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Full Length Article

Morphological and Genetic Diversity of Cereal Genotypes in Kingdom of Saudi Arabia

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Abstract

Cereals are rich in carbohydrates and offer a major source of daily calorie intake. Among cereals, wheat (*Triticum aestivum* L.), barley (*Hordeum vulgare* L.), maize (*Zea mays* L.) and sorghum (*Sorghum bicolor* L.) are the leading crops grown across the globe. The utilization of exotic and diverse germplasm of a crop is a useful tool to increase the genetic diversity among the genotypes. In this study, we collected 11 wheat, 4 barley, 15 sorghum and 6 maize genotypes from farmer's fields of Saudi Arabia and evaluated, for their morphological and genetic diversity potential. Significant differences were observed in the morphological characters of tested wheat, barley, sorghum and maize genotypes under field conditions. Sequence-related amplified polymorphism showed substantial genetic diversity in the tested genotypes of all the cereal crops. All the genotypes of wheat and barley significantly differed for the plant height, productive tillers, 1000 grain weight, and days to 50% flowering and maturity. Similarly, sorghum and maize genotypes differed significantly for the leaf area and plant height. All genotypes of wheat, barley, sorghum and maize differed for the number of alleles; maximum alleles were 156 in wheat, 172 in barley, 127 in sorghum and 73 in maize, per primer combination. Polymorphism of all of tested genotypes of wheat, barley, sorghum and maize was 100% in all the tested genotypes. Existence of genetic diversity of these tested wheat, barley, sorghum and maize genotypes offers opportunities to exploit favourable alleles for use in the breeding program aimed at yield improvement.

Keywords: Cereals; Crop improvement; Genetic diversity; Sequence-related amplified polymorphism

Introduction

Cereal crops such as wheat (*Triticum aestivum* L.), barley (*Hordeum vulgare* L.), sorghum (*Sorghum bicolor* L.) and maize (*Zea mays* L.) are consumed for food and feed in many parts of the world. The importance of these crops in the food security is vital, as they play a significant role in poverty alleviation, environmental protection and sustainable development, by acting as a source of daily calories intake for both the human and animals (Ureta *et al*., 2012).

In commercial crop production systems and natural ecosystems, the genetic variation and diversity in crop plants is being lost continuously (Adnan, 2011; Gergana, 2014). In this context, the gene banks are an important source of alleles and reservoir of the biodiversity that can be easily utilized for the genetic improvement of the target plants (Pecetti *et al*., 2001). Research endeavors are underway to collect the threatened landraces and the genotypes that have obsolete genetic stocks, as the crop improvement through breeding approaches rely largely on the extent of genetic variation in the respective crop gene pools (Ibrahim *et al*., 2011). Utilization of the genetic resources and their efficient conservation need ample knowledge regarding the amount of genetic variation in germplasm arrays and genetic relationships between genotypes (Lekgari and Dweikat, 2014).

The morphological characterization and evaluation of the diversity of the wheat genetic resources is often useful to improve the wheat breeding for its adaptation to optimal and suboptimal environments (Pecetti *et al*., 2001; Zaharieva *et al*., 2010). In a big group of wheat genotypes, originating from several countries, the wheat was divided according to the origins through simple sequence repeat (SSR) markers-assisted analysis. However, the combined effects of genotypic adaptability to diverse set of conditions and the breeding methods led to the diversity within each geographical group (Balfourier *et al*., 2007). Polymorphism in some morphological traits indicated a wide range of variability

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in the Turkish durum wheat landraces (Zencirci and Karago, 2005).

Analysis of 224 barley genotypes indicated significant genotypic variation for grain weight, plant height and flowering time (Haseneyer *et al*., 2010). Seed quality and the quantitative trait analysis of 3191 genotypes of the barley landraces of Oman also showed considerable phenotypic diversity for spike glaucousness (0.50–0.15) and spikelets per spike (0.85) (Jaradat *et al*., 2004). Rajeev *et al.* (2007) described that EST-derived single nucleotide polymorphism (SNP) was the best class of markers for characterizing and conserving the gene bank materials, and the amplified fragments length polymorphism (AFLP) and SSR markers were more suitable for diversity analysis and fingerprinting in barely.

Drought tolerance is one of the most important traits in sorghum, enabling the growth of sorghum in harsh environments (Pammi *et al*., 1994) such as the subtropical desert region of Saudi Arabia. Although, there are numerous international and national collections of sorghum cultivars, however, much of the diversity of the sorghum genotypes remained uncharacterized (Kimber *et al*., 2013). In a study on maize germplasm, a significant difference among morphological characters was observed, thus indicating high genetic diversity (Marker and Krupakar, 2009). A high level of variation among and within 41 Mexican maize races for climatic and ecological adaptation was found (Corral *et al*., 2008).

