ASSESSMENT OF GENETIC VARIABILITY AND DIVERSITY FOR YIELD, BIOCHEMICAL AND NUTRITIONAL COMPONENTS OF LABLAB BEAN *(Lablab purpureus* (L.) Sweet)

THESIS

Submitted in partial fulfilment of the requirements
for the Degree of

MASTER OF SCIENCE
IN
AGRICULTURE
(GENETICS AND PLANT BREEDING)

By

Miss. SANGALE GAYATRI KAMALAKAR
(ADPM/22/2884)

DEPARTMENT OF AGRICULTURAL BOTANY
COLLEGE OF AGRICULTURE, DAPOLI

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SEPTEMBER, 2024

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Under the Guidance of

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DECLARATION OF STUDENT

I hereby declare that the experimental work and its interpretation of the Thesis entitled **"Assessment of genetic variability and diversity for yield, biochemical and nutritional components of lablab bean (*Lablab purpureus* (L.) Sweet)."** or part thereof has neither been submitted for any other degree or diploma of any University, nor the data have been derived from any thesis/publication of any University or scientific organization. The source of materials used and all assistance received during the course of the investigation have been duly acknowledged and the part of the thesis has been submitted for any other degree or diploma.

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This is to certify that the thesis entitled, **"Assessment of genetic variability and diversity for yield, biochemical and nutritional components of lablab bean (*Lablab purpureus* (L.) Sweet)."** submitted for the degree of M. Sc. (Agri.) in Genetics and Plant Breeding, of the College of Agriculture, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, is a bonafide research work carried out by **Miss. Sangale Gayatri Kamalakar (ADPM/22/2884)** under my supervision and that no part of this thesis has been submitted for any other degree. The student had completed all the Course and Research requirements as per the norms in regular mode and has published/submitted one research paper from her M. Sc. Work.

The assistance and help received during the course of investigation have been fully acknowledged.

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THESIS APPROVAL BY THE STUDENT'S ADVISORY COMMITTEE INCLUDING EXTERNAL EXAMINER

This is to certify that the thesis entitled, **"Assessment of genetic variability and diversity for yield, biochemical and nutritional components of lablab bean (*Lablab purpureus* (L.) Sweet)"** submitted by **Miss. Sangale Gayatri Kamalakar (ADPM/22/2884)** of the College of Agriculture, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, in partial fulfilment of the requirements for the degree of M.Sc. (Agriculture) in the subject Genetics and Plant Breeding having, Plant Physiology of Department of Agril. Botany as minor subject has been approved by the Student's Advisory Committee, Board of Studies of the Department and Evaluated by One External Examiner after an open Viva Voice examination in the presence of External Examiner on the same held on dated 06 / 12 /2024.

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Place : Dapoli
Date :18/12/2024

(Miss. Sangale Gayatri Kamalakar)

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List of Abbreviations

Fig.	:	Figure
%	:	Per cent
/		Per
>	:	Greater than
<	:	Less than
*	:	Significant at 5 % level of significance
**	:	Significant at 1 % level of significance
ANCOVA	:	Analysis of covariance
ANOVA	:	Analysis of variance
@	:	At the rate
^{0}C	:	Degree Celsius
C.D.	:	Critical Difference
cm	:	Centimeter
d.f.	:	Degree of freedom
EMS	:	Error mean sum of squares
Err.	:	Error
et al.	:	And others
G	:	Genotype
mg	:	Milligram
g	:	Grams
kg	:	Kilograms
NS	:	Non-significant
ha	:	Hectare
h^2	:	Heritability
i.e.,	:	That is
GCV	:	Genotypic coefficient of variance
PCV	:	Phenotypic coefficient of variance
K_2O	:	Potassium

MSS	:	Mean sum of squares
N	:	Nitrogen
P_2O_5	:	Phosphorus
S.E.	:	Standard error
SS	:	Sum of squares
RBD	:	Randomized Block Design
viz.,	:	Namely
GAM	:	Genetic advance as per percentage of mean

Glossary

Genetic Variability : Genetic variability is either the presence of, or the generation of genetic differences.

Heritability : Heritability is the amount of phenotypic (observable) variation in a population that is attributable to individual genetic differences.

Genotype : Genotype is the genetic makeup of an individual cell or organism that determines or contributes to its phenotype.

Genetic advance : Genetic advance is a measure of how much gain you may get from phenotypic selection for a trait.

Path analysis : Path analysis is a method to discern and assess the effects of a set of variables acting on a specified outcome via multiple causal pathways.

Genetic diversity : Genetic diversity is the biological variation that occurs within species.

Konkan : Konkan is the 700 km long rugged section of the western coastline of Arabian Sea which extends from Damon in the North to western side land of Maharashtra and Goa.

CHAPTER I : INTRODUCTION

Background Information

Pulse crop plays an important role in Indian economy. They are source of high-quality protein and occupy an important place in human's food and nutritional requirements. They are very important constituents in the diets of a very large number of people and are good source of protein which helps to supplement cereal diets, improving their nutritive values. The presence of different types of proteins and their smaller molecules, including alkaloids, isoflavones, polyphenols and a variety of oligosaccharides, make legumes seeds unique in providing nutraceuticals. For centuries a combination of cereals and pulses has been good source of improved nutrition for people all over world. Besides, pulses are also important for increasing soil health through biological nitrogen fixation with sustainability of cropping system, crop diversification and natural resource management.

Among various pulses grown, lablab bean (*Labalab purpureus* (L.) is one of the important pulse crop, belonging to family fabaceae, with chromosome number 2n = 22. It is a self -pollinated crop. It is a semi-erect, bushy perennial herb with no inclination to climb, according to its morphology (Vaijanthi *et al*., 2019). Although there is a lot of genetic variation in the plant due to cultivation, in general it is either annual or have a brief lifespan. This wild species is evergreen. Their undersides might have hairs. Several flower racemes make up the inflorescence. There are cultivars with white flowers and others with blue or purplish flowers. The legume pod that bears fruit varies in size, shape, and colour. It has four seeds or more in it. Depending on the cultivar, the seeds can be white, brown, red, or black. Occasionally, they have a white hilum.

Lablab bean is called by an array of names *viz*., Indian bean, Dolichos bean (Davari *et al*., 2018), Wal, Hyacinth bean, Field bean, Country bean, Bonavista Bean, Egyptian Bean, Musical Bean and locally called as in Marathi-Wal or Pavata, Gujarat-Wal, Bengali-Sheem, Hindi-Sem, Tamil-Avarai, Malayalam-Amara, Telugu-Chikkudu etc.

Since 2500 BC, lablab bean has been grown in India. Lablab bean is a native to India or South East Asia. Verdcourt (1979) placed hyacinth bean in a separate genus Lablab from Dolichos and designated it as *Lablab purpureus* (L.) (*Lablab niger, Dolichos lablab, Dolichos purpureus, Lablab vulgaris*) which is now widely accepted. Various wild forms are found in India. India is major pulse growing country in the world. The cultivation of it has expanded globally to subtropical areas, after colonisation brought it to Central and South America.

According to Kimani *et al*., 2012, it can adapt to a broad range of climatic conditions, including arid, semi-arid, subtropical, and humid regions with temperature fluctuations between 22^0 C and 35 °C and pH ranges between 4.4 and 7.8. As a legume, it possesses the capacity to stabilise atmospheric nitrogen (nitrogen fixation). Compared to other warm-season forages like cowpea or velvet bean (*Mucuna pruriens*), it is more suited to the cold.

Major portion of India is under rainfed conditions and the pulses have adapted well in different mixed and intercropping crop rotations. In India, the area under total pulses cultivation during the year 2021-22 was 31.03 million hectares with the production of 27.69 million tonnes and productivity of 892 kg per hectare. India ranks first in the world in terms of pulse production (25% of the total world's production) (FAOSTAT, 2022). Major pulse producing states in India are Rajasthan, Madhya Pradesh, Uttar Pradesh, Maharashtra, Karnataka and Andhra Pradesh. These six states contribute 80 per cent of total pulse production and area. During the year 2021-22 Maharashtra had 5.22 million hectare area and 5.19 million tonnes total pulses production with 995 kg per hectare productivity of pulses (Anonymous, 2022).

Lablab bean is a multipurpose crop, mainly grown for its young pods, green immature seeds for vegetable purpose while dry seeds are used in many food preparations. It is also used for fodder, hay, silage, green manure and cover crop. It's cultivated as a nutrient-dense food crop for human consumption and as animal feed because it's a legume with a high protein content. Intercropping Lablab with maize has been shown to increase crop yields while preventing erosion and providing fodder for livestock. Its drought resistance may make it an even more important crop as climate change advances. In the United States and Europe, it is grown mostly as an ornamental vine instead of a food crop.

Lablab bean is rich in nutritive value. The proximate and mineral composition of lablab bean shows that the protein content ranged from 20.46 to 25.47 per cent, crude lipid 2.69 to 4.17 per cent, ash 3.97 to 4.48 per cent and carbohydrates 60.63 to 66.32 per cent. The energy level of the seed (1524.20 to 1604.34 kJ /100g DM) was comparable with commonly consumed Indian pulses (Kamatchi *et al*., 2010). The approximate composition of the dry pulse is 24.9 per cent protein with 9.6 per cent moisture, 60.1 per cent carbohydrates, 0.8 per cent fat, 1.4 per cent fibre and 3.2 per cent ash content. (Kay, 1975).

Importance and need of the study

The potential of underutilized legumes like Lablab bean in improving food and nutrition security is of importance. Lablab is known among nutritious underutilized diversified legumes, which is drought tolerant relative to other legumes. However, it is less popular as human food. The nutritional potential of underutilized Lablab varieties can be used for food availability,

accessibility and satisfactorily utilization for improved livelihood. So far research attention has been focusing on good agronomic performance with less information on their nutritional quality and its contribution to the wellbeing of people. Both wild and cultivated Lablab accessions do differ morphologically and across diverse habitat environments. This may make them less known, untapped and underutilized despite its promising potential as a food resource in developing countries where malnutrition still exists. Efforts are needed to popularize high-quality nutritional accessions, enhancing their consumption and commercialization for feeding the ever-increasing population in the future.

Being economic crop of the region, research on wal has it's own significance and needs to put on priority. It has been dibbled in the standing fields of rice at the time of maturity of rice crop in the month of Oct- Nov. In the Konkan region, it is grown on residual moisture after harvesting rice (Ingle *et al.,* 2020). During early phase of crop growth, soil moisture is sufficient for germination and vegetative growth but during later phase of growth soil moisture decreases and plant goes under the stress. Lablab bean is grown in small pockets on the residual moisture after the rice fallow in Konkan region by the farmers accounting 80 percent of total area under lablab bean in Maharashtra which is about 60,000 ha (Sawant and Bendale, 2006). Lablab bean is grown in all the districts of Konkan region of Maharashtra *viz.*, Thane, Palghar, Raigad, Ratnagiri and Sindhudurg with gram, lentil, horse gram with an average productivity of 537 kg/ha (Karwade, 2023). All India Co-ordinated Research Project has made mandate of research for *kharif* crops like moth bean, rice bean and *rabi* crops like Pea, Lathyrus and Lentil.

Objectives of the study

An attempt was made with specific objective to examine the genetic parameters of variability to identify major characters for achieving higher yield. One of the main thrust in any crop improvement programme is to enhance yield. In the present studies, these techniques were employed and keeping in view, the above important aspects, the present investigation entitled "**Assessment of genetic variability and diversity for yield, biochemical and nutritional components of Lablab Bean (*Lablab purpureus* (L.) Sweet)"** was carried out with following objectives:

1. To evaluate genetic variability and diversity for yield and yield related components of Lablab bean.
2. To evaluate biochemical and nutritional components.
3. To select superior genotypes of Lablab bean based on yield and quality.

Hypothesis

This study will help to select prominent genotype for future breeding programme. This research will help to utilize information related to genetic variability, heritability and genetic advanced for different traits. Correlation and path analysis will serve as a path for future breeding programmes by determining the interrelationship between yield and its contributing characters in lablab bean. Nutritionally superior genotypes determined will be helpful.

Scope and limitations of the study

Scope

Studying the degree of variability found in crop species is a prerequisite for any crop improvement programme because it offers the framework for both effective selection and the selection of desirable genotypes for crop improvement. Greater the variation in material, better is the chance for selecting desired types. It is essential to calculate the proportion of genetic and non-genetic variability displayed by the traits under study. Since, many of the plant characters are governed by polygenes and greatly influenced by environmental conditions; the progress of breeding is, however, conditioned by the magnitude, nature and interrelationship of genotypic and non-genotypic variation. This suggests a redundancy need to partition the overall variability into heritable and non-heritable components.

Plant breeders can select superior genotypes based on various genetic parameters, such as genotypic variation, heritability, genetic gain, etc., by having a clear understanding of the variability in various quantitative characters present in the breeding material. This understanding also aids in understanding the type and magnitude of variation available in the population. Genetic diversity is another important parameter helps in development of genotypes and gives idea about genetical distance among the genotypes under study. The knowledge of characters influencing divergence is an important aspect for a plant breeder. Information on the nature and degree of divergence would help the plant breeder to choose right parents for breeding programmes.

For the success of the crop improvement programme, the characters for which variability is present, it should be highly heritable as progress due to selection depends on heritability, selection intensity and genetic advance of the character. Heritability and genetic advance estimates for different targeted traits help the breeder to apply appropriate breeding methodology in the crop improvement programme. It helps in determining the influence of environment on the expression of the genotypic variation and reliability of direct selection for fixation of characters in further generations. Yield is a complex trait and is dependent on many other ancillary

characters which are mostly inherited quantitatively. Meagre information is available for genetic variability in Dolichos bean addressing the morphological and yield traits.

Genetic improvement of a crop is a continuous demand for higher yield and yield attributing characters for different agroclimatic regions. Possibility of achieving improvement in any crop plant depends on the magnitude of genetic variability. Improvement of economic characters like yield through selection is conditioned by the nature and magnitude of variability existing in such populations. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm.

Correlation studies are helpful to determine the components of complex traits like yield. But they do not provide direct & indirect influence of each of component characters towards the yield. Path coefficient analysis is helpful to recognize direct and indirect causes of correlation and also enables us to compare the causal factors on the genetic basis of their contribution.

Limitations

1. Although Lablab bean is an excellent pulse crop with tremendous nutritional value, the plant faces some productivity limitations which occur due to improper cultivation practices, poor growing techniques and improper soil management. Systemic cultivation of this crop should be practiced.

2. Lablab bean can fetch higher price as compared to many other pulses and cereals which can improve and bring economical stability to farmers. But due to lack of proper cultivation practices and knowledge the potential of this crop is not fully exploited.

3. The labour available is not used well commercially as well as agronomically leading to effect on the production.

4. On the other hand, due to lack of variation plants cannot be able to adapt with change environment or escape from potential pathogen attacks. Pod borer and Lablab bean mosaic virus can affect the crop severely in Konkan region of Maharashtra.

5. In Konkan region, lablab bean local types are of long duration (135-145 days) and being grown on residual moisture thus, improvement of this crop in this region is crucial.

6. Seedlings can be affected under prolonged water logging conditions. Hence, the crop cannot be cultivated in *Kharif* season. Thus, the low grain yield (4-5 q/ha) is ultimately caused by the biotic and abiotic stresses.

Therefore, it is imperative to create the genotypes with short duration and high yields.

CHAPTER II : REVIEW OF LITERATURE

Any successful crop improvement programme requires a thorough understanding of the genetic variation present in the germplasm for various traits, their heritability, relationship to yield, and extent of genetic diversity. Attempts have also been made to investigate the genetic variability of Lablab beans for a variety of quantitative traits, as well as the correlation and path analysis between yield and its constituent parts. The potential of underutilized legumes Dolichos Lablab in improving food and nutrition security is of importance. The following heading provides a review of the literature that is currently available on these topics in *Lablab purpureus* (L.) Sweet and other related pulse crops.

2.1 Genetic variability, heritability and genetic advance.

2.2 Correlation studies.

2.3 Path coefficient analysis.

2.4 D^2 analysis.

2.5 Biochemical and nutritional analysis.

2.1 Genetic variability, heritability and genetic advance

The amount of genetic variability that is available to crop plants determines how much genetic improvement they can achieve. The variation in phenotype that is caused by a genotype or set of genotypes in any species that can be divided into components that are phenotypic and genotypic. The heritable portion of total variability, the genotypic component, influences the selection strategies to be used by breeders based on its component characters and its impact on yield.

Joshi (1971) examined twenty lablab bean types for key characteristics such as the weight of a hundred seeds, the number of pods per plant, the number of seeds per pod, and the seed production per plant. In contrast to the number of branches and seed weight, the number of seeds per plant displayed a high degree of genetic heterogeneity. The highest heritability values were found in the weight of 100 seeds and the number of branches per plant. The weight of the seeds, the number of pods, and the number of seeds per pod all showed high genetic advance.

Muralidharan (1980) observed a significant degree of variation in lablab bean across all 20 features examined in 81 native collections. For every character under study, the PCV was greater than the GCV. This demonstrates that the environment has a significant impact on the phenotypic. For both the number of pods per plant and the seed production per plant, high

heritability and high genetic gain were noted. Days to blooming, days to maturity, and seed protein, on the other hand, showed minimal genetic advancement but significant heritability.

Basavarajappa and Gowda (2004) found wide variations 144 field bean genotypes for pods per plant, pod production per plant, and grain output per plant. Additionally, these features showed substantial genetic progress and high heritability, suggesting that additive gene effects were at work for these traits.

Bendale *et al.* (2004) studied 32 genotypes of lablab beans. The parameters number of pods per plant, seed yield per plant, and number of branches exhibited high estimates of heritability related with larger magnitude of genetic advance as percentage of mean. The number of branches and pods per plant had high GCV values, whereas the number of seeds produced per plant had intermediate GCV values.

Hotti (2010) assessed lablab bean for genetic parameters such as PCV, GCV, heritability, and genetic advance. It was discovered that the number of pods per plant and seed yield per plant were high, indicating a wide range of genetic variability in the material evaluated.

Parmar *et al.* (2013) investigated thirty genotypes of Dolichos bean (*Lablab purpureus*) which were evaluated to study the genetic variability on yield, yield contributing and related characters *viz*. days to 50 per cent flowering, days to first pod set, days to maturity, number of pods per cluster, pod length, width of pod, weight of 10 green pods, number of single podded clusters per plant, number of pods per plant and protein content. The range, heritability, genetic advance, and correlation were calculated, as well as the genotypic and phenotypic coefficients of variation. For each attribute, the genotypes shown a considerable degree of variability.

Salim *et al.* (2013) studied variability, correlation, and path analysis in lablab bean and observations on characters as number of pods per plant, pod yield per plant (g), number of seeds per pod, number of seeds per plant, seed yield per plant (g). High heritability coupled with high expected genetic advance in percentage of mean were observed for most of the characters.

Ajay Kumar *et al.* (2014) aimed to determine the genetic variability, heritability, and anticipated genetic advancement for eighteen traits in dolichos beans. Twelve genotypes of *Lablab purpureus* made up the experimental material. Based on the mean pod yield, the genotypes GL 243, Culture 47, and GL 671 are superior. Plant height, number of secondary branches per plant, number of pods per inflorescence, number of inflorescences per plant, mean pod weight, number of pods per plant, weight of 100 seeds, pod yield per plant, and pod yield

per hectare were found to be more variable. High genetic advancement and heritability were also noted for each of these characters. Selection for these qualities will therefore be successful.

Mohan *et al*. (2014) analysed fifty seven pole-type vegetable dolichos bean (*Lablab purpureus* (L.) Sweet) germplasm lines and evaluated them for genetic variability, heritability and genetic advance. Results showed that GCV was comparatively high in days to 50 per cent flowering, days to pod maturity, pod length, pod weight, number of pods per cluster, number of pods per plant, pod yield per plant and pod width. High heritability estimates were observed for number of pods per plant, pod yield per plant, pod weight, days to 50per cent flowering, pod length, days to pod maturity, pod width and number of pods per cluster. High genetic advance, along with relatively high heritability percent, was observed for number of pods per cluster and pod width. Existence of wide variation along with high heritability and genetic advance for number of pods per cluster, pod length, pod width and pod yield per plant indicate that selection would be effective for these traits.

Choudhary *et al.* (2016) examined sixty four genotypes of Indian bean (*Lablab purpureus* (L.) Sweet) for green pod yield and its contributing characters. Plant height, seed yield per plant, seed yield (q) per ha, green pod yield per plant, green pod yield (q) per ha, pod width, weight of 10 pods, number of green pod per plant, pericarp thickness and days to first flowering exhibited high GCV and PCV values indicating large amount of variation. The highest heritability estimate was observed for days to last picking (99.60 per cent).

Kambale *et al.* (2016) in the F_4 generation, examined the genetic variability of ninety-one progenies for yield and characteristics associated with yield, as well as one check of Lablab beans. The hundred seed weight and days to maturity showed the greatest and lowest coefficients of variance, respectively. There was little to no difference seen between PCV and GCV in the expression of many features, such quantity of seeds produced by each plant. PCV was generally greater than GCV in magnitude. The characteristics of plant height, number of peduncles per plant, number of pods per plant, number of seeds produced per plant, and hundred seed weight showed high to moderate values of GCV and PCV.

Sadak *et al.* (2018) studied twenty nine genotypes of field bean (*Lablab purpureus* L.) and evaluated to study the genetic variability on yield, yield contributing and related 18 attributes. The range, genotypic and phenotypic coefficient of variation, heritability, genetic advance and correlation were calculated. The genotypes showed considerable amount of variability for all the traits. Wide range of variability was recorded for fresh pod yield per plant, dry seed yield per plant, days to 50 per cent flowering and days to first pod set. The genotypic and phenotypic coefficients of variation were high (>20per

cent) for fresh pod yield per plant, number of pods per plant. The characters *viz*., number of pods per plant, days to last pod harvest, weight of 10 green pods, dry seed yield per plant and fresh pod yield per plant had high genetic high heritability coupled with high genetic advance and GA as per cent of mean indicating the predominance of additive gene action.

Shailaja *et al.* (2021) conducted an experiment to determine the genetic variability, heritability, genetic advance for yield and yield-related traits in dolichos bean. The experimental material comprises six bush-type dolichos bean genotypes with two local checks were evaluated for 12 morpho-metric characters in randomized block design with three replications. The mean performance of all the characters analyzed was found significant. High PCV and GCV were observed for the number of pods/plant, pod length (cm), and pod width (cm), indicating the higher magnitude of variability for these traits and consequently more scope for their improvement through selection. High heritability coupled with high genetic advance as percent of mean was recorded for all the characters except for days to 50 per cent flowering, primary branches/plant and plant height (cm). These results indicate these characters are under the influence of additive gene action; hence simple selection based on the phenotypic performance of these traits would be more effective.

Lahari *et al.* (2022) investigated Dolichos bean (*Lablab purpureus* L.) genotypes and studied genetic variability, heritability and genetic advance. Total thirty three genotypes of Dolichos bean were evaluated in Randomized Block Design in two replications. Considerable amount of genotypic and phenotypic coefficient of variation was observed for all characters studied. Phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the characters. Highest genotypic and phenotypic coefficient of variation were noted in the character pod yield per plant (68.79 per cent, 68.86 per cent). Heritability was observed high in all the characters. Highest heritability was reported in the characters number of pods per plant (99.83 per cent) and protein content (99.83 per cent). Genetic advance as percent of mean were recorded high in all characters except in plant height. Highest genetic advance as per cent mean was observed in pod yield per plant (141.59 per cent).

Patel *et al.* (2022) studied genetic variability in which the ANOVA depicted sufficient variability present among the genotypes for all traits in lablab bean. Plant height, racemes per plant, pods per raceme, pod weight, pods per plant, pod width, and seed yield per plant showed moderate to high GCV (Genotypic coefficient of variation) and PCV (Phenotypic coefficient of variation), moderate to high heritability and moderate to high genetic advance as a per cent of mean.

Samsuzzaman *et al.* (2023) conducted study for the genetic evaluation and traits association in hyacinth bean. The analysis of variance revealed that significant differences were found among the genotypes. The selection based on no. of green pods per plant, days to 50per cent flowering, and green pod yield might be efficient since they hold high values of genotypic and phenotypic variance. High heritability combined with high genetic advance was observed for the weight of green pod per plant, no. of green pod per plant, and green pod yield.

Singh *et al.* (2024) carried out an experiment to evaluate the magnitude of variability in dolichos bean (*Lablab purpureus* (L.) Sweet) genotypes for important horticultural traits and their associations. The observed range and mean variations of the studied traits revealed a significant genetic diversity among the genotypes. The narrow gap in the genotypic (GCV) and the phenotypic coefficient of variation (PCV) for delineated characters indicated that they are governed by genetic factors, and environmental factors had little or no impact on the phenotypic expression of these traits. The traits including pod yield, days taken to first flowering, weight of pod, plant height, and pod width, showed positive GCV, indicating the presence of additive genes action. Traits such as pod weight, days taken to first flowering, and pod width displayed high heritability and moderate genetic advance, suggesting that the high heritability of these traits is due to the effects of additive genes and that genetic gain can be expected through the phenotypic selection.

2.2 Correlation studies

Lad *et al*. (2010) reported that among other component traits, the harvest index, hundred seed weight, number of seeds per pod, pod length, and number of inflorescences per plant demonstrated the strongest positive direct and indirect effects on seed yield. This suggests that breeding for these traits will be effective in increasing the breeding efficiency for seed yield in wal.

Salim *et al.* (2013) studied about correlation in dolichos bean and found that days to first pod setting exhibited negative direct effects on seed yield. It was concluded that days to first flowering, days to 50per cent flowering, number of pods/plant, pod yield/plant, number of seeds/pod, number of seeds/plant, 100-seed weight are the most important yield contributing characters as they influenced pod yield and seed yield directly in positive direction.

Choudhary *et al*. (2016) studied correlation in sixty four genotypes of Indian bean (*Lablab purpureus* (L.) Sweet) and reported that green pod yield per plant exhibited positive and significant correlation with green pod yield (q) per ha, seed yield (q) per ha, plant height at 60 days, days to first flowering, days to first picking, days to last picking, weight of 10 pods, weight of hundred seed, number of green pods per plant, pod length, pericarp thickness, moisture percentage and seed yield per plant at both genotypic and phenotypic levels.

Gupta *et al*. (2017) conducted study to the estimation of correlation analysis for quantitative traits in Dolichos bean (*Lablab purpureus* L.). The experiment was conducted in Randomized Block Design having thirty eight genotypes in three replications. Green pod yield per plant was significantly positive correlated with pod length, pod width, pod weight, seeds per pod, 100 seed weight, protein content, while non-significant and positively correlated with carotenoids, moisture content, number of flower per inflorescence, total chlorophyll while non-significant and negative correlated with inflorescence length, days to 50 per cent flowering, fiber content, days to first flowering, at genotypic and phenotypic level.

Radhelal *et al*. (2018) laid out an investigation in RBD with three replications to study character association between different genotypes. The results showed that green pod yield per plant was significantly positive correlated with pod length, pod width, pod per inflorescence, seeds per pod, pod weight, number of green pod picking and days to last green pod harvest, at genotypic as well as phenotypic level. Inflorescence length exhibited highly significant and positively correlated with number of flowers per inflorescence, days to last green pod harvest. Number of flowers per inflorescence exhibited highly significant and positively correlated with number of pods per inflorescence. Number of flowers per inflorescence exhibited highly significant and positively correlated with number of pods picking, green pod yield per plant, 100 seed weight.

Thorat *et al*. (2020) studied correlation for 9 different sowing dates. The experiment was laid out in Randomized Block Design (R.B.D.) with ten pole type genotypes and three replication. The results of the investigation clearly showed that pod setting percent, number of pods, number of pods per inflorescence, pod length, length of inflorescence and pod width significantly positive association with green pod yield. Also days to first flowering, days to 50 per cent flowering and days to first picking showed significantly negative association with green pod yield.

