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Full Length Article

Agro-Morphological Characterization of Lentil Genotypes in Dry Environments

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Abstract

This study aimed to assess genetic variability among lentil genotypes at the agro-morphological level and to identify the most promising genotypes for cultivation in dry environments. Our field evaluation included 36 lentil genotypes collected from Yemen, Bangladesh, Egypt, Saudi Arabia, and International Center for Agriculture Research in the Dry Areas (ICARDA), in a triple Lattice experiment. Twenty-four agro-morphological traits were evaluated. Analyses of variance showed highly significant inter and intra block differences for all genotypes tested. On average, the genotypes required 74 days to flowering and 135 days to maturity. Genotype BD-Barimasur-6 (57 days to flower) was the earliest flowering genotype, but YE35016, YE35038, BD-Barimasur-3, BD-Barimasur-7 and BD-Barimasur-6 were the earliest maturating genotypes. The EG-Giza 9 and EG-Giza 51 produced the highest number of pods per plant, while the highest seed weight at both locations was recorded for SA-KSUYellow1, 2 and 3. Genotype SA-KSURed out yielded the all genotypes at both locations and surpassed overall locations mean. Principal component analysis (PCA) supported by hierarchical cluster analysis based on quantitative and qualitative traits- distributed the 36 genotypes according to geographical origin for both locations. Broad diversity was found among the tested lentil genotypes for different characters. The potential genotypes of lentil were identified for their use in genetic analysis and lentil breeding programmes for dry areas.

Keywords: Maturity; Flowering; Variabilty; Selection; Multivarince analysis

Introduction

Lentil (*Lens culinaris* Medik.) is one of the oldest and most appreciated grain legumes in the world. It is an annual, herbaceous, diploid (2n = 2x = 14), self-pollinating species (Sharma *et al*., 1995), which originated in the Near East (Zohary, 1972) and spread to the north of Africa, east of Ethiopia, south of Europe, North America, Oceania and South Asia (Duke, 2012). Lentil was domesticated along with wheat (*Triticum aestivum* L.) and barley (*Hordeum vulgare* L.) approximately 9000 years ago from the wild progenitor *Lens culinaris* subspp. *orientalis* (Boiss.) (Zohary and Hopf, 2000). It is planted as a major cool season crop, growing in North Africa, West Asia, the Middle East, Indian subcontinent, and North America (Erskine, 1997). Lentil is cultivated in over 4.52 million hectares around the world, with a total production of 4.88 million metric tons (FAOSTAT, 2014). Worldwide average lentil seed yield was only 1.08 metric tons ha^{-1} in 2014, which was much lower than the average yield of many other legumes.

Cultivated lentil shows close morphological, cytogenetic and molecular similarities with wild *L. orientalis* (Boiss.) (Ladizinsky and Muehlbauer, 1993; Oss *et al*., 1997). It is chromosomally uniform and fully homologous with the standard orientalis race. Hybrids between this wild *orientalis* of chromosomal type and the culinary cultivars are fully fertile.

Lentil is rich in fibre and low in fat and the total soluble fibre are greater than peas (*Pisum sativum* L.) and chickpea (*Cicer arietinum* L.) (Brummer *et al*., 2015). The dietary fibre is also higher than chickpeas and broad beans and protein contents ranged between 20.6 to 31.4% (Urbano *et al*., 2007). The protein in lentil contains low percentage of sulphur-containing amino acids. The nutritional benefits of lentil in humans include lipid and cholesterol lowering effects along with reducing intensity of type-2 diabetes and colon cancer (Roy *et al*., 2010).

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Analysis of the genetic variability of lentil is considered as one of the main activities in breeding programs for sustainable utilization of this crop. The genetic diversity can be characterised by using agro-morphological traits or molecular markers. Lentil varieties showed a considerable variation in plant height, number of branches, number of pods per plant, number of seeds per plant and biological yield (Chakraborty and Haque, 2000; Sarker and Erskine, 2001). A considerable genetic variability was revealed and recorded for the different agro-morphological traits of lentil (Bacchi *et al*., 2010; Al-Ghzawi *et al*., 2011; Alghamdi *et al*., 2013; Aslam *et al*., 2017). Consequently, numerous true breeding lines and aggregates of landraces have evolved in this crop. This study aimed to assess the genetic variability among 36 lentil genotypes at the agro-morphological level and to identify the best-suited genotypes for cultivation in dry environments.

Materials and Methods

Plant Materials

Thirty-six lentil genotypes, used in this study, were collected from Yemen, Bangladesh, Egypt and Saudi Arabia. The list of lentil genotypes and their origin is shown in Table 1.

Field Experiment

The field experiment was carried out at the Experimental Station, National Agriculture and Animal Resources Research Centre, Riyadh (24°34′46.1″N 46°43′04.8″E), Saudi Arabia and at Dirab Agricultural Research Station (24°25′04.6″N 46°39′13.2″E), King Saud University, Riyadh, Saudi Arabia. Lentil genotypes were planted at both experiment sites on 20 November 2015 and 24 November 2016, during first and second growing seasons, in a triple Lattice design. The experimental unit consisted of two lines, each of 4 m in length and 25 cm apart, with 10 cm spaced hills for a population density of 40 plants m^{-2}. All agronomic practices were performed according to the Agricultural Research Station Management. Fertilizers were applied as 90, 100 and 120 kg NPK ha^{-1} using diammonium phosphate (18% N, 46% P_2O_5), urea (46% N) and potassium sulphate (50% K), respectively, as sources. Plots were immediately irrigated after planting and were subsequently irrigated according to plant demand. Weeds were removed manually to keep plots clean during the growing season. Crop was harvested on 11 April 2016 and 15 April 2017 during 1st and 2nd growing seasons, respectively at maturity.

Morphological Characterization

Data on morphological and phenotypic traits was measured based on the descriptors proposed by the International Plant Genetic Resources Institute (IPGRI) and the International Union for the Protection of New Varieties of Plants (UPOV). All data were recorded from ten plants per row in each experimental plot. Procedure to record the data are given in Table 2.

Table 1: The list and the origin of lentil genotypes used in this study

S. No.	Genotypes	Cod	Origin
1	BD-Barimasur-3	BD-1	Bangladesh
2	BD-Barimasur-7	BD-2	Bangladesh
3	BD-Barimasur-6	BD-3	Bangladesh
4	EG-Giza 370	EG-1	Egypt
5	EG-Giza 9	EG-2	Egypt
6	EG-Sina 1	EG-3	Egypt
7	EG-Giza 51	EG-4	Egypt
8	ILL 11022	ILL-1	ICARDA
9	ILL 11193	ILL-2	ICARDA
10	SA-KSURed	SA-1	Alqaseem, Saudi Arabia
11	SA-KSUYellow1	SA-2	Gaizan, Saudi Arabia
12	SA-KSUYellow2	SA-3	Gaizan, Saudi Arabia
13	SA-KSUYellow3	SA-4	Alqaseem, Saudi Arabia
14	SA-PGRB 291	SA-5	Aseer, Saudi Arabia
15	SA-PGRB 295	SA-6	Aseer, Saudi Arabia
16	SA-PGRB 297	SA-7	Aseer, Saudi Arabia
17	YE35005	YE-1	Sanaa, Yemen
18	YE35006	YE-2	Haja, Yemen
19	YE35008	YE-3	Dhamar, Yemen
20	YE35012	YE-4	Marib, Yemen
21	YE35014	YE-5	Dhamar, Yemen
22	YE35016	YE-6	Dhamar, Yemen
23	YE35017	YE-7	Amran, Yemen
24	YE35018	YE-8	Taiz, Yemen
25	YE35021	YE-9	Albedha, Yemen
26	YE35034	YE-10	Dhamar, Yemen
27	YE35037	YE-11	Taiz, Yemen
28	YE35038	YE-12	Dhamar, Yemen
29	YE35039	YE-13	Dhamar, Yemen
30	YE35040	YE-14	Dhamar, Yemen
31	YE35048	YE-15	Albedha, Yemen
32	YEDhamar-1	YE-16	Dhamar, Yemen
33	YEDhamar-2	YE-17	Dhamar, Yemen
34	YEHaymi	YE-18	Sanaa, Yemen
35	YEMatri	YE-19	Sanaa, Yemen
36	YESabri	YE-20	Taiz, Yemen

Data Analysis

Data recorded for both growing seasons were pooled before analysis. Mean and standard deviation values of the morphological traits were analysed by Statistical software SAS 9.3 (in the partially balance Lattice design). Means were compared by the least significant difference (LSD) test at 0.05 probability level. Test of variance homogeneity for seed yield was generated using Bartlett test. Principal component analysis (PCA) and phenological dendrogram were constructed based on Euclidean distance coefficients using PAST 3.11 (Hammer *et al*., 2001).