Usually, the genetic diversity is estimated by measuring the differences in the morphological traits of the genotypes (Upadhaya *et al*., 2007). However, assessment of genetic diversity on the basis of morphological traits is mostly limited by the environmental factors due to their direct influence on the expression of the quantitative traits. In this scenario, the use of molecular markers such as sequence-related amplified polymorphism (SRAP) and AFLP, which are insensitive to environmental variables, might be used as a pragmatic tool to elucidate the inter- and intra-species variations (Kumar, 1999; Hartings *et al*., 2008; Khan *et al*., 2016).

Although, the assessment of cereal genotypes on physiological, biochemical and morphological basis has been widely reported; few reports include the information regarding genetic diversity on morphological and molecular basis in wheat, barley, sorghum and maize genotypes of the Kingdom of Saudi Arabia using SRAP. This study was, therefore, conducted to evaluate the genetic diversity among the wheat, maize, sorghum and barley genotypes of Saudi Arabia on agronomic, morphological and phenological basis using SRAP molecular marker techniques.

Materials and Methods

Germplasm Collection

Genotypes of major cereal crops wheat (11), barley (4), sorghum (15) and maize (6) were collected from different locations in the Kingdom of Saudi Arabia. The collected seeds were purified, cleaned, packed and sealed. Each sample was labelled according to the gene bank serial number starting with the initials of the King Saud University (KSU) followed by the initials of the English name of the crop, and the serial number of the genotype.

Field Performance

This study was conducted at the Dirab Experimental Station (24º 43' 34" N, 46º 37' 15" E) of the King Saud University, Riyadh, Kingdom of Saudi Arabia during the growing seasons of 2013–2014 and 2014–2015. Sorghum and maize were planted on July 18, 2013, and July 21, 2014 during first and second years, respectively; whereas wheat and barley were planted on October 28, 2013 and November 01, 2014 during first and second years, respectively.

The experimental soil was sandy clay loam having pH of 8.15 and EC_e of 2.1 dS m^{-1}. The plot length was 5 m and the planted row length was 4 m. The experimental plot had four rows for each genotype and the rows were 0.5 m apart from each other. The distance between plants was 15 cm for wheat and barley, and 40 cm for sorghum and maize.

Fertilizers were applied at 120, 100 and 60 kg ha^{-1}, 100, 90 and 50 kg ha^{-1}, 150, 120 and 70 kg ha^{-1}, and 100, 80 and 50 kg ha^{-1} nitrogen (as urea), phosphorus (as triple super phosphate) and potassium (as potassium sulphate) for wheat, barley, maize and sorghum, respectively.

The plots were protected using plastic net to avoid bird attack. Sorghum was harvested on September 08, 2013, and September 13, 2014 during first and second years, respectively; whereas maize was harvested on September 12, 2013 and September 18, 2014 during first and second years respectively. Wheat was harvested depending on the maturity of each genotype during both years of the study; however, barley was harvested was harvested on May 08, 2014 and May 12, 2015 during first and second years, respectively.

Data on ten plants from each replication were recorded for each of the parameters. For all cereals, the plant height was recorded with a meter rod from the base of plant to the tip of the inflorescence. For wheat and barley, the total and productive tillers were counted for each of the plant, and averaged. For recording the 1000 grain weight, 1000 seeds were counted and weighed on a digital weighing balance. Days from sowing to 50% flowering and 95% maturity were recorded as days to flowering and maturity, respectively by visual observation. Leaf area (per plants) of sorghum and maize was recorded, at heading stage, with portable leaf area meter (LI-3100C, LI-COR, Lincoln, Nebraska USA).

Molecular Characterization

For molecular analysis, DNA was extracted following as detailed by Alghamdi *et al*. (2012). The SRAP primer combinations were tested on randomly selected genotypes

of each crop included in the study. As consistently reproducible polymorphism was noted, the primer combinations were selected to analyse the genotypes included in the study.

Statistical Analysis

All phenotypic variables were tested for normal distribution. As the year effect was not significant, data on morphological parameters of two years were pooled. The data have been presented as mean of replications and years. The GeneMapper Analysis Software v3.7 was used for the fragment analysis. The threshold for allele calling was set at 200 relative florescence units (rfu) following Wooten and Tolley-Jordan (2009). Data generated by the SRAP analysis were analyzed by Jaccard similarity coefficient following Jaccard (1908), and the dendrograms were constructed following Alghamdi *et al.* (2014).

