant indirect effects of traits namely panicle width, panicle length and leaf length on grain yield confirmed that these traits should be prioritized during selection for ensuring higher genetic gain in grain yield in yellow sorghum improvement programs. The negative direct effect of days to 50% flowering and days to maturity on grain yield at the phenotypic and genotypic levels respectively implied that medium-flowering genotypes were more favourable for *rabi* situations.

**KEYWORDS:** yellow sorghum, correlations, path analysis, test weight

**Citation (VANCOUVER):** Sujatha et al., Correlation and Path Coefficient Analysis for Yield and Contributing Traits in Yellow Sorghum (*Sorghum bicolor* (L.) Moench). *International Journal of Bio-resource and Stress Management*, 2025; 16(12), 01-10. [HTTPS://DOI.ORG/10.23910/1.2025.6656](https://doi.org/10.23910/1.2025.6656).

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**Data Availability Statement:** Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

**Conflict of interests:** The authors have declared that no conflict of interest exists.

## 1. INTRODUCTION

Sorghum (*Sorghum bicolor* (L.) Moench) is the fifth most important cereal crop globally, following rice, wheat, maize, and barley in terms of production and utilization (Anonymous, 2021). It is a multipurpose crop providing food, feed, fodder and fuel, in Africa and India where it is extensively cultivated (Reddy et al., 2006; Upadhyaya et al., 2017). In India, sorghum is grown in an area of 4.35Mha with a production of 4.63Mtons and an average productivity of 1064 kg ha<sup>-1</sup>. In Telangana, it occupies an area of 78,000 ha with 120 lakh tonnes production and 1296 kg ha<sup>-1</sup> average productivity during the *rabi* season (Anonymous, 2022).

Sorghum grain color is determined by the genes that control the pericarp color (R and Y gene), pericarp thickness (Z gene), presence of pigmented testa (B1 and B2 genes), spreader (S gene) and the color intensifier (I gene). The genes RR and YY are related epistatically and act in a complementary way. According to the color, sorghum was classified into five types: white, yellow, red, brown, and black sorghums. White sorghum has a white or colorless pericarp when the Y gene is recessive, and irrespective of the R gene (rryy or R yy). Yellow sorghum has a yellow pericarp when the R gene is recessive and Y gene is dominant (rrY<sup>+</sup>). The dominant allele of the intensifier gene (I<sup>+</sup>), acts over the pericarp color intensifying the red color and the lemon yellow color, but the white color appears opaque. If the spreader gene (S<sup>+</sup>) is present in the dominant form the brown pigments of dominant gene B1\_B2<sup>+</sup> are spread throughout the pericarp and when the homozygous recessive gene (ss) is present the brown color occurs only in the testa layer. The dominant gene Z<sup>+</sup> results in a thin pericarp and white color grain while the recessive homozygous gene (zz) causes a thick pericarp with a chalky appearance (Rooney and Waniska, 2000).

Yellow pericarp sorghum is a specialty sorghum and has a higher market demand owing to its nutritional value and good roti-keeping quality. It is rich in protein, betacarotene, and iron (Maheshwaramma et al., 2023) when compared to white sorghum. It has higher levels of flavanones and phenolics, which act as antioxidants and play a crucial role in enhancing the immune system. It serves as a balanced diet and plays a vital role in dietary diversification, biofortification, and addressing nutritional security (Dykes and Rooney, 2006; Awika and Rooney, 2004; Reddy et al., 2022). The yellow sorghum varieties have less bird damage (owing to phenols) and are tolerant to grain molds, which occur frequently when grain maturity coincides with showers in the rainy season. Currently cultivated yellow sorghum cultivars are low-yielding local land races which are generally cultivated in patches in tribal areas for subsistence under poor management conditions. Correlation

and path coefficient analyses help in understanding the interrelationships among traits and in identifying both primary and secondary traits governing yield (Dewey and Lu, 1959). Correlation analysis reveals the degree and direction of association among traits, while path analysis partitions these correlations into direct and indirect effects, assisting breeders to prioritize traits for yield enhancement in sorghum (Singh and Chaudhary, 1985; Ayana and Bekele, 1999). Keeping in view the nutritional superiority and the rising consumer demand for yellow sorghum, an attempt was made in the present study to evaluate the performance of 52 yellow sorghum genotypes for yield and its contributing traits through Correlation and Path analysis and to identify the target traits on which selection can be based for yield enhancement.

