



## **Genetic Association of Root and Yield Traits in Two Recombinant Inbred Populations of Sorghum Under Terminal Drought Condition**

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### **ABSTRACT**

Root traits are key determinants of the ability of a plant to access water and nutrients to support growth. Yet, the root system in general has been studied far less intensively than the shoot. Thus, in the present investigation two Recombinant Inbred Populations (RIPs) developed from crosses viz., E36-1 x Basavanapada (RIP1) and E36-1 x SPV70 (RIP2) segregating for high root volume and root length respectively, were characterized to study genetic basis for root and yield related traits and to determine relationships among contributing traits towards drought tolerance and yield of sorghum under water limited condition. Analysis of variance revealed significant difference among the Recombinant Inbred Lines (RILs) of both the populations and the high values of PCV, GCV, heritability coupled with genetic advance as per cent of mean were evident for early seedling vigour, panicle exertion, 100 seed weight, seed yield per plant and for root traits in both the populations indicating that simple selection would be sufficient to bring genetic improvement of these traits. Correlation analysis exhibited highly significant positive association among the root related traits; and root traits with days to 50 per cent flowering and panicle length in RIP1; and early seedling vigour in RIP2 populations; suggests that these traits could be improved simultaneously and might be reliable selection criteria for drought tolerance in sorghum. However, the lack of significant negative association of root related traits and seed yield per plant in both populations provides the scope for improvement of root and yield simultaneously.

**Key words:** Sorghum, Variability, Correlation, Heritability, Genetic Advance, Root traits

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### **INTRODUCTION**

Sorghum is an important staple food crop for millions of people and good cattle feed in the arid and semi-arid regions of the world, including India. Due to its adaptation to arid environments, diverse germplasm, and relatively small genome (760 Mbp), sorghum is considered as an excellent model crop of choice for studying the genetic and physiological mechanisms of drought tolerance. In India, *rabi* (post-rainy) sorghum is a major form of sorghum grain preferred for human consumption due to superiority of the grain largely owing to its maturation under dry and cloud free conditions. Although sorghum has an ability to cope up with many types of stresses, including heat, drought, salinity and flooding [1], in arid and semi-arid regions this crop is usually affected by water stress at the reproductive stage particularly post flowering stage [2, 3]. Thus, drought is a major constraint limiting *rabi* sorghum productivity under post-rainy situations.

Drought stress has diverse effects on yield in sorghum depending on the development stage at which it occurs. Incidence of water stress in sorghum during flowering and anthesis lead to the failure of fertilization because of the impairment of pollen and ovule function, reduces leaf area, causes death of florets, reduces seed yield *via* reduction of seed weight and/or number of seeds per panicle and also causes premature leaf senescence which in-turn leads to stalk lodging, stalk rot disease and significant yield loss [2-5]. Therefore, drought tolerance has been a prime breeding objective in *rabi* sorghum

improvement programmes.

The traits such as prolific root system, high osmotic adjustment, and stay-green are the target traits in sorghum to achieve economic yields in drought-prone environments. The best characterized form of drought tolerance during terminal stage of sorghum growth is the “stay-green” traits, which is defined as the ability to resist premature plant senescence, retain green leaf area, fill grain normally and resist lodging under conditions of post-flowering drought stress [6]. The concerted efforts have been made in the past to identify stay-green genotypes and mapping of QTLs associated with this trait [2, 3, 7, 8]. However, root system architecture and root distribution are key determinants of the ability of a plant to access water and nutrients to support shoot growth in water limiting conditions [9]. Despite of its importance root has received less attention than the shoot as a trait either for screening or selection for drought resistance and hence, there is currently little understanding of the potential role of root system architecture for improving drought tolerance of sorghum. This appears partly due to the limited knowledge of the morphological and architectural development of the sorghum root system, and the lack of fast and effective root screening techniques. Further, simulation of field situations in artificial structures like rhizotron can greatly aid in understanding the traits related to root system.

