Stability Analysis in Grass Pea [*Lathyrus sativus* (L.)]

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Thesis

Master of Science in Agriculture

(Plant Breeding & Genetics)

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DEPARTMENT OF PLANT BREEDING AND GENETICS
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Dated: / /2007

This is to certify that **Mr. Kanhaiya Lal Raiger** has successfully completed the Comprehensive/Preliminary Examination held on 09-07-2007 as required under the regulation for degree of **Master of Science in Agriculture.**

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Dated: / /2007

This is to certify that the thesis entitled **"Stability analysis in grass pea [*Lathyrus sativus* (L.)]"** submitted for the degree of **Master of Science in Agriculture** in the subject of **Plant Breeding and Genetics,** embodies bonafied research work carried out by **Mr. Kanhaiya Lal Raiger** under my guidance and supervision and that no part of this thesis has been submitted for any other degree. The assistance and help received during the course of investigation have been fully acknowledged. The draft of this thesis was also approved by the advisory committee on 10-11-2006.

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ABSTRACT

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The present study entitled **"Stability analysis in grass pea [*Lathyrus sativus* (L.)]"** was carried-out with sixteen diverse varieties/strains for seed yield, its components and quality parameters. The material was planted under two locations in four environments during *rabi*, 2005-06 and 2006-07 at Udaipur and Kota.

Observations were recorded for eight yield contributing characters and one quality trait. Variability parameters, correlations and path analysis were computed for each environment and over pooled basis. Stability parameters were analyzed using the model (Eberhart and Russell, 1966).

Superior varieties L-18, I-30 and R-33 were identified on the basis of their consistent *per se* performance in each environment and over pooled basis for seed yield and its component traits. I-18, I-30 and R-31 exhibited high seed protein content while I-30 displayed superiority for seed yield as well as quality characters. Large genetic advance as percentage of mean coupled with high GCV and heritability were recorded for pods per plant and plant height in at least one environment and over pooled basis suggesting that selection for these traits would be effective for seed yield in grass pea.

Association studies revealed that seed yield per plant was positively correlated at genotypic levels with branches per plant in at least one environment.

Path analysis studies indicated that seed protein content contributed to seed yield indirectly with negative effect.

A joint regression analysis of variance based over four environments indicated that genotypes differed significantly for almost all the characters except plant height and branches per plant. Environmental effects were also significant for all characters. Both linear and non-linear components were significant for all the characters. However, linear component was of higher magnitude for pods per plant, days to maturity, branches per plant, 100-seed weight, days to flowering, seed yield per plant and plant height.

Superior varieties were identified with respect to their phenotypic stability for per plant and its components. For quality character varieties R-29, I-22, R-33, and L-07 had high *per se* performance for seed protein content under high management practices

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indicating that these entries could be exploited for solving malnutrition problem in developing country like India. Thus aforesaid these grass pea varieties appeared the most promising.

To conclude the present study conducted in four environments at two locations in two years based over various estimates viz. variability parameters, correlations, path analysis and stability parameters. Grass pea varieties I-30, L-08 and I-22 appeared to be the most promising for seed yield as they were not only stable but also had high per se for pods per plant, 100-seed weight and branches per plant. Among these, R-29, I-22, R-33 and L-07 also possessed high protein content. The results so obtained were critically discussed to give an impetus to grass pea breeding programme. Thus, stability of seed yield per plant in L-08 and I-30 varieties was imparted by the stability of its component characters like pods per plant, seeds per pod, 100-seed weight, days to flower and days to maturity.

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INTRODUCTION

Grass pea [*Lathyrus sativus* (L.)] belongs to family Leguminosae and sub family *Palilionoideae*. It is a self-pollinated crop with 2n = 14 chromosomes and is native of South Europe and West Asia. It commonly known as Khesari or chickling vetch, is also called Teora in Hindi, Khesari in Bengali and Kisara in Nepali.

Grass pea is grown during winters in India, Iran, Nepal, Bangladesh, Middle East and Southern America and Europe. At global level it is a minor crop while in some countries like Bangladesh and Nepal, it is a major one. In India it occupies 1.6 mha with annual production of 0.58 m tonnes which accounts for 4.0% of the total area and 0.3% of total pulse production of the country. An average crop at the seed rate of 40 kg per ha yields about 925 kg per ha of pulse and 3.2 tones per ha of forage in India (FAO, 2001). In India grass pea is grown in the plains as well as in the hills up to an altitude of 1220 m. The major area of *Lathyrus* lies in the region of Indo-gangetic plains, Chhatisgarh, Madhya Pradesh, Bihar, Uttar Pradesh, Maharashtra, Orissa and West Bengal. Although its output is highest in Madhya Pradesh, but its yield is higher in Bihar and West Bengal (Rathore *et al.*, 2003).

Grass pea is a drought hardy grain legume rich in proteins and possesses good qualities of essential amino acids. However, Government of India has imposed a ban on its cultivation and sale since 1961 because the seeds contain a neurotoxin 3-N-oxalyl-2,3-diaminopropionic acid or beta-ODAP which causes *Lathyrisum* in human beings when its dal is consumed in larger quantity for a longer period of time (Roy *et al.*, 1963). The varieties generally have low yield potential, poor plant type and high neurotoxin content which instable over environments (Ramanujan *et al.*, 1980). The seeds containing less than 0.2% ODAP are safe for human consumption but it has 0.1 – 2.5% ODAP (Grela *et al.*, 2000).

It is generally cultivated as a relay crop locally called *Paira* or *Utera* viz., broadcasting *Lathyrus* seeds in standing rice crop 7-10 days before harvesting (Dutta *et al.*, 1999). It is also grown as mixed/intercrop with mustard, barley and gram. *Lathyrus* is raised on the residual moisture. It is tolerant to adverse climatic conditions and can be grown on the lands which are suited to no other pulse crop.

The main drawback of Khesari is the anti- nutritional factor *Lathyrogen*, which can be overcome through several detoxification methods viz., stepping the dehusked seed overnight and boiling for 30 minutes removes all toxic substances, or roasting the seeds at 140°C for 15-20 minutes, or par boiling of seeds also make its seeds free of neurotoxin, or spraying of certain micronutrients like cobalt nitrate (0.5 mg per litter) and ammonium molybdate (20 mg

per litter) at flowering reduced ODAP content by 33 and 19 per cent, respectively (Rathore *et al.*, 2003). Later on ICAR appointed high powered committee which found that there was no incidence of paralysis due to this pulse crop (Singhal, 2003).

The dried seeds of *Lathyrus* contain 31.9% protein, 53.9% carbohydrates, 0.9% oil and 3.2% ash (Rajendra, 2002). The seeds can be used in dal preparation and bread making. These are made into paste balls, put in curry, or boiled and eaten like a pulse. It can be used in making local beverages and its leaves can be used as a post herb and vegetables after boiling. Seeds are dehusked and parched before use (Kay, 1979). Plants are also valued as green manure. Seeds are used as a nutritive feed for poultry and live stock. Primarily grass pea is cultivated as cold weather forage crop. Oil from seeds is a powerful and dangerous cathartic that contains a poisonous salt (3-N-oxalyl-2,3-diaminopropionic acid)of phytic acid. The seeds are used locally in homeopathic medicine (Duke, 1981). The pulse is also reported to be widely used in adultering masoor dal because of its marked resemblance (Singhal, 2003).

The crop has a little area in Rajasthan but due to its drought tolerance capacity, it can be successfully grown in marginal undulated hilly conditions as a rainfed crops during winter season. Rajasthan has frequent famines and under such situations this crop can thrive well in areas of wasteland where nothing grows. Hence this crop not only provides good economic returns but will also improve the soil fertility, being leguminous in nature. So far no systematic work has been done in Rajasthan with respect to varietal evaluation of *Lathyrus*.

The genetic improvement in a crop is primarily conditioned by the nature, magnitude and interrelation of genotypic and non genotypic variation of plant characters. Seed yield as well as the quality characters are polygenic in nature and influenced by environment. Information on association of component characters with seed yield and among themselves and the extent to which they are influenced by the environment should be known. Further, characterization of genotype – environment interaction is immensely helpful and leads to successful evaluation of stable genotypes which could be used in future breeding programme.

Therefore keeping aforesaid consideration in view, the present study was undertaken by growing sixteen diverse varieties/strains of grass pea in two crop seasons at two locations with following objectives:

1) To estimate various variability parameters for seed yield, its components and seed protein content.
2) Correlation and path analysis for seed yield, its components and seed protein content, and
3) Estimation of genotype – environment interaction and stability parameters over four environments.

