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Determination of genetic diversity in lentil germplasm based on quantitative traits

S. Roy[1], M.A. Islam[2], A. Sarker[3], M.A. Malek[*1, 4], M.Y. Rafii[4] and M.R. Ismail[4]

[1]Plant Breeding Division, Bangladesh Institute of Nuclear Agriculture, Mymensingh-2202, Bangladesh
[2]Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh-2202, Bangladesh
[3]International Center for Agricultural Research in the Dry Areas (ICARDA), New Delhi, India
[4]Institute of Tropical Agriculture, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia

***Corresponding author: mamalekbina@yahoo.com**

Abstract

Genetic diversity present in a gene pool is an important determination for breeding programs and characterization is useful of building crop plant collections primarily based on the knowledge of the presence of valuable genes and traits. In Bangladesh, one of the most common problems in lentil is the narrow genetic base, which must be broadened to enhance production. So, a detailed morphological study based on quantitative traits was under taken to assess the genetic diversity in 110 lentil germplasm, including landraces, popular varieties, phenologically adapted exotic lines and selected advanced lines of lentil of diverse origin. The main aim was to identify superior genotypes to be used for future breeding program in Bangladesh. The experiments were carried out during 2006-07 and 2007-08 and eight quantitative characters were studied under international standard of characterization. The UPGMA dendrogram segregated lentil accessions into six clusters. Genotypes fell in different clusters irrespective of their origin and accessions. The accession from ICARDA gene bank showed high diversity. Group B3, B4 and F were important as they comprised accessions with higher yield per plant, higher number of pods per plant and higher number of seeds per pod separated by higher inter cluster distance, which warrant their use in the breeding program.

Keywords: Lentil accessions; quantitative characters; genetic diversity; UPGMA dendrogram; varietal improvement.
Abbreviations: ICARDA- International Center for Agricultural Research in the Dry Areas; UPGMA- Unweighted pair group method of arithmetic means; BARI-Bangladesh Agricultural Research Institute.

Introduction

Lentil has been domesticated in West Asia then introduced into the Indo-Gengetic plain around 2000 BC (Cubero, 1981). It is a major source of protein (28%) for human consumption and its straw is a valued animal feed consisted of minerals (2%) and carbohydrates (59%) (Frederick et al., 2006). The worldwide lentil production in 2007 was 3.78 million ton (Mt) from an area of 3.78 million hectares with an average productivity 1000 kg/ha of which 60% produced in South Asia (FAOSTAT, 2008). Lentil producing countries of South Asia are Bangladesh, Burma, India, Nepal and Pakistan. The other major lentil producing regions are West Asia-North African region. Lentil is one of the important pulses in Bangladesh. It ranks second in area (77, 330 ha) and production (71,000 tons) (BBS, 2009) but first in consumers preference and a daily dietary constituent of the people in Bangladesh. It is traditionally grown during the dry winter months (rabi season) on residual soil moisture under rain fed conditions. It faces serious competition with wheat, boro rice, oil seeds, potatoes and other profitable winter crops, particularly where irrigation is available. As a result, the crop has been pushed to marginal and sub-marginal lands and area under lentil has been declined from 1254760 ha in 1997-98 to 432250 ha in 2007-08 (BBS, 2010).

Main concern with lentil is low yield potential because of narrow genetic base of the local cultivars. Therefore, the key to increase lentil yield in South Asia including Bangladesh is through widening the available genetic base (Erskine and Saxena, 1993). Indian lentils are exclusively of pilose type and show limited variations. This narrow genetic variability among indigenous germplasm has restricted breeding progress. Lentil is a short, slender, self-pollinated annual diploid (2n = 2x = 14) which exhibits a wide range of morphological variations. Considerable variations among the characters for use in breeding and selection programmes have been reported for various morphological characters (Sindhu and Mishra, 1982; Ramgiry et al., 1989; Sarker and Erskine, 2001). The knowledge of genetic variation and relationships between populations is important to understand the available genetic variability and its potential use in breeding programs. Genetic variation between and within populations of crop species is a major interest of plant breeders and geneticists (Hayward & Breese, 1993). The breeders must have the idea of choosing the accession that most likely possess the trait of interest. Quantitative traits provide an estimate of genetic diversity. Various numerical taxonomic techniques have been successfully used to classify and measure the pattern of phenotypic diversity in the relationship of germplasm collections in a variety of crops by many scientists in lentil (Fratini et al., 2007 and Tullu et al., 2008), pea (Amurrio et al., 1995) and alfalfa (Smith et al., 1995). Rubeena et al. (2006) identified markers closely linked to the major QTLs that may be useful for future marker-assisted selection for crop improvements. Many workers emphasized the importance of genetic divergence in selection of parents for hybridization. The more diverse the parents, within the reasonable range the more would be the chance of improving

Table 1. Mean squares for yield, yield components and other characters at four different environments