Results

Wheat

Field performance of wheat showed significant variability in plant height, total tillers, productive tillers, 1000-grain weight, days to flowering and days to maturity. Variability among plant height ranged from 50.3 cm in genotype KSU-WH1 (lowest) to 105.7 cm (highest) in genotype KSU-WH5 with an average of 69.4 cm. The maximum total tillers were observed in genotype KSU-WH11, and the minimum total tillers were recorded in genotype KSU-WH1 (Table 1). However, the maximum productive tillers were recorded in genotype KSU-WH11, and were the lowest in genotype KSU-WH1. Wheat genotypes also showed high variability in 1000-grain weight; maximum 1000 grain weight was recorded in genotype KSU-WH2 (43.2 g), and the lowest was noted in genotype KSU-WH1 (26.5 g) (Table 1). Genotype KSU-WH4 took less days (95 and 129 days), while genotype KSU-WH2 took more days (139 and 179 days) to reach 50% flowering and maturity, respectively (Table 1).

The dendrogram constructed by UPGMA cluster analysis, of the tested genotype based on the morphological data, was cut at a genetic distance of 0.22 units. This generated two main cluster groups, one cluster group consisted of the genotypes KSU-WH2, KSU-WH3, and KSU-WH10, and other cluster group consisted of the genotypes KSU-WH6, KSU-WH7, KSU-WH8, KSU-WH9 and KSU-WH11. The genotypes KSU-WH1, KSU-WH4 and KSU-WH5 failed to form any cluster, thus were individually separated (Fig. 1). However, at 50% distance (0.30), nine genotypes were grouped in one cluster and the genotypes KSU-WH1 and KSU-WH4 were individually separated (Fig. 1). Genotype KSU-WH10 surpassed all other genotypes in 1000 grain weight. This genotype could be elite genotype for improving the yield components. Jaccard genetic similarity index among genotypes ranged from 1.0 to 0.17 (Table 2).

In wheat genotypes, a total of 593 polymorphic alleles were generated using five primer combinations, ranging from 65 to 156 alleles per primer combination, with an average of 119 alleles per primer set (Table 3). The highest number of alleles (156) was observed in the primer combination P1×P4. The size of amplification products ranged from 100 to 500 bp. All the primer combinations displayed 100% polymorphism (Table 3) which indicated high genetic diversity among all the tested wheat genotypes. All primers generated 2465 amplified fragments with an average of 493 fragments per primer combination and 244 fragments per genotype (Table 3).

Barley

In barley genotypes, a wide range of variability was observed for plant height, total number of tillers, productive tillers, 1000 grain weight, days to flowering and days to maturity. Variability among plant height ranged from a minimum of 56.20 cm in KSU-BA4 to a maximum of 80.00 cm in KSU-BA2 (Table 4). Maximum total and productive tillers were recorded with genotype KSU-BA4, and they were the minimum in genotype KSU-BA1. Maximum 1000 grain weight was recorded with genotype KSU-BA1, and the minimum was recorded in genotype KSU-BA3 (Table 4). The genotype KSU-BA4 took less time to complete 50% flowering compared with other genotypes, while the genotype KSU-BA3 took less days to reach the maturity (Table 4).

The dendrogram constructed by the UPGMA cluster analysis, of the genotypes based on the morphological data, was cut at a genetic distance of 0.54 units. This generated one main cluster group with two genotypes *viz.* KSU-BA1 and KSU-BA3. The genotypes KSU-BA4 and KSU-BA2 failed to form any cluster and were individually separated (Fig. 2). Genetic similarity index among the genotypes ranged from 0.1 among genotypes KSU-BA3 and KSU-BA4 to 0.36 among genotypes KSU-BA1 and KSU-BA3 (Table 5).

In barley genotypes, a total of 605 polymorphic alleles were generated using five primers combination, ranging from 78 to 172 alleles per primer combination, with an average of 121 alleles per primer set. The highest number of alleles i.e. 172 was recorded in primer combination P1×P2 (Table 3). The size of amplification region ranged from 100 to 500 bp. All the primer combinations displayed 100 % polymorphism (Table 3) with highest genetic diversity. All primers generated 1928 amplified fragments with an average of 386 fragments per primer combination and 482 fragments per genotype (Table 3).