Based on the study of superior *Lathyrus sativus* L. variety for seed yield, its components and seed protein content were identified for different environmental situations.

REVIEW OF LITERATURE

The genetic improvement of crop can be achieved by breeding high yielding varieties with the improved quality. A detailed knowledge of nature and magnitude of genetic variability and its heritable portion in economic traits and information regarding inter-relationship among the component characters and direct and indirect contribution of important characters towards yield are the prime requisite of any efficient breeding programme. Studies on genotype-environment interaction lead to successful evaluation of stable genotype which could be used in the breeding programme. Thus present investigation was conducted to estimate variability parameters, correlation, path coefficient analysis and stability parameters for yield, its components and seed protein content in grass pea [*Lathyrus sativus* (L)]. The information regarding present investigation has been reviewed under following heads:

1. Variability parameters
2. Correlation and path coefficient analysis, and
3. Stability parameters

1. Variability Parameters :

A detailed study of the extent of variability for grain yield and its contributing characters is the prime requisite for an efficient breeding programme. The magnitude of variability may be measured by genetic variance into three components (a) additive genetic variance, (b) dominance components, and (c) epistatic component. Accordingly additive genetic variance can be exploited for genetic advance through selection. Grain yield as well as protein content are complex characters being governed by different kinds of gene actions and are highly influenced by environment. Environment plays an important role in expression of a phenotypic and the genetic factors are inferred from phenotypic observation. Hence, the observed variability can be divided into heritable and non-heritable variations. Information about these genetic parameters can be obtained through the parameters like genotype coefficient of variation (GCV), heritability (broad sense) and genetic gain. This would help the breeder in developing and formulating selection programme for genetic improvement of crop plant.

Islam *et al.* (1989) assessed 23 strains of grass pea for 7 yield related characters. The highest phenotypic and genotypic coefficient of variation was obtained for pods per plant followed by seed yield per plant and branches per plant. Pods per plant, 100-seed weight and

branches per plant were estimated to have a high heritability and pods per plant were calculated to have the highest potential of genetic advance.

Deshpande *et al.* (1992) reported genotypic variability in the neurotoxin beta –N-Oxalyl-amino-L-alanine (BOAA), condensed tannins and phenolics, and protein inhibiters of trypsin, chymotrypsin and alpha-amylase in 100 lines of *Lathyrus sativus* (L.).

Dixit *et al.* (1995) reported the variability in protein content and its association with 100-seed weight, days to flowering and days to maturity in 19 exotic and 7 indigenous lines of *Lathyrus* (24 *L. sativus* and 2 *L. cicera* lines). Range and mean for protein content were higher in the exotic lines, while coefficient of variability was higher in the indigenous lines.

Kumari *et al.* (1995) determined genetic variability and heritability for 12 characters in 16 genotypes of *Lathyrus sativus* (L.). Heritability values were generally higher in the low-ODAP genotypes.

Kumar *et al.* (1996) determined coefficients of variability for yield and its components at phenotypic, genotypic and environmental levels in 25 induced mutants of grass pea. Yield per plant, pods per plant and seeds per plant were more variable than the other traits studied.

Panday *et al.* (1997) reported variability for 13 yield components, including seed yield and ODAP (beta-N-Oxalyl-L- alpha –beta-diamino propionic acid) content in 1187 accessions of *Lathyrus sativus* (L). A wide range of variability was observed for all the traits, indicating opportunities for selection.

Kumari and *et al.* (1997) studied genetic variability and heritability derived from data on 7 different characters in 15 populations of *Lathyrus sativus* (L.). Seed yield per plant, pods per plant and 100-seed weight showed considerable variation as revealed by high phenotypic and genotypic coefficients of variation. High narrow sense heritability accompanied by high genetic advance was observed for pods per plant.

Pandey *et al.* (2002) evaluated 126 genotypes of grass pea for 15 characters including neurotoxin (ODAP) content. High magnitude of GCV was noted for grain yield, pod per plants and seeds per pod. High heritability coupled with high genetic gain was found for branches per plant, pods per plant, 100-seed weight and ODAP content.

Rybinski (2000) recorded wide variability for pods per plant, seeds per pod, 100-seed weight and seed yield per plant of two polish cultivars of *Lathyrus sativus* (L.).

Mitra *et al.* (2001) reported variability for pods per plant, seeds per pod, 100-seed weight and yield per plant in two grass pea crosses viz., RED X P 28 and RED X EC 242692 up to the F_5 generation through single seed descent, pedigree and random bulk methods. The single seed descent method proved to be superior over the others for high variability.

Sharma *et al.* (2001) reported higher magnitude of genetic variability among 270 genotypes of grass pea. The coefficient of variations for pods per plant, seed yield per plant, neurotoxin content (ODAP), plant height, 100-seed weight and branches per plant were high. Maximum variability was observed for seed yield per plant followed by pods per plant, ODAP (beta-N-Oxalyl-L- alpha–beta-diamino propionic acid) content, plant height and 100-seed weight indicating that selection for these traits may lead to development of desirable genotypes.

Pandey *et al*. (2002) investigated 4 grass pea crosses viz., BioL-203 X BioL-222; BioL-203 X RLS-9; BioL-222 X BioR-231 and BioL-222 X Pusa-24 to study the genetics of seed yield and neurotoxin (ODAP) content. Both additive and dominance components in general were significant for almost all the traits except days to flowering, seed size and ODAP content.

Wuletaw *et al.* (2002) determined morphological variability in 50 land race population of grass pea for plant and yield characters. Phenotypic coefficient of variation (PCV) was slightly higher than genotypic coefficient of variation (GCV) for all the characters signifying that genotypic factors exerted reasonable effect in estimating the variation. The wide difference between PCV (22.4 %) and GCV (13.0 %) for seed yield per plant indicated the complexity of this trait and the important role of other factors such as environment in influencing yield potential in addition to the genetic factors.

Polignano *et al.* (2003) evaluated 280 entries represented by *Lathyrus sativus* (L.), *L. cicera* and *L. ochrus* for 18 quantitative and qualitative descriptors. The presence of high diversity within the *Lathyrus sativus* (L.) and *L. cicera* confirmed the use of both species as valuable sources of genetic material for grass pea improvement.

Amarshettiwar *et al.* (2004) evaluated 11 genotypes of *Lathyrus sativus* (L.) to study the comparative performance under drilled and Utera conditions in rice based cropping system. Drilled sowing method gave the highest emergence count, plant height, days to flowering, days to maturity, pods per plant, 100-seed weight and seed yield, irrespective to cultivars.

2. Correlation and Path Coefficient Analysis :

Correlation studies are important in framing selection programme. Further, path coefficient analysis (simple standardized partial regression analysis) breaks correlations between traits into their direct and indirect effect, thereby permitting a critical examination of specific forces acting to produce a given correlation and measures the relative importance of

each casual factor. Path analysis was initially suggested by Wright (9121) but was applied for first time in plant breeding by Dewey and Lu (1959).

Microshnichenko *et al.* (1979) studied 436 genotypes of *Lathyrus sativus* (L.) for 11 characters, including yield components. The closest correlation was found between pods per plant and seeds per pod which are also closely correlated with branches per plant.

Sethi *et al.* (1981) evaluated 60 land races of *Lathyrus sativus* (L.) for beta-N-Oxalyl-aminoalanine (BOAA) content and 100-seed weight and recorded significant positive correlation between BOAA content and 100-seed weight.

Kavuncu *et al.* (1985) studied 10 ecotypes of grass pea for seed yield and 8 related traits. Branches per plant was significantly correlated with seed yield per plant.

Somaroo (1988) evaluated 397 accessions of of *Pisum sativum, Vicia sativa, Lathyrus sativus (L.), Medicago aculeate* and *M. rigidula* and found positive and significant correlation coefficient between dry matter yield and seed yield per plant.

Kolotilov *et al.* (1991) studied 750 accessions of *Lathyrus sativus* (L.) for seed yield, pods per plant, seed size, seed protein content and shoot growth period. Coefficients of variation for various economic characters showed correlation with notable seed yield.

Kumari *et al*. (1995) determined yield correlations from data on 12 characters in 16 genotypes groups of *Lathyrus sativus* (L.). Correlation analysis from pooled data showed that seed ODAP content was positively correlated with biomass per plant, plant height, flowers per plant, pod length and seed size, and was negatively correlated with yield per plant.