Source of variation	df	First flower (days)	Maturity (days)	Plant height (cm)	Branches/ plant (no.)	Pods/plant (no.)	Seeds/ pod (no.)	100-seed weight (g)	Seed yield/plant (g)
Environment-1 Ishurdi, 2006-07									
Replication	2	2.22	1.64	24.36	0.114	279.33	0.0099	0.104	0.014
Genotype	109	318.9**	173.00**	17.53**	0.674**	3097.99**	0.071**	1.31**	2.00**
Error	191	2.338	1.4799	8.132	0.2106	494.89	0.010	0.051	0.381
Environment-2 Magura, 2006-07									
Replication	2	11.73	26.748**	5.388	0.296	260.25	0.010	0.516	0.215
Genotype	109	310.33**	211.39**	22.88**	0.503**	421.82**	0.049**	1.176**	0.482**
Error	191	1.81	2.75	6.87	0.282	100.297	0.009	0.077	0.074
Environment-3 Ishurdi, 2007-08									
Replication	2	11.9	1.78	87.48**	10.61**	697	0.13**	0.27	0.351
Genotype	109	453.9**	352.9**	26.81**	2.90**	1742**	0.040**	1.60**	0.95**
Error	191	2.13	3.06	11.19	0.56	452	0.01	0.05	0.338
Environment-4 Magura, 2007-08									
Replication	2	5.73	5.664	80.40	5.885	271	0.09	0.30	0.24
Genotype	109	294.78**	181.48**	28.39	0.991	912**	0.04**	1.09**	0.95**
Error	191	3.52	2.123	34.28	0.904	332	0.03	0.07	0.34

** indicates significant at 1% level of probability.

the characters of question. Barulina (1930) first recorded detailed morphological descriptions of lentil landraces and species from Asia. The main characters in her study to define subspecies were pods, seeds and distinct differences in the length of flowers and secondary characters included size of leaflets, length of vegetation and height of plants. Erskine and Witcombe (1984) classified the world collection of lentil germplasm on the basis of morphological variations as days to flowering, days to maturity, plant height, seed yield, biomass yield, straw yield and 100-seed weight. Tullu et al. (2001) suggested that there was considerable genetic variation for phenological and morphological traits in the core collection of lentil that can be used to breed higher biomass and seed yielding cultivars.

The traditional approach of characterization and evaluation involves cultivation of accession sub samples and their morphological and agronomical description; a procedure facilitated by the use of internationally recognized descriptor lists (Erskine and Williams, 1980). Morphological characterization is the first step in the classification and description of any crop germplasm (Smith and Smith, 1989). One of the approaches for gene pool assembly is to collect material from diverse geographical origins with a concentration of accessions from proposed centres of diversity in individual samples (Laghetti et al., 1998). Germplasm collection of crop plants is an excellent source of economically useful plant characters. However, in many crops the number of available accessions greatly surpasses the time a breeder can devote to a screening operation. The breeders must have a means of choosing the accessions that most likely possess the traits of interest. Targeted and more efficient utilization of germplasm by plant breeders can be achieved if the trait characteristics of accessions are known. Therefore, present study was undertaken to access and evaluate the genetic diversity in lentil germplasm collected from diverse origin on the basis of quantitative traits and to identify superior genotypes for future use.

Result and Discussion

Germplasm characterization and evaluation

Significant differences were found among 110 lentil accessions for all eight characters for days to first flowering, days to maturity, plant height, number of branches, number of pods per plant, number of seeds per pod, 100-seed weight and seed yield per plant except plant height and number of branches per plant in environment 4 for individual and combined data (Table 1 and 2). The incidence of highly significant variation among the accessions for the majority of the studied morphological traits is a sign of the presence of high degree of genetic variation implying great potential of the accessions in future breeding programs through selection. Grand mean, range and standard error of 110 accessions are presented in Table 3. Days to first flowering of accessions showed a range 37.3 to 83.0 days, grand mean was 59.6 and standard error was ± 1.5. The accession BLx98006-3 was the earliest for first flowering and maturity. Days to maturity displayed a range of 98 to 135 days. This material could be used to develop early maturing variety, which is the prime need for lentil improvement programme in Bangladesh. Values of plant height varied from 34 to 44 cm, grand mean was 39 cm and standard error was ± 3.8. Number of branches per plant ranged 1.7 to 3.9, grand mean was 2.6 and standard error was ± 0.69. Grand mean for number of pods per plant was 69, mean values of number of pods per plant varied from 33 to 114 and standard error was ± 18.5. Seeds per pod ranged 1.20 to 1.70 and 100-seed weight was 1.30 to 5.50 g. Lentil pod containing one to two seeds per pod was common. These results further indicated the existence of variability among the accessions for these traits. Seed yield was dependent on number of seeds per pod in lentil mutant (Sinha and Chowdhury, 1991; Rajput and Sarwar, 1989). Dewan (2005) also found significant variation in number of seeds per pod in lentil. Rahman and Ali (2004) found wide range of variability in existing lentil cultivars in 100-seed weight which was in supportive of this present study.

