



Short Communication

Inheritance of qualitative and quantitative traits in interspecific crosses of lentil

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Abstract

Inheritance of qualitative and quantitative traits was studied in six inter-sub-specific crosses (*Lens culinaris* × *Lens culinaris* ssp. *orientalis*) of lentil. Leaf pigmentation, leaf pubescence and seed cotyledon color was controlled by single gene while tendril formation and seedling stem pigmentation was controlled by two genes. Wide range of genetic variation was observed for agronomically important quantitative traits in the segregating populations. Transgressive segregants were also observed for various traits. Moderate (52.5%) to high heritability (97.5%) observed for the quantitative traits indicated possible effectiveness of selection for these traits in later generations.

Key words: Genetics; agronomic traits; wide cross; lentil

Introduction

Lentil is one of the important cool season food legume crops cultivated globally on 6.58 mha area and produces 7.59 mt of grains with an average yield of 1153 kg/ha (FAOSTAT, 2019). In India, lentil is cultivated in about 1.49 m ha area with a production of about 1.61 mt and productivity of 1006 kg/ha, which is lower than global average. The low productivity could be ascribed to biotic and abiotic stresses, narrow genetic bases and poor management practices, etc. Wide hybridization is expected to widen the genetic base of cultivated gene pool (Singh et al. 2014a; Singh et al. 2018) and breakdown the yield plateau (Gorim and Vandenberg 2018). For that matter, it is essential to have knowledge about mode of inheritance of the traits. Genetics of several morphological traits in lentil have been reported (Fratini and Ruiz 2006; Singh et

al. 2013, 2014; Emami and Sharma 2000; Shrama 2009). The present study was therefore, aimed to study the genetics of five agro-morphological traits viz., leaf pigmentation, leaf pubescence, tendril formation, seedling stem pigmentation and seed cotyledon color in six wide crosses involving two genotypes (DPL 62 and DPL 58) of cultivated species (*Lens culinaris*) and six accessions of *L. culinaris* ssp. *orientalis*, namely, ILWL 118, ILWL 7, ILWL 189, ILWL 248, ILWL 366, and ILWL 425. The DPL 62 is a widely adapted lentil variety in India and DPL 58 is an improved breeding line carrying many desirable traits. The accessions of wild annual *Lens* taxa were obtained from the Biodiversity and Integrated Gene Management Unit at the International Centre for Agricultural Research in Dry Areas (ICARDA), Aleppo, Syria.

Six crosses, viz., DPL58 × ILWL7, DPL62 × ILWL189, DPL 58 × ILWL248, DPL58 × ILWL366, DPL62 × ILWL425 and DPL58 × ILWL118 were made in 2012-2013 season and their F₁, F₂ and F₃ progenies were raised during 2013-2014, 2014-2015 and 2015-2016, respectively at ICAR-IIPR, Kanpur. The parental lines, F₁, F₂ and F₃ progenies derived from the above crosses were sown in separate experiments in single-row plots (3.0 × 0.3 m). The parental lines of each cross were replicated and the data for days to 50% flowering (no.), days to podding (no.), plant height (cm), secondary branches (no.), pods/plant (no.) and 100 seed weight (g) were recorded on 10 randomly selected plants of parental lines and each plant of F₂ and F₃ progenies. To determine the genetics of a morphological trait, observed frequency of F₂ plants

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in each class of a trait was subjected to χ^2 test to test the goodness of fit to the expected segregating ratio. The p -value of chi-square at 0.05 probability was calculated using online tools (<http://www.socscistatistics.com/pvalues/chidistribution.aspx>). The range, mean and coefficient of variation were used to assess the level of phenotypic variability for six quantitatively inherited traits. F test used to know the significant differences between the parental lines and its progenies of each cross for quantitative traits at the significance level of $P < 0.05$ using Excel software. Heritability in the broad-sense (H^2b) was estimated as per Allard (1960). Genotypic variance (σ^2G) was calculated by subtracting the average variance of parents (σ^2E) from the variance of F_2 (σ^2p).