Kumar and dubey (1996) reported correlation between yield and its component in 25 induced mutants of grass pea. Yield per plant, pods per plant and seeds per plant showed significant positive associations among themselves**.**

Tiwari and Campbell (1996) studied parents (ie L720060, L900436 and LS82046), F_1 and F_2 progenies of grass pea. The F_1 and F_2 progenies had intermediate seed weights. 100-seed weight and seed yield were positively correlated with each other.

Waghmare *et al.* (1996) reported genetic divergence and yield correlations from data on 8 yield components in 50 genotypes of *Lathyrus sativus* (L.). Pods per plant, plant height, seeds per pod and 100-seed weight had significant and positive correlation with seed yield whereas days to 50% flowering had a negative correlation with seed yield. Path analysis revealed that pods per plant and 100-seed weight had large positive and direct effects on seed yield while the remaining characters exhibited direct negative effects on seed yield.

Sharma *et al.* (1997) while evaluating 80 genotypes of grass pea indicated that ODAP content and 100-seed weight were negatively correlated with each other, while 100-seed showed positive correlation with days to maturity.

Sharma and Yasin (1997) evaluated 10 grass pea genotypes for seed and seedling vigour. Seedling growth rate exhibited positive significant correlation with seedling dry weight.

Mitra and Mehra (1999) studied F_3, F_4 and F_5 progenies of 2 crosses of grass pea for yield and its components. Significant and positive correlations among F_3, F_4 and F_5 progenies in all three possible combinations were observed only for pods per plant.

Pandey *et al.* (2000) reported that grain yield was positively associated with days to maturity, plant height, branches per plant, pods per plant and seeds per plant in grass pea.

Sabanci and Ozpinar (2000) evaluated 15 genotypes of grass pea [*Lathyrus sativus* (L.)] for days to flowering, 100-seed weight, seed and biomass yield. 100-seed weight was correlated with maximum seed and biomass yield.

Zode *et al.* (2000) reported correlation coefficient for morpho-physiological, biochemical and yield related traits such as seeds per pod, pods per plant and seed yield per plant in 10 genotypes of *Lathyrus sativus* (L.). Seed yield showed positive correlation with seeds per pod and pods per plant.

Chauhan *et al.* (2001) studied correlation in 17 characters of lentil genotypes. Seed yield was positively correlated with number of secondary branches per plant, plant spread and number of fruiting nodes per plant.

Das and Kundagrami (2001) reported that 100-seed weight was significantly negative correlated to ODAP content indicating that large seed size had low ODAP content. Exotic Bold and P-28 grass pea genotypes had large flower size, high 100-seed weight and low ODAP content.

Das and Kundagrami (2002) evaluated 9 grass pea [*Lathyrus sativus* (L.)] genotypes for pods per plant, seeds per pod, 100-seed weight, days to flowering, seed protein content and seed yield per plant. Pods per plant and seeds per pod showed negative association with seed yield per plant. A negative correlation was also observed between 100-seed weight and protein content. Days to flowering and days to maturity maintained a positive correlation with seed protein content.

Kundagrami and Das (2002) evaluated 9 genotypes of grass pea to investigate relationship between seed characters and protein content. The correlation between seed size

and protein content showed that 100-seed weight was significantly and positively correlated with protein content indicating that large and bold seed has higher protein content.

Tadesse and Bekele (2002) studied land race populations of grass pea to determine morphological characters association. The strong positive association of pods per plant, 100-seed weight and primary branches per plant with seed yield indicated the possibility of selecting lines for yield improvement based on these characters at the very early stage of breeding programme.

While analysing correlation and path coefficient in grass pea [*Lathyrus sativus* (L.)], Das *et al.* (2002) reported that pods per plant and seeds per pod showed consistent high positive correlation both at phenotypic and genotypic levels with seed yield per plant. However, 100-seed weight showed negative association with seed yield. Significant positive correlations were observed between pods per plant and seeds per pod, and days to flowering and maturity, while negative correlations were observed between pods per plant and 100-seed weight, pods per plant and days to flowering, and pods per plant and days to maturity.

Wuletaw *et al.* (2003) studied 50 grass pea race populations. The association of ODAP with grain yield, plant height and seed size was negative, suggesting that the selection of tall and late maturing varieties with large seed size and high grain yield potential would enable the development of varieties with low ODAP content.

Polingnano *et al.* (2005) reported that there was no significant correlation between beta-ODAP and other morphological traits.

3. Stability Analysis :

The phenotypic response for a change in environment may not be the same for all the genotypes. Thus interplay in the effects of genetic and environmental factors on development is called genotype-environment interaction. The genotype-environment interaction signifies that the relative performance of various genotypes is affected by environment. The performance of all the genotypes may not be influenced by the environment to some extent. A specific change in environment may have a greater effect on some genotypes than the others. The magnitude of genotype-environment interaction can be estimated by growing the experimental material over a number of years, locations, controlled conditions, growth conditions and different cultural practices.

The phenotypic stability may be defined as the ability of a genotype to produce a narrow range of phenotypes in different environments. Phenotypically stable varieties are desirable for commercial production of crop plants. In a breeding programme, it is also important to screen and identify the phenotypically stable genotypes which could perform

more or less uniformly under environmental conditions. Stability studies are not only important in finding out the most stable genotypes for varied environmental conditions but are also equally useful in screening the different genotypes for their comparative performance under a particular set of environment. Lewis (1955) measured the phenotypic stability in terms of a stable factor (SF) calculated as

$$SF = \frac{Mean\ performance\ in\ high\ yielding\ environment}{Mean\ performance\ in\ low\ yielding\ environment}$$

However, a better way of ascertaining phenotypic stability was given by Finlay and Wilkinson (1963). They considered linear regression slope as a measure of stability. Eberhart and Russell (1966) emphasized the need of considering both linear (b) and non-linear (S_2d) component of genotype-environment interaction in judging the stability of genotypes. Breese (1969) and Paroda and Hayes (1971) advocated that linear regression could simply be regarded as a measure of response of a particular genotypes, where as the deviation around the regression line was considered as a measure of stability, genotypes with the lowest deviation being the most stable.

Dahiya and Jeswani (1974) investigated 18 varieties of *Lathyrus sativus* (L.) for seed yield and its components over 12 environments. The differences in mean performance of the different varieties were significant only for 100-seed weight. Varieties with above average phenotypic stability were generally low in mean yield and those with below average gave above average yield. 5 varieties gave a high yield combined with maximum phenotypic stability. Stability for seed yield per plant was positively correlated with stability for pods per plant and 100-seed weight. Krarup (1983) reported stability for *Lathyrus sativus* (L.) in 5 different sowing dates and 3 sowing densities.

El-Moneim and Cocks (1993) studied 16 promising races of *Lathyrus* spp. comprising 11 *L. sativus* (L.), 4 *L. ochrus* and 1 *L. cicera* under rainfed conditions. Two locations in each of 4 years were treated as separate environment to give 8 environments altogether. There was considerable variation in herbage and seed yield within both lines and environments. The most stable herbage and seed yields were obtained from *L. sativus* (L.).

Angelova and Yancheva (1995) studied 2 varieties of each of the crops winter and spring pea, *Lathyrus sativus* (L.), *Lupinus albus* and *Vicia ervilia.* The varieties of *V. ervilia* and *L. sativus* (L.) showed high stability for drought resistance and seed yield per plant.

Sharma *et al*. (1997) reported stability of 80 grass pea varieties grown over 3 years for ODAP content, days to maturity, 100-seed weight and seed yield per plant. Varieties RLS1 and LSD3 showed high stability for low ODAP content while selections 505 and JRL 115 for 100-seed weight.

Albelwafa *et al.* (1999) revealed highly significant differences among genotypes, environment and G X E interaction for plant height, seeds per pod, pods per plant and seed yield per plant of *Lens culinaris* (Medik). Stability parameters for the genotypes in 12 environments confined the fact that high yielding genotypes are more likely to have lower stability and vice versa.

Hunberry *et al.* (1999) evaluated 407 and 96 genotypes of *Lathyrus sativus* (L.) and *Lens cicera* (Medik), respectively for phenology and seed yield over 3 environments to examine genotype-environment interactions on seed yield and ODAP concentration in the seed of the two *Lathyrus* species. Genotype-environment interactions had no effect on seed ODAP concentrations. In terms of seed yield, both species showed substantial potential in the environments tested.

Siddique *et al.* (1999) studied the adaptation of grain legumes by measuring crop phenology, growth and yield at total of 36 environments over 3 seasons, with the aim of identifying species with suitable adaptation and seed yield for specific environments.

Jones and Singh (2000) estimated stability in terms of mean seed yield per plant, production stability and yield trends of four relations of barley with vetch (*Vicia sativa* and *Lathyrus sativus* (L.) in two different environments over two years.