Results

Quantitative traits

The analysis of variance on the agro-morphological traits of

Table 2: Morphological and phenotypic qualitative traits measured based on the descriptors proposed by the International Plant Genetic Resources Institute (IPGRI) and the International Union for the Protection of New Varieties of Plants (UPOV)

Quantitative agronomic traits	
Vegetative growth traits	
Plant height	In cm, from the soil surface to the upper part of the plant canopy
Biological yield	[g/plant], yield of dried, mature plants after harvesting.
Inflorescence and fruit	
Days to 50% flowering	Number of days from sowing to 50% flowering
Days to 90% maturity	Number of days from sowing to stage when 90% pods turned golden brown
Number of flowers	Number of flowers per raceme
Height of lowest pod	In cm, from the soil surface to the first pod
Number of pods	Number of pods per plant
Yield-related traits	
Number of seeds/pod	Measured as a mean of 10 dry pods
100 seed weight	In gram, average weight of two samples of 100 randomly chosen seeds.
Seed yield	[g/plant], seed yield after drying
Qualitative phenotypic traits	
Vegetative growth traits	
Seedling stem pigmentation	0 = Absent, + = present) observed two weeks after the emergence
Leaf pubescence	0 = Absent, 3 = slight, 7 = Dense. Observed before maturity
Leaflet size	3 = Small, 5 = Medium, 7 = Large. Observed on fully expanded leaves on lower flowering nodes
Tendril length	1 = Rudimentary, 2 = Prominent. Observed during pod filling.
Intensity of ramification	3 = Weak, 5 = Medium, 7 = Strong. Observed at maturity.
Lodging susceptibility	0 = None, 3 = Low, 5 = Medium, 7 = High. Observed at maturity.
Anthocyanin coloration	0 = Absent, + = present. Observed before maturity.
Inflorescence and fruit	
Flower ground color	Ground color of standard petal – flag. 1= White, 2= White with blue veins, 3= Blue , 4= Violet , 5= Pink , 6= White with violet veins , 7= Violet with white veins
Pod pigmentation	0 = Absent, + = present
Pod shedding	0 = None, 3 = Low, 5 = Medium, 7 = High. Scored a weak after maturity.
Seeds traits	
Ground color testa	1=Green, 2=Grey, 3= Brown, 4=Black, 5=Pink. Observed on seed less than 3 months old.
Pattern testa	0 = Absent, 1= Dotted, 2= Spotted, 3= Marbled, 4= Complex. Observed on seed less than 3 months old.
Color of pattern on testa	0= Absent, 1= Olive, 2= Grey, 3=Brown, 4= Black. Observed on seed less than 3 months old.
Cotyledon color	1= Yellow, 2= Orange /red, 3= Olive /green. Observed on seed less than 3 months old

the tested lentil genotypes grown at two locations showed highly significant inter and intra-block differences. The descriptive values with the best performing (25%) of the genotypes for the quantitative traits of the 36 lentil genotypes grown at the two locations showed that genotype SA-KSUYellow2 (SA-3) had the highest plant height (46.27 and 48.9 cm), while genotypes introduced from Bangladesh had the minimum plant height (Table 3). Overall, biological yield (BY) ranged from 5.43 to 40.07 g plant^{-1} and the highest BY (40.07 g plant^{-1}) was recorded in genotype SA-KSURed (SA-1), while genotype YE35012 produced the lowest value. At National Center, genotype SA-KSUYellow3 was considered the latest flowering genotype (114 days), however, genotype BD- Barimasur-6 was considered the earliest flowering genotype (56 days). Four genotypes, YE35016, BD- Barimasur-7, YE35037 and BD-Barimasur-6 had the lowest number of days to flowering at both locations and did not differ significantly from the earliest flowering genotypes. Genotypes ILL11022, SA-KSUYellow1, 2 and 3 had the maximum number of flowers per raceme and genotypes BD-Barimasur-7 and 6 produced the minimum flowers at both locations (Table 3).

The number of days to maturity (DM) ranged 116.67 to 160 at National Center and from 118.33 to 160 at Dirab. Genotypes SA-KSUYellow1, 2, 3 and YEMatri displayed the highest number of days to maturity and were considered the latest maturing genotypes. In contrast, genotypes YE35016, YE35038 and BD-Barimasur-3, 7, 6, had the lowest number of days to maturity and were considered the earliest maturating genotypes at both locations (Table 3). Mean values for height of the lowest pod (HLP) ranged 6.67 to 21.39 cm with genotype SA-KSUYellow2 ranked at first in this trait (Table 3). Genotypes BD-Barimasur-3, 7, 6, YE35016 and YE35017 ranked lowest at both locations.

The highest numbers of pods plant^{-1} (PD/P) were recorded in genotypes EG-Giza 9 and EG-Giza 51 at both locations. The highest seeds pod^{-1} (S/PD) were observed in genotypes EG-Giza 370, YE35017 and YE35040 at National Center, while genotypes EG-Giza 370, YE35017, YE35018 and EG-sina1 at Dirab. The genotypes SA-KSUYellow1, 2 and 3 produced the heaviest seeds (100-seed weight) at both locations, while genotype SA-PGRB 295 recorded the smallest seed weight at both locations (Table 3).

For homogeneity variance the Bartlett test was performed and there were non-significant differences among the variances at both locations. However, both locations showed a highly significant difference in seed yield. Genotypes SA-KSURed and YE35012 produced maximum and minimum seed yield at both locations, respectively. The eight genotypes SA-KSURed, EG-Giza 51, EG-Giza 9, SA-

Table 3: Means, maximum, minimum and the standard deviations for the quantitative traits of tested lentil genotypes grown at two locations