## 2. MATERIALS AND METHODS

### 2.1. Experimental site

The study was conducted during *rabi* season 24–25 (October 2024 to February 2025) at Agriculture Research Station, Tandur, Vikarabad district operating under Professor Jayashankar Telangana Agricultural University, Telangana state. Tandur is located at 17°14' North latitude and 77°34' East longitude and at an altitude of 461 m above mean sea level, representing the Southern Telangana zone. The experimental material consisted of 49 yellow sorghum genotypes evaluated along with 3 checks (Table 1) for yield and yield component traits in a Randomized block design with three replications. A healthy crop was raised following the standard package of practices in deep black soil. Each entry was sown in two rows of 2 m length with inter-row spacing of 45 cm and intra-row spacing of 15 cm.

### 2.2. Method of data collection

Data was collected on five competitive plants per plot for ten traits such as days to 50% flowering, days to maturity, plant height, number of leaves per plant, leaf length, leaf width, panicle length, panicle width, number of grains per panicle and 100 seed weight (test weight) and their means were used for statistical analysis. Observations on grain yield and fodder yield were recorded on a plot basis and converted to kg ha<sup>-1</sup>. Correlations at genotypic and phenotypic levels were calculated following the method suggested by Al-Jiobouri et al. (1958). The genotypic and phenotypic correlations were further analyzed using path analysis, as per Wright (1921) and expanded by Dewey and Lu (1959). The data was statistically analysed for correlations and path coefficients using INDOSTAT software version 9.1.

## 3. RESULTS AND DISCUSSION

### 3.1. Correlation analysis

Correlation studies give insight into the interconnections

Table 1: List of yellow sorghum genotypes studied

Sl. No.	Genotype	Pedigree	Sl. No.	Genotype	Pedigree
1.	ICSV 17214	YPS-1	27.	ICSV 17252	GP (4)-7-2
2.	ICSV 17215	YPS-4	28.	ICSV 17253	GP (4)-38-1
3.	ICSV 17217	YPS-6	29.	ICSV 17255	GP (4)-20-1
4.	ICSV 17220	YPS-15	30.	ICSV 17256	GP (4)-50
5.	ICSV 17222	GP (4)-20-3	31.	ICSV 17257	GP (4)-57-1
6.	ICSV 17225	MBNR-58 994121	32.	ICSV 17258	GP (4)-16-5
7.	ICSV 17229	GP (4) Sweet-2652	33.	ICSV 17259	GP (4)-33 B2
8.	ICSV 17230	GP (4) (Insipid)-2648	34.	ICSV 17260	GP (4)-46
9.	ICSV 17232	GP (4)-7-1	35.	ICSV 17261	GP (4)-2567
10.	ICSV 17233	GP (4)-23	36.	ICSV 17262	GP (4)-2443
11.	ICSV 17234	GP (4)-2654	37.	ICSV 17263	GP (4)-17-3
12.	ICSV 17235	GP (4)-2658	38.	ICSV 17264	GP (4)-28-2
13.	ICSV 17236	GP (4)-40-1	39.	ICSV 17265	GP (4)-CSM-13
14.	ICSV 17237	GP (4)-4-2	40.	ICSV 17266	MBNR-S9 994122
15.	ICSV 17238	GP (4)-2655	41.	PYPS 1	PSLRC 2×PSLRC 3
16.	ICSV 17240	GP (4)-55	42.	PYPS 2 (Palem pacha jonna)	PSLRC 2×PSLRC 4 Check, released variety from Regional Agricultural Research Station, Palem, Telangana
17.	ICSV 17241	GP (4)-58-1	43.	PYPS 4	PSLRC 2×PSLRC 6
18.	ICSV 17242	GP (4)-2646	44.	PYPS 5	PSLRC 21×PSLRC 7
19.	ICSV 17243	GP (4)-48	45.	PYPS 6	PSLRC 3×PSLRC 6
20.	ICSV 17244	GP (4)-2653	46.	PYPS 7	PSLRC 3×PSLRC 7
21.	ICSV 17245	GP (4)-64-1	47.	PYPS 10	PSLRC 9×PSLRC 10
22.	ICSV 17246	GP (4)-32-2	48.	PYPS 11	PSLRC 4×PSLRC 6
23.	ICSV 17247	GP (4)-2446	49.	PYPS 13	PSLRC 2×PSLRC 21
24.	ICSV 17248	GP (4)-8e-5	50.	PYPS 14	PSLRC 20×PSLRC 21
25.	ICSV 17250	GP (4)-65-1	51.	N14	Check, Yellow sorghum variety released variety from Regional Agricultural Research Station, Nandyal, Andhra Pradesh
26.	ICSV 17251	GP (4)-34-1	52.	N15	Check, Yellow sorghum variety released variety from Regional Agricultural Research Station, Nandyal, Andhra Pradesh