Sorghum

In all fifteen sorghum genotypes, a wide range of variability was observed in leaf area and plant height. The genotypes

Table 1: Descriptive statistics of morphological, agronomic and phenological traits of some wheat genotypes of Saudi Arabia

Genotype No.	Origin	Plant height (cm)	Total tillers (per plant)	Productive tillers (per plant)	1000- grain weight (g)	Days to flowering	Days to maturity
KSU-WH1	Qaseem	50.3	04.3	03.5	26.5	135.0	172.0
KSU-WH2	Qaseem	71.9	10.9	10.4	43.2	139.0	179.0
KSU-WH3	Qaseem	64.5	08.5	07.4	38.8	137.6	176.9
KSU-WH4	Najran	59.0	10.1	8.6	29.9	095.7	129.5
KSU-WH5	Najran	105.7	11.6	11.0	39.3	137.2	172.0
KSU-WH6	Najran	68.9	09.1	09.0	34.4	112.3	152.0
KSU-WH7	Old landrace (Samma)	61.6	10.2	09.2	37.8	113.1	151.6
KSU-WH8	Old landrace (Samma)	71.3	10.2	09.9	34.9	132.2	169.5
KSU-WH9	Old landrace (Luquimi)	70.0	09.0	08.7	36.1	123.9	159.1
KSU-WH10	Wadi-e-Dwaser	63.5	10.1	7.9	40.8	128.3	166.9
KSU-WH11	Commercial cultivar (Yoko)	77.1	12.2	11.5	38.7	129.7	157.5
Mean		69.4	9.7	8.8	36.4	125.8	162.4
Max		105.7	12.2	11.5	43.2	139.0	179.0
Min		50.3	4.3	3.5	26.5	95.7	129.5
Standard error		4.2	0.6	0.7	1.5	4.1	4.4
Variance		198.0	4.4	4.7	23.4	184.4	208.3
Standard deviation		14.1	2.1	2.2	4.8	13.6	14.4
Median		68.9	10.1	9.0	37.8	129.7	166.9
Coefficient of variance		20.3	21.6	24.6	13.3	10.8	8.9

Table 2: Jaccard similarity index among wheat genotypes of Saudi Arabia generated using SRAP markers

	KSU-WH1	KSU-WH2	KSU-WH3	KSU-WH4	KSU-WH5	KSU-WH6	KSU-WH7	KSU-WH8	KSU-WH9	KSU-WH10	KSU-WH11
KSU-WH1	1.00										
KSU-WH2	0.29	1.00									
KSU-WH3	0.30	0.38	1.00								
KSU-WH4	0.33	0.45	0.33	1.00							
KSU-WH5	0.29	0.43	0.38	0.43	1.00						
KSU-WH6	0.26	0.31	0.22	0.32	0.28	1.00					
KSU-WH7	0.32	0.39	0.32	0.44	0.39	0.36	1.00				
KSU-WH8	0.32	0.35	0.22	0.34	0.35	0.31	0.43	1.00			
KSU-WH9	0.28	0.33	0.28	0.35	0.34	0.39	0.37	0.42	1.00		
KSU-WH10	0.34	0.34	0.30	0.31	0.33	0.31	0.36	0.44	0.38	1.00	
KSU-WH11	0.19	0.22	0.17	0.22	0.19	0.18	0.20	0.18	0.21	0.23	1.00

Table 3: DNA polymorphism generated using five SRAP primer combinations in barley and wheat genotypes of Saudi Arabia

Primer pair combination		Wheat	Barley
P1×P1	Number of alleles	65	87
	Total fragments	298	284
	Polymorphism (%)	100	100
P1×P2	Number of alleles	145	172
	Total fragments	696	640
	Polymorphism (%)	100	100
P1×P3	Number of alleles	122	78
	Total fragments	553	268
	Polymorphism (%)	100	100
P1×P4	Number of alleles	156	132
	Total fragments	444	342
	Polymorphism (%)	100	100
P1×P5	Number of alleles	105	136
	Total fragments	474	394
	Polymorphism (%)	100	100
Total alleles		593	605
Total fragments		2465	1928
Average alleles/primer pairs combination		118.6	121
Average fragments/primer pairs combination		493	385.6

KSU-SO5 and KSU-SO6 had the maximum plant height of 275 cm, while the genotypes KSU-SO1 and KSU-SO1 had the shortest plants with average height of 195 cm (Table 6).

