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A Thamizhiniyan
Department of Plant Breeding and Genetics, TNAU, AC&RI, Madurai, Tamil Nadu, India

R Chandirakala
Department of Millets, TNAU, Coimbatore, Tamil Nadu, India

A Yuvaraja
Department of Plant Breeding and Genetics, TNAU, Tapioca & Castor Research Station, Yethapur, Tamil Nadu, India

S Vellaikumar
Department of Biotechnology, Centre of Innovation, TNAU, AC&RI, Madurai, Tamil Nadu, India

Corresponding Author:
A Thamizhiniyan
Department of Plant Breeding and Genetics, TNAU, AC&RI, Madurai, Tamil Nadu, India

Genetic analysis of quantitative traits in the F_4 population of *Red sorghum* (*Sorghum bicolor* (L.) Moench)

A Thamizhiniyan, R Chandirakala, A Yuvaraja and S Vellaikumar

Abstract
Sorghum is an important tropical crop, which is a major food crop in poor parts of the world. A study was conducted to identify the best performing genotypes in F_4 generation of *Red sorghum* cross *viz.*, Paiyur 2 X Kottathur local-5 through variability and association analyses. Thirteen quantitative traits from 200 plants were recorded *i.e.*, days to fifty percent flowering, days to maturity, plant height, number of leaves per plant, leaf length, leaf width, stem girth, number of primary branches per panicle, panicle length without peduncle, panicle width, panicle weight, test weight and single plant yield. Variability analysis revealed that low level of variation was observed for plant height, number of leaves, leaf length, days to maturity, days to fifty percent flowering and panicle weight while a moderate level of PCV and GCV values were recorded for traits like leaf width, stem girth, panicle length, panicle width, number of primary branches, test weight and single plant yield. High heritability accompanied with high genetic advance was observed for leaf width, stem girth, panicle length, panicle width, number of primary branches, test weight and single plant yield. Association analysis revealed that plant height was positively correlated with number of leaves, stem girth and single plant yield. Days to maturity was positively correlated with single plant yield and Test weight was positively correlated with panicle width. Panicle weight, number of primary branches per panicle and test weight were also positively correlated with single plant yield. Pathway estimates illustrated that days to maturity hold the highest positive direct effect followed by number of leaves, number of primary branches per panicle, test weight and panicle length.

Keywords: Quantitative, population, *Red sorghum, Sorghum bicolor* L.

Introduction
Sorghum is the fourth most important world food crop following wheat, rice and maize. It is a staple food in the drier parts of tropical Africa, India and China. Sorghum because of its drought resistance grows well in dry regions and areas with unreliable rainfall. In Tamil Nadu, sorghum occupies around 3.86 lakh hectares of cultivable land under which 1 lakh hectare is under *Red sorghum* (Indiastat, 2020-21). In Tamil Nadu, Namakkal is the largest sorghum producing district, followed by Thiruppur, Dindigul, Salem, Coimbatore, Trichy, Karur, Thoothukudi, and Virudunagar. Namakkal district has recorded the highest production (1.644 lakh tonnes), whereas Dindigul district has recorded the highest productivity (2551 kg/ha) (APY, 2021) *Red sorghum* contains a high amount of phenolic compounds (phenolic acids, flavonoids and condensed tannins) and it is well known for its unique anthocyanin content *viz*., 3-deoxyanthocyanidin which is resistant to high pH of 7-9 and temperature of 65-75 ºC. Hence, it can be a promising food colorant for replacing synthetic colorants in Brewery Industries (Xiong *et al*., 2019) [25]. Sorghum is gluten-free and has bioactive compound-rich properties serving as an alternative food substitute to cereals. It has higher content of dietary fiber and a low-glycemic index which make it suitable for diabetic patients. It is also rich in protein, fiber and micronutrients, making it preferable for people in different parts of the country. The phytoalexin characteristics of the polyphenols enable them to protect the grain from microbial assaults like mould. Due to these distinguished properties, *Red sorghum* is mostly used by food-based industries as a principle component as well additional component of their products.in this study, identification of the best performing genotypes in the F_4 generation of *Red sorghum* genotypes was carried out based on their quantitative characters through variability and association analyses.