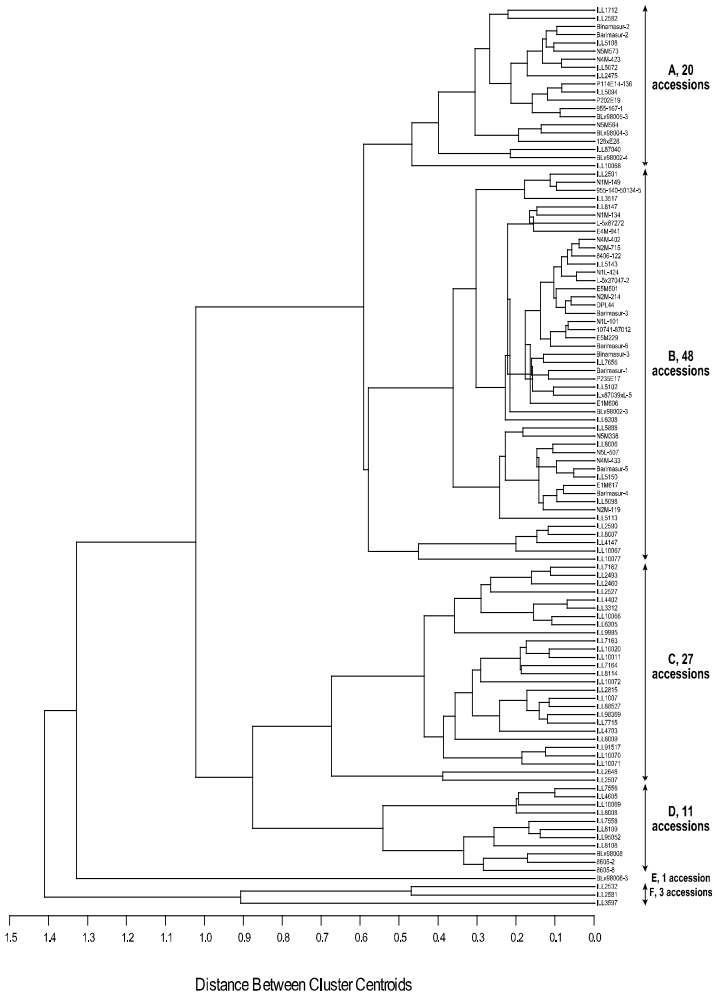

Fig 1. UPGMA dendrogram showing the genetic relationships among 110 accessions of lentil.

Mondal et al. (2007) reported that seed yield in lentil depends on seed size. Seed yield per plant varied from 1.30 to 3.11 g.

Yield performance of the accessions in four individual environments revealed that accession ILL7656 performed consistently better in three environments and ILL4605, ILL5150, ILL8006, 40-50134-5, ILL2581 performed better at least two environments (Table 4). From combined performance of genotypes over two years at two locations, top yielding 20 accessions were identified (Table 5). Accession ILL5150 produced the highest seed yield of 3.11 g per plant. Accessions ILL2532, ILL4605, ILL2581, ILL8006, Barimasur-4, ILL7656, DPL-44 and 40-50134-5 produced good seed yield of 2.83, 2.97, 2.80, 2.68, 2.79, 2.98, 2.62, and 2.72 g, respectively. Malik et al. (1984) found sufficient genetic variability in lentil germplasm in traits like days to flowering, days to maturity, plant height, pods per plant and seed yield per plant. Among the accessions, the top yielding early maturing two accessions, ILL5150 and ILL7656 ranked the first and second position due to their higher number of pods per plant and higher number of seeds per pod. Other good performing accessions were ILL4605, ILL2532 and ILL2581. These precious accessions could be used in lentil improvement programme of Bangladesh.

There is a scope for selection of desirable genotypes, where variability exists. Genetic variability of germplasm resources is necessary to sustain long-term genetic improvement of cultivars. The assessment of genetic variation and the behaviour of different genotypes in the germplasm with specific phenological responses provide the basis for adaptation to the climatic variables of the prevailing environment. The result of morphological evaluation of the characters showed significant genetic variation of different yield and yield contributing characters in the accessions indicating the scope and their warranty to use in the breeding programmes (Tullu et al., 2001).

Genetic diversity and relatedness

The genetic distance analysis using unweighted pair group method of arithmetic means (UPGMA) dendrogram was constructed for measuring genetic diversity and relatedness among the accessions (Fig. 1). Cluster analysis indicated the extent of genetic diversity that is of practical use in plant breeding (Sultana et al., 2006). Lentil accessions used in this study were grouped into six clusters (A, B, C, D, E and F) (Table 6) showing existence of considerable genetic diversity among 110 lentil accessions. The highest genetic distance was found between two accessions, ILL1712 and ILL3597, where they held the first and last position of the dendrogram. The former one originated from Ethiopia and the latter from India. On the other hand, the lowest genetic distance was found between the lentil accessions ILL1712 and ILL2582 in the same group. These two accessions were also originated from Ethiopia and India, respectively.