The first study on sorghum root system under field conditions was reported by Miller [10]. He recorded sorghum root growth up to a depth of 180 cm and lateral distance of about 90 cm. Few reports have presented evidence of genotypic variation for root traits and potential importance for drought adaptation in sorghum [11-15], based on studies involving a limited number of genotypes. Salih *et al.* [16] reported that the roots of a drought tolerant sorghum line grew at least 40 cm deeper than a drought sensitive one. Further, most of the research endeavors to study root system were conducted using solution culture [17] or in small pots [18] in greenhouses/growth chambers and rhizotrons (rarely) that too for a limited number of traits at early stages of plant growth in general. Further, Dhanda *et al.* [19] and Khan *et al.* [20] reported that drought adapted plants often characterized by deep and vigorous root system. Correlation and path coefficient analysis using seventeen sorghum land races by Ali *et al.* [21] demonstrated that fresh root shoot weights, dry shoot weight and root to shoot ratio were important criteria for drought tolerance as well as higher grain yield at seedling stage. Further, Girish *et al.* [22] using twenty three advanced sorghum lines reported moderate to high heritability along with genetic advance as percent of mean for root volume and fresh root weight along with significant positive correlation between root traits. However, evaluation of large population under simulation of field situations in artificial structures (rhizotron) can greatly aid in understanding the traits related to root system. Therefore, two large Recombinant Inbred Populations (RIPs) developed from a crosses viz., E36-1 x Basavanapada (RIP1) and E36-1 x SPV70 (RIP2) segregating for high root volume and root length respectively, were characterized under natural drought condition (*rabi*) in an above ground rhizotron structure, to study genetic basis for root and yield related traits and determination of the relationships among contributing traits towards drought tolerance and yield of sorghum under water limited condition.

## MATERIAL AND METHODS

**Plant material:** Experiment material consisted of two RIPs consisting of 226 F<sub>9</sub> lines and 184 F<sub>8</sub> lines of RIP1 and RIP2, respectively. E36-1, a female parent for root trait in these RIPs, is a high yielding line from guinea-caudatum hybrid race with Ethiopian origin, well adapted to tropical environment but has thin and short roots. The Basavanapada and SPV570, pollen parents have high root volume and root length respectively besides known for better adaptability, quality grain and fodder of *rabi* sorghum in North Karnataka, India [23].

**Field experiment and Phenotyping of root traits:** RI populations along with parents and a check (RS-29) were evaluated in a 19×12 and 16×12 simple lattice design with three replications. Recommended package of practices were followed throughout the cropping season. Three randomly selected plants from each replication for each RIL (Recombinant Inbred Line) was used for recording observation on early seedling vigour (ESV), days to 50 per cent flowering (DF), plant height (cm) (PH), number of leaves (NL), panicle length (cm) (PL), panicle exertion (cm) (PE), number of spikelets per plant (NSP), plant girth (cm) (PG), 100-seed weight (g) (SW) and seed yield per plant (SYP) (g) as described in descriptor for sorghum [24].

The rhizotron, an above ground type was constructed (25 m long, 4 m wide and 1.5 m height) with collapsible walls on all four sides with cement block. The rhizotron was filled with a mixture of the local alluvial clay and sandy loam soil. The soil was wetted completely and allowed to settle and drain to achieve the required compaction. Both RIPs along with the parents and check were evaluated under rhizotron structure. Recommended practices were followed throughout the cropping season to raise crop. Irrigation water was applied to field capacity until flowering, (up to 55 DAS) and thereafter, daily irrigation was applied only to wet the treatment until harvest. Roots were sampled for observation of

root traits on 110 DAS (days after sowing). One side of the rhizotron wall was collapsed and the whole root system of each line was carefully taken out by loosening the soil around the root profile and the soil adhered to root was carefully washed using a very slow water spray to minimize disturbance of the root system. After all soil had been removed, the intact washed root system was separated from shoot and the following root parameters were recorded *viz.*, root length (cm) (RL), root volume (cm<sup>3</sup>) (RV), number of roots per plant (NR), root to shoot ratio (RS), root fresh weight (g) (RFW) and root dry weight (g) (RDW) (after drying fresh roots in hot air oven at 80 °C for 48 h).

**Statistical analysis:** The mean data recorded for root and yield traits were subjected to the analysis of variance (ANOVA). The phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were calculated as per the method suggested by Burton and Devane [25]. Heritability in broad sense expressed in percentage as suggested by Hanson *et al* [26] and genetic advance was estimated by using the formula given by Johnson *et al.* [27]. The GCV and PCV values and genetic advance as per cent of mean (as per Johnson *et al.* (27) were categorized as low (0-10%), moderate (11-20%) and high (>20%). While, heritability (h<sup>2</sup>) was classified into low (0-30%), medium (30-60%) and high (>60%) as suggested by Robinson *et al.* [28]. Genotypic and phenotypic correlation coefficients for all the characters were estimated using method suggested by Singh and Choudhary [29].