Genetic analysis of qualitative and quantitative traits

The segregation for the morphological characters observed in F_2 population (Table 1) was used to find out the mode of inheritance of the six traits. The inheritance of leaf pigmentation was studied DPL 58 \times ILWL 118. In F_1 , the leaves were pigmented indicating it to be dominant. In the F_2 , the pigmented (161) and non-pigmented (68) plants segregated in a ratio that fit to 3:1 ratio indicating that leaf pigmentation is controlled by a single dominant gene (Table 1). Emami and Sharma (1996) also reported single dominant gene for leaf pigmentation. The genetics of leaf pubescence was studied in the same cross combination and found that leaf pubescence is controlled by a single dominant gene (Table 1). The results have been supported by earlier workers (Hoque et al. 2002; Kumar et al. 2005; Khosravi et al. 2012). In case of stem pigmentation, the parental lines DPL 58 and ILWL 118 did not have pigmentation at seedling stage; however the F_1 plants produced stem pigmentation in the stem at seedling stage indicating that the stem pigmentation at seedling stage is the result of complementation between two genes. In F_2 , the plants segregated in 9 pigmented: 7 non-pigmented ratio confirming that the seedling stem pigmentation is governed by two dominant complementary genes (Table 1). However, in contrast to this, earlier workers reported that a single dominant gene (G_s) is responsible for green epicotyls (Ladizinsky 1979; Emami and Sharma 1996; Kumar et al. 2005). Seed cotyledon color viz., bright, orange, red and yellow is an important trait influencing market price. Orange cotyledon is preferred over yellow by the consumers of south Asian countries. DPL 58 producing yellow cotyledon was

crossed with three accessions of *L. culinaris* ssp. *orientalis* viz., IL WL118, IL WL 7 and IL WL 366, all having orange cotyledon. The F_1 of all the 3 cross combinations had orange cotyledon indicating it to be dominant over yellow cotyledon. The cotyledon colour in each F_2 segregated in 3 orange (Yc): 1 yellow (yc) cotyledon indicating the cotyledon color to be governed by single dominant gene. Similar inheritance pattern of seed cotyledon color was reported earlier (Singh et al. 2014; Kumar et al. 2005; Vandenberg and Slinkard 1989). However, two to three genes controlling cotyledon color in lentil has also been reported (Emami and Sharma 1996; Sharma et al. 2004). The inheritance of tendrils was studied in the cross DPL 58 \times ILWL 118, where both the genotypes were tendril-less, however, the F_1 plants produced tendrils indicating complementary gene action for the trait. In the F_2 , plants with tendrils (135) and no-tendrils (94 plants) segregated in the 9:7 ratios which confirmed involvement of two dominant complementary genes for the trait. Sharma (2009) indicated involvement of tendrilless plants into tendrilless class for confirming the mode of inheritance. However, Khosravi et al. (2012) reported involvement of single gene for tendril (*Tnl*). has been proposed for the tendril formation (Vandenberg and Slinkard 1989).

Wild relatives of crop species are often used to improve simply inherited qualitative traits (Tullu et al. 2013). To improve quantitatively inherited complex traits is a rare instance, because wild species are generally inferior for these traits. Although phenotypically poor wild species do have favorable genes, which often remain cryptic due to their low-frequency, presence of deleterious alleles and negative epistatic interactions (Peng and Khush 2003). In lentil, earlier studies also demonstrated that introgression of genes from wild relatives help to widen the genetic base of the cultivated gene pool (Singh et al. 2013, 2017, 2018). In the present study, the mean, range, standard error of the mean, coefficient of variation (%) and heritability were estimated for six agronomic traits to estimate the level of genetic variability existing in the F_2 and F_3 plant of the six crosses (Table 2). A wide range of variability was observed for days to 50% flowering, pod formation as well as for other traits in the F_2 and F_3 plants of each cross. The coefficient of variation for these traits in each cross was also higher in F_2 and F_3 as compared to the parental genotypes. In general, the estimates of heritability had a wider range from lowest for 100-seed weight (52.5 %) to highest for days to flowering (98.1%) among the six

Table 1. Inheritance of morphological traits in wild x cultivated crosses of lentil

