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Multi-Trait Diverse Germplasm Sources from Mini Core Collection for Sorghum Improvement

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Abstract: Sorghum is a multipurpose crop cultivated in over 100 countries, but its productivity is constrained by several biotic and abiotic stresses. Therefore, sorghum improvement programs largely focus on developing high-yielding cultivars with multiple traits including stress resistance, bioenergy and nutritional quality. This study was undertaken to meet breeders' needs to develop such cultivars and identify diverse germplasm sources with multiple traits. The 242 sorghum mini core accessions were evaluated for agronomic traits (yield, maturity, 100-seed weight) in two post-rainy seasons under optimally irrigated and drought conditions and identified 21 accessions as a sources for agronomic traits. The evaluation of mini core revealed 70 accessions resistant to biotic stress, 12 to abiotic stress, 13 for bioenergy traits and 27 for nutritional traits. The 13,390 single nucleotide polymorphism markers on mini core were used to identify genetically diverse accessions with desirable agronomic traits: IS 23684 (nutrition traits, diseases, insect pests), IS 1212 (earliness, nutrition traits, drought, seedling vigor, diseases), IS 5094 (yield, drought, diseases, insect pests), IS 473 (earliness, diseases), IS 4698 (yield, Brix %, insect pests) and IS 23891 (greater seed weight, yield, Brix %, drought, diseases). These are useful genetic resources that meet breeders needs to develop agronomically superior sorghum cultivars with desirable combinations of multiple traits and a broad genetic base.

Keywords: agronomic traits; biotic and abiotic stresses; genetic diversity; mini core; sorghum; trait-specific germplasm

1. Introduction

Sorghum (*Sorghum bicolor* (L.) Moench) is a C₄ multipurpose crop with high photosynthetic efficiency, which is a staple food crop for millions of the poorest and most food-insecure people in the semi-arid tropics. Sorghum is the fifth most important cereal after maize (*Zea mays* L.), rice (*Oryza sativa* L.), wheat (*Triticum aestivum* L.), and barley (*Hordeum vulgare* L.). Africa (46.7%), the Americas (36.1%) and Asia (12.5%) are the major sorghum producing regions of the world that together contributed 95% of the world's sorghum production during 2016 (<http://www.faostat.fao.org>; data accessed in April, 2018). Globally, sorghum is cultivated on 44.8 m ha in 110 countries with an annual production

of 63.9 m t. The global yield of sorghum in 2016 was only 1428 kg ha⁻¹, which is rather low. There were severe regional imbalances in the yield of sorghum which varied from 977 kg ha⁻¹ in Africa, 1091 kg ha⁻¹ in Asia to 3840 kg ha⁻¹ in the Americas. Country-wise yields vary much more drastically; 39 countries of the world covering over 50% of the area (26.2 m ha) have yields ranging from 152 kg ha⁻¹ in Eritrea to 1000 kg ha⁻¹ in Ghana. Further, of the top 10 countries area-wise, five countries, Sudan (9.2 m ha), India (5.8 m ha), Niger (3.6 m ha), Mali (1.6 m ha) and Chad (1.2 m ha), had yields ranging from 502 kg ha⁻¹ in Niger to 706 kg ha⁻¹ for Sudan, 780 kg ha⁻¹ for India, and 832 kg ha⁻¹ for Chad to 893 kg ha⁻¹ for Mali. Nigeria (5.8 m ha) and Burkina Faso (1.7 m ha) had yields of 1193 kg ha⁻¹ and 1055 kg ha⁻¹, respectively (<http://www.faostat.fao.org>; data accessed in April, 2018).

Sorghum production is constrained by several biotic (diseases: downy mildew, grain mold, anthracnose, rust, leaf blight, etc.; insect pests: stem borer, shoot fly, midge, aphids, etc.) and abiotic (drought, heat, salinity, cold, aluminium toxicity, nutrient deficiency, etc.) stresses, resulting in low productivity of sorghum. Available scientific evidences indicated that the improved sorghum hybrids and cultivars were less diverse as compared to wild and weedy relatives and landraces [1,2]. The improved sweet sorghum lines in the USA were originally derived from six landraces, indicating that the majority of lines have similar genes/alleles for high Brix % and plant height [3]. The genetic diversity assessment of USA sorghum hybrids that were widely cultivated from 1980 to 2008 revealed that the hybrids released during the 2000s had the least number of new alleles as compared to the previous two decades [4]. Similarly, in Australian sorghum breeding programs, a strong selection for resistance to sorghum midge, stay-green (a drought resistance trait) and other agronomic traits have been associated with a decline in genetic diversity [5,6].

The low diversity of crop cultivars is mainly because most crop breeders use their working collections containing limited numbers of adapted and improved materials that have the most desirable traits and avoid using wild and weedy relatives and unadapted landraces in the hybridization program. Such a narrow genetic base of cultivars might result in increased risk of crop vulnerability, i.e., crop failure, due to insect pests and disease epidemics or unpredictable climatic effects. History has witnessed numerous epidemics caused by low levels of nuclear and cytoplasmic genetic diversity, including the late blight that affected temperate potatoes in the northern hemisphere in the 1840s, wheat stem rust which devastated wheat fields in 1917, the Bengal famine in India in 1943 due to rice brown spot disease and the southern corn leaf blight epidemic of maize in the USA in 1970 [7]. There are several recent incidences of disease outbreak and re-occurrences, including the outbreak of wheat rust disease in Germany in 2013 and 2016, the United Kingdom in 2013, Ethiopia and Sicily in 2016 [8,9], indicates that the disease is re-emerging as a threat to wheat production. Lewis [9] reported that about 80% of current UK wheat varieties are susceptible to the stem rust isolate UK-01. This demands identification and utilization of germplasm for introduction of new variability for disease resistance and other traits.

The identification of trait-specific germplasm from large ex situ collections is key to successful introgression of new diversity into the crop improvement programs [10]. Greater use of such diversity in sorghum breeding programs so as to develop cultivars with a broad genetic base will result in sustainable sorghum production. The aim of the present investigation was to assess the agronomic performance of sorghum mini core collection [11], a germplasm diversity panel representative of the global sorghum collection, and identify genetically diverse multi-trait-specific germplasm sources, considering agronomic performance and published information on the response of sorghum mini core accessions to biotic [12–17] and abiotic [17–19] stresses, and for grain nutritional [20] and bioenergy traits [21,22].

2. Materials and Methods

2.1. Description of Materials

The sorghum mini core collection consisting of 242 accessions [11], originating from 57 countries, and three controls (IS 33844, IS 2205, and IS 18758) were used in this study. The mini core collection accessions included all the five basic races (*caudatum* 16.1%, *durra* 12.4%, *guinea* 12%, *kafir* 8.7%, and

bicolor 8.3%) and 10 intermediate races (*caudatum-bicolor* 12.4%; *guinea-caudatum* 11.2%; *durra-caudatum* 7.9%; *durra-bicolor* and *kafir-caudatum* each 2.9%; *kafir-durra* 1.7%; *guinea-kafir* 1.2%; and *guinea-bicolor*, *guinea-durra*, and *kafir-bicolor* each 0.8%) of sorghum [11]. The controls: IS 33844 (Parbhani Moti) is the most popular sorghum cultivar grown under receding soil moisture conditions during the post-rainy season in India, is tolerant to terminal drought, and possesses excellent grain quality attributes [18]; IS 18758 is cultivated in Burkina Faso and Burundi [23]; IS 2205, a *durra-bicolor* landrace from India, is resistant to shoot fly (*Atherigona soccata* (Rondani)) and stem borer (*Chilo partellus* (Swinhoe)) [24].