Geetha *et al*. (2021) aimed and to carried out correlation studies in Dolichos Bean genotypes. The field experiment was carried out using twenty-six genotypes of field bean in Randomized Block Design with three replications. The results concluded that at both phenotypic and genotypic levels, green pod yield recorded moderately significant and positive correlation with plant height and number of branches/plant and the traits *viz*., number of pod/plant and grain yield (g) exhibited an extremely significant and positive correlation with green pod yield. Days to maturity showed the first maximum positive direct effect on green pod yield, followed by number of pod/plant and number of branches/plant. Whereas the other characters *viz.*, days to fifty percent flowering, plant height and grain yield recorded direct negative effect on green pod yield.

Patel *et al.* (2022) studied about correlation in lablab bean. They concluded that plant height, racemes per plant, pods per plant, pod weight, and pods per raceme were significantly and positively associated with seed yield per plant at the genotypic level. Pods per plant had the most favorable direct effects (0.736) on seed yield per plant, subsequently by pod weight, seeds per pod, pods per raceme, pod length, pod width, plant height and days to maturity.

Sirina *et al.* (2022) used twenty one genotypes to study the correlation and path coefficient analysis for growth and yield related traits during *Rabi*, 2020-21. Green pod yield per plant had positive and significant association with traits like number of flowers per inflorescence, number of pods, pod length and average weight of 10 fresh pod at both genotypic and phenotypic level. Since, these associations of characters are in the desirable direction, it indicates that simultaneous selection for these characters would be rewarding for improving the green pod yield per plant. Path analysis revealed that the some traits had positive effect on green pod yield per plant.

Samsuzzaman *et al.* (2023) conducted study for the genetic evaluation and traits association in hyacinth bean. Green pod yield showed significant positive correlation with weight of green pod per plant at genotypic and phenotypic levels. The analysis of variance revealed that significant differences were found among the genotypes. The selection based on no. of green pods per plant, days to 50 per cent flowering, and green pod yield might be efficient since they hold high values of genotypic and phenotypic variance. High heritability combined with high genetic advance was observed for the weight of green pod per plant, number of green pod per plant, and green pod yield.

Singh *et al.* (2024) conducted an experiment to evaluate the magnitude of variability in dolichos bean (*Lablab purpureus* (L.) Sweet) genotypes for important traits and their associations. The narrow gap in the genotypic (GCV) and the phenotypic coefficient of variation (PCV) for delineated characters indicated that they are governed by genetic factors, and environmental factors had little or no impact on the phenotypic expression of these traits. The higher genotypic correlations revealed an inherent association between the traits. Therefore, the selection criterion for high yield was proposed based on the strong character association between plant height, number of pods/cluster, pod width, and pod weight. The number of pods/plant, followed by the number of clusters/plant had the highest direct positive effect on yield. Consequently, pod yield may be increased through selection of heavier pods, more clusters/ plant, and more pods/cluster.

2.3 Path coefficient analysis

Wright (1921) and Dewey and Lu (1959) developed Path coefficient analysis, which is a standardized partial regression analysis. Path coefficient analysis makes it possible to divide

correlation coefficients into direct and indirect effects, providing a more accurate portrayal of the character relationships and aiding in the identification of the key elements. A brief overview is given of the literature that is currently available on the route analysis of seed yield with their component qualities in lablab beans and other comparable pulses.

Patel *et al.* (2011) revealed that path coefficient analysis among the developmental characters *viz.*, green pod yield/plant (kg), hundred seed weight, number of pods/plant, number of pods/inflorescence, pod length, leaf width and inflorescence length showed high direct effect with seed yield.

Gondhalekar *et al.* (2013) conducted the path coefficient analysis in eight Lablab bean parents and 24 selected progenies in F_2 generation and observed that the characters, number of pods per plant, days to first flowering, days to overall maturity and hundred seed weight bearing direct positive effect on grain yield could be the selection criteria for genetic improvement of grain yield per plant in Lablab bean population under study.

Pawar *et al.*(2013) reported that path analysis had highest positive direct effect of number of pods per plant followed by number of seeds per pod, days to 50 per cent flowering, number of inflorescences per plant and 100-seed weight on grain yield per plant, while days to maturity and pod length exhibited high negative direct effects on grain yield per plant.

Salim *et al.* (2013) studied lablab bean and estimated range, mean, genetic parameter, correlation co-efficient and path coefficient. Path coefficient analysis showed that days to first flowering, days to 50 per cent flowering, number of pods/plant, 20 pod weight (g), pod yield/plant, pod length, number of seeds/pod, number of seeds/plant, 100-seed weight influenced seed yield/plant directly in positive direction.

Gadakh *et al.* (2014) reported that the characters, number of pods per plant, number of peduncles per plant, hundred seed weight and days to first flowering bearing direct positive effect on grain yield could be the selection criteria for genetic improvement of grain yield per plant in lablab bean population under study.

Ravinaik *et al.* (2014) examined 9 genotypes of dolichos bean and revealed that pod yield per plant had highest positive direct effect on number of flowers per cluster followed by number of pods per cluster, pod width, days to 50 per cent flowering, number of branches per plant and pod length but number of pods per plant, plant height, average weight of pods and number of seeds per pod had negative effect on pod yield per plant at genotypic levels. Whereas at phenotypic levels number of pods per plant had direct effect on pod yield per plant followed by number of branches per plant, pod width, average weight of pods, days to 50 per cent flowering on the other hand, number of pods per plant, number of flowers per cluster, plant height, pod length and number of seeds per pod had negative effect on pod yield per plant.

Radhelal *et al.* (2018) examined and reported that green pod yield per plant was significantly positive correlated with 100 seed weight, pod length, pod width, pod per inflorescence, seeds per pod, pod weight, number of green pod picking and days to last green pod harvest, at genotypic as well as phenotypic level. Hence direct selection for these traits may lead to the development of high yielding genotypes of dolichos bean**.**

Noorjahan *et al.* (2019) reported that green pod yield per plant was significantly and had positively direct effect with 50 per cent flowering, length of inflorescence, number of grains per pod, pod yield per hectare and negative direct effect with days to first flowering, number of flowers per inflorescence, number of pods per inflorescence, first pod harvest, pod length, pod width, mean pod weight. Hence direct selection for these traits may lead to the development of high yielding genotypes of dolichos bean.

Ingle (2020) studied forty three F_5 of lablab bean and observed the direct positive effect of days to initiation of flowering, days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant and 100 seed weight on seed yield per plant.

Pallavi *et al.* (2021) conducted an investigation on lablab bean for path coefficient analysis of M_3 generation and revealed that the number of fresh pod per plant exhibited high positive direct effect on pod yield followed by fresh pod shelling percentage, average weight of fresh pod, days to fresh pod harvest, number of locules per fresh pod, leaflet length, number of nodes per raceme, raceme length, number of buds per nodes, fresh pod width, and fresh seed length at phenotypic level, while fresh seed yield per vine exhibited high positive direct effect on fresh pod yield followed by days to fresh pod harvest, number of seeds per fresh pod, number of fresh pods per vine, leaf length, fresh 100 seed weight, fresh seed length, number of nodes per raceme, number of buds per nodes, pod setting per cent, fresh pod width and average weight of fresh pod at genotypic level.

2.4 D^2 analysis

Nandi *et al.* (2000) conducted study to analyse the genetic diversity using Mahalanobis D^2 statistic. The genotypes were grouped into 5 clusters, Cluster I had 22 genotypes. The analysis further indicated that the genotypes of common geographic origin or same location were grouped into different clusters which suggested a lack of relationship between genetic and geographic diversity. The average intercluster D^2 values indicated maximum statistical divergence between cluster II and V followed by I and V and I and IV, Cluster V recorded highest mean pod length, pod weight, seeds/pod and green pod yield/plant. The first 2 canonical vectors accounted for 73.09 per cent of total genetic variation.

Gnanesh *et al.* (2007) evaluated for sixty four genotypes for their genetic diversity using Mahalanobis D^2 statistic and were grouped in to eleven clusters. Geographical and genetic diversity were observed to be unrelated as genotypes from diverse geographical regions were placed in the same cluster, while genotypes from the same centre were grouped into different clusters. It was observed that pod yield per plant and plant height contributed the maximum towards genetic divergence.

Sankaran *et al.* (2008) suggested that Mahalanobis D^2 statistics which is based on the multivariate analysis of quantitative trait is a powerful tool for measuring divergence among a set populations and therefore made an to study the multivariate analysis of genetic divergence in local landraces of lablab bean.

Chaitanya *et al.* (2013) used Mahalanobis D^2 statistics to study the genetic divergence of Indian bean. Genotypes were grouped in to eight clusters on the basis of relative magnitude of D^2 values. The highest number of genotypes (14) appeared in cluster III. The maximum inter cluster distance was observed between cluster IV and cluster VI followed by cluster IV and VIII. The minimum inter cluster distance was observed between cluster I and cluster IV. Among the yield contributing characters, the maximum contribution towards divergence was made by protein content.

Salim *et al.* (2013) concluded that the inter-cluster distances (D^2) were higher than the intra-cluster distances. The inter-cluster D^2 values varied from 2059.094 to 19302.6. The intracluster distance (8502.795) observed in cluster VII revealed maximum diversity among themselves. Data on the contribution of individual characters towards divergence suggested that no. of pods per plant contributed maximum (34.033%). Results of the study suggested that selection for these traits in these genotypes might be effective. By strategically using this diversity, the breeder can develop high yielding varieties of lablab bean.

Ananya *et al.* (2015) investigated genetic diversity present among 90 Indian bean genotypes using D^2 statistic. Cluster analysis grouped 90 germplasm into sixteen clusters based on the degree of divergence between the genotypes. The results revealed that number of green pods yield per plant, number of green pods per branch, number of green pods per plant, and green pod weight contributed 80.68 % to total divergence. Maximum inter-cluster distance was recorded between clusters XV and XVI followed by clusters VII and XV indicating wide genetic diversity and it may be used in Indian bean hybridization programme for improving yield.

Nidhin *et al.* (2021) carried out Mahalanobis D^2 analysis. The accessions were grouped into six clusters. The highest inter cluster distance was exhibited between the clusters IV and V

(3929.71) which indicated that maximum variability existed between the accessions present in these clusters and hence they can be used as parents in a hybridization programme.

Shulee *et al.* (2021) studied divergence which revealed that pod yield per plant contributed maximum per cent to the diversity followed by number of branches per plant, plant height, number of cluster per plant, green pod crude protein, days to 50 per cent flowering, number of flower per cluster and number of pods per cluster. Maximum inter cluster distance was observed between cluster II and V which indicated that the genotypes within these clusters were highly divergent and desirable to select for further crop improvement programme.

Islam *et al.* (2023) conducted an experiment with 150 accessions of Hyacinth bean. The accessions were grouped into ten clusters ranging from 8 to 25 accessions. Accessions collected from the same districts in Bangladesh or countries were distributed into different clusters. The results obtained by D^2 analysis were also confirmed by canonical analysis.

Sathuri *et al.* (2023) grouped the lines of lablab bean into five clusters using modified tocher method for cluster analysis, which has been shown to be superior to tocher method. Cluster-I and cluster-IV showed the highest inter-cluster distance (124.92) and crossing between genotypes from these two clusters was suggested to get desirable segregants. The study also suggested that PCA and D^2 analysis can be used alternatively to assess the genetic diversity pattern among genotypes.

Subashri *et al.* (2023) grouped twenty three genotypes into seven clusters on the basis of the relative magnitude of D^2 values. The results revealed that the maximum inter-cluster distance was observed between cluster III and cluster VI followed by clusters V and VI. The minimum inter-cluster distance was observed between cluster I and cluster VII. The maximum intra-cluster distance was in cluster VI followed by cluster IV. The mean value for most of the traits was highest in cluster V. Pod yield plant-1 followed by crude fibre, crude protein and number of seeds pod-1 and green pod girth contributed higher towards genetic divergence. Hence, that the genotypes from cluster V and cluster I could be selected for crop enhancement.

2.5 Biochemical and nutritional analysis

Soetan *et al.* (2010) studied the proximate and mineral composition of three varieties of lablab beans (*Lablab purpureus*). Rongai brown variety had the highest concentration of crude protein, crude fat, ash and of gross energy. There were significant differences ($P< 0.05$) in the crude protein, crude fibre and the nitrogen free extracts in all the three varieties of the lablab beans. Potassium, phosphorus, magnesium and iron were appreciably high in all the three varieties while calcium and sodium concentrations were low. It is concluded that the lablab beans can be used as a source of dietary proteins especially in developing and under developed

countries where consumption of animal protein may be limited as a result of economic, social, cultural or religious factors.

Shaahu *et al.* (2015) analysed proximate chemical, amino acid, anti- nutritional factors (ANF) and mineral composition of different varieties of *Lablab purpureus* . *Lablab purpureus* seed irrespective of the variety was lower in crude protein but higher in crude fibre. The three varieties of lablab seed analyzed in the study contained between 7.22-9.23 % of crude fibre while the crude protein content ranged between 24.88-34.33g/100g.

Shahdat *et al*. (2016) studied lablab bean to generate awareness that *L. purpureus* could also act as a good source of food components essential for good health. Proximate analysis revealed that the seed powder contained 8.47 ± 0.52% moisture; 3.50 ± 0.0.07% ash; 1.02 ± 0.06% total fat; 23.95 ± 0.15% total protein; 1.21 ± 0.16% total dietary fiber; 61.86 ± 0.70% total carbohydrate and 352.4 ± 2.66 kcal/100 g energy. Phytic acid content (%) was 1.014 ± 0.048. Also, it is a good source of proteins and fatty acids.

Davari *et al.* (2018) conducted study on *Lablab purpureus* using twenty five promising genotypes. The results of proximate analysis concluded that, genotype DPLW15 was found to be beneficial for increasing the content of N, K, Ca, Mg, S and protein. Among the twenty five genotypes, the genotype DPLW15 and DPLW46 content high percentage of protein. While genotype DPLW46 observed to be high in fat, grain yield and protein yield as compared to all other genotypes. These genotypes appeared to be comparatively superior in respect of high grain yield and could therefore be encouraged for.

Mohammad *et al.* (2021) reported significant variations and also noted for the nutrient compositions among the lablab bean genotypes under study. The analytical experiment shows the auto had the highest proportion of Cu (15.28 ppm), Fe (122.22 ppm), Mn (40.74 ppm), B (60.60 ppm), S (0.158 %) and Ca (1.67 %). In contrast, the genotype of SB003 had the highest amount of Zn (61.86 ppm) and SB011 had Mg (7.85%) content.

Nidhin *et al.* (2021) examined lablab bean samples and reported highest calcium in the accession LP-13 (152.66 mg/100g) and lowest content in LP-15 (88.89 mg/100g). Iron content was maximum in LP-11 (18.14 mg/100g) and minimum in LP-27 (11.02 mg/100g). Total phenols recorded was maximum in LP-19 (9.64 mg/100g) and minimum in LP-30 (2.06 mg/100g). Highest crude protein content was recorded in LP-12 (20.65%) and lowest crude protein was recorded in LP-17 (15.82%). Maximum crude fibre was recorded in LP-10 (17.81%) and minimum in LP-17 (8.98%). Phytic acid content was minimum in LP-27 (550.90 mg/100g) and maximum in LP-11 (906.88 mg/100g).

Dileep Kumar *et al.* (2022) analysed nutritional and anti-nutritional components and found considerable variations for each of the characters under the study. All accessions had good nutritional content and very low anti-nutritional elements, particularly the phytic acid was extremely low (1.77–2.43 mg/100gm) in the tender pod when compared to the lablab accessions of south Indian states as well as of common leguminous vegetables. These local accessions of lablab also represent an agronomically and nutritionally important pool for *L. purpureus* improvement/breeding.

Vishnu *et al.* (2022) analysed nutritional and anti-nutritional factors using the standard protocol, revealed significant variations for all the characters studied. Compared to the popular leguminous vegetables, the nutritional content of all accessions was found to be high, whereas anti-nutritional factors were very low and giving importance to neglected and underutilized crops effectively maintain a diverse and healthy diet and combat micronutrient deficiencies.

Debarati *et al.* (2023) studied morphological parameters in distinct genotypes of *Lablab purpureus* L. It revealed wide variation in morphological parameters among the genotypes. Biochemically, genotype DCP 11 possessed the highest amounts of protein (32.33±0.50 g /100mg), phenol (3.77±0.12g/100g) and flavonoids (8.32±0.05 mg/100g) as well as exhibited the highest antioxidant activity (IC50 value 27.36±0.61µg/mL), and DCP 12 had the highest iron (15.24±0.10mg/100g) and zinc (5.54±0.04mg/100g) and lowest tannin (0.59±0.02g/100g) content.

Maksuratun *et al*. (2024) revealed the results that stated that the country bean retained the highest vitamin C (90.15 %) and protein (96.48) when dried in box solar dryer. Country bean seeds have noteworthy proximate compositions.

CHAPTER III : MATERIAL AND METHODS

The information pertaining to the experimental details and analytical methodology followed during the present investigation entitled "**Assessment of genetic variability and diversity for yield, biochemical and nutritional components of Lablab Bean (*Lablab purpureus* (L.) Sweet)**" was carried out at Research and Education Farm, Department of Agril. Botany, College of Agriculture, Dapoli, Dist. Ratnagiri during *rabi* 2023-2024. The details of the material used and the methodology adopted during this course of the investigation are given in this chapter under the following objectives:

1. To evaluate genetic variability and diversity for yield and yield related components of Lablab bean.
2. To evaluate biochemical and nutritional components.
3. To select superior genotypes of Lablab bean based on yield and quality.

3.1 Material required

3.1.1 Inputs used

The material for the present experiment comprised of twenty five different genotypes of Wal and one check. Konkan Wal-2 was used as check in the following research work. The twenty six genotypes used for the study and their source are given in Table 1.

Table 3.1 List of genotypes and their source

Sr.No.	Genotype	Source	Sr.No.	Genotype	Source
1	DPLW-22-1	Dapoli	14	DPLW-22-33	Dapoli
2	DPLW-22-2		15	DPLW-22-45	
3	DPLW-22-3		16	DPLW-22-48	
4	DPLW-22-4		17	DPLW-22-54	
5	DPLW-22-5		18	DPLW-22-61	
6	DPLW-22-6		19	Pavata	
7	DPLW-22-7		20	Goda Wal	
8	DPLW-22-8		21	Kadva Wal	
9	DPLW-22-9		22	Local Kadva	
10	DPLW-22-10		23	Local Alibaug	Sagaon
11	DPLW-22-12		24	Local Pen	Jambhoshi
12	DPLW-22-13		25	Kelshi Wal	Kelshi
13	DPLW-22-14		26	Konkan Wal-2	Dapoli

3.1.2 Machines and equipment used

Machines used

- Mould board plough
- Rotovator
- Land leveler
- Tractor/ Power tiller
- Kjeldahl apparatus
- Atomic Absorption Spectrophotometer (AAS)

Equipment used

- Knapsack sprayer
- Measuring scale
- Weighing balance
- Meter tape

3.2 Methods adopted

The present investigation was carried out at Research and Education Farm, Department of Agril. Botany, College of Agriculture, Dapoli, Dist. Ratnagiri during *rabi* 2023-2024. The experimental details are presented in Table 2.

3.2.1 Experimental details

The experiment was conducted in Randomized Block Design with three replications. The plot size was 3.0m X 0.9 m. Three rows were planted with each row having ten plants thus, constituted thirty plants per replication with the spacing of 30 x 30 cm. A general view of experimental plot is shown in plate I.

Table 3.2 Details of the experimental plot

1	Crop	:	Lablab bean
2	Spacing (cm)	:	30 x 30
3	Experimental design	:	Randomized Block Design (RBD)
4	No. of genotypes	:	25 + 1 check
5	No. of plants per line	:	10
6	Plot size	:	3.0 x 0.9 m
7	Recommended fertilizer dose	:	25 kg N: 50 kg P_20_5: 50 kg K_2O / ha
8	Season	:	*Rabi* 2023-24
9	Date of sowing	:	30 October, 2023

Plate I : General view of the experimental plot

3.2.2 Cultural practices

The experiment was conducted at the normal fertility level on lateritic soil. The preliminary tillage operations were carried out properly in order to bring the soil at fine tilth.

Sowing was done on 30th October 2023. One seed was dibbled at each hill. Gap filling was done ten days after sowing. Two weeding were done at 20 days and 50 days after sowing. The recommended fertilizer dose applied @ 25 kg N: 50 kg P_20_5: 50 kg K_2O per hectare. Other cultural practices were carried out as per the standard recommendations.

3.2.3 Observations recorded

The observations were recorded on randomly selected five plants per replication for different characters. The mean of observations of the five plants were used for statistical analysis.

1. Days to 50 per cent flowering:

The number of days were recorded from the date of sowing to, till flowering of 50 per cent population.

2. Days to maturity:

The number of days from the date of sowing to the date on which more than 90 per cent plants showed physiological maturity was recorded.

3. Plant height (cm):

Plant height was measured in centimeter from ground level to the tip of the main axis of the plant at maturity.

4. Number of primary branches per plant:

Number of primary branches per plant were counted as the total number of primary branches on the main stem.

5. Number of peduncles per plant:

Number of peduncles per plant were counted as the total number of peduncles present on the plant at maturity.

6. Number of pods per plant:

Number of pods per plant were counted as the total number of pods present on the plant at the time of harvest.

7. Pod length (cm):

Pod length was measured in cm from the base to the tip of the pod.

8. Number of seeds per pod:

Number of seeds were counted from each of the selected five pods and mean of these pods were calculated as the number of seeds per pod.

9. Seed yield per plant:

Seed yield per plant was recorded in gram as the weight of the total seeds per plant.

10. Hundred seed weight (g):

Weight of the randomly selected 100 seeds were recorded in gram.

11. Harvest index (%):

Harvest index of all genotypes was calculated by the formula given by Donald (1962). It is the ratio of the seed yield to the total biological yield of the plant and expressed in per cent.

$$\text{Harvest index} = \frac{\text{Economic yield (kg/ha)}}{\text{Biological yield (kg/ha)}} \text{ x } 100$$

12. Protein content (%):

Total nitrogen was determined using macro-khjeldhal method. The protein content was estimated by multiplying the nitrogen content by conversion factor 6.25 (because protein contains 16% nitrogen).

13. Calcium content (mg/100g):

Calcium contents were determined using versanate titration method using muroxide indicator.

14. Potassium content (mg/100g):

Potassium from the filtrate was determined using systronics flame photometer.

15. Phosphorus content (mg/100g):

Vandomolybdate method was used for determination of the total phosphorus content.

16. Iron content (mg/100g):

Iron content was analysed using atomic absorption spectroscopic method.

17. Ascorbic acid(mg/100g):

Volumetric method was used for the estimation of ascorbic acid.

18. Phenols (mg/100g):

Phenols were estimated using the method given by Malick C.P. and Singh M.B. (1980).

3.3 Statistical analysis

The data collected on individual characters was subjected to the statistical analysis for randomized block design. The statistical analysis of the data was done by the standard method known as analysis of variance described by Panse and Sukhatme (1967). The standard error (SE) of mean and critical difference (CD) at 5 per cent level of significance was worked out, wherever the results were significant. The ANOVA is given below.

3.3.1 Analysis of variance (ANOVA)

Source of variation	d.f.	SS	MSS	Expected MS
Replication	(r-1)	RSS	RMS	σ^2 + $g\sigma$^2 r
Genotype	(g-1)	GSS	GMS	σ^2 $e + r\sigma$^2 g
Error	(r-1)(g-1)	ESS	EMS	σ^2 e
Total	(rg-1)			

Where,

r = Number of replications

g = Number of genotypes

3.3.2 Estimation of statistical parameters

i) Mean

Mean value for each character was worked out by dividing the total by corresponding number of observations.

$$\bar{x} = \frac{\Sigma x_i}{n}$$

Where,

$\bar{x}$ = Mean of the character

Σx_i = Total of the character

n = Number of observation

ii) Range

The lowest and the highest value from the mean of each character were taken as the range of that character.

iii) Standard error of mean

SEm $\pm$ = $\sqrt{\sigma e^2}/_r$

iv) Standard error of difference

Standard error of difference between two mean (SEd) = SEm x $\sqrt{2}$

v) The **critical difference** between any two means was calculated as SEd x 't' value at error degrees of freedom.

3.3.3 Estimation of genetic parameters

A) Estimation of variance

The environmental ($\sigma^2 e$), phenotypic ($\sigma^2 p$) and genotypic ($\sigma^2 g$) variances were calculated as,

1) **Environmental variance**

$\sigma^2 e$ =EMS

2) **Genotypic variance**

$$\sigma^2 g = \frac{GMS - EMS}{r}$$

3) **Phenotypic variance**

$$\sigma^2 p = \sigma^2 g + \sigma^2 e$$

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean sum of squares

r = Number of replications

B. Estimation of coefficient of variation

The genotypic and phenotypic coefficients of variations were calculated as per the formulae given by Burton and De vane (1953).

a. Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\bar{x}$ = Mean of the characters

b. Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sqrt{\sigma^2 p}}{\bar{x}} \times 100$$

Where,

$\sigma^2 p$ = Phenotypic variance

$\bar{x}$ = Mean of the characters

Categorization of range of variation as proposed by Sivasubramanian and Menon (1973).

<10 (%) : Low

10-20(%) : Moderate

>20 (%) : High

C. Estimation of broad sense heritability (h^2bs)

Heritability in broad sense estimated for various characters by the formulae suggested by Lush (1949),

$$h^2bs\ (\%) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

Heritability in broad sense was estimated by method suggested by Stansfield (1969), as given below.

0-20(%) : Low

20-50(%) : Medium

50 (%) & above : High

D. Estimation of genetic advance (GA)

The genetic advance was calculated in per cent by the formula suggested by Johnson *et al*. (1955).

a. Genetic advance

$$GA = \frac{\sigma^2 g}{\sigma^2 p} \times \sigma_p \times k$$

b. GA as percentage of mean

$$GAM = \frac{GA}{\bar{x}} \text{ X } 100$$

Where,

$\sigma^2 p$ = Phenotypic variance

$\sigma^2 g$ = Genotypic variance

σ_p = Phenotypic standard deviation

k = Selection differential at 5 per cent selection intensity (2.06)

$\bar{x}$ = Mean of the character

The range of genetic advance as percent of mean was classified as method suggested by Johnson *et al.* (1955).

<10(%) : Low

10-20 (%) : Moderate

>20(%) : High

3.3.4 Estimation of correlation coefficient

Analysis of co-variance was carried out by taking two characters at a time and plot error was used as environmental co-variance. The phenotypic and genotypic co-variances were derived as detailed below.

ANCOVA for phenotypic and genotypic co-variance

Source	d.f.	Mean products
Replication	(r-1)	-
Treatments	(t-1)	GMP
Error	(r-1)(t-1)	EMP
Total	(rt-1)	-

Where,

r = Number of replications

t = Number of treatments

GMP = Genotypic mean sum of product

EMP = Error mean sum of product

The genotypic and phenotypic co-variances were worked out as per the formulae given by Singh and Chaudhary (1977).

Environmental co-variance = $(C_0Ve\ x1\ x2)$ =EMP

Genotypic co-variance = $(C_0Vg\ x1\ x2) = \frac{GMP-EMP}{r}$

Phenotypic co-variance = $(C_0Vp\ x1\ x2) = (C_0Ve\ x1\ x2) + (C_0Vg\ x1\ x2)$

The appropriate variances and co-variances were used for calculating phenotypic and genotypic correlation coefficients (Johnson *et al*., 1955).

a) **Phenotypic correlation coefficients (rp)** was derived as

$$rpx_1x_2 = \frac{C_0Vpx_1x_2}{\sqrt{(\sigma^2p_1)(\sigma^2p_2)}}$$

Where,

rpx_1x_2 = Phenotypic correlation between character x1 and x2

$C_0Vpx_1x_2$ = Phenotypic co-variance between character x1 and x2

σ^2p1 & σ^2p_2 = Phenotypic variance of character x1 and x, respectively.

b) **Genotypic correlation coefficients (rg)** were derived as

$$rgx_1x_2 = \frac{C_0Vgx_1x_2}{\sqrt{(\sigma^2g_1)(\sigma^2g_2)}}$$

Where,

rgx_1x_2 = Genotypic correlation between character x1 and x2

$C_0Vgx_1x_2$ = Genotypic co-variance between character x1 and x2

σ^2g_1 & σ^2g_2= Genotypic variance of character X_1 and X2 respectively

The significance of phenotypic and genotypic correlation coefficients were tested by using 't' test.

