RESEARCH NOTE

Determination of gene action for some biometrical traits in *Lens culinaris* Medik. under mid-hill conditions of northwestern Himalayas

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Introduction

Lentil ($2n = 14$) is a highly nutritious food legume cultivated for its grain and is mostly eaten as *dal* in south Asia. High protein percentage (22–34.6%) along with significant concentration of limiting amino acid lysine and its fast cooking characteristics make it an important part of diet in many parts of the world, especially west, south and southeast Asia. This crop is valued for its role in the cropping system as it needs few inputs and has beneficial effects on the soil fertility, because of symbiotic nitrogen fixation. The contribution of India to global lentil area and production is 39.52 and 42.42%, respectively. However, the productivity of lentil in India is very low (619 kg per ha) in comparison to the world average of 887 kg per ha because it is normally grown under rainfed conditions by resource-poor farmers with dearth of potential high yielding cultivars.

Being an autogamous crop, recombinant breeding is the most appropriate approach to combine various desirable attributes like high yield and other important yield contributing and quality attributes. The choice of most suitable breeding procedure, among several available, depends to a large extent on the nature of gene action involved in the control of character(s) in which the plant breeder is interested (Cockerham 1961). The detection, estimation and interpretation of epistasis has progressed much faster at the level of first degree statistics (Mather and Jinks 1982) which has certain limitations due to the cancellation of genic effects. An experimental method known as triple test-cross to overcome these limitations has been developed by Kearsey and Jinks (1968), which besides overcoming these limitations has many other advantages. Keeping in view the above considerations, the genetic amelioration of lentil genotypes with respect to some important biometrical traits was carried out by using the triple test-cross model suggested by Kearsey and Jinks (1968) and Jinks *et al.* (1969) except that the testers were crossed to a number of lines instead of F_2 individuals. This simplified version of the triple test-cross (Jinks *et al.* 1969) retains many of the advantages of being unambiguous, statistically reliable and universal in applicability. The main limitation of this design is that if the testers do not differ at all loci for which the lines under test differ, the test for epistasis is no longer unambiguous and the estimates of additive and dominance components of variation are biased (Virk and Jinks 1977). In order to test and allow for such biases, a modification of the simplified triple test-cross analysis has been suggested by Jinks and Virk (1977).

Materials and methods

The present investigation was carried out in the experimental farm of the Department of Crop Improvement, CSK HPKV, Palampur, Himachal Pradesh, India. The experimental farm is situated at 32°8′N latitude and 76°3′E longitude at an elevation of 1290.8 m above mean sea level. Agro climatically, the location represents the mid-hill zone (zone-II) of Himachal Pradesh and is characterized by humid subtemperate climate with high rainfall (2500 mm). The soil is acidic in nature with pH ranging from 5.0 to 5.6.

Experimental materials and methods

Two genotypes, viz., Vipasa (*macrosperma*) and PL-406 (*microsperma*) were used as testers with designation as L_1 and L_2, respectively. The F_1 (resulting from hybridization

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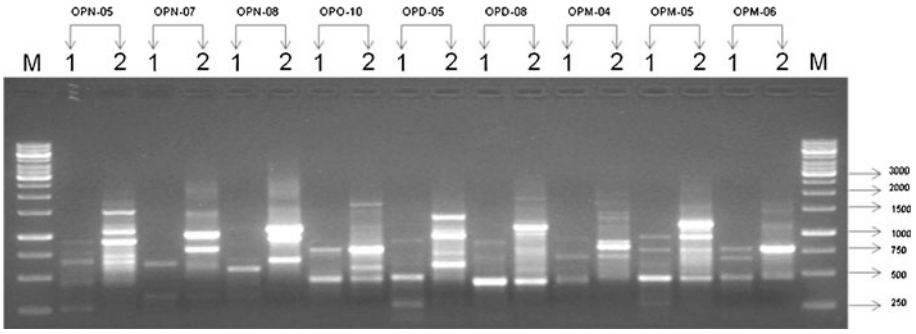

