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Full Length Article

Genetic Diversity and Field Performance of Mung Bean, Faba Bean and Lentil Genotypes in the Kingdom of Saudi Arabia

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Abstract

Grain legumes are grown for their high proteins and biological nitrogen fixation ability. In this study, 3 mung bean, 4 lentil and 20 faba bean genotypes from the Kingdom of the Saudi Arabia were evaluated for genetic diversity. There were significant differences in the morphological and molecular characteristics in the tested mung bean (*Vigna radiata* L.), lentil (*Lens culinaris* Medik.) and faba bean (*Vicia faba* L.) genotypes. The sequence-related amplified polymorphism (SRAP) and amplified fragments length polymorphism (AFLP) markers exhibited a considerable genetic diversity among the tested genotypes of all three legume crops. The genotypes differed for plant height, primary branches, pod length, pods per plant, grain per pod and 100-grain weight. All the tested genotypes of mung bean, lentil and faba bean differed in the number of alleles. Maximum number of alleles per primer combination was 112 in mung bean, 72 in lentil and 126 in faba bean. Polymorphism percentage of all the tested genotypes of the mung bean and lentil was 100% and in faba bean, it ranged from 97 to 100%. Existence of genetic diversity of these tested mung bean, lentil and faba bean genotypes offers opportunities to exploit favourable alleles for use in the breeding program aimed at yield improvement.

Keywords: Legumes; Alleles; Genetic diversity; Polymorphism; SRAP; AFLP

Introduction

The legumes are vital for humans and livestock for use as food and forage, and their biological nitrogen fixing ability to improve the soil fertility. In production, worldwide, grain legumes rank third after cereals and oilseeds but have a major impact on agriculture, the environment, animal and human health, and nutrition (Graham and Vance, 2003; Dita *et al*., 2006; Mantri *et al*., 2013). The legumes increase biological nitrogen fixation, reduce energy costs and improve soil physical conditions (Courty *et al*., 2015; Peix *et al*., 2015).

The agro-biodiversity is the most important component of plant genetic resources, which exists in the primitive forms of cultivated plant species and landraces, obsolete and modern cultivars, weedy types, wild species, genetic stocks, and breeding lines (Abbas *et al*., 2010; Kumar *et al*., 2011). For the selection and improvement of crops through breeding to ensure the food security needs, the genetic resource is a basic material (Duc *et al*., 2010). The genetic variation among genotypes of various legume crops is being vastly eroded as the modern cultivars are replacing the traditional cultivars over large areas across the globe (Duc *et al*., 2010; Alghamdi *et al*., 2012). On the other hand, the genetic diversity is threatened for breeding the crops for future generations due to the destruction of wild relatives of the cultivated crop species (Wang *et al*., 2012; Baloch *et al*., 2014).

Various studies have been carried out to characterize the legumes genotypes on morphological and biochemical basis (Raturi *et al*., 2014; Alghamdi *et al*., 2015). For instance, 374 mung bean genotypes significantly differed for the morphological and yield related traits (Divyaramakrishnan and Savithramma, 2014). A wide diversity among faba bean genotypes was also found for earliness and stem architectures, time to flowering, variability for nitrogen-fixing activity, biotic stresses (Duc, 1997), and grain composition (Duc *et al*., 1999). In lentil germplasm, there was large variation for different agro-morphological traits (flowering, maturity, plant height, pods per plan) and tolerance against biotic stresses (root-knot nematode, *Ascochyta* blight, rust and powdery mildew diseases) (Gautam *et al*., 2013). Roy *et al*. (2012) also assessed the genetic diversity in 110 lentil germplasm and found very high genetic diversity for number of pods per plant, number of seeds per pod and yield per plant.

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A population of 802 faba bean landraces and varieties from different geographical locations of China and abroad were examined for genetic diversity and relationships among them by using inter simple sequence repeat markers (Wang *et al*., 2012). The maximum genetic diversity was detected among the accessions from North China, while the central China accessions showed low level of diversity and Chinese winter faba bean germplasm was clearly separated from Chinese spring faba bean genotypes (Wang *et al*., 2012).