Cluster B was the largest of all clusters containing 48 accessions. The second largest cluster was C which included 27 accessions, cluster A had 20 accessions and cluster D comprised of 11 accessions. Cluster E was formed with one accession and F included three. Cluster A could be subdivided into five sub clusters. Sub cluster A1 comprised of only two accessions, ILL1712 and ILL2582. These two accessions originated from Ethiopia and India. Binamasur-2, Barimasur-2, ILL5108, N5M-573, N4M-423, ILL5072, ILL2475, P114E14-136, ILL5094, P202xE19 and BLx98005-3 were in sub cluster A2. Most of these accessions were developed at BINA and BARI, Bangladesh. Accessions N5M-564, BLx98004-3 and 128xE28 included in sub cluster A3. These accessions were also developed at BARI. Accessions ILL87040 and BLx98002-4 were developed in Bangladesh formed the sub cluster A4. Only one accession, ILL10068 from ICARDA formed the sub cluster A5 with bold seed. Majority of cluster A represented by 20 accessions were developed in Bangladesh. So, the inclusion of the accessions in same cluster is very justified. The cluster B could be subdivided into five sub clusters. Accessions ILL2501, N1M-149, 955-140-50134-5 and ILL3517 formed the sub cluster B1. These accessions were developed in Bangladesh and India. Accessions ILL8147, N1M-134, L5x87272 and E4M-941 were included in sub cluster B2. Most of the accessions of this sub cluster were developed in Bangladesh. Accessions E4M-402, N2M-715, 8406-122, ILL 5143, N1I-424, L5x37047-2, E5M-501, N2M-214, DPL-44, Barimasur-3, N1I-101, 107-41-87012, E5M 229, Barimasur-6, Binamasur-3 and ILL7656, Barimasur-1, P235E17, ILL 5102, ILx87039xL-5, E1M-606, BLx98002 and ILL6308 comprised the sub cluster B3. Most of the accessions of this sub cluster were from Bangladesh, India and Pakistan. Accessions ILL5888, N5M-338, ILL8006, N5I-507, N4M-433, Barimasur-5, ILL5150, E1M-617, Barimasur-4, ILL5098 and N2M-119 were included in sub cluster B4. They were developed at BARI and BINA. Most of the accessions of B3 and B4 clusters showed a high yield

Table 2. Mean squares for yield and yield components over two locations (Ishurdi and Magura) from 2006-07 to 2007-08.

Source of variation	df	First flowering (days)	Maturity (days)	Plant height (cm)	Branches/ plant (no.)	Pods/ plant (no.)	Seeds/ pod (no)	100-seed wt. (g)	Seed yield (g)
Environment	3	21412**	12776**	4083**	24.7**	162742**	0.65**	0.70**	94.9**
Genotype	109	1211**	776**	36**	2.23**	2475**	0.12**	4.69**	1.42**
Genotype× environment	327	55.6**	47.4**	20**	0.94**	1239**	0.03**	0.16**	0.98**
Pooled error	758	2.45	2.35	15	0.49	344	0.01	0.06	0.28

** indicates significant at 1% level of probability.

Table 3. Mean, range and standard error of 110 lentil accessions.

Items	First flowering (days)	Maturity (days)	Plant height (cm)	Branches/ plant	Pods/ plant (no.)	Seeds/ pod (no.)	100-seed wt. (g)	Seed yield/ plant (g)
Mean	59.7	114.3	39	2.6	69	1.62	2.00	2.13
Range	37-83	98-135	34-44	1.7-3.9	33-114	1.20-1.70	1.30-5.50	1.30-3.11
Standard error(±)	1.56	1.53	3.88	0.69	18.5	0.12	0.248	0.53

Table 4. Top yielding 20 lentil accessions identified in four individual environments.

Environment-1		Environment-2		Environment-3		Environment-4	
Accessions	Seed yield/ plant (g)	Accessions	Seed yield/ plant(g)	Accessions	Seed yield/ plant (g)	Accessions	Seed yield/plant (g)
ILL5150	6.09	ILL4605	3.02	Barimasur-5	3.48	ILL4605	3.68
ILL2581	5.18	ILL7164	2.85	ILL7656	3.35	ILL7558	3.53
ILL2532	5.08	ILL7656	2.46	N2M-119	3.29	ILL8109	3.35
ILL8605-2	4.45	ILL1712	2.44	40-50134-5	3.23	N1M-149	3.16
ILL7656	4.26	ILL2648	2.40	ILL4147	3.22	DPL-44	2.88
Binamasur-2	4.19	ILL3597	2.37	ILL5113	3.21	P235E17	2.84
P202E19	4.16	ILL6305	2.36	N4M-433	3.19	N1I-424	2.90
40-50134-5	4.12	ILL10072	2.33	Barimasur-4	3.17	ILL8605-8	2.76
ILLx5102	4.00	ILLx87040	2.31	P235E17	3.07	ILL95052	2.72
N1M-134	3.97	ILL8006	2.27	ILL8008	2.99	ILL2527	2.67
ILL5888	3.91	ILL8108	2.27	L-5x37047	2.95	N5I-507	2.66
N4M-402	3.82	Barimasur-1	2.29	BLx98002-3	2.90	128xE28	2.62
ILL8006	3.70	Barimasur-4	2.29	DPL-44	2.89	ILL8114	2.60
BLx8005-3	3.65	N2M-214	2.26	N2M-715	2.88	ILL8605-2	2.58
8406-122	3.62	ILL5150	2.20	E1M-606	2.79	ILL10067	2.57
ILL8007	3.58	ILL1007	2.12	ILL2507	2.77	Barimasur-3	2.55
N5M-564	3.57	BLx98008	2.10	x87039xL-5	2.75	ILL3517	2.54
ILL1007	3.56	Binamasur-3	2.09	ILL 2581	2.72	ILL8114	2.60
ILL5108	3.54	ILL2582	2.04	ILL7556	2.64	N1I-101	2.47
ILL10072	3.52	ILL8605-2	2.06	ILL 8006	2.56	ILL5113	2.39
Average of 110 lentil accessions	2.88		1.63		2.10		1.90