## RESULT AND DISCUSSION

**Variance components, heritability and genetic advance:** The data of all studied 16 traits followed normal distribution, therefore used directly for analysis without transformation. Analysis of variance revealed highly significant differences among RILs and respective parents for all the 16 traits studied (Table 1) indicated high genetic variability thus provides ample scope for selection. Such genetic variability among these RILs would be obvious as these populations were developed from deliberately selected, phenotypically distinct parents for high root volume (RIP1) and root length (RIP2), respectively. A wide range of variation for the investigated traits in these RILs, normal phenotypic distribution, higher value of PCV than GCV for both populations, suggested polygenic inheritance of traits and the utility of the RILs for genetic investigations. The extent of variability in terms of range, mean, PCV, GCV, heritability and genetic advance as per cent of mean were worked out for all the traits and the results are presented in the Table 2. In both the RIPs high values of PCV and GCV were evident for early seedling vigour, panicle exertion, 100 seed weight, seed yield per plant and root traits, *viz.*, root volume, number of roots per plant, root fresh weight and root dry weight emphasizes that variation in these characters contributed markedly to the total variability and represents the potentiality of these traits for improvement. High values of variability for yield traits were also reported in earlier studies Rajkumar *et al.* (30) and Gebre (31); and for root related traits by Thudi [23] and Girish *et al.* [22].

**Table 1: Mean phenotypic values of parental lines and mean sum of squares for root and yield related traits in recombinant inbred lines of RIP1 and RIP2**

Traits	RIP2 (E36-1 x SPV570)			RIP1 (E36-1 x Basavanapada)			Parental lines		
	CD 5 %	Error MSS	Replication MSS	CD 5 %	Error MSS	Replication MSS	SPV570	Basavanapada	E36-1
	0.95	0.21	3.48**	1.04	0.24	2.92	1.67	2.00	3.33
	12.16	33.44	140.60**	10.19	23.48	133.03	67.67	75.33	54.67

50.53	2.33	3.74	5.18	14.81	1.71	0.81	26.29	26.59	12.69	16.3	8.68	0.29	22.6
577.16	1.23	3.17	6.06	49.58	0.66	0.15	156.19	159.8	36.4	60.03	17.05	0.02	115.41
4770.78**	2.87**	75.55**	20.90**	160.22**	1.38**	1.39**	722.45**	1855.33*	799.72**	1541.01**	1239.15**	0.07**	1813.81**
4728.38	185.52	7.71	32.46	1667.53	26.81	10.04	11372.14	784.49	225.66	2513.84	54.49	0.21	2690.52
54.69	2.38	5.36	7.05	15.47	1.61	0.62	35.65	25.26	12.67	13.54	9.53	0.21	12.53
676.02	1.29	6.51	11.23	54.07	0.58	0.09	287.32	144.22	36.26	41.43	20.54	0.01	35.49
4520.45**	3.77**	40.87**	16.77**	111.39**	1.72**	1.82**	1752.60**	5098.37*	1230.89**	1415.79**	1562.90**	0.09**	1372.41**
1843.83	63.20	19.90	98.89	2376.52	0.72	0.32	3081.39	670.76	591.51	1972.82	307.23	0.02	1125.96
207.78	7.22	17.44	14.22	24.78	3.78	2.23	175.00	89.00	50.00	78.67	54.00	0.81	34.33
266.67	8.33	18.33	15.22	35.11	4.22	2.97	155.67	136.33	66.00	93.67	64.33	0.59	40.33
153.89	10.00	6.11	23.67	53.11	5.78	3.50	141.67	56.00s	36.00	54.00	21.33	0.85	65.00
Plant height (cm)	Number of leaves	Panicle exertion (cm)	Panicle length (cm)	Number of spikelets per plant	Plant girth (cm)	100 seed weight (g)	Root length (cm)	Root volume (cm <sup>3</sup> )	Number of roots per plant	Root fresh weight (g)	Root dry weight (g)	Root to shoot ratio	Seed yield per plant

