



Heterosis for seed yield and its relationship with genetic divergence in grasspea (*Lathyrus sativus* L.)

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Abstract

Heterosis has been a phenomenon of great interest for Plant Breeders and its utilization has led to the considerable yield improvement in crop plants. Keeping in view, the present investigation was conducted to study the nature and extent of genetic diversity available in this crop under northwestern Himalayas. Twenty-four landraces were collected from different agroclimatic locations and raised in Randomized Complete Block Design with three replications in the experimental farm of Himachal Pradesh Krishi Vishvavidyalaya, Palampur, during *rabi* 1994-95. To study the relationship between heterosis over the better parent and genetic divergence, five genetically diversified parents (LSP-1, LSP-2, LSP-3, LSP-4 and LSP-5) were crossed in a half-diallel fashion. All the fifteen populations were raised in randomised complete block design with three replications during *rabi* 1995-96. The observations on plant height, number of branches, days to flower, days to podding, days to maturity, pods/plant, seeds/pod, 100-seed weight, seed yield/plot and seed neurotoxin content were recorded at appropriate stages. The seeds were analyzed biochemically as per the standard procedure. The analysis of variance revealed the presence of considerable genetic variability for all characters except for days to maturity. Using Tocher's procedure, twenty four lines could be grouped into five clusters, three of which contained only a single line each. Cluster I contained the maximum number of 19 lines. LSP-19 (white flower) and LSP-20 (pink flower) clustered with blue flowered lines. Likewise, LSP-20 (lowest ODAP) clustered with other high ODAP lines including LSP-11 (highest ODAP) which suggested that the flower color and ODAP content were not the cause for genetic diversification in *Lathyrus sativus* L. The study revealed an appreciable heterotic response over better parent in desired direction for a number of characters. A highest positive and significant heterosis for seed yield (28.7%) was exhibited by the cross LSP-2 \times LSP-5 followed by the crosses LSP-3 \times LSP-5 (23.0%) and LSP-2 \times LSP-3 (16.7%). The cross LSP-2 \times LSP-5 also recorded highest heterosis (53.6%) for pods/plant. An examination of the clustering behavior of fifteen populations revealed that seven clusters could be formed, two of which contained only single member each. The cross LSP-2 \times LSP-5 though, showed highest heterosis for seed yield yet, its parents did not record maximum divergence. On the other hand, the

cross LSP-2 \times LSP-3 showed maximum divergence (148.0) between its parental clusters, but, indicated considerable heterotic response for seed yield. This suggested that divergence between parents and percent heterosis in crosses did not have one-to-one correspondence for seed yield.

Key words: Grasspea, *Lathyrus sativus*, heterosis, multivariate D^2 -statistic

Introduction

Lathyrus sativus L. commonly known as *Khesari*, is a drought hardy grain legume rich in proteins (28-32%) and possesses good qualities of essential amino-acids. However, Government of India has imposed a ban on its cultivation and sale since 1961 because it contains neurotoxin (α - β -oxaly-L-diamino propionic acid or ODAP) which causes *Lathyrism* in man when its *dal* is consumed in larger quantities for a longer period of time (1). The varieties generally have low yield potential, a poor plant type and high neurotoxin content which is unstable over environments (2). The cause of relatively poor success in grain legumes in achieving substantial progress is the lack in genetic diversity. On the other hand, there have been reports where heterosis is not observed even when divergent parents are crossed.

An estimate of heterosis over better parent (heterobeltiosis) may provide valuable genetic information on seed yield and its component characters as well as neurotoxin content to facilitate selection of desirable parents and cross-combinations in an efficient breeding programme in *Lathyrus sativus* L. Keeping in view the importance of this crop as a rich source of proteins, low input requirement for its cultivation and tolerance to various biotic and abiotic stresses, the present investigation was undertaken to assess the nature of heterosis observed in the crosses in relation to the genetic divergence among parents through multi-variate D^2 analysis.