Maler *et al.* (2000) evaluated environmental conditions under which grass pea [*Lathyrus sativus* (L.)] is grown and assessed for days to 50% flower, days to maturity, pod length and seeds per pod. It was concluded that grass pea could be grown after harvesting of lowland, rain fed rice. Low toxin, bold-seeded and high yielding varieties suitable for relay cropping and dual-purpose varieties were considered priorities for breeding programme.

Kumari (2000) reported stability for 10 grass pea genotypes for 5 yield components and low ODAP content over two years.

Solanki (2001) evaluated 72 genotypes of lentil for stability analysis of seed yield and its components. The stability of genotypes for grain yield in the superior or inferior environment was impaired by the stability of different yield contributing traits.

Kumari (2001) studied 18 land races of grass pea for days to flowering, days to maturity, pods per plant, seeds per pod, 100-seed weight and seed yield. Environment played a major role in developing genetic variation for seed yield. Partitioning of genotype-environment interaction into its linear (G X E linear) component showed that the linear responses of genotype to environments differed significantly for days to flowering, pods per plant and seeds per pod. The genotype LSP-6 and LSP-7 could be considerable as stable genotypes with predictable performance for more seeds per pod as they showed stable response over the environmental variation.

Tadesse (2003) studied 20 grass pea genotypes over two years and reported that ODAP content is significantly affected by both the genotypes and environmental components. Stable genotype for seed yield per plant may not be stable for ODAP content and vice versa.

Mundada *et al*. (2004) evaluated 8 *Lathyrus sativus* (L.) genotypes for their morph-physiological characteristics under two different environments. The effect of location was non-significant for root nodules and leaf area at 90 days after sowing, but significant for leaf area at 70 DAS. The genotypes performed better and had significantly high root nodules, leaf area, seed yield and dry matter content at both locations.

Tovoletti *et al.* (2005) revealed high genetic variation among population and negligible genotype-environment interaction while studying 16 genotypes of grass pea for morphological and agronomic traits and ODAP content under two locations.

MATERIALS AND METHODS

The present investigation entitled "Stability Analysis in Grass pea [*Lathyrus sativus* (L.)]" was carried-out in 4 environments at 2 locations in viz., Rajasthan College of Agriculture, Udaipur and Agricultural Research Station, Kota. Udaipur is situated at an elevation of 582.17 metres above mean sea level on latitude 24°34' North, longitude 74°42' East while Kota is situated at latitude 24°42' North and Longitude 70°56' East.

Material and Design of Experiment :

The experimental material for the present study consisted of diverse 16 varieties/strains of *Lathyrus sativus* (L.) namely R-15, I-18, I-30, G-164, I-22, R-31, R-29, R-33, G-158, L-08, L-54, R-02, L-07, L-212, L-57 and R-09. These were obtained from Vivekanand Pravartiya Krishi Ausandhan Prayogasala, Indian Council of Agricultural Research, Almora. The hilly agro-ecological situation of Almora where this material is being grown appeared to be similar to soil-climatic-hilly-conditions of zone IV A of Rajasthan during winters. This was also one of the reasons of evaluating the germplasm of Almora region here.

These entries were planted in *rabi*, 2005-06 at Udaipur and Kota and again in *rabi*, 2006-07 at Udaipur and Kota. Each entry was sown in six row plot. Row to row and plant to plant distances were maintained as 40 cm and 10 cm at each location respectively.

The crop was raised under conserved moisture condition in each environment. Recommended and uniform agronomical and plant protection measures were followed to raise the crop in each environment. Week-wise average of meteorological data during crop growth for each environment at locations is given in Table (1, 2, 3, and 4).

The details of environments are given as under :

Details of Environments :

Environments	Location	Agroclimatic Zone	Soil type	Irrigation	Sowing season	Fertilizers application N P K
E_1	Udaipur	IV A	Lithosols	2	*Rabi*, 2005-06	20:20:0
E_2	Kota	V	Black soils	3	*Rabi*, 2005-06	20:20:0
E_3	Udaipur	IV A	Lithosols	2	*Rabi*, 2006-07	20:20:0
E_4	Kota	V	Black soils	3	*Rabi*, 2006-07	20:20:0

Characters Studied :

Observations were recorded on ten randomly selected plants of each variety in each replication for each environment. The detailed procedure adopted for recording eight morphological/agronomical and one biochemical quality characters is given below:

(A) Morphological/Agronomical Characters :

1. **Days to flower –** Data on which 50 per cent of plants in each plot showed flowering initiation were noted and from sowing date, days required for flowering were estimated.
2. **Days to maturity –** Number of days to attaining maturity of 75 per cent plants per plot (pods turned dark golden brown to yellow in colour) were counted.
3. **Plant height –** Height of the plants was measured in centimeters from the ground level to the top of the plant at the time of maturity.
4. **Branches per plant –** Number of branches were counted from ten randomly selected plants for each line and averaged.
5. **Pods per plant –** Total number of fully matured pods on ten plants were counted and average to obtain pods per plant.
6. **Seeds per pod** - Number of seeds were counted in 10 randomly selected pods and averaged.
7. **100 – Seed Weight –** The weight of 100-seeds from the produce of each line in each replication was recorded on Electronic Single Pan Balance in grams..
8. **Seed yield per plant –** Total seeds of each plant were weighed in grams on Single Pan Electronic Balance

(B) Biochemical Analysis :

Bulk seeds of ten plants of each entry from each replication only for E_1 and E_3 (Udaipur location) were taken for the purpose of biochemical analysis. These seeds were crushed and the flour was used for estimating seed protein.

9. **Seed protein content –** Nitrogen content of seeds was estimated in duplicate by the standard micro kjeldahl method. Value of N so obtained were converted to crude protein percentage by multiplying with a factor 6.25 (Appendix-I)

Statistical Methodology :

The data recorded for all aforesaid quantitative and quality characters were analysed to get plot means. A brief outline of different statistical calculations studied is mentioned below :

i. Analysis of variance

To test the variation among the treatments under each location analysis of variance was carried out as per standard methodology in individual as well as pooled over four environments. Skelton ANOVA is given as under :

Source	d.f.	S.S.	MSS	Expected MSS
Replication	(r – 1)	a	al	$\sigma^2e + \sigma^2r$
Genotype	(g– 1)	b	bl	$\sigma^2e + \sigma^2g$
Error	(r – 1)(g – 1)	c	cl	σ^2e
Total	r.g - 1			

Analysis of variance pooled over environments

Source of variation	d.f.	S.S.	M.S.	Expected M.S.
Environment	(s-1)	SS_1	M_1	$\sigma^2 + r\sigma^2_{GE} + glr\sigma^2_E$
Rep./Env.	s(r-1)	SS_2	M_2	$\sigma^2 + g\sigma^2_R$
Genotype	(g-1)	SS_3	M_3	$\sigma^2 + r\sigma^2_{GE} + rs\sigma^2_G$
G x E	(g-1)(s-1)	SS_{15}	M_{15}	$\sigma^2 + r\sigma^2_{GE}$
Pooled error	s(g-1)(r-1)	SS_{27}	M_{27}	σ^2

where,

r = number of replication, and

g = number of genotypes

Standard error for differences between treatment means was Calculated as

$$SE(diff.) = \frac{\sqrt{2\,EMS}}{r}$$

Where, EMS = Error mean sum of square for the experiment, and

r = number of replication

Coefficient of variation was calculated as

$$CV = \frac{\sqrt{2\,EMS}}{\overline{X}} \times 100$$

Where, CV = coefficient of variation, and

$\overline{X}$ = population mean

ii. Estimation of variability parameters :

(a) Genetic variability: It is the variance contributed by genetic causes or the genetic occurrence of difference among the individuals due to their genetic make up. It was calculated by using formula given by Panse and Sukhatme (1978).

$$Vg = \frac{MSV - Ve}{r} = \frac{bl - cl}{r}$$

Where, V_g = Genotypic variance

MSV = Mean sum of square for varieties,

Ve = Error variance, and

r = Number of replication

(b) Phenotypic variability: It is the sum of variances contributed by genetic causes and environmental factors and was computed as :

$$V_{ph} = V_g + Ve$$

where, V_{ph} = Phenotypic variance,

V_g = Genotypic variance and

Ve = Error variance

(c) Genotypic coefficient of variation (GCV): The magnitude of genetic variation existing in a character was estimated by the formula given by the Burton (1952) :

$$GCV = \frac{\sqrt{Vg}}{\overline{X}} \times 100$$

Where, V_g = Genotypic variance, and

$\overline{X}$ = Population mean of the character

(d) Phenotypic coefficient of variation (PCV): The magnitude of phenotypic variation existing in a character was estimated by using the following formula (Singh and Choudhary, 1979):

$$PCV = \frac{\sqrt{Vph}}{\overline{X}} \times 100$$

Where, V_{ph} = Genotypic variance, and

$\overline{X}$ = Population mean of the character

(e) **Heritability:** It is the proportion of total variability which is heritable in nature. It was estimated in broad sense by using following following suggested by Burton and De Vane (1953) and Johnson *et al.* (1955).

$$h = \frac{Vg}{Vph} \times 100$$

Where, h = Heritability in broad sense,

Vg = Genotypic variance, and

V_{ph} = Phenotypic variance

(f) **Genetic gain:** It is the percentage of expected genetic advance based on the mean of a compound using following formula suggested by Johnson *et al.* (1955).