between various traits. Factors such as genetic linkage, pleiotropy and the association of genes located on the same chromosome can also lead to trait correlations (Walsh and blows, 2009). These correlations often reflect coordinated physiological and developmental processes, which are regulated by genetic mechanisms (Mackay et al., 2009). It is essential to consider the relationship between yield and its related traits while making selections in plant breeding. The direction (positive or negative) and strength of these relationships are important for understanding how traits

influence each other. The estimates of genotypic and phenotypic correlation coefficients indicated that genotypic correlation coefficients were consistently higher than their phenotypic counterparts. This suggests a strong inherent association among the various traits and minimum influence of environment on the phenotypic expression of these correlations (Dabi et al., 2016).

Correlation analysis among the twelve yield related traits at the phenotypic level revealed highly significant positive association of grain yield with fodder yield (0.657\*\*)

followed by number of grains plant<sup>-1</sup> (0.373\*\*), number of leaves (0.372\*\*), leaf width (0.355\*\*), test weight (0.287\*\*) and panicle width (0.255\*\*). Also significant correlations

of grain yield were observed with plant height (0.205\*), leaf length (0.190\*), days to maturity (0.183\*) and days to 50% flowering (0.158\*) (Table 2, Figure 1 and Figure 2).

Table 2: Phenotypic and genotypic correlations between yield and yield contributing characters

Trait	DFF	DM	PH	NL	LL	LW	PL	PW	NGP	TW	Fy kg ha <sup>-1</sup>	Gy kg ha <sup>-1</sup>
DFF	1	0.987**	-0.127	-0.073	0.144	-0.063	0.088	0.306**	-0.234**	0.314**	0.073	0.158*
DM	1.008**	1	-0.130	-0.063	0.152	-0.056	0.080	0.314**	-0.225**	0.329**	0.076	0.183*
PH	-0.151	-0.146	1	0.075	-0.003	0.240**	0.099	0.165*	0.168*	-0.026	0.456**	0.205*
NL	-0.071	-0.065	0.211**	1	0.085	0.362**	0.066	-0.049	0.056	0.244**	0.199*	0.372**
LL	0.179*	0.159*	0.031	0.120	1	0.152	-0.003	0.080	-0.130	0.259**	-0.034	0.190*
LW	-0.059	-0.052	0.389**	0.661**	0.250**	1	0.036	0.165*	0.239**	0.074	0.355**	0.355**
PL	0.150	0.144	0.178*	-0.149	0.042	-0.113	1	0.084	0.015	-0.023	0.019	0.068
PW	0.425**	0.426**	0.165*	-0.069	0.202*	0.164*	0.193*	1	-0.099	0.314**	0.307**	0.255**
NGP	-0.247**	-0.237**	0.224**	0.076	-0.165*	0.317**	0.083	-0.161*	1	-0.625**	0.363**	0.373**
TW	0.352**	0.354**	-0.022	0.332**	0.269**	0.104	-0.025	0.429**	-0.654**	1	0.212**	0.287**
Fy kg ha <sup>-1</sup>	0.103	0.108	0.586**	0.352**	-0.015	0.443**	0.201*	0.369**	0.375**	0.259**	1	0.657**
Gy kg ha <sup>-1</sup>	0.195*	0.203*	0.320**	0.556**	0.215**	0.500**	0.174*	0.378**	0.393**	0.312**	0.798**	1