Where, \* and \*\*= significant at P>0.05 and P>0.01, respectively, CD: critical difference, MSS: Mean sum of square

**Table 2: Range, mean and estimates of variability parameters for root and yield related traits in recombinant inbred lines of RIP1 and RIP2**

RIP2 (E36-1 x SPV570)	GAM		78.42	15.37	32.29	12.22	71.20	19.77	24.57	15.23	42.88	26.28
	h <sup>2</sup> (%)		94.10	76.21	87.90	57.20	95.80	70.99	69.06	51.92	89.45	78.38
	GCV (%)		39.24	8.55	16.72	7.84	35.31	11.39	14.35	10.26	22.01	14.93
	PCV (%)		40.45	9.79	17.83	10.37	36.08	13.52	17.27	14.24	23.27	10.08
	Mean		2.66	70.00	223.65	9.00	13.91	19.53	42.00	4.76	2.93	153.91
	Range	Max.	5.00	91.00	350.00	13.00	25.00	27.00	76.33	8.00	5.00	210.00
		Min.	1.00	50.00	97.67	6.00	2.00	1.64	16.67	2.33	1.00	90.00
	GAM		63.54	19.88	29.91	17.41	43.50	8.38	13.44	20.23	43.02	34.63
	h <sup>2</sup> (%)		91.23	86.53	85.05	65.94	84.08	33.04	51.46	66.02	95.30	83.61
	GCV (%)		32.29	10.37	15.75	10.41	23.03	7.08	9.10	12.09	21.39	18.39
RIP1 (E36-1 x Basavanapada)	PCV (%)		33.81	11.15	17.07	12.82	25.11	12.32	12.68	14.88	21.91	20.11
	Mean		2.84	68.00	227.34	8.00	14.70	19.19	48.06	5.08	3.56	120.20
	Range	Max.	5.00	90.00	350.00	13.00	33.67	35.67	74.33	8.00	5.80	165.00
		Min.	1.00	49.00	81.67	5.00	3.33	6.00	22.00	2.33	1.50	85.00
	Trait		Early seeding vigor	Days to 50 % flowering	Plant height (cm)	Number of leaves	Panicle exertion (cm)	Panicle length (cm)	Number of spikelets per plant	Plant girth (cm)	100 seed weight (g)	Root length (cm)

56.34	62.13	55.22	76.42	28.03	68.90
91.39	95.45	96.10	98.62	73.27	93.64
28.61	30.87	27.35	37.36	15.89	34.56
29.93	31.60	27.89	37.61	18.57	35.72
83.10	51.67	81.25	54.03	0.82	68.84
142.65	96.00	135.00	97.00	1.64	136.00
22.25	10.00	39.00	9.00	0.41	14.00
69.64	64.44	46.57	72.42	53.20	64.79
97.17	97.05	97.07	98.69	88.58	97.41
34.29	31.75	22.94	35.39	27.44	31.86
34.79	32.23	23.29	35.63	29.15	32.28
118.50	62.85	93.29	64.07	0.59	66.25
220.00	114.00	150.00	109.00	1.73	138.00
30.00	14.00	40.00	11.00	0.04	20.00
Root volume (cm <sup>3</sup> )	Number of roots per plant	Root fresh weight (g)	Root dry weight (g)	Root to shoot ratio	Seed yield per plant

Where, GCV – Genotypic coefficient of variance; PCV – Phenotypic coefficient of variance;  $h^2$  – Heritability in broad sense; GAM – Genetic advance as per cent of mean;

**Table 3a: Coefficient of genotypic (upper diagonal) and phenotypic (lower diagonal) correlation among root and yield related traits in the recombinant inbred lines (RILs) derived from the cross E36-1 x Basavanapada (RIP1)**