Using amplified fragment length polymorphisms (AFLP) markers, Chinese faba bean germplasm of spring (Zong *et al*., 2010) and winter (Zong *et al*., 2009) ecotypes were separately compared with accessions from the rest of the world. AFLP markers were effective to describe the genetic diversity among the tested genotypes (Zong *et al*., 2009; Zong *et al*., 2010). Using simple sequence repeat markers (SSR) the genetic relationship among 20 mung bean genotypes was studied and among that 78% genic SSR markers showed polymorphism and the number of alleles ranged from two to six with average polymorphic information content (PIC) value of 0.34. The wild and cultivated genotypes were separated clearly into groups with cluster analysis (Gupta *et al*., 2014). To study molecular diversity among 21 mung bean genotypes, Bharti *et al*. (2013) used sequence-related amplified polymorphism (SRAP) markers and out of 29 SRAP primers six primers were more useful in fingerprinting mung bean genotypes. This indicated that SRAP markers were efficient for the assessment of genetic relationships among the mung bean genotypes (Bharti *et al*. 2013). To study amplification of genomic DNA of the 24 popular Indian mung bean cultivars, the random amplified polymorphic DNA (RAPD) markers were used which yielded polymorphism average of 90% and the genotypes were grouped in two major groups indicating the narrow genetic base in the Indian mung bean cultivars (Datta *et al*., 2012).

The assessment of legumes genotypes, on the morphological and chemical composition basis, has been widely reported; however, little efforts have been done to access the genetic diversity among the mung bean, faba bean and lentil genotypes of Kingdom Saudi Arabia at morphological and molecular levels using newly developed molecular markers. Thus, this study was conducted to explore the genetic diversity among Saudi mung bean, faba bean and lentil genotypes at morphological and molecular levels using AFLP and SRAP markers.

Materials and Methods

Germplasm Collection

For the collection of germplasm of all legumes species, 20 regions were surveyed. A total of 3 of mung bean, 4 of lentil and 20 of faba bean genotypes were collected from different sites of the Kingdom of Saudi Arabia. The collected seeds were purified, cleaned and packaged. Each sample was labelled according to gene bank serial number started with the initials of the King Saud University (KSU) followed by initials of English name of the crop and serial number of the accession.

Field Performance

All the collected genotypes were evaluated at "Dirab Research and Agricultural Experiments Station" (24º 43' 3'4" N, 46º 37' 15" E), King Saud University, Riyadh, Saudi Arabia for two consecutive growing seasons during 2013–2014 and 2014–2015. The experimental soil was sandy clay loam having pH 8.15 and EC_e 2.1 dS m^{-1}. Mung bean was planted on April 13, 2013 and April 07, 2014; whereas lentil and faba bean were planted on October 28, 2013 and November 1, 2014.

The plot length was 5 m with the planted row length of 4 m. There were three rows per plot with 0.15 m and 0.5 m plant to plant and row to row distance, respectively in all the genotypes of all studied crops. For all tested legumes, 200:150 kg NP ha^{-1} were applied using ammonium sulphate as sources for nitrogen and calcium super phosphate as source for phosphorus, respectively. One third of nitrogen and whole of phosphorus were applied as basal dose whereas remaining nitrogen was split into two equal splits applied each at flowering and pod filling stage.

The plots were protected using plastic net to avoid bird attack. Mung bean was harvested on June 18, 2013 and June 09, 2014 during 1st and 2nd years of study, respectively; whereas lentil was harvested on April 05, 2014 and April 12, 2015 during 1st and 2nd years, respectively. Faba bean was harvested on April 18, 2014 and May 23, 2015 during 1st and 2nd years, respectively.

Data on ten plants from each replication were recorded for each of the parameters. Leaf area (per plant) of mung bean was recorded with portable leaf area meter (LI-3100C, LI-COR, Lincoln, Nebraska USA) at flowering. For all studied crops, the plant height was recorded at harvest maturity with the help of meter rod from the base of plant to the terminal leaf tip. The numbers of pods per plant, primary and secondary branches was counted for each of the plant, and were averaged. Pod length was measured with a ruler. Number of grains in each pod were separated and counted to record grains per pod, and grains per plant were recorded as product of pods per plant and grains per pod. For recording the 100 grain weight and 1000 grain weight in faba bean and lentil genotypes, respectively number of grains were counted and weighed on a digital weighing balance. To record the grain yield per plant, the number of grains on each plant were weighed.

Molecular Characterization

Second top leaves were collected from the two-week old seedlings of genotypes of all legume crops and were

stored liquid nitrogen. The DNA was isolated using Modified SDS protocol as described by Alghamdi *et al*. (2012).