Genetic gain (genetic advance as percentage of mean)

$$= \frac{GA}{\overline{X}} \times 100$$

Where GA = Genetic advance is the shift in a population towards superior side under some selection pressure. It was measured by the following formula suggested by Lush (1949) and Johnson *et al.* (1955) at 5 per cent selection pressure using the constant K as 2.06 given by Allard (1960).

$$GA = K \frac{\overline{X}}{\bar{i}} \frac{Vg}{Vph} \frac{\overline{X}}{\bar{i}} \sqrt{Vph}$$

Where, Vg = Genotypic variance,

Vph = Phenotypic variance,

K = Selection differential at 5 per cent and

$\overline{X}$ = Population mean of the character under study

iii. Correlation coefficients :

Genotypic and phenotypic correlation coefficients of seed yield with its contributing characters namely days to flower, days to maturity, plant height, branches per plant, pods per plant, seed per pod, 100-seed weight, seed protein content and seed yield per plant and among themselves were calculated by using the genotypic and phenotypic variance and covariance values in the formula suggested by Fisher (1954) and Al Jibouri *et al.* (1958). These genotypic and phenotypic covariances were worked-out between pairs of characters with the

analysis techniques as used for variance calculation. Mean product expectations of covariance analysis are analogues of the mean square expectation of the analysis of variance.

(a) Genotype correlation coefficient :

$$r_{xy}(g) = \frac{Cov.xy(g)}{\sqrt{Vx(g).Vy(g)}}$$

(b) Phenotypic correlation coefficient :

$$r_{xy}(ph) = \frac{Cov.xy(ph)}{\sqrt{Vx(ph).Vy(ph)}}$$

Where,

$r_{xy}(g)$	=	Genotypic correlation between x and y traits
$r_{xy}(ph)$	=	Phenotypic correlation between x and y traits
Cov. xy (g)	=	Genotypic covariance for x and y traits
Cov. xy (ph)	=	Phenotypic covariance for x and y traits
$V_x(g)$	=	Genotypic variance for x traits
$V_y(g)$	=	Genotypic variance for y traits
V_x (ph)	=	Phenotypic variance for x traits
V_y (ph)	=	Phenotypic variance for y traits

The significance of correlation was tested by formula –

$$t = \frac{r}{\sqrt{1-r^2}}.\sqrt{n-2}$$

Where,

r	=	Correlation coefficient
t	=	Test of significance, and
n	=	Total no. of observations.

The calculated value of ‘t’ (cal.) were tested against the tabulated values of ‘t’ with (n-2) d.f. at 0.1 and 0.5 level of significance.

iv. Path coefficient analysis :

Path coefficient can be defined as the ratio of the standard deviation of the effect due to given cause to the total standard deviation of the effect i.e. if y is the effect and x is the cause, the path coefficient for the path from cause X_1 to the effect Y_1 is $\sigma x_1/\sigma y_1$.

The principle and technique suggested by Wright (1921), Li (1955) and Dewey and Lu (1959) to assess that direct and indirect effect of 8 variables on seed yield are followed. These 8 variables were days to flower, days to maturity, plant height, branches per plant, pods per plant, seeds per pod, 100-seed weight and seed protein content and path coefficients were calculated at genotypic level only for E_1, E_2 and E_3 sets.

Nine simultaneous equations generated were presented in matrix form and solved as per procedure given below :

$r_{1\,12}$ $r_{1\,1}\, r_{1\,2}$ ……$r_{1\,8}$ $P_{1\,12}$

$r_{1\,12}$ $r_{1\,1}\, r_{2\,2}$ ……$r_{2\,8}$ $P_{2\,12}$

. ….. …

. ….. …

. ….. …

$R_{8\,12}$ $R_{8\,1}\, r_{8\,2}$ ……$r_{8\,8}$ $P_{8\,12}$

or

$A = B.C.$

Value of C vectors were obtained as $C = B^{-1}.A$

Where B^{-1} is the inverse of mutual correlation matrix of character. The inversion matrix was carried out by pivotal condensation method.

The residual effect was computed from the following algebric relationship.

$$1 = R^2 + r_{1\,12}\,P_{1\,12} + r_{2\,12}\,P_{2\,12} + r_{3\,12}\,P_{3\,12} + r_{4\,12}\,P_{4\,12} + r_{5\,12}\,P_{5\,12} + r_{6\,12}\,P_{6\,12} + r_{7\,12}\,P_{7\,12} + r_{8\,12}\,P_{8\,12}$$

$$R = \sqrt{1 - (r_{1\,12}\,P_{1\,12} + r_{2\,12}\,P_{2\,12} + r_{3\,12}\,P_{3\,12} + r_{4\,12}\,P_{4\,12} + r_{5\,12}\,P_{5\,12} + r_{6\,12}\,P_{6\,12} + r_{7\,12}\,P_{7\,12} + r_{8\,12}\,P_{8\,12}}$$

where,

R = Residual effect

v. Stability parameters :

In the present study the data obtained for 9 characters for 4 environments were analyzed to estimate the stability parameters following the model of Eberhart and Russell (1966).

According to this model a variety is said to be stable with unit regression coefficient ($b \approx 1.0$) and the deviation from regression not significantly different from zero ($S^2d = 0$) with high mean value. Eberhart and Russell used the following model to study the stability of varieties under different environments (Singh and Choudhary, 1979).

$$Y_{ij} = \mu_i + B_i l_j + \delta_{ij}$$

Where, Y_{ij} = Mean of ith variety in jth environment

μ_i = Mean of ith variety over all environment

B_i = The regression coefficient of ith variety on the environmental index which measures the response of this variety to varying environments.

δ_{ij} = The deviation from regression of the ith variety at the jth environment.

I_j = The environmental index which is defined as the deviation of all the varieties at a given location from the overall mean, and it can be obtained as the mean of all the varieties at the jth environment minus the grand mean.

$$I_j = \frac{\sum_i Y_{ij}}{V} - \frac{\sum_i \sum_{ij} Y_{ij}}{V_N} \text{ with } \sum_j \sum_i = 0$$

Where, $\sum_i Y_{ij}$ = Total of all the varieties at jth location

$\sum_i \sum_j Y_{ij}$ = Grand total

V = Number of varieties

n = Number of locations, and

δ_{ij} = The deviation from regression of ith and variety at jth location.

The two parameters of stability were computed as follows :

(a) Regression coefficient (b):

The regression coefficient is the regression of the performance of each variety under different environments on the environmental means over all the genotypes. It was estimated as follows:

$$b = \sum Y_{ij} l_j / l^2 j$$

Where, b = Regression coefficient of ith variety

$\sum_j y_{ij}$ = Sum of products of replication mean of ith variety in the varying environment with corresponding environmental index. (i.e. $\sum Y_{ij}.l_j = |X||l_j|$, and

$\sum_j l^2 j$ = Sum of squares of environmental index

(b) Mean square deviation (S^2d) from mean regression:

This parameter of stability was estimated as follows:

$$S^2 d = \frac{\sum_j ij}{n-2} - \frac{S^2 e}{r}$$

Where,

$$\sum_j \delta^2 ij = \left[\sum_j Y^2 ij - Y^2 i / n \right] - \frac{\left(\sum_j Y_{ij} I_j \right)^2}{\sum_j I^2 j} \wedge$$

$\delta^2 e$	=	The estimate of pooled error.
$\sum_j Y^2 ij$	=	Sum of square of replication mean values of ith variety over all the environments.
r	=	Number of replications
$Y^2 i$	=	Square of sum of ith variety over all environment
n	=	Number of environments

This model provides the mean of partitioning the genotype x environment interaction of each variety into two components.

(i) The variation due to response of a variety to varying environmental index (sum of squares due to regression), and

(ii) The unexplainable deviation from the regression on the environmental index.