The UPGMA cluster analysis of sorghum genotypes based at morphological data was cut at the distance of 0.10 units (which represented 33% of the distance from the maximum distance of 0.28 units to the minimum of 0.01

Table 4: Descriptive statistics of morphological, agronomic and phenological traits of some barley genotypes of Saudi Arabia

Genotype No.	Origin	Plant height (cm)	Total tillers (per plant)	Productive tillers (per plant)	1000- grain weight (g)	Days to flowering	Days to maturity
KSU-BA1	Jazan	58.90	07.90	06.70	47.70	134.70	180.40
KSU-BA2	Jazan	80.00	13.30	12.20	42.40	142.00	189.00
KSU-BA3	Jazan	64.50	08.50	07.40	38.80	137.60	176.90
KSU-BA4	Commercial cultivar (Gosto)	56.20	20.80	12.60	41.30	133.30	179.30
Mean		64.90	12.60	09.70	42.55	136.90	181.40
Max		80.00	20.80	12.60	47.70	142.00	189.00
Min		56.20	07.90	06.70	38.80	133.30	176.90
Standard error		5.3	3.0	1.6	1.9	1.9	2.6
Variance		113.3	35.5	9.6	14.1	14.8	27.8
Standard deviation		10.6	6.0	3.1	3.7	3.8	5.3
Median		61.7	10.9	9.8	41.9	136.2	179.9
Coefficient of variance		16.4	47.2	31.9	8.8	2.8	2.9

Table 5: Jaccard similarity index among barley genotypes of Saudi Arabia generated using SRAP markers

	KSU-BA1	KSU-BA2	KSU-BA3	KSU-BA4
KSU-BA1	1.00			
KSU-BA2	0.13	1.00		
KSU-BA3	0.36	0.22	1.00	
KSU-BA4	0.15	0.06	0.10	1.00

Table 6: Descriptive statistics of leaf area and plant height of some sorghum and maize genotypes of Saudi Arabia

Sorghum					Maize				
Genotype No.	Origin	Sorghum type	Leaf area (mm^2)	Plant height (cm)	Genotype No.	Origin	Maize type	Leaf area (mm^2)	Plant height (cm)
KSU-SO1	Jazan	Red sorghum	477.8	195.0	KSU-MA1	Jazan	White maize	450.0	152.5
KSU-SO2	Jazan	Red sorghum	164.1	195.0	KSU-MA2	Jazan	White maize	382.6	127.5
KSU-SO3	Jazan	Red sorghum	344.7	235.3	KSU-MA3	Jazan	White maize	416.5	131.3
KSU-SO4	Jazan	Red sorghum	319.0	210.0	KSU-MA4	Jazan	Yellow maize	442.5	194.0
KSU-SO5	Jazan	Red sorghum	165.8	275.0	KSU-MA5	Jazan	Yellow maize	229.4	175.0
KSU-SO6	Jazan	Red sorghum	216.8	275.0	KSU-MA6	Jazan	Yellow maize	309.9	185.2
KSU-SO7	Jazan	White sorghum	359.0	232.5	Mean			371.8	160.9
KSU-SO8	Jazan	White sorghum	186.2	214.0	Max			450.0	194.0
KSU-SO9	Jazan	White sorghum	287.2	217.2	Min			229.4	127.5
KSU-SO10	Jazan	White sorghum	341.1	205.0	Standard error			35.3	11.5
KSU-SO11	Jazan	White sorghum	136.9	230.0	Variance			7467.6	789.4
KSU-SO12	Jazan	White sorghum	316.4	205.0	Standard deviation			86.4	28.1
KSU-SO13	Jazan	Yellow sorghum	196.2	209.0	Median			399.6	163.8
KSU-SO14		Yellow sorghum	185.0	251.0	Coefficient of variance			23.2	17.5
KSU-SO15		Yellow sorghum	245.9	239.3					
Mean			262.8	225.9					
Max			477.8	275.0					
Min			136.9	195.0					
Standard error			24.8	6.7					
Variance			9193.1	665.6					
Standard deviation			95.9	25.8					
Median			245.9	217.2					
Coefficient of variance			36.5	11.4					

units), which clustered the data into four different clusters. The first cluster grouped six genotypes i.e. KSU-SO3, KSU-SO4, KSU-SO7, KSU-SO9, KSU-SO10 and KSU-SO12. The genotypes KSU-SO2, KSU-SO8 and KSU-SO13 form one cluster, while the genotypes KSU-SO5 and KSU-SO14 were grouped into another separate cluster. The genotypes KSU-SO6 and KSU-SO15 were grouped together in one cluster. The genotypes KSU-SO1 and, KSU-SO11 were individually separated (Fig. 3). Genetic similarity index among genotypes ranged from 0.14 among genotypes KSU-SO9 and KSU-SO10 to 0.61 among genotypes KSU-SO5 and KSU-SO6 (Table 6). The KSU-SO10 genotype was the most diverted among all the tested sorghum genotypes in this study (Table 7).