A consistently reproducible polymorphism observed when tested genotypes were selected randomly through SRAP primer combinations. Five SRAP primer combinations were selected to analyze all the tested genotypes of mung bean and lentil, whereas six AFLP primer combinations were used in faba bean The PE Biosystems plant mapping kit (Applied Biosystems, Foster city, CA, USA) following the modified procedure of Vos *et al.* (1995) was used for AFLP analysis as detailed in Alghamdi *et al.* (2014) for faba bean. SRAP and AFLP primers used in the study are listed in Tables 1 and 2.

Statistical Analysis

Morphological data of both growing seasons were pooled, and were presented as mean of four replications. Means of genotypes were planted for descriptive statistics and dendrogram was developed by Past software (Hammer, 2001). Gene Mapper Analysis Software v3.7 (ABI) was used for AFLP and SRAP fragments analysis, and the markers showing single alleles across genotypes were eliminated. To perform the fragment analysis, the Gene Mapper Analysis Software v3.7 (ABI) was used as detailed in Alghamdi *et al.* (2014). The threshold for the allele calling was set at 200 relative florescence units (rfu) (Wooten and Tolley-Jordan, 2009). Jaccard similarity coefficient (Jaccard, 1908) was used on the data generated from AFLP and SRAP analysis using PAST software program (Hammer, 2001).

Results

Mung Bean

The mung bean genotypes significantly differed for the leaf area, number of grains per pod, and pod length (Table 3). The variability among the leaf area ranged from 55.8 cm^2 for genotype KSU-MB2 to 102.9 cm^2 for the genotype KSU-MB1. Likewise, maximum pod length (10.1 cm) was recorded in the genotype KSU-MB1 and minimum pod length (8.6 cm) was recorded in the accession KSU-MB3 (Table 3). However, maximum grains per pod (9.0) were recorded in the genotype KSU-MB2 and minimum (7.5) in the genotype KSU-MB1 (Table 3).

On the basis of morphological data of genotypes, the UPGMA cluster analysis was cut at a genetic distance of 50% (distance from the maximum 0.8 to the minimum of 0.4 units). With the cutting of dendrogram at 50% value, KSU-MB2 and KSU-MB3 were grouped in a cluster, while the genotype KSU-MB1 was individually separated (Fig. 1). The genetic similarity index among the tested genotypes ranged from 0.23 between KSU-MB1 and KSU-MB2/KSU-MB3 to 0.28 between the KSU-MB2 and KSU-MB3 genotype (Table 4). Among 3 mung bean accessions, a total of 330 polymorphic alleles, ranging from 37 to 112 alleles per primer combination, with an average of 66 alleles per primer set were generated using five SRAP primer pair combinations (Table 5). The amplification products size ranged from 100–500 bp. The polymorphism was 100% with all the primer combinations. A total of 557 amplified fragments were generated with all primers, with an average of 111.4 fragments per primer combination and 186 fragments per genotype (Table 5).

Table 1: Name and sequence of SRAP primers used in the study

Forward primers 5'--------3'	Reverse primers 5'--------3'
(P1F): TGAGTCCAAACCGGTAA	(P1R): GACTGCGTACGAATTATG
	(P2R): GACTGCGTACGAATTCAA
	(P3R): GACTGCGTACGAATTCAT
	(P4R): GACTGCGTACGAATTGTA
	(P5R): GACTGCGTACGAATTTAA

Table 2: Name and sequence of AFLP primers used in the study

Adaptors	Pre-selective primers
AFLP adaptors and primers	
EcoRI 5 -CTCGTAGACTGCGTACC-3 3 - CATCTGACGCATGGTTAA-5	EcoRI 5 - GACTGCGTACCAATTCA-3
MseI 5 -GACGATGAGTCCTGAG-33 - TACTCAGGACTCAT-5	MseI 5 - GATGAGTCCTGAGTAAC-3
AFLP selective primers	
EcoRI	MseI
E-CA	M-CTT
E-CA	M-CAA
E-CA	M-CAC
E-AA	M-CTA
E-AA	M-CTC
E-AA	M-CTT

Table 3: Descriptive statistics for morphological traits of some mung bean genotypes of Saudi Arabia

Genotype	Leaf area (cm^2)	Plant height (cm)	Pod length (cm)	Grains/pod
KSU-MB1	102.9	34.0	10.1	7.5
KSU-MB2	55.8	34.0	08.7	9.0
KSU-MB3	74.8	32.0	08.6	8.8
Mean	77.8	33.3	09.1	8.4
Max	102.9	34.0	10.1	9.0
Min	55.8	32.0	08.6	7.5
Standard error	13.7	0.7	0.5	0.5
Variance	561.5	1.3	0.7	0.7
Standard deviation	23.7	1.2	0.8	0.8
Coefficient of variance	30.4	3.5	9.2	9.7