2.2. Experimental Details

The experiment was conducted in Patancheru (17.53° N, 78.27° E, and 545 m above sea level), India, in precision fields on Vertisol Kasireddipally series isohypothermic Typic Pellustert [25] during the 2010–2011 and 2011–2012 post-rainy seasons. The experiment was planted in a split-plot design in three replications using drought stress and control (optimally irrigated) treatments as the main plot and genotypes as the subplots in five maturity groups (G1—extra early, flowered <60 day after sowing (DAS); G2—early, flowered 61–70 DAS; G3—medium, flowered 71–80 DAS; G4—late, flowered 81–90 DAS; and G5—extra late, flowered >90 DAS) based on days to 50% flowering observations recorded during the 2009–2010 post-rainy season at Patancheru. This duration grouping became necessary, as the grain yield of a genotype under terminal drought was consistently confounded by the flowering time [26]. Drought stress was imposed on each accession by withholding irrigation from about 30 days prior to anthesis in each flowering group, while accessions grown under optimally irrigated conditions were used as control. The experimental fields in both the years were kept fallow during the rainy seasons. The precision fields at the ICRISAT center have uniform fertility and have irrigation facilities with a gentle slope of 0.5%. The experimental materials were planted in the second week of October each year. Each accession was planted in a single-row, 4 m in length, with a row-to-row spacing of 75 cm, and plant-to-plant spacing within a row of 10 cm. Seeds were sown at a uniform depth of 2 to 3 cm using a tractor-mounted four-cone planter, and crop-specific agronomic practices, including plant protection measures, were followed. Diammonium phosphate was applied at the rate of 150 kg ha⁻¹ as a basal dose, and urea was applied at the rate of 100 kg ha⁻¹ as topdressing 3 weeks after planting. A ridge and furrow system of cultivation was adopted and, each time, the experimental plots received about 7 cm of irrigation water. Observations on days to 50% flowering (the day when 50% or more of the plants had reached anthesis in a plot), 100-seed weight (from bulk seed samples of each accession), and grain yield (from panicles including tillers if any, of five representative plants in a plot at harvest maturity) were recorded.

2.3. Statistical Analysis

Analysis of variance was performed using a split-plot design for individual post-rainy seasons and combined of two post-rainy seasons using GenStat 17th Edition (<https://www.vsni.co.uk/>) and means were obtained for each accession. The single nucleotide polymorphism (SNP) markers data on sorghum mini core collection generated from the genotyping-by-sequencing (GBS) approach in our earlier study [27], was utilized to estimate the genetic distance between accessions following Tajima–Nei [28] using the software MEGA 7 [29], and accessions clustered following the neighbor-joining method [30] using the software DARwin 6.0.14 [31].

2.4. Trait-Specific Sources and Their Agronomic Performance

On the basis of sorghum mini core accessions grown in two post-rainy seasons under optimally irrigated and drought-stressed conditions, the sources for earliness (flowered <60 DAS), greater seed size, and high grain yielding accessions were identified. Further, published information on the response of sorghum mini core accessions [11] to biotic [12–17] and abiotic [17–19] stresses, and for grain nutritional [20] and bioenergy traits [21,22] (Table 1) were used to identify genetically diverse trait-specific sources for use in sorghum breeding globally.

Table 1. Germplasm sources identified in sorghum mini core collection for grain nutritional and bioenergy traits and for biotic and abiotic stress tolerance.

Trait	Mini Core Accession	Reference
Grain nutritional traits		
Fe, 40.3 to 48.6 mg kg ⁻¹ seed	IS# 16382, 23992, 28313, 28389, 28849, 20743, 21645, 21863, 28747, 30508, 31681	Upadhyaya et al. [20]
Zn, 32.2 to 36.4 mg kg ⁻¹ seed	IS# 30460, 602, 17980, 19859, 28451, 30466, 30536, 5301, 8774, 4951, 25249, 24139, 24175, 24218	Upadhyaya et al. [20]
Fe, 40.8 to 48.9 mg kg ⁻¹ seed and Zn, 32.8 to 42.6 mg kg ⁻¹ seed	IS# 1219, 1233, 30450, 30507, 1212, 27786, 30383, 31651, 24503	Upadhyaya et al. [20]
Protein (12.2 to 13.8%)	IS# 2902, 4951, 19975, 23684, 25249, 25910, 25989, 26025, 26046	http://genebank.icrisat.org/
Lysine (3.1 to 4.3%)	IS# 3971, 25836, 5386	http://genebank.icrisat.org/
Bioenergy traits		
Stalk sugar content (Brix: 14.0 to 15.2%)	IS# 13294, 13549, 23216, 23684, 24139, 24939, 24953	Upadhyaya et al. [21]
Dual purpose (grain and sweet stalk)	IS# 1004, 4698, 23891, 28141	Upadhyaya et al. [21]
High saccharification yield	IS# 2872, 27887, 19262, 3158, 7305, 33353, 4951	Wang et al. [22]
Biotic stresses		
Downy mildew	IS# 28747, 31714, 23992, 27697, 28449, 30400; 1212, 2413, 3121, 4060, 4360, 4372, 4613, 4631, 5094, 7305, 9745, 12302, 12804, 12883, 12965, 13549, 15170, 15478, 15945, 16528, 20625, 20632, 21083, 22294, 22720, 23216, 24453, 24462, 24463, 26222, 26484, 26617, 26749, 27557, 29239, 29314, 29358, 29392, 29606, 29627, 29654, 30092, 30383, 30443, 30466, 30562, 31557	Sharma et al. [12]; Radwan et al. [14]
Grain mold	IS# 602, 603, 608, 1233, 2413, 3121, 12697, 12804, 20727, 20740, 20743, 20816, 30562, 31681, 2379, 2864, 12302, 13971, 17941, 19389, 23992, 26694, 29335, 21512, 21645, 12945, 22294, 995, 2426, 12706, 16151, 24453, 26701, 29326, 30383, 30533, 30536, 20956, 29314, 30092, 10969, 23590, 29187, 29269, 473, 29304, 1212, 13893, 29241, 29568	Sharma et al. [12]
Anthracnose	IS# 473, 5301, 6354, 7679, 10302, 16382, 19153, 20632, 20956, 23521, 23684, 24218, 24939	Sharma et al. [13]
Leaf blight	IS# 473, 2382, 7131, 9108, 9177, 9745, 12937, 12945, 14861, 19445, 20743, 21083, 23521, 23644, 23684, 24175, 24503, 24939, 24953, 26694, 26749, 28614, 29187, 29233, 29714, 31557, 33353,	Sharma et al. [13]
Charcoal rot	IS# 24463; 4515, 13549, 29582, 25301, 12735, 30533, 23514, 29950, 14010, 14090, 29358, 19859, 16528, 22986, 5094, 26046, 23590, 24503, 21512, 29269, 27697, 19676, 19389, 22294, 7250, 17941, 602, 30092, 29733, 31557, 23216, 10757, 12945, 29606, 12697, 31651, 7679, 23891, 32787, 29091, 29335, 30466, 4631, 29233, 28451, 24218, 1041, 30507, 29627, 2379	Borphukan [15]; Kapanigowda et al. [17]
Rust	IS# 473, 23521, 23684, 24503, 26737, 33023	Sharma et al. [13]
<i>Potyvirus</i> spp.	IS# 7679 and 20740	Seifers et al. [16]
Shoot fly	IS# 2205, 4515, 4698, 5094	ICRISAT Unpublished
Spotted stem borer	IS# 4698, 5094, 1041, 18039, 19445, 23992	ICRISAT Unpublished
Sugarcane Aphid	IS# 2205, 4515, 4698, 18039, 1004, 3121, 4581, 5386, 12937, 15744, 16528, 20625, 20632, 23514, 23521, 23586, 23684, 24492, 24939, 25089, 25249, 25301, 25548, 27034, 27887, 28614, 29314, 29654, 29772, 31446, 31557, 33023	ICRISAT Unpublished
Abiotic stress		
Drought	IS# 14779, 23891, 31714, 4515, 5094, 9108, 15466, 1212	Upadhyaya et al. [18]; Kapanigowda et al. [17]
Seedling vigor under low temperature stress	IS# 1212, 14779, 15170, 22986, 7305, 7310	Upadhyaya et al. [19]
Germinability under low temperature stress	IS# 602, 1233, 7305, 10302, 20956	Upadhyaya et al. [19]