	Plant height (cm)		Biological yield (g)		Days to 50% flowering		Flowers/raceme		Days to maturity	
	National Center	Dirab Station	National Center	Dirab Station	National Center	Dirab Station	National Center	Dirab Station	National Center	Dirab Station
Min	21.23	23.45	5.43	4.98	56.33	58	1.59	1.60	116.67	118.33
Max	46.27	48.90	40.07	38.29	114	112	2.97	3.00	160.00	160.00
Mean	31.28	34.68	13.96	15.03	74.54	74.70	2.21	2.27	134.72	134.37
SD	7.60	7.64	8.05	8.63	15.64	15.35	0.37	0.37	11.39	12.13
	The best performed 25% of the genotypes									
	SA-3	SA-3	SA-1	EG-3	BD-3	BD-3	ILL-1	ILL-1	BD-3	YE-3
	EG-1	EG-3	EG-3	SA-1	YE-11	YE-11	SA-4	SA-3	BD-1	BD-3
	EG-2	EG-1	EG-2	SA-7	BD-2	BD-2	SA-3	SA-2	YE-12	BD-1
	SA-4	SA-4	SA-7	SA-5	YE-6	YE-6	SA-2	SA-4	BD-2	BD-2
	SA-2	SA-2	SA-5	EG-2	BD-1	YE-18	SA-7	YE-19	YE-6	YE-6
	EG-4	EG-2	YE-20	YE-20	YE-18	YE-13	YE-19	SA-7	YE-4	YE-4
	EG-2	EG-4	EG-4	EG-4	YE-13	YE-12	SA-1	ILL-2	YE-1	YE-12
	YE-19	KSU291	YE-18	YE-18	YE-3	YE-1	EG-3	SA-1	YE-16	YE-1
	YE-17	YE-19	ILL-2	YE-17	YE-4	BD-1	ILL-2	EG-3	YE-11	YE-11
					YE-16	YE-8				
	Height of lowest pod (cm)		Pods/Plant		Seeds/pod		100-seed weight (g)		Seed yield/Plant (g)	
	National Center	Dirab Station	National Center	Dirab Station	National Center	Dirab Station	National Center	Dirab Station	National Center	Dirab Station
Min	6.67	3.33	57.44	61.45	1	1.03	1.48	1.23	1.69	1.70
Max	21.39	22.22	267.28	303.43	1.9	1.93	5.08	4.61	14.03	12.95
Mean	11.29	9.79	123.16	143.13	1.62	1.62	2.59	2.47	4.68	4.96
SD	3.61	4.56	53.46	69.06	0.23	0.22	0.85	0.71	2.58	2.71
	The best performed 25% of the genotypes									
	SA-3	SA-3	EG-3	EG-3	YE-7	EG-1	SA-4	SA-3	SA-1	SA-1
	YE-19	YE-19	EG-2	EG-2	YE-14	YE-7	SA-2	SA-4	EG-2	SA-5
	SA-4	SA-2	SA-7	SA-5	EG-1	YE-8	SA-3	SA-2	EG-3	EG-3
	SA-2	SA-4	YE-20	YE-20	YE-8	EG-4	SA-1	SA-1	SA-5	EG-2
	EG-3	SA-7	SA-5	SA-7	YE-18	YE-14	ILL-1	ILL-1	YE-20	YE-20
	SA-7	EG-3	SA-6	EG-4	YE-5	YE-18	ILL-2	YE-19	SA-7	SA-7
	EG-2	EG-1	SA-1	SA-1	YE-20	YE-1	YE-19	YE-17	YE-18	EG-4
	SA-6	ILL-1	EG-4	SA-6	BD-3	SA-1	SA-5	ILL-2	EG-4	YE-17
	ILL-1	SA-6	YE-18	YE-18	EG-2	BD-3	YE-16	SA-5	ILL-2	YE-18

BD: Bangladesh, EG: Egypt, ILL: International Legume Lentil, KSU: King Saud University, SA-PGRB Saudi Plant Genetic Resources Bank, YE: Yemen

PGRB291, YESabri, SA-PGRB297, YEHaymi and EG-Sina1 recorded the highest seed yield at both locations and across locations.

Qualitative Traits

The different qualitative trait scores as for pigmentation of seedling stem, leaf pubescence, leaflet size, tendril length, lodging susceptibility, intensity of ramification and anthocyanin colouration are given in Table 4. Seedling stem pigmentation was present in 35 genotypes and absent in only one genotype (YEMatri). The leaf pubescence divided the genotypes to 21 out of 36 with six genotypes as dense pubescence and seventeen out of 20 (Yemeni genotypes) as slight leaf pubescence. Most of the Saudi genotypes (5 out of 7) were characterised by the absence of leaf pubescence (Table 4). Twenty-three genotypes showed small sized leaflets, of which 18 were Yemeni. Nine genotypes showed medium sized leaflets and four large sized leaflets. The genotypes from Egypt had medium leaflets; however, 3 out of 6 of the Saudi genotypes had large size leaflets (Table 4). Genotypes BD-Barimasur-3, BD-Barimasur-6 and EG-Giza 370, showed a rudimentary tendril, while 33 genotypes had prominent tendrils. Genotype susceptibility to lodging varied significantly. Twenty-one of them (18 from Yemen and three from Bangladesh) showed high resistance to lodging, while 12 genotypes showed intermediate. The intensity of ramification ranged from weak, in 15 genotypes, to medium in 12 genotypes, to strong ramification shown by 9 genotypes. Five out of six of the Saudi genotypes showed strong ramification, while the Yemeni genotypes were classified into the three categories mentioned, 10 weak, eight medium and two, with strong ramification. All Bangladeshi genotypes showed week ramification. Thirty genotypes showed absence of anthocyanin. However, six of the genotypes, YEHaymi, EG-Giza 370, EG-Giza 51, ILL11022, SA-KSUYellow3 and SA-KSUYellow1, showed anthocyanin colouration (Table 4).

Inflorescence and Fruit Traits

The colour of the flower ground, pod pigmentation, pod shedding, colour of the testa ground, pattern on the testa and colour of pattern on testa are listed in Table 5. The colour of the flower ground was white in eleven genotypes and white with blue veins in three genotypes. One genotype showed a violet colour (SA-PGRB297). Nineteen genotypes showed a white colour with violet veins. Two genotypes (YEDhamar-1 and SA-PGRB291) were violet with white veins. Most of the Yemeni genotypes (14) and all the Egyptian genotypes (4) were off white colour with violet veins of flowers. The Bangladeshi genotypes showed white flowers. Four

Table 4: Seedling stem pigmentation (SSP), leaf pubescence (LP), leaflet size (LS), tendril length (TL), lodging susceptibility (LOS), intensity of ramification (IOR) and anthocyanin coloration (AC) of tested lentil genotypes

Genotypes	SSP*[1]	LP*[2]	LS*[3]	TL*[4]	LOS*[5]	IOR*[6]	AC*[7]
BD-Barimasur-3	+	7	3	1	0	3	0
BD-Barimasur-7	+	3	3	2	0	3	0
BD-Barimasur-6	+	7	5	1	0	3	0
EG-Giza 370	+	7	5	1	5	3	+
EG-Giza 51	+	7	5	2	5	3	+
EG-Giza 9	+	3	5	2	7	7	0
EG-Sina 1	+	0	5	2	5	5	0
ILL11022	+	3	5	2	5	5	+
ILL11193	+	7	3	2	5	7	0
SA-KSURed	+	7	5	2	3	5	0
SA-KSUYellow1	+	0	7	2	7	7	+
SA-KSUYellow2	+	0	7	2	5	7	0
SA-KSUYellow3	+	0	7	2	7	7	+
SA-PGRB 291	+	3	3	2	5	7	0
SA-PGRB 295	+	0	3	2	3	5	0
SA-PGRB 297	+	0	5	2	5	7	0
YE35005	+	3	3	2	0	5	0
YE35006	+	3	3	2	0	3	0
YE35008	+	3	3	2	0	3	0
YE35012	+	3	3	2	0	5	0
YE35014	+	3	5	2	0	3	0
YE35016	+	3	3	2	0	5	0
YE35017	+	0	3	2	0	3	0
YE35018	+	0	3	2	0	5	0
YE35021	+	3	3	2	0	5	0
YE35034	+	3	3	2	0	3	0
YE35037	+	3	3	2	0	3	0
YE35038	+	3	3	2	0	3	0
YE35039	+	3	3	2	0	5	0
YE35040	+	3	3	2	0	5	0
YE35048	+	3	3	2	0	7	0
YEDhamar-2	+	3	3	2	0	3	0
YEDhamar-1	+	3	3	2	0	3	0
YEHaymi	+	3	3	2	0	3	+
YEMatri	0	3	7	2	7	5	0
YESabri	+	0	3	2	3	7	0

BD: Bangladesh, EG: Egypt, ILL: International Legume Lentil, KSU: King Saud =absent 0University, SA-PGRB Saudi Plant Genetic Resources Bank, *1: +=present, =dense *3: 3=small, 5=medium, 7=large *4: 1=rudimentary, 7=slight, 3=absent, 0*2: 2=prominent *5: 0=none, 3=low, 5=medium, 7=high *6: 3=Weak, 5=Medium, =absent07=Strong *7: +=present,