Materials and Methods

The plant material consisted of single plant populations derived from an inter-specific cross of *Red sorghum viz.,* Paiyur 2 X Kottathur local-5 and was evaluated in the F_4 generation. The female parent paiyur 2 had characteristics *viz.,* high yielding, dual-purpose (fodder and grain), high protein. Whereas Kottathur local 5 had possessed high tannin, polyphenol and protein content.

The single plant populations were raised in the *rabi* 2021, at Agricultural College and Research Institute, Madurai. Each cross was raised in ten rows of 6m in length with a spacing of 45 cm x 15 cm. The crop was raised by adapting proper agronomic and crop protection management. Among the single plant populations, well-performing and nearly homozygous populations were selected. For the selected population observations for the following thirteen quantitative traits *viz.,* days to fifty percent flowering (DFF), days to maturity (DM), plant height (PH), number of leaves per plant (NL), leaf length (LL), leaf width (LW), stem girth (SG), number of primary branches per panicle (NPB), panicle length without peduncle (PL), panicle width (PWd), panicle weight (PWt), test weight (TW), single plant (SPY) were recorded.

Descriptive statistics were computed for the thirteen quantitative characters using Microsoft Excel 2021. Variability parameters *viz.,* (genotypic coefficient of variation, phenotypic coefficient of variation, genetic advance and heritability) were computed using TNAUSTAT. Correlation analysis was carried out through OPSTAT software and path analysis was done through TNAUSTAT statistical package.

Result and Discussion

All the proginies in the cross Paiyur 2 X Kottathur local-5 recorded high mean, standard error and standard deviation for plant height and a high coefficient of variation for leaf length (Table 1). Crop development was primarily based on the level of variation since it determines the performance and quality of the crop population. In this study the level of variation between GCV and PCV was low, hence it could be inferred that the influence of environmental variation on the quantitative traits was negligible. Plant height, number of leaves, leaf length, days to maturity, days to fifty percent flowering and panicle weight recorded low PCV & GCV values. Similar results for plant height was observed by Eniola *et al*. (2019) [6]; Ahmed and Rajab (2017) [1]. Moderate level of PCV and GCV values were recorded for traits like leaf width, stem girth, panicle length, panicle width, number of primary branches and single plant yield. Swamy *et al.* (2018) [21] also observed similar results with moderate variation for panicle length. Moderate variation for stem girth was also observed by Shivaprasad *et al.* 2019 [17] and Shamini and Selvi *et al.* 2018 [16].

High heritability accompanied with high genetic advance was observed for leaf width, stem girth, panicle length, panicle width, number of primary branches, test weight and single plant yield, which indicated that heritability was due to additive gene action and selection could be most effective for such traits. High heritability with moderate genetic advance was observed for number of leaves, leaf length, days to fifty percent flowering and panicle weight, which was exhibited due to environmental effects where selection could be effective for further crop improvement. Shamini and Selvi (2018) [16] and Kavipriya *et al.* (2020) [11] also observed similar results for traits having high heritability coupled with high genetic advance. (Table 2)

Correlation analysis was necessary to understand the relationship among the traits for crop improvement and to produce well-performing lines. The correlation coefficient analysis was carried out to study the relationship between the thirteen observed traits. Plant height was positively correlated with the number of leaves, stem girth and single plant yield. Days to maturity was positively correlated with single plant yield. Test weight was positively correlated with panicle width. Panicle weight, number of primary branches per panicle and test weight were also positively correlated with single plant yield. For a further selection of progenies factors like plant height, number of leaves, panicle weight, number of primary branches per panicle and test weight should be considered for developing high-yielding progenies since they were positively correlated with the single plant yield **(**Table 3). The above results were in accordance with results reported by Mengesha (2019) [7] and Swamy *et al*. (2018) [21] for plant height and days to maturity. Nirosh *et al.* (2021) [15] observed high positive correlation between single plant yield and plant height. Sweta Sinha and Kumaravadivel (2016) [18] reported that single pant yield had positive correlation with number of leaves and leaf width.