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

Where,

r = Correlation coefficients

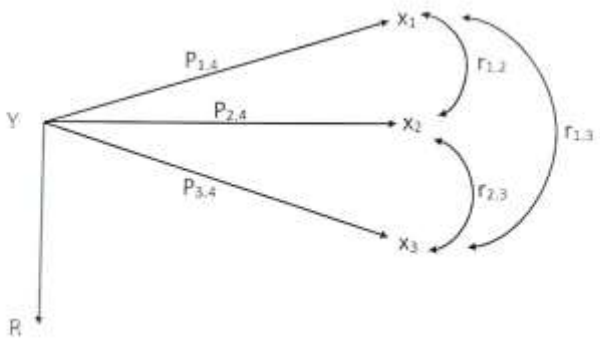
$n =$ Total number of observations

The calculated 't' value is tested with table 't' value for respective (n-2) degrees of freedom for significance.

3.3.5 Path coefficient analysis

To establish a cause and effect relationship, the genotypic and phenotypic correlation coefficients were partitioned in direct and indirect effect by path analysis as suggested by Dewey and Lu (1959). The first step in path analysis is to prepare a path diagram based on cause and effect relationship.

The concept behind this is that yield is the combined function of various components like x_1, x_2, x_3 then these components show following type of association with one another.



From this figure, it is obvious that yield is the result of x1, x2 and x3 some other undefined factors designated by 'R'. The double arrowed lines indicate mutual association as measured by correlation coefficients and the single arrowed line represented direct influence as measured bypath coefficients Pij.

Path coefficients were obtained by solving a set of simultaneous equation of the form,

$$r_{ny} = p_{ny} + r_{n2} + 4n_2p_y + 4n_3 + \ldots\ldots$$

Where,

r_{ny} = Represented correlation between one component and yield

p_{ny} = Represented path coefficient between one component and yield

r_{n2} = Represented correlation between that character and each of the other yield components in turn

Matrix A Matrix B

$$\begin{pmatrix} r_{1y} \\ r_{2y} \\ r_{nY} \end{pmatrix} \qquad \begin{pmatrix} 1 & r_{1.2} & r_{1.3}\ldots\ldots & r_{1n} \\ r_{2.3} & 1 & r_{2.3}\ldots\ldots & r_{2n} \\ r_{n1} & r_{n2} & r_{n3}\ldots\ldots & 1 \end{pmatrix}$$

Where,

$r_{1.2} = r_{1.2}$ and so on

r_{1y} = Correlation between one component character and yield.

The 'B' matrix (P_{ij}) were obtained as

$(P_{ij}) = A \times (B^{-1})$

The indirect effect of a particular character through other characters was obtained by multiplication of direct path and particular correlation coefficients between these characters separately.

Indirect effect = $r_{ij} \times P_{ij}$

Where,

i = 1 to n

j =1 to n

$P_{ij} = P_1Y_1, P_2Y_2,$-----P_nY_n

Path coefficient (P_{ij}) correlation coefficient (r_{ij}) and residual factor (s) were diagrammatically presented.

The residual factors i.e. variation in yield unaccounted for by these association was calculated from the following formula,

Residual factor (x) = $1-R^2$

Where,

$$R^2 = P_{1y}r_{1y} + P_{2y}r_{2y} + P_{3y}r_{3y}\ldots\ldots + P_{nyrny}$$

Where,

P_{1y}, $P_{2y}\ldots\ldots$ P_{ny} = Path values

r_{1y}, $r_{2y}\ldots\ldots..$ r_{ny} = Correlation coefficents

The path coefficient is rated based on the scales given below: (Lenka and Mishra, 1973).

0.00-0.09 = Negligible

0.10-0.19 = Low

0.20-0.29 = Moderate

0.30-0.99 = High

>1.00 = Very high

3.3.6 Genetic divergence

The genetic divergence between twenty six genotypes was estimated using Mahalanobis (1936) using D^2 statistic techniques D^2 value between i^{th} and j^{th} genotypes for 'P' characters was calculated as

$$D^2_{ij} = \sum_{t-1} (\underline{Y}it - \underline{Y}jt)^2$$

Where,

$\underline{Y}it$ = Uncorrelated mean values of i^{th} genotype for 't' character

$\underline{Y}jt$ = Uncorrelated mean values of j^{th} genotype for 't' character

D^2ij = D^2 between i^{th} and j^{th} genotype

The various steps involved in estimation of D^2 values are given below.

3.3.6.1 Test of significance

Variance was calculated for all fourteen characters investigated and test of significance was carried. Analysis of covariance (ANOVA) for the character pairs was estimated on the basis of mean values. From these estimates, a dispersion table was prepared. After testing the differences between the genotypes for each of the characters, a simultaneous test of significance of differences between the mean values of a number of correlated variables was done by using V statistic which in turn utilize Wilk's criterion (Rao, 1952).

Wilk's criterion '^' $|E|/|E + V|$

= Determination of error matrix

= Determination of (genotypes + error) sum of squares and sum of product matrix.

Then the value of 'V' statistic was worked out using Wilk's lambda criterion V' (stat)-m loge'^'.

$$Z = \frac{\sqrt{pq}}{n}$$

Where,

p = number of characters

q = number of genotypes

n = degree of freedom (for error+ genotypes)

e = 2.7183

'V' (stat) is distributed as x^2 with pq degrees of freedom.

3.3.6.2 Transformation of correlated variables

In the present model, computation of D^2 values were reduced to simple summation values of the difference in mean values of various characters of the two genotypes i.e. d^2ij. Therefore, transformation of correlated variables to uncorrelated one was done before working out the D^2 values. Transformation was done by using pivotal consideration method.

3.6.6.3 Computation of D^2 values

For given a combination of 'i' and 'j' genotype, the mean deviation *i.e.*$\underline{Y}it - \underline{Y}jt$ for t= 1, 2.....p variables were computed and D^2 values were calculated as sum of squares deviations p.

$$D^2_{ij} = \sum_{t-1} (\underline{Y}it - \underline{Y}jt)^2$$

Where,

$\underline{Y}it$ = Uncorrelated mean values of i^{th} genotype for 't' character

$\underline{Y}jt$ = Uncorrelated mean values of j^{th} genotype for 't' character

D^2_{ij} = D^2 between i^{th} and j^{th} genotype

3.3.6.4 Testing the significance of D^2 values

The D^2 value obtained for a pair of genotypes was taken as the calculated value of x^2 and tested against tabulated x^2 at p degree of freedom where, "*P*" is the number of character considered.

3.6.6.5 Contribution of individual characters towards divergence

In all the combinations each character was ranked on the basis of their contribution toward divergence between two entries (di= yit-yjt).

Rank 1^{st} was given to the highest mean difference and rank p to the lowest difference, where P is the total number of characters considered percentage contribution of each character towards genetic divergence was calculated using the formula:

Percentage contribution of character = $\frac{N}{M} \times 100$

Where,

N = Number of genotype contributions where the character was ranked first

M = All possible combinations of genotypes considered

3.3.6.6 Grouping of genotypes into various clusters

Grouping of genotypes into different clusters was done by using Tocher's method. The criterion used in clustering by this method was that any two genotypes belonging to the same cluster should have a smaller D^2 value among themselves than those belonging to different clusters.

The first step in grouping the genotype into different clusters was to arrange the genotypes. in the order of their relative distance from each other. For this purpose, D^2 values of all the combinations for each genotype were arranged in the increasing order of their magnitude. To start with two genotypes having the smallest distance from each other was considered first to which third population having the smallest average D^2 value from the first two genotypes was considered and so on. At certain stage when it was felt that after adding a particular variety, there was a disrupt increase in the average D^2 value, then that genotype was not considered for inclusion in that cluster. Similarly, a second cluster was formed. The process was continued till all the genotypes were included in one or the other clusters.

3.3.6.7 Intra and inter cluster distance

Average intra cluster distance

For the measurement of intra cluster distance, the formula used was

$$\frac{\sum Di^2}{n}$$

Where,

$\sum Di^2$ = Sum of distance between all possible combinations (n) of the populations included in a cluster

n = Number of cluster

Average inter cluster distance

Clusters were taken one by one and their distance from other clusters was calculated. The distance between the two clusters as the sum of D^2 value between the number one clusters to each of the member of each cluster divided by the product of number of genotypes in both the clusters under consideration. The square root of the average D^2 value gave the genetic distance 'D' between the clusters. Based on D value (inter cluster distance), the scale given by Rao (1952) for rating of the distance was adopted and the cluster diagram was prepared.

$$\text{Average inter cluster distance} = \frac{D^2}{n1\ X\ n2}$$

When n_1 and n_2 are the number of genotypes in cluster 1 and cluster 2, respectively. Based on the 'D' values, the genotypes were categorized as indicated.

3.4 Experimental site

The present investigation was carried out at Research and Education Farm, Department of Agril. Botany, College of Agriculture, Dapoli, Dist. Ratnagiri during *rabi* 2023-2024.

The Research and Education Farm, Department of Agril. Botany comes under the Dapoli taluka. Geographically, Dapoli is situated in the tropical region on the $17^0$45.119'' North latitude and $73^0$12'' East longitude having elevation of 240 meters above the mean sea level with warm and humid conditions throughout the year. Average minimum temperature ranges from 21^0C to 25^0C and maximum temperature of this place ranges from 31°C to 35°C. The mean annual precipitation is 3000 to 4000 mm which is generally received during the month from June to September at the location. The soil of the experimental site was lateritic.

The weather data of Dapoli collected from Meteorological observatory, Department of Agronomy, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli is presented in Appendix.

CHAPTER IV : RESULTS AND DISCUSSION

An experiment entitled, "**Assessment of genetic variability and diversity for yield, biochemical and nutritional components of Lablab bean (*Lablab purpureus* (L.) Sweet)"** was undertaken at the Research and Education farm, Department of Agricultural Botany, College of Agriculture, Dapoli during *rabi* 2023-24. The results and discussion of the experiment are presented in this chapter under following headings.

4.1 Genetic variability

4.2 Correlation

4.3 Path analysis

4.4 Genetic divergence

4.1 Genetic variability

The most important prerequisite for a crop breeding programme is genetic variability. Plant breeders are therefore constantly interested in gathering or generating variety through research and recombination. Furthermore, before implementing new techniques, plant breeders should have a solid understanding of the range of variability, as well as the nature and expression of various traits, within a crop population. Therefore, evaluating population variability becomes a fundamental prerequisite for any breeding program.

For every trait of the lablab bean that was the subject of this analysis, the genotypes showed a wide range of variation. The results of the analysis of variance showed the variations in the genotypes were significant for every character that was examined. But the extent of variability varied considerably in different characters. The genotypic sum of squares was highly significant which for all characters which made the genotypes under study suitable.

4.1.1 Analysis of variance

The analysis of variance for twenty five genotypes and one check replicated in three replications was carried out for eighteen different characters in randomized block design. The mean sum of squares due to replications and treatments for all characters are given in Table 4.1. The mean sum of squares for treatments (genotypes) were significant for all the characters that were studied. The mean sum of squares for replications were non-significant for all the characters that were studied. The genotypic and error mean sum of squares were further used for analysis of genotypic and phenotypic variances.

Table 4.1 Analysis of variance for different characters studied in Lablab bean.

ANOVA Summary				
Sr. No.	**Source**	**Mean Sum of Squares (MSS)**		
		Replication	**Treatment**	**Error**
	Degrees of freedom	**2**	**25**	**50**
1	Days to 50% flowering	0.3590	24.382**	2.359
2	Days to maturity	3.6280	52.478**	2.242
3	Plant height (cm)	0.870	413.917**	12.837
4	No. of Primary branches	0.0140	0.383**	0.016
5	No. of peduncles	0.0990	1.652**	0.113
6	Pods/plant	5.4340	35.534**	2.824
7	Pod Length (cm)	0.0050	0.336**	0.012
8	No. of seeds/pod	0.020	0.152**	0.012
9	Test weight(g)	0.1370	14.801**	0.173
10	Harvest Index (%)	0.3940	10.086**	1.219
11	Seed yield / plant (g)	0.990	8.485**	0.743
12	Protein Content (%)	0.130	11.747**	0.398
13	Calcium content (mg/100g)	2.0130	214.166**	5.786
14	Iron content (mg/100g)	0.0110	2.243**	0.007
15	Potassium content (mg/100g)	88.9540	13401.065**	139.289
16	Phosphorus content (mg/100g)	96.6750	2518.657**	88.296
17	Ascorbic Acid (mg/100g)	0.040	1.206**	0.031
18	Phenols content (mg/100g)	0.0210	5.235**	0.013

* Significant at 5 percent level of significance

** Significant at 1 percent level of significance

4.1.2 Mean performance and range of variability

The variability parameters such as mean performance, range, general mean, standard error, coefficient of variance and critical difference obtained through statistical analysis for twenty five genotypes and one check of lablab bean for 18 characters are presented in Table 4.2.

1. Days to 50 per cent flowering

Days to 50 per cent flowering ranged from 64.33 to 74 days with general mean of 68.37 days for the character. Among genotypes, twenty genotypes flowered late as compared to check Konkan Wal-2. Among the genotypes, DPLW-22-6 and DPLW-22-10 express same for days to 50 per cent flowering as check Konkan wal-2 (65.33 days). The genotype DPLW-22-54 (64.33 days) and Kelshi Wal (64.33 days) were found early than the check Konkan Wal-2 whereas, Local Kadwa (74 days) and DPLW-22-8 (72 days) were found late as compared to check Konkan Wal-2 (65.33). Significant variation was also reported by Verma *et al*. (2015), Kambale *et al.* (2016), Ingle *et al*. (2016), Shailaja *et al.* (2021) in Lablab bean.

Table 4.2 Mean performance for different characters in Lablab bean.

Sr. No.	Genotypes	DFF	DTM	PH	NPBP	NPPP	PPP	PL	NSPP	TW	HI	SYPP	PRC	Ca	Fe	K	P	AA	PHC
1.	**DPLW-22-1**	66.33	100	68.95	3.33	5.73	28.47	4.25	3.93	16.17	30.27	10.54	20.15	104.67	2.77	725.22	371.88	9.11	2.52
2.	**DPLW-22-2**	71	101.33	93.01	3.73	6.87	30.60	4.57	3.93	17.20	31.08	12.11	22.88	105.33	4.06	625.77	353.44	8.31	3.15
3.	**DPLW-22-3**	69	102	86.03	3.27	7.07	32.40	4.42	3.67	14.39	34.35	15.30	18.67	95.00	3.07	570.77	336.56	10.28	4.20
4.	**DPLW-22-4**	66.33	99	84.14	3.87	7.53	34.67	4.75	4.00	22.03	31.37	15.33	25.37	96.33	2.50	599.11	395.66	10.34	4.75
5.	**DPLW-22-5**	66.67	96	65.98	3.33	4.80	21.93	4.63	3.93	18.75	33.63	13.43	24.83	95.00	2.54	666.00	367.00	8.92	5.30
6.	**DPLW-22-6**	65.33	100.67	98.98	3.40	6.53	29.07	4.43	3.80	19.55	32.39	12.84	22.93	100.00	3.31	765.00	336.00	10.24	2.30
7.	**DPLW-22-7**	70.67	105.33	84.44	3.33	4.60	21.47	5.04	3.93	17.62	33.83	10.47	22.69	109.67	3.12	676.11	374.89	9.52	1.67
8.	**DPLW-22-8**	72	98.33	84.18	3.60	5.47	27.53	4.56	4.00	17.26	32.89	13.50	21.53	95.33	4.67	569.56	359.89	10.34	4.76
9.	**DPLW-22-9**	68.33	109.67	91.35	3.67	5.20	24.73	4.67	3.80	14.92	35.08	11.27	19.15	121.00	2.35	727.22	400.33	9.53	2.59
10.	**DPLW-22-10**	65.33	101.67	96.54	3.73	5.13	24.13	4.44	3.80	16.00	34.79	11.87	21.47	100.33	5.33	746.89	355.89	10.44	5.53

Note: DFF-Days to 50% flowering, DM-Days to maturity, PH-Plant height (cm) , NPBP-Number of primary branches per plant, NPPP-Number of peduncles per plant, PPP- Pods per plant, PL-Pod length (cm) , NSPP-Number of seeds per pod, TW-Test weight (g), HI-Harvest index (%) , SYPP-Seed yield/plant, PRC- Protein content (%) , Ca-Calcium (mg/100g), Fe-Iron (mg/100g), K-Potassium (mg/100g), P-Phosphorus (mg/100g), AA-Ascorbic Acid (mg/100g), PHC-Phenol content (mg/100g).

Continued Table 4.2...

Sr. No.	Genotypes	DFF	DTM	PH	NPBP	NPPP	PPP	PL	NSPP	TW	HI	SYPP	PRC	Ca	Fe	K	P	AA	PHC
11.	**DPLW-22-12**	71.67	110	69.23	3.53	5.40	26.20	4.66	4.00	14.97	35.97	11.75	23.32	119.33	2.66	684.78	337.22	9.87	4.16
12.	**DPLW-22-13**	65.67	104.67	74.14	3.47	5.73	26.20	3.81	3.67	17.31	31.39	12.05	21.46	112.67	4.36	702.89	406.33	8.23	5.24
13.	**DPLW-22-14**	69.33	103.33	78.36	3.73	5.47	23.60	4.84	4.00	16.17	32.30	10.12	22.27	102.67	2.85	617.00	312.33	9.10	3.64
14.	**DPLW-22-33**	71.33	102	88.49	3.93	5.00	21.87	4.64	4.00	18.62	31.33	10.84	22.65	106.00	1.66	719.78	375.56	9.32	2.98
15.	**DPLW-22-45**	72	98.33	78.30	3.33	5.60	24.07	4.14	3.53	19.72	36.00	11.77	20.51	104.33	3.72	575.56	364.00	10.15	3.63
16.	**DPLW-22-48**	66	98	65.38	3.40	6.13	27.27	4.63	4.00	18.50	32.55	11.30	20.52	94.33	3.48	612.11	403.33	9.19	6.27
17.	**DPLW-22-54**	64.33	96.33	69.67	3.53	5.47	25.47	4.79	3.93	19.30	35.03	13.23	20.54	108.67	3.55	634.77	357.11	9.72	5.61
18.	**DPLW-22-61**	65	100.33	90.55	3.27	6.33	25.07	4.63	3.93	19.38	32.40	13.11	20.75	105.00	2.81	649.33	333.22	10.02	3.67
19.	**Pavata**	67.67	105.67	103.58	3.33	7.13	33.80	5.42	4.73	21.30	35.41	14.93	24.83	103.00	4.24	662.67	417.67	9.14	6.63
20.	**Local Pen**	69.67	111.33	74.75	3.13	5.87	25.47	4.54	4.00	19.17	30.33	9.77	25.01	117.00	2.62	775.67	322.78	9.24	5.20
21.	**Local Kadwa**	74	109	83.19	3.27	5.33	24.33	4.05	4.00	14.91	30.07	9.25	20.63	104.00	4.48	791.33	347.22	10.44	3.83

Note: DFF-Days to 50% flowering, DM-Days to maturity, PH-Plant height (cm) , NPBP-Number of primary branches per plant, NPPP-Number of peduncles per plant, PPP- Pods per plant, PL-Pod length (cm) , NSPP-Number of seeds per pod, TW-Test weight (g), HI-Harvest index (%) , SYPP-Seed yield/plant, PRC-Protein content (%) , Ca-Calcium (mg/100g), Fe-Iron (mg/100g), K-Potassium (mg/100g), P-Phosphorus (mg/100g), AA-Ascorbic Acid (mg/100g), PHC-Phenol content (mg/100g).

Continued Table 4.2...

Sr. No.	Genotypes	DFF	DTM	PH	NPBP	NPPP	PPP	PL	NSPP	TW	HI	SYPP	PRC	Ca	Fe	K	P	AA	PHC
22.	**Local Alibaug**	70.67	106	58.50	2.53	5.73	23.74	4.11	3.53	16.85	30.24	9.67	23.30	97.33	2.55	665.89	319.77	9.07	6.20
23.	**Kadwa Wal**	71.33	102	60.53	2.47	6.20	27.93	4.24	3.67	16.05	33.56	11.00	25.12	104.00	3.67	657.45	344.67	10.22	3.48
24.	**Kelshi Wal**	64.33	100.33	78.62	3.40	6.53	25.67	4.83	4.00	20.90	31.66	13.53	24.67	126.33	2.73	793.22	350.67	10.06	5.60
25.	**Goda Wal**	68.33	104	76.56	2.73	5.60	27.93	4.30	4.00	13.47	32.18	12.48	19.91	105.00	4.15	700.89	320.56	10.00	3.72
26.	**Konkan Wal-2**	65.33	101	80.74	3.27	5.87	26.07	4.62	4.00	18.37	32.56	11.49	20.81	111.00	3.83	719.33	338.78	9.76	4.61
General Mean		68.37	102.55	80.16	3.37	5.86	26.53	4.54	3.92	17.65	32.79	12.04	22.15	105.51	3.35	678.24	357.8	9.64	4.28
CV %		2.25	1.46	4.47	3.75	5.73	6.33	2.41	2.8	2.36	3.37	7.16	2.85	2.28	2.46	1.74	2.63	1.84	2.63
SE_m		0.89	0.86	2.07	0.07	0.19	0.97	0.06	0.06	0.24	0.64	0.5	0.36	1.39	0.05	6.81	5.43	0.1	0.06
CD at 5%		2.52	2.46	5.88	0.21	0.55	2.76	0.18	0.18	0.68	1.81	1.41	1.04	3.94	0.14	19.36	15.41	0.29	0.18
CD at 1%		3.36	3.27	7.83	0.28	0.73	3.67	0.24	0.24	0.91	2.41	1.88	1.38	5.26	0.18	25.8	20.54	0.39	0.25
Minimum		64.33	96	58.50	2.47	4.60	21.47	3.81	3.53	13.47	30.07	9.25	18.67	94.33	1.66	569.56	312.33	8.23	1.67
Maximum		74	111.33	103.58	3.93	7.53	34.67	5.42	4.73	22.02	36	15.33	25.37	126.33	5.33	793.22	417.67	10.44	6.63

Note: DFF-Days to 50% flowering, DM-Days to maturity, PH-Plant height (cm) , NPBP-Number of primary branches per plant, NPPP-Number of peduncles per plant, PPP- Pods per plant, PL-Pod length (cm) , NSPP-Number of seeds per pod, TW-Test weight (g), HI-Harvest index (%), SYPP-Seed yield/plant, PRC-Protein content (%) , Ca-Calcium (mg/100g), Fe-Iron (mg/100g), K-Potassium (mg/100g), P-Phosphorus (mg/100g), AA-Ascorbic Acid (mg/100g), PHC-Phenol content (mg/100g).

2. Days to maturity

Days to maturity ranged from 96 to 111.33 days with general mean of 102.55 days for the character. Fifteen genotypes were late in maturity as compared to check. The genotype DPLW-22-5 (96 days) and DPLW-22-54 (96.33 days) were early maturing than the check Konkan wal-2 (101 days). The genotypes Local Pen (111.33 days) and DPLW-22-12 (110 days) had late maturity.

Days to maturity showed significant variation, suggesting that the genotypes varied for this character. For cultivation during the *rabi* season in the Konkan region, early genotypes are necessary. Compared to the check Konkan Wal-2, two genotypes in the current study DPLW-22-5 and DPLW-22-54 exhibited earlier maturity. Verma *et al*. (2015), Kambale *et al.* (2016), Ingle *et al*. (2016), Shailaja *et al.* (2021) also reported the variation for this characters in Lablab bean.

3. Plant height (cm)

Plant height ranged from 58.50 to 103.58 cm with the general mean 80.16 cm for plant height for the character. Thirteen genotypes were dwarf and 12 genotypes were tall than the check for plant height. Among the genotypes, Pavata (103.58 cm) and DPLW-22-6 (98.98 cm) were found tall than the check Konkan Wal-2 (80.74cm). The genotypes Local Alibaug (58.50 cm) and Kadwa Wal (60.53 cm) were found dwarf. In this crop, the determinate type plant habit is most preferred. Topare (1994), Gadakh (2014), Chaudhari *et al.* (2016), Kambale *et al*. (2016), Patel *et al.* (2022) have also documented a wide range of variation for plant height in lablab beans.

4. Number of primary branches per plant

The number of primary branches per plants ranged from 2.47 to 3.93 with the general mean 3.37 for the character. Eighteen genotypes recorded higher, four genotypes recorded lower and three genotypes recorded same number of primary branches per plant as check Konkan Wal-2 (3.27). Highest number of primary branches per plant were recorded in DPLW-22-33 (3.93) followed by DPLW-22-4 (3.87). Lowest number of primary branches per plant were recorded in Kadwa Wal (2.47) followed by Local Alibaug (2.53).

Research on lablab beans has indicated that a plant with a higher number of peduncles and pods per plant would be preferred; this could be accomplished by adjusting the number of primary branches on each plant. Significant differences were reported by Pandey and Dubey (1972), Kurane (1997), Basavrajappa and Gowda (2004), Gondhalekar (2013), Gadakh (2014), Kambale *et al*. (2016), Ingle *et al.* (2016), Patel *et al.* (2022) and Singh *et al.* (2024).

5. Number of peduncles per plant

The general mean for the character was 5.86 which ranged from 4.60 to 7.53 for number of peduncles per plant. Nine genotypes had more number of peduncles per plants as compared to the check Konkan Wal-2. Fifteen genotypes showed lesser number of peduncles per plants as compared to the check. Same number of peduncles per plant were recorded in Local Pen and check Konkan wal-2 (5.87). Maximum number of peduncles per plant were recorded in DPLW-22-4 (7.53) followed by Pavata (7.13). DPLW-22-7 (4.60) and DPLW-22-5 (4.80) showed lowest number of peduncles per plant. Significant variation have been reported by Pandey and Dubey (1972), Kurane (1997), Basavrajappa and Gowda (2004), Gondhalekar (2013), Gadakh (2014), Kambale *et al*. (2016), Ingle *et al.* (2016), Patel *et al.* (2022) and Singh *et al.* (2024).

6. Number of pods per plant

Number of pods per plant ranged from 21.47 to 34.67 with general mean 26.53 for the character. Twelve genotypes had higher number of pods per plant as compared to check Konkan Wal-2 (26.07) and thirteen genotypes had lower. Maximum number of pods per plant were recorded in DPLW-22-4 (34.67) followed by Pavata (33.80). DPLW-22-7 (21.47) and DPLW-22-33 (21.87) showed lowest number of pods per plant. For improvement in yield number of pods has positive correlation.

Significant variations were also reported by Pandey and Dubey (1972), Kurane (1997), Basavrajappa and Gowda (2004), Gondhalekar (2013), Gadakh (2014), Kambale *et al*. (2016), Ingle *et al.* (2016), Patel *et al.* (2022) and Singh *et al.* (2024).

7. Pod length (cm)

The general mean for the character was 4.54 cm and pod length ranged from 3.81 to 5.42 cm for pod length. Among the genotypes twelve genotypes had higher pod length than check. Genotype Pavata (5.42) recorded maximum pod length while minimum was observed in DPLW-22-13 (3.81 cm).

Similar differences have been reported by results have been reported by Pandey and Dubey (1972), Kurane (1997), Basavrajappa and Gowda (2004), Gondhalekar (2013), Gadakh (2014), Kambale *et al*. (2016), Ingle *et al.* (2016), Patel *et al.* (2022) and Singh *et al.* (2024).