SYP	-0.178**	-0.001	0.115**	0.035	0.046
RS	0.128**	0.146**	-0.092*	0.016	-0.023
RDW	0.063	0.099**	-0.048	-0.156**	0.066
RFW	0.054	0.092*	-0.028	-0.131**	0.066
NR	0.011	0.090*	-0.045	-0.124**	0.127**
RV	0.02	0.086*	-0.045	-0.114**	0.105**
RL	0.069	0.078*	-0.113**	0.053	0.168**
SW	-0.185**	-0.017	0.113**	0.112**	-0.001
PG	0.035	-0.023	-0.054	0.090*	0.091*
NSP	-0.075*	-0.156**	0.233**	0.392**	0.036
PL	-0.255**	-0.246**	0.145**	-0.277**	0.242**
PE	-0.005	0.039	-0.054	-0.135**	1
NL	-0.327**	0.109**	0.227**	1	-0.092*
PH	-0.124**	0.089*	1	0.200**	-0.046
DF	0.063	1	0.075	0.086*	0.043
ESV	1	0.068	-0.108**	-0.270**	0.002
Traits	ESV	DF	PH	NL	PE

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0.067	0.208**	0.004	0.193**	-0.013	-0.012	-0.024	-0.055	-0.053	-0.034	1
0.174**	-0.391**	-0.080*	-0.174**	0.761**	0.618**	0.595**	0.574**	0.574**	1	0.029
0.265**	-0.306**	-0.128**	-0.148**	0.724**	0.933**	0.967**	0.998**	1	0.538**	-0.052
0.274**	-0.289**	-0.111**	-0.130**	0.740**	0.940**	0.975**	1	0.995**	0.535**	-0.055
0.270**	-0.200**	-0.071	-0.094*	0.792**	0.978**	1	0.947**	0.941**	0.550**	-0.025
0.328**	-0.260**	-0.042	-0.099**	0.832**	1	0.953**	0.914**	0.914**	0.5753**	-0.012
0.191**	-0.206**	0.053	-0.154**	1	0.756**	0.714**	0.668**	0.6586**	0.732**	-0.011
-0.027	0.126**	0.005	1	-0.126**	-0.094*	-0.090*	-0.122**	-0.143**	-0.152**	0.185**
-0.134**	-0.017	1	-0.001	0.047	-0.033	-0.058	-0.095*	-0.101**	-0.054	-0.001
-0.124**	1	0.018	0.095*	-0.107**	-0.179**	-0.161**	-0.197**	-0.217**	-0.242**	0.142**
1	-0.038	-0.036	-0.012	0.100**	0.179**	0.153**	0.138**	0.147**	0.080*	0.038
0.163**	0.031	0.064	-0.002	0.135**	0.095*	0.115**	0.064	0.059	-0.013	0.034
-0.135**	0.233**	0.059	0.080*	0.037	-0.094*	-0.095*	-0.102**	-0.126**	0.015	0.027
0.089*	0.163**	-0.055	0.101**	-0.092*	-0.039	-0.036	-0.024	-0.042	-0.080*	0.104**
-0.140**	-0.117**	-0.022	-0.012	0.067	0.081*	0.087*	0.084*	0.094*	0.131**	0.001
-0.141**	-0.07	0.017	-0.170**	0.059	0.014	0.016	0.045	0.059	0.111**	-0.166**
PL	NSP	PG	SW	RL	RV	NR	RFW	RDW	RS	SYP

Where, \* and \*\*= significant at  $P>0.05$  and  $P>0.01$  respectively, ESV: Early seedling vigour; DF: Days to 50 per cent flowering; PH: Plant height (cm); NL: Number of leaves; PL: Panicle length (cm); PE: Panicle exertion (cm), NSP: Number of spikelets per plant; PG: Plant girth (cm); SW: 100-seed weight (g) and SYP: seed yield per plant (g).

**Table 3b: Coefficient of genotypic (upper diagonal) and phenotypic (lower diagonal) correlation among root and yield related traits in the recombinant inbred lines (RILs) derived from the cross E36-1 x SPV50 (RIP21)**