Figure 1. Genetic diversity between testers Vipasa (1) and PL-406 (2) observed using RAPD primers. M, molecular weight marker.

between Vipasa and PL-406) provided the third tester designated as L_3. Fifteen true breeding genotypes/lines viz., L-652, L-651, L-658, L-635, L-407, L-630, L-617, L-666, L-649, L-620, L-354, L-403, L-412, L-642 and L-737 were crossed with the three testers (L_1, L_2 and L_3) during *rabi* 2006–07 and also during summer (off-season) 2007 at HAREC, Kukumseri (Himachal Pradesh, India). The experiment comprising 15 inbred lines, 3 testers, 30 single crosses and 15 three-way crosses was conducted in a randomized complete block design with two replications at the experimental farm of the Department of Crop improvement, CSK HPKV, Palampur, on 16th November 2007 (see table 1 in electronic supplementary material at http://www.ias.ac.in/jgenet/). Each cross/parent was raised in two rows, 2-m long with row to row and plant to plant spacing of 30 cm and 5 cm, respectively.

Recording of observations

Ten plants were tagged randomly from each entry and in each replication to record observations for 15 traits, days to 50% flowering, days to 75% maturity, plant height (cm), primary branches per plant, fertile nodes per plant, pods per plant, seeds per pod, 100-seed weight (g), seed yield per plant (g), biological yield per plant (g), harvest index (%), crude protein content (micro-Kjeldhal method, AOAC, 1970), methionine content (Horn *et al.* 1946), tryptophan content (Mertz *et al.* 1975) and polyphenol oxidase activity (Bastin and Unluer 1972).

Statistical analysis

The statistical analysis for all triple test-cross calculations were performed using the window stat software developed by Indian Agricultural Statistical Research Institute, New Delhi, India.

Results and discussion

The genetic diversity between the two testers (Vipasa and PL-406) used in the present study was found to be 79.37% as estimated by using RAPD markers and the testers were extreme selections from the population of inbred lines being tested, thus fulfilling the basic requirement of triple test-cross analysis (figure 1). The analysis of variance revealed the presence of sufficient genetic variability in the material for exploitation through recombination breeding. The significant influence of nonallelic interaction was observed for all the traits under study indicating the presence of epistasis for these traits and suggesting one would not have obtained a clear picture about the genetic systems controlling these traits if a procedure assuming no epistasis would have been used (Subbaraman and Rangaswamy 1989). Epistasis was detected as integral part of genetic system for all the 15 traits studied (table 1). Distribution of total epistasis into additive × additive (*i* type), additive × dominance and dominance × dominance (*j* and *l* type) interactions showed the existence of *i* type for all traits except seeds per pod; and *j* and *l* type epistasis for all characters. The predominant effect of *i* type epistasis than *j* and *l* type was observed for all traits except 100-seed weight and tryptophan content. This has a special significance in lentil, being a highly selfpollinated crop where a linear directional and fixable component (*i* type epistasis) of genetic variation can be most easily exploited compared with unfixable component (*j* and *l* type epistasis). The *i* type epistasis has also been found important in wheat (Singh and Singh 1976) and rice (Saleem *et al.* 2005).

The significance of mean square due to sums and differences provide a direct test of significance of additive and dominance components of variation. The significance of mean squares due to sums (except days to 75% maturity, primary branches per plant, seeds per pod and methionine content) and differences (except seeds per pod and methionine content) for most of the traits observed in the present study indicates the importance of both additive and dominance variance in controlling the expression of these traits in lentil (table 2). Sharma *et al.* (2008) also recorded significant values of both D and H for most of the traits in peas. Both additive and dominance gene action were observed to be equally important for most of the traits (table 3). The magnitude of additive variance was higher for plant height, biological yield per plant, harvest index, protein content and tryptophan content whereas all other traits exhibited higher dominance

Table 1. Analysis of variance for the detection of epistasis ($\bar{L}_{1i} + \bar{L}_{2i} - 2\bar{L}_{3i}$) for different traits in lentil.