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Materials and methods

The experimental material for the present investigation comprised of twenty three local landraces collected from farmers fields from Kangra district and one exotic collection (LSP-24) obtained from Division of Genetics, Indian Agricultural Research Institute, New Delhi. All the germplasm lines were raised in Randomised Complete Block Design (RCBD) with three replications at the experimental farm of Himachal Pradesh Krishi Vishvavidyalaya, Palampur (32°N 6' and altitude of 1290 metres) during *rabi* 1994-95. Each genotype was raised in 1.5 × 1.4 m² plot with inter- and intra-row spacings of 30cm and 15cm, respectively. For heterotic studies, the experimental material comprised of five distinct genotypes viz., LSP-1, LSP-2, LSP-3, LSP-4 and LSP-5. The genotypes were crossed in all possible combinations excluding reciprocals. All the parents along with their ten F₁ crosses were raised in Randomised Complete Block Design (RCBD) with three replications during *rabi*, 1995-96. Palampur has a temperate wet type of climate, characterized by wet summers and cold winters. The season was endowed with wide range of temperature variation (2.8°C to 35.4°C) and rainfall of 240.2mm. Only 9.7 mm of rainfall was received during the first two months of sowing. It rained 40.7, 59.4 and 80.1 mm during January, February and March, respectively. The ultimate plot size consisted of single row of one metre each with inter-row and inter-plant spacings of 30 cm and 15 cm, respectively. Recommended cultural practices were followed to raise the crop. The observations on various morphological and yield components such as plant height, number of branches, days to flower, days to podding, days to maturity, pods per plant, seeds per pod, 100-seed weight, seed yield per plot were recorded on five random plants in parents and all plants in hybrids during flowering and maturity stages. The seeds of parents as well as crosses were analyzed biochemically following the standard procedure [3]. The data were subjected to statistical analysis using Mahalanobis's D² analysis [4]. Grouping of genotypes into various clusters was carried out following Tocher's procedure [5] and the relative contribution of different characters to total D² distance was calculated as per Singh and Chowdhury [6]. The magnitude of heterosis as the difference in F₁ performance over better parent (heterobeltiosis) in percentage was calculated as per Hayes *et al.* [7]. Depending upon the desirability of the character, first or second parent was treated as better parent.

Results and discussion

The analysis of variance for all characters revealed highly significant differences among all genotypes suggesting the presence of substantial genetic variability. However for days to maturity, no significant differences among genotypes were observed indicating that all

genotypes matured almost in the same duration. Using Tocher's procedure, all the twenty-four genotypes could be grouped into five clusters, three of which contained only a single line each. Cluster I contained the maximum number of nineteen lines followed by cluster III which contained only two lines. LSP-19 (White flower) and LSP-20 (Pink flower) clustered with blue flower colored lines. Like wise, LSP-20 (lowest seed ODAP content) clustered with other high ODAP lines including LSP-11 (highest seed ODAP) which suggested that the flower color and ODAP content were not the cause for genetic diversification of lines in *Lathyrus sativus* L. (Table 1). The results are in agreement with earlier findings of Kumari *et al.* [8]. They also observed

Table 1. Distribution of twenty-four genotypes of *Lathyrus sativus* L. into different clusters

Cluster	Number	Genotypes
I	19	LSP-1, LSP-3, LSP-4, LSP-6, LSP-7, LSP-8, LSP-9, LSP-10, LSP-11, LSP-12, LSP-13, LSP-14, LSP-15, LSP-16, LSP-17, LSP-18, LSP-19, LSP-20, LSP-21
II	1	LSP-2
III	2	LSP-22, LSP-23
IV	1	LSP-24
V	1	LSP-5

that seed ODAP content and flower color were in no way involved in genetic diversification in natural evolution. The clustering pattern revealed that the local landraces and exotic collection were not grouped into a single cluster e.g. the exotic collection (LSP-24) formed a separate cluster IV. However, Waghmare *et al.* [9] while studying fifty genotypes of *Lathyrus sativus* L., observed that all lines could be grouped into seven clusters which did not agree to their geographical origins.

The maximum inter-cluster divergence (108.4) was recorded between clusters IV and V with one genotype each suggesting that these genotypes were highly divergent from each other (Table 2). Likewise, the minimum inter-cluster divergence (35.8) was recorded between clusters II and IV indicating that genotypes of these clusters were very close to each other. The intracluster divergence was comparable in clusters I and III while for clusters II, IV and V, it was zero as the clusters were constituted by a single line each.

Table 2. Intra-(diagonal) and inter-cluster divergence for five clusters in *Lathyrus sativus* L.

Cluster	I	II	III	IV	V
I	13.8	41.3	60.6	73.3	52.9
II		0	65.0	35.8	93.6
III			12.3	63.1	77.8
IV				0	108.4
V					0

The mean values for different characters of five clusters indicated the superior expression of some characters in different clusters (Table 3). Cluster I had the genotypes having highest values for number of

An examination of the clustering behavior of fifteen populations (five parents and ten crosses) revealed that seven clusters could be formed, two of which contained only single member each. Cluster I contained the

Table 3. Cluster means and percent contribution of different characters in *Lathyrus sativus* L.