3. Results

3.1. Analysis of Variance

Analysis of variance following the split-plot design on individual post-rainy seasons data indicated a significant effect of genotype (G), and genotype and drought (G–D) for days to 50% flowering, 100-seed weight and grain yield (except G–D for 100-seed weight in G 4) in all flowering groups in both the post-rainy seasons, indicating the presence of significant variation in sorghum mini core collection, and that genotypes interacted significantly with the drought treatment. The main effect due to D was significant for days to 50% flowering only in G3 in 2010–2011 and G2, G3 and G5 in 2011–2012; the 100-seed weight was significant in all flowering groups in both seasons; grain yield was significant in all flowering groups except G2 and G3 in 2010–2011 and G5 in 2011–2012 post-rainy seasons, indicating significant influence of drought on the traits studied. Pooled analysis showed that the main effects, namely D, G, and year (Y), were significant in all flowering groups for days to 50% flowering (except in G4), 100-seed weight (except in G5), and grain yield. The D–G, D–Y, G–Y and D–G–Y interactions were significant for all traits except D–Y for days to 50% flowering in G1, and D–G for 100-seed weight and D–Y for days to 50% flowering and grain yield in G5 (data not shown).

3.2. Trait-Specific Sources and Their Agronomic Performance

3.2.1. Agronomic Traits

Sorghum mini core accessions showed a wide range of variation for days to 50% flowering (from 52 to 121 DAS), 100-seed weight (from 0.42 to 5.15 g) and grain yield (from 3.72 to 43.32 g plant⁻¹). Eighty-two accessions flowered significantly earlier (<69 DAS) than the early-flowering control cultivar IS 18758 (69 to 71 DAS). However only 13 accessions flowered in <60 DAS, of which 10 accessions (IS 1233, IS 2379, IS 2864, IS 12706, IS 14861, IS 16382, IS 17941, IS 20298, IS 28313, IS 28849) also had good yields (11.12–18.63 g) and 100-seed weight (1.64–3.33 g) and thus were regarded as sources for early flowering (Table 2). For the 100-seed weight, ten accessions, two each in G1 (IS 14861, IS 26484) and G2 (IS 23891, IS 31714) and six accessions in G3 (IS 11473, IS 15466, IS 15744, IS 28141, IS 30838, IS 31706) that had significantly higher 100-seed weights (3.72–5.15 g) than the control IS 33844 (3.44 to 3.61 g) were selected. These 10 accessions flowered from 58 to 80 DAS and yielded 16.17 to 40.91 g plant⁻¹. For grain yield, four accessions were identified (IS 4698 in G1, IS 23590 and IS 23891 in G2 and IS 28141 in G3) as significantly high grain yielding (38.39 to 43.32 g plant⁻¹) as compared to the high grain yielding control, IS 33844 (33.49 to 35.99 g plant⁻¹). These accessions took 74 to 77 DAS to flower and had a 100-seed weight of 2.99 to 5.15 g compared to IS 33844, in which the 100-seed weight ranged from 3.44 to 3.61 g and flowering from 77 to 78 DAS (Table 2). However, considering all three agronomic traits together, 21 mini core accessions were identified as promising sources, and days to 50% flowering of these accessions ranged from 52 to 80 DAS, 100-seed weight from 1.64 to 5.15 g and grain yield from 11.12 to 43.32 g plant⁻¹ (Table 2).

Table 2. Germplasm sources for early flowering, greater seed weight, and high grain yield identified in sorghum mini core collection evaluated under optimally irrigated and post-flowering drought-stressed conditions during two post-rainy seasons (2010–2011 and 2011–2012) at Patancheru, India.

IS#	Origin	Race	Combined Data over Two Seasons and Two Conditions (Optimally Irrigated and Post-Flowering Drought Stress)		
			Days to 50% Flowering	100-Seed Weight (g)	Grain Yield (g Plant ⁻¹)
Group 1					
1233	China	Bicolor	54 *	1.64	11.74
2379	South Africa	Caudatum	58 *	2.11	13.92
2864	South Africa	Caudatum	59 *	2.03	17.88
4698	India	Durra	77	3.18	43.32 *
12706	USA	Caudatum-bicolor	53 *	3.33	12.08
14861	Cameroon	Caudatum	58 *	3.94 *	18.63
16382	Cameroon	Guinea	58 *	3.24	11.12
17941	India	Caudatum	56 *	2.31	15.30
20298	Niger	Caudatum-bicolor	54 *	2.85	12.88
26484	Benin	Guinea	72	4.25 *	24.85
28313	Yemen	Durra-caudatum	52 *	2.88	11.88
28849	Yemen	Durra-caudatum	52 *	3.17	15.41
Control					
2205	India	Durra-bicolor	80	2.03	26.16
18758	Ethiopia	Guinea-caudatum	71	2.51	29.74
33844	India	Durra	78	3.44	35.25
Trial Mean			62	2.60	18.46
Trial Range			52–77	1.64–4.25	9.08–43.32
LSD (P 0.05)			1.08	0.17	2.29
CV (%)			2.50	9.30	19.30
Group 2					
23590	Ethiopia	Guinea-caudatum	74	2.99	38.39 *
23891	Yemen	Durra	76	5.14 *	40.91 *
31714	Yemen	Durra-caudatum	67 *	4.45 *	30.80
Control					
2205	India	Durra-bicolor	80	2.11	24.39
18758	Ethiopia	Guinea-caudatum	69	2.42	27.26
33844	India	Durra	77	3.61	33.49
Trial mean			68	2.41	21.02
Trial range			53–86	1.27–5.14	10.29–40.91
LSD (P 0.05)			1.21	0.17	2.78
CV (%)			2.30	8.80	17.10
Group 3					
11473	Ethiopia	Caudatum	67 *	4.49 *	16.17
15466	Cameroon	Caudatum	80	3.78 *	37.72
15744	Cameroon	Durra-caudatum	74	3.94 *	36.96
28141	Yemen	Durra-caudatum	76	5.15 *	40.20 *
30838	Cameroon	Guinea	71	3.72 *	23.01
31706	Yemen	Durra	76	4.69 *	35.93
Control					
2205	India	Durra-bicolor	80	2.11	26.32
18758	Ethiopia	Guinea-caudatum	70	2.32	26.74
33844	India	Durra	77	3.53	35.99
Trial mean			76	2.40	23.20
Trial range			67–95	0.42–5.15	7.23–40.20
LSD (P 0.05)			1.25	0.17	3.51
CV (%)			2.10	8.20	18.00