Pathway estimates illustrated that days to maturity hold the highest positive direct effect (0.3535) followed by number of leaves (0.3276), number of primary branches per panicle (0.3006), test weight (0.2371) and panicle length (0.2117). Number of leaves recorded positive direct effect and positive indirect effect which was majorly contributed by days to maturity. It also had positive indirect effect with panicle length. Lokesh Kumar Verma and Biradar (2021) [24] reported similar results for positive indirect effect for number of leaves.

Days to maturity was another trait that had positive direct effect with high phenotypic correlation with single plant yield (0.6384) and it also had positive indirect effect which was contributed by number of leaves and test weight. Chavhan *et al.* (2022) [4] reported similar results for positive indirect effect where days to maturity contributed by test weight. Panicle length had positive direct effect and positive phenotypic correlation with single plant yield. Its positive indirect effect was majorly contributed by number of leaves and test weight. This was in accordance to result observed by Arunkumar (2013) [3].

Number of primary branches per panicle revealed positive direct effect and positive indirect effect which was majorly contributed by test weight. Test weight was also chiefly contributed by number of primary branches per panicle for its positive indirect effect, which also recorded positive direct effect and moderate positive phenotypic correlation with single plant yield (0.5542). Lokesh Kumar Verma and Biradar (2021) [24] also reported positive indirect effect between primary branch per panicle and test weight.

Table 1: Descriptive statistical estimates of the thirteen quantitative traits in F_4 population of *Red sorghum*

Character	Mean	Standard Deviation	Std. Error
PH	203.305	9.407	0.660
NL	10.050	0.759	0.239
LL	27.455	3.702	0.707
LW	3.760	0.342	0.177
SG	3.215	0.388	0.217
DM	105.300	1.031	0.100
DFF	66.000	2.052	0.253
PL	18.975	1.102	0.253
PWt	34.880	1.075	0.182
PWd	4.450	0.199	0.094
NPB	34.700	2.598	0.441
TW	18.555	0.777	0.180
SPY	27.940	1.092	0.207

(Days to fifty percent flowering (DFF), Days to maturity (DM), Plant height (PH), Number of leaves per plant (NL), Leaf length (LL), Leaf width (LW), Stem girth (SG), Number of primary branches per panicle (NPB), Panicle length without peduncle (PL), Panicle width (PWD), Panicle weight (PWT), Test weight (TW), single plant (SPY).

Table 2: Genetic variability estimates of the thirteen quantitative traits in F_4 population of *Red sorghum*

Character	PCV (%)	GCV (%)	h^2 (%)	GAM (%)
PH	2.7135	2.2346	67.8185	3.7910
NL	6.1788	6.1488	99.5710	12.6664
LL	9.9757	8.3346	69.8053	14.3449
LW	17.5772	16.0604	83.4862	30.2295
SG	12.5000	12.2475	96.0000	24.7200
DM	2.3310	2.2839	96.0000	4.6098
DFF	7.8451	7.8103	99.1150	16.0179
PL	17.2253	17.1197	98.7772	35.0503
PWt	6.9086	6.8744	99.0130	14.0912
PWd	11.5169	11.3384	96.9231	22.9949
NPB	14.3411	14.3211	98.0483	29.5016
TW	24.3876	24.3784	99.9251	50.2007
SPY	15.6787	15.6053	99.0661	31.9965

(Days to fifty percent flowering (DF), Days to maturity (DM), Plant height (PH), Number of leaves per plant (NL), Leaf length (LL), Leaf width (LW), Stem girth (SG), Number of primary branches per panicle (NPB), Panicle length without peduncle (PL), Panicle width (PWD), Panicle weight (PWT), Test weight (TW), single plant (SPY).

Table 3: Correlation analysis estimates of thirteen quantitative traits in F_4 population of *Red sorghum*.