Cross	Character	Parents DPL 58 ILWL 118/ ILWL7/ILWL 366	F1	F2		Expected ratio	χ^2	P value
				Class	Frequency			
DPL 58 x ILWL 118	leaf pigmentation	absent	present	present absent	161 68	3:1	2.69(1)	0.10
DPL 58 x ILWL 118	leaf pubescence	absent	present	absent present	52 177	3:1	2.76(1)	0.10
DPL 58 x ILWL 118	tendrill formation	absent	prominent	absent prominent	94 135	7:9	0.41(1)	0.50
DPL 58 x ILWL 118	seedling stem pigmentation	absent	present	present absent	127 102	9:7	0.06(1)	0.81
DPL 58 x ILWL 118	seed cotyledon color	yellow	orange	orange yellow	160 69	3:1	3.21(1)	0.07
DPL58 x ILWL7	seed cotyledon color	yellow	orange	orange yellow	85 37	3:1	0.25(1)	0.61
DPL 58 x ILWL 366	seed cotyledon color	yellow	orange	orange yellow	87 28	3:1	0.02(1)	0.89
Pooled data (DPL 58 x ILWL 118/ILWL7/ILWL 366)	seed cotyledon color	yellow	orange	orange yellow	332 134	3:1	3.51(1)	0.06

**non-significant at $P < 0.05$ and respective d.f. is given in parenthesis.

crosses. Genetic variability for pods/plant was significantly higher in the F_2 and F_3 progenies and moved to both negative and positive directions. These findings indicated that the use of wild species has broadened the genetic variability through introgression of alleles from wild accessions as also reported earlier (Singh et al. 2013; Singh et al. 2017). A few segregants showed higher value over the parents for some desirable traits in F_2 generation and F_3 progeny indicated accumulation of favorable genes in recombinants. Tanskey and Nelson (1996) had also observed transgressive segregants in the progenies derived from wide crosses. Identification of transgressive segregants in segregating populations with poor value for some traits as compared the poor parental lines may be a result of negative epistatic interaction among alleles contributed by the wild species. These results are supported by previous results reported by Peng and Khush (2003) in rice. High heritability for the economic traits is desirable for making genetic improvement in quantitatively inherited traits through selection. The estimation of heritability distinguishes the proportion of total phenotypic variances that is caused by genotype x environmental factors and reveals the extent of response to selection exercised in segregating population over the initial breeding pool. The present study showed high broad-sense heritability estimates for each trait studied in all the crosses. These findings are also supported by earlier reports published on wide crosses (Singh et al. 2013, 2014a; 2017). Thus, the genetic improvement in plant types with respect to the studied traits can be effectively brought in by efficient selection in segregating and subsequent generations. The results obtained demonstrate that wild *Lens* taxa can be successfully exploited for lentil

Table 2. Mean, range, coefficient of variation (CV) and heritability (%) of agronomically important traits in wild × cultivated crosses of lentil

Cross/parent	Parents/ generation	Day to 50% flowering (no.)				Day to podding (no.)			
		Range	Mean±SE	CV	h^2 (%)	Range	Mean±SE	CV	h^2 (%)
DPL 58	P1 (10)	79-83	81.1±0.4	1.7		90-93	91.9±0.4	1.5	
ILWL7	P2(10)	90-93	91.4±0.3	0.9		113-116	114.6±0.3	0.7	
DPL58 × ILWL7	F2 (90)	74-90	82.3±0.3	4.6	91%	88-166	99.6±0.6	7.2	97.5
	F3(59)	75-95	83.8±0.2	5.6		87-164	100.0±0.5	6.2	
DPL 62	P1 (10)	80-83	81.4±0.3	1.0		89-93	91.2±0.5	1.8	
ILWL189	P2 (10)	104-107	105.5±1.1	3.5		117-127	121.5±1.0	2.6	
DPL62 × ILWL189	F2 (136)	77-90	83.4±0.3	4.5	88.1	76-110	100.5±0.6	6.7	89.5
	F3(68)	70-92	85.4±0.3	5.5		78-108	99.1±0.5	5.3	
DPL 58	P1(10)	79-83	81.1±0.4	1.7		90-93	91.9±0.4	1.5	
ILWL248	P2(10)	90-92	91.1±0.3	1.1		98-108	99.5±0.4	1.2	
DPL 58 × ILWL248	F2 (160)	76-110	83.5±0.4	6.5	95.1	80-112	100.9±0.5	6.0	95.6
	F3(156)	75-112	85.5±0.4	8.5		75-110	100.0±0.5	7.0	
DPL 58	P1(10)	79-83	81.1±0.4	1.7		90-93	91.9±0.4	1.5	
ILWL-366	P2(10)	102-106	104.8±0.4	1.3		115-118	116.0±0.3	0.9	
DPL58 × ILWL366	F2 (120)	76-88	82.6±0.4	4.4	85.3	88-103	96.1±0.5	4.3	91.2
	F3(114)	72-90	80.6±0.3	6.4		86-110	99.1±0.5	6.3	
DPL62	P1(10)	80-83	81.4±0.3	1.0		89-93	91.2±0.5	1.8	
ILWL425	P2(10)	104-107	105.6±0.3	0.8		115-119	118.0±0.4	1.1	
DPL62 × ILWL425	F2 (150)	66-99	86.4±0.5	7.0	98.1	90-110	101.7±0.4	4.4	92.4
	F3(103)	65-102	87.4±0.4	7.3		85-113	103.2±0.3	6.9	
DPL58	P1(10)	79-83	81.1±0.4	1.7		90-93	91.9±0.4	1.5	
ILWL118	P2(10)	52-56	54.0±0.4	2.3		70-73	71.3±0.4	5.4	
DPL58 × ILWL118	F2 (120)	55-85	65.2±0.6	10.3	96.2	67-97	81.5±0.5	6.5	93.2
	F3 (120)	55-84	63.2±0.3	12.3		70-100	91.5±0.5	7.9	