(c) Pooled analysis of variance:

The appropriate pooled analysis of variance is given in Table 5. In this analysis, the sum of square due to location and genotype x locations are partitioned into location (linear) genotype × location (linear) and deviation from regression (i.e. pooled deviation).

The significance of the above estimates were tested as follows (Singh and Choudhary, 1979).

a) The significance of the difference among variety/genotype means i.e.

$H_o = \mu_1 = \mu_2 = \ldots\ldots\ldots\ldots = \mu_v$

It can be tested by the appropriate 'F' test

F = MS1/MS2

b) To test, that the varieties/genotypes do not differ from their regression on environmental index

$H_o = b_1 = b_2 = \ldots\ldots\ldots\ldots = b_v$

$$\text{Pooled error} = \frac{(n_i + 1)(\text{M.S. error } E_i) + \ldots + (n_i - 1)(\text{M.S. error } E_j)}{(n_1 - 1) + (n_2 + 1) + \ldots + (n_j - 1)}$$

Where, $(n_i - 1)$ = d.f. of error in environment i

$(n_j - 1)$ = d.f. of error in environment j

M.S. error E_j = M.S. due to error for j^{th} location.

It can be tested by appropriate 'F' test.

F = MS3/MS4

(c) An appropriate test of the deviation from regression for each variety was tested by

$$F = \left[\left(\sum_j \delta^2_{ij}\right) / n - 1\right] / \text{pooled error}$$

(d) To test that the individual regression coefficient (bi) do not differ from unity (Ostle, Bernard, and Richard W. Mensing, 1975) i.e.,

$H_o = b_o = 1$

It can be tested by appropriate 't' test as :

$$t = \frac{b_i - b_o}{\text{SE of } b} \text{ with } (n - 2) \text{ d.f.}$$

Where,

n = number of location

Assuming homogeneity between all individual regression coefficients SE of b in place of SE of b is used to test the significance of b where b is overall regression coefficient considering all the varieties together.

Table 5. Analysis of variance for estimating stability parameters (Eberhart and Russell, 1966)

Source	d.f.	S.S.	MS
Genotypes	(v – 1)	$1/n\sum_i y_i^2 - C.F.$	MS_1
Locations	(n – 1)	$1/v\sum_j y_j^2 - C.F.$	
Genotype × location	(v – 1)(n-1)	$1/v\sum_i\sum_j y_{ij}^{\ 2} - \sum Y_i^2/n\sum y_j^2/v + C.F.$	MS_2
Location + (Genotype x location)	v(n-1)	$\sum_i\sum_j y_i^2 - \left(\sum y_i^2/n\right) - \left(\sum y_i^2/n\right)$	
Location (Linear)	1	$1/v\left(\sum_i y\sum_j ij\right)^2 / \sum_j l^2 j$	
Genotype x location (Linear)	(v-1)	$\sum_i\left(\sum_j Y_{ij} l_j\right)^2 / \sum_j l^2{}_j - Env.\,Linear\,S.S.$	MS_3
Pooled deviation	v(n-2)	$\sum_i\sum_j \delta^2{}_{ij}$	MS_4
Pooled deviation due to genotype	(n-2)	$\sum_j Y^2{}_{ij} - (Y_i)^2/n - \left(\sum_j Y_j l_j\right)^2 / \sum_j l^2{}_j - \sum_j \delta^2{}_{ij}$	
Pooled error	n(r-1)(v-1)		

RESULTS AND DISCUSSION

An attempt has been made in the present study to estimate various genetic parameters which will not only help in framing an effective breeding programme but also result in making certain improvements in the yield levels and quality of *Lathyrus sativus* (L.). Further this would lead to successful evaluation of phenotypically stable and superior varieties which could be used for commercial production.

The results obtained in the present study are discussed here under following heads:

1. Variability parameters
2. Correlation coefficient
3. Path coefficient analysis, and
4. Stability parameters

1. Variability Parameters :

Success of a breeding programme largely depends on the extent of genetic variability present in the material, greater the diversity in the material better are the chances for evolving promising and desired types. The genetic facts are inferred from phenotypic observations which are the result of the interaction of genotype and environment. Since environment has a great influence on many quantitative and quality characters, the observed variability can be grouped under heritable and non-heritable components and this can be estimated by the parameters like genetic coefficient of variation (GCV), heritability and genetic gain. This would help the breeder in developing and formulating selection programme for the genetic improvement of crop plants.

Mean performance of the best grass pea varieties/ strains at each location as well as their consistent and high *per se* performance in all the four sets of experiments and over pooled basis for nine characters are given in Appendices II to IV. The overall performance of the varieties/strains were superior in environment E_2 followed by E_4 (both locations) at Kota, E_1 and E_3 at Udaipur. This might be on account of less winter, heavy soils of Kota and better water holding capacity of this soil. Wide range of variability was conspicuous for almost all the characters including seed yield. Varieties I-18, I-30 and R-33 exhibited high *per se*

performance for seed yield and L-08 and L-07 for 100-seed weight. Varieties R-29, I-22 and L-54 exhibited high *per se* performance for seed protein content. Over and above, I-22 and I-18 displayed superiority for seed as well as quality characters. Therefore, these entries could be gainfully utilized in breeding programme.

Analysis of variance (Table 7) revealed significant differences among the genotypes for different characters indicated presence of sufficient variability in the material.

Mean, standard error (SE), range, genotypic and phenotypic coefficient of variation (GCV and PCV), heritability (broad sense) and genetic gain (GG) analyzed for each location and over pooled basis are shown in Table 9.

The PCV estimated was slightly higher than GCV for all the characters in all the set of environments. There was little difference between PCV and GCV estimates in most of the sets for days to flowering, days to maturity indicating that the variability was primarily due to genotypic differences. On other hand, environmental influences were predominant for the remaining traits. Therefore, selection based on the days to flower, days to maturity are expected to be effective while for other traits selection must be performed carefully considering environmental factors.

High GCV and PCV were recorded for pods per plant and seed yield per plant in at least three environments and over pooled basis. So selection for these characters would be effective. Moderate GCV and PCV were in general, recorded for branches per plant and 100-seed weight for at least two environments and over pooled basis. Analysis of variance for pooled over environments, genotypes and G × E interactions showed significant differences among most of the genotypes for different characters, indicated presence of sufficient variability in the material shown in Table 8(a) and seed protein content also showed significant differences among genotypes and G × E interactions in E_1 and E_3 (Udaipur location) as depicted in Table 8(b).

High estimates of GCV were also reported by Islam *et al*. (1989) for pods per plant, seed yield per plant and branches per plant, Dixit *et al.* (1995) for protein content, 100-seed weight, days to flowering and days to maturity, Kumar *et al.* (1996) for seeds per pod, pods per plant and yield per plant, Kumari *et al.* (1997) for seed yield per plant, pods per plant and 100-seed weight, Pandey *et al.* (1997) for seed yield per plant and ODAP content, Rybinski (2000) for pods per plant, seeds per pod, 100-seed weight and seed yield per plant Wuletaw *et al.* (2002) for seed yield per plant and its components.

However, characters like days to flower, days to maturity and seed protein content showed comparatively low estimates of GCV and PCV indicated that these characters were highly influenced by the location/environmental effects.

Estimates of genotypic and phenotypic coefficient of variation alone do not assess the amount of heritable variation which in turn can be estimated by heritability. High heritability in broad sense (above 80%) was recorded for days to flower for two environments and over pooled basis. Seed yield per plant, branches per plant, pods per plant and seeds per pod had high heritability in at least one environment. Similar findings for one or other characters were also reported by Wuletaw *et al.* (2002), Kumari *et al*. (1995), Vedna *et al*. (1997) and Pandey *et al.*(2000) in grass pea.

Burton (1952) suggested that GCV along with heritability estimates would give a better idea about the efficiency of selection as it simply depicts the amount of genetic variation while heritability measures the proportion to which the variability of a character is transmitted to its progenies. However, Johanson *et al.* (1955) suggested that variability and genetic advance when calculated together would become more useful in predicting the resultant effect of selection on phenotypic expression.

While assessing the over all situation over environments and pooled basis, the present study revealed high estimates of genetic advance as percentage of mean (genetic gain) along with high estimates of heritability and GCV for pods per plant and seed yield per plant in at least three environments. Characters like plant height, branches per plant, 100-seed weight showed moderately high GCV and genetic gain with high heritability in at least two environments. Similar to the present findings high estimates of GCV, heritability and genetic gain were also reported by Kumari *et al.* (1997) for pods per pant, 100-seed weight and seed yield per plant, Islam *et al.* (1989) for pods per plant, 100-seed weight and branches per plant, Pandey *et al.* (2000) for pods per plant, seeds per pod and seed yield per plant.