* Significant at $p \leq 0.05$ compared to the control.

3.2.2. Grain Nutritional Contents

Our previous study identified 11 accessions with high grain Fe content, 14 accessions for high grain Zn content, and nine accessions for both high grain Fe and Zn contents [20] (Table 1, Table S1). From the ICRISAT genebank database, we selected nine mini core accessions as sources for high protein (12.2 to 13.8%) and three accessions (IS 25836, IS 5386 and IS 3971) for high lysine content of 3.1, 3.1

and 4.3%, respectively (Table S1). Among the nutrient dense accessions, we identified 27 accessions that have good grain yields and 100-seed weights. Eight (IS 2902, IS 26046, IS 25910, IS 4951, IS 23684, IS 25249, IS 25989, IS 26025) out of nine accessions selected as sources for high protein content also had significantly higher Fe and/or Zn; while high lysine content accessions (IS 3971, IS 25836, IS 5386) also had 27.87 to 36.51 mg kg⁻¹ of Fe and 19.46 to 28.50 mg kg⁻¹ of Zn, IS 3971 had significantly high Zn content, 28.50 mg kg⁻¹. Thirteen of the high grain nutrients content accessions were significantly earlier in flowering than the earliest flowering control IS 18758 (69 to 71 DAS), and also had significantly higher Fe and/or Zn. The selected accessions could be utilized for enhancing grain nutritional content in sorghum.

3.2.3. Bioenergy Traits

Eighteen accessions have been reported as sources for bioenergy traits in sorghum mini core collection (Table 1) [21,22], including sources for high Brix % (seven accessions), high Brix % and grain yield (four accessions), and high saccharification yield (seven accessions). Of the 18 accessions, we have selected 13 accessions including dual purpose (high Brix % plus high grain yields) accessions (IS 4698, IS 1004, IS 23891, IS 28141, IS 23216, IS 13549, IS 24939, IS 24953, IS 24139), and high saccharification yield with Brix % ranging from 10 to 13% (IS 7305, IS 4951, IS 27887, IS 33353) as sources for bioenergy traits improvement in sorghum. Days to 50% flowering of these accessions ranged from 74 to 95 DAS. Three (IS 1004, IS 23891, IS 28141) of these had significantly higher 100-seed weight (3.78 to 5.15 g) and four (IS 4698, IS 1004, IS 23891, IS 28141) were significantly high grain yielding, 12 to 23% higher than the high grain yielding control IS 33844 (Table S1).

3.2.4. Biotic Stress Tolerance

Sorghum mini core accessions have been extensively evaluated for resistance to diseases [12–17], and insect pests (ICRISAT Unpublished), and the identified sources of resistance are listed in Table 1. These includes 53 accessions with resistance to downy mildew (three accessions, IS 28747, IS 28449 and IS 30400, for Patancheru isolate of *Peronosclerospora sorghi* and 47 accessions for pathotype 6 (P6), a new virulent pathotype of *P. sorghi* in Texas and three accessions, IS 23992, IS 27697 and IS 31714, resistant to both Patancheru isolate and P6), 50 for grain mold, 27 for leaf blight, 13 for anthracnose, six for rust, 32 for sugarcane aphid (*Melanaphis sacchari*), six for spotted stem borer (*Chilo partellus*) and four for shoot fly (*Atherigona soccata*). Many of these accessions were resistant to more than one disease and/or insect pest. Among these biotic stress-resistant accessions, we selected 70 accessions that were resistant to multiple diseases and/or insect pests and had high grain yields as ideal sources that can be utilized in crop improvement (Table S1). Accessions resistant to both disease and insect pests were: IS 1041 for charcoal rot and stem borer; IS 3121 for downy mildew, grain mold and aphids; IS 4515 for charcoal rot, shoot fly and aphids; IS 5094 for downy mildew, charcoal rot, stem borer and shoot fly; IS 12937 and IS 28614 for leaf blight and aphids; IS 16528 for downy mildew, charcoal rot and aphids; IS 19445 for leaf blight and stem borer; IS 20632 for downy mildew, anthracnose and aphids; 23514 for charcoal rot and aphids; IS 23521 for anthracnose, leaf blight, rust and aphids; IS 23684 for anthracnose, leaf blight, rust and aphids; IS 23992 for downy mildew, grain mold and stem borer; IS 24939 for anthracnose, leaf blight and aphids; IS 25301 for charcoal rot and aphids; IS 29314 for downy mildew, grain mold and aphids; IS 29654 for downy mildew and aphids; IS 31557 for downy mildew, leaf blight, charcoal rot and aphids; and IS 33023 for rust and aphids. Fourteen of the biotic stress-resistant accessions flowered earlier than the earliest control, IS 18758 (69 to 71 DAS), and four accessions (IS 4698, IS 1004, IS 23590, IS 23891) were significantly high yielding compared to the highest yielding control, IS 33844.

3.2.5. Abiotic Stress Tolerance

Sorghum mini core accessions tolerant to abiotic stresses such as post-flowering drought stress and low temperature stress have been reported [17–19]. Seven accessions (IS 14779, IS 23891, IS 31714, IS 4515, IS 5094, IS 9108, IS 15466) reported as post-flowering drought tolerant were chosen as desirable

for use in breeding, as these were expected to have much wider adaptability because they were selected based on a drought tolerance index [26] which is free from the effects of yield potential and flowering time [18]. Upadhyaya et al. [19] have reported six and five accessions with high seedling vigor and germinability, respectively, under low temperature stress (Table 1). Of these 11 accessions, we have selected six top yielding accessions (IS 14779, IS 1212, IS 22986, IS 7305, IS 10302, IS 20956; grain yield 16.14–25.30 g plant⁻¹) as desirable sources for use in crop improvement. Thus, considering tolerance to all the abiotic stresses, 12 accessions were selected, of which IS 14779 and IS 1212 were found to be tolerant to both post-flowering drought and low temperature stress, four accessions (IS 14779, IS 1212, IS 22986, IS 31714) were significantly early flowering (63–67 DAS) as compared to the earliest flowering control IS 18758, and IS 23891 was significantly high grain yielding (40.91 g plant⁻¹) compared to the control IS 33844 (33.49 g plant⁻¹) (Table S1).