Cross/parent	Parents/ generation	Plant height (cm)				Secondary branches (no.)			
		Range	Mean±SE	CV	h^2 (%)	Range	Mean±SE	CV	h^2 (%)
DPL 58	P1(10)	32.0-43.0	38.6±1.0	8.6		10-14	11.7±0.6	15.1	
ILWL7	P2(10)	16.0-22.0	18.8±0.6	9.6		29-38	33.4±1.1	10.2	
DPL58 × ILWL7	F2 (90)	20.0-40.0	30.4±0.8	13.0	82.5	3-44	18.1±0.9	54.8	95.1
	F3(59)	11-37	25.2±0.5	21.3		14.0-40.0	24.0±0.6	13.0	
DPL 62	P1(10)	41.0-46.0	43.8±0.7	4.8		8-14	10.2±0.5	16.5	
ILWL189	P2(10)	20.0-25.0	22.3±0.5	6.7		16-19	17.7±0.3	6.0	
DPL62 × ILWL189	F2 (136)	15.0-46.0	29.9±0.4	16.6	89.7	2-43	16.6±0.8	53.3	96.4
	F3(68)	19-42	29.3±0.6	17.9		10-32	22.6±0.6	21.2	
DPL 58	P1(10)	32.0-43.0	38.6±1.0	8.6		10-14	11.7±0.6	15.1	
ILWL248	P2(10)	21.0-25.0	22.9±0.3	4.8		9-20	15.2±1.1	22.7	
DPL 58 × ILWL248	F2 (160)	15.0-45.0	30.5±0.4	16.8	73.0	2-37	14.3±0.5	40.4	77.5
	F3(156)	14-43	29.5±0.5	22.3		11-30	19.7±0.3	21.2	
DPL 58	P1(10)	32.0-43.0	38.6±1.0	8.6		10-14	11.7±0.6	15.1	
ILWL-366	P2(10)	12.0-19.0	15.7±0.6	12.4		6-12	8.7±0.5	18.8	

DPL58 × ILWL366	F2 (120)	11.0-48.0	29.5±0.6	17.7	73.0	5-28	12.9±0.6	42.7	94.7
	F3(114)	16-44	30.0±0.6	20.5		12-29	19.7±0.4	24.1	
DPL62	P1(10)	41.0-46.0	43.8±0.7	4.8		8-14	10.2±0.5	16.5	
ILWL425	P2(10)	15.0-21.0	18.5±0.5	9.3		22.0-23.0	21.1±0.5	8.2	
DPL62 × ILWL425	F2 (150)	14.0-48.0	29.8±0.5	21.2	92.7	6-40	14.0±0.6	50.9	90.5
	F3(103)	16-38	30.3±0.5	15.3		12-25	18.3±0.3	18.1	
DPL58	P1(10)	32.0-43.0	38.6±1.0	8.6		10-14	11.7±0.6	15.1	
ILWL118	P2(10)	23.0-30.0	25.2±0.7	9.5		23-30	25.2±0.7	9.5	
DPL58 × ILWL118	F2 (120)	20.0-90.0	31.8±0.7	23.2	84.6	8-58	27.1±1.0	42.1	97.2
	F3 (120)	16-39	30.1±0.5	18.6		10.0-44.0	19.8±0.5	25.5	