Table 5: Flower ground color (FGC), pod pigmentation (PDPI), pod shedding (PSh), ground color testa (GCT), pattern of testa (PT), color pattern on testa (CPT) and cotyledon color (CotCo) for tested lentil genotypes

Genotypes	FGC*[1]	PDPI*[2]	PSh*[3]	GCT*[4]	PT*[5]	CPT*[6]	CotCo*[7]
BD-Barimasur-3	1	0	0	3	1	4	2
BD-Barimasur-7	1	0	0	1	1	4	2
BD-Barimasur-6	1	0	0	1	1	4	2
EG-Giza 370	6	0	0	3	0	0	2
EG-Giza 51	6	0	0	3	0	0	2
EG-Giza 9	6	+	3	3	0	0	2
EG-Sina 1	6	0	0	3	0	0	2
ILL11022	1	0	7	5	0	0	2
ILL11193	2	0	0	3	1	4	2
SA-KSURed	1	0	3	3	0	0	2
SA-KSUYellow1	1	+	7	1	0	0	1
SA-KSUYellow2	6	+	3	1	0	0	1
SA-KSUYellow3	1	0	0	1	0	0	1
SA-PGRB 291	7	0	3	3	4	2	2
SA-PGRB 295	1	0	3	3	4	4	2
SA-PGRB 297	4	0	3	3	4	2	2
YE35005	6	0	3	3	4	4	2
YE35006	6	0	3	3	4	4	2
YE35008	6	0	5	3	4	4	2
YE35012	6	0	3	3	4	4	2
YE35014	6	0	0	3	4	4	2
YE35016	2	0	7	3	4	4	2
YE35017	6	0	5	3	4	4	2
YE35018	6	0	5	3	4	4	2
YE35021	1	0	5	3	4	4	2
YE35034	6	0	3	3	4	4	2
YE35037	6	0	5	3	4	4	2
YE35038	6	0	3	3	4	4	2
YE35039	6	0	3	3	4	4	2
YE35040	6	0	3	3	4	4	2
YE35048	1	+	3	3	4	4	2
YEDhamar-2	6	0	3	3	2	4	2
YEDhamar-1	7	0	0	3	4	4	2
YEHaymi	2	0	5	3	4	4	2
YEMatri	1	0	5	5	0	0	2
YESabri	6	0	5	3	4	4	2

BD: Bangladesh, EG: Egypt, ILL: International Legume Lentil, KSU: King Saud white =white, 2=University, SA-PGRB Saudi Plant Genetic Resources Bank. *1:1 + violet, 6=white with violet veins, 7=violet. White veins *2:=with blue veins, 4 = absent *3: 0=none, 3=low, 5=medium, 7=high *4:1=green, 3=brown, 0present, = 5=pink *5: 0= absent, 1=dotted, 2= spotted, 4= complex *6: 0= absent 2= grey 4= black *7: 1= yellow, 2= orange/red

genotypes, namely, YE35048, SA-KSUYellow1, SA-KSUYellow2 and EG-Giza 9, showed that there were distinct pigments on the pod coat, while there was no pigment in the other genotypes (Table 5).

Genotypes from Bangladesh and Egypt were characterised by the non-pod-shedding trait, while three genotypes ILL11022, YE35016 and SA-KSUYellow1 showed high pod-shedding. The rest of the genotypes were medium level pod-shedding (Table 5). Most of the genotypes (29) showed brown ground testa, five genotypes green and two genotypes (YEMatri and ILL11022) pink colour. The pattern of the testa was complex in 21 genotypes and spotted in one genotype (YEDhamar-2). The Bangladeshi genotypes, along with one ICARDA genotypes (ILL11193) showed dotted testa. Ten genotypes showed clear testa without any pattern and were all the SA-KSU and Egyptian genotypes, in addition to one Yemeni (YEMatri) and one ICARDA ILL11022. All genotypes showed patterns on the testa (26 genotypes); twenty-four genotypes showed a black coloured pattern while, two genotypes (SA-PGRB297 and SA-PGRB291) showed a grey coloured pattern on the testa. While genotypes SA-KSUYellow1, SA-KSUYellow2 and SA-KSUYellow3, showed yellow cotyledons, all other genotypes showed orange/red cotyledons (Table 5).

Principal Component for Quantitative Traits

Principal component analysis showed that at National Center station, the first four PCs explained most of the total variance, which was 84.77% with individual values (47.43, 20.91, 9.31 and 7.12% for PC1, 2, 3, and 4, respectively) (Table 6). Traits such as DF and the seed yield plant^{-1} (0.37

Table 6: Eigenvalue, percent of variance, cumulative variance and loading of the traits of the first four principal components (PCs) of tested lentil genotypes grown at at two locations

	PC 1		PC 2		PC 3		PC 4	
	NC	DE	NC	DE	NC	DE	NC	DE
Eigenvalue	9.36	8.51	4.13	4.62	1.84	1.51	1.41	1.4
Variance (%)	47.43	44.47	20.91	24.15	9.31	7.89	7.12	7.31
Cumulative variance	47.43	44.47	68.33	68.62	77.64	76.51	84.77	83.83
DF	0.38	0.40	-0.19	-0.06	0.10	0.26	0.38	-0.21
NF	0.25	0.32	-0.16	-0.15	0.75	0.28	0.08	0.6
DM	0.36	0.45	-0.21	-0.14	-0.47	0.14	0.05	-0.39
PH	0.37	0.4	-0.17	-0.11	-0.36	-0.17	-0.18	0.32
HLP	0.33	0.45	-0.30	-0.11	-0.06	0.16	0.37	-0.23
PD/P	0.37	0.22	0.31	0.38	0.01	-0.33	-0.20	-0.04
S/PD	0.11	0.01	0.73	0.72	-0.10	0.61	0.60	0.16
BY	0.34	0.22	0.28	0.32	0.07	-0.34	-0.28	-0.14
SY/P	0.37	0.20	0.21	0.4	0.16	-0.33	-0.41	-0.02
100-SW	0.12	0.19	-0.17	-0.03	0.17	-0.27	0.18	0.49

PH: plant height, BY: Biological yield, DF: No. of days to flowering, NF: No. of flower/raceme, DM: No. of days to maturity HLP: Height of lowest pod, PD/P No. of pods/plant, S/PD: Seeds/pod, SY/P: Seed yield /plant, 100-SW: Hundred seeds weight

in PC1 and 0.21 in PC2) contributed the most of total variation. The scatter biplot of the first two PCs distributed the 36 genotypes across four quarters. The first PC grouped 53% of the genotypes and separated the genotypes that were introduced from ICARDA and Egypt, along with Saudi genotypes, except SA-KSUYellow2 from other genotypes from Yemen and Bangladesh. The PD/P, BY and SY/P were the main traits that were aggregated in genotypes YE35037, YE35012, YE35016, YEDhamar-2, YE35006, YE35021, YE35039, YE35008, SA-KSUYellow2 and YE35018. However, in the second quarter of the positive PC1, PH, DF and the number of days to maturity, were the main traits that were aggregated in genotypes BD-Barimasur-7, BD-Barimasur-6, YE35014, BD-Barimasur-3, YE35038, YE35005, YE35034, YE35048 and YE35017. The second PC grouped 47% of the genotypes and separated Saudi from Bangladeshi genotypes, while the two ICARDA genotypes were separated from each other. The number of seeds pod^{-1} was the main trait that was aggregated in genotypes SA-KSUYellow3, ILL11022, SA-KSUYellow1, YEMatri, EG-Giza 9, SA-PGRB295, EG-Giza 370 and SA-KSURed.