To study the molecular traits in sorghum, six SRAP primer pairs combinations were used, and a total of 552 polymorphic alleles, ranging from 59 to 127 alleles per primer combination, with an average of 92 alleles per primer set were generated (Table 8). The size of amplification products ranged from 100 to 500 bp. All the

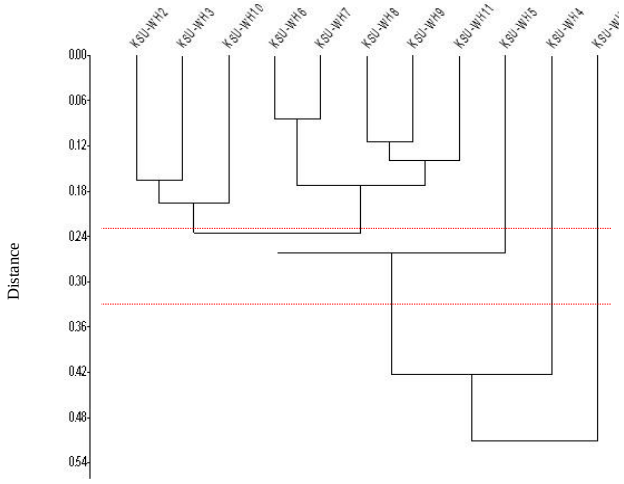

Fig. 1: Dendrogram produced by Euclidean distance coefficient and the UPGMA clustering method based on morphological, agronomic and phenological traits of some wheat genotypes of Saudi Arabia

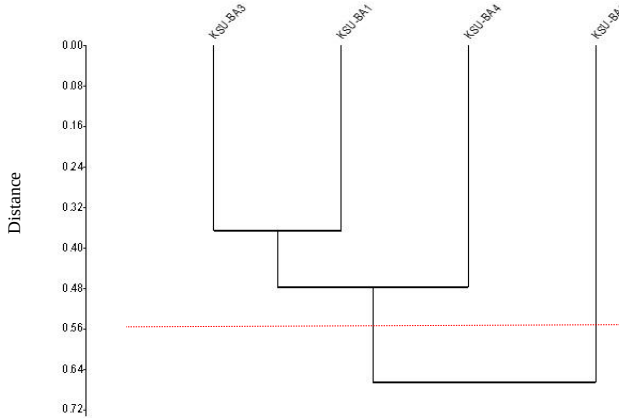

Fig. 2: Dendrogram produced by Euclidean distance coefficient and the UPGMA clustering method based on Morphological, agronomic and phenological traits of some wheat genotypes of Saudi Arabia

primer combinations displayed 100% polymorphism. All primers generated 1779 amplified fragments with an average of 297 fragments per primer combination and 119 fragments per genotype (Table 8).

Maize

In all maize genotypes, a variety of diversity was recorded in leaf area, plant height and number of heads per plant. Highest leaf area was recorded in the genotype KSU-MA1 and minimum leaf area was recorded with genotype KSU-MA5 (Table 6). The maximum plant height was recorded in genotype KSU-MA4, and that of minimum in genotype KSU-MA2 (Table 6).

The UPGMA cluster analysis of maize genotypes based at morphological data was cut at the distance of

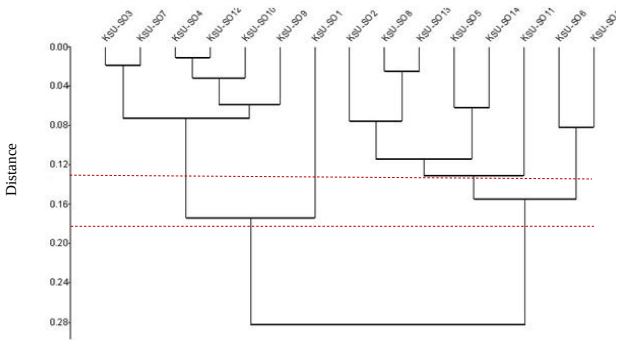

Fig. 3: Dendrogram produced by Euclidean distance coefficient and the UPGMA clustering method based on leaf area and plant height of some sorghum genotypes of Saudi Arabia