Table 4: Jaccard similarity index among mung bean genotypes of Saudi Arabia generated using SRAP markers

	KSU-MB1	KSU-MB2	KSU-MB3
KSU-MB1	1.00		
KSU-MB2	0.23	1.00	
KSU-MB3	0.23	0.28	1.00

Table 5: DNA polymorphism generated using five SRAP primers combinations in mung bean and lentil genotypes

Primer pair combination		Mung bean	Lentil
P1×P1	Number of alleles	53	47
	Total fragments	93	57
	Polymorphism (%)	100	100
P1×P2	Number of alleles	112	72
	Total fragments	189	80
	Polymorphism (%)	100	100
P1×P3	Number of alleles	37	42
	Total fragments	59	42
	Polymorphism (%)	100	100
P1×P4	Number of alleles	80	14
	Total fragments	140	17
	Polymorphism (%)	100	100
P1×P5	Number of alleles	48	41
	Total fragments	76	46
	Polymorphism (%)	100	100
Total alleles		330	216
Total fragments		557	242
Average alleles/primer pair combination		66	43.2
Average fragments /primer pair combination		111.4	48.4

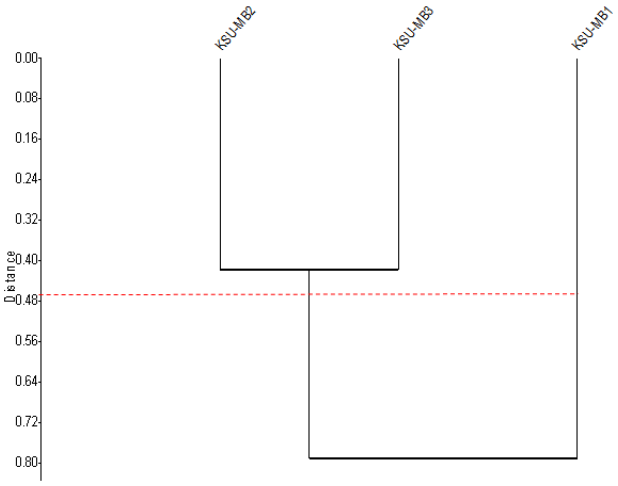

Fig. 1: Dendrogram produced by Euclidean distance coefficient and the UPGMA clustering method based on morphological traits of some mung bean genotypes of Saudi Arabia

Lentil

High genetic variability among the morphological and molecular characters was observed among the lentil accessions (Table 6). Maximum plant height (56.6 cm), primary (7.3) and secondary branches (16), grains per pod (2), grains per plant (87.8), 1000-grain weight (62.9 g) and grain yield per plant (5.5 g) were recorded in the genotype KSU-LE1 (Table 6). However, the minimum plant height (39.7 cm), primary (3.4) and secondary branches (11.2), grains per pod (1.3), grains per plant (39.1) and grain yield per plant (1.8 g) were recorded in the genotype KSU-LE2. Number of pods per plant was maximum in genotype KSU-LE3 (Table 6).

Based on the morphological data of the genotypes the UPGMA cluster analysis was cut at a genetic distance of 0.26 units (showed 50% genetic distance from maximum 0.38 to minimum 0.14 units), which grouped the genotypes (KSU-LE3 and KSU-LE4) into one cluster and the other two accessions KSU-LE1 and KSU-LE2 failed to form cluster and individually separated (Fig. 2). Genetic similarity index among accessions ranged from 0.14 among KSU-LE2 and KSU-LE4 to 0.38 among KSU-LE2 and KSU-LE3 (Table 7).

In lentil genotypes, the genetic diversity among the accessions was assessed using five SRAP primer pair combinations. A total of 216 polymorphic alleles, ranging from 14 to 72 alleles per primer combination, 43 alleles per primer set on an average were generated with five primers set (Table 5). The amplification product size ranged from 100 to 500 bp with 100% polymorphism on all primer combinations. All primers generated 242 amplified fragments with 65 fragments per accession and 48 fragments per primer combination on an average (Table 5).