Characters like days to maturity and seed protein content exhibited low estimates of GCV and genetic gain with moderately high heritability, hence these characters seemed to be greatly affected by location effects and strong evaluation programme might result into their exploitation.

Therefore, characters like pods per plant, seed yield per plant and seeds per pod might be exhibiting predominance of additive gene effects. The single seed descent proved to be superior over the others for high variability. Thereby selection for these traits would be effective for genetic improvement of seed yield in grass pea as also advocated by Pandey *et al.* (2002) and Singh *et al.* (2003). While 100-seed weight and seeds per pod were not

effective for genetic improvement of seed yield as advocated by Islam *et al*. (1989) and Kumari *et al.*, (1997).

2. Correlation Coefficient :

The knowledge of genetic correlation for seed yield, its components and various quality characters become very important when the breeder is confronted with problems of combining high yield potential with desirable agronomic and quality parameters. Association studies would provide reliable information on nature, extent and direction of selection.

Genotypic and phenotypic correlation coefficient of different characters with seed yield, and among themselves was estimated in the present study for each location using variance techniques.

Table 10 clearly indicated that, in general, a close agreement existed between genotypic and phenotypic correlation for at least 8 characters in E_1 and E_3, 7 characters in E_4 and 3 characters in E_2 environment. It was further noticed that almost all characters exhibited slightly higher genotypic correlation in comparison to their corresponding phenotypic correlation in all the sets of experiments. This revealed that the environmental factors affected both variables taken at a time at random indicating lack of correlation at environmental level.

In the present study as obvious from Table 10 seed yield per plant was positively correlated with branches per plant at genotypic level in E_4 environment. Pods per plant showed significant positive genotypic correlation with days to maturity and branches per plant. Seeds per pod showed significant positive correlation with branches per plant and pods per plant at least one environment.

Variable results were observed with respect with mutual correlations between different characters in all the four environments and over pooled basis [Table 10]. Pods per plant and seeds per pod, showed association with each other in E_3 environment Branches per plant showed genotypic correlation with days to maturity in E_1 and plant height and days to flower in at least one environment.

Seed protein content showed significant positive genotypic correlation with plant height and seed yield per plant in E_3 and branches per plant in E_1 as also reported by Kundarami and Das (2002).

Seed yield per plant showed significant and negative association with plant height, branches per plant and days to maturity in at least one environment at genotypic level as also reported by Sharma *et al.* (1997) and Das and Kundagrami (2002) in grass pea.

On the basis of association studies, it could be concluded that seed yield per plant in grass pea was correlated with days to maturity, plant height and branches per plant in at least one environment. Most of these characters were also mutually correlated. Hence simultaneous selection for all these would result in the genetic improvement of seed yield in grass pea.

3. Path Coefficient Analysis :

Information obtained from correlation studies does not provide a clear picture of contribution of each component characters. At the same time as more variables are included in association studies, the direct associations become complex and important. Under such situations path coefficient analysis has been useful in partitioning direct and indirect causes of correlation and allows a detailed examination of specific forces acting to produce a given correlation. Path analysis at the same time also measures the relative importance of each causal factor. Hence this study provides a realistic basis for allocation of weight age to each attribute in deciding a suitable criterion for genetic improvement.

Path coefficient were computed for seed yield per plant using genotypic correlation only for three environments at two location in two years [Table 11]. The characters analyzed for this study were days to flowering, days to maturity, plant height, branches per plant, pods per plant, seeds per pod and 100-seed weight.

As observed from correlation study branches per plant, plant height and days to maturity were associated with seed yield at genotypic levels in at least one environment.

However, Table 11 reveals direct and indirect contribution of component traits on seed yield per plant. Maximum direct effects on seed yield were recorded by plant height in E_3 environment followed by seeds per plant in E_1 and E_3 environments and pods per plant in E_1 environment as also reported by Waghmare *et al.* (1996). These characters showed positive genotypic correlations and high direct effects because of their indirect contribution through one another and also through 100-seed weight, plant height, protein content in at least one environment.

Days to flowering also showed positive indirect effect with branches per plant and pods per plant in E1and E3 environments. Plant height showed positive indirect effect with days to flower, branches per plant, pods per plant, seeds per pod, 100-seed weight and protein content in at least one environment. Pods per plant and seeds per pod also showed positive indirect effect with branches per plant in at least one environment and 100-seed weight with branches per plant in at least two environments.

Characters like seeds per pod plant height and branches per plant showed negative indirect effect with protein content in E_1 environment. Negative effects of plant height were on account of indirect contribution to majority of characters towards negative direction and its insignificant association with seed yield.

Therefore, on the basis of path coefficient analysis seeds protein content contributed to seed yield indirectly with negative effect. Further, on the basis of variability parameters, correlations and path analysis pods per plant, seeds per pod and branches per plant turned out to be the most important contributing traits for enhancing yield in grass pea as they showed high to moderate GCV as well as high heritability at all the environments. Hence due emphasis should be given to these traits.

4. Stability Parametrs :

Phenotypically stable varieties are usually sought for commercial production of crop plants. In breeding programme also it is necessary to screen and identify phenotypically stable genotypes. Stability of a genotype refers to its performance with respect to changing environmental factors over time with given environments. Several workers have emphasized the importance of evaluating the materials under more than one environment to get information on the relative magnitude of components of variance. The interaction between genotypes and environment gives rise to an additional variance component of the total phenotypic variance. The different source of variation including the genotypes-environment interaction variance are of great practical importance to the plant breeder for deciding the appropriate testing and selection procedure for planning an efficient breeding programme.

The component of genotype x environment interaction are linked with genetic variance and exhibit an upward bias in the estimation of genetic variance and heritability when evaluated only in one environment, which leads to discrepancies between expected and realized response to selection (Allard and Bradshaw, 1964). Further the contribution of micro-environment in the final expression of a genotype is usually very small. Moreover, owning to the unpredictable and uncontrollable nature of the micro environment its interaction with genotype can't be properly and precisely assessed. Thus it is only the macro environment and its interaction with the genotype that can be isolated and studied (Prabhakaran and Jain, 1992).

Stability of seed yield is an important consideration in *Lathyrus sativus* (L.) also which is highly influenced by agro climatic conditions Deka and Talukdar(1997). Thereby

sixteen diverse varieties/ strains of grass pea were evaluated for their stability performance in four environments at two locations for eight quantitative and one quality characters using the Eberhart and Russell (1966).

As evident from Table 12 mean squares due to genotypes were significant for all the characters, revealing sufficient variability among the genotypes included. However, genotypic differences were significant for all characters in each environment.

G x E interaction variance were significant for all the characters, revealing that genotype responded differentially by planting them at different environments. Significant G x E interaction of different characters were also reported by El-Moneim and Cocks (1993), Hunberry *et al.* (1999), Kumari (2001) and Mundada *et al.*(2004) in grass pea.

The pooled analysis of variance (Table 12) also exhibited significant linear as well as non-linear components of G x E for almost all the characters. This indicated that genotypes differed considerably with respect to their stability and the prediction of their performance over locations would be difficult.

The prediction of performance with regards to different environment was made on the basis of assumption laid by Eberhart and Russell (1966) considering both linear (b) and non-linear (S^2d) components of G x E interaction in judging stability of genotypes. Accordingly, an ideal adaptable variety would be one having high mean value, $b \approx 1$ and $S^2d = 0$. However, other measures of stability have also been used by various scientists. Earlier, Finlay and Wilkinson (1963) used simple linear regression as a quantitative measure of stability. Later Breese (1969), Samual *et al.* (1970) and Paroda and Hayes (1971) emphasized that 'b' could simply be regarded as a measure of response of a particular genotype whereas S^2d is the most suitable measure of stability. This approach has been followed in the present study.

A perusal of Table 13 revealed that all genotypes attained flowering within 70.67 (I-22) to 78.08 (L-57) after sowing. Six genotypes showed non-significant deviation and thus were considered stable. Of these R-02, G-164, I-18, I-30 and L-54 showed $b > 1$ and flowered earlier. While L-08 depicted ($b < 1$) and was found to be early and promising (Table 15). Thus these genotypes would show variation over the varying environments for days to flower in grass pea.

For days to maturity, thirteen genotypes showed non significant deviation and thus were considerable stable (Table 13) of these L-212, G-158, L-08, I-18 and R-31 showed early maturing with high responsiveness ($b > 1$) and were stable, suited for favourable environmental conditions while R-02 and R-33 with low responsiveness ($b < 1$) and was stable, suitable for unfavourable/stress environments.