performance. Again, accessions ILL2590, ILL8007, ILL4147, ILL10067 and ILL10077 formed the sub cluster B5 which were from Bangladesh, ICARDA, India and Pakistan. Accessions ILL7162, ILL2493, ILL2460, ILL2527, ILL4402, ILL3312, ILL10066, ILL6305 and ILL9995 formed the sub cluster C1. Most of the accessions of this sub cluster were originated from India, ICARDA and Pakistan. The sub cluster C2 comprised of accessions ILL7163, ILL10020, ILL10011, ILL7164, ILL8114 and ILL10072. They originated from Pakistan and ICARDA. Accessions ILL2815, ILL1007, ILL88527, ILL98369, ILL7715, ILL4703, ILL8009 were in sub cluster C3. The sub cluster C3 contained accessions originated from India, Pakistan, Nepal and ICARDA. The sub cluster C4 included the accessions ILL91517, ILL10070, ILL10071, ILL2698 and ILL2507. They originated from India, ICARDA, and Pakistan. Accessions ILL7556, ILL4605, ILL10069 and ILL8008 consisted of the sub cluster D1. They originated from India, ICARDA and Argentina. ILL7558, ILL8109, 95052, ILL8108, BLx98008, ILL8605-2 and ILL8605-8 accessions formed the sub cluster D2 and originated from Argentina. Furthermore, the accessions of cluster D were with yellow cotyledon, larger seed size and were grouped as macrosprma type. Therefore, the inclusion of the accessions in same cluster is very much justified. Only one accession, BLx98006-3 formed the cluster E which was developed in Bangladesh, a cross material of BARI which was extra early type with bold seed. Cluster F included the three accessions viz., ILL2532, ILL2581 and ILL3597. They originated from India with high pod and seed yield. It is explicit that there is no relationship between geographic distribution and genetic diversity of lentil in this study.

No definite correspondence between geographic origin and genetic diversity of lentil has been observed in other crops like field pea (Gemechu et al., 2005) and safflower (Khan et

Table 5. Performance of 20 top yielding lentil accessions identified in combined environments.

Accessions	First flower (days)	Maturity (days)	Plant height (cm)	Branches/ plant (no.)	Pods/ plant (no.)	Seeds/ pod (no.)	100-seed wt. (g)	Seed yield/ plant (g)
ILL5150	50	108	38	2.3	87	1.73	1.72	3.11
ILL7656	52	110	38	2.5	81	1.70	1.97	2.98
ILL4605	60	115	39	2.0	52	1.46	3.95	2.97
ILL2532	62	115	38	3.1	114	1.68	1.85	2.83
ILL2581	58	113	38	2.4	101	1.69	1.70	2.80
Barimasur-4	54	109	37	2.8	86	1.62	2.24	2.79
40-50134-5	55	113	40	2.8	74	1.70	2.25	2.72
ILL8605-2	55	111	37	1.9	45	1.53	3.52	2.62
DPL-44	53	109	38	2.9	76	1.60	1.98	2.62
ILL5113	58	108	34	3.0	85	1.69	1.47	2.55
Barimasur-5	50	109	38	2.6	87	1.68	2.06	2.58
P235E17	49	106	37	2.6	84	1.70	2.13	2.55
BLx98002-3	46	106	37	2.6	77	1.70	2.19	2.49
ILLx5102	48	106	41	2.5	79	1.58	1.83	2.43
N1M-134	49	107	37	2.6	72	1.70	1.64	2.43
ILL3597	79	131	41	3.4	106	1.61	1.43	2.41
Barimasur-3	53	107	39	2.3	76	1.70	2.16	2.41
N5M-338	51	105	37	2.7	91	1.72	1.70	2.41
N5I-507	54	109	39	2.6	88	1.70	1.64	2.39
ILL5888	53	108	38	2.4	93	1.69	1.62	2.39
Average of 110 accessions	60	114	39	2.6	69	1.62	2.00	2.13

Table 6. Brief description of A, B, C etc.