The hierarchical cluster gathered the 36 genotypes at a distance value of 5.9 (Fig. 1a). The first cluster grouped 33% of the genotypes and this cluster was further sub-divided into three sub-clusters and one of the ICARDA genotypes (ILL11193) was individually separated. The first sub-cluster contained all the Egyptian genotypes. The second sub-cluster contained three Saudi genotypes: SA-PGRB291, SA-PGRB297 and SA-KSURed and the third sub-cluster contained four of the Yemeni genotypes. The second cluster included 50% of the genotypes and was further subdivided into three sub-clusters. Two sub-clusters were dominated by Yemeni genotypes, and one sub-cluster was mixed with Bangladeshi genotypes. The third cluster was classified into two sub-clusters. The Saudi genotypes: SA-KSUYellow1, SA-KSUYellow2 and SA-KSUYellow3, were gathered in the first sub-cluster. However, the second sub-cluster contained genotypes ILL11022 and YEMatri.

At Dirab station, the first four PCs explained most of the total variance, which was 83.83%. Number of days to maturity, height of lowest pod, DF, and PH, were the most relevant contributors in the case of PC1, which explained 44.47% of the total variance. In PC2, the most relevant contributors which explained 24.15% of the total variance were S/PD, yield of seed plant^{-1}, PD/P and BY.

The third principal component explained 7.89% of the total variance and the traits; S/PD, number of flowers per raceme and DF showed the highest contribution in the PC3. The loading of the traits showed that the maximum values were recorded for the number of days to maturity, height of lowest pod (0.45), DF and PH (0.40) in PC1. However, in PC2, the traits that recorded maximum values were S/PD (0.72), seed yield plant^{-1} (0.40) and PD/P (0.38). In PC3, the maximum values were recorded for S/PD (0.61), number of flowers per raceme (0.28) and DF (0.26). In PC4, maximum value was recorded for the number of flowers per raceme (0.60), 100-seed weight (0.49) and PH (0.32). DF, number of flowers per raceme, PH and S/PD contributed at least in two of the first four PCs.

The scatter biplot of the first two PCs distributed the 36 genotypes across four quarters. In the first PC, most of the Yemeni genotypes (16 out of 20) and all Bangladeshi genotypes were separated from Saudi, Egyptian and ICARDA genotypes. All traits were directed toward positive ordination of the PC1. On this ordination, the YE35012, YE35014, YE35037, BD- Barimasur-3, BD-Barimasur-7 and BD- Barimasur-6 were the most diverse genotypes, which were further separated in PC2, in which Bangladeshi genotypes were separated from Yemeni genotypes. It was also noted that PC2 separated the two genotypes introduced from ICARDA. The BY, PD/P and seed yield plant^{-1} were the main traits that were aggregated in genotypes YE35012, YE35014, YE35037, YE35008, YE35016, YE35039, YE35006, YE35021 and YE35017, in the positive part of the first PC1and PC2. However, in the second quarter, the number of days to maturity and height of the lowest pod were the main traits that were aggregated in genotypes BD-Barimasur-3, BD-Barimasur-7, BD-Barimasur-6, YE35005, YE35034, YEDhamar-2, YE35048, YE35038 and YEHaymi. In PC2, S/PD was the main trait that was aggregated in genotypes SA-KSUYellow2, SA-KSUYellow1, ILL11022, SA-KSUYellow3, and YEMatri.

The hierarchical cluster clustered the thirty-six genotypes were gathered in four main clusters (Fig. 1b). Fifty percent of all genotypes were grouped in the first cluster, with most of the Yemeni (15 out of 20) and Bangladeshi genotypes were gathered in this cluster, which was further subdivided into three sub-clusters. Two genotypes (BD-Barimasur-6, YE35018) failed to be grouped together and they were individually separated. The

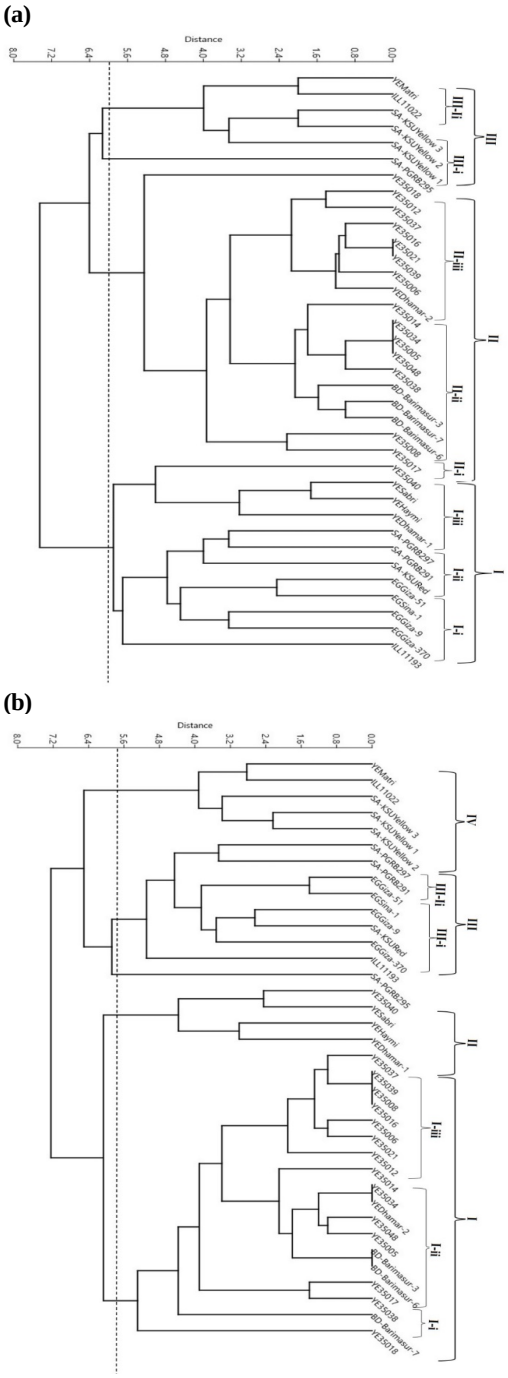

Fig. 1: UPGMA clustering of 36 genotypes of lentil growing at (**a**) National Center and (**b**) Dirab station according to Euclidean estimated from agronomic traits

first sub-cluster included two genotypes from Yemen (YE35017 and YE35038). Seven genotypes were grouped in the second sub-cluster and the third sub-cluster grouped seven Yemeni genotypes with most diverse genotype YE35012. The second cluster included four genotypes. Nine genotypes were grouped in the third cluster and this cluster was further subdivided into two sub-clusters and two

Table 7: Eigenvalue, percent of variance and Cumulative variance of the first 3 principal components (PCs) of fourteen traits in tested lentil genotypes at two locations

Traits	PC 1	PC 2	PC 3
Eigen value	9.95	5.06	2.72
Variance (%)	47.85	24.32	13.07
Cumulative variance	47.85	72.17	85.24
SSP	0.017	0.003	0.005
FGC	0.440	0.878	-0.002
LS	-0.377	0.177	-0.034
TL	0.012	0.018	0.088
LP	0.001	-0.052	-0.235
PDPI	-0.040	0.021	0.068
PSh	0.004	-0.078	0.239
IOR	-0.244	0.066	0.826
AC	-0.060	0.010	-0.046
LOS	-0.299	0.187	0.147
PT	0.514	-0.133	0.406
CPT	0.490	-0.362	0.049
Cot.Co	0.049	-0.019	-0.039
GCT	0.050	0.018	0.011

SSP: Seedling stem pigmentation, FGC: Flower ground color, LS: Leaflet size, TL: Tendril length, LP: Leaf pubescence, PDPI: Pod pigmentation, PSh: Pod shedding, IOR: Intensity of ramification, AC: Anthocyanin coloration, LOS: Lodging susceptibility, PT: Pattern testa, CPT: Color of pattern on testa, Cot.Co: Cotyledon color, GCT: Ground color testa

genotypes (SA-KSA295 and ILL11193) were individually separated. Egyptian genotypes and genotype SA-KSURed formed the first sub-cluster. The second sub-cluster contained two Saudi genotypes (SA-PGRB291 and SA-PGRB297). The fourth cluster contained five genotypes.