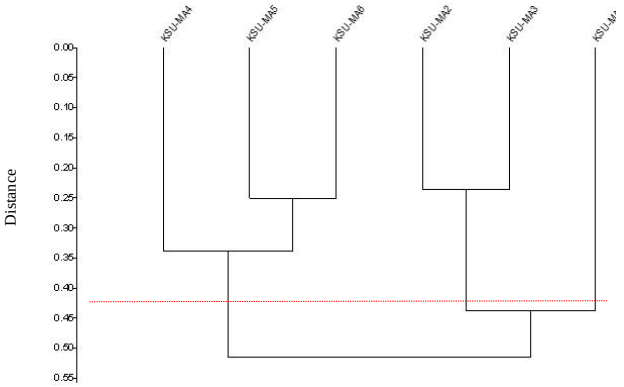

Fig. 4: Dendrogram produced by Euclidean distance coefficient and the UPGMA clustering method based on leaf area and plant height of some maize genotypes of Saudi Arabia

0.10 units, which generated two clusters. The genotypes KSU-MA2 and KSU-MA3 formed one cluster, while genotypes KSU-MA4, KSU-MA5 and KSU-MA6 formed the second cluster. The genotype KSU-MA1 failed to form any cluster and was individually separated (Fig. 4). Genetic similarity index among genotypes ranged from 0.1 between KSU-MA3 and KSU-MA4 to 0.63 between KSU-MA2 and KSU-MA3 (Table 9).

Using six SRAP primer combinations a total of 316 polymorphic alleles were generated, ranging from 18 to 73 alleles per primer combination, with an average of 53 alleles per primer set. The size of amplification products ranged from 100 to 500 bp. All the primer combinations displayed 100 % polymorphism. All primers generated 673 amplified fragments with an average of 112 fragments per primer combination and 112 fragments per genotype (Table 8).

Discussion

Cereals have been the principal food and energy source for

Table 7: Jaccard similarity index among sorghum genotypes of Saudi Arabia generated using SRAP markers

	KSU-SO1	KSU-SO2	KSU-SO3	KSU-SO4	KSU-SO5	KSU-SO6	KSU-SO7	KSU-SO8	KSU-SO9	KSU-SO10	KSU-SO11	KSU-SO12	KSU-SO13	KSU-SO14	KSU-SO15
KSU-SO1	1.00														
KSU-SO2	0.45	1.00													
KSU-SO3	0.46	0.41	1.00												
KSU-SO4	0.27	0.28	0.27	1.00											
KSU-SO5	0.25	0.31	0.30	0.54	1.00										
KSU-SO6	0.18	0.24	0.21	0.52	0.61	1.00									
KSU-SO7	0.32	0.36	0.39	0.41	0.36	0.35	1.00								
KSU-SO8	0.25	0.27	0.23	0.31	0.36	0.35	0.33	1.00							
KSU-SO9	0.29	0.25	0.25	0.27	0.32	0.27	0.20	0.15	1.00						
KSU-SO10	0.24	0.27	0.26	0.18	0.23	0.18	0.22	0.20	0.14	1.00					
KSU-SO11	0.27	0.23	0.22	0.20	0.15	0.19	0.38	0.23	0.21	0.17	1.00				
KSU-SO12	0.34	0.31	0.26	0.20	0.19	0.17	0.26	0.18	0.21	0.22	0.32	1.00			
KSU-SO13	0.37	0.40	0.34	0.43	0.45	0.41	0.44	0.30	0.26	0.30	0.25	0.22	1.00		
KSU-SO14	0.37	0.38	0.36	0.35	0.43	0.38	0.41	0.27	0.24	0.25	0.25	0.27	0.36	1.00	
KSU-SO15	0.38	0.40	0.40	0.47	0.49	0.45	0.48	0.32	0.30	0.30	0.20	0.25	0.45	0.34	1.00

Table 8: DNA polymorphism generated using five SRAP primer combinations in sorghum and maize genotypes of Saudi Arabia

Primer pair combination		Sorghum	Maize
P2×P6	No. alleles	127	68
	Total fragments	392	177
	Polymorphism%	100	100
P2×P7	No. alleles	107	73
	Total fragments	297	150
	Polymorphism%	100	100
P2×P8	No. alleles	76	66
	Total fragments	167	130
	Polymorphism%	100	100
P3×P9	No. alleles	75	44
	Total fragments	227	69
	Polymorphism%	100	100
P3×P10	No. alleles	108	47
	Total fragments	395	92
	Polymorphism%	100	100
P3×P11	No. alleles	59	18
	Total fragments	301	55
	Polymorphism%	100	100
Total alleles		552	316
Total fragments		1779	673
Average alleles/primer pair combination		92	53
Average fragments /primer pair combination		297	112

