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Genetic variability and diversity for various agro morphological traits in lentil (*Lens culinaris* M.)

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Abstract
The present study was undertaken at DARS, Budgam to study the variability and diversity in exotic accessions of lentil. A set of 45 genotypes of Lentil comprising 44 accessions from ICARDA BIGM nursery and a local variety Shalimar Masur 1 as check were evaluated for various agro-morphological and quality traits. Significant variability was found for all the traits under study. Large differences between phenotypic and genotypic variances were found for these two traits, which means environment has a role in these traits. Plant height was correlated with days to maturity and flowering, which means late flowering due to temperate conditions, can affect plant height. Primary branches per plant, pods per plant and seeds per pod were positively and significantly correlated with seed yield per plant. The said set of 45 genotypes was divided into 7 clusters, the check was found in cluster IV. Considerable inter and intra cluster distances were found. In cluster VI two genotypes were placed which were bold seeded but exhibited higher yield than the check. The above set was also morphologically characterized for stem, flower and seed traits as per PPV&FR guidelines. Considerable variability was found for seed characters also.

Keywords: diversity, genotype, lentil, protein content, variability, yield

Introduction
Pulses are a type of leguminous crop that are harvested solely for the dry seed. Dried beans, lentils and peas are the most commonly known and consumed types of pulses. pulses are not merely a source of food. They have nutritional importance. They are an alternate to meat, they are one of best green manure crops, they can be used for green fodder, animal cake, catch cropping, oils and can be cultivated on low fertility soils. The lentil or daal or Masoor dal (*Lens culinaris* Medik) is a bushy annual plant of the legume family, grown for its lens-shaped seeds. It is about 15 inches tall and the seeds grow in pods, usually with two seeds in each. The plant originated in the Near East and has been part of the human diet since the aceramic (non-pottery producing) Neolithic times, being one of the first crops domesticated in the Near East. It is one of the oldest and an important seed legume crop, cultivated worldwide as human food in the fertile crescent 7000-9000 years ago (Zohary and Hopf,2000) [12]. Production of this cool season annual crop spread from the Near East to the Mediterranean area, Asia, Europe and finally the Western Hemisphere (Oplinger *et al.*, 1990) [6]. It is an annual, diploid (2n=14) and autogamous species (Sharma *et al*., 1995) [9]. It grow well in limited rainfall areas of the world (Oplinger *et al.*, 1990) [6]. With 26% protein, lentils have the third highest level of protein from any plant-based food after soybeans and hemp and it is an important part of the diet in many parts of the world, especially in Indian subcontinent which have large vegetarian populations. Lentil seeds are valued as a food of both high quality plant proteins and fiber. It plays an important role in rain-fed cropping systems, providing an alternative to cereal grains (Hamayun *et al*., 2011) [4]. It is cultivated mainly for its seed and only cotyledon is used as food in India. It has ability to fix symbiotically with certain bacteria atmospheric nitrogen and thus contributes greatly to soil fertility (Anjum *et al*., 2005) [3].

Materials and Methods
Location of experiment
The field experiment was laid at DARS, Budgam using Randomized Block Design, and laboratory experiment was carried out at Biofertilizer lab at FoA Wadura.

Plant Materials
Forty five genotypes including local variety Shalimar Masur 1 of Lentil obtained from ICARDA BIGM Nursery were evaluated for various vegetative and yield associated traits in the field experiment and protein content in laboratory.

Characters studied and observational procedure

Observations were recorded on 10 randomly selected and tagged competitive plants from each experimental plot in each replication for plant height, primary branches per plant, secondary branches per plant, pods per plant, seeds per pod, pods per plant, test weight and seed yield per plant. Days to 50 percent flowering and days to maturity were recorded on the whole plot basis. Mean values for all the characters and median values for days to 50 percent flowering were worked out for analysis of variance**. P**rotein content (%) was estimated using Nitrogen Auto Analyser by Kjeldahl method as described by Peach and Tracey (1956).

Table 1: Analysis of variance for different morphological, maturity and yield component traits in Lentil.

Source of variation	D.F	Days to 50 (%) flowering	Days to maturity	Plant height (cm)	Primary branches Plant^{-1}	Secondary branches Plant^{-1}	Pods Plant^{-1}	Seeds Pod^{-1}	100 Seed Weight (g)	Yield Plant^{-1} (g)	Protein content (%)
Replication	2	1.11	3.80	2.43	0.29	10.75	2.33	0.002	0.032	0.002	0.15
Genotypes	44	26.33*	14.68*	93.28*	0.55*	53.96*	311.16*	0.065*	1.250*	1.090*	25.70*
Error	88	8.07	2.95	11.22	0.03	8.38	5.26	0.002	0.027	0.012	0.06

* Significant at 5% level

Table 2: Estimates of mean, range, phenotypic and genotypic variance, phenotypic and genotypic coefficient of variation for different morphological, maturity and yield component traits in Lentil