Characters/Clusters	Plant height (cm)	Number of branches	Days to flower	Days to podding	Days to maturity	Pods/plant	Seeds/pod	100-seed weight (g)	Seed yield/plot (g)	Seed ODAP content (%)
I	54.1	15.6	132.8	160.7	180.3	45.4	2.94	7.04	204.2	0.63
II	76.5	10.0	131.3	158.7	179.7	26.3	3.03	7.63	123.1	0.47
III	31.3	10.0	128.5	156.8	182.2	22.6	2.05	5.93	23.1	0.32
IV	64.1	11.5	132.3	161.3	180.3	19.5	2.23	11.21	60.9	0.33
V	56.7	11.1	133.0	167.0	179.3	51.6	3.02	6.70	180.4	0.73
Percent contribution to genetic divergence	8.3	6.9	6.5	13.4	3.3	14.5	10.14	10.87	25.7	0.36

branches and seed yield per plot. It had moderately high values for plant height, days to flower, days to podding, days to maturity, pods per plant, seeds per pod and seed ODAP content. Cluster II was represented by a genotype (LSP-2) with highest values for plant height and seeds per pod accompanied by minimum branch number. The genotypes having minimum height, days to flower, days to podding, seeds per pod, 100-seed weight and seed yield were observed in cluster III. The lines in this cluster also exhibited lowest seed ODAP content. Cluster IV was comprised of a genotype (LSP-24, a bold seeded line) with highest 100-seed weight and low neurotoxin content. Likewise, the genotype failing in cluster V (LSP-5) was late in flowering and podding. It exhibited highest pods per plant and seeds per pod but, also showed highest seed ODAP content.

The relative contribution of different characters towards the expression of genetic divergence revealed that seed yield per plot contributed maximum (25.72%) towards genetic divergence followed by pods per plant (14.5%) and days to podding (13.4%). Namboodiri *et al.* [10] while studying genetic divergence reported pods per plant to be the most important character contributing towards genetic divergence (Table 3).

maximum number of five populations in which hybrids as well as one parent clustered together thus, indicating that parent-hybrid differentiation was not the cause for genetic divergence in this crop. Clusters II, III, IV and V had two lines each while clusters VI and VII had only one member each. Out of five parents, LSP-1 and LSP-3 clustered together in cluster V. The remaining three parents occupied separate clusters. LSP-2 and LSP-4 appeared to carry mostly the dominant genes for characters contributing to genetic divergence as seen from the clustering behavior of their offspring's, which generally clustered with respective parents. LSP-5, a genotype with highest seed ODAP content, clustered separately (Table 4).

The maximum genetic divergence (154.1) was observed between clusters VI and VII suggesting that the genotypes falling in these clusters were highly divergent from each other. It was further followed by divergence value of 148.0 between clusters IV and V. Cluster I and II were the closest ones with genetic distance of 34.2. The intra-cluster divergence was comparable in 5 clusters whereas for clusters VI and VII, it was zero as both clusters were constituted by lone member each. Genotypes belonging to clusters separated by high genetic distance may be used in hybridization programme to obtain a wide spectrum of

Table 4. Intra-(diagonal) and inter-cluster divergence, cluster composition following multivariate D^2 analysis

Clusters	I	II	III	IV	V	VI	VII	No. of populations	Population description
I	22.3	34.2	91.5	78.8	46.7	35.1	85.4	5	LSP-1 × LSP-4, LSP-1 × LSP-5, LSP-1 × LSP-3, LSP-4 × LSP-5, LSP-4
II		19.1	67.6	111.9	59.8	42.0	88.4	2	LSP-3 × LSP-4, LSP-3 × LSP-5
III			25.3	68.6	139.2	127.0	36.8	2	LSP-2 × LSP-4, LSP-2 × LSP-5
IV				28.3	148.0	118.5	40.5	2	LSP-2, LSP-1 × LSP-2
V					41.4	88.3	111.6	2	LSP-1, LSP-3
VI						0	154.1	1	LSP-5
VII							0	1	LSP-2 × LSP-3

variation among the segregates [11]. Cluster I was represented by the populations having moderately higher values for most of the character components. Cluster II had the crosses exhibiting highest seed yield which might have been contributed by the highest pods per plant, seeds per pod and test weight but also showed higher toxicity. The populations in cluster III were tall and medium in maturity. Higher pods per plant and test-weight could contribute to seed yield in these crosses. The genotypes belonging to cluster IV had the populations with tall plant type, moderate seed yield and lowest neurotoxin content. Cluster VI was comprised of LSP-5, a genotype with moderate plant height, medium in flowering and podding with late maturity and very high seed ODAP content. The bold-seeded (high test-weight) cross requiring the least days to podding was grouped in cluster VII (Table 5).