Faba Bean

In faba bean, high genetic variability among all the accessions was detected for all morphological, agronomic and molecular traits. Plant height ranged from a minimum of 45.1cm for the genotype KSU-FB7 to a maximum of 93.6 cm for the genotype KSU-FB7 with mean of 66.7 cm (Table 8). The maximum number of pods and grains per plant were recorded in the genotype KSU-FB17; 100-grain weight (208.68 g) in the genotype KSU-FB9. The minimum 100-grain weight (45.01 g) was recorded in the genotype KSU-FB1 (Table 8). The maximum pod length (8.99 cm) was recorded in the genotype KSU-FB16; and the minimum (4.85 cm) in the genotypeKSU-FB18 (Table 8). Grain yield ranged from 6.6 g for KSU-FB14 to 110 g for KSU-FB17 with an average yield of 38.5 g (Table 8).

Based on the morphological and agronomic data of the genotypes the UPGMA cluster analysis was cut at a genetic distance of 0.60 units, which showed 50% genetic distance (from maximum 1.20 to minimum 0.0 units), which grouped all the accessions into five main clusters. The accessions KSU-FB2, KSU-FB4, KSU-FB5, KSU-FB10, KSU-FB11 and KSU-FB12 formed the first cluster. The second cluster grouped the genotypes KSU-FB3, KSU-FB6, KSU-FB13 and KSU-FB17. The third cluster grouped the accession KSU-FB19 and KSU-FB20. In the fourth cluster, the accessions KSU-FB1, KSU-FB14 and KSU-FB15 were grouped and the accessions KSU-FB7, KSU-FB8 and KSU-FB9 were grouped in the fifth cluster (Fig. 3). Genetic similarity index among accessions ranged from 0.17 in the genotype KSU-FB5 and KSU-FB18 to 0.59 among KSU-FB3 and KSU-FB7 and between KSU-LRU-54 and KSU-FB16 (Table 9).

Table 6: Descriptive statistics for morphological and agronomic traits of some lentil genotypes of Saudi Arabia

Genotype	Plant height (cm)	Primary branches	Secondary branches	Pods/plant	Grains/pod	Grains/plant	1000-grain weight (g)	Grain yield/plant (g)
KSU-LE1	56.6	7.3	16.0	43.9	2.0	87.8	62.9	5.5
KSU-LE2	39.7	3.4	11.2	30.1	1.3	39.1	45.3	1.8
KSU-LE3	56.5	4.8	11.6	52.4	1.6	83.8	56.0	4.7
KSU-LE4	49.2	5.1	12.1	45.7	1.7	77.7	44.8	3.5
Mean	50.5	5.2	12.7	43.0	1.7	72.1	52.3	3.9
Max	56.6	7.3	16.0	52.4	2.0	87.8	62.9	5.5
Min	39.7	3.4	11.2	30.1	1.3	39.1	44.8	1.8
Standard error	4.0	0.8	1.1	4.7	0.1	11.2	4.4	0.8
Variance	63.8	2.6	4.9	87.6	0.1	501.2	77.1	2.6
Standard deviation	8.0	1.6	2.2	9.4	0.3	22.4	8.8	1.6
Coefficient of variance	15.8	31.3	17.4	21.8	17.5	31.1	16.8	41.5

Table 7: Jaccard Similarity index generated using SRAP markers among lentil genotypes

	KSU-LE1	KSU-LE2	KSU-LE3	KSU-LE4
KSU-LE1	1.00			
KSU-LE2	0.29	1.00		
KSU-LE3	0.21	0.38	1.00	
KSU-LE4	0.22	0.14	0.15	1.00

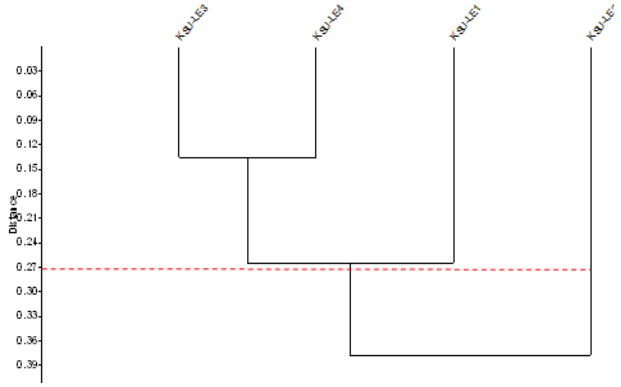

Fig. 2: Dendrogram produced by Euclidean distance coefficient and the UPGMA clustering method based on morphological and agronomic traits of some lentil genotypes of Saudi Arabia