For plant height three grass pea varieties/strain showed significant deviation and were highly unstable. Plant height ranged from 47.92 cm (R-09) to 53.81 cm (R-15) with a population mean of 50.63 cm (Appendix II). L-54, I-22 and G-158 showed b > 1 highly stable.

Thirteen genotypes had greater branches per plant than the population mean 7.11 with R-29 securing the top position. Nine entries showed significant S^2d values and were thus unstable (Table 13). L-54 was highly responsive to environmental changes (b > 1) with high *per se* performance hence suitable to high fertility conditions. L-07 showed poor response to environmental changes (b < 1) with high *per se* performance.

For pods per plant, twelve grass pea entries showed significant regression coefficient ranging from 0.74 (I-18) to 1.35 (I-22), while two genotypes showed significant deviation. Both the components of G x E interaction were significant (Table 12). I-22, R-29 and L-08 had higher pods per plant with greater responsiveness and non significant deviation (Table 15). Dahiya and Jeswani (1974) and Krarup (1983) also identified stable varieties for different environmental conditions in grass pea.

For seeds per pod from Table 15, a single genotype showed significant deviation. L-07 had higher seeds per pod with greater responsiveness (b > 1) and high *per se* performance while I-30, L-57, R-02 and L-08 showed high *per se* performance with (b < 1) responsiveness. Kumari (2001), and Das and Kundagrami (2002) also identified stable varieties for different environmental conditions in grass pea.

For 100-seed weight four varieties exhibited significant deviation while twelve genotypes exhibited non-significant regression coefficient (Table 14). Both linear and non-linear components were significant with the higher magnitude of linear component (Table 12). L-08 showed high *per se* performance with greater responsiveness (b > 1) and was identified as stable for high management condition while I-22 high *per se* performance with low responsiveness (b < 1) and was stable, suited for unfavourable/stress environments. Dahiya and Jeswani (1974), Sharma *et al.* (1997) and Das and Kundagrami (2002) also identified stable varieties for different environmental conditions in grass pea.

For seed yield per plant six grass pea genotypes showed significant S^2d and nine exhibited significant regression coefficient (Table 14). Further the linear component of G x E interaction exhibited its predominance over non-linear component (Table 12), hence prediction could be made for seed yield.

As evident from (Table 14) seven genotype yielded more than population mean ($\bar{X}$ = 6.98 g) ranging from 5.44g (R-29) to 8.53g (I-30). I-30 and R-33 were evaluated superior and stable for their high degree of responsiveness (b > 1) under high fertility condition (Table 15)

while R-15 and R-02 were considered as stable with high *per se* performance and below average response ($b < 1$). Dahiya and Jeswani (1974), El-Moneim and Cocks (1993), Jones and Singh (2000), Kumari (2000) and Tadesse (2003) also identified stable varieties for different environmental conditions in grass pea.

Hence from the present study (Table 15) it could be concluded that varieties I-30, L-08 and I-22 displayed high *per se* performance, above average response and stability for at least two important characters like pods per plant, seeds per pod, 100-seed weight, branches per plant and plant height while R-02 displayed high *per se* performance, below average response and stability at least two important characters like seed yield per plant, seeds per pod and days to maturity. It is interesting to note that each variety exhibited its superior performance for other important response yield contributing characters besides above which revealed that stability is imparted by its component traits as also highlighted by Sharma *et al.* (1997) and Das and Kundagrami (2002).

Overall conclusion of the present study based on stability parameters which classified the varieties for different situation revealed superiority of I-30, L-08 and I-22 for seed yield as well as their important components under varying climatic conditions. While I-18, L-212, G-164 and R-09 could be gainfully utilized in grass pea quality improvement programmes. Therefore, these grass pea varieties/strains could be recommended for direct cultivation or could be used in hybridization programme for different management practices.

To conclude the present study conducted in four environments at two locations over various estimates viz. variability parameters, correlations, path analysis and stability parameters. Varieties I-30, L-08 and I-22 appeared to be the most promising for increasing seed yield levels in grass pea as they were not only stable but had high *per se* performance for pods per plant, seeds per pod and 100-seed weight. Among 16 varieties R-29, I-22, R-33 and L-07 possessed high protein content. Thus, stability of seed yield per plant in L-08 and I-30 varieties was imparted by the stability of its component characters like pods per plant, seeds per pod, 100-seed weight days to flower and days to maturity.

SUMMARY

The present investigation was carried-out to elicit information on different variability parameters, correlation, path coefficient and stability parameters in grass pea [*Lathyrus sativus* (L.)] for seed yield, its components and quality characters.

The experimental material comprised sixteen diverse varieties/strains of grass pea. The material was planted during rabi, 2005-06 at two locations (Udaipur: E_1, and Kota: E_2) and rabi, 2006-07 at same locations (Udaipur: E_3, and Kota: E_4) under irrigated conditions. The experiment was conducted in randomized block design with three replications following uniform and recommended agronomical practices at all the location.

Observation were recorded on ten randomly selected plants at each location for eight yield characters viz. days to flowering, days to maturity, plant height, branches per plant, pods per plant, seeds per pod, 100-seed weight and seed yield per plant. Quality character like seed protein content was analysed for E_1 and E_3 at Udaipur location only.

Variability parameters, correlation and path coefficient were computed for each of the four environments separately as well as over pooled basis. While stability parameters were analyzed using the model proposed by Eberhart and Russell (1966) over four environments. The important findings were as follows:

1.i. Superior varieties L-08, I-30 and R-33 were identified on the basis of their consistent *per se* performance in all the environments and over pooled basis for seed yield and its components.

ii. Similarly I-18, I-22 and R-31 exhibited high *per se* performance for seed protein content.

iii. Variety I-30 displayed superiority for seed yield as well as quality characters.

2.i. Analysis of variance for at least three environments clearly showed presence of sufficient variability among the varieties for the quantitative and quality characters.

ii. Pods per plant, and seed yield per plant exhibited high estimates of genotypic and phenotypic coefficient of variation in at least three environments and over pooled basis. Moderate GCV and PCV were recorded for branches per plant and 100-seed weight in at least two environments.

iii. High heritability (broad sense) was observed for days to flower in at least two environments. Pods per plant, seed yield per plant and branches per plant had high heritability in at least one environment.

iv. Large genetic advance as per cent of mean coupled with high GCV and heritability were recorded for pods per plant and plant height in at least one environment suggesting that selection for these traits would be effective in genetic improvement of seed yield in *Lathyrus sativus* (L.).

3.i. Association studies revealed a close agreement between genotypic and phenotypic correlations. The genotypic correlations were slightly higher than their respective phenotypic correlations.

5.i. A join regression analysis of variance based over four environments indicated that genotypes differed significantly for almost all the characters except plant height and branches per plant.

ii. The mean squares due to environments were significant for almost all the characters except seeds per pod. MS due to E + (G x E) were significant for all the characters. Both linear and non-linear (predictable and unpredictable) components showed significant G x E interaction. However, magnitude of linear component was higher for pods per plant, days to maturity, branches per plant, 100-seed weight, days to flowering, seed yield per plant and plant height.

6.i. Superior varieties were identified with respect to their phenotypic stability. I-30, L-08 and I-22 displayed high per se performance, above average response and stability for seed yield per plant and its components. It is interesting to note that each variety exhibited its superior performance for other important yield contributing characters i.e. pods per plant, 100-seed weight etc. which revealed that stability is imparted by its component traits.

ii. R-15 and R-02 had high seed yield below average response and appeared stable under stress conditions.

iii. Fulfilling the assumptions laid by Eberhart and Russell (1966) variety L-57 exhibited high mean performance, average response and stability for their seed yield. Thus appeared the most promising and could be gainfully utilized.

iv. For quality characters varieties R-29, I-22, R-33 and L-07 were considered promising for seed protein content.

To conclude the present study conducted in four environments at two locations in two years based over various estimates viz. variability parameters, correlations, path analysis and stability parameters. Grass pea varieties I-30, L-08 and I-22 appeared to be the most

promising for increasing seed yield levels in grass pea as they were not only stable but also had high per se performance for pods per plant, 100-seed weight and branches per plant. Among 16 varieties, R-29, I-22, R-33 and L-07 also possessed high protein content. Thus, stability of seed yield per plant in L-08 and I-30 varieties was imparted by the stability of its component characters like pods per plant, seeds per pod, 100-seed weight, days to flower and days to maturity.

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