8. Number of seeds per pod

The general mean for the character was 3.92 and number of seeds per pod ranged from 3.53 to 4.73. Maximum number of seeds per pod was recorded Pavata (4.73). Check Konkan Wal-2 had 4.00 seeds per pod. Minimum number of seeds per pod were recorded in Local

Alibaug and DPLW-22-45 (3.53). The number of seeds per plant has the crucial role in maximization of yield. Gadakh (2014) and Kambale *et al*. (2016) reported variation in the character seed per pod in lablab beans.

9. Test weight (g)

Test weight ranged from 13.47 to 22.02 g with the general mean 17.65 g for the character. Eleven genotypes recorded higher test weight than the check. Maximum test weight was recorded in DPLW-22-4 (22.02 g) and minimum test weight was observed in Goda Wal (13.47). As per the consumer preference, small seeds of lablab bean are also liked in some urban areas. Salim *et al.* (2013) also reported variation for test weight.

10. Harvest index (%)

Harvest index ranged from 30.07 to 36 % with general mean 32.79 % for the character. Eleven genotypes showed higher harvest index compared to the check. Maximum harvest index was recorded in DPLW-22-45 (36 %) followed by DPLW-22-12 (35.97%), Pavata (35.41%). Minimum harvest index was recorded in Local Kadwa (30.07 %). Similar variation was reported by results have been reported by Pandey and Dubey (1972), Kurane (1997), Basavrajappa and Gowda (2004), Gondhalekar (2013), Gadakh (2014), Kambale *et al*. (2016), Ingle *et al.* (2016), Patel *et al.* (2022) and Singh *et al.* (2024).

11. Seed yield per plant (g)

The general mean for the character was 12.04 g and seed yield per plant ranged from 9.25 to 15.33 g. Higher seed yield per plant was recorded in fifteen genotypes as compared to the check. The maximum seed yield per plant was observed in DPLW-22-4 (15.33 g) followed by DPLW-22-3 (15.30 g) and Pavata (14.93 g). Minimum seed yield per plot was recorded in Local Kadwa (9.25 g). Higher seeds yield is the ultimate aim of breeder to improve the crop.

Gadakh (2014) and Kambale *et al*. (2016) reported similar types of variation in the character seed yield per plant in lablab beans. Similar trends in variance for this property in lablab bean were also documented by Pandita *et al*. (1980) and Basavarajappa and Gowda (2004).

12. Protein content (%)

Protein content ranged from 18.67 to 25.37 % with general mean 22.15 % for the character. Highest protein content was recorded in the genotype DPLW-22-4 (25.37%) followed by Kadwa Wal (25.12%) and Local Pen (25.01%). Minimum protein was recorded in DPLW-22-3 (18.67%). Pulses are the richest source of protein and wal is one of the most important crop.

Significant differences were reported by Davari *et al*. (2018), Nidhin *et al.* (2021) and Mohammad *et al.* (2021) for various components.

13. Calcium content (mg/100g)

Calcium content ranged from 94.33 to 126.33 mg/100g with general mean 105.51 mg/100g for the character. Calcium content of 111 mg/100g was recorded in check Konkan Wal-2. Highest calcium content was recorded in Kelshi Wal (126.33 mg/100g) followed by DPLW-22-9 (121 mg/100g) and DPLW-22-12 (119.33 mg/100g). DPLW-22-48 (94.33 mg/100g) recorded minimum calcium content. Calium is one of important nutrients. Similar significant variations were reported by Davari *et al*. (2018), Nidhin *et al.* (2021) and Mohammad *et al.* (2021) for various components.

14. Iron content (mg/100g)

Iron content ranged from 1.66 to 5.33 mg/100g with the general mean 3.35 mg/100g for the character. Highest iron content was recorded in DPLW-22-10 (5.33 mg/100g) followed by DPLW-22-8 (4.67 mg/100g) and Local Kadwa (4.48 mg/100g). Minimum iron content was recorded in DPLW-22-33 (1.66 mg/100g). Similar variation in the results were reported by Davari *et al*. (2018), Nidhin *et al.* (2021) and Mohammad *et al.* (2021) for various components.

15. Potassium content (mg/100g)

The general mean for the character was 678.24 mg/100g and the potassium content ranged from 569.56 to 793.22 mg/100g. Maximum potassium content was recorded in Kelshi Wal (793.22 mg/100 g) followed by Local Kadwa (791.33 mg/100g) and Local Pen (775.67 mg/100g). Minimum potassium content was observed in DPLW-22-8 (569.56 mg/100g). Similar differences were reported by Davari *et al*. (2018), Nidhin *et al.* (2021) and Mohammad *et al.* (2021) for various components.

16. Phosphorus content (mg/100g)

The general mean for the character was 357.8 mg/100g and the phosphorus content ranged from 312.33 to 417.67 mg/100g. Genotype Pavata (427.67 mg/100g) recorded highest phosphorus content followed by DPLW-22-13 (406.33 mg/100g) and DPLW-22-48 (403.33). Minimum phosphorus content was recorded in DPLW-22-14 (312.33 mg/100g). Similar variation in results were reported by Davari *et al*. (2018), Nidhin *et al.* (2021) and Mohammad *et al.* (2021) for various components.

17. Ascorbic acid (mg/100g)

Ascorbic acid content ranged from 8.23 to 10.44 mg/100g with the general mean 9.64 mg/100g for the character. Local Kadwa (10.44 mg/100g) and DPLW-22-10 (10.44 mg/100g)

recorded highest ascorbic acid content followed by DPLW-22-4, DPLW-22-8 and DPLW-22-3 with 10.34 mg/100g, 10.34 mg/100g and 10.28 mg/100 g of ascorbic acid. Minimum ascorbic acid content was recorded in DPLW-22-13 (8.23 mg/100g). Debarati *et al.* (2023) also reported similar variation for results for phenol content.

18. Phenols content (mg/100g)

The general mean for the character was 4.28 mg/100g and phenols content ranged from 1.67 to 6.63 mg/100g. Highest phenols content was observed in Pavata (6.63 mg/100g) followed by DPLW-22-48 (6.27 mg/100g) and Local Alibaug (6.20 mg/100g). Minimum phenols content was recorded in DPLW-22-7 (1.67 mg/100g). Phenols are crucial for both plant and human health due to their protective and functional properties. Debarati *et al.* (2023) also reported significant variation for phenol content.

4.1.3 Components of variation

The total variation of the population was divided into genotypic, phenotypic and environmental variance. The estimates of variance due to these three components for different characters are presented in Table 4.3.

The phenotypic variance ranged from 0.12 to 4559.88, genotypic variance ranged from 0.05 to 4420.59 and environmental variance ranged from 0.01 to 139.29 for various characters. Phenotypic variance was higher in magnitude than genotypic variance. The phenotypic variance was maximum for potassium content (4559.88) followed by phosphorus content (898.42) and minimum pod length (0.12) followed by number of primary branches per plant (0.14).

The magnitude of genotypic variance was maximum in potassium content (4420.59) followed by phosphorus content (810.12) and minimum for number of seeds per pod (0.05) followed by pod length (0.11). The magnitude for environmental variance was higher in potassium content (139.29) followed by phosphorus content (88.30) and minimum for pod length (0.01), number of seeds per pod (0.01), iron content (0.01), phenols content (0.01) followed by ascorbic acid content (0.03). Ingle (2020) reported the findings that phenotypic variance was higher than the genotypic variance.

4.1.4 Coefficient of variation

Table 4.4 represents the estimates of coefficient of variation at phenotypic and genotypic levels.

Phenotypic coefficients of variation were greater in magnitude over the respective genotypic coefficient of variation. Highest phenotypic coefficient of variation was exhibited by the phenols content (30.95%), followed by iron content (25.89%), seed yield per plant (15.15%)

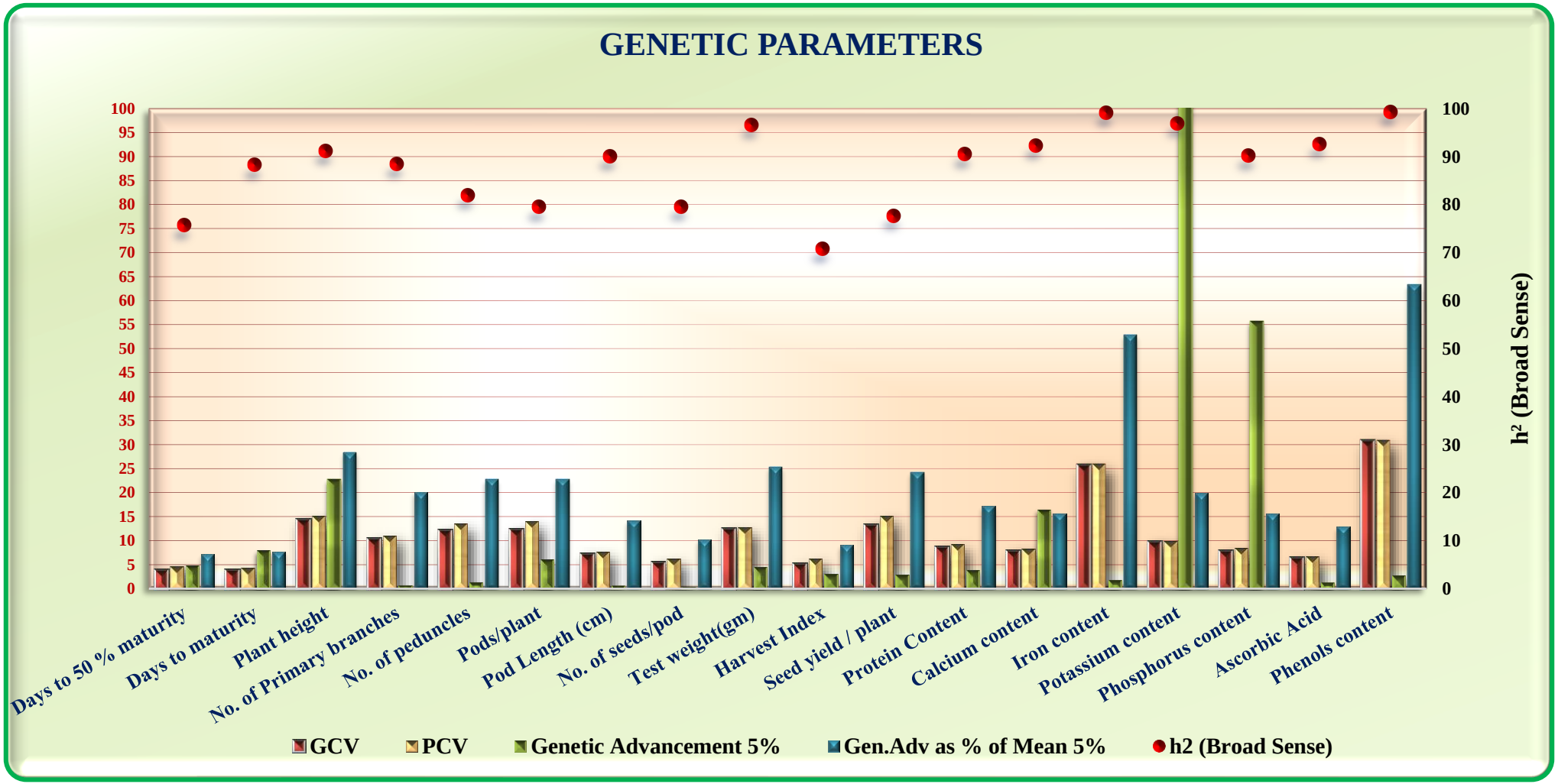


Fig. 4.1. Graphical representation of genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as a percentage of the mean

and plant height (15.10%). The phenotypic coefficient of variation for the other characters were – number of pods per plant (13.97%), number of peduncles per plant (13.50%), test weight (12.73%), number of primary branches (11.04%), potassium content (9.96%), protein content (9.23%), phosphorus content (8.38%), calcium content (8.22%), pod length (7.62%), ascorbic acid content (6.75%), harvest index (6.23%), number of seeds per pod (6.19%), days to 50 per cent flowering (4.56%) and days to maturity(4.25%).

Table 4.3 Estimates of phenotypic (σ^2_p), genotypic (σ^2_g) and environmental (σ^2_e) variance for different characters of Lablab bean.

Sr. No.	**Characters**	σ^2_p	σ^2_g	σ^2_e
1	Days to 50% flowering	9.70	7.34	2.36
2	Days to maturity	18.99	16.75	2.24
3	Plant height (cm)	146.53	133.69	12.84
4	No. of Primary branches	0.14	0.12	0.02
5	No. of peduncles	0.63	0.51	0.11
6	Pods/plant	13.73	10.90	2.82
7	Pod Length (cm)	0.12	0.11	0.01
8	No. of seeds/pod	0.06	0.05	0.01
9	Test weight(g)	5.05	4.88	0.17
10	Harvest Index (%)	4.17	2.96	1.22
11	Seed yield / plant (g)	3.32	2.58	0.74
12	Protein Content (%)	4.18	3.78	0.40
13	Calcium content (mg/100g)	75.25	69.46	5.79
14	Iron content (mg/100g)	0.75	0.75	0.01
15	Potassium content (mg/100g)	4559.88	4420.59	139.29
16	Phosphorus content (mg/100g)	898.42	810.12	88.30
17	Ascorbic Acid (mg/100g)	0.42	0.39	0.03
18	Phenols content (mg/100g)	1.75	1.74	0.01

Genotypic coefficient of variation represents the amount of genetic variation present in the population under study. Phenols content (30.83%) exhibited highest genotypic coefficient of variation followed by iron content (25.77%), plant height (14.42%), seed yield per plant (13.35%) and test weight (12.51%). Lowest GCV was observed in days to 50 per cent flowering (3.96%) followed by days to maturity (3.99%). The GCV for remaining characters were as, plant height (14.42%), seed yield per plant (13.35%), test weight (12.51%), number of pods per plant (12.45%), number of peduncles per plant (12.22%), number of primary branches per plant (10.38%), potassium content (9.80%), protein content (8.78%), phosphorus content (7.96%),

calcium content (7.90%), pod length (7.23%), ascorbic acid content (6.49%), number of seeds per pod (5.52%) and harvest index (5.24%).

The study found that the total variability in each of the eighteen characters could be divided into three components: phenotypic, genotypic, and environmental variation. This allows researchers to identify the heritable and non-heritable portion of variation in relation to the characters under investigation. The character days to maturity, days to 50% flowering, and number of pods per plant showed moderate variability, which is consistent with findings from studies conducted on lablab beans by Kurane (1997), Bapat (1999), Gondhalekar (2013), Kambale (2016), and Ingle (2016).

Both the phenotypic coefficient of variation (PCV) and the genotypic coefficient of variation (GCV) quantify the degree of variation observed in the population for a given character. In general, the PCV was found to be larger than the genotypic coefficient of variation in the current analysis for all the characters studied. It shows how the environment affects genotypes, which may have some bearing on how the genotypes express themselves. The PCV recorded of seed yield per plant, plant height, the number of pods per plant, indicated that environmental influences had an impact on these characteristics. The days to maturity had the lowest value. Muralidharan (1980), Patil and Lad (2007), Hotti (2010), Chaudhary *et al.* (2016), Kambale *et al.* (2016) and Shailaja *et al.* (2021) all reported findings that were similar.

Comparing the amount of variation and evaluating genetic variability for different features are made possible by the genotypic coefficient of variation (GCV). The GCV recorded for the characters plant height, test weight, number of pod, seed yield and number of peduncles, whereas the character days to 50 per cent flowering and days to maturity showed the lowest GCV.

In terms of lablab beans, these findings concur with those of Bendale *et al.* (2004), Gondhalekar (2013), Pawar and Prajapati (2013), and Gadakh (2014). The highest GCV was recorded in phenols content followed by iron content.

4.1.5 Heritability and genetic advance

Heritability in broad sense range from 70.81 to 99.28 per cent. Phenols content (99.28%) exhibited highest estimates of heritability followed by iron content (99.10%), potassium content (96.95%), test weight (96.57%) and ascorbic acid content (92.58%). Harvest index (70.81%) recorded the lowest estimates of heritability.

The very high heritability was observed for test weight (96.57%), plant height (91.24%), pod length (90.03%), number of primary branches (88.45%), days to maturity (88.19%), number

of peduncles (81.97%). High heritability in broad sense was observed for number of seeds per pod (79.55%), number of pods per plant (79.43%), seed yield per plant (77.65%), days to 50 per cent flowering (75.68%) and harvest index (70.81%). These findings in the lablab bean are consistent with those of Joshi (1971), Muralidharan (1980), Topare (1994), Bapat (1999), Basavarajappa and Gowda (2004), Bendale (2004), Patil and Lad (2007), Gondhalekar (2013), Pawar and Prajapati (2013), Gadakh (2014), Ingle (2016), Samsuzzaman *et al.* (2023). Heritability provides insight into the role that genotype plays in a character's expression, as a result, selection pressure may be given to such characteristics.

Table 4.4 Estimates of genetic parameters for different characters in Lablab bean.

Sr. No.	Genetic Parameters	PCV (%)	GCV (%)	h^2bs (%)	GA (%)	GAM (%)
1	Days to 50% flowering	4.56	3.96	75.68	4.86	7.10
2	Days to maturity	4.25	3.99	88.19	7.92	7.72
3	Plant height (cm)	15.10	14.42	91.24	22.75	28.38
4	No. of Primary branches	11.04	10.38	88.45	0.68	20.12
5	No. of peduncles	13.50	12.22	81.97	1.34	22.80
6	Pods/plant	13.97	12.45	79.43	6.06	22.86
7	Pod Length (cm)	7.62	7.23	90.03	0.64	14.13
8	No. of seeds/pod	6.19	5.52	79.55	0.40	10.14
9	Test weight (g)	12.73	12.51	96.57	4.47	25.33
10	Harvest Index (%)	6.23	5.24	70.81	2.98	9.09
11	Seed yield / plant (g)	15.15	13.35	77.65	2.92	24.23
12	Protein Content (%)	9.23	8.78	90.47	3.81	17.20
13	Calcium content (mg/100g)	8.22	7.90	92.31	16.50	15.63
14	Iron content (mg/100g)	25.89	25.77	99.10	1.77	52.86
15	Potassium content (mg/100g)	9.96	9.80	96.95	134.86	19.88
16	Phosphorus content (mg/100g)	8.38	7.96	90.17	55.68	15.56
17	Ascorbic Acid (mg/100g)	6.75	6.49	92.58	1.24	12.87
18	Phenols content (mg/100g)	30.95	30.83	99.28	2.71	63.29

Very high heritability in broad sense was observed for phenols content (99.28%), iron content (99.10%), potassium content (96.95%), ascorbic acid content (92.58%), calcium content (92.31%), protein content (90.47%) and phosphorus content (90.17%).

The estimates of genetic advance ranged from 0.40 to 134.86 per cent. Highest estimates of genetic advance were observed in potassium content (134.86%) followed by phosphorus content (55.68%). Lowest estimates of genetic advance was observed in number of seeds per pod (0.40%).

The quantitative character inheritance pattern is revealed by the heritability estimates; however, the amount of genetic gain derived from the selection of the best individual within the best group is not indicated. Therefore, selection benefits more from heredity in combination with genetic advancement than from heritability alone. In yield and yield attributing characters, plant height had the highest estimates of genetic advancement as a percentage of mean, followed by test weight, seed yield per plant, number of pods per plant, number of peduncles per plant and number of primary branches. These results suggested that selection had a role in improving these characters. Bendale *et al.* (2004) also observed high genetic advance in lablab beans expressed as a percentage of mean seed yield per plant.

The range of genetic advance as per cent of mean was from 7.10 to 63.29 per cent. The highest value was observed in phenols content (63.29%) followed by iron content (52.86%) whereas, lowest value for genetic advance as per cent of mean was observed in days to 50 per cent flowering (7.10%) followed by days to maturity (7.72%). According to Gadakh (2014), Lahari *et al.* (2022) the lablab bean showed a remarkable genetic progress as a percentage of mean in plant height, hundred seed weight, and seed yield per plant.

For plant height (in cm), number of peduncles per plant, number of pods per plant, test weight (g) and seed yield per plant, high heritability estimates and high genetic advance as a percentage of mean were observed. Similar findings were also reported by Bendale (2004), Pawar and Prajapati (2013), Gadakh (2014), and Ingle (2016) in lablab beans.

High heritability combined with high genetic advance as a percent of mean suggests that the heritability is most likely due to additive gene effects and selection may be effective. The influence of non-additive gene action was suggested by high heritability estimates with low genetic advance observed in days to 50 per cent flowering days to maturity, number of seeds per pod and pod length. Selections for such traits may not be effective. Similar results were also reported by Muralidharan (1980) and Topare (1994).

4.2 Correlation

It is crucial to understand the correlation between the yield and its component characters since the seed yield is dependent on several independent characters. Finding the reciprocal relationship between yield and its constituent characters can be accomplished with the use of the correlation analysis. The phenotypic and genotypic correlation estimates offer a useful method for anticipating the selection response and separating attractive individuals from the breeding population. To investigate the phenotypic and genotypic associations between characteristics for every feasible combination of characters, the correlation coefficients were calculated. Tables 4.5 and 4.6, respectively, show the phenotypic and genotypic correlation between the 18 characters.

4.2.1 Phenotypic correlation coefficient

The results provided in Table 4.5 indicated that days to 50 per cent flowering showed positive highly significant correlation with days to maturity (0.922), plant height (0.537), number of primary branches per plant (0.632), number of peduncles (0.536), number of pods per plant (0.536), pod length (0.737), number of seeds per pod (0.801), test weight (0.517), harvest index (0.805), protein content (0.734), calcium content (0.740), iron content (0.379), potassium content (0.661), phosphorus content (0.704), ascorbic acid content (0.805) and seed yield per plant (0.430). Positive non-significant correlation was recorded for phenols content (0.219).

Days to maturity showed positive highly significant correlation with plant height (0.589), number of primary branches per plant (0.632), number of peduncles (0.576), number of pods per plant (0.549), pod length (0.773), number of seeds per pod (0.840), test weight (0.529), harvest index (0.806), protein content (0.742), calcium content (0.855), potassium content (0.804), phosphorus content (0.727), ascorbic acid content (0.786) and seed yield per plant (0.438). Positive significant correlation was recorded for phenols content (0.281) and iron content (0.350).

Plant height had positive highly significant correlation with number of primary branches per plant (0.708), number of peduncles (0.552), number of pods per plant (0.530), pod length (0.669), number of seeds per pod (0.672), test weight (0.525), harvest index (0.582), protein content (0.418), calcium content (0.483), iron content (0.417), potassium content (0.513), phosphorus content (0.582), ascorbic acid content (0.590) and seed yield per plant (0.568). Positive non-significant correlation was recorded for phenols content (0.029).

Number of primary branches per plant showed positive highly significant correlation with number of peduncles (0.439), number of pods per plant (0.452), pod length (0.729), number of seeds per pod (0.705), test weight (0.597), harvest index (0.671), protein content (0.519), calcium content (0.603), potassium content (0.503), phosphorus content (0.728), ascorbic acid content (0.588) and seed yield per plant (0.537). Positive significant correlation was recorded for iron content (0.244) and positive non-significant correlation was recorded for phenols content (0.1737).

Number of peduncles per plant showed positive highly significant correlation with number of pods per plant (0.877), pod length (0.601), number of seeds per pod (0.647), test weight (0.635), harvest index (0.524), protein content (0.593), calcium content (0.462), potassium content (0.368), phosphorus content (0.569), ascorbic acid content (0.573), phenols content (0.397) and seed yield per plant (0.695). Positive significant correlation was recorded for iron content (0.303).

4.5 Estimates of phenotypic correlation coefficient between different characters in Lablab bean.

Phenotypic Correlation Matrix																		
Characters	**DFF**	**DTM**	**PH**	**NPBP**	**NPPP**	**PPP**	**PL**	**NSPP**	**TW**	**HI**	**PRC**	**Ca**	**Fe**	**K**	**P**	**AA**	**PHC**	**SYPP**
DFF	1	0.922**	0.537**	0.632**	0.536**	0.536**	0.737**	0.801**	0.517**	0.805**	0.734**	0.740**	0.379**	0.661**	0.704**	0.805**	0.219	0.430**
DTM		1	0.589**	0.632**	0.576**	0.549**	0.773**	0.840**	0.529**	0.806**	0.742**	0.855**	0.350*	0.804**	0.727**	0.786**	0.281*	0.438**
PH			1	0.708**	0.552**	0.530**	0.669**	0.672**	0.525**	0.582**	0.418**	0.483**	0.417**	0.513**	0.582**	0.590**	0.029	0.568**
NPBP				1	0.439**	0.452**	0.729**	0.705**	0.597**	0.671**	0.519**	0.603**	0.244*	0.503**	0.728**	0.588**	0.1737	0.537**
NPPP					1	0.877**	0.601**	0.647**	0.635**	0.524**	0.593**	0.462**	0.303*	0.368**	0.569**	0.573**	0.397**	0.695**
PPP						1	0.584**	0.651**	0.504**	0.539**	0.536**	0.393**	0.373**	0.309*	0.611**	0.576**	0.319*	0.709**
PL							1	0.907**	0.731**	0.813**	0.746**	0.711**	0.2167	0.577**	0.748**	0.701**	0.329*	0.632**
NSPP								1	0.706**	0.771**	0.765**	0.730**	0.384**	0.689**	0.789**	0.730**	0.403**	0.612**
TW									1	0.583**	0.754**	0.536**	0.1538	0.475**	0.691**	0.542**	0.470**	0.610**
HI										1	0.641**	0.727**	0.412**	0.558**	0.762**	0.811**	0.319*	0.645**
PRC											1	0.653**	0.1948	0.640**	0.626**	0.621**	0.413**	0.487**
Ca												1	0.2039	0.817**	0.646**	0.662**	0.198	0.390**
Fe													1	0.269*	0.363*	0.425**	0.337*	0.295*
K														1	0.560**	0.650**	0.1907	0.248*
P															1	0.608**	0.357*	0.607**
AA																1	0.241*	0.595**
PHC																	1	0.399**
SYPP																		1

*Significant at 5 % level **Significant at 1 % level

Note: DFF-Days to 50% flowering, DM-Days to maturity, PH-Plant height (cm), NPBP-Number of primary branches per plant, NPPP-Number of peduncles per plant, PPP- Pods per plant, PL-Pod length (cm), NSPP-Number of seeds per pod, TW-Test weight (g) , HI-Harvest index (%), SYPP-Seed yield/plant, PRC-Protein content (%), Ca-Calcium (mg/100g), Fe-Iron (mg/100g), K-Potassium(mg/100g), P-Phosphorus (mg/100g), AA-Ascorbic Acid(mg/100g), PHC-Phenol content (mg/100g)

Number of pods per plant showed positive highly significant correlation with pod length (0.584), number of seeds per pod (0.651), test weight (0.504), harvest index (0.539), protein content (0.536), calcium content (0.393), iron content (0.373), phosphorus content (0.611), ascorbic acid content (0.576) and seed yield per plant (0.709). Positive significant correlation was recorded for potassium content (0.309) and phenols content (0.319).

Pod length showed positive highly significant correlation with number of seeds per pod (0.907), test weight (0.731), harvest index (0.813), protein content (0.746), calcium content (0.711), potassium content (0.577), phosphorus content (0.748), ascorbic acid content (0.701) and seed yield per plant (0.632). Positive significant correlation was recorded for phenols content (0.329) and positive non-significant correlation for iron content (0.2167).

Number of seeds per pod showed positive highly significant correlation with test weight (0.706), harvest index (0.771), protein content (0.765), calcium content (0.730), iron content (0.384), potassium content (0.689), phosphorus content (0.789), ascorbic acid content (0.730), phenols content (0.403) and seed yield per plant (0.632).