Groups	No. of accessions	Accessions
A	20	A1=ILL1712, ILL2582 A2= Binamasur-2, Barimasur-2, ILL5108, N5M-573, N4M-423, ILL5072, ILL2475, P114E14-136, ILL 5094, P202xE19, 955-167-1, BLx98005-3 A3=N5M-564, BLx98004-3 A4=128xE28, ILL87040, BLx98002-4, ILL10068
B	48	B1=ILL2501, N1M-149, 955-140-50134-5, ILL3517 B2=ILL8147, N1M-134, L5x87272, E4M-941 B3=E4M-402, N2M-715, 8406-122, ILL5143, N1I-424, L5x37047-2, E5M-501, N2M-214, DPL-44, Barimasur-3, N1I-101, 107-41-87012, E5M 229, Barimasur-6, Binamasur-3, ILL7656, Barimasur-1, P235E17, ILL5102, ILx87039xL-5, E1M-606, BLx98002-3, ILL6308 B4=ILL5888, N5M-338, ILL8006, N5I-507, N4M-433, Barimasur-5, ILL5150, E1M-617, Barimasur-4, ILL5098, N2M-119, B5=ILL5113, ILL2590, ILL 8007, ILL4147, ILL10067, ILL10077
C	27	C1=ILL7162, ILL2493, ILL2460, ILL2527, ILL4402, ILL3312, ILL10066, ILL6305, ILL9995 C2= ILL7163, ILL10020, ILL10011, ILL7164, ILL8114, ILL10072 C3=ILL2815, ILL1007, ILL88527, ILL98369, ILL7715, ILL4703, ILL8009 C4=ILL91517, ILL10070, ILL10071, ILL2698, ILL2507
D	11	D1=ILL7556, ILL4605, ILL10069, ILL8008 D2=ILL7558, ILL8109, 95052, ILL8108, BLx98008, ILL8605-2, ILL8605-8
E	1	BLx98006-3
F	3	ILL2532, ILL2581, ILL3597

al., 2008) suggesting that parental selection should be made on the basis of systematic assessment of genetic distance in a specific population rather than on geographic difference. Crop improvement is made through generating variability in desired traits followed by selection. Continued success in crop improvement can only be realized when new substantial variability is found and used in a population. Divergence between any two parents expresses the allelic differences between them (Dias et al., 2003). The genotypes grouped into the same cluster presumably diverge very little from one another. Crossing of genotypes belonging to the same cluster is not expected to yield desirable segregants. Consequently, a crossing program should be conducted with putative parents belonging to different characters. Therefore, crosses between the members of clusters separated by inter-cluster distances are likely seemed to be beneficial for further improvement. Significant differences among the accessions for different characters indicated variations among the accessions favorable for their use in the breeding programs. Crosses between parents with maximum divergence would be more responsive to improvement since they are likely to produce higher heterosis and desirable genetic recombination.

Table 7. Source and country of origin of 110 lentil accessions with main characteristic(s).

Accessions	Source of collection	Origin	Main characteristic(s)
ILL4605 and ILL8108	ICARDA, Syria	Argentina	Yellow cotyledon and large seed
ILL5888, ILL8006, ILL8007, ILL8147, 955-167-1, 8406-122, BLx98005-3, x87039xL-5 and 40-50134-5	ICARDA, Syria	Bangladesh	Red cotyledon
ILL1712 and ILL2501	ICARDA, Syria	Ethiopia	Red and yellow cotyledon
ILL8605-8, ILL8605-2, ILL9995, ILL10011, ILL10020, ILL10066, ILL10067, ILL10068, ILL10069, ILL10070, ILL10071, ILL10072, ILL10073 and ILL10077	ICARDA, Syria	ICARDA	Red and yellow cotyledon
ILL2532, ILL2581, ILL2582, ILL2590, ILL2648, ILL2815, ILL3312, ILL3517, ILL3597, ILL4147 ILL5094, ILL7556, ILL7558, ILL7715, ILL8008 and ILL8109	ICARDA, Syria	India	Red and yellow cotyledon
ILL 8009	ICARDA, Syria	Nepal	Red cotyledon
ILL4402, ILL7162, ILL7163, ILL7164, ILL8114, ILL88527, ILL91517 and ILL98369	ICARDA, Syria	Pakistan	Red cotyledon
Binamasur-2, Binamasur-3, N1I-101, N1I- 424, N1M-134, N1M-149, N2M-119, N2M-214, N2M -715, N4M-402, N4M-423, N4M-433, N5I-507, N5M-338, N5M-564, E1M-606, E1M-617, E4M-941, E5M-229, E5M-501 and N5M-573	BINA, Bangladesh	Bangladesh	Red cotyledon and white flower
Barimasur-1, Barimasur-3, Barimasur-5, Barimasur-6, BLx98002-3, BLx98002-4, BLx98004-3, BLx98006-3, BLx98008, ILLx87040, L-5x37047, L-5x87272 and 10741-87012	BARI, Bangladesh	Bangladesh	Red cotyledon
ILL4703, ILL5072, ILL5098, ILL5102, ILL5108, ILL5143, ILL6305 and ILL7656	BARI, Bangladesh	ICARDA	Red cotyledon
ILL2460, ILL2475, ILL2493, ILL2507, ILL2527, ILL5113, ILL5150, DPL-44, 128xE28, P202E19 and P235E17	BARI, Bangladesh	India	Red cotyledon
Barimasur-2 and Barimasur-4	BARI, Bangladesh	Nepal	Red cotyledon
ILL6308 and ILL95052	BARI, Bangladesh	Pakistan	Red cotyledon
P114E14-136	BARI, Bangladesh	USA	Red cotyledon

Note: Bangladesh accessions were developed either by mutation or by hybridization at BINA or BARI

Table 8. Recording of data on different quantitative characters (ICARDA and IBPGR, 1985).