Cross/parent	Parents/ generation	Pods/plant (no.)				100 seed wt. (g)			
		Range	Mean±SE	CV	h^2 (%)	Range	Mean±SE	CV	h^2 (%)
DPL 58	P1(10)	57-120	84.2±6.4	24.3		3.0-3.3	3.2±0.0	3.4	
ILWL7	P2(10)	30-75	42.2±5.3	40.5		1.0-1.1	1.0±0.0		
DPL58 × ILWL7	F2 (90)	2-418	93.0±7.7	92.6	95.21	1.0-3.6	2.3±0.2	18.0	97.9
	F3(59)	21-397	131.4±9.5	13.0		1.0-3.4	2.2±0.1	13.0	
DPL 62	P1(10)	65-140	95.1±7.1	23.9		3.0-3.6	3.3±0.1	5.7	
ILWL189	P2(10)	35-98	62.5±7.0	35.9		1.1-1.3	1.2±0.0	5.2	
DPL62 × ILWL189	F2 (136)	5-336	74.7±5.3	83.4	86.9	1.0-3.8	2.2±0.1	28.0	94.5
	F3(68)	25-410	170.0±11.6	56.1		1.0-4.0	2.2±0.1	29.5	
DPL 58	P1(10)	57-120	84.2±6.4	24.3		3.0-3.3	3.2±0.0	3.4	
ILWL248	P2(10)	56-120	92.7±5.6	19.4		1.1-1.6	1.2±0.1	14.3	
DPL 58 × ILWL248	F2 (160)	10-326	79.4±3.4	54.6	80.23	1.8-3.9	2.9±0.0	15.8	77.8
	F3(156)	10-398	128.1±7.1	69.7		1.6-3.5	2.7±0.0	12.2	
DPL 58	P1(10)	57-120	84.2±6.4	24.3		3.0-3.3	3.2±0.0	3.4	
ILWL-366	P2(10)	12-70	32.6±7.0	68.4		0.6-1.1	0.8±0.0	18.0	
DPL58 × ILWL366	F2 (120)	1-218	53.5±4.1	66.7	62.68	1.2-4.6	2.7±0.1	25.0	95.0
	F3(114)	17-388	117.2±8.0	72.6		1.5-4.8	2.8±0.1	21.3	
DPL62	P1(10)	65-140	95.1±7.1	23.9		3.0-3.6	3.3±0.1	5.7	
ILWL425	P2(10)	35.0-80.0	51.3±5.1	32.1		0.9-1.0	0.9±0.0	5.5	
DPL62 × ILWL425	F2 (150)	2-403	80.7±5.5	83.0	91.25	1.8-3.7	2.6±0.0	16.0	52.5
	F3(103)	27-288	129.4±5.9	45.8		2.0-3.4	2.5±0.0	7.9	
DPL58	P1(10)	57-120	84.2±6.4	24.3		3.0-3.3	3.2±0.0	3.4	
ILWL118	P2(10)	70-123	98.6±5.6	18.0		3.2-3.6	3.4±0.0	4.6	92.8
DPL58 × ILWL118	F2 (120)	8-493	169.1±10.0	65.1	96.9	1.9-3.9	2.7±0.0	16.7	
	F3 (120)	17-389	127.5±7.1	61.6		1.3-3.8	2.6±0.0	19.1	

Note: The variances in F₂ and F₃ progenies of each cross were significantly different from the variances of parental lines at P<0.05; population size is given in parenthesis.

improvement programs, and the variations generated could be easily utilized for broadening the genetic base of the cultivated lentil gene pool for improving yield.

Authors' contribution

Conceptualization of research (JK); Designing of the experiments (JK); Contribution of experimental

materials (JK); Execution of field/lab experiments and data collection (SG); Analysis of data and interpretation (JK); Preparation of manuscript (JK).

Declaration

The authors declare no conflict of interest.

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