	PH	NL	LL	LW	SG	DM	DFF	PL	PWt	PWd	NPB	TW	SPY
PH	1.000												
NL	0.705^{**}	1.000											
LL	0.218	0.018	1.000										
LW	0.423	0.028	0.236	1.000									
SG	0.609^{**}	0.337	0.184	0.579^{**}	1.000								
DM	0.535^{*}	0.383	0.179	0.453^{*}	0.593^{**}	1.000							
DFF	0.087	-0.068	0.276	0.330	0.357	-0.100	1.000						
PL	0.280	0.222	0.263	-0.067	0.158	-0.076	0.005	1.000					
PWt	0.446^{*}	0.240	0.400	0.412	0.197	0.167	0.305	0.154	1.000				
PWd	0.448^{*}	0.332	0.199	0.101	0.235	0.308	-0.155	0.114	0.052	1.000			
NPB	0.303	0.141	-0.149	0.246	0.026	0.134	-0.039	-0.056	0.162	0.041	1.000		
TW	0.418	0.093	0.388	0.448^{*}	0.179	0.162	-0.007	0.158	0.241	0.459^{*}	0.431	1.000	
SPY	0.738^{**}	0.543^{*}	0.406	0.569^{**}	0.573^{**}	0.638^{**}	0.103	0.319	0.498^{*}	0.245	0.476^{*}	0.554^{*}	1.000

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

(Days to fifty percent flowering (DF), Days to maturity (DM), Plant height (PH), Number of leaves per plant (NL), Leaf length (LL), Leaf width (LW), Stem girth (SG), Number of primary branches per panicle (NPB), Panicle length without peduncle (PL), Panicle width (PWD), Panicle weight (PWT), Test weight (TW), single plant (SPY).

Table 4: Pathway estimates of the thirteen quantitative traits in F_4 population of *Red sorghum*

	PH	NL	LL	LW	SG	DM	DFF	PL	PWt	PWd	NPB	TW	SPY
PH	-0.0879	0.2308	0.0416	0.0487	0.0899	0.1893	-0.0024	0.0592	0.0558	-0.0777	0.0912	0.0992	0.7376
NL	-0.062	0.3276	0.0034	0.0033	0.0496	0.1355	0.0019	0.0469	0.03	-0.0575	0.0425	0.0221	0.5433
LL	-0.0191	0.0058	0.1910	0.0271	0.0271	0.0632	-0.0076	0.0558	0.0501	-0.0346	-0.0449	0.0920	0.4060
LW	-0.0372	0.0093	0.045	0.1151	0.0853	0.1602	-0.0091	-0.0142	0.0516	-0.0174	0.0740	0.1062	0.5688
SG	-0.0536	0.1102	0.0351	0.0666	0.1475	0.2096	-0.0098	0.0335	0.0247	-0.0408	0.0077	0.0423	0.5730
DM	-0.0471	0.1255	0.0342	0.0522	0.0874	0.3535	0.0027	-0.0162	0.0209	-0.0535	0.0402	0.0385	0.6384
DFF	-0.0076	-0.0221	0.0527	0.0379	0.0526	-0.0352	-0.0276	0.001	0.0382	0.0269	-0.0119	-0.0016	0.1033
PL	-0.0246	0.0726	0.0503	-0.0077	0.0234	-0.027	-0.0001	0.2117	0.0193	-0.0198	-0.0169	0.0376	0.3187
PWt	-0.0392	0.0786	0.0765	0.0474	0.0291	0.0591	-0.0084	0.0326	0.1252	-0.009	0.0486	0.0572	0.4976
PWd	-0.0394	0.1086	0.0381	0.0116	0.0347	0.109	0.0043	0.0242	0.0065	-0.1735	0.0123	0.1087	0.2450
NPB	-0.0267	0.0463	-0.0285	0.0283	0.0038	0.0472	0.0011	-0.0119	0.0202	-0.0071	0.3006	0.1022	0.4756
TW	-0.0368	0.0305	0.0742	0.0516	0.0263	0.0574	0.0002	0.0335	0.0302	-0.0795	0.1296	0.2371	0.5542

Residual effect = 0.2737

Days to fifty percent flowering (DFF), Days to maturity (DM), Plant height (PH), Number of leaves per plant (NL), Leaf length (LL), Leaf width (LW), Stem girth (SG), Number of primary branches per panicle (NPB), Panicle length without peduncle (PL), Panicle width (PWD), Panicle weight (PWT), Test weight (TW), single plant (SPY)

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