Trait	Source of variation					
	Epistasis (DF = 15)	*i* Type interaction (DF = 1)	(*j* + *l*) Type interaction (DF = 14)	Epistasis × replication (DF = 30)	*i* Type × replication (DF = 2)	(*j* + *l*) Type × replication (DF = 28)
Days to 50% flowering	89.87**	202.80*	81.80**	3.80	4.27	3.77
Days to 75% maturity	43.40**	136.53*	36.75**	5.23	3.27	5.37
Plant height (cm)	112.82**	517.09*	83.94**	7.85	8.45	7.81
Primary branches/plant	8.14**	47.58*	5.32**	0.44	0.30	0.45
Fertile nodes/plant	13134.31**	61798.57**	9658.30**	82.46	489.53**	53.39
Pods/plant	56928.03**	299979.67**	39567.17**	208.05	1724.04**	99.76
Seeds/pod	0.28**	0.31	0.28**	0.03	0.02	0.03
Biological yield/plant (g)	309.73**	2189.66**	175.45**	1.45	8.97	0.91
Seed yield/plant (g)	51.63**	228.97**	38.96**	0.28	1.07*	0.23
100-seed weight (g)	0.75**	0.05**	0.80**	0.02	8.00E-05	0.03
Harvest index (%)	0.04**	0.10**	0.04**	9.20E-04	4.00E-05	9.90E-04
Protein content (%)	200.10**	297.61**	193.13**	1.10	0.46	1.14
Tryptophan content (g/16 g N)	3.85**	0.03**	4.12**	2.90E-04	2.40E-04	2.90E-04
Methionine content (g/16 g N)	2.39**	17.10**	1.34**	0.04	8.90E-04	0.04
PPO (ΔAbs./min.)	1.26E-03**	1.41E-02**	3.40E-03**	2.00E-05	1.00E-05	2.00E-05

*Significant at $P \leq 0.05$; **significant at $P \leq 0.01$; DF, degree of freedom.

variance. Although D values are expected to be higher for most of the traits in a self-pollinated crop like lentil but the environment may influence the gene action. Jinks and Perkins (1970) observed that the components of variance changed to different degrees over environments if different kind of gene action were not equally sensitive to the environment. Generally the presence of common alleles in the testers increase the magnitude of additive component by adding the dominance effect of common alleles in testers along with the cross product effects of dominance and additive effects for the common alleles. Moreover, the dominance effect will be estimated for noncommon loci only, reducing the magnitude of dominance variance.

The high magnitude of additive variance for most of the traits indicated the relative importance of fixable type of gene action in their inheritance. The presence of higher magnitude of additive gene action for seeds per pod and plant height has also been reported by Sharma *et al.* (2008) in peas, and for plant height and protein content by Verma *et al.* (2007) in barley. The magnitude of dominance variance was higher for

Table 2. Analysis of variance for sums ($\bar{L}_{1i} + \bar{L}_{2i}$) and differences ($\bar{L}_{1i} - \bar{L}_{2i}$) for different traits in lentil.

Trait	Mean squares			
	Sums (DF = 14)	Sums × replication (DF = 14)	Differences (DF = 14)	Differences × replication (DF = 14)
Days to 50% flowering	16.90*	3.42	47.99**	1.70
Days to 75% maturity	3.75	2.59	3.75*	1.35
Plant height (cm)	13.39**	1.96	12.06**	2.34
Primary branches/plant	0.86	0.50	0.64**	0.14
Fertile nodes/plant	896.21**	26.54	939.35**	15.19
Pods/plant	2719.14**	101.41	2922.87**	59.54
Seeds/pod	0.09	0.042	0.03	0.03
Biological yield/plant (g)	14.37**	0.91	13.13**	0.97
Seed yield/plant (g)	2.71**	0.15	3.33**	0.28
100-seed weight (g)	0.33**	0.02	0.33**	0.02
Harvest index (%)	0.01**	8.80E-04	0.01**	1.97E-03
Protein content (%)	14.21**	1.00	12.59**	0.49
Tryptophan content (g/16 g N)	0.54**	1.00E-04	0.26**	2.00E-04
Methionine content (g/16 g N)	0.09	0.08	0.09	0.06
PPO (ΔAbs./min.)	2.00E-05**	0	3.00E-05*	1.00E-05

*Significant at $P \leq 0.05$; **significant at $P \leq 0.01$; DF, degree of freedom.