Principal Component for Qualitative Traits

Principal component analysis of the first three PCs explained most of the total variance, which was 85.24% with contribution of 47.85%, 24.32% and 13.07% for PC1, PC2 and PC3, respectively (Table 7). The PC1 includes pattern on testa, colour of pattern on testa and flower ground colour, with loading of 0.51, 0.49 and 0.44 respectively. In PC2, the flower ground colour, lodging susceptibility and leaflet size were the main contributors. In PC3, intensity of ramification, pattern on testa, pod-shedding, and lodging susceptibility showed the highest contribution with loading of 0.83, 0.41, 0.24 and 0.15, respectively. The pattern on testa and the flower ground colour were the only two traits that contributed at least in two of the three PCs.

The scatter biplot of the first two PCs distributed the 36 genotypes in four quarters. The colour of flower ground was the main trait that was aggregated in most of the Yemeni genotypes (15 out of 20 genotypes). However, the pattern on testa and the colour pattern of testa were the main traits that were aggregated in the genotypes SA-PGRB295, YE35021, YE35016 and YEHaymi, in the second quarter of PC1. In PC2, flower ground colour, leaflet size and lodging of susceptibility were the main traits aggregated in Egyptian genotypes (EG-Giza 370, EG-Giza 51 EG-Sina1 and EG-Giza 9) and in Saudi genotype SA-KSUYellow2.

The hierarchical cluster of thirty-six genotypes was classified into four main clusters (Fig. 2). The first main

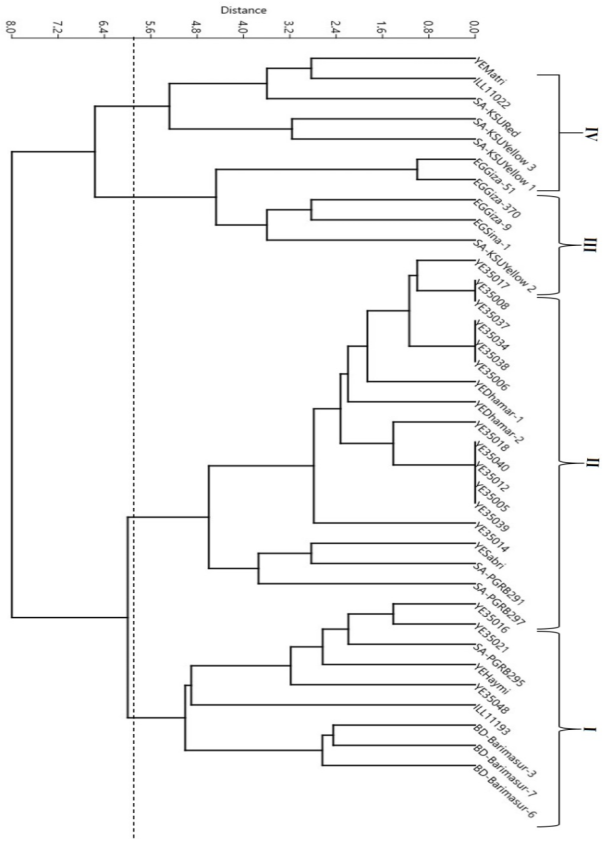

Fig. 2: UPGMA clustering of 36 genotypes of lentil according to Euclidean estimated from fourteen morphological traits

cluster (cluster I) included 25% of the genotypes, with an average of 4.13. This cluster was further subdivided into two sub-groups, in which the first group included genotypes BD-Barimasur-3, BD-Barimasur-7 and BD-Barimasur-6. The second group contained genotypes YE35048, YEHaymi, SA-PGRB295 YE35021, YE35016 and ILL11193. In this cluster, the most distant genotypes were BD- Barimasur-6 and YE35048.

Cluster II, which included 47% of all genotypes, was sub-divided into two sub-clusters. The first sub cluster contained genotypes SA-PGRB291, SA-PGRB297 and YESabri. The remaining genotypes, (YE35005, YE35008, YE35012, YE35014, YE35017, YE35018, YE35034, YE35037, YE35038, YE35039, YE35040, YE35006, YEDhamar-1 and YEDhamar-2), formed the second sub-cluster. The most distant genotypes were SA-PGRB297 from the first sub-cluster and the Genotypes YEDhamar-1 from e second sub-cluster. Notably, most of the Yemeni genotypes were included in this cluster and that the lowest distance value recorded in this cluster was zero. Cluster III, contained all Egyptian genotypes in addition to one genotype from Saudi Arabia (SA-KSUYellow2). Genotypes Giza 370 and SA-KSUYellow2 were the most distant ones in this cluster. In cluster IV, three out of five genotypes were from Saudi Arabia and one genotype from both Yemen and ICARDA. The most distant genotypes in this cluster were SA-KSUYellow3 and ILL11022 (Fig. 2).

Discussion

The analysis of genetic variability at the agro-morphological level is considered the main activity in breeding programs for sustainable utilization of lentil crop. Morphological diversity has been used to characterise the germplasm in a range of plant species, including lentil. It allows assessment of genetic diversity among and within genotypes, populations, accessions and breeding lines. The analysis of variance showed that there were highly significant differences among lentil genotypes at both locations, indicating a high degree of genetic variation and had great potential of the genotypes in future breeding programs through selection. Plant height of lentil genotypes used in this study showed a wide variation, which exceeded that of many previous studies (Alghamdi *et al*., 2013; Dugassa *et al*., 2014; Paliya *et al*., 2015). Biological yield range (5.43–40 g plant^{-1}) in this study was higher than values recorded in previous studies (Cristobal *et al*., 2014; Paliya *et al*., 2015). A considerable genetic variability if existed had a greatly significant role in the breeding program as well as in the improvement of these traits through selection (Bhartiya *et al*., 2015). The improvement in biomass at the vegetative growth stage prior to flowering, leads to further increase in N-assimilation and thereby in seed yield (Whitehead *et al*., 2000).

A wide variation among genotypes was recorded for days to flowering and maturity as the time of flowering is considered as an effective mechanism for escaping drought; and early flowering and seed set before the onset of terminal drought is an important trait in grain legumes (Thomson *et al*., 1997). Developing early maturing cultivars is one of the breeding approaches most commonly used for drought escape in crops in general and in lentil, in particular. Although water scarcity affects productivity of legumes at any growth stage, its occurrence during the reproductive and grain filling stages (terminal drought) is more critical and usually results in a significant loss of grain yield (Farooq *et al*., 2009). Hence, terminal drought has strong negative effects on the capacity to produce a large number of flowers and thus, to set seeds, thereby substantially reducing the grain yield (Pushpavalli *et al*., 2014).

Genotypes varied in the number of flowers per raceme, which is coincide with results of Ruisi *et al*. (2015), who recorded an average of 2.3 for flowers per raceme. Flower production is highly affected by environmental conditions, especially drought and heat stress. Water stress reduced flower production by about two-thirds in chickpea genotypes and seed yields reduced by 58–95%, compared to irrigated plants, indicating that both, flower and pod abortion are important in determining seed yield (Fang *et al*., 2010). The date of flower initiation significantly affected flower and pod development, with late-initiated flowers and pods being largely

aborted. The results of present study are supported by the Fang *et al*. (2010), whose finding indicated that the duration from the time of the first flower and the development of water deficit played an important role in determining the number of flowers and pods that produced seed.

The importance of the number of pods per plant and seeds per pod in determining grain yield was reported and was higher in microsperma than macrosperma (Bacchi *et al*., 2010). In this study, the pods per plant averaged 123.16 and 143.13 at National Center and Dirab stations, respectively. In many studies, a wide variation was found for the number of pods per plant and had positive association with grain yield (Gupta *et al*., 2012; Ahamed *et al*., 2014; Babayeva *et al*., 2014). A consistent regional difference among the lentil landraces of Ethiopia regarding number of pods per plant and seeds per pods have been reported by Bacchi *et al*. (2010) and Mekonnen *et al*. (2014). An average of 2.59 g and 2.47 g was registered for 100-seed weight, coupled with a wide variation, at both National Center and Dirab stations. This trait is highly influenced by the environment and regional differences, because the trait is highly affected by abiotic stress, especially drought (Kumar and Solanki, 2014).