Traits	ESV	DF	NL	PH	PE	PL	NSP	PG	SW	RL
<b>SYP</b>	0.029	-0.038	0.102**	0.135**	-0.175**	0.079	0.195**	0.243**	0.579**	-0.072
<b>RS</b>	0.181**	-0.076	-0.013	0.024	-0.086*	-0.198**	-0.177**	0.038	0.027	0.284**
<b>RDW</b>	0.143**	0.04	-0.098*	-0.08	0.044	-0.120**	-0.108*	-0.136**	0.069	0.985**
<b>RFW</b>	0.148**	0.009	-0.095*	-0.072	0.029	-0.136**	-0.150**	-0.152**	0.064	0.988**
<b>NR</b>	0.077	0.005	-0.101*	-0.086*	0.03	-0.109**	-0.082	-0.110**	0.098*	0.978**
<b>RV</b>	0.103*	0.062	-0.084*	-0.100*	0.031	-0.155**	-0.113**	-0.137**	0.046	0.998*
<b>RL</b>	0.117**	-0.007	-0.106*	-0.085*	0.076	-0.074	-0.064	-0.098*	0.093*	1
<b>SW</b>	0.038	0.067	0.140**	0.042	-0.094*	-0.123**	0.052	0.276**	1	0.08
<b>PG</b>	0.031	0.131**	0.403**	0.352**	-0.153**	0.093*	0.439**	1	0.212**	-0.106*
<b>NSP</b>	-0.085*	0.247**	0.359**	0.186**	-0.037	0.389**	1	0.307**	0.031	-0.034
<b>PL</b>	-0.193**	-0.110**	0.176**	0.321**	0.215**	1	0.256**	0.075	-0.091*	-0.061
<b>PE</b>	-0.157**	0.106*	-0.133**	0.063	1	0.192**	-0.032	-0.119**	-0.084*	0.076
<b>PH</b>	-0.089*	-0.005	0.560**	1	0.057	0.254**	0.140**	0.279**	0.028	-0.07
<b>NL</b>	-0.142**	0.130**	1	0.426**	-0.097*	0.153**	0.247**	0.288**	0.089*	-0.063
<b>DF</b>	0.07	1	0.090*	-0.002	0.091*	-0.081	0.114**	0.076	0.05	-0.002
<b>ESV</b>	1	0.062	-0.112**	-0.076	-0.149**	-0.159**	-0.049	0.032	0.033	0.108*

-0.014	-0.017	0.008	-0.022	-0.01	1
0.356**	0.400**	0.372**	0.332**	1	-0.005
0.976**	0.937**	0.998**	1	0.282**	-0.023
0.990**	0.978**	1	0.980**	0.310**	0.003
0.994**	1	0.931**	0.918**	0.328**	-0.023
1	0.916**	0.949**	0.928**	0.284**	-0.012
0.874**	0.943**	0.891**	0.882**	0.270**	-0.064
0.046	0.088*	0.065	0.063	0.038	0.522**
-0.114**	-0.095*	-0.118**	-0.108*	0.038	0.199**
-0.073	-0.055	-0.091*	-0.076	-0.078	0.134**
-0.114**	-0.098*	-0.108*	-0.105*	-0.149**	0.049
0.025	0.029	0.025	0.041	-0.07	-0.169**
-0.090*	-0.082	-0.063	-0.072	0.009	0.118**
-0.054	-0.069	-0.066	-0.071	-0.024	0.071
0.063	0.002	0.005	0.031	-0.054	-0.037
0.095*	0.071	0.139**	0.133**	0.135**	0.027
RV	NR	RFW	RDW	RS	SYP

Where, \* and \*\*= significant at  $P>0.05$  and  $P>0.01$  respectively, ES:V: Early seedling vigour; DF: Days to 50 per cent flowering; NL: Number of leaves; PH: Plant height (cm); PL: Panicle length (cm); PE: Panicle exertion (cm), NSP: Number of spikelets per plant; PG: Plant girth (cm); SW: 100-seed weight (g) and SYP: seed yield per plant (g).

Moderate PCV and GCV were noticed for traits such as plant height and plant girth in both the populations. Moderate values for plant height was in agreement with previous reports of [31, 32] and for plant girth by Mukri [33]. The moderate variability values for the above traits indicated considerable influence of environment on these traits. Thus, these traits are restrictedly amenable for further improvement. Among all the 16 traits studied in both the populations, variability was comparatively low for days to 50 per cent flowering in RIP2. This could be because of less variation for days to 50 per cent flowering between the parents (57 days for E36-1, 67 days for SPV570).