For seed yield per plot, all crosses deviated significantly from their respective superior parents, one of them showed negative heterosis. A highest positive significant heterosis was exhibited by the cross LSP-2 × LSP-5 (28.7%) followed by LSP-3 × LSP-5 (23%) and LSP2 × LSP-3 (16.7%). The cross LSP-2 × LSP-5 also recorded highest heterosis (53.6%) for pods per plant. In general, characters like lesser days to podding and maturity, increased pods per plant and 100-seed

weight influenced the heterosis for seed yield. This was further indicated by parallel behavior of *per se* performance of the crosses. Quader [12] also revealed a considerable heterotic response over better parents for seed yield in grasspea. The cross LSP2 × LSP-5 although, showed best heterosis for seed yield yet, its parents did not record maximum divergence in D² analysis. On the other hand, LSP-1 × LSP-2 and LSP-2 × LSP-3 recorded maximum divergence between parental clusters but, did not indicate best heterosis (Table 6). This suggested that the divergence between parents and percent heterosis observed in crosses did not have one-to-one correspondence for seed yield. However, Srivastava [13] had reported a fair agreement between the relationship of heterosis and genetic divergence in *Lathyrus sativus* L. For seed ODAP content, none of the crosses exhibited desirable heterosis for the character suggesting that probably more genotypes with much more variation in seed ODAP content are required to be included in the present investigation.

Since not much work on heterosis has been carried out in this crop, the present information may prove useful in future breeding programmes aimed at the development of the high yielding and low neurotoxin lines/varieties of grasspea.

Table 5. Cluster means for different characters in fifteen populations of *Lathyrus sativus* L.

Cluster	Characters									
	Plant height (cm)	Number of branches	Days to flower	Days to podding	Days to maturity	Pods/plant	Seeds/pod	100-seed weight (g)	Seed yield/plot (g)	Seed ODAP content (%)
I	56.4	13.3	123.1	148.9	212.9	51.3	3.5	7.7	194.7	0.54
II	56.7	17.2	124.0	148.2	214.0	63.5	4.0	8.2	213.5	0.55
III	72.5	18.9	112.3	143.2	209.2	57.6	3.4	8.0	210.1	0.44
IV	72.3	12.6	112.4	140.9	188.2	39.6	3.3	7.7	185.3	0.41
V	48.8	15.1	127.9	152.0	214.9	43.5	3.3	8.0	199.4	0.55
VI	59.3	13.2	118.0	150.3	217.0	56.2	3.7	7.6	176.8	0.68
VII	66.3	17.5	115.3	140.0	206.3	40.3	3.4	8.2	210.6	0.43

Table 6. Parental divergence and heterosis over better parent in crosses of *Lathyrus sativus* L.

Cross	Characters									
	Divergence between parental clusters	Plant height	Number of branches	Days to flower	Days to podding	Days to maturity	Pods/plant	Seeds/pod	100-seed weight	Seed yield/plot
1 × 2	148.0	39.7*	-12.7*	6.7**	4.6**	-12.4**	3.4	-16.7**	2.6	5.4*
1 × 3	0.0	2.1	34.2**	-4.5**	0	-0.7	21.0**	0.90	-3.7**	-5.1*
1 × 4	46.7	-13.7**	-12.3*	-3.4**	0.5	-0.6	29.6**	6.1	-3.8**	7.4**
1 × 5	88.3	19.1**	8.5	2.3	-0.2	-1.7	25.4**	-11.6	2.6	9.3**
2 × 3	148.0	35.3**	30.6**	6.1**	1.7	2.8	-16.7**	-5.6	9.2**	16.7**
2 × 4	78.8	23.3**	55.4**	3.3**	3.3**	2.8	38.6**	-14.0**	2.6	6.8*
2 × 5	118.5	20.4**	32.6**	3.3**	-4.2**	-2.4	53.6**	2.8	6.6**	28.7**
3 × 4	46.7	18.2**	33.1**	0	-0.9	-0.1	26.4**	18.2**	6.6**	13.4**
3 × 5	88.3	13.1**	29.5**	1.7	-0.7	-0.2	36.0**	21.2**	7.9**	23.0**
4 × 5	35.1	6.7*	6.9	1.1	-0.9	-0.5	4.6	11.8**	5.3**	16.4**

*Significant at P ≤ 0.05; **Significant at P ≤ 0.01; 1: LSP-1; 2: LSP-2; 3: LSP-3; 4: LSP-4; 5: LSP-5

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