3.3. Multi-Trait-Specific Sources

The availability of germplasm that are agronomically desirable and are also sources for resistance to multiple stresses is most desirable for use in breeding programs. In this study, we have identified 110 accessions resistant to one or more stresses and that have good agronomic performance. Among these, 28 accessions were found to be sources for multiple traits (Table 3). The flowering duration of these multi-trait-specific accessions varied from 52 to 97 DAS, and they produced grain yields of 6.82 to 43.32 g plant⁻¹. Multi-trait-specific accessions include combinations of two trait groups: high grain nutrients and agronomically desirable (IS 1233, IS 16382, IS 28313), resistant to biotic stress and agronomically desirable (IS 14861, IS 15744, IS 17941, IS 23590, IS 26484), high grain nutrients and bioenergy traits (IS 4951, IS 24139), high grain nutrients and biotic stress resistance (IS 602, IS 20743, IS 23684, IS 30383), bioenergy traits and resistance to biotic stress (IS 1004, IS 13549, IS 23216, IS 24939), biotic and abiotic stress tolerance (IS 4515, IS 5094, IS 20956), and three or four trait groups (IS 4698 for grain yield, Brix %, resistant to stem borer, shoot fly, aphids; IS 31714 for greater seed weight, tolerant to drought and resistant to downy mildew; IS 1212 for Fe, Zn, drought tolerance, high seedling vigor under low temperature, resistance to downy mildew and grain mold, and IS 23891 for greater seed weight, high grain yield, high Brix %, tolerance to drought and resistance to charcoal rot). Among multi-trait-specific accessions, IS 1004, IS 4698, IS 23590, IS 23891, and IS 28141 were significantly high grain yielding with one or more other desirable traits such as greater seed weight, bioenergy traits, drought tolerance, resistance to grain mold, charcoal rot, stem borer, shoot fly and aphids (Table 3).

Table 3. Multi-trait-specific sources identified in sorghum mini core collection and their agronomic performance based on experiments conducted under optimally irrigated and drought-stressed conditions during two post-rainy seasons (2010–2011 and 2011–2012) at Patancheru, India.

IS#	Origin	Race	Traits	Combined Data over Two Seasons and Two Conditions (Optimally Irrigated and Post-Flowering Drought)					
				Days to 50% Flowering	100-Seed Weight (g)	Grain Yield (g Plant ⁻¹)	Fe (mg kg ⁻¹)	Zn (mg kg ⁻¹)	Brix (%)
602	USA	Bicolor	High Fe and Zn, resistant to grain mold and charcoal rot	67	1.27	13.74	42.79	35.98	9.19
1004	India	Durra	High Brix % and resistant to aphids	86	3.78	38.71	28.51	27.38	12.28
1212	China	Kafir-bicolor	High Fe and Zn, tolerance to drought and low temperature stress (high seedling vigor), and resistant to downy mildew and grain mold	63	2.26	16.14	43.57	38.21	10.06
1233	China	Bicolor	Early flowering and high Fe and Zn contents	54	1.64	11.74	48.46	39.05	8.98
4515	India	Durra	Tolerant to drought, and resistant to charcoal rot, shoot fly and aphids	75	2.99	34.28	28.36	20.47	12.43
4698	India	Durra	High Brix %, high grain yielding and resistant to stem borer, shoot fly and aphids	77	3.18	43.32	23.91	20.35	12.75
4951	India	Guinea	High Fe, Zn, protein contents and high saccharification yield	83	1.64	14.19	41.90	33.11	12.08
5094	India	Durra	Tolerant to drought, and resistant to downy mildew, charcoal rot, stem borer and shoot fly	77	2.46	31.27	32.57	22.39	14.23
7305	Nigeria	Caudatum	High saccharification yield and tolerant to low temperature stress (high germinability and vigor)	74	3.04	24.37	37.25	25.63	10.73
13549	Mexico	Caudatum-bicolor	High Brix %, and resistant to downy mildew and charcoal rot	87	1.75	15.91	30.04	29.15	13.99
14861	Cameroon	Caudatum	Early flowering, greater seed weight, and resistant to leaf blight	58	3.94	18.63	33.13	20.28	9.22
15466	Cameroon	Caudatum	Greater seed weight, high grain yielding and tolerant to drought	80	3.78	37.72	28.07	13.53	13.23
15744	Cameroon	Durra-caudatum	Greater seed weight and resistant to aphids	74	3.94	36.96	27.23	15.40	11.61
16382	Cameroon	Guinea	Early flowering and high Fe content	58	3.24	11.12	46.55	23.66	9.19
17941	India	Caudatum	Early flowering and resistant to grain mold and charcoal rot	56	2.31	15.30	29.83	19.73	8.38
20743	USA	Bicolor	High Fe and Zn, and resistant to grain mold and leaf blight	63	1.80	15.18	46.18	29.74	8.19

Table 3. Cont.

IS#	Origin	Race	Traits	Combined Data over Two Seasons and Two Conditions (Optimally Irrigated and Post-Flowering Drought)					
				Days to 50% Flowering	100-Seed Weight (g)	Grain Yield (g Plant ⁻¹)	Fe (mg kg ⁻¹)	Zn (mg kg ⁻¹)	Brix (%)
20956	Indonesia	Durra-caudatum	Tolerant to low temperature stress (high germinability) and resistant to grain mold and anthracnose	72	2.97	24.38	35.06	25.72	11.71
23216	Zambia	Caudatum-bicolor	High Brix % and resistant to downy mildew and charcoal rot	86	1.89	12.28	33.36	24.49	14.69
23590	Ethiopia	Guinea-caudatum	High grain yielding and resistant to grain mold and charcoal rot	74	2.99	38.39	30.38	20.06	12.01
23684	Mozambique	Guinea	High protein and Brix % and resistant to anthracnose, leaf blight, rust and aphids	97	1.60	6.82	39.14	29.55	14.53
23891	Yemen	Durra	Greater seed weight, high yielding, high Brix %, tolerant to drought and resistant to charcoal rot	76	5.14	40.91	31.59	27.23	11.72
24139	Tanzania	Guinea	High Zn and Brix %	95	1.65	13.75	41.84	35.32	15.16
24939	Zambia	Bicolor	High Brix %, and resistant to anthracnose, leaf blight and aphids	85	1.76	12.18	42.13	29.65	14.61
26484	Benin	Guinea	Greater seed weight and resistant to downy mildew	72	4.25	24.85	41.00	27.98	10.73
28141	Yemen	Durra-caudatum	High grain yielding, greater seed weight and high Brix %	76	5.15	40.20	34.41	26.98	11.80
28313	Yemen	Durra-caudatum	Early flowering and high Fe content	52	2.88	11.88	47.93	29.16	10.15
30383	China	Caudatum-bicolor	High Fe and Zn contents, and resistant to downy mildew and grain mold	65	1.99	15.88	45.05	38.56	9.77
31714	Yemen	Durra-caudatum	Greater seed weight, tolerant to drought and resistant to downy mildew	67	4.45	30.80	32.99	21.36	10.93