The coefficient of variation indicates only the extent of variability present in different characters and do not indicate the heritability portion. Thus, Johnson *et al.* [27] suggested that heritability in conjunction with genetic advance is more effective and reliable in predicting resultant effect of selection than heritability alone. High heritability coupled with high genetic advance as per cent of mean was noticed for early seeding vigour, plant height, panicle exertion, 100 seed weight, seed yield per plant, and for root traits in both populations. From, this it would be inferred as the genotypic variance for these traits were primarily due to additive genetic effect and selection based on phenotypic performance could be worth in achieving desired results. Thus, the high genotypic potentiality of root traits studied contributes to drought tolerance, as the efficiency of soil water uptake is determined by the root system. Therefore, root traits are key factor in determining the tolerance to drought. This kind of trend for yield related traits was already known in sorghum [32, 33] and for root related trait was reported earlier [14, 15, 21-23].

**Correlation among the root and yield related traits:** Drought being a complex character and its expression depends on interplay of several component characters. Thus, information regarding the nature and extent of association between any two pairs of metric characters is of much importance. The phenotypic and genotypic correlation coefficients are worked out among different characters (Table 3a for RIP1 and Table 3b for RIP2) revealed that genotypic correlations coefficients were higher than phenotypic correlations. The higher genotypic correlation coefficient suggests the inherent relationship

between characters and its contribution to the relative stability of the RILs under study.

Correlation coefficients among 16 traits in both the populations revealed a lot of significant and practical associations. A total of 79 and 72 significant correlation coefficients were observed among the traits in RIP1 and RIP2, respectively. The highest correlation coefficient was observed among root fresh weight and root dry weight ( $r = 0.998$ ) followed by root volume and number of roots per plant ( $r = 0.978$ ) in RIP1. Likewise, a highest correlation of  $r = 0.998$  between root length and root volume; and root fresh weight and root dry weight was recorded in RIP2. However, highly significant positive correlation observed among all the root related characters in both the populations was obvious, as these populations have reached the homozygous status for these traits. Girish *et al.* [22] also reported significant positive correlation between root traits such as root weight and root length, root volume and root length; and dry root weight and root length.

In RIP1 the root traits revealed significant positive association with days to 50 per cent flowering and panicle length on the contrary significant negative relation with number of spikelets per plant and 100 seed weight. Likewise, root length and root to shoot ratio displayed negative association with plant height. Root volume, number of roots per plant, root fresh weight and root dry weight showed negative association with number of leaves. While, root length, root volume, number of roots per plant positively associated with panicle exertion, on the contrary plant girth found to be negatively related with root fresh weight, root dry weight and root to shoot ratio. Similarly, in RIP2 all the root related traits were positively associated with early seedling vigour (except root volume), while negatively with number of spikelets per plant and number of leaves (except root shoot ratio). Root length and number of roots per plant positively associated with 100 seed weight. Likewise, root length, root volume, number of roots per plant negatively associated with plant height, in a similar way root volume, root fresh weight, root dry weight and root to shoot ratio negatively associated with plant girth and panicle length.

The above correlation results implicated that the root related parameter along with days to 50 per cent flowering and panicle length in RIP1; and early seedling vigour in RIP2 could be selected simultaneously due to absence of negative relationship among these traits and this also points out that these parameters could be utilized as selection criteria for drought tolerance. Further, root related traits did not show any significant negative correlation with seed yield per plant in both populations. Thus, provides opportunity for simultaneous improvement of root and yield related traits. Turner [34] reported positive correlations between seed yield and root development in cereals, especially in barley, wheat and sorghum. Matsuura *et al.* [35] also reported a positive relation between drought tolerance and root length in four gramineous crops (barnyard millet, maize, pearl millet and sorghum).

The significant positive correlation of seed yield per plant with plant height, number of spikelets per plant and 100 seed weight in RIP1; and number of leaves, plant height, plant girth, number of spikelets per plant and 100 seed weight in RIP2 implicates that increased grain yield in these populations can be achieved through improvement in one or more of the above character. Earlier studies in germplasm and other mapping populations also reported similar positive association of yield with these traits [8, 36, 37].

## CONCLUSION

The significant positive association among the root related traits supported with high estimates of heritability coupled with genetic advance in both the populations clearly paves the way for improvement of drought tolerance by selecting these root related traits. However, lack of significant negative correlation between the root related traits and seed yield per plant in both populations, indicated that the selection for both root (drought) and yield related traits will not have unforeseen consequences. It is thus possible to combine higher grain yield and desirable root morphological traits, favorably, to enhance productivity of sorghum under receding moisture condition.

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