\*, \*\* significant at  $p=0.05$  and  $p=0.01$  level respectively; The upper diagonal indicates phenotypic correlations and the lower diagonal indicates genotypic correlations; DFF: Days of 50% flowering; DM: Days to maturity; PH: Plant height in cm; NL: Number of leaves plant<sup>-1</sup>; LL: Leaf length in cm; LW: Leaf width in cm; PL: Panicle length in cm; PW: Panicle width in cm; NGP: Number of grains panicle<sup>-1</sup>; TW: Test weight (100 grain wt) in g; Fy kg ha<sup>-1</sup>: Fodder yield in kg ha<sup>-1</sup>; Gy kg ha<sup>-1</sup>: grain yield in kg ha<sup>-1</sup>

At the genotypic level, highly significant positive association of grain yield was recorded with fodder yield (0.798\*\*) followed by number of leaves (0.556\*\*), leaf width (0.500\*\*), number of grains plant<sup>-1</sup> (0.393\*\*), panicle width (0.378\*\*), plant height (0.320\*\*), test weight (0.312\*\*) and leaf length (0.215\*\*). A strong correlation of these traits with grain yield indicated that simultaneous improvement of all the characters is possible. This is in agreement with the reports of Hundekar et al. (2016), Shivaprasad et al. (2019) and Vinodhini et al. (2022). Significant correlations of grain

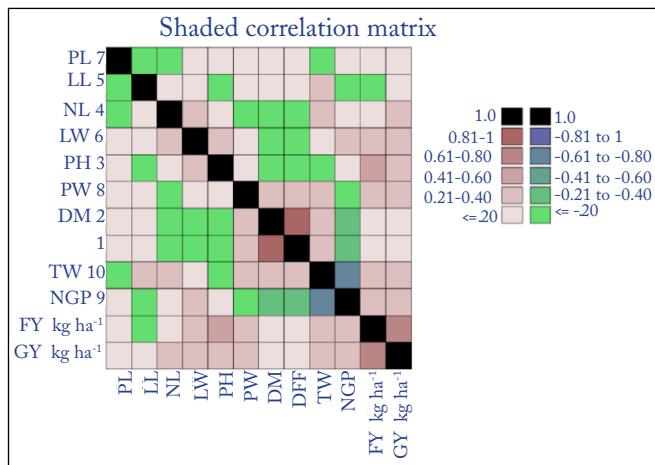


Figure 1: Phenotypic correlation matrix

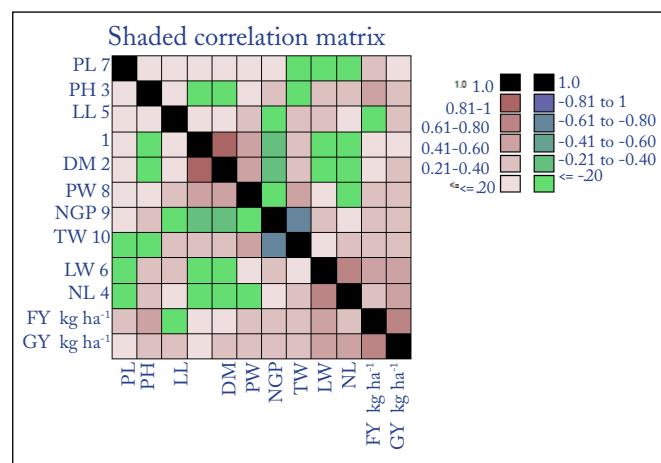


Figure 2: Genotypic correlation matrix

yield were also recorded with days to maturity (0.203\*), days to 50% flowering (0.195\*) and panicle length (0.174\*) as reported by Sheetal et al. (2021), Mamo and Worede, (2020) and Thant et al. (2021). At the phenotypic level, a significant positive association of fodder yield was recorded with plant height (0.456\*\*) followed by number of grains plant<sup>-1</sup> (0.363\*\*), leaf width (0.355\*\*), panicle width (0.307\*\*), test weight (0.212\*\*) and number of leaves (0.199\*). Significant positive association of fodder yield was observed with plant height (0.586\*\*), leaf width (0.443\*\*), number of grains

plant<sup>-1</sup> (0.375\*\*), panicle width (0.369\*\*), number of leaves (0.352\*\*), test weight (0.259\*\*), and panicle length (0.201\*) at the genotypic level. Similar findings were reported in sorghum by Goswami et al. (2020), Sahane et al. (2024) and Somu et al. (2024).