3.4. Genetic Distance Among Trait-Specific Sources

The SNP data on sorghum mini core collection [27] were utilized to estimate the genetic distance between accessions following the Tajima–Nei model [28], and clustered following the neighbor-joining method [30]. A neighbor-joining tree based on 13390 SNPs broadly grouped 110 accessions of selected trait-specific accessions into three major clusters. Cluster I and II represent largely accessions originating from Africa, while Cluster III represents accessions originating from Asia (Figure 1a), and traits distributed in both Asia and Africa (Figure 1b). The genetic distance between 5995 pairs involving 110 trait-specific sources varied from 0.008 (between IS 20956 originating from Indonesia of intermediate race *durra-caudatum* and IS 10302 originating from Thailand of race *caudatum*) to 0.540 (IS 25989 originating from Mali of race *guinea* and IS 5094 originating from India of race *durra*) (Table S2). Similarly, pair-wise genetic distance of accessions within sources for agronomic traits (genetic distance range 0.038 to 0.455), grain nutrient contents (genetic distance range 0.020 to 0.526), bioenergy traits (genetic distance range 0.104 to 0.457), biotic stress (genetic distance range 0.031 to 0.499), abiotic (genetic distance range 0.008 to 0.427) and multiple trait-specific (genetic distance range 0.043 to 0.478) sources were estimated, and identified the top 20 most diverse pairs of accessions from each group (Table 4). Further, genetic distances between trait groups of accessions were estimated to identify highly diverse pairs of accessions. This included IS 16382 and IS 28313 having high grain nutrients and agronomically desirable accessions (genetic distance 0.355), IS 17941 and IS 26484 having biotic stress-resistant and agronomically desirable accessions (genetic distance 0.344), IS 4951 and IS 24139 with high grain nutrients and bioenergy traits accessions (genetic distance 0.207), IS 23684 and IS 30383 with high grain nutrients and biotic stress resistance accessions (genetic distance 0.466), IS 13549 and IS 24939 with bioenergy traits and resistance to biotic stress accessions (genetic distance 0.375), and IS 5094 and IS 20956 having biotic and abiotic stress tolerance accessions (genetic distance 0.361). Four accessions, IS 4698, IS 31714, IS 1212, and IS 23891, were identified as sources for three or four trait groups, and the highest genetic distance (0.273) was observed between IS 1212 and IS 4698.

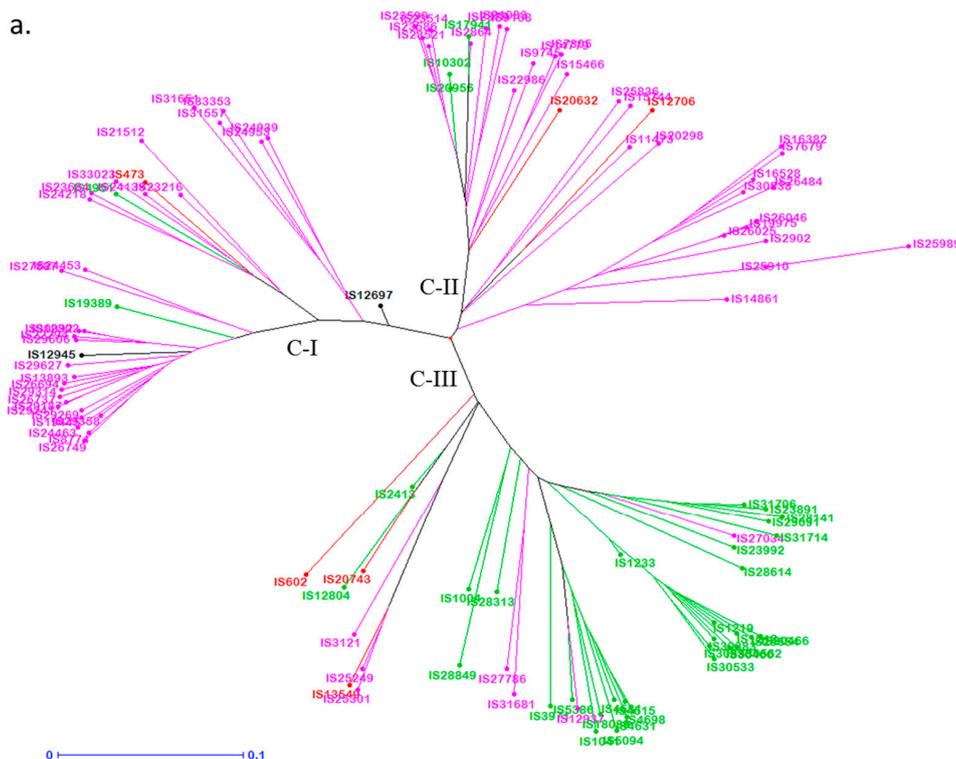


Figure 1. Cont.