Characters	Data recorded
Days to 1st flower	Time in days from sowing to when at least one plant flowered in each plot.
Days to maturity	It was recorded from sowing to when 90% pods turned into were golden brown.
Plant height (cm)	It was measured from the ground to the tip of the extended foliage in late pod-filling stage.
Primary branches/plant	Number of branches in main stem
Pods/plant	Total number of pods in a plant
Seeds/pod	Number of seeds counted from 100 dry pods and then averaged
100-seed weight (g)	Average weight of two samples of 100 randomly chosen seeds
Yield/plant (g)	Weight of total seeds of 10 randomly chosen plants and averaged.

Note: The characters were recorded from ten randomly selected plants for each accession and the values were averaged.

Materials and methods

Plant materials

The present study was comprised of 110 landraces, popular varieties, phenologically adapted exotic lines and selected advanced lines of lentil of diverse origin (Table 7). The fifty one accessions were selected from the collection of ICARDA germplasm bank and the others were provided by Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh, Bangladesh and BARI, Gazipur, Bangladesh included released popular cultivars and selected advanced lines.

Experimental site and design, cultural management and data recording

The experiments were conducted at the farms of BINA sub-stations at Ishurdi and Magura, representative lentil growing areas of Bangladesh in two consecutive years 2006-07 and 2007-08, which is situated between 24.01º N latitude and 89.55º E longitude. Urea, muriate of potash and triple super phosphate were applied during land preparation at 32, 77 and 32 kg ha^{-1}, respectively. The experiments were carried out following an *Alpha lattice* design with three replicates. Unit plot size was 2 m × 0.6 m. Row to row and plant to plant distances were 30 and 6-8 cm, respectively. Seeds were sown on 9 November 2006 and 12 November 2007 at Ishurdi and on 10 November 2006 and 13 November 2007 at Magura for two consecutive years 2006-07 and 2007-08, respectively. Intercultural operations were done when necessary for proper growth and development of the plants. Data were recorded in two consecutive years following Bioversity International and ICARDA guidelines on days to first flower, days to maturity, plant height, number of branches and pods per plant, seeds per pod, 100-seed weight and seed yield per plant (Table 8).

Statistical Analysis

All analyses were done using SAS software (SAS, 2003). The analysis of variance for all eight quantitative characters

was done using data for individual and based on combined data (two locations and two years). Diversity analysis was done for UPGMA for combined data.

Conclusion

Genotypes divided into different clusters irrespective of their origin. Accessions from ICARDA gene bank showed high genetic diversity. Group B3, B4 and F were important because they comprised of accessions with high yield per plant, high pods per plant and high number of seeds per pod separated by high inter cluster distance. This implies a great potential for breeding programmes through hybridization or direct used as variety for successful lentil production in Bangladesh.

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References

Amurrio JM, De Ron AM, Zeven AC (1995) Numerical taxonomy of Iberian pea landraces based on quantitative and qualitative characters. Euphytica 82: 195-205

Barulina H (1930) Lentils of USSR and other countries. Bulletin of Applied Botany, Genetics and Plant Breeding, Leningrad Supplement 40: 265-304 (Russian, English summary)

BBS (2009) Statistical Year Book of Bangladesh. Bangladesh Bureau of Statistics, Statistics Division, Ministry Planning, Government of the People's Republic of Bangladesh p. 126

BBS (2010) Statistical Year Book of Bangladesh. Bangladesh Bureau of Statistics, Statistics Division, Ministry Planning, Government of the People's Republic of Bangladesh p. 126

Cubero JI (1981) Origin, taxonomy and domestication. pp. 15-38. *In*: C. Webb and G. Hawtin (eds.), Commonwealth Agricultural Bureau, Slough, United Kingdom

Dewan MA (2005) Characterization of lentil mutants in respect of their morphological and yield attributes. MS thesis, submitted to Dept. Crop Botany, Bangladesh Agricultural University, Mymensingh, Bangladesh

Dias LAS, Marita J, Cruz CD, Barros EG, Salomão TMA (2003) Genetic distance and its association with heterosis in cacao. Braz Arch Biol Technol 46: 339-347

Erskine W, Williams JT (1980) The principles, problems and responsibilities of the preliminary evaluation of genetic resources samples of seed-propagated crops. FAO/1BPGR Plant Genet Resour News l 41: 19-32