Table 3. Estimates of additive (D) and dominance (H) components of genetic variance, average degree of dominance $(H/D)^{1/2}$, direction of dominance ($r_{s,d}$) and narrow sense heritability for different traits in lentil.

Trait	D	H	$(H/D)^{1/2}$	$r_{s,d}$	h^2_{ns} (%)
Days to 50% flowering	26.96**	92.57**	1.85	0.03	22
Days to 75% maturity	2.32	4.80*	1.44	−0.73**	27
Plant height (cm)	22.86**	19.37**	0.92	−0.50	51
Primary branches/plant	0.71	1.01**	1.19	0.14	38
Fertile nodes/plant	1739.32**	1848.34**	1.03	0.25	48
Pods/plant	5235.46**	5726.65**	1.05	0.24	48
Seeds/pod	0.09	1.00E−03	0.11	0.21	74
Biological yield/plant (g)	26.90**	24.32**	0.95	0.23	52
Seed yield/plant (g)	5.13**	6.12**	1.09	−0.04	45
100-seed weight (g)	0.62**	0.64**	1.02	−0.05	49
Harvest index (%)	0.02**	0.02**	0.95	−0.01	50
Protein content (%)	26.42**	24.20**	0.96	0.50	52
Tryptophan content (g/16 g N)	1.09**	0.52**	0.69	0.17	68
Methionine content (g/16 g N)	0.03	0.06	1.60	−0.35	17
PPO (ΔAbs. /min.)	2.40E-05	4.00E-05	1.29	0.29	32

*Significant at $P \leq 0.05$; **significant at $P \leq 0.01$.

days to 50% flowering, fertile nodes per plant, pods per plant, seed yield per plant and 100-seed weight signifying thereby the relative importance of nonfixable type of gene action. The preponderance of additive component of genetic variance for the expression of plant height, biological yield per plant, harvest index, protein content and tryptophan content indicates the possibility of improvement of these traits through pedigree method of selection procedure. But the existence of substantial amount of nonadditive components for rest of the traits indicates the use of diallel selective mating/biparental mating or recurrent selection for their improvement as also suggested in linseed by Sood *et al.* (2007).

The average degree of dominance was in the range of over dominance to partial dominance. The negative and significant correlation between sums and differences for days to 75% maturity was observed which indicate the genes with positive effects are more predominant. All other traits showed non-significant correlation indicating that these traits did not supply any evidence for directional dominance in lentil, and alleles with increasing and decreasing effects appear to be dominant and recessive to the same extent.

The heritability estimates were low to moderate with highest value recorded for seeds per pod, tryptophan content, protein content, biological yield per plant, plant height and harvest index (>50%) and moderate (30–50%) for 100-seed weight, fertile nodes per plant, pods per plant, seed yield per plant and primary branches per plant and lowest value (<30%) for days to 75% maturity, days to 50% flowering, methionine content and polyphenol oxidase activity. The high estimates of heritability indicate the characters are largely governed by additive genes and simple selection for improvement of such characters would be rewarding. The low estimates indicate that there is preponderance of nonadditive gene action and recombinant breeding may thus be useful.

The nonallelic interactions played an important role in the inheritance of all the traits in the present study suggesting recurrent selection for the improvement of these traits to develop high yielding genotypes in lentil. Recurrent selection has also been suggested for nonallelic inherited traits in rice (Subbaraman and Rangaswamy 1989; Vijayakumar *et al.* 1996) and wheat (Sharma *et al.* 1995) and mungbean (Khattak *et al.* 2001). Since both additive and dominance gene effects were significant for most of the traits simple selection procedures in the early generations may not contribute significantly to the improvement of these traits and deferred selection in later generations of segregating populations will improve the secondary yield components and seed yield in lentil.

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