Significant negative correlations were recorded between the number of grains panicle<sup>-1</sup>, with test weight (-0.625\*\*), days to 50% flowering (-0.234\*) and days to maturity (-0.225\*) at the phenotypic level. At the genotypic level, significant negative correlation of number of grains panicle<sup>-1</sup> was recorded with test weight (-0.654\*\*), days to 50% flowering (-0.247\*\*), days to maturity (-0.237\*\*), leaf length (-0.165\*\*) and panicle width (-0.161\*) as reported by Godbharle et al. (2010).

Days to 50% flowering showed significant positive correlation with days to maturity both at genotypic (0.987\*\*) and phenotypic level (1.00\*), indicating that sorghum genotypes that flower later tend to mature later, consistent with the physiological growth duration. It also had a significant positive association with panicle width (0.306\*, 0.425\*\*) and test weight (0.314\*, 0.352\*\*), both at genotypic and phenotypic levels, respectively, as reported by Chibvongodze et al. (2025) and Enyew et al. (2021).

Days to maturity reflected significant positive correlation with test weight (0.329\*, 0.354\*) and panicle width (0.314\*, 0.426\*\*) both at phenotypic and genotypic levels, respectively as reported by Enyew et al. (2021) suggesting that medium duration types are high yielding with larger panicles and bold grains than early duration types. It was significantly and positively correlated with leaf length (0.159) at the genotypic level.

Plant height recorded a significant positive association with leaf width (0.240\*\*, 0.389\*\*), number of grains panicle<sup>-1</sup> (0.168\*, 0.224\*) and panicle width (0.165\*, 0.165\*), both at phenotypic and genotypic levels. These results are in accordance with Hundekar et al. (2016), Mamo and Woreda (2020), and Deshmukh et al. (2021) and Vinodhini et al. (2022). Plant height showed significant positive genotypic association with the number of leaves (0.211\*\*) and panicle length (0.178\*) as reported by El-Raheem et al. (2020).

Number of leaves plant<sup>-1</sup> had a significant positive correlation, leaf width (0.362\*\*, 0.661\*\*), test weight (0.244, 0.332\*\*) both at phenotypic and genotypic levels as reported by Srinivas et al. (2010) and Rao et al. (2014). Similar correlations were obtained by Shivaprasad et al. (2019) for panicle length, Lokesh and Biradar (2021) for fodder yield, and Vinoth et al. (2021) for test weight.

Leaf length showed a significant positive correlation with test weight (0.259\*\*, 0.269\*\*), both at the phenotypic and genotypic level. It also showed significant positive correlation with leaf width (0.250\*) and panicle width

(0.202\*) at the genotypic level and significant negative correlation with number of grains panicle<sup>-1</sup> (-0.165\*) at the genotypic level. These results were in conformity with those reported by Patil et al. (2015).

Leaf width was significantly positively correlated with the number of grains panicle<sup>-1</sup> (0.239\*, 0.317\*\*) and panicle width (0.165\*, 0.164\*), both at genotypic and phenotypic levels as reported by Somu et al. (2024). Panicle length showed significant positive correlation with panicle width (0.193\*) at the genotypic level as reported by Thant et al. (2021) and Deshmukh et al. (2021). Panicle width exhibited significant positive correlations with test weight (0.314\*\*, 0.429\*) at both phenotypic and genotypic levels as reported by Tesso et al. (2011), Kavipriya et al. (2020); Endalemaw and Semahegn (2020), Kumar et al. (2023) and Sahane et al. (2024).