Parameters	Day to 50 (%) flowering	Days to maturity	Plant height (cm)	Primary branches Plant^{-1}	Secondary branches Plant^{-1}	Pods Plant^{-1}	Seeds Pod^{-1}	100 seed Weight (g)	Yield Plant^{-1} (g)	Protein content (%)
Mean	171.36	218.86	38.61	1.96	19.71	48.88	1.69	2.40	2.18	23.08
Range	165.33-179	214.66-227	25.50-48.23	1.15-2.66	10.33-27.33	27.27-55.48	1.39-1.94	1.55-3.56	1.10-3.52	18.42-29.79
Phenotypic variance	14.15	6.86	38.58	0.20	23.57	107.22	0.02	0.43	0.37	8.61
Genotypic variance	6.08	3.91	27.35	0.17	15.19	101.96	0.02	0.40	0.36	8.54
PCV	2.19	1.19	16.08	24.34	24.63	21.18	9.04	27.47	28.00	12.71
GCV	1.44	0.90	13.54	22.34	19.77	20.65	8.48	26.60	27.54	12.66

Table 3: Heritability and Genetic Gain in Lentil Genotypes

Traits	Heritability (Broad sense)	Expected genetic gain (per cent of mean)
Day to 50 (%) flowering	0.43	1.944
Days to maturity	0.57	1.406
Plant height (cm)	0.70	23.491
Primary branches Plant^{-1}	0.84	42.231
Secondary branches Plant^{-1}	0.64	32.701
Pods Plant^{-1}	0.95	41.496
Seeds pod^{-1}	0.88	16.394
100 Grain weight (g)	0.93	53.062
Yield Plant^{-1}(g)	0.96	55.809
Protein content (%)	0.99	25.984

Table 4: Analysis of variance for dispersion of Lentil genotypes

Source of variation	D.F	Mean squares
Genotypes	44	8.48*
Error	87	4.52
Total	131	0.00

*, significant at 5% level of significance
Wilk's criterion= 129.5

Table 5: Distribution of different Lentil genotypes into clusters based on D^2 statistics

Cluster	Number of genotypes in the cluster	Variety/accession number of the genotypes
I.	10	LSN-2016-(185, 191, 174, 226, 209, 153, 171, 237, 144, 202)
II.	19	LSN-2016-(237, 152, 219, 189, 139, 224, 186, 196, 190, 142, 194, 221, 229, 183, 172, 220, 148, 195, 173,)
III.	7	LSN-2016-(192, 181, 137, 166, 201,136, 203)
IV.	5	LSN-2016-(216, 140, 239), SM1
V.	1	LSN-2016-228
VI.	1	LSN-2016-199
VII.	2	LSN-2016-(227, 214)

Table 6: Average inter-cluster (above diagonal) and intra-cluster (diagonal) D^2 values among different genotypes

Cluster	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
1	34.15	210.46	80.55	92.95	154.06	263.10	110.05
2		39.96	331.49	81.02	59.58	76.88	132.03
3			32.26	153.95	308.12	467.78	282.06
4				36.58	93.13	160.28	112.20
5					0.00	36.18	65.30
6						0.00	81.38
7							20.38

Table 7: Cluster means for different traits in different clusters of lentil genotypes

Clusters	Days to 50 (%) flowering	Days to maturity	Plant height (cm)	Primary branches Plant^{-1}	Secondary branches Plant^{-1}	Pods Plant^{-1}	Seeds Pod^{-1}	100 Seed Weight (g)	Yield Plant^{-1} (g)	Protein content (%)
1	171.90	219.57	38.60	1.42	16.33	39.40	1.52	3.01	1.64	24.97
2	171.02	219.40	40.33	2.15	22.40	58.15	1.83	1.94	2.63	20.82
3	171.24	217.86	36.14	1.56	17.05	38.59	1.64	2.48	1.48	27.89
4	172.33	217.73	36.03	2.17	20.20	52.21	1.68	2.65	2.59	23.51
5	171.00	216.67	43.43	1.68	16.67	43.86	1.53	1.63	1.99	20.41
6	168.67	216.00	33.93	2.33	25.33	46.43	1.76	1.97	2.23	18.42
7	171.50	219.17	37.53	1.64	17.83	39.71	1.64	3.48	2.12	20.94

Table 8: Percent contribution of different quantitative traits towards genetic diversity

Traits	Number of times appearing first in ranking	Per cent contribution towards total divergence
Day to 50(%) flowering	3	0.30
Days to maturity	6	0.61
Plant height(cm)	9	0.91
Primary branches Plant^{-1}	16	3.81
Secondary branches Plant^{-1}	1	0.10
Pods Plant^{-1}	130	12.02
Seeds pod^{-1}	100	11.13
100 seed weight (g)	55	5.21
Yield Plant^{-1}(g)	425	45.67
Protein content (%)	198	20.24

Results and Discussion

The study of Analysis of variance revealed significant differences among characters. This indicates presence of substantial amount of genetic variability for all traits under study. High estimates for yield and its component traits indicate a better scope for selection of desirable combinations for segregant population or successive generation. (Table1)