In this study, seed yield per plant registered higher values and showed a wide variation (from 1.7 to 14.03 g plant^{-1}) and a highly genotypic variability among tested genotypes. However, Hussain *et al*. (2014) reported seed yield variation (13.80 to 27.95 g plant^{-1}) among 14 candidate lentil lines and two high yielding check varieties. Low yield variability was observed among 25 lentil accessions over three years, showing high adaptability of the tested germplasm to a semi-arid environment and differences between macro and microsperma groups were not found, nor did yield level appear to be influenced by geographic origin (Bacchi *et al*., 2010). Tullu *et al*. (2001) reported that large-seed types contributed 7% of the seed yield, compared to the small-seed and red-cotyledon lentils, indicated that there was a considerable genetic variation in the phenological and morphological traits that can be used to breed higher biomass and seed-yielding cultivars.

Improvement of a target character can be achieved by indirect selection via other characters that are more heritable and easier to select. This strategy of selection requires understanding the interrelationships among the characters and with the target character (Dugassa *et al*., 2014). A high and significant correlation between seed yield and most of the agro-morphological traits was recorded at both locations in this study. The study of correlation between yield and its components, the traits (biological yield, number of pods per plant and number of days to maturity) were found to be major contributing traits to yield and can be given due emphasis during the development of the improved genotypes of lentil for rainfed conditions (Bhartiya *et al*., 2015). Depar *et al*. (2016) concluded that the increase in seed yield per ha was mainly associated with the increase in the percentage of the seed germination, pods per plant and seed index, while prolonged flowering and maturity of the lentil crop had an adverse effect on yield. Number of seeds per plant followed by the number of pods per plant had the highest positive direct effect on seed per plant yield and selection for these traits may be useful in improving the seed yield of lentil (Abo-Hegozy *et al*., 2012).

Slight leaf pubescence with small-sized leaflet and prominent tendril was found in most of genotypes studied and showed high resistance to lodging. Pigmentation of seedling stems was present in 35 genotypes and was absent in only one of them. These results were fully consistent with those of Toklu *et al*. (2009), who reported that a collection of Turkish lentil landraces had a seedling-stem pigmentation with a low degree of pod-shedding and pod dehiscence. Moreover, Dixit *et al*. (2011) reported that stem pigmentation was present in most varieties. Our results were consistent with those of Toklu *et al*. (2009), who reported that almost all landraces had a prominent tendril. It has also been reported that pubescent leaves, white flowers with blue veins, as well as taller plants and large seeds characterise the Mediterranean collections (Lázaro *et al*., 2001). Only four genotypes showed distinct pigments on the pod coat, while the pigment was absent from other genotypes. Only three genotypes showed the high pod-shedding trait. Most of the genotypes (29) showed a brown ground testa and 21 of them had a complex test pattern. Twenty-four genotypes showed a pattern of black colour on testa. A wide range of flower colour variation was recorded, which ranged from white to violet (Roy *et al*., 2013). Toklu *et al*. (2009) reported two groups of the flower colour; white flowers with blue veins, and violet flowers. The result of this study is consistent with that of Dixit *et al*. (2011), who recorded 4 out of 29 varieties showed pigments on the pod coat and the colour of ground testa was brown in all varieties. The dominant colour of cotyledons in all evaluated genotypes in this study was red/orange, except in three Saudi genotypes, which bore yellow cotyledons. Genetic diversity of cotyledon colour in 13 of the Turkish lentil cultivars was assessed (Erdoğan, 2015), significant differences in the colour parameters of cotyledons were observed.

Principal component analysis (PCA) of the quantitative traits showed that the yield and its components contributed positively to the first principal components, mainly PC1 and PC2. The PC1 was positively correlated with biological yield, weight of pods/plant, number of the pods/plant, number of seeds/plant and seed weight/plant. In Spain, the morpho-agronomical characters of 27 lentil landraces showed that the first five components of PCA explained 83.7% of the cumulative variance and seed production contributed the most to the first factor (Cristobal *et al*., 2014). Yield and yield components accounted for 73.13% of the total variance in the first three components of PCA (Toklu *et al*., 2009). The seed yield, number of pods per plant, height of the lowest pod, days to flowering, number of secondary branches and number of seeds per pod are main traits in genotypes, because they represent most of

the variability (~82%) in each principle component (Al-Ghzawi *et al*., 2011). Bhartiya *et al*. (2015) reported that the first four principal components (PCs) expressed 83.50% of total variation. Harvest index, number of pods per plant, days to maturity, yield of seed per plant and days to 50% flowering were highly significant and positively correlated with PC1, which accounted for 34.73% of the total variation. Moreover, PCA showed maximum contribution from pods per plant, days to 50% flowering, plant height and days to maturity to total diversity among the lentil accessions studied (Kumar and Solanki, 2014).

The scatter plot of the first two PCs distributed the 36 genotypes according to their geographical origin and their qualitative traits. These results were also supported by the hierarchical cluster analysis based on the agronomic and qualitative traits under the conditions at the National Center and Dirab stations. The first two PCs, contributed with 61.87% of the total variation, formed two distinct groups that distinguished the lentil genotypes possessing a high (>5 g plant^{-1}) or a low (<5 g plant^{-1}) biological yield per plant (Bhartiya *et al*., 2015). In a study, Bacchi *et al*. (2010) reported that lentil populations from Algeria, Cyprus, Egypt, Morocco, Tunisia, Pakistan and Ethiopia, were separated according to the type of seeds rather than to climatic zones.

Conclusion

In thirty-six germplasm accessions of lentil of diverse origin, a wide range of diversity was registered for agro-morphological characters of both qualitative and quantitative traits and these can be used in selection breeding for development of lentil cultivars. The information obtained at seed and plant levels may be useful for discrimination and verification of varieties and maintenance of genetic purity during seed production and certification programs. Several potential genotypes were identified, which can be used in genetic analysis and lentil improvement programmes.

References

Abo-Hegozy, S., T. Selim and E. El-Enam, 2012. Correlation and path coefficient analysis of yield and some yield components in lentil. *Egypt. J. Plant Breed*., 16: 147–159

Ahamed, K., B. Akhter, M. Islam, M. Humaun and M Alam, 2014. Morphological characterization and genetic diversity in lentil (*Lens culinaris* medikus sspp. *culinaris*) germplasm. *Intl. J. Agric. Res. Innov. Technol*., 4: 70–76

Al-Ghzawi, A.L.A., E. Bsoul, Z. Al-Ajlouni, M. Al-Azzam and M.M. Ajlouni, 2011. Genetic variation for quantitative traits in Jordanian lentil landraces. *Adv. Environ. Biol.,* 5: 3676–3681

Alghamdi, S.S., A.M. Khan, M.H. Ammar, E.H. El-Harty, H.M. Migdadi, S.M.A. El-Khalik, A.M. Al-Shameri, M.M. Javed and S.A. Al-Faifi, 2013. Phenological, nutritional and molecular diversity assessment among 35 introduced lentil (*Lens culinaris* Medik.) genotypes grown in Saudi Arabia. *Intl. J. Mol. Sci*., 15: 277–295

Aslam, M., M.A. Maqbool, Q.U. Zaman, M. Shahid, M.A. Akhtar, A.S. Rana, 2017. Comparison of different tolerance indices and PCA biplot analysis for assessment of salinity tolerance in lentil (*Lens culinaris*) genotypes. *Intl. J. Agric. Biol.,* 19: 470–478

Babayeva, S., Z. Akparov, A. Damania, V. Izzatullayeva, G. Aslanova and M. Abbasov, 2014. Genetic diversity for drought tolerance in lentils from Central Asia and the Caucasus: CACLentil. *Alban. J. Agric. Sci.,* 13: 1–8