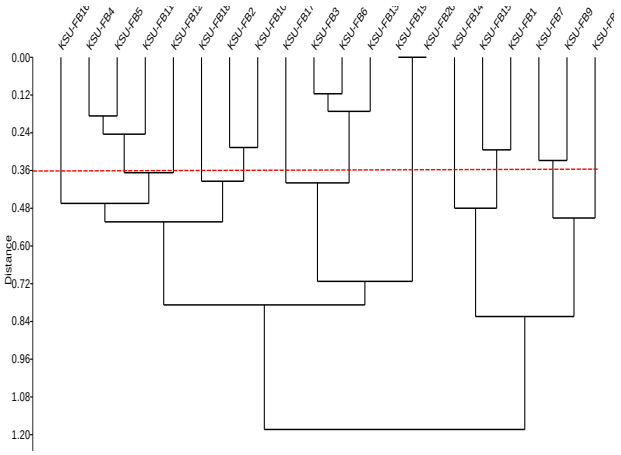

Fig. 3: Dendrogram produced by Euclidean distance coefficient and the UPGMA clustering method based on morphological and agronomical traits of some faba bean genotypes of Saudi Arabia

The genetic variability was assessed among 20 faba bean accessions using six AFLP primer combinations. By using the six primer combinations a total of 516 polymorphic alleles were produced, with 26 to 126 alleles per primer combination, and with average of 86 alleles per primer set. The product of amplification size ranged from 100 to 500 bp. The polymorphism was 97–100% for all the primer combinations. All primers generated 3478 amplified fragments with an average of 580 fragments per primer combination and 174 fragments per accession (Table 10).

Discussion

The landraces are one of the most important sources of genetic resource because of their ability to evolve adaptation against various environmental conditions (Asins and Carbonell, 1989; Karaköy *et al*., 2014). These landraces are an outcome of natural and farmer's selection and are an important source of genetic diversity for the existing breeding programs (Asins and Carbonell, 1989; Baloch *et al*., 2014). However, the rapid and continual destruction of the genetic variability in landraces and traditional cultivars has reduced the possibilities to improve the crop output (grain yield) with enhancement in the susceptibility to the diseases, and sensitivity to the adverse climatic variables (Asins and Carbonell, 1989).

This study revealed a high genetic variability in various genotypes of legumes (mung bean, lentil and faba bean) for morphological, agronomic and molecular traits (Tables 3–10). In mung bean genotypes, the highest leaf area was recorded in the genotype KSU-MB1, which indicated the ability of this genotype to harvest more solar radiation against those genotypes having minimum leaf area. Thus, the plants of this genotype attained maximum plant height and pod length. While the maximum

Table 8: Descriptive statistics for morphological and agronomic traits of some faba bean genotypes of Saudi Arabia

Genotype designation	Genotype name	Plant height (cm)	Pods/plant	Pod length (cm)	Grains/pod	Grains/plant	100- grain weight (g)	Grain yield (g/plant)
KSU-FB1	Hassawi1	48.53	10.67	7.25	2.27	23.47	45.01	11.72
KSU-FB2	Hassawi2	53.20	19.67	7.03	3.00	37.60	50.55	20.79
KSU-FB3	Hassawi3	74.53	35.67	6.33	2.60	70.13	102.66	77.10
KSU-FB4	Goff1	83.80	16.33	7.63	2.80	28.60	120.62	38.23
KSU-FB5	Gazira 1	77.00	14.00	8.82	2.60	36.00	92.15	36.80
KSU-FB6	Gazira 2	71.00	33.00	7.76	2.80	74.20	99.25	85.86
KSU-FB7	T.W	45.07	7.00	5.89	2.27	15.9	196.31	31.2
KSU-FB8	T.Wrsc	48.00	8.00	6.38	2.16	17.3	164.35	28.4
KSU-FB9	H3	86.40	7.33	6.83	2.40	17.6	208.68	36.7
KSU-FB10	H5	67.00	19.67	5.45	2.13	33.20	73.13	25.95
KSU-FB11	H8	73.20	10.67	8.35	2.80	27.80	146.49	42.10
KSU-FB12	L. 4	53.67	12.67	6.01	2.60	32.9	140.78	46.4
KSU-FB13	L. 21	53.80	32.00	7.55	2.60	78.13	88.10	72.74
KSU-FB14	Pop. 3	67.87	7.33	5.92	2.60	10.27	59.19	6.58
KSU-FB15	Pop. 4	58.67	16.33	5.86	2.40	16.47	53.77	21.1
KSU-FB16	H4	71.33	17.33	8.99	3.60	58.20	83.86	51.72
KSU-FB17	H7	74.80	57.00	6.15	2.47	130.53	79.76	104.1
KSU-FB18	Line 9	78.20	27.00	4.85	2.33	59.60	56.16	36.44
KSU-FB19	Line 5	93.60	45.33	7.08	2.27	116.53	62.51	72.8
KSU-FB20	Line 22	93.60	45.33	7.08	2.27	116.53	62.51	72.8
Mean		68.66	22.1	6.9	2.5	51.2	99.3	45.8
Max		93.60	57.0	9.0	3.6	130.5	208.7	104.1
Min		45.07	7.0	4.9	2.1	10.3	45.0	6.6
Standard error		3.3	3.3	0.2	0.1	8.1	10.9	5.9
Variance		222.6	215.9	1.2	0.1	1305.7	2372.4	704.0
Standard deviation		14.9	14.7	1.1	0.3	36.1	48.7	26.5
Coefficient of variance		21.7	66.4	16.2	13.5	70.6	49.1	57.7