### 3.2. Path coefficient analysis

Path coefficient analysis partitions the total correlation coefficient into direct and indirect effects and measures the relative importance of the causal factor individually. Among the eleven component traits, significant positive

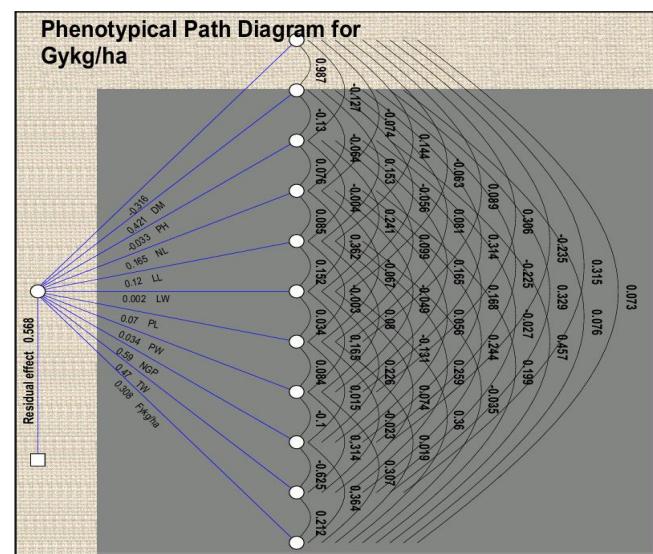


Figure 3: Phenotypic path diagram depicting direct and indirect effects on grain yield

direct effects were exhibited by number of grains panicle<sup>-1</sup> (0.590), followed by test weight (0.470), days to maturity (0.421), fodder yield (0.308), and number of leaves plant<sup>-1</sup> (0.164) on grain yield at the phenotypic level (Table 3, Figure 3). Conversely, days to maturity (-0.199) and leaf width (-0.195) showed negative direct effects on grain yield. At the genotypic level, a significant positive direct effect was exhibited by the number of grains panicle<sup>-1</sup> (0.577), followed by the number of leaves plant<sup>-1</sup> (0.426), fodder yield (0.401), test weight (0.316), days to 50% flowering (0.276)

Table 3: Phenotypic path coefficients of yield contributing characters in yellow sorghum

Character	DFF	DM	PH	NL	LL	LW	PL	PW	NGP	TW	FY
DFF	-0.315**	-0.311**	0.040	0.023	-0.045	0.019	-0.028	-0.096	0.074	-0.099	-0.023
DM	0.415	0.421**	-0.054	-0.026	0.064	-0.023	0.034	0.132	-0.094	0.138	0.032
PH	0.004	0.004	-0.033	-0.002	0.0001	-0.007	-0.003	-0.005	-0.005	0.0009	-0.015
NL	-0.012	-0.010	0.012	0.164*	0.014	0.059	-0.011	-0.008	0.009	0.040	0.032
LL	0.017	0.018	-0.0005	0.010	0.120	0.018	-0.0004	0.0009	-0.015	0.031	-0.004
LW	-0.0001	-0.0001	0.0004	0.0007	0.0003	0.0018	0.0001	0.0003	0.0004	0.0001	0.006
PL	0.006	0.005	0.007	-0.004	-0.0002	0.002	0.070	0.005	0.001	-0.001	0.001
PW	0.010	0.010	0.005	-0.001	0.002	0.005	0.002	0.033	-0.003	0.010	0.010
NGP	-0.138	-0.133	0.099	0.033	-0.077	0.133	0.008	-0.059	0.590**	-0.368**	0.214**
TW	0.148	0.154	-0.012	0.114	0.121	0.034	-0.010	-0.147	-0.294	0.470**	0.098
FY	0.022	0.023	0.140	0.061	-0.010	0.110	0.005	0.094	0.112	0.065	0.308**