Erskine W, Witcombe JR (1984) Lentil Germplasm Catalog. ICARDA, Aleppo, Syria

Erskine W, Saxena, M.C. (1993) Breeding lentil at ICARDA for southern latitudes. In: Lentils in South Asia. Eds. Erskine W, Saxena MC Roush S. International Center for Agricultural Research in the Dry Areas(ICARDA), Aleppo, Syria

FAOSTAT database (2008) http://faostat.fao.org/

Frederick M, Cho S, Sarker A, McPhee K, Coyne C, Rajesh P, Ford P (2006) Application of biotechnology in breeding lentil for resistance to biotic and abiotic stress. Euphytica 147: 149-165

Fratini R, Durán Y, García P, Pérez de la Vega M (2007) Identification of quantitative trait loci (QTL) for plant structure, growth habit and yield in lentil. Spanish J Agric Res 5(3): 348-356

Gemechu K, Mussa J, Tezera W, Getinet D (2005) Extent and pattern of genetic diversity for morpho-agronomic traits in Ethiopian highland pulse landraces. 1. Field pea (*Pisum sativum L*.). Genet Resour Crop Evol 52: 801-808

Hayward MD, Breese EL (1993) Population structure and variability. *In*: Hayward MD, Bosemark NO, Romayosa I (Eds), Plant Breeding: Principles and Prospects, Chapman and Hall, London. pp: 7-29

IBPGR, ICARDA (1985) International Board for plant Genetic Resources and International Center for Agricultural Research in Dry Areas. Lentil Descriptors

Khan MA, Witzke-Ehbrecht SV, Maass BL, Becker HC (2009) Relationships among different geographical groups, agro-morphology, fatty acid composition and RAPD marker diversity in Safflower (*Carthamus tinctorius*). Genet Resour Crop Evol 56: 19-30

Laghetti G, Pienaar BL, Pasdulosi S, Perrino P (1998) Ecogeographical distribution of *Vigna savi* in southern Africa and some areas of the Mediterranean basin. Plant Genet Resour Newsl 115: 6-12

Malik BA, Tahir M, Haqani AN, Anwar R (1984) Documentation, characterization and preliminary evaluation of lentil (*Lens culinaris*) germplasm in Pakistan. Lens Newsl 11(20): 8-11

Mondal MMA, Howlader MHK, Akter MB, Dutta RK (2007) Evaluation of five advanced lentil mutants in relation to morphophysiological characters and yield. Bangladesh J Crop Sci 18(2): 367-372

Rahman MA, Ali MO (2004) The causes of decreases in pulse production and its remeady. Krishi Biplob (A fortnightly magazine in Bengali). Published on 15 Nov. 2004. Published by M.N. Nabi, 279, East Hazipara, Rampura, Dhaka-1219, Bangladesh. p. 5

Rajput MA, Sarwar G (1989) Genetic variability, correlation studies and their implication in selection of high yielding lentil mutants. Lens Newsl 16: 5-8

Ramgiry SR, Paliwal KK, Tomar SK (1989) Variability and correlation of grain yield and other qualitative characters in lentil. Lens Newsl 16: 19-21

Rubeena PW, Taylor J, Ades PK, Ford R (2006) QTL mapping of resistance in lentil (*Lens culinaris* ssp. *culinaris*) to ascochyta blight (*Ascochyta lentis*). Plant Breeding 125(5): 506- 512

Sarker A, Erskine W (2001) Utilization of genetic Resources in lentil improvement. p. 42 *In*: Proceedings of the Genetic Resources of Field Crops: Genetic Resources Symposium, EUCARPIA, Poznam, Poland

SAS (2003) SAS User's Guide. Statistics. SAS Inst., Cary, NC

Sindhu JS, Mishra HO (1982) Genetic variability in Indian microsperma type lentil. Lens Newsl 9: 10-11

Sinha RP, Choudhury SK (1991) Induced co-dominent mutation for dwarfness in lentil. Indian J Genet Plant Breed 51: 370-372

Smith JSC, Smith OS (1989) The description and assessment of distances between inbred lines of maize: The utility of morphological, biochemical and genetic descriptors and a scheme for the testing of distinctiveness between inbred lines. Maydica 34: 151-161

Smith SE, Guarino L, Doss AA, Conta DM (1995) Morphological and agronomic affinities among Middle Eastern alfalfas accessions from Oman and Yemen. Crop Sci 35: 1118-1194

Sultana T, Ghafoor A, Ashraf M (2006) Geographic pattern of diversity of cultivated lentil germplasm collected from Pakistanas assessed by protein assays. Acta Biologica Cracoviensia, Series Botanica, Poland. 48: 77-84

Tullu A, Kusmenoglu I, McPhee KE, Muehlbauer FJ (2001) Characterization of core collection of lentil germplasm for phenology, morphology, seed and straw yields. Genet Res Crop Evol 48: 143-152

Tullu A, Tar'an B, Warkentin T and Vandenberg A (2008) Construction of an intraspecific linkage map and QTL analysis for earliness and plant Height in lentil. Crop Sci. 48(6): 2254-2264