Test weight showed positive highly significant correlation with harvest index (0.583), protein content (0.754), calcium content (0.536), potassium content (0.475), phosphorus content (0.691), ascorbic acid content (0.542), phenols content (0.470) and seed yield per plant (0.610). Iron content showed positive non-significant correlation (0.1538).

Harvest index showed positive highly significant correlation with protein content (0.641), calcium content (0.727), iron content (0.412), potassium content (0.558), phosphorus content (0.762), ascorbic acid content (0.811) and seed yield per plant (0.645). Positive significant correlation was observed with phenols content (0.319).

Protein content showed positive highly significant correlation with calcium content (0.653), potassium content (0.640), phosphorus content (0.626), ascorbic acid content (0.621), phenols content (0.413) and seed yield per plant (0.487). Positive non-significant correlation was observed with iron content (0.1948).

Calcium content showed positive highly significant correlation with potassium content (0.817), phosphorus content (0.646), ascorbic acid content (0.662) and seed yield per plant (0.390). Positive non-significant correlation was observed with iron content (0.2039) and phenols content (0.198).

Iron content showed positive highly significant correlation with ascorbic acid content (0.425). Positive significant correlation was observed with potassium content (0.269), phosphorus content (0.363), phenols content (0.337) and seed yield per plant (0.295).

Potassium content showed positive highly significant correlation with phosphorus content (0.560), ascorbic acid content (0.650) and seed yield per plant (0.248). Positive non-significant correlation was observed with phenols content (0.1907).

Phosphorus content showed positive highly significant correlation with ascorbic acid content (0.608) and seed yield per plant (0.607). Positive significant correlation was observed with phenols content (0.357).

Ascorbic acid content showed positive highly significant correlation with seed yield per plant (0.595). Positive significant correlation was observed with phenols content (0.241).

Phenols content showed positive highly significant correlation with seed yield per plant (0.399).

Determining the relationship between yield and yield contributing characters is made easier with an understanding of correlation. To ascertain the strength and direction of the link between the features, correlation analyses were conducted in the current study at the genotypic and phenotypic levels. When compared to their genotypic correlation values, the majority of the characteristics exhibited higher phenotypic correlation coefficients overall.

Days to 50 per cent flowering showed positive highly significant correlation with days to maturity at phenotypic level. Basavarajappa and Gowda (2004), Pawar and Prajapati (2013) and Salim *et al*. (2013) also reported similar findings for seed yield per plant. Positive highly significant correlation was observed at phenotypic level for plant height, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, harvest index, protein content, calcium content, iron content, potassium content, phosphorus content, ascorbic acid content and seed yield per plant. Positive non-significant correlation was recorded for phenols content at phenotypic levels.

Days to maturity showed positive highly significant correlation with plant height, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, harvest index, protein content, calcium content, potassium content, phosphorus content, ascorbic acid content and seed yield per plant at phenotypic levels. Bendale (2008), Gondhalekar (2013) and Gadakh (2014) quoted similar results mentioned above.

At phenotypic levels plant height had positive highly significant correlation with number of primary branches per plant, pod length, number of seeds per pod and seed yield per plant. Positive non-significant correlation was recorded for phenols content. Bagade *et al.* (2004), Bendale (2008), Pawar and Prajapati (2013) and Ravinaik *et al*. (2014) recorded similar findings.

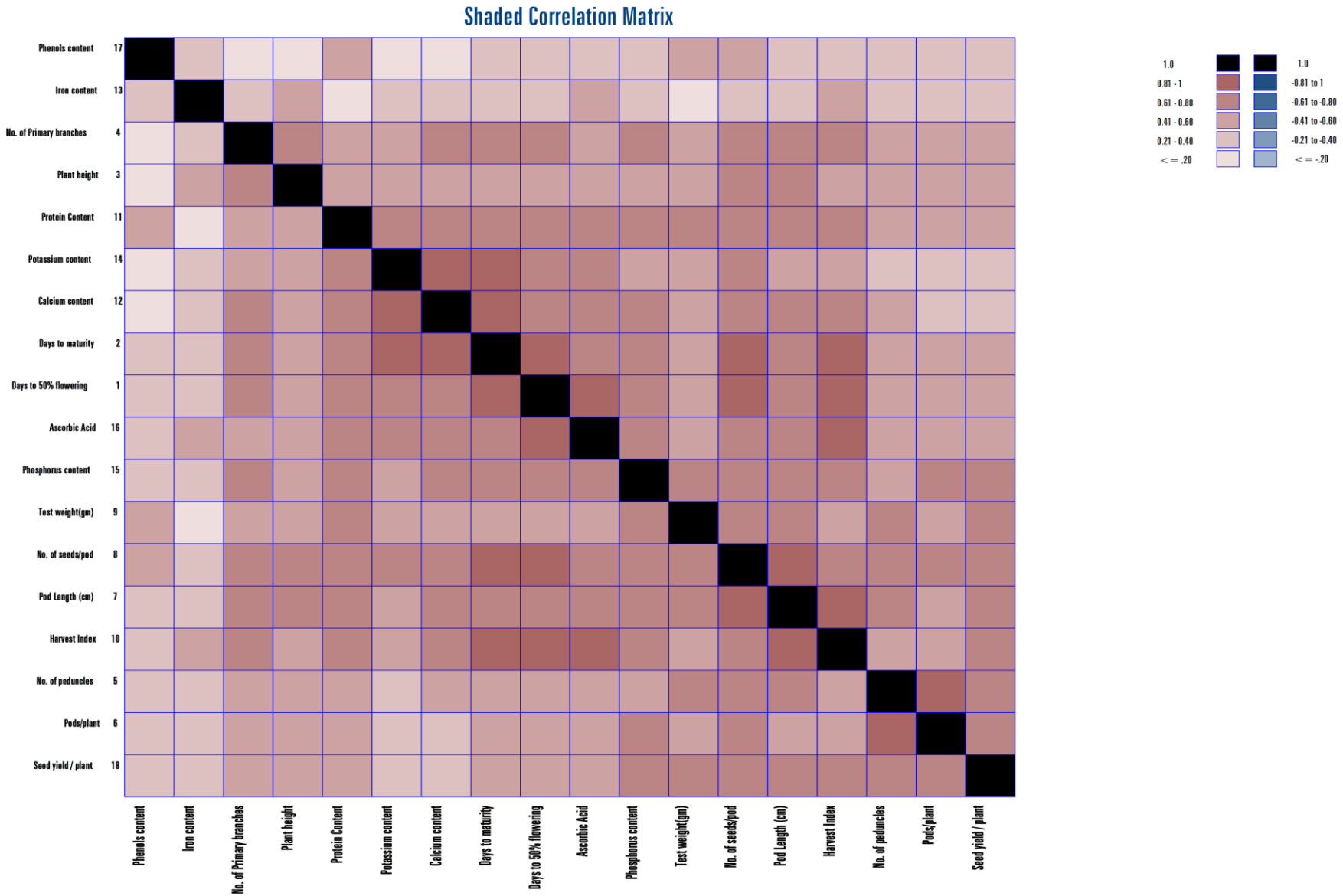


Fig. 4.2. Shaded phenotypic correlation matrix

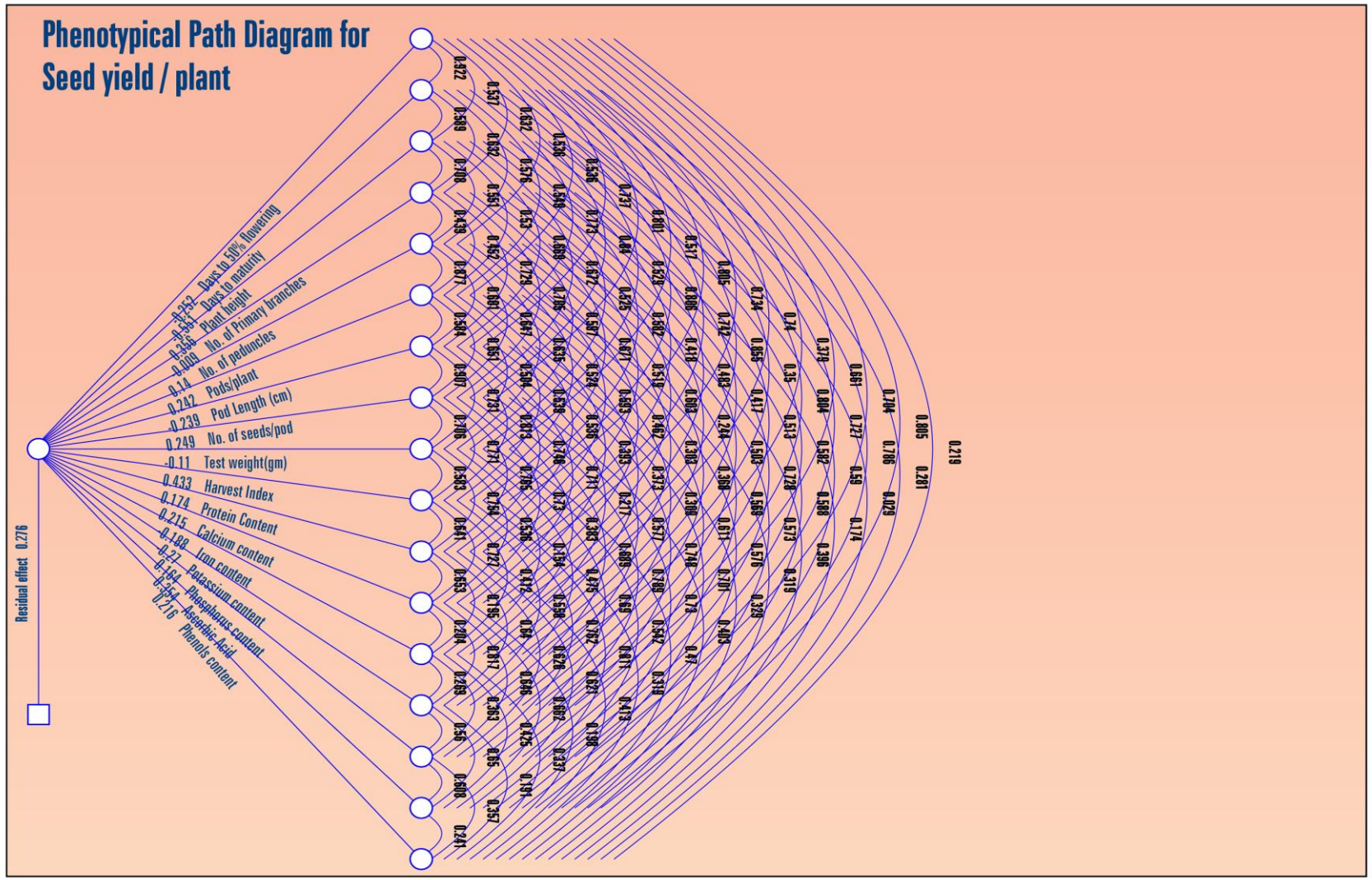


Fig. 4.3. Phenotypic path diagram for grain yield per plant

Number of primary branches per plant showed positive highly significant correlation with test weight, harvest index and seed yield per plant. Kurane (1997), Bendale (2008), Gadakh (2014) reported similar findings.

Number of peduncles per plant showed positive highly significant correlation with number of pods per plant and seed yield per plant at phenotypic level. Similar results were also reported by Basarvarajappa and Gowda (2004) in field bean and Gadakh (2014) in Lablab bean.

Number of pods per plant showed positive highly significant correlation with pod seed yield per plant at phenotypic level. Similar results were reported by Topare (1994), Bendale *et al.* (2008), Gadakh *et al.* (2014), Geetha et al. (2021), Samsuzzaman *et al.* (2023) in Lablab bean.

Pod length showed positive correlation with the number of seeds per pod. Singh *et al.* (2011) also gave similar results. Test weight showed positive highly significant correlation with seed yield per plant. Kabir and Sen (1989) and Ingle *et al.* (2016) reported similar results. Harvest index showed positive highly significant correlation with seed yield per plant.

Protein content showed positive highly significant correlation with phenols content at phenotypic level. Calcium content showed positive highly significant correlation with potassium content at phenotypic level. Iron content showed positive highly significant correlation with ascorbic acid content at phenotypic level. Positive significant correlation was observed with potassium content, phosphorus content and phenols content at phenotypic level. Potassium content showed positive highly significant correlation with phosphorus content, ascorbic acid content, seed yield per plant at phenotypic level. Phosphorus content showed positive highly significant correlation with seed yield per plant at phenotypic level. Positive significant correlation was observed with phenols content. Ascorbic acid content showed positive highly significant correlation with seed yield per plant at phenotypic level. Phenols content showed positive highly significant correlation with seed yield per plant at phenotypic level.

4.2.2 Genotypic correlation coefficient

Table 4.6 represents the results that days to 50 per cent flowering showed positive highly significant correlation with days to maturity (0.634). Positive significant correlation was observed in harvest index (0.260) and protein content (0.280). Positive non-significant correlation was observed in number of primary branches per plant (0.018), number of pods per plant (0.0761), phosphorus content (0.1278) and ascorbic acid content (0.1364). Negative significant correlation was observed in test weight (-0.327) and phenols content (-0.289). Negative non-significant correlation was observed in plant height (-0.0263), number of

peduncles (-0.0934), pod length (0.0683), number of seeds per pod (-0.0072), calcium content (-0.1303), iron content (-0.0703), potassium content (-0.1902) and seed yield per plant (-0.1212).

Days to maturity showed positive significant correlation with protein content (0.249), calcium content (0.333) and potassium content (0.327). Positive non-significant correlation was observed in plant height (0.0733), number of pods per plant (0.085), number of seeds per pod (0.0288), harvest index (0.0516) and phosphorus content (0.0882). Negative highly significant correlation was observed in test weight (-0.475). Negative significant correlation was observed in iron content (-0.245) and seed yield per plant (-0.271). Negative non-significant correlation was observed in number of primary branches (-0.0889), number of peduncles (-0.0747), pod length (-0.0617), ascorbic acid content (-0.2027) and phenols content (-0.2064).

Plant height showed positive highly significant correlation with number of primary branches per plant (0.527), pod length (0.394), number of seeds per pod (0.388) and seed yield per plant (0.406). Positive significant correlation was observed in number of peduncles (0.322), number of pods per plant (0.336) and phosphorus content (0.240). Positive non-significant correlation was observed in test weight (0.181), harvest index (0.1943), iron content (0.2014), potassium content (0.0571) and ascorbic acid content (0.1632). Negative significant correlation was observed in phenols content (-0.278). Negative non-significant correlation was observed in protein content (-0.0658) and calcium content (-0.086).

Number of primary branches showed positive highly significant correlation with pod length (0.405) and phosphorus content (0.476). Positive significant correlation was observed in number of seeds per pod (0.308), test weight (0.227) and seed yield per plant (0.323). Positive non-significant correlation was observed in number of pods per plant (0.1133), harvest index (0.2087) and calcium content (0.0262). Negative non-significant correlation was observed in number of peduncles (-0.0383), protein content (-0.0044), iron content (-0.1342), potassium content (-0.1402), ascorbic acid (-0.1902) and phenols content (-0.143).

Number of peduncles showed positive highly significant correlation with number of pods per plant (0.931), test weight (0.396) and seed yield per plant (0.670). Positive significant correlation was observed in number of seeds per pod (0.318), protein content (0.279) and phenols content (0.241). Positive non-significant correlation was observed in pod length (0.2011), iron content (0.0171), phosphorus content (0.176) and ascorbic acid content (0.0183). Negative significant correlation was observed in calcium content (-0.282), potassium content (-0.309). Negative non-significant correlation was observed in harvest index (-0.0122).

Table 4.6 Estimates of genotypic correlation coefficient between different characters in Lablab bean.

Genotypic Correlation Matrix																		
Characters	**DFF**	**DTM**	**PH**	**NPBP**	**NPPP**	**PPP**	**PL**	**NSPP**	**TW**	**HI**	**PRC**	**Ca**	**Fe**	**K**	**P**	**AA**	**PHC**	**SYPP**
DFF	1	0.634**	-0.0263	0.018	-0.0934	0.0761	-0.0683	-0.0072	-0.327*	0.260*	0.280*	-0.1303	-0.0703	-0.1902	0.1278	0.1364	-0.289*	-0.1212
DTM		1	0.0733	-0.0889	-0.0747	0.085	-0.0617	0.0288	-0.475**	0.0516	0.249*	0.333*	-0.245*	0.327*	0.0882	-0.2027	-0.2064	-0.271*
PH			1	0.527**	0.322*	0.336*	0.394**	0.388**	0.181	0.1943	-0.0658	-0.086	0.2014	0.0571	0.240*	0.1632	-0.278*	0.406**
NPBP				1	-0.0383	0.1133	0.405**	0.308*	0.227*	0.2087	-0.0044	0.0262	-0.1342	-0.1402	0.476**	-0.1092	-0.143	0.323*
NPPP					1	0.931**	0.2011	0.318*	0.396**	-0.0122	0.279*	-0.282*	0.0171	-0.309*	0.176	0.0183	0.241*	0.670**
PPP						1	0.2171	0.450**	0.2018	0.1602	0.2024	-0.301*	0.1687	-0.318*	0.336*	0.183	0.1513	0.740**
PL							1	0.747**	0.409**	0.409**	0.379**	-0.0386	-0.369**	-0.295*	0.335*	-0.1604	0.0324	0.469**
NSPP								1	0.308*	0.0593	0.398**	-0.249*	-0.0802	-0.1123	0.423**	-0.371**	0.1886	0.416**
TW									1	-0.0475	0.531**	-0.1705	-0.266*	-0.1991	0.370**	-0.2218	0.318*	0.434**
HI										1	0.0365	-0.0863	0.0511	-0.496**	0.378**	0.257*	-0.0159	0.512**
PRC											1	0.0851	-0.255*	0.1538	0.1739	-0.0801	0.227*	0.2023
Ca												1	-0.436**	0.452**	-0.0349	-0.434**	-0.276*	-0.267*
Fe													1	-0.1789	0.028	0.0579	0.2029	0.0745
K														1	-0.1189	-0.1958	-0.1941	-0.435**
P															1	-0.2054	0.1281	0.392**
AA																1	-0.2196	0.346*
PHC																	1	0.284*
SYPP																		1

*Significant at 5 % level **Significant at 1 % level

Note: DFF-Days to 50% flowering, DM-Days to maturity, PH-Plant height (cm), NPBP-Number of primary branches per plant, NPPP-Number of peduncles per plant, PPP- Pods per plant, PL-Pod length (cm), NSPP-Number of seeds per pod, TW-Test weight (g) , HI-Harvest index (%), SYPP-Seed yield/plant, PRC-Protein content (%), Ca-Calcium (mg/100g), Fe-Iron (mg/100g), K-Potassium(mg/100g), P-Phosphorus (mg/100g), AA-Ascorbic Acid(mg/100g), PHC-Phenol content (mg/100g)

Number of pods per plant showed positive highly significant correlation with number of seeds per pod (0.450) and seed yield per plant (0.740). Positive significant correlation was observed in phosphorus content (0.336). Positive non-significant correlation was observed in pod length (0.2171), test weight (0.2018), harvest index (0.1602), protein content (0.2024), iron content (0.1687), ascorbic acid content (0.183) and phenols content (0.1513). Negative significant correlation was observed in calcium content (-0.301) and potassium content (-0.318).

Pod length showed positive highly significant correlation with number of seeds per pod (0.747), test weight (0.409), harvest index (0.409), protein content (0.379) and seed yield per plant (0.469). Positive significant correlation was observed in phosphorus content (0.335). Positive non-significant correlation was observed in phenols content (0.0324). Negative highly significant correlation was observed in iron content (-0.369) and potassium content (-0.295). Negative non-significant correlation was observed in calcium content (-0.0386) and ascorbic acid content (-0.1604).

Number of seeds per pod showed positive highly significant correlation with protein content (0.398), phosphorus content (0.423) and seed yield per plant (0.416). Positive significant correlation was observed in test weight (0.308). Positive non-significant correlation was observed in harvest index (0.0593) and phenols content (0.1886). Negative highly significant correlation was observed in ascorbic acid (-0.371). Negative significant correlation was observed in calcium content (-0.249). Negative non-significant was observed in iron content (-0.0802) and potassium content (-0.1123).

Test weight showed positive highly significant correlation with protein content (0.531), phosphorus content (0.370) and seed yield per plant (0.434). Positive significant correlation was observed in phenols content (0.318). Negative significant correlation was observed in iron content (-0.266). Negative non-significant was observed in harvest index (-0.0475), calcium content (-0.1705), potassium content (-0.1991) and ascorbic acid content (-0.2218).

Harvest index showed positive highly significant correlation with phosphorus content (0.378) and seed yield per plant (0.512). Positive significant correlation was observed in ascorbic acid content (0.257).

Positive non-significant correlation was observed in protein content (0.0365) and iron content (0.0511) Negative highly significant correlation was observed in potassium content (-0.496). Negative non-significant was observed in calcium content (-0.0863) and phenols content (-0.0159).

Protein content showed positive significant correlation with phenols content (0.227) while, positive non-significant correlation with calcium content (0.0851), potassium content (0.1538),

phosphorus content (0.1739) and seed yield per plant (0.2023). Negative significant correlation was observed in iron content (-0.255). Negative non-significant correlation was observed in ascorbic acid content (-0.0801).

Calcium content showed positive highly significant correlation with potassium content (0.452). Negative highly significant correlation was observed in iron content (0.436) and ascorbic acid content (0.434). Negative significant correlation was observed in phenols content (-0.276) and seed yield per plant (-0.267). Negative non-significant correlation was observed in phosphorus content (-0.0349).

Iron content showed positive non-significant correlation with phosphorus content (0.028), ascorbic acid content (0.0579), phenols content (0.2029) and seed yield per plant (0.0745). Negative non-significant correlation was observed in potassium content (-0.1789).

Potassium content showed negative highly significant correlation with seed yield per plant (0.435). Negative non-significant correlation was observed in phosphorus content (-0.1189), ascorbic acid content (-0.1958) and phenols content (-0.1941).

Phosphorus content showed positive highly significant correlation with seed yield per plant (0.392). Positive non-significant correlation was observed in phenols content (0.1281). Negative non-significant correlation was observed in ascorbic acid content (-0.2054).

Ascorbic acid content showed positive significant correlation with seed yield per plant (0.346). Negative non-significant correlation was observed in phenols content (-0.2196).

Phenols content showed positive significant correlation with seed yield per plant (0.284).

A grasp of correlation facilitates the process of determining the relationship between yield and yield contributing features. In the current investigation, both genotypic and phenotypic correlation studies were carried out to determine the direction and degree of the relationship between the traits.

At genotypic level, days to 50 per cent flowering showed positive highly significant correlation with days to maturity. Results reported by Basavarajappa and Gowda (2004), Pawar and Prajapati (2013) and Salim *et al*. (2013) were also similar. At genotypic levels negative significant correlation was observed for test weight.

Days to maturity showed positive non-significant correlation with harvest index. Similar results of association of maturity with seed yield were reported by Bendale (2008), Gondhalekar (2013) and Gadakh (2014). At genotypic levels, plant height had significant positive correlation with number of peduncles per plant. Similar results of association of plant height with seed yield

were reported by Bagade *et al.* (2004), Bendale (2008), Pawar and Prajapati (2013) and Ravinaik *et al*. (2014).

Number of primary branches had positive highly significant correlation with pod length at genotypic levels as per Chaudhari *et al.* (2013). It had negative non-significant correlation with number of peduncles and protein content at genotypic levels.

At genotypic level, number of peduncles per plant showed positive highly significant correlation with number of pods per plant and seed yield per plant. In field bean Basarvarajappa and Gowda (2004) and in Lablab bean Gadakh (2014) found similar results. At genotypic level it had negative non-significant correlation with harvest index.

Number of pods per plant had positive highly significant correlation with pod seed yield per plant at genotypic level. Results reported by Topare (1994), Bendale *et al*. (2008), Gadakh *et al.* (2014), Geetha *et al.* (2021), Samsuzzaman *et al.* (2023) in Lablab bean were similar.

Pod length showed positive correlation with harvest index at genotypic level. Bendale *et al.* (2008) reported similar findings. Pod length had positive highly significant correlation with seeds per pod and test weight at genotypic level. Test weight indicated positive highly significant correlation with seed yield per plant at genotypic level. Kabir and Sen (1989) and Ingle *et al.* (2016) reported similar results. At genotypic level, harvest index had positive highly significant correlation with seed yield per plant.

Protein content indicated positive highly significant correlation with phenols content at genotypic level. Calcium content had positive highly significant correlation with potassium content at genotypic level and positive non-significant correlation with seed yield per plant, ascorbic acid and phenols content at genotypic level. At both levels, phosphorus content and seed yeild per plant exhibited a positive and very significant association. There was a substantial positive connection seen with the phenol content. At both levels, ascorbic acid content and seed yeild per plant exhibited a favourable and very significant correlation.

The majority of the characteristics, including the number of pods per plant, peduncles per plant, primary branches per plant, test weight, harvest index, and pod length had demonstrated favourable associations at both the phenotypic and genotypic levels for seed yield per plant. This indicates that while the number of seeds in the pod has little bearing on increasing output, the size of the seed has a significant impact. Therefore, it is recommended to apply selection pressure on the number of pods per plant, the hundred seed weight, the number of peduncles per plant, and the number of primary branches per plant in order to increase the seed yield.