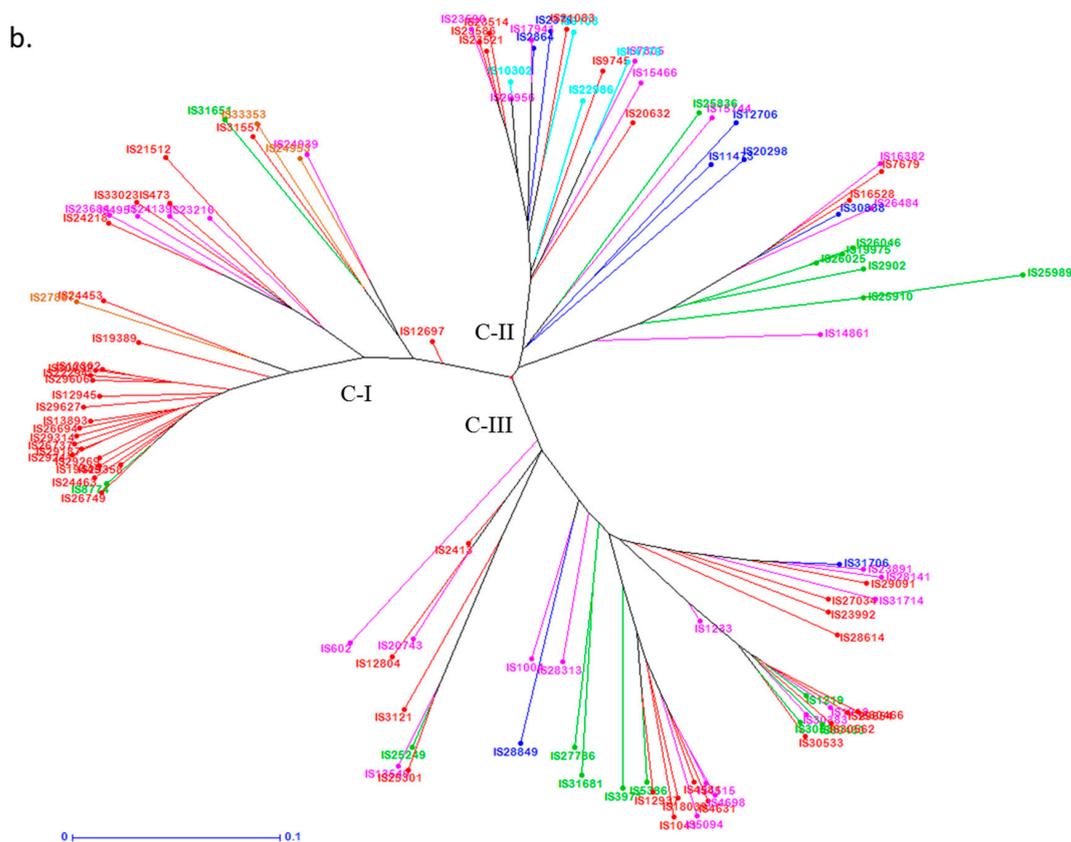


Figure 1. Neighbor-joining tree based on 13390 single nucleotide polymorphism markers and 110 trait-specific accessions: (a) mini core trait-specific accessions, color based on region: Africa—pink; Asia—green; the Americas—red; Oceania—black; and (b) mini core trait-specific accessions, color based on traits: agronomic—blue; grain nutrients—green; bioenergy—brown; biotic—red; abiotic—sky blue; multi-trait-specific—pink.

Table 4. Most genetically diverse pairs of accessions identified in sorghum mini core collection for agronomic, grain nutrition and bioenergy traits, biotic and abiotic stress tolerance and for multiple trait-specific sources.

Pair of Accessions	Genetic Distance	Pair of Accessions	Genetic Distance
Agronomically desirable sources			
IS 28141 and IS 16382	0.455	IS 30838 and IS 28141	0.413
IS 16382 and IS 4698	0.452	IS 31714 and IS 2379	0.411
IS 23891 and IS 16382	0.443	IS 28849 and IS 16382	0.410
IS 26484 and IS 4698	0.438	IS 31714 and IS 30838	0.410
IS 31714 and IS 16382	0.432	IS 26484 and IS 23891	0.407
IS 31706 and IS 16382	0.428	IS 23891 and IS 2379	0.406
IS 28141 and IS 26484	0.424	IS 28141 and IS 23590	0.406
IS 30838 and IS 4698	0.419	IS 31714 and IS 26484	0.406
IS 28141 and IS 2379	0.415	IS 4698 and IS 2864	0.403
IS 23590 and IS 4698	0.413	IS 4698 and IS 2379	0.402
Mean distance of 0.311 among 276 pairs of accessions; Minimum 0.038 between IS 17941 and IS 2864; Maximum 0.455 between IS 28141 and IS 16362			
Grain nutrient rich sources			
IS 30460 and IS 25989	0.526	IS 25989 and IS 25836	0.461
IS 25989 and IS 5386	0.521	IS 23684 and IS 1212	0.460
IS 25989 and IS 3971	0.516	IS 25989 and IS 8774	0.458
IS 25989 and IS 1212	0.515	IS 24139 and IS 1212	0.456
IS 30383 and IS 25989	0.508	IS 30460 and IS 24139	0.454
IS 25989 and IS 1219	0.505	IS 25989 and IS 602	0.453
IS 30536 and IS 25989	0.502	IS 23684 and IS 1219	0.452

Table 4. Cont.

Pair of Accessions	Genetic Distance	Pair of Accessions	Genetic Distance
IS 27786 and IS 25989	0.491	IS 30536 and IS 23684	0.451
IS 31681 and IS 25989	0.479	IS 25989 and IS 23684	0.448
IS 30460 and IS 23684	0.465	IS 30536 and IS 24139	0.448
Mean distance of 0.329 among 351 pairs of accessions; Minimum 0.020 between IS 26025 and IS 19975; Maximum 0.526 between IS 30460 and IS 25989			
Bioenergy traits			
IS 27887 and IS 4698	0.457	IS 28141 and IS 23216	0.427
IS 28141 and IS 24139	0.456	IS 28141 and IS 24939	0.427
IS 24139 and IS 4698	0.448	IS 27887 and IS 13549	0.421
IS 24139 and IS 23891	0.443	IS 24939 and IS 4698	0.420
IS 27887 and IS 28141	0.435	IS 24939 and IS 23891	0.419
IS 33353 and IS 4698	0.434	IS 24953 and IS 23891	0.418
IS 23216 and IS 4698	0.433	IS 33353 and IS 23891	0.418
IS 28141 and IS 24953	0.431	IS 28141 and IS 7305	0.416
IS 27887 and IS 23891	0.431	IS 24953 and IS 4698	0.407
IS 33353 and IS 28141	0.430	IS 13549 and IS 4951	0.407
Mean distance of 0.338 among 78 pairs of accessions; Minimum 0.104 between IS 28141 and IS 23891; Maximum 0.457 between IS 27887 and IS 4698			
Biotic stress resistance sources			
IS 30466 and IS 21512	0.499	IS 30562 and IS 23684	0.479
IS 29654 and IS 21512	0.498	IS 23684 and IS 5094	0.478
IS 30562 and IS 21512	0.497	IS 30466 and IS 23684	0.475
IS 30466 and IS 24218	0.488	IS 29654 and IS 24218	0.475
IS 21512 and IS 1212	0.486	IS 30533 and IS 24218	0.475
IS 21512 and IS 5094	0.486	IS 31714 and IS 21512	0.474
IS 30533 and IS 21512	0.485	IS 33023 and IS 29654	0.474
IS 30562 and IS 24218	0.485	IS 29091 and IS 24218	0.473
IS 33023 and IS 30466	0.482	IS 24218 and IS 1212	0.472
IS 24218 and IS 5094	0.479	IS 21512 and IS 4631	0.472
IS 30383 and IS 21512	0.479		
Mean distance of 0.332 among 2415 pairs of accessions; Minimum 0.031 between IS 29241 and IS 29187; Maximum 0.499 between IS 30466 and IS 21512			
Abiotic stress tolerance sources			
IS 9108 and IS 5094	0.427	IS 14779 and IS 31714	0.404
IS 9108 and IS 1212	0.419	IS 7305 and IS 4515	0.401
IS 9108 and IS 31714	0.417	IS 14779 and IS 5094	0.398
IS 7305 and IS 5094	0.416	IS 9108 and IS 23891	0.397
IS 7305 and IS 31714	0.415	IS 14779 and IS 23891	0.397
IS 10302 and IS 5094	0.407	IS 10302 and IS 23891	0.392
IS 7305 and IS 1212	0.405	IS 10302 and IS 4515	0.391
IS 14779 and IS 1212	0.405	IS 7305 and IS 23891	0.39
IS 9108 and IS 4515	0.405	IS 10302 and IS 31714	0.389
IS 10302 and IS 1212	0.404	IS 15466 and IS 1212	0.387
Mean distance of 0.301 among 66 pairs of accessions; Minimum 0.008 between IS 20956 and IS 10302; Maximum 0.427 between IS 9108 and IS 5094			
Multi-trait-specific sources			
IS 23684 and IS 5094	0.478	IS 16382 and IS 4698	0.452
IS 28141 and IS 23684	0.465	IS 31714 and IS 23684	0.452
IS 24139 and IS 5094	0.462	IS 23891 and IS 23684	0.452
IS 23684 and IS 1212	0.460	IS 23684 and IS 4515	0.451
IS 23684 and IS 4698	0.458	IS 24139 and IS 4698	0.448
IS 31714 and IS 24139	0.457	IS 30383 and IS 23684	0.446
IS 24139 and IS 1212	0.456	IS 16382 and IS 4515	0.444
IS 16382 and IS 5094	0.456	IS 24139 and IS 4515	0.444
IS 28141 and IS 24139	0.456	IS 23891 and IS 16382	0.443
IS 28141 and IS 16382	0.455	IS 24139 and IS 23891	0.443
Mean distance of 0.328 among 378 pairs of accessions; Minimum 0.043 between IS 4698 and IS 4515; Maximum 0.478 between IS 23684 and IS 5094			