Residual effect: 0.568; Direct effects are bold values on the diagonal; Indirect effects are values above the diagonal

and panicle width (0.190) on grain yield (Table 4, Figure 4). In the present study, days to 50% flowering were found to be positively correlated with grain yield. However, it showed a significant negative direct effect (-0.0.315) and a significant negative indirect effect (-0.311) through days to maturity on grain yield at the phenotypic level. This suggests that medium flowering types, rather than long duration types, are preferable for maximizing yield. This is consistent with earlier reports of Ali et al. (2011), Akatwijuka et al. (2019), Shivaprasad et al. (2019), Tafere et al. (2018), and El-Raheem et al. (2020), Sahane et al. (2024) where days to 50% flowering had a negative direct effect on grain yield. At the genotypic level, it showed a significant positive direct effect (0.276) on grain yield and a significant positive indirect effect through panicle width (0.543), test weight (0.449), days to maturity (0.277), leaf length (0.228), panicle

length (0.192), and negative indirect effect through number of grains panicle<sup>-1</sup> (-0.315).

Days to maturity exhibited a significant positive direct effect (0.421) and negative indirect effect through days to maturity (-0.311) on grain yield at the phenotypic level, confirming that medium duration genotypes allow better grain filling and yield performance. At the genotypic level, it had a significant negative direct effect (-0.199), positive indirect effects through number of grains panicle<sup>-1</sup> (0.285), plant height (0.175), and negative indirect effects through panicle width (-0.512), test weight (-0.425) and panicle length (-0.172). Similar results were reported by Akatwijuka et al. (2019) and Tafere et al. (2018).

Plant height recorded a negative direct effect (-0.033) on grain yield at the phenotypic level, suggesting that height alone does not directly improve yield. Comparable results

Table 4: Genotypic path coefficient analysis of yield and yield contributing characters in yellow sorghum

Character	DFF	DM	PH	NL	LL	LW	PL	PW	NGP	TW	FY
DFF	0.276**	0.277**	-0.19	-0.090	0.228**	-0.076	0.192*	0.543**	-0.315**	0.449**	0.132
DM	0.200	-0.199*	0.175*	0.078	-0.191	0.062	-0.172*	-0.512**	0.285**	-0.425**	-0.130
PH	0.011	0.011	-0.079	-0.016	-0.002	-0.030	-0.014	-0.013	-0.017	0.001	-0.046
NL	-0.030	-0.027	0.089	0.426**	0.051	0.281**	-0.063	-0.029	0.032	0.141	0.150
LL	0.027	0.024	0.004	0.018	0.155	0.038	0.003	0.031	-0.025	0.041	-0.002
LW	0.011	0.010	-0.076	-0.129	-0.049	-0.195*	0.022	-0.032	-0.062	-0.020	-0.086
PL	0.007	0.007	0.008	-0.007	0.001	-0.005	0.048	0.009	0.004	-0.001	0.009
PW	0.081	0.081	0.031	-0.013	0.038	0.031	0.036	0.190	-0.030	0.081	0.070
NGP	-0.142	-0.137	0.129	0.044	-0.095	0.183	0.048	-0.092	0.577**	-0.377**	0.219**
TW	0.111	0.112	-0.007	0.105	0.085	0.033	-0.007	0.135	-0.206	0.316**	0.081
FY	0.041	0.043	0.235	0.141	-0.006	0.178	0.081	0.148	0.152	0.104	0.401**

Residual effect: 0.568; Direct effects are bold values on the diagonal; Indirect effects are values above the diagonal

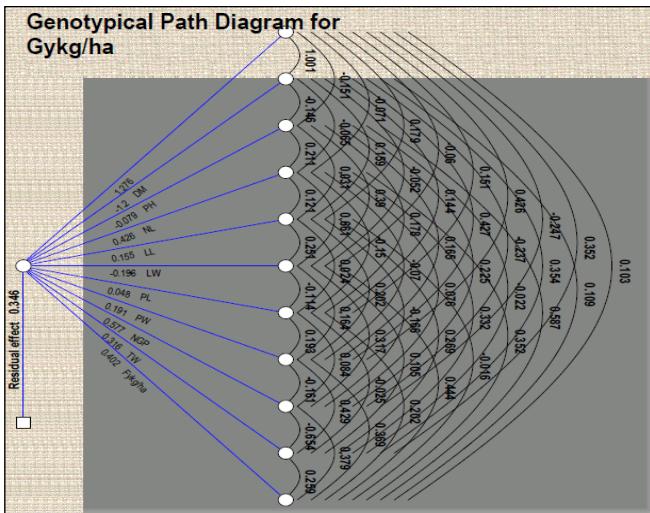


Figure 4: Genotypic path diagram depicting direct and indirect effects on grain yield