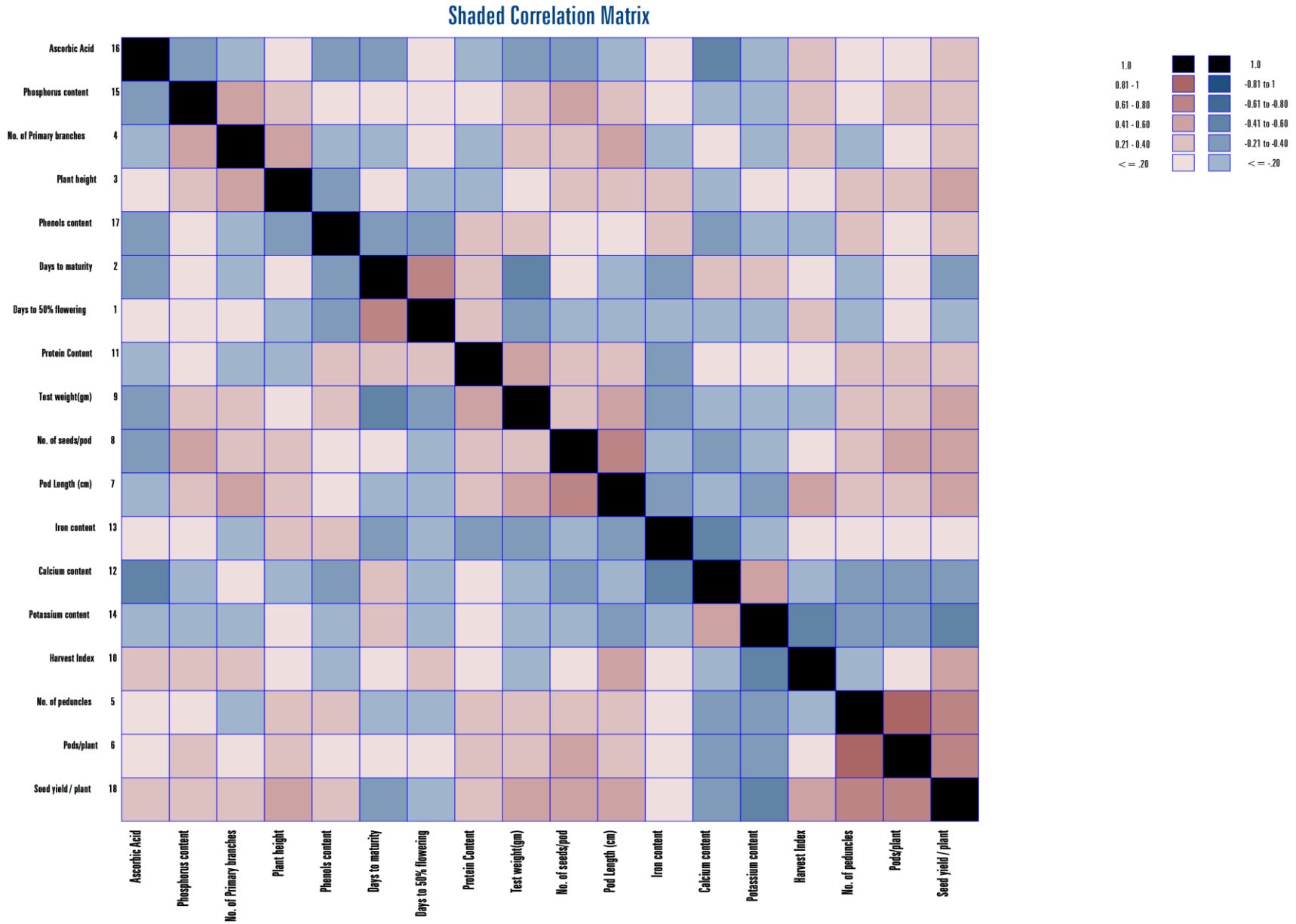


Fig. 4.4. Shaded genotypic correlation matrix

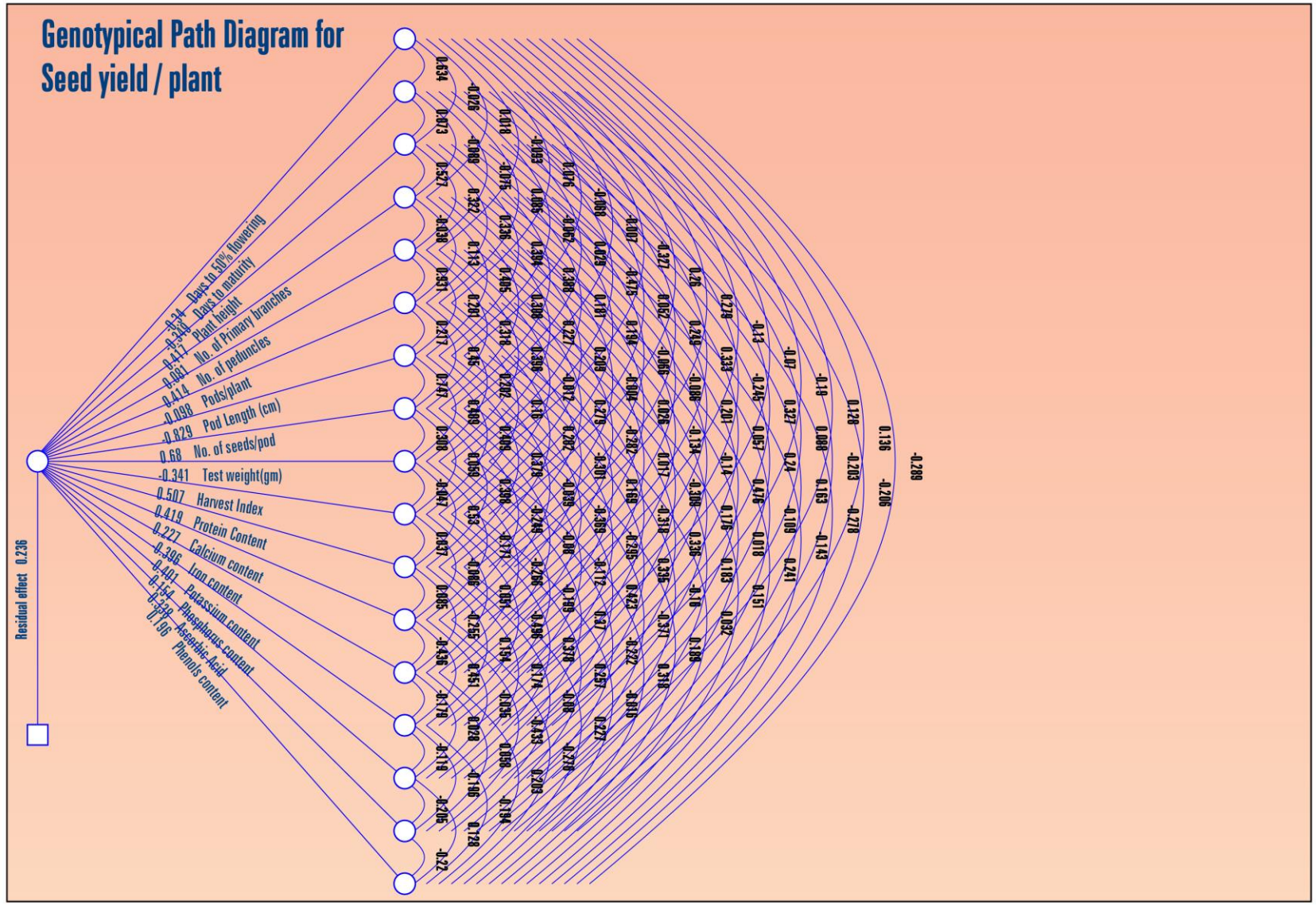


Fig. 4.5. Genotypic path diagram for grain yield per plant

4.3 Path coefficient analysis

The direct and indirect contributions for each character towards seed yield per plant revealed by path analysis at phenotypic level and genotypic level are presented in Table 4.7 and Table 4.8 respectively. Studies using correlations show a relationship between yield and yield components, but they do not give a clear picture of the direct and indirect effects. causes of this correlation, which path analysis may be able to reveal. As a result, path coefficient analysis is a highly helpful method for highlighting the crucial yield components that are used to suggest selection indices. This provides a clear picture of how different characteristics affect yield both directly and indirectly (Dewey and Lu, 1959).

4.3.1 Phenotypic correlation coefficient portioned for path coefficient analysis

The phenotypic correlation coefficients were divided into direct and indirect effects and are presented in Table 4.7. The results show that, days to 50 per cent flowering (-0.2522) had negative direct effect on seed yield per plant. Its indirect effect via days to maturity, plant height, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, harvest index, protein content, calcium content, iron content, potassium content, phosphorus content, ascorbic acid content and phenols content were negative. The character had positive highly significant correlation (0.430) with seed yield per plant.

The character days to maturity (-0.5515) had negative direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, plant height, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, harvest index, protein content, calcium content, iron content, potassium content, phosphorus content, ascorbic acid content and phenols content were negative. The character had positive highly significant correlation (0.438) with seed yield per plant.

Plant height (0.3565) had positive direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, harvest index, protein content, calcium content, iron content, potassium content, phosphorus content, ascorbic acid content and phenols content were positive. The character had positive highly significant correlation (0.568) with seed yield per plant.

The character number of primary branches (-0.0087) had negative direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test

weight, harvest index, protein content, calcium content, iron content, potassium content, phosphorus content, ascorbic acid content and phenols content were negative. The character had positive highly significant correlation (0.537) with seed yield per plant.

The character number of peduncles per plant (0.14) had positive direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, pod length, number of seeds per pod, test weight, harvest index, protein content, calcium content, iron content, potassium content, phosphorus content, ascorbic acid content and phenols content were positive. The character had positive highly significant correlation (0.695) with seed yield per plant.

The character number of pods per plant (2418) had positive direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of peduncles, pod length, number of seeds per pod, test weight, harvest index, protein content, calcium content, iron content, potassium content, phosphorus content, ascorbic acid content and phenols content were positive. The character had positive highly significant correlation (0.709) with seed yield per plant.

The character pod length (-0.2393) had negative direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of peduncles, number of pods per plant, number of seeds per pod, test weight, harvest index, protein content, calcium content, iron content, potassium content, phosphorus content, ascorbic acid content and phenols content were negative. The character had positive highly significant correlation (0.632) with seed yield per plant.

The character number of seeds per pod (0.2493) had positive direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, test weight, harvest index, protein content, calcium content, iron content, potassium content, phosphorus content, ascorbic acid content and phenols content were positive. The character had positive highly significant correlation (0.612) with seed yield per plant.

The test weight (-0.1099) had negative direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, number of seeds per pod, harvest index, protein content, calcium content, iron content, potassium content, phosphorus content, ascorbic acid content and phenols content were negative. The character had positive highly significant correlation (0.610) with seed yield per plant.

Table 4.7 Path analysis for different characters at phenotypic level in Lablab bean.

Phenotypic Path Matrix																		
Characters	**DFF**	**DM**	**PH**	**NPBP**	**NPPP**	**PPP**	**PL**	**NSPP**	**TW**	**HI**	**PRC**	**Ca**	**Fe**	**K**	**P**	**AA**	**PHC**	**SYPP**
DFF	**-0.2522**	-0.2324	-0.1353	-0.1593	-0.1352	-0.1353	-0.1858	-0.202	-0.1304	-0.2029	-0.1851	-0.1865	-0.0956	-0.1666	-0.1775	-0.2029	-0.0552	0.430**
DTM	-0.5084	**-0.5515**	-0.3245	-0.3487	-0.3176	-0.3029	-0.4265	-0.4633	-0.2919	-0.4447	-0.4094	-0.4713	-0.1931	-0.4435	-0.401	-0.4335	-0.1548	0.438**
PH	0.1913	0.2098	**0.3565**	0.2525	0.1966	0.1888	0.2386	0.2397	0.1872	0.2074	0.1491	0.1721	0.1486	0.1827	0.2075	0.2102	0.0103	0.568**
NPBP	-0.0055	-0.0055	-0.0062	**-0.0087**	-0.0038	-0.0039	-0.0063	-0.0061	-0.0052	-0.0058	-0.0045	-0.0052	-0.0021	-0.0044	-0.0063	-0.0051	-0.0015	0.537**
NPPP	0.0751	0.0807	0.0772	0.0615	**0.14**	0.1228	0.0841	0.0906	0.0889	0.0734	0.0831	0.0647	0.0425	0.0515	0.0797	0.0803	0.0555	0.695**
PPP	0.1297	0.1328	0.1281	0.1094	0.212	**0.2418**	0.1412	0.1574	0.1219	0.1303	0.1297	0.095	0.0901	0.0748	0.1477	0.1392	0.077	0.709**
PL	-0.1763	-0.1851	-0.1602	-0.1744	-0.1437	-0.1397	**-0.2393**	-0.217	-0.175	-0.1945	-0.1785	-0.1702	-0.0519	-0.1381	-0.179	-0.1677	-0.0787	0.632**
NSPP	0.1996	0.2094	0.1676	0.1757	0.1612	0.1622	0.226	**0.2493**	0.1759	0.1922	0.1906	0.1819	0.0956	0.1718	0.1966	0.182	0.1004	0.612**
TW	-0.0568	-0.0582	-0.0577	-0.0656	-0.0698	-0.0554	-0.0803	-0.0776	**-0.1099**	-0.0641	-0.0828	-0.0589	-0.0169	-0.0521	-0.0759	-0.0595	-0.0516	0.610**
HI	0.3484	0.3491	0.2519	0.2903	0.2268	0.2333	0.3518	0.3338	0.2525	**0.433**	0.2777	0.3148	0.1786	0.2416	0.3301	0.351	0.1382	0.645**
PRC	0.128	0.1294	0.0729	0.0906	0.1034	0.0935	0.1301	0.1333	0.1314	0.1118	**0.1743**	0.1138	0.034	0.1116	0.1092	0.1082	0.072	0.487**
Ca	0.1592	0.184	0.1039	0.1298	0.0995	0.0846	0.1531	0.1571	0.1154	0.1565	0.1405	**0.2153**	0.0439	0.1759	0.1391	0.1426	0.0426	0.390**
Fe	-0.0714	-0.0659	-0.0785	-0.046	-0.0571	-0.0702	-0.0408	-0.0722	-0.029	-0.0777	-0.0367	-0.0384	**-0.1883**	-0.0507	-0.0684	-0.08	-0.0635	0.295*
K	-0.1783	-0.2169	-0.1383	-0.1356	-0.0992	-0.0835	-0.1556	-0.1859	-0.128	-0.1505	-0.1727	-0.2204	-0.0726	**-0.2697**	-0.151	-0.1754	-0.0514	0.248*
P	0.1156	0.1194	0.0956	0.1195	0.0935	0.1003	0.1228	0.1295	0.1134	0.1252	0.1028	0.1061	0.0596	0.0919	**0.1642**	0.0999	0.0586	0.607**
AA	0.2849	0.2782	0.2087	0.2083	0.2029	0.2038	0.248	0.2585	0.1918	0.2869	0.2198	0.2344	0.1503	0.2302	0.2154	**0.3539**	0.0855	0.595**
PHC	0.0472	0.0605	0.0063	0.0375	0.0855	0.0687	0.0709	0.0869	0.1013	0.0688	0.089	0.0427	0.0727	0.0411	0.077	0.0521	**0.2156**	0.399**
SYPP	0.430**	0.438**	0.568**	0.537**	0.695**	0.709**	0.632**	0.612**	0.610**	0.645**	0.487**	0.390**	0.295*	0.248*	0.607**	0.595**	0.399**	

*Significant at 5 % level **Significant at 1 % level

Note: Bold figures indicate direct effect.

Note: DFF-Days to 50% flowering, DM-Days to maturity, PH-Plant height (cm), NPBP Number of primary branches per plant, NPPP-Number of peduncles per plant, PPP- Pods per plant, PL Pod length (cm), NSPP-Number of seeds per pod, TW-Test weight (g) , HI-Harvest index (%), SYPP-Seed yield/plant, PRC-Protein content (%), Ca-Calcium (mg/100g), Fe-Iron (mg/100g), K-Potassium(mg/100g), P-Phosphorus (mg/100g), AA-Ascorbic Acid(mg/100g), PHC-Phenol content (mg/100g).

The character harvest index (0.433) had positive direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, protein content, calcium content, iron content, potassium content, phosphorus content, ascorbic acid content and phenols content were positive. The character had positive highly significant correlation (0.645) with seed yield per plant.

The character protein content (0.1743) had positive direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, harvest index, calcium content, iron content, potassium content, phosphorus content, ascorbic acid content and phenols content were positive. The character had positive highly significant correlation (0.487) with seed yield per plant.

The character calcium content (0.2153) had positive direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, harvest index, protein content, iron content, potassium content, phosphorus content, ascorbic acid content and phenols content were positive. The character had positive highly significant correlation (0.390) with seed yield per plant.

The character iron content (0.1743) had negative direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, harvest index, protein content, calcium content, potassium content, phosphorus content, ascorbic acid content and phenols content were negative. The character had positive significant correlation (0.295) with seed yield per plant.

The character potassium content (-0.2697) had negative direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, harvest index, protein content, calcium content, iron content, phosphorus content, ascorbic acid content and phenols content were negative. The character had positive significant correlation (0.248) with seed yield per plant.

The character phosphorus content (0.1642) had positive direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, harvest index, calcium content, iron content, potassium

content, phosphorus content, ascorbic acid content and phenols content were positive. The character had positive highly significant correlation (0.607) with seed yield per plant.

The character ascorbic acid content (0.3539) had positive direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, harvest index, protein content, calcium content, iron content, potassium content, phosphorus content and phenols content were positive. The character had positive highly significant correlation (0.595) with seed yield per plant.

The character phenols content (0.2156) had positive direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, harvest index, calcium content, iron content, potassium content, phosphorus content, ascorbic acid content and ascorbic acid content were positive. The character had positive highly significant correlation (0.399) with seed yield per plant.

The residual effect of path analysis at phenotypic level was found to be **0.276**.

The path coefficient demonstrated a direct positive relationship between seed yield, number of peduncles per plant and number of seeds per pod. Negative direct effect on seed yield per plant was seen because of days to 50 per cent flowering and days to maturity at phenotypic level. Similar results were also observed by Topare (1994), Kurane (1997), Gondhalekar (2013), Salim *et al*. (2013) and Ingle *et al*. (2016).

The days to 50 per cent flowering exhibited a negative direct influence at the phenotypic level on seed yield per plant. This suggests that early blossoming plants may be preferred and may help them survive conditions of moisture stress. Chaitanya *et al.* (2014) had found similar results.

Days to 50 per cent flowering had negative direct effect on seed yield per plant but, it had indirect effect on days to maturity, number of primary branches per plant, number of pods per plant, harvest index, protein content, phosphorus content, ascorbic acid content which were negative.

The days to maturity all exhibited a negative direct influence at the phenotypic level on seed yield per plant at phenotypic level. Pawar and Prajatpati (2013) also reported results which were similar.

Days to maturity showed negative direct effect on seed yield per plant and indirect effect on days to 50 per cent flowering, number of primary branches per plant, number of peduncles

per plant, number of pods per plant and harvest index. Also, it had negative significant correlation with seed yield at genotypic levels. Pawar (1998) also reported similar results in Lablab bean.

Plant height had indirect effect via days to maturity, number of peduncles per plant, number of seeds per pod and harvest index which were positive. Pawar (1998) also reported similar results in Lablab bean. Plant height had positive direct effect on seed yield per plant and positive significant correlation with seed yield per plant.

Higher positive direct effect exhibited by number of peduncles per plant and number of seeds per pod show that these are the important characters influencing yield. Gondhalekar (2013), Salim *et al*. (2013), Gadakh (2014) and Ingle *et al*. (2016) also presented similar results in lablab bean.

The character number of pods per plant had positive direct effect on seed yield per plant. Patel *et al*. (2022), Thorat *et al.* (2020) also reported similar results.

Pod length had negative direct effect on seed yield per plant. For this character similar results were put forward by Salim *et al.* (2013).

Number of seeds per pod showed positive direct effect on seed yield per plant while negative indirect effect through days to maturity, plant height, number of peduncles per plant, number of pods per plant, test weight and harvest index resulted into negative non- significant correlation with grain yield per plant. Lad *et al*. (2010), Pawar and Prajapati (2013) and Salim *et al.* (2013) also reported similar reports.

The test weight had negative direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, number of seeds per pod, harvest index content were negative at genotypic level.

Harvest index had positive direct effect on seed yield per plant but indirect positive effect through days to 50 per cent flowering, plant height, number of primary branches per plant, number of pods per plant, pod length, number of seeds per pod and test weight resulted into highly positive significant correlation with seed yield per plant at phenotypic level.

The path coefficient demonstrated a direct positive relationship between seed yield and protein content, calcium content, phosphorus content, ascorbic acid content and phenols content.

4.3.2 Genotypic correlation coefficient portioned for path coefficient analysis

The genotypic correlation coefficients portioned into direct and indirect effects are represented in Table 4.8. The results reveal that, days to 50 per cent flowering (-0.3402) had negative direct effect on seed yield per plant. Its indirect effect via plant height, number of peduncles, pod length, number of seeds per pod, test weight, calcium content, iron content, potassium content and phenol content were positive. Its indirect effect via days to maturity, number of primary branches per plant, number of pods per plant, harvest index, protein content, phosphorus content and ascorbic acid content were negative. The character had negative non-significant correlation (-0.1212) with seed yield per plant.

Days to maturity (-0.3489) had negative direct effect on seed yield per plant. Its indirect effect via number of primary branches per plant, pod length, test weight, iron content, ascorbic acid content and phenols content were positive. Its indirect effect via days to 50 per cent flowering, plant height, number of pods per plant, number of seeds per pod, harvest index, protein content, calcium content, potassium content and phosphorus content were negative. The character had negative significant correlation (-0.271) with seed yield per plant.

The character plant height (0.4173) had positive direct effect on seed yield per plant. Its indirect effect via days to maturity, number of primary branches, number of peduncles, number of pods per plant, number of seeds per plant, test weight, harvest index, iron content, potassium content, phosphorus content and ascorbic acid content were positive. Its indirect effect via days to 50 per cent flowering, protein content, calcium content and phenols content were negative. The character had positive highly significant correlation (0.406) with seed yield per plant.

The character number of primary branches per plant (0.0814) had positive direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, plant height, number of pods per plant, pod length, number of seeds per plant, test weight, harvest index, calcium content, potassium content and phosphorus content were positive. Its indirect effect via days to maturity, number of peduncles, protein content, iron content, potassium content, ascorbic acid content and phenols content were negative. The character had positive significant correlation (0.323) with seed yield per plant.

The character number of peduncles (0.4139) had positive direct effect on seed yield per plant. Its indirect effect via plant height, number of pods per plant, pod length, number of seeds per pod, test weight, protein content, iron content, phosphorus content, ascorbic acid content and phenols content were positive. Its indirect effect via days to 50 per cent flowering, days to maturity, number of primary branches, harvest index, calcium content and potassium content were negative. The character had positive highly significant correlation (0.670) with seed yield per plant.

The character number of pods per plant (-0.0981) had negative direct effect on seed yield per plant. Its indirect effect via calcium content and potassium content were positive. Its indirect

effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of peduncles per plant, pod length, number of seeds per pod, test weight, harvest index, protein content, iron content, phosphorus content, ascorbic acid content and phenols content were negative. The character had positive highly significant correlation (0.740) with seed yield per plant.

The character pod length (-0.8286) had negative direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, calcium content, iron content, potassium content and ascorbic acid content were positive. Its indirect effect via plant height, number of primary branches per plant, number of peduncles per plant, number of pods per plant, number of seeds per pod, test weight, harvest index, protein content, phosphorus content and phenols content were negative. The character had positive highly significant correlation (0.469) with seed yield per plant.

The character number of seeds per pod (0.6795) had positive direct effect on seed yield per plant. Its indirect effect via days to maturity, plant height, number of primary branches, number of peduncles per plant, number of pods per plant, pod length, test weight, harvest index, protein content, phosphorus content and phenols content were positive. Its indirect effect via days to 50 per cent flowering, calcium content, iron content, potassium content and ascorbic acid content were negative. The character had positive highly significant correlation (0.416) with seed yield per plant.

The character test weight (-3408) had negative direct effect on seed yield per plant. Its indirect effect via days to maturity, harvest index, calcium content, iron content, potassium content and ascorbic acid content were positive. Its indirect effect via plant height, number of primary branches, number of peduncles, number of pods per plant, number of seeds per pod, protein content, phosphorus content and phenols content were negative. The character had positive highly significant correlation (0.434) with seed yield per plant.

The character harvest index (0.5073) had positive direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, pod length, number of seeds per pod, protein content, iron content, phosphorus content and ascorbic acid content were positive. Its indirect effect via number of peduncles, test weight, calcium content, potassium content and phenols content were negative. The character had positive highly significant correlation (0.512) with seed yield per plant.

The character protein content (0.4193) had positive direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, harvest index, calcium content, potassium content, phosphorus content and phenols content were positive. Its indirect via plant height, number of primary branches, iron content and ascorbic acid content were negative. The character had positive non-significant correlation (0.2023) with seed yield per plant.

Table 4.8 Path analysis for different characters at genotypic level in Lablab bean.

Genotypic Path Matrix																		
Character	**DFF**	**DTM**	**PH**	**NPBP**	**NPPP**	**PPP**	**PL**	**NSPP**	**TW**	**HI**	**PRC**	**Ca**	**Fe**	**K**	**P**	**AA**	**PHC**	**SYPP**
DFF	**-0.3402**	-0.2157	0.009	-0.0061	0.0318	-0.0259	0.0232	0.0024	0.1111	-0.0886	-0.0951	0.0443	0.0239	0.0647	-0.0435	-0.0464	0.0984	-0.1212
DTM	-0.2213	**-0.3489**	-0.0256	0.031	0.0261	-0.0297	0.0215	-0.0101	0.1656	-0.018	-0.0869	-0.1161	0.0856	-0.1142	-0.0308	0.0707	0.072	-0.271*
PH	-0.011	0.0306	**0.4173**	0.2199	0.1342	0.1403	0.1645	0.1618	0.0756	0.0811	-0.0274	-0.0359	0.084	0.0238	0.1002	0.0681	-0.1158	0.406**
NPBP	0.0015	-0.0072	0.0429	**0.0814**	-0.0031	0.0092	0.033	0.025	0.0185	0.017	-0.0004	0.0021	-0.0109	-0.0114	0.0387	-0.0089	-0.0116	0.323*
NPPP	-0.0387	-0.0309	0.1331	-0.0158	**0.4139**	0.3853	0.0832	0.1316	0.1638	-0.005	0.1155	-0.1169	0.0071	-0.1278	0.0729	0.0076	0.0997	0.670**
PPP	-0.0075	-0.0083	-0.033	-0.0111	-0.0913	**-0.0981**	-0.0213	-0.0441	-0.0198	-0.0157	-0.0199	0.0295	-0.0165	0.0312	-0.033	-0.018	-0.0148	0.740**
PL	0.0566	0.0511	-0.3265	-0.3358	-0.1666	-0.1799	**-0.8286**	-0.619	-0.3387	-0.3388	-0.3138	0.032	0.3057	0.2441	-0.2772	0.1329	-0.0268	0.469**
NSPP	-0.0049	0.0196	0.2635	0.209	0.216	0.3058	0.5077	**0.6795**	0.2095	0.0403	0.2704	-0.1692	-0.0545	-0.0763	0.2874	-0.2522	0.1282	0.416**
TW	0.1113	0.1617	-0.0617	-0.0773	-0.1349	-0.0688	-0.1393	-0.1051	**-0.3408**	0.0162	-0.1808	0.0581	0.0906	0.0679	-0.126	0.0756	-0.1083	0.434**
HI	0.1321	0.0262	0.0986	0.1059	-0.0062	0.0813	0.2074	0.0301	-0.0241	**0.5073**	0.0185	-0.0438	0.0259	-0.2516	0.192	0.1303	-0.0081	0.512**
PRC	0.1172	0.1044	-0.0276	-0.0019	0.117	0.0849	0.1588	0.1669	0.2224	0.0153	**0.4193**	0.0357	-0.1069	0.0645	0.0729	-0.0336	0.095	0.2023
Ca	-0.0296	0.0755	-0.0195	0.0059	-0.0641	-0.0683	-0.0088	-0.0565	-0.0387	-0.0196	0.0193	**0.2269**	-0.0989	0.1025	-0.0079	-0.0984	-0.0627	-0.267*
Fe	0.0278	0.0971	-0.0797	0.0531	-0.0068	-0.0668	0.1461	0.0318	0.1053	-0.0202	0.1009	0.1725	**-0.3959**	0.0708	-0.0111	-0.0229	-0.0803	0.0745
K	0.0762	-0.1312	-0.0229	0.0562	0.1237	0.1273	0.1181	0.045	0.0798	0.1987	-0.0616	-0.1809	0.0717	**-0.4007**	0.0477	0.0785	0.0778	-0.435**
P	0.0197	0.0136	0.037	0.0734	0.0271	0.0518	0.0516	0.0652	0.057	0.0583	0.0268	-0.0054	0.0043	-0.0183	**0.1541**	-0.0317	0.0197	0.392**
AA	0.0461	-0.0685	0.0551	-0.0369	0.0062	0.0618	-0.0542	-0.1253	-0.0749	0.0867	-0.027	-0.1464	0.0195	-0.0661	-0.0693	**0.3376**	-0.0742	0.346*
PHC	-0.0566	-0.0404	-0.0544	-0.028	0.0472	0.0296	0.0063	0.0369	0.0622	-0.0031	0.0444	-0.0541	0.0397	-0.038	0.0251	-0.043	**0.1958**	0.284*
SYPP	-0.1212	-0.271*	0.406**	0.323*	0.670**	0.740**	0.469**	0.416**	0.434**	0.512**	0.2023	-0.267*	0.0745	-0.435**	0.392**	0.346*	0.284*	

*Significant at 5 % level **Significant at 1 % level **Note:** Bold figures indicate direct effects.