Table 9: Jaccard similarity index among faba bean genotypes of Saudi Arabia generated using AFLP markers

	KSU-FB1	KSU-FB2	KSU-FB3	KSU-FB4	KSU-FB5	KSU-FB6	KSU-FB7	KSU-FB8	KSU-FB9	KSU-FB10	KSU-FB11	KSU-FB12	KSU-FB13	KSU-FB14	KSU-FB15	KSU-FB16	KSU-FB17	KSU-FB18	KSU-FB19	KSU-FB20
KSU-FB1	1.00																			
KSU-FB2	0.51	1.00																		
KSU-FB3	0.57	0.47	1.00																	
KSU-FB4	0.51	0.44	0.56	1.00																
KSU-FB5	0.38	0.48	0.44	0.36	1.00															
KSU-FB6	0.25	0.43	0.31	0.24	0.46	1.00														
KSU-FB7	0.41	0.41	0.59	0.44	0.37	0.28	1.00													
KSU-FB8	0.32	0.30	0.38	0.36	0.40	0.29	0.39	1.00												
KSU-FB9	0.32	0.27	0.40	0.34	0.39	0.31	0.42	0.46	1.00											
KSU-FB10	0.23	0.21	0.28	0.24	0.35	0.23	0.32	0.42	0.46	1.00										
KSU-FB11	0.25	0.29	0.29	0.26	0.39	0.38	0.35	0.40	0.45	0.47	1.00									
KSU-FB12	0.31	0.31	0.36	0.32	0.50	0.33	0.42	0.44	0.57	0.54	0.53	1.00								
KSU-FB13	0.50	0.37	0.54	0.40	0.42	0.30	0.51	0.38	0.51	0.33	0.32	0.44	1.00							
KSU-FB14	0.36	0.36	0.37	0.39	0.28	0.21	0.39	0.24	0.22	0.21	0.21	0.27	0.39	1.00						
KSU-FB15	0.38	0.27	0.42	0.41	0.35	0.27	0.48	0.42	0.58	0.38	0.37	0.48	0.54	0.31	1.00					
KSU-FB16	0.33	0.23	0.41	0.33	0.27	0.22	0.45	0.31	0.47	0.34	0.33	0.40	0.47	0.29	0.59	1.00				
KSU-FB17	0.26	0.23	0.29	0.26	0.36	0.24	0.36	0.45	0.48	0.58	0.49	0.52	0.35	0.19	0.45	0.38	1.00			
KSU-FB18	0.27	0.19	0.24	0.24	0.17	0.20	0.32	0.27	0.37	0.25	0.27	0.30	0.38	0.28	0.45	0.56	0.34	1.00		
KSU-FB19	0.23	0.21	0.25	0.26	0.34	0.26	0.30	0.41	0.46	0.50	0.47	0.43	0.28	0.18	0.39	0.29	0.54	0.26	1.00	
KSU-FB20	0.21	0.20	0.25	0.22	0.27	0.31	0.33	0.37	0.46	0.51	0.53	0.43	0.30	0.19	0.41	0.39	0.45	0.35	0.51	1.00

number of grains per pod was recorded in the genotype KSU-MB2 (Table 3). As number of grains per pod is an important yield contributing traits, which indicated the ability of this genotype to enhance the yield of mung bean using this genotype in future breeding programs. The existence of high level of genetic diversity, for morphological and yield contributing traits in mung bean genotypes indicates the potential for use in the future breeding programs aimed to tailor the genotypes for target set of parameters (Rahim *et al*., 2008; Abna *et al*., 2012; Divyaramakrishnan and Savithramma, 2014).