Table 9: Jaccard similarity index among maize genotypes of Saudi Arabia generated using SRAP markers

	KSU-MA1	KSU-MA2	KSU-MA3	KSU-MA4	KSU-MA5	KSU-MA6
KSU-MA1	1.00					
KSU-MA2	0.49	1.00				
KSU-MA3	0.50	0.63	1.00			
KSU-MA4	0.15	0.15	0.10	1.00		
KSU-MA5	0.38	0.42	0.47	0.14	1.00	
KSU-MA6	0.44	0.52	0.54	0.19	0.50	1.00

the human being. However, the demand is continuously increasing owing to exponentially rising global population. Although the plant breeding efforts are aimed at yield improvement in crop plants mainly the cereals. Nonetheless breeding programs focused on yield enhancement have narrowed the genetic basis of modern crop plants (Fu *et al*., 2015). This necessitates exploring the inter- and intra-species genetic diversity to exploit the desirable allelic combination (Litrico and Violle, 2015). In this regard, this study, for the very first time, indicated existence of high genetic variability and diversity for morphological and yield related traits in the tested wheat, barley, sorghum and maize genotypes of Saudi Arabia (Tables 1–9; Figs. 1–4). This variation provides a great scope for use of these genotypes

of wheat, barley, sorghum and maize in breeding programs to improve the production and resilience against suboptimal growth environments (Talebi *et al*., 2008).

Some morphological and yield parameter such as grain weight, productive tillers and the days to flowering and maturity distinguished the wheat and barley genotypes very efficiently. Apart from the yield related traits, the time required by the crop to reach at the stages of flowering and maturity is vital for their adaption to different agro-ecological regions. For instance, Kumar *et al.* (2011) indicated that the time to flowering is very crucial part of life cycle of plant due to its strong association with the phenotypic plasticity and early maturity in case of terminal drought and/heat stresses (Farooq *et al*., 2011; 2014). This study was also able to identify some good genotypes of wheat and barley for their large scale commercial production in the Kingdom of Saudi Arabia. For example, the genotype KSU-WH10, KSU-WH11, KSU-WH5, KSU-WH4, and KSU-WH2 of wheat produced the more productive tillers. The genotypes KSU-WH10 and KSU-WH2 of wheat produced the bolder grains, which may be used in the future wheat breeding programs for improvement in wheat grain yield (Farooq *et al*., 2011). In barely, KSU-BA4 and KSU-BA2 produced the highest productive tillers while KSU-BA1 and KSU-BA2 produced the bolder grain which are useful for cultivation to maximize yield as well for the future barely breeding programs in the kingdom of Saudi Arabia.

Among sorghum genotypes, the highest leaf area was recorded in genotype KSU-SO1. In maize the highest leaf area was recorded in KSU-MA1 and KSU-MA4. More leaf area in these genotype of sorghum and maize might be due to broader leaves and these genotype might be used in the future breeding programs aimed at producing the sorghum/maize plants which possess more leaf surface area to harvest the photosynthetically active radiations (Farooq *et al*., 2010).

In wheat genotypes, a total of 593 polymorphic alleles; in barley, a total of 605 polymorphic alleles; in sorghum, a total of 552 polymorphic alleles; and in maize, a total of 316 polymorphic alleles were generated using AFLP and SRAP marker technique. Polymorphism percentage was (100%) in all the primer combination which depicted the high genetic diversity and broad genetic basis of the collected genotypes (Table 3). Indeed, the molecular markers, such as SRAP, are powerful tools for the assessment of genetic variations in crop genotypes due to their high polymorphism rate (as observed in this study), and high degree of discriminatory and reproducibility power (Alghamdi *et al*., 2015). Moreover, the highest polymorphism rates in tested cereal genotypes might be attributed to the use of very sensitive laser-based genetic analyzer detection system. This laser-based system may detect even one base pair difference among the amplicons (Tavoletti and Iommarini, 2007; Altintas *et al*., 2008). This highest polymorphism rate along with low values of genetic similarity index suggest that there was very high level of heterogenic in the tested cereal genotypes for the recorded traits.

The future crop production systems depend upon the available genetic diversity to reutilize these resources for crop improvement. This great variation existed in the tested wheat, maize, sorghum and barely genotypes for various morphological and yield related traits offers opportunities to exploit favourable alleles for use in the breeding program aimed at yield improvement to meet the ever increasing food demand of the world population, and to increase the adaptability of cereal genotypes under changing climate in various agro-ecological regions.

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