4. Discussion

Sorghum is one of the major staple food crops in many developing countries and represents an important subsistence crop for millions of people in the semi-arid tropics of Africa, Asia, and Central America. Sorghum crops experience multiple stresses, i.e., one or more diseases and/or insect pests and abiotic stresses, during different crop growth stages resulting in severe crop losses.

Therefore, crop improvement programs largely focus on developing high-yielding cultivars with multiple traits including stress tolerance, bioenergy and nutritional quality. To meet such needs, appropriate genetically diverse germplasm sources preferably, with multiple traits, are required by breeders.

The sorghum mini core collection [11], consisting of 242 accessions representing global diversity, provides breeders with much of the available genetic diversity in a substantially manageable size. In this study, the evaluation of sorghum mini core collection under optimally irrigated and drought-stressed conditions during two post-rainy seasons resulted in the identification of 21 germplasm as sources for important agronomic traits namely early flowering, greater seed weight and high grain yield, for their utilization in crop improvement. The sorghum mini core collection has been extensively evaluated by researchers globally and sources for various traits identified for use in sorghum breeding programs [12–22]. The agronomic performance of these trait-specific accessions is a key factor to utilize them in breeding programs. Therefore, agronomic performance of sorghum mini core accessions grown under optimally irrigated and drought-stressed conditions together with genotyping information [27], response to biotic [12–17] and abiotic [17–19] stresses, grain nutritional contents [20] and bioenergy traits [21,22] were used to identify subsets of genetically diverse trait-specific sources for use in sorghum improvement. This study has resulted in the identification of 110 accessions (Table S1) that are superior among the trait-specific sources reported in terms of grain yield and some of them yielded greater than more than the best controls.

Neighbor-joining tree based on 13390 SNP loci was used to group the 110 accessions into three major clusters on the basis of region and country of origin, and racial structure. Accessions originated in Africa were clustered into two major groups, while accessions of Asia were separately clustered, and trait-specific accessions were distributed in both Asia and Africa providing opportunity to select diverse pair of accessions for use in the sorghum breeding program. Furthermore, the top 20 most diverse pairs of accessions within each group of agronomic, grain nutritional and bioenergy trait, and for biotic and abiotic stress tolerance were identified for their utilization in sorghum breeding. Diverse germplasm with multiple trait-specific sources in agronomically desirable backgrounds offer breeders opportunities to combine several genes [10]. Therefore, we have identified a set of 28 accessions as sources for two or more traits and listed the top 20 most diverse pairs of accessions (Table 4). Utilization of these diverse multi-trait sources in hybridization broadens the genetic base of sorghum cultivars.

Sorghum diversity is structured according to geographic regions and races within the regions [27,32]. This has reflected in their adaptation to various biotic and abiotic stresses and for quality traits. Among the 110 accessions identified as trait-specific sources, accessions of races *bicolor* and *guinea* were found to be sources for high grain nutrients and resistance to biotic stress; *caudatum-bicolor* for bioenergy traits and biotic stress tolerance; *durra* for bioenergy traits, biotic and biotic stress tolerance; and *kafir* for biotic stress tolerance. Previous studies have revealed that the race *durra* and *caudatum* possess high transpiration efficiency and, therefore, the frequency of identifying drought tolerant accessions is high [18,33]. Sharma et al. [12] found the maximum number of accessions that are resistant to grain mold from the race *bicolor*. This could be due to the loose panicles and dark grain color. Similarly, the *guinea* and *caudatum* races were reported to be good sources for anthracnose and leaf blight resistance, respectively [13].

The introduction of new diversity from exotic, unadapted germplasm and/or wild relatives in breeding is an important way of combating the narrow genetic base of crop cultivars, but it is challenging due to the linkage load of many undesirable genes and their associated problems. Jordan et al. [34] have used a range of sorghum lines (with geographic or racial diversity, phenotypic diversity for key traits, elite lines from breeding programs in other countries, and cross-compatible wild species) that were unadapted to Australian conditions, and introduced new alleles from unadapted germplasm into elite breeding materials. The sources identified in this study are not only highly diverse for traits, regions, and races, and sources for different biotic and abiotic stress, grain nutritional, bioenergy and agronomic traits, but also are agronomically desirable. Thus, they may carry less or no linkage drag.

These lines could be utilized in developing populations and subsequently in cultivar development, and for genomic investigations.

In conclusion, this study aimed to identify genetically diverse multi-trait-specific sorghum accessions by considering the agronomic performance of sorghum mini core accessions evaluated during two post-rainy seasons under optimally irrigated and drought-stressed conditions with existing published information on the response of accessions to biotic and abiotic stress tolerance, grain nutritional and bioenergy traits. This has resulted in the identification of 110 genetically diverse trait-specific sources, and 28 of them were multi-trait-specific with good agronomic performances and meet the needs of sorghum researchers. Trait-specific accessions were distributed in both Africa and Asia and were from different race/intermediate races, offering breeders the opportunity to choose diverse parents in different combinations of traits/regions/races for breeding improved cultivars for enhancing grain yield and quality, in addition to the improved adaptation of sorghum cultivars to environmental challenges. These accessions could be utilized in genetic and genomic investigations to understand the mechanisms underlying multiple stress tolerance, and mapping genes. Sorghum researchers can obtain seed samples of these accessions from the ICRISAT genebank (<http://genebank.icrisat.org/>) for research purposes through a Standard Material Transfer Agreement (SMTA).

Supplementary Materials: The following are available online at <http://www.mdpi.com/2077-0472/9/6/121/s1>, Table S1: Sorghum mini core accessions identified as sources for agronomic traits (early maturity, greater seed size, high grain yield), grain nutrients (high Fe, Zn, protein and Lysin), bioenergy (high Brix %, high saccharification yield, dual purpose), Table S2: Genetic distance among the trait-specific sources identified in the sorghum mini core collection.

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