Note: DFF-Days to 50% flowering, DM-Days to maturity, PH-Plant height (cm), NPBP-Number of primary branches per plant, NPPP-Number of peduncles per plant, PPP- Pods per plant, PL-Pod length (cm), NSPP-Number of seeds per pod, TW-Test weight (g) , HI-Harvest index (%), SYPP-Seed yield/plant, PRC-Protein content (%), Ca-Calcium (mg/100g), Fe-Iron (mg/100g), K-Potassium(mg/100g), P-Phosphorus (mg/100g), AA-Ascorbic Acid(mg/100g), PHC-Phenol content (mg/100g

The character calcium content (0.2269) had positive direct effect on seed yield per plant. Its indirect effect via days to maturity, number of primary branches, protein content and potassium content were positive. Its indirect effect via days to 50 per cent flowering, plant height, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, harvest index, iron content, phosphorus content, ascorbic acid content and phenols content were positive. Its indirect via plant height, number of primary branches, iron content and ascorbic acid content were negative. The character had negative significant correlation (-0.267) with seed yield per plant.

The character iron content (-0.3959) had negative direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, number of primary branches, pod length, number of seeds per pod, test weight, protein content, calcium content and potassium content were positive. Its indirect effect via plant height, number of peduncles, number pods per plant, harvest index, phosphorus content, ascorbic acid content and phenols content were negative. The character had positive non-significant correlation (0.0745) with seed yield per plant.

The character potassium content (-0.4007) had negative direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, number of primary branches, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, harvest index, iron content, phosphorus content, ascorbic acid content and phenols content were positive. Its indirect effect via days to maturity, plant height, protein content, calcium content were negative. The character had negative highly significant correlation (-0.435) with seed yield per plant.

The character phosphorus content (0.1541) had positive direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, harvest index, protein content, iron content and phenols content were positive. Its indirect effect via calcium content, potassium content and ascorbic acid content were negative. The character had positive highly significant correlation (0.392) with seed yield per plant.

The character ascorbic acid content (0.3376) had positive direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, plant height, number of peduncles, number of pods per plant, harvest index and iron content were positive. Its indirect effect via days to maturity, number of primary branches, pod length, number of seeds per pod, test weight, protein content, calcium content, potassium content, phosphorus content and phenols content were negative. The character had positive significant correlation (0.346) with seed yield per plant.

The character phenols content (0.1958) had positive direct effect on seed yield per plant. Its direct effect via number of peduncles, number of pods per plant, pod length, number of seeds per pod, test weight, protein content, iron content and phosphorus content were positive. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches, harvest index, calcium content, potassium content and ascorbic acid content were negative. The character had positive significant correlation (0.284) with seed yield per plant.

The residual effect of path analysis at genotypic level was found to be **0.236**.

The character days to 50 per cent flowering and the days to maturity indicated a negative direct influence at the genotypic level. Pawar (1998) and Pawar and Prajapati (2013) also reported similar results. Days to 50 per cent flowering had negative direct effect on seed yield per plant but, it had indirect effect on plant height, number of peduncles, number of seeds per pod, harvest index, protein content, calcium content, potassium content and phosphorus content which were negative.

Days to maturity showed negative direct effect on seed yield per plant and indirect effect on number of primary branches per plant which was positive. Also, it had negative significant correlation with seed yield at genotypic levels. Pawar (1998) also reported similar results in Lablab bean.

Plant height had indirect effect via days to maturity, number of peduncles per plant, number of seeds per pod and harvest index were positive. Pawar (1998) also reported similar results in Lablab bean. Plant height had positive direct effect on seed yield per plant and positive significant correlation with seed yield per plant.

The character number of pods per plant showed negative direct effect on seed yield per plant. Number of seeds per pod showed positive direct effect on seed yield per plant. Lad *et al*. (2010), Pawar and Prajapati (2013) and Salim *et al.* (2013) also reported similar reports.

The test weight reflected negative direct effect on seed yield per plant. Its indirect effect via days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of peduncles, number of pods per plant, pod length, number of seeds per pod, harvest index content were negative at genotypic level.

Harvest index indicated positive direct effect on seed yield per plant but indirect positive effect through days to initiation of flowering, days to 50 per cent flowering, plant height, number of primary branches per plant, number of pods per plant, pod length, number of seeds per pod and test weight resulted into highly positive significant correlation with seed yield per plant at genotypic level.

The path coefficient demonstrated a direct positive relationship between seed yield and protein content, calcium content, phosphorus content, ascorbic acid content and phenols content whereas it showed direct positive relationship at phenotypic level and negative direct relationship at genotypic level.

4.4 Genetic divergence

The estimation of genetic distance is the key aspect that determines the vast potential for crop development for character of interest that arises from the presence of genetic distance among accessible material. The genetic divergence can be assessed using a statistical method, Mahalanobis D^2 statistics, which provides a details about the diversity of genotypes. Clusters were formed using Rao's (1952) Tocher technique. The results are mentioned below.

4.4.1 Grouping of genotypes into various clusters

Table 4.9 shows the genotype distribution into different groupings. 25 genotypes and 1 check were divided into six groups based on the magnitude of D^2 values.

Table 4.9 Grouping of Lablab bean genotypes into different clusters by Tocher method.

Cluster Group	No. of Genotypes	List of Genotypes
I	16	Local Kadwa, Goda Wal, Konkan Wal-2, DPLW-22-2, DPLW-22-3, DPLW-22-14, DPLW-22-12, Kadwa Wal, DPLW-22-61, DPLW-1, DPLW-22-9, DPLW-22-6, DPLW-22-45, DPLW-22-54, DPLW-22-8 and DPLW-22-5
II	1	DPLW-48
III	6	Local Pen, Kelshi Wal, Local Alibaug, Pavata, DPLW-22-13 and DPLW-22-4
IV	1	DPLW-22-7
V	1	DPLW-22-33
VI	1	DPLW-22-10

Based on the magnitude of D^2 values, the 26 genotypes of lablab bean were grouped in 6 clusters. Cluster I with 16 genotypes was obtained as the cluster having largest genotypes followed by cluster III with 6 genotypes whereas the cluster II, IV, V were solitary.

4.4.2 Average inter and intra cluster distance

Tables 4.10 and 4.10.a show the average intra and inter cluster D^2 and D values for each of the six clusters. The highest divergence was observed between clusters V and VI (1294.10), followed by cluster IV and cluster VI (1130.29), cluster II and cluster IV (875.43), cluster III and

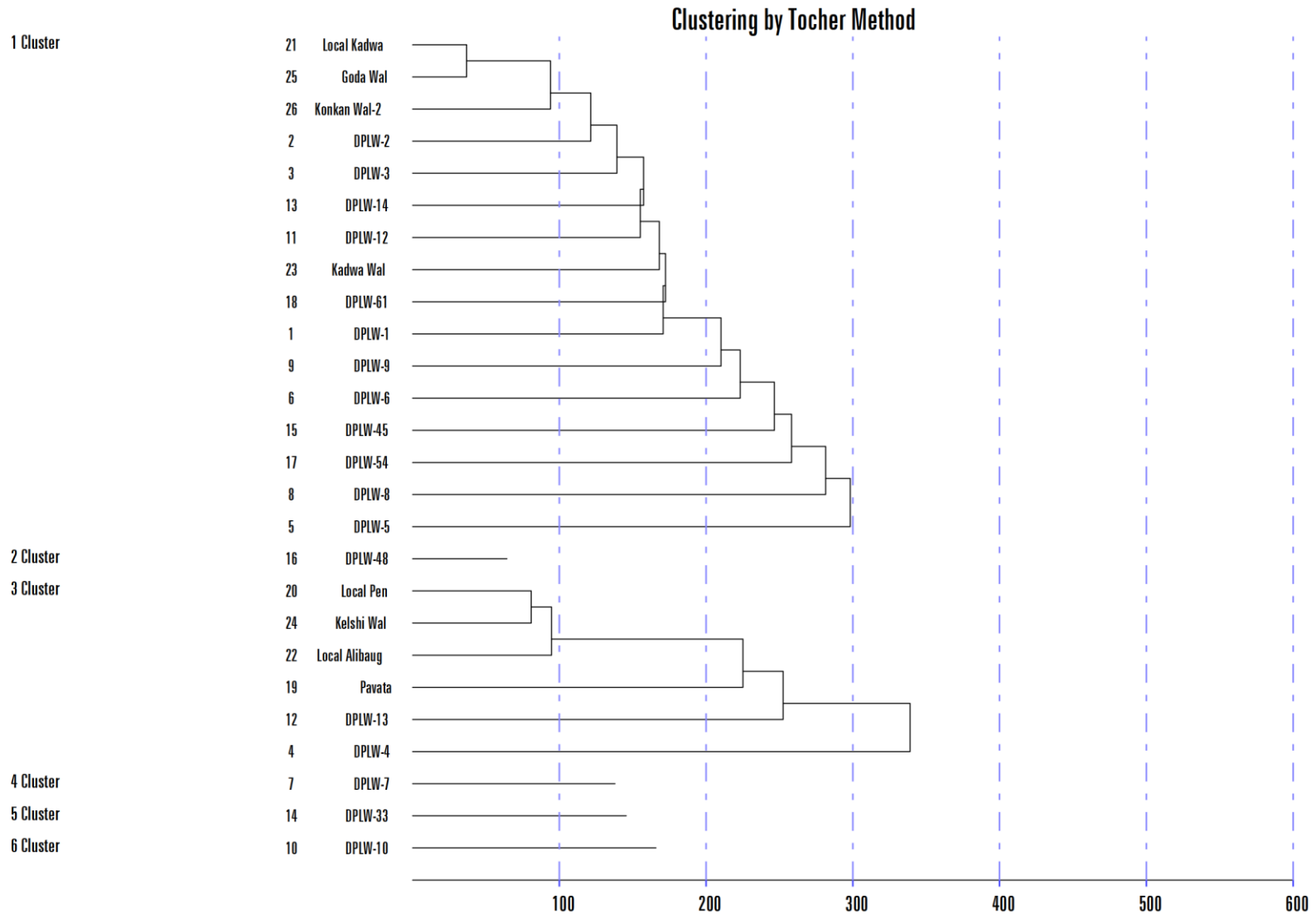


Fig. 4.6. Clustering by Tocher method (Dendrogram)

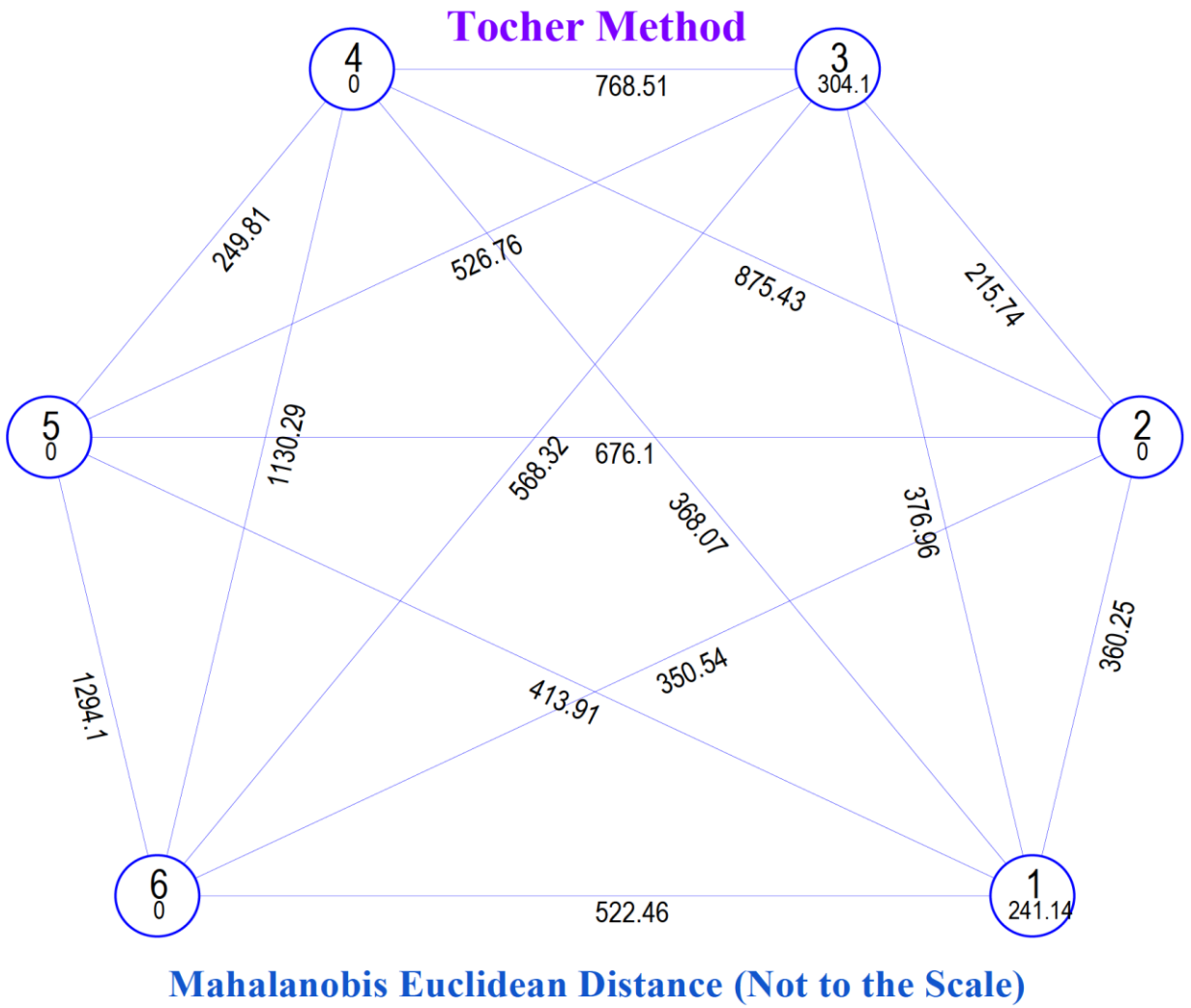


Fig. 4.7. Cluster Diagram (Tocher method)

cluster IV (768.51), cluster II and cluster V (676.10), cluster III and cluster VI (568.32), cluster III and cluster V (526.76), cluster I and cluster VI (522.46). The minimum divergence was observed between cluster II and cluster III (215.74) followed by cluster IV and cluster V (249.81), cluster II and cluster V (350.54), cluster I and cluster II (360.25), cluster I and cluster IV (368.07), cluster I and cluster III (376.96), cluster I and cluster V (413.91). This suggests that the genotypes in these clusters may have different genomic architecture. Cluster III has the maximum intra cluster distance (304.10), followed by cluster I (241.14). Clusters II, cluster IV, cluster V and cluster VI have the shortest distance (0.00). Cluster III was the most diversified, as it shared the most inter-cluster distance with several other clusters.Chaitanya *et al.* (2013), Nidhin *et al.* (2021), Islam *et al.* (2023) and Subashri *et al.* (2023) reported similar results in lablab bean.

Table 4.10 Average intra and inter cluster D^2 values in 6 clusters in 25 genotypes and 1 check of Lablab bean

Cluster Distances						
	I	**II**	**III**	**IV**	**V**	**VI**
I	**241.14**	360.25	376.96	368.07	413.91	522.46
II		**0.00**	215.74	875.43	676.10	350.54
III			**304.10**	768.51	526.76	568.32
IV				**0.00**	249.81	1130.29
V					**0.00**	1294.10
VI						**0.00**

Note: Diagonal values (**Bold**) are intra- cluster distances. Off-diagonal values are inter cluster distances.

Table 4.10.a Average intra and inter cluster $\sqrt{D^2}$ values (D Values) values in 6 clusters in 25 genotypes and 1 check of Lablab bean

Cluster Distances						
	I	**II**	**III**	**IV**	**V**	**VI**
I	**15.52**	18.98	19.41	19.18	20.34	22.85
II		**0.00**	14.68	29.58	26.01	18.72
III			**17.43**	27.72	22.95	23.84
IV				**0.00**	15.80	33.62
V					**0.00**	35.97
VI						**0.00**

Note: Diagonal values (**Bold**) are intra- cluster distances. Off-diagonal values are inter cluster distances.

4.4.3 Cluster mean for different characters

Table 4.11 represents the cluster mean for different characters. The cluster mean performance for days to 50 per cent flowering ranged from 66.00 days (Cluster II) to 71.33 days (Cluster V), with a mean population of 68.02 days. Cluster II genotypes showed early 50 per cent flowering, but cluster V genotypes showed late 50 per cent flowering.

The cluster mean performance for days to maturity varied from 99.94 days (Cluster I) to 105.33 days (Cluster IV) with population mean of 101.90 days. The genotypes from cluster I recorded early maturity whereas genotypes from cluster IV were reported for late maturity.

The cluster mean performance for plant height was ranged from 65.38 cm (Cluster II) to 96.54 cm (Cluster VI) with the mean population of 81.98 cm. The genotypes from cluster II were dwarf plant stature whereas genotypes from cluster VI were reported for tallness among all.

The cluster mean performance for the number of primary branches per plant ranged from 3.28 (Cluster I) to 3.93 (Cluster V), with a population mean of 3.49. The genotypes from Cluster I had fewer branches per plant, whereas the genotypes from Cluster V had more branches per plant.

The cluster mean performance for number of peduncles per plant ranged from 4.60 (Cluster IV) to 6.42 (Cluster III), with a population mean of 5.49. Cluster IV genotypes had fewer peduncles per plant, whereas genotypes from Cluster III produced more peduncles per plant.

The cluster mean performance for number of pods per plant ranged from 21.47 (Cluster IV) to 28.26 (Cluster III), with a population mean of 24.83. Cluster IV genotypes produced fewer pods per plant, whereas genotypes from Cluster III produced more pods per plant.

The cluster mean pod length performance ranged from 4.40 cm (Cluster I) to 5.04 cm (Cluster IV), with a population mean of 4.62 cm. Cluster I genotypes were found to have shorter pod lengths, whereas cluster IV genotypes had longer pod lengths.

The cluster mean performance in terms of number of seeds per pod ranged from 3.80 seed per pod cluster (Cluster I & VI) to 4.00 seed per pod cluster (Cluster II & V), with a population mean of 3.92. Cluster I & cluster VI genotypes were documented for a lower number of seed per pod, whereas cluster II & cluster V genotypes were reported for a higher number of seed per pod.

The cluster mean performance for test weight ranged from 16.00 g (Cluster VI) to 19.59 g (Cluster III), with a population mean of 17.81 g. Cluster VI genotypes were documented for low test weight, while cluster III genotypes were reported for high test weight.

Table 4.11 Mean performance of clusters with their contribution towards total divergence.

Sr. No.	Characters	Clusters						Mean population	Contribution towards divergence (%)	Times ranked first
		I	II	III	IV	V	VI			
1	Days to 50% flowering	67.40	66.00	67.39	70.67	71.33	65.33	68.02	4.00	13
2	Days to maturity	99.94	98.00	104.50	105.33	102.00	101.67	101.90	4.76	15
3	Plant height (cm)	78.06	65.38	78.95	84.44	88.49	96.54	81.98	2.80	9
4	No. of Primary branches	3.28	3.40	3.29	3.33	3.93	3.73	3.49	6.11	19
5	No. of peduncles	5.68	6.13	6.42	4.60	5.00	5.13	5.49	5.21	16
6	No. of pods/plant	26.00	27.27	28.26	21.47	21.87	24.13	24.83	4.83	15
7	Pod Length (cm)	4.40	4.63	4.58	5.04	4.64	4.44	4.62	4.40	14
8	No. of seeds/pod	3.80	4.00	3.99	3.93	4.00	3.80	3.92	7.21	23
9	Test weight (g)	16.53	18.50	19.59	17.62	18.62	16.00	17.81	4.62	15
10	Harvest Index (%)	32.42	32.55	31.73	33.83	31.33	34.79	32.78	8.50	27
11	Seed yield / plant(g)	11.82	11.30	12.55	10.47	10.84	11.87	11.48	13.50	44
12	Protein Content (%)	21.09	20.52	24.06	22.69	22.65	21.47	22.06	9.87	32
13	Calcium content (mg/100g)	102.75	94.33	108.78	109.67	106.00	100.33	103.64	4.30	14
14	Iron content (mg/100g)	3.32	3.48	3.17	3.12	1.66	5.33	3.34	5.32	17
15	Potassium content (mg/100g)	652.53	612.11	699.91	676.11	719.78	746.89	684.55	2.00	6
16	Phosphorus content (mg/100g)	341.73	403.33	368.81	374.89	375.56	355.89	370.04	3.21	10
17	Ascorbic Acid (mg/100g)	9.55	9.19	9.35	9.52	9.32	10.44	9.56	2.15	7
18	Phenols content (mg/100g)	3.73	6.27	5.60	1.67	2.98	5.53	4.30	7.21	23

The cluster mean performance for harvest index varied from 31.33 % (Cluster V) to 34.79 % (Cluster VI) with mean population of 32.78 %. The genotypes from cluster V were reported for low harvest index whereas genotypes from cluster VI were observed for high harvest index.

The cluster mean performance for seed yield per plant ranged from 10.47 g (Cluster IV) to 12.55 g (Cluster III), with a mean population of 11.48 g. Cluster IV genotypes had low seed yield per plant, but cluster III genotypes had good seed yield per plant.

The cluster mean performance for protein content varied from 20.52 % (Cluster II) to 24.06 % (Cluster III) with mean population of 22.06 %. The genotypes from cluster II were recorded for less protein content whereas genotypes from cluster III were reported for more protein content.

The cluster mean performance for calcium content varied from 94.33 mg/100g (Cluster II) to 109.67 mg/100g (Cluster IV) with mean population of 103.64 mg/100g. The genotypes from cluster II were recorded for less calcium content whereas genotypes from cluster IV were reported for more calcium content.

The cluster mean performance for iron content varied from 1.66 mg/100g (Cluster V) to 5.33 mg/100g (Cluster VI) with mean population of 3.34 mg/100g. The genotypes from cluster V were recorded for less iron content whereas genotypes from cluster VI were reported for more iron content.

The cluster mean performance for potassium content varied from 621.11 mg/100g (Cluster II) to 746.89 mg/100g (Cluster VI) with mean population of 684.55 mg/100g. The genotypes from cluster II were recorded for less potassium content whereas genotypes from cluster VI were reported for more potassium content.

The cluster mean performance for phosphorus content varied from 341.73 mg/100g (Cluster I) to 403.33 mg/100g (Cluster II) with mean population of 370.04 mg/100g. The genotypes from cluster I were recorded for less phosphorus content whereas genotypes from cluster II were reported for more phosphorus content.

The cluster mean performance for ascorbic acid content varied from 9.19 mg/100g (Cluster II) to 10.44 mg/100g (Cluster VI) with mean population of 9.56 mg/100g. The genotypes from cluster II were recorded for less ascorbic acid content whereas genotypes from cluster VI were reported for more ascorbic acid content.

The cluster mean performance for phenols content varied from 1.67 mg/100g (Cluster IV) to 6.27 mg/100g (Cluster II) with mean population of 4.30 mg/100g. The genotypes from cluster

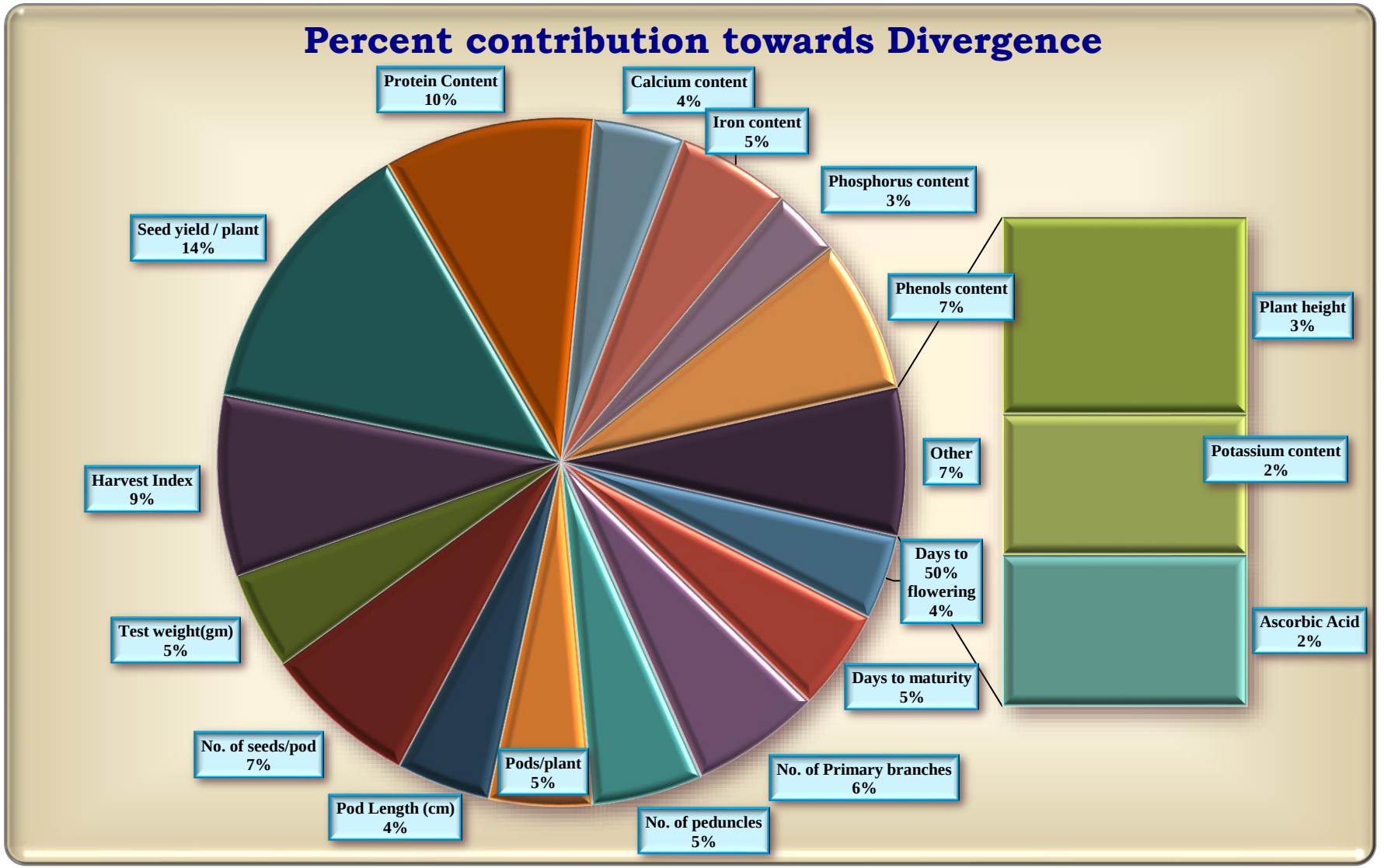


Fig.4.8. Character contribution towards divergence

IV were recorded for less phenols content whereas genotypes from cluster II were reported for more phenols content.

4.4.4 Character contribution towards divergence

Table 4.11 represents how different characters contributed to total deviation. Seed yield per plant (13.50 %, 44) had the greatest contribution to divergence, with its respective times placed first, followed by protein content (9.87%, 32), harvest index (8.50%, 27), number of seeds per pod (7.21%, 23), phenols content (7.21%, 23), number of primary branches (6.11%, 19), iron content (5.32, 17), number of peduncles (5.21%, 16), number of pods per plant (4.83%, 15), days to maturity (4.76%, 15), test weight (4.62%, 15), pod length (4.40%, 14), calcium content (4.30%, 14), days to 50 per cent flowering (4.00%, 13), phosphorus content (3.21%, 10), plant height (2.80%, 9), ascorbic acid content (2.15%, 7) and potassium content (2.00%, 6).

The success of the breeding program, which entails selecting the best genotypes, is influenced by its variability and diversity. Selection based on a wide range of genetic variation has its own relevance. As a result, the diversity of 25 distinct genotypes and 1 check of lablab bean were evaluated in the current study. This study provided significant information that might be used to select effective genotypes for introduction as a variety.

The high variability in quantitative character appears to be driving the wide range of genetic variation among biological genotypes. As a result, D^2 analysis was performed using Mahalanobis statistics to quantify the magnitude of divergence among the genotypes, taking into account the relative contribution of different components to overall divergence at the intra and inter cluster levels. (Mahalonobis, 1936).