were reported by Shivaprasad et al. (2019), Tafere et al. (2018), El-Raheem et al. (2020) and Maiga et al. (2022). The number of leaves had a significant positive direct effect (0.164) on grain yield at the phenotypic level, and a significant positive direct effect (0.426) and indirect effect through leaf width (0.281) at the genotypic level. This reflects the role of leaf area in increasing photosynthetic capacity (source size) and productivity. Similar findings were documented by Shivaprasad et al. (2019), highlighting the importance of leaf area in improving source strength.

Leaf length displayed a positive direct effect (0.120) at the phenotypic level on grain yield. These results agree with Lokesh and Biradar (2021), who observed that longer leaves contribute to increased light interception and improved grain filling. Leaf width had a very small positive direct effect (0.001) at the phenotypic level, indicating minimal independent influence on yield, as reported by Patil et al. (2015), suggesting that it is a supportive rather than primary yield-determining trait. Panicle length recorded a small positive direct effect (0.0704) on grain yield at the phenotypic level, as against Deshmukh et al. (2021), where panicle length contributed modestly but positively to yield through increased grain-bearing capacity. Similar results were reported by Deepalakshmi and Ganesamurthy (2007), Lokesh and Biradar (2021) and Sheetal et al. (2021). Panicle width had a small positive direct effect (0.033) on grain yield at the phenotypic level as reported by Shivaprasad et al. (2019) and El-Raheem et al. (2020).

The number of grains panicle<sup>-1</sup> exhibited a significant positive direct effect (0.590) on grain yield at the phenotypic level, making it the most important yield determinant. Significant positive indirect effects came through fodder yield (0.214) and negative indirect effects were noted via test weight (-0.368) at the phenotypic level. At the genotypic

level, it exhibited a significant positive direct effect (0.577) on grain yield, a significant positive indirect effect through fodder yield (0.219) and a negative indirect effect via test weight (-0.377). This is in agreement with Lata and Shailesh (2001), Adane et al. (2018), Lokesh and Biradar (2021) and Maiga et al. (2022), Sahane et al. (2024) who consistently reported the number of grains panicle<sup>-1</sup> as the trait with the largest positive direct effect in sorghum.

Test weight recorded the significant positive direct effect on grain yield at both the phenotypic (0.470) and genotypic (0.316) levels and a significant indirect effect through the number of grains per panicle at both levels (-0.368 and -0.377). Thus, grain size exhibits an inverse relationship with grain number as seen in studies of Kole et al. (2008) Santhiya et al. (2021) and Deshmukh et al. (2021) and Sahane et al. (2024).

Fodder yield had a significant positive direct effect (0.308) and positive indirect effect through the number of grains panicle<sup>-1</sup> (0.214) on grain yield at the phenotypic level. At the phenotypic level, it had a significant positive direct effect (0.401) and positive indirect effect through the number of grains panicle<sup>-1</sup> (0.219) on grain yield. These intricate relationships emphasize the need for multi-trait selection strategies, as advocated by Hundekar et al. (2016).

## 4. CONCLUSION

Significant positive correlations of grain yield with fodder yield, number of grains panicle<sup>-1</sup>, number of leaves plant<sup>-1</sup>, leaf width, test weight, and panicle width suggested that selection for these traits would result in grain yield improvement in yellow sorghum. Significant positive direct effects of number of grains panicle<sup>-1</sup>, test weight, days to maturity, fodder yield and significant indirect effects of panicle width, panicle length and leaf length confirmed these traits to be critical determinants of grain yield.

## 5. ACKNOWLEDGEMENT

The authors are thankful to the Indian Institute of Millets Research (IIMR) and Professor Jayashankar Telangana Agricultural University (PJTAU) for providing funding to carry the research work, and ICRISAT for the supply of seed material of sorghum genotypes.

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