In the present study PCVs were higher than GCVs for all traits. Traits like days to 50% flowering and days to maturity showed smaller values of GCV and PCV, as well as the differences between PCV and GCV were higher for these traits. Such differences were higher due to larger effect of environment on these traits. Similar trend was reported by Singh *et al.* (2012) and Firas and Al-Aysh (2014). The maximum PCV and GCV were recorded for yield per plant followed by hundred seed weight and pods per plant, primary branches per plant and seeds per pods also showed high FCV and PCV values. GCV is also a reliable criterion for estimating genetic variability. The maximum PCV and GCV were recorded for yield per plant followed by hundred seed weight and pods per plant, primary branches per plant and seeds per pods also showed high FCV and PCV values. GCV is also a reliable criterion for estimating genetic variability. (Table 2)

Heritability and genetic advance

In this study heritability estimates in broad sense were higher for protein content, yield, 100 seed weight, pods per plant, seeds per pods, primary branches. Moderate estimates of heritability and secondary branches were recorded. Traits like days to 50% flowering and days to maturity showed lower values for heritability in broad sense. High heritability coupled with genetic advance were recorded for yield, pods per plant, primary branches per plant and protein content. Similar trends have been reported by Sharaan *et al.* (2003). Seeds per pod, secondary branches and plant height showed considerable values of heritability but low genetic advance suggesting action of non additive genetic variation governing these characaters. Similar trends have been reported by Panday *et al.* (2015) [7], Rajput *et al.* (1989). Days to 50% flowering and days to maturity showed low heritability couples with low genetic advance revealing additive genetic variation governing these characters. (Table 3).

Genetic divergence

Divergence analysis of 45 lentil genotypes was carried out and results are presented in the Table 4, 5, 6, 7 and 8. In all breeding programmes genetic diversity has been considered as an important factor which is also an essential prerequisite for hybridization programme for obtaining high yielding progenies. The critical review of these tables indicates that the studied genotypes exhibited significant variation for the studied traits. Percent contribution of different quantitative traits towards genetic diversity is presented in Table 8. Pods per plant, seeds per pod contributed 12.02% and 11.13 % towards genetic diversity. Hundered seed weight, yield and protein content contributed 5.21%, 45.67% and 20.24% respectively towards the genetic diversity. In the present investigation 45 genotypes wore grouped into 7 clusters using D^2 value in such way that the genotypes within a cluster had a smaller D^2 value than those of another cluster. On the basis of these estimates genotypes were grouped to in cluster

indication, sufficient genetic diversity present in the experimental material. 10 genotypes were included in 1 cluster, 19 genotypes in cluster 2, 7 genotypes were in cluster 3, 5 genotypes were in cluster 4, 1 genotype each in clusters 5 and six and 2 genotypes in cluster 7.

In the present study the magnitude of inter cluster distance was higher than intra cluster distance. This is close harmony with the finding of Viramgama and Goyal (1994) and Rao *et al*. (2010). Highest intra cluster distance was reported in cluster 2 and lowest intra cluster distance reported in cluster 5 and 6. Maximum inter cluster distance was found between cluster 3 and 6 and the minimum inter cluster distance between 5 and 6. Similar findings were reported by Majumdar *et al.* (2011). The highest cluster mean value for seed yield per plant, pod per plant and biological yield per plant were found in cluster 2. Similar trend was reported by Konda *et al.* (2007).

Seed yield per plant (45.67) exhibited maximum contribution in genetic diversity followed by protein content (20.24) pods per plant (12.02) and seeds per pod (11.13). Hence, characters like Period of reproductive phase. Primary branches per plant, days to physiological maturity, days to flowering initiation were negligible contributed in genetic diversity. These finding are in close harmony with the results obtained by Singh *et al.* (2012); Venkatesan *et al.* (2003).

Morphological characterization

In the present investigation 45 Lentil genotypes were characterized (Annexure-II) on the basis of DUS guidelines of PPV&FR (Singh *et al*. 2006). The characters studied were stem colour, flower colour, seed coat colour, colour pattern on seed coat, cotyledon colour, seed size and tendril formation. Out of these seven characters studied, stem colour, flower colour and tendril formation were not variable as all the genotypes possessed green stems with white flowers and persistent tendrils. From the study of seeds of genotypes, 19 genotypes possessed green seeds, 9 genotypes had brown seed coats and 17 genotypes were with grey colour seeds. 11 genotypes had spotted seed coats, 3 genotypes had marbled seed coats and seeds of 31 genotypes possessed no pattern. 37 genotypes had yellow cotyledon and 8 genotypes had orange coloured cotyledons. From the study of seed size 20 genotypes were large seeded (>2.6 g/100-seeds), seeds of 10 genotypes were medium sized (2.1-2.5 g/100-seeds) and 15 genotypes were small seeded (≤2 g/100-seeds).

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