High genetic variability among all the lentil genotypes was observed for morphological and yield parameters using the SRAP markers. Highest grains per pod and grain weight was recorded in the genotype KSU-LE1; while the genotype KSU-LE3 produced the maximum number of pods per plant

(Table 6), and both genotypes may be utilized to improve the grain yield of lentil by the future breeding programs. In another study, Gautam *et al*. (2013) recorded a great genetic difference in the agro-morphological traits (flowering, maturity, plant height, pods per plant, primary branches/plant) in lentil germplasm. Some other studies have separated the different lentil accessions based on number of pods per plant, number of grains per pod and yield per plant, irrespective of their origin (Roy *et al*., 2012).

Using the AFLP markers, there was found a wide genetic diversity in tested faba bean genotypes for the morphological, agronomic and molecular traits. In this regard, the genotype KSU-FB6 (Table 8), produced the maximum grain yield, which can be attributed to higher grains number per pod/plant and more grain weight. The highest number of pods and number of grains per plant were recorded in genotype KSU-FB17; while 100 grain weight was the highest in genotype KSU-FB9. These genotypes may be the priority of the future crop breeder to develop high yielding faba bean genotypes. Analysis of agro-morphological diversity of faba bean germplasm showed highly significant differences among the populations for most of the morphological and yield related traits at several locations in Tunisia (Yahia *et al*., 2012). In another study, to assess the genetic diversity and relationship among 58 faba bean genotypes fourteen SRAP primer combinations were used and found a wide genetic diversity for morphological and molecular traits (Alghamdi *et al*., 2012).

Although, great efforts to enhance the production of forage and grain legumes through the conventional breeding approaches have been made (Ahmad *et al*., 2010). However, due to existence of the wide genotype × environment interactions, which impacts the grain yield and the related traits, these genetic improvements approach of conventional breeding are slow (Kumar and Ali, 2006). Use of molecular markers can assist accelerating the crop genetic improvement program. Indeed, not only for crop improvement but also for the conservation and efficient management of plant genetic resources, the assessment of genetic diversity with the use of molecular markers is important and need of the time (Alghamdi *et al*., 2011, 2015). The molecular characterization through AFLP and SRAP markers showed very high polymorphism rate among the tested legume genotypes in this study. This high polymorphism with the use of AFLP and SRAP markers among the tested legume genotypes might be attributed to the use of more sensitive laser based genetic analyzer detection system. This most advanced system even may detect a difference of one per base pair between the amplicons (Tavoletti and Iommarini, 2007; Altintas *et al*., 2008). Moreover, for the differentiation of the relationship among various traits of legume genotypes, the molecular markers (AFLP and SRAP) were very useful. The significant correlations in the data based on morphological matrix in this study based on the SRAP/AFLP markers indicated the coherent pattern of genetic diversity for the studied legume genotypes. The cluster analysis grouped all the legume genotypes into various clusters. The genotypes placed in the same cluster might have same parentage or have similar features to be adopted to an area.

Table 10: DNA polymorphism generated using six AFLP primers combinations in faba bean genotypes

Primer pair combination		Faba bean
E-TA /M-CTC	Number of alleles	75
	Total fragments	244
	Polymorphism (%)	97.3
E-TC /M-CTA	Number of alleles	106
	Total fragments	1034
	Polymorphism (%)	97.2
E-TC /M-CAA	Number of alleles	126
	Total fragments	792
	Polymorphism (%)	99.2
E-TT /M-CTC	Number of alleles	107
	Total fragments	509
	Polymorphism (%)	99.1
E-GA /M-CTT	Number of alleles	26
	Total fragments	121
	Polymorphism (%)	100
E-TT /M-CAA	Number of alleles	76
	Total fragments	778
	Polymorphism (%)	100
Total alleles		516
Total fragments		3478
Average alleles/primer pair combination		86
Average fragments /primer pair combination		580

In conclusion, this study of genetic diversity of Saudi landraces and genotypes of faba bean, mung bean and lentils based on AFLP and SRAP markers was very useful for the identification of the superior traits for future plant breeding programmes to meet the ever-increasing food demand of the world through crop improvement and to increase the adaptability of genotypes under climate change.

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