Bacchi, M., M. Leone, F. Mercati, G. Preiti, F. Sunseri and M. Monti, 2010. Agronomic evaluation and genetic characterization of different accessions in lentil (*Lens culinaris* Medik.). *Ital. J. Agron*., 5: 303–314

Bhartiya, A., J. Aditya and S. Singh, 2015. Assessment of variability for agro-morphological traits in elite lentil (*Lens culinaris*) lines using multivariate analysis. *Ind. J. Agric. Res*., 49: 539–543

Brummer, Y., M. Kaviani and S.M. Tosh, 2015. Structural and functional characteristics of dietary fibre in beans, lentils, peas and chickpeas. *Food Res. Intl*., 67: 117–125

Chakraborty, M. and M.F. Haque, 2000. Genetic variability and component analysis in lentil (*Lens culinaris* Medik). *J. Res. Birsa Agric. Univ*., 12: 199–204

Cristobal, M.D., V. Pando and B. Herrero, 2014. Morphological characterization of lentil (*Lens culinaris* medik.) landraces from Castilla Y Leon, Spain. *Pak. J. Bot*., 46: 1373–1380

Depar, M.S., N.A. Soomro, A.S. Chandio, H.A. Samoon, B.L. Meghwar, A.K. Pathan and M.W. Kalroo, 2016. Evaluation of morpho-yield traits and their correlation with seed yield in lentil (*Lens culinaris*) genotypes. *Sci. Intl*., 28: 2675–2678

Dixit, G., P. Katiyar and B. Singh, 2011. Characterization of lentil (*Lens culinaris* Medik.) varieties based on morphological traits. *J. Food Legume*, 24: 194–197

Dugassa, A., H. Legesse and N. Geleta, 2014. Genetic variability, yield and yield Associations of lentil (*Lens culinaris* Medic.) genotypes grown at Gitilo Najo, Western Ethiopia. *Sci. Technol. Arts Res. J.*, 3: 10–18

Duke, J., 2012. *Handbook of Legumes of World Economic Importance*. Springer Science & Business Media, Berlin, Germany

Erdoğan, C., 2015. Genetic characterization and cotyledon color in lentil. *Chil. J. Agric. Res*., 75: 383–389

Erskine, W., 1997. Lessons for breeders from land races of lentil. *Euphytica*, 93: 107–112

Fang, X., N.C. Turner, G. Yan, F. Li, K.H.M. Siddique, 2010. Flower numbers, pod production, pollen viability and pistil function are reduced and flower and pod abortion increased in chickpea (*Cicer arietinum* L.) under terminal drought. *J. Exp. Bot*., 61: 335–345

FAOSTAT, 2014. Available online: http://faostat3.fao.org/download/Q/QC/E [accessed on 12 November 2016]

Farooq, M., A. Wahid, N. Kobayashi, D. Fujita and S.M.A. Basra, 2009. Plant drought stress: effects, mechanisms and management. *Agron. Sustain. Dev.,* 29: 185–212

Gupta, M., B. Verma, N. Kumar, R.K. Chahota, R. Rathour, S.K. Sharma, S. Bhatia and T.R. Sharma, 2012. Construction of intersubspecific molecular genetic map of lentil based on ISSR, RAPD and SSR markers. *J. Genet*., 91: 279–287

Hammer, O., D.A.T. Harper and P.D. Ryan, 2001. PAST: Paleontological statistics software package for education and data analysis. *Palaeontol. Electr.,* 4: 1–9

Hussain, N., M. Yaqoob and A. Rashid, 2014. Genetic competition among lentil (*Lens culinaris*) candidate lines for yield and yield components under rainfed conditions. *J. Agric. Res*., 52: 53–66

Kumar, J. and R. Solanki, 2014. Evaluation of lentil germplasm for agro-morphological traits. *J. Food Legume,* 27: 302–306

Ladizinsky, G. and F. Muehlbauer, 1993. Wild lentils. *Crit. Rev. Plant Sci*., 12: 169–184

Lázaro, A., M. Ruiz, L.D.L. Rosa and I. Martín, 2001. Relationships between agro/morphological characters and climatic parameters in Spanish landraces of lentil (*Lens culinaris* Medik.). *Genet. Resour. Crop Evol*., 48: 239–249

Mekonnen, F., F. Mekbib, S. Kumar, S. Ahmed and T.R. Sharma, 2014. Agromorphological traits variability of the ethiopian lentil and exotic genotypes. *Adv. Agric*., 2014: 1–15

Oss, H.V., Y. Aron and G. Ladizinsky, 1997. Chloroplast DNA variation and evolution in the genus *Lens* Mill. *Theor. Appl. Genet*., 94: 452–457

Paliya, S., A. Saxena, A. Tikle, M. Singh and A. Tilwari, 2015. Genetic divergence and character association of seed yield and component traits of lentil (*Lens culinaris* M.). *Adv. Biores*., 6: 53–59

Pushpavalli, R., M. Zaman-Allah, N.C. Turner, R. Baddam, M.V. Rao and V. Vadez, 2014. Higher flower and seed number leads to higher yield under water stress conditions imposed during reproduction in chickpea. *Funct. Plant Biol*., 42: 162–174

Roy, F., J. Boye and B. Simpson, 2010. Bioactive proteins and peptides in pulse crops: pea, chickpea and lentil. *Food Res. Intl*., 43: 422**–**432

Roy, S., M. Islam, A. Sarker, M. Ismail, M. Rafii, M. Mondal and M. Malek, 2013. Morphological characterization of lentil accessions: Qualitative characters. *Bangl. J. Bot*., 41: 187–190

Ruisi, P., M. Longo, F. Martinelli, G.D. Miceli, A. Frenda, S. Saia, F. Carimi, D. Giambalvo and G. Amato, 2015. Morpho-agronomic and genetic diversity among twelve sicilian agro-ecotypes of lentil (*Lens culinaris*). *J. Anim. Plant Sci*., 25: 716–728

Sarker, A. and W. Erskine, 2001. Utilization of genetic resources in lentil improvement. *In: Proceedings of the Genetic Resources of Field Crops: Genetic Resources Symposium*, pp: 16–20. Eucarpia, Poznam, Poland

Sharma, S.K., I.K. Dawson and R. Waugh, 1995. Relationships among cultivated and wild lentils revealed by RAPD analysis. *Theor. Appl. Genet*., 91: 647–654

Thomson, B., K.H.M. Siddique, M. Barr and J. Wilson, 1997. Grain legume species in low rainfall Mediterranean-type environments I. Phenology and seed yield. *Field Crops Res*., 54: 173–187

Toklu, F., B. Biçer and T. Karaköy, 2009. Agro-morphological characterization of the Turkish lentil landraces. *Afr. J. Biotechnol*., 8: 4121–4127

Tullu, A., I. Kusmenoglu, K.E. McPhee and F.J. Muehlbauer, 2001. Characterization of core collection of lentil germplasm for phenology, morphology, seed and straw yields. *Genet. Resour. Crop Evol*., 48: 143–152

Urbano, G., J.M. Porres, J. Frıas and C. Vidal-Valverde, 2007. Nutritional value. *In*: *Lentil: An Ancient Crop for Modern Times*, pp: 47–93. Yadav, S.S., D. McNeil and P.C. Stevenson (Eds.). Berlin: Springer

Whitehead, S., R. Summerfield, F. Muehlbauer, C. Coyne, R. Ellis and T. Wheeler, 2000. Crop improvement and the accumulation and partitioning of biomass and nitrogen in lentil. *Crop Sci*., 40: 110–120

Zohary, D., 1972. The wild progenitor and the place of origin of the cultivated lentil: *Lens culinaris*. *Econ. Bot*., 26: 326–332

Zohary, D. and M. Hopf, 2000. *Domestication of plants in the Old World. The origin and spread in West Asia, Europe and the Nile Valley*. Oxford University Press, Oxford, UK

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