Thus, the 25 genotypes and 1 check were divided into six clusters with a large range of variance. The clustering pattern of 25 genotypes and 1 check of lablab bean followed no definite pattern and was completely random. Cluster I contain 16 genotypes along with check Konkan Wal-2, cluster II contain 1 genotype, cluster III contains 6 genotypes, cluster IV contain 1 genotype, cluster V contain 1 genotype and cluster VI contain only 1 genotype. Clusters II, IV, V and VI were mono-genotypic. The diversity present between the lablab bean genotypes measured by inter-cluster distances was adequate for the improvement of lablab bean by selection. The genotypes clustered in these six clusters may be used to develop a promising variety.

Maximum mean for cluster was recorded for potassium content followed by phosphorus content whereas minimum cluster mean was observed for iron content followed by number of primary branches per plant.

Seed yield per plant had the greatest contribution to divergence, with its respective times placed first, followed by harvest index, number of seeds per pod, number of primary branches number of peduncles, number of pods per plant days to maturity, test weight, pod length, days to 50 per cent flowering and plant height. Similar results were reported by Ananya *et al.* (2015), Shulee *et al.* (2021) in lablab bean.

DPLW-22-1

DPLW-22-4

DPLW-22-3

Plate II : Variation in plant height

Plate III : Variation in pod length

Plate IV : Seeds per pod

CHAPTER V : SUMMARY AND CONCLUSION

The present investigation, entitled **"Assessment of genetic variability and diversity for yield, biochemical and nutritional components of Lablab bean (*Lablab purpureus* (L.) Sweet)"**, was conducted at Research and Education farm, Department of Agriculture Botany, College of Agriculture, Dapoli., Dist. Ratnagiri, during the *rabi* 2023-24 with the following objectives:

1. To evaluate genetic variability and diversity for yield and yield related components of Lablab bean.
2. To evaluate biochemical and nutritional components.
3. To select superior genotypes of Lablab bean based on yield and quality.

To achieve success in any strategic crop improvement programme depends on extent of variability present and effective skills applied under selection. Therefore, present research was performed for evaluation of the performance of promising genotypes by estimating their mean and coefficient of variation, genetic variability, path analysis, genetic divergence heritability, genetic advance, genetic advance as percent of mean and character association with lablab bean.

The experimental material consisted of 25 genotypes and 1 check (Konkan Wal-2). These material were evaluated in randomized block design during *rabi* 2023-24 at Educational and Research farm, Department of Agricultural Botany, College of Agriculture, Dapoli. The observations were recorded days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of peduncles per plant, number of pods per plant, pod length(cm), number of seeds per pod, test weight (g), harvest index(%), seed yield per plant (g), protein content(%), calcium content (mg/100g), iron content (mg/100g), potassium content (mg/100g), phosphorus content(mg/100g), ascorbic acid (mg/100g) and phenol content (mg/100g). The data was taken for suitable analysis and findings summarized below which could be utilized for further improvements in lablab bean:

- The analysis of variance revealed the presence of sufficient variability among the genotypes for different characters indicating the presence of sufficient genetic variability in the experimental material.
- A wide range of variation was observed for almost all the characters studied. A wide range of variation was observed for potassium content, phosphorus content, plant height, calcium content, days to maturity and days to 50 per cent flowering while less range was seen for number of seeds per pod, pod length and number of primary branches per plant.

- Based on the mean performance, the genotypes *viz*., DPLW-22-4 and pavata were found elite genotypes. These, genotypes can be used for further varietal improvement.

- In Konkan region, Wal is grown on residual moisture after rice fallow thus early maturing varieties like DPLW-22-5 and DPLW-22-54 can be beneficial.

- The estimates of the phenotypic, genotypic and environmental variances indicated that the value of phenotypic variances were slightly higher than genotypic variances indicating the less influence of environmental factor in most of the characters. The data indicated that genetic components (genetic variances) played a greater role in expression of characters as compared to environmental variances.

- For all the characters, phenotypic coefficient of variation was higher than the respective genotypic coefficient of variation. Varying per cent of phenotypic and genotypic coefficient of variation were observed. Higher genotypic and phenotypic coefficient of variations were observed for phenols content, iron content, seed yield per plant, plant height, number of pods per plant and number of peduncles per plant while they were low for days to maturity, days to 50 per cent flowering and number of seeds per pod.

- Heritability was the highest for phenol content followed by iron content, potassium content, test weight, ascorbic acid content. This suggested that heritability may be due to higher contribution of the genotypic component in these characters.

- High estimates of genetic advance expressed as per cent of mean were found for phenol content followed by iron content, plant height, test weight and seed yield per plant . Whereas, moderate value of genetic advance expressed as per cent of mean were observed phosphorus content, calcium content which indicated the predominance of additive gene action and direct selection could be effective for improvement of this character.

- High heritability coupled with high genetic advance expressed as per cent of mean were observed for phenol content, iron content, plant height, seed yield per plant. This indicates the presence of additive genes and less environmental influence on the characters and existence of sufficient heritable variation and wider scope for effective selection.

- The seed yield per plant showed significant and positive association (correlation) with number of branches per plant, plant height, number of pods per plant, pod length, number of seeds per pod, test weight, number of peduncles per plant and harvest index at simple level, which indicated the dependency of these characters with each other were considered as useful selection criteria.

- The path coefficient demonstrated a direct positive relationship between seed yield and plant height, number of peduncles per plant, number of seeds per pod, harvest index, protein content, calcium content, phosphorus content, ascorbic acid content and phenols content at both levels. Number of pods per plant, pod length and iron content had positive direct effect with seed yield at phenotypic level but negative direct effect at genotypic level.

- Total 26 genotypes were grouped into 6 different clusters on the basis of magnitude of D^2 values evaluated by Mahalanobis D^2 analysis. Among 26 genotypes, 16 were clustered into first (I) cluster, followed by cluster (III) with 6 genotypes and cluster (II) ,cluster (IV), cluster (V), cluster (VI) had 1 genotype each.

- The highest divergence was observed between clusters V and VI, followed by cluster IV and cluster VI, cluster II and cluster IV. The minimum divergence was observed between cluster II and cluster III followed by cluster IV and cluster V, cluster II and cluster V.

- Cluster III has the maximum intra cluster distance. Cluster III was the most diversified, as it shared the most inter-cluster distance with several other clusters. Clusters II, cluster IV, cluster V and cluster VI had the shortest distance.

- Maximum cluster mean was recorded for potassium content followed by phosphorus content whereas minimum cluster mean was observed for iron content followed by number of primary branches per plant.

- Seed yield per plant had the greatest contribution to divergence, with its respective times placed first, followed by protein content and harvest index. Potassium content had least contribution to divergence followed by ascorbic acid content and plant height.

Conclusion

- In conclusion, it is to be confessed that, broad range of variability was present between the genotypes studied for the different quantitative characters.
- High heritability coupled with high genetic advance per cent mean was observed for phenol content followed by iron content. The higher estimates of heritability coupled with high genetic advance as percent of mean shows additive gene action and make in suitable for direct selection.
- On the basis of correlation and path analysis studied, seed yield per plant could be improved through simultaneously selection of number of pods per plant, number of peduncles per plant, harvest index, number of primary branches per plant, plant height, pod length, test weight, days to maturity and number of seeds per pod. It is desirable to give more magnitude of weightage to these characters during selection programme.
- The genotype DPLW-22-4 was found with best performance in all genotypes studied for yield and yield attributing characters.
- DPLW-22-4 was found the good yielder with the contributing character i.e., seed yield per plant.
- Pavata was also found to be elite with contributing character i.e., number of seeds/pod, phosphorus and phenols content.
- Among all the genotypes studied, highest protein content was reported in DPLW-22-4.
- Highest calcium content was observed in Kelshi wal followed by DPLW-22-9 among all genotypes studied.
- DPLW-22-10 showed highest iron content followed by DPLW-22-8 among all genotypes.
- Local Kadwa had highest potassium content followed by Kelshi wal from genotypes studied.
- Among all genotypes under study, phosphorus content was highest in Pavata followed by DPLW-22-13.
- Highest ascorbic acid content was observed in Local Kadwa and DPLW-22-10.
- Phenols content was maximum in Pavata followed by DPLW-22-48 among all genotypes.
- Genotypes found superior *viz.*, DPLW-22-4, Pavata, DPLW-22-9, DPLW-22-10 and DPLW-22-48 for yield and nutritional contents may be used as promising genetic material in future breeding programmes for the improvement of specific traits in this crop.

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APPENDIX I

Meteorological observation during the period of experiment

Rabi, 2022-2023 at Dapoli

Period	MW	T_{max}	T_{min}	RH-I	RH-II	Wind speed	Rain	RD	BSS	E_{pan}
		(°C)	(°C)	(%)	(%)	(Kmph)	(mm)	day	(hrs.)	(mm)
12.11 – 18.11	**46**	33.9	17.9	91	51	2.2	0.0	0	8.1	4.0
19.11 – 25.11	**47**	34.1	17.7	91	46	2.5	0.0	0	8.0	4.0
26.11 – 02.12	**48**	32.1	18.4	94	53	3.1	1.4	0	6.5	3.7
03.12 – 09.12	**49**	32.6	16.6	94	56	2.8	0.0	0	7.2	3.7
10.12 – 16.12	**50**	32.8	14.8	91	49	2.7	0.0	0	8.5	3.8
17.12 – 23.12	**51**	32.0	15.4	88	47	3.1	0.0	0	4.4	3.5
24.12 – 31.12	**52**	33.8	12.9	93	42	2.1	0.0	0	8.1	3.7
01.01 - 07.01	**1**	32.2	13.9	94	48	2.7	0.0	0	7.0	3.5
08.01 - 14.01	**2**	32.7	16.0	91	52	3.0	0.5	0	6.3	3.4
15.01 - 21.01	**3**	29.7	11.6	90	46	3.0	0.0	0	9.2	3.2
22.01 - 28.01	**4**	31.3	11.2	91	42	2.7	0.0	0	9.4	3.4
29.01 - 04.02	**5**	31.9	12.6	92	43	3.1	0.0	0	8.0	3.3
05.02 - 11.02	**6**	33.6	12.7	89	44	3.1	0.0	0	9.0	3.5
12.02 - 18.02	**7**	33.8	12.5	90	38	3.2	0.0	0	9.7	3.7
19.02 - 25.02	**8**	31.7	11.2	88	50	4.3	0.0	0	10.5	3.4
26.02 - 04.03	**9**	33.7	15.6	88	47	3.6	0.0	0	10.3	3.7
05.03 - 11.03	**10**	33.1	11.6	83	43	4.5	0.0	0	10.0	3.6
Mean/Total		32.6	14.3	90.5	46.9	3.0	1.9	0.0	8.2	3.6

BSS* : Bright Sun Shine hours

RH I : Morning Relative Humidity

RH II : Evening Relative Humidity

T_{max} : Temperature Maximum

T_{min} : Temperature minimum

APPENDIX II

- **Determination of protein content**

The protein content of dry pods was determined by estimating the nitrogen content as per the modified Kjeldhal method and multiplying the nitrogen content with a factor 6.25 and expressed on percent basis for each genotype.

Methodology for the Determination of Protein by Kjeldhal Method

- **Principle**

The protein content is determined from the organic Nitrogen content by Kjeldahl method. The various nitrogenous compounds are converted into ammonium sulphate by boiling with concentrated sulphuric acid. The ammonium sulphate formed is decomposed with an alkali (NaOH) and the ammonia liberated is absorbed in excess of standard solution of acid and then back titrated with standard alkali.

- **Apparatus**

a. Kjeldahl digestion flask - 500 or 800 ml

b. Kjeldahl distillation apparatus, - same digestion flask fitted with rubber stopper through which passes lower end of efficient rubber bulb or trap to prevent mechanical carryover of NaOH during distillation or apparatus as shown below:

c. Conical flask, 250 ml

d. Burette 50 ml.

- **Reagents**

a. Concentrated Sulphuric acid – sp. gr. 1.84

b. Sodium Hydroxide solution - 45%. Dissolve 450 gm of Sodium Hydroxide In 1000 ml water

c. Standard Sulphuric acid solution – 0.1 N

d. Standard Sodium Hydroxide solution – 0.1 N

e. Methyl Red Indicator solution - Dissolve 0.5 gm methyl red in 100 ml of Alcohol

- **Procedure**

Weigh quickly about 0.5 g of the sample and transfer to a 500 or 800 ml Kjeldahl flask taking care to see that no portion of the sample clings to the neck of the flask. Add 0.7 gm of Mercuric oxide, 15 gm of Potassium Sulphate and 40 ml of concentrated sulphuric acid. Add two to three glass beads. Place the flask in an inclined position on the stand in the digestion chamber and digest. Heat the flask gently at low flame until the initial frothing ceases and the mixture boils steadily at a moderate rate.

During heating rotate the flask several times. Continue heating for about an hour or more until the colour of the digest is pale blue. Cool the digest and add slowly 200 ml of water. Cool, add a piece of granulated Zinc or anti bump granules and carefully pour down from the side of the flask sufficient Sodium Hydroxide solution (450gm/ litre) to make the contents strongly alkaline (about

110 ml) before mixing the acid and alkaline layer. Connect the flask to a distillation apparatus incorporating an efficient flash head and condenser. To the condenser fit a delivery tube which dips just below the surface of the pipette volume of standard acid contained in a conical flask receiver. Mix the contents of the digestion flask and boil until 150 ml have distilled into the receiver. Add 5 drops of methyl red indicator and titrate with 0.1 N Sodium hydroxide solutions.

A blank was also run through all steps as above. Percent crude protein content of the sample was calculated by using the following formula:

% Crude Protein = 6.25* x %N (*. Correction factor)

$$\%N = \frac{(S - B) \times N \times 0.014 \times D \times 100}{\text{Wt. of the sample} \times V}$$

Where,

S = Sample titration reading

B = Blank titration reading

N = Normality of HCl

D = Dilution of sample after digestion

V = Volume taken for distillation

0.014 = Milli equivalent weight of Nitrogen

APPENDIX III

- **Estimation of Calcium using titration method**
- **Reagents**
    1) Buffer solution

       67.5 g NH_4Cl + 200 ml distilled water + 570 ml of conc. NH_4OH. Make the volume 1 litre with distilled water.
    2) Std. EDTA (0.01 N)

       Take 1.86 g of disodium EDTA and make the volume to 1 litre.
    3) Std. Ca solution (0.01 N)

       0.50 g $CaCO_3$ in 5 ml of approximate 6N HCl and make the volume to 1 litre.
    4) NaOH solution (10%)

       Take 100 g of NaOH and make the volume of 1 litre by adding distilled water.
    5) Muroxide indicator

       Add 0.2 g ammonium purpurate with 40 g finely grind potassium sulphate. Grind using mortar and pestle.
- **Procedure**
    1) Take 5 ml extract in porcelain basin.
    2) Add 5 ml 10 % NaOH solution to attain pH 12 or more.
    3) Add half spatula of muroxide indicator (50 mg).
    4) Titrate with std. EDTA till colour changes from pink to violet (Purple).
- **Calculation**

$$\text{Ca (meq/100g)} = \frac{\text{TV1 X N of EDTA X Extract volume X 100}}{\text{Weight of sample X Aliquot taken}}$$

APPENDIX IV

- **Determination of Iron from plant sample by AAS**
- **Principle**

The principle that almost of metallic elements which normally remain in ground state under flame conditions absorb energy when subjected to radiation of specific wavelength absorb energy when subjected to radiations of specific wavelength. The absorption of radiation is proportional to the concentration of atoms of that element. The AAS has a distinct advantage over flame emission spectroscopy because the absorption of radiation by the atoms is independent of the wavelength of the radiations and temperature of the atoms. It also has greater sensitivity and accuracy.

- **Method:**
- **Digestion of plant material**

Wet Di-acid digestion by Nitric Acid and Perchloric acid plant material is digested either in an HNO_3-$HCIO_4$, mixture and dissolved in acid. Also carry blank digestion using all steps, excluding the plant material to avoid any impurity in the reagents being used.

1. Acid mixture-dilute two parts HNO_3 with one part $HCLO_4$ or nine part HNO_3 with four parts $HCLO_4$.

2. Weight 0.2 to 0.5 gm of plant material into a 50 ml digestion tube.

3. Add 5ml of acid mixture.

4. Place the small dry funnel into the tube and put the tube into block digester.

5. Heat sample at 60°C for 15 min or until reaction is complete.

6. Increase heat to 120°C and digestion for 75 min or until sample clear.

7. Remove tube from block digester when sample is clear. Cool and add sufficient distilled water to bring solution up to 100 ml.

- **Analysis of plant digest**

Fe concentration in plant digest can be determined by atomic absorption spectrophotometer as follows.

1. Read operator's manual prior to start instrument.

2. Set zero of the instrument with blank.

3. Feed standard of element to be determined to the AAS to standardize the instrument for element in sample. Feed plant digest and record the absorbance/concentration of the element in question.

4. Repeat the above steps for every element.

5. In case the instrument shows a sign of over for some element in a particular sample then make further dilution of the sample and feed again to record absorbance or concentration.

- **Calculation**

$$Fe = \frac{R \times \text{Final volume acid extract} \times \text{dilution factor}}{\text{Wt. of plant tissue (g)}}$$

Where,

R- Read from AAS-in µg/ml

APPENDIX V

- **Estimation of Total Potassium using flame photometer**
- **Principle of Flame Photometer:**

The principle of flame photometers is based on the measurement of the emitted light intensity when metal is introduced into the flame. The wavelength of the color gives information about the element and the color of the flame gives information about the amount of the element present in the sample.

- **Reagents**
- **Preparation Standard Solutions for Standardizing the Flame Photometer:**

A) Ammonium acetate solution:

1. Dissolve 77g of ammonium acetate in 900ml D.W.
2. Adjust pH to 7.0 by adding 3N Sodium hydroxide solution
3. Makeup volume up to 1 Liter

B) Standard Potassium Chloride Solution (1000 ppm):

1. Dissolve 1.908 g Potassium Chloride in 1 liter D.W. to get a 1000 ppm solution of Potassium Chloride.
2. From the above solution pipette out 1ml, 3ml, 5ml, and 10ml separately into different flasks and makeup volume to 100ml with D.W. We will get 10 ppm, 30ppm, 50ppm, and 100ppm standard solutions of Potassium Chloride.

- **Procedure**

Step-I : Digestion

1) Weigh 0.5 g sample
2) Add 15 ml di-acid in conical flask (Di-acid = HNO_3 : $HClO_4$= 9:4).
3) Put it overnight for pre-digestion.
4) Put conical flask on hot plate till colourless solution is obtained.
5) Add 20 ml water for dilution.
6) Filter through Whatman number 42 filter paper.
7) Make up the volume 50 ml.

Step – II : Estimation

Take readings of digested samples flame photometer

- **Calculations**

Total K = ppm X 0.01

APPENDIX VI

- **Estimation of Total phosphorus using Vandomolybdate method**
  - **Reagents**

Ammonium molybdate-vanadte solution

1) Dissolve 22.5 g ammonium molybdate in 400 ml distilled water.
2) Dissolve 1.25 g ammonium vanadate in 300 ml of boiling water in a beaker.\
3) Add ammonium vanadate solution to the ammonium molybdate solution.
4) Cool it at room temperature.
5) Add 250 ml of conc. Nitric acid.
6) Make up the volume to 1 litre.

Primary phosphate standard solution (50 ppm)

1) Weight 0.2195 g of potassium dihydrogen phosphate (KH_2PO_4).
2) Dissolve in 400 ml of distilled water.
3) Add 25 ml pf 7N H_2SO_4.
4) Make volume to 1 litre.
5) Prepare the standard series from 50 ppm KH_2PO_4. Pipette out 1ml, 2ml, 3ml, 4ml, 5ml separately into different flasks and makeup volume to 100ml with D.W. We will get 10 ppm, 20ppm, 30ppm, 40ppm and 50ppm standard solutions of KH_2PO_4.

- **Procedure**
- **Step-I : Digestion**

1) Weigh 0.5 g sample
2) Add 15 ml di-acid in conical flask (Di-acid = HNO_3 : $HClO_4$= 9:4).
3) Put it overnight for pre-digestion.
4) Put conical flask on hot plate till colourless solution is obtained.
5) Add 20 ml water for dilution.
6) Filter through Whatman number 42 filter paper.
7) Make up the volume 50 ml.

- **Step-II : Estimation**

1) Pipette out 10 ml extract in 50 ml volumetric flask.
2) Add 10 ml ammonium molybdate-vanadate reagent.
3) Make up the volume 50 ml.
4) Wait for 30 minutes until yellow colour developed.
5) Measure absorbance at 420 nm by spectrophotometer.

- **Calculations**

1) Graph factor = $\frac{x1/y1 + x2/y2 + x3/y3 \ldots\ldots xn/yn}{\text{Number of point (n)}}$

2) Total phosphorus =

$$\frac{\text{(Graph factor X absorbance) X 100 X Volume of extract made at colour development (50ml)}}{10^6 \text{ ml of aliquot taken (10 ml)}} \text{ X } \frac{\text{Volume made (50 ml)}}{\text{Weight of sample(0.5g)}}$$

3) **Total phosphorus** = (Graph factor X Absorbance) X 0.05

APPENDIX VII

- **Estimation of Ascorbic Acid by volumetric method**
- **Materials**

1. Oxalic Acid (4%)

2. Dye Solution: Weigh 42mg sodium bicarbonate into a small volume of distilled water. Dissolve 52mg 2,6-dichlorophenal indophenol in it and make up to 200ml with distilled water.

3. Stock Standard Solution: Dissolve 100mg ascorbic acid in 100ml of 4% oxalic acid solution in a standard flask (1mg/ml).

4. Working Standard: Dilute 10ml of stock solution to 100ml with 4% oxalic acid. The concentration of working standard is 100ug/ml

- **Principle**

Ascorbic acid reduces the 2. 6-dichlorophenol indophenol dye to a coloriss leuco-base. The ascorbic acid gets oxidized to dehydroascorbic acid. Though the dye is a blue coloured compound, the end point is the appearance of pink colour. The dye is pink colour in acidic medium. Oxalic acid is used as the titrating medium.

- **Procedure**

1. Pipette out 5ml of the working standard solution into a 100ml of conical flask.

2. Add 10ml of 4% oxalic acid and titrate against the dye (V_1 ml). End point is the appearance of pink colour which persists for a few minutes. The amount of dye consumed is equivalent to the amount of ascorbic acid.

3. Extract the sample (0.5-5g depending on the sample) in 4% oxalic acid and make up to a known volume (100ml) and centrifuge. 4. Pipette out 5ml of this supernatant, add 10ml of 4% oxalic acid and titrate against the dye (V_2ml).

- **Calculations**

Amount of ascorbic acid mg/100ml sample

$$\frac{0.5\text{mg X } V_2\text{ ml X 100 ML X 100}}{V_1\text{ ml x 5ml X Wt. of the sample}}$$

APPENDIX VIII

- **Estimation of phenols**
- **Reagents**
  1) 30% Ethanol
  2) Folin-Ciocalteus's reagent
  3) Na_2CO_3-20%
  4) Standard (100 mg catechol in 100 ml water) – Dilute 10 times for working standard.
- **Preparation of standard solution**
  1) 0.1 g of catechol diluted in 1000 ml of water. Use this solution for standards.
  2) Take 0.2 ml to 2 ml of standard solution in test tubes.
  3) Add 3 ml distilled water and then 0.5 ml Folin-Ciocalteus's reagent.
  4) After 3 minutes add 2 ml 20% Na_2CO_3.
  5) Mix thoroughly and place the test tubes in boiling water bath for 2 minutes.
  6) Take the reading at 650 nm against blank and plot a graph.
- **Procedure**

1) Weigh 0.5 to 1 g sample and grind it with a pestle and mortar for 10 times volume of 80% ethanol.
2) Centrifuge the homogenate at 10000 r.p.m. for 20 minutes. Save the supernatant, re-extract the residue with five times the volume of 80 % ethanol, centrifuge and pool the supernatant.
3) Evaporate the supernatant to dryness.
4) Dissolve the residue in known volume of distilled water (5 ml).
5) Pipette out different aliquots (0.2 to 2 ml) into test tubes.
6) Make up the volume in each tube to 3 ml with distilled water. Add 0.5 ml Folin-Ciocalteu's reagent.
7) After 3 minutes, add 2 ml of 20% Na_2CO_3 solution to every test tube.
8) Mix thoroughly place the test tubes in boiling water for exactly one minute. Cool and measure the absorbance at 650 nm against blank.
9) Prepare a standard curve using different concentration of Catechol.

- **Calculations**

$$\textbf{Phenol (mg/g)} = \frac{\text{Graph factor X Reading X 3}}{\text{0.5 (Weight of sample)}}$$

THESIS ABSTRACT

a)	Title of the thesis	: "Assessment of genetic variability and diversity for yield, biochemical and nutritional components if Lablab bean (*Lablab purpureus* (L.) Sweet)."
b)	Full name of the student	: Miss. Sangale Gayatri Kamalakar
c)	Name and address of the major advisor	: Dr. R. L. Kunkerkar Head, Department of Agril. Botany, College of Agriculture, Dapoli.
d)	Degree to be awarded	: M.Sc. (Agri.)
e)	Year of award of degree	: 2024
f)	Major subject	: Genetics and Plant Breeding
g)	Total number of pages in the thesis	: 86
h)	Number of words in the abstract	: 297
i)	Signature of student	:
j)	Signature, Name and address of forwarding authority	:

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The investigation titled "Assessment of Genetic Variability and Diversity for Yield, Biochemical and Nutritional Components of Lablab Bean (*Lablab purpureus* (L.) Sweet)" was conducted at the College of Agriculture, Dapoli, during the *rabi* season of 2023-24 with the objectives : To evaluate genetic variability and diversity for yield and yield related components of Lablab bean, To evaluate biochemical and nutritional components and To select superior genotypes of Lablab bean based on yield and quality. The study aimed to evaluate genetic variability and diversity among 25 Lablab bean genotypes and one check variety (Konkan Wal-2) for yield and nutritional components.

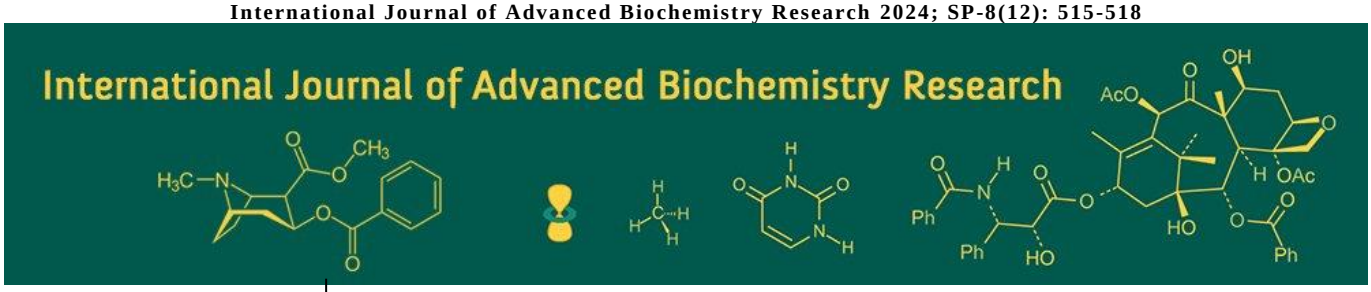
The experimental design was randomized block, with observations recorded for key traits including days to flowering and maturity, plant height, number of pods, test weight, and biochemical components such as protein and mineral content. Analysis of variance revealed significant variability among genotypes, with a wide range of variation noted particularly for potassium and phosphorus content.

Estimates of phenotypic and genotypic variances indicated a strong genetic influence on most traits, with high phenotypic coefficients of variation observed for phenol and iron content. High heritability was recorded for several traits, suggesting effective selection potential. Correlation and path analysis showed that seed yield per plant positively correlated with traits such as plant height and harvest index, indicating interdependency.

Cluster analysis grouped the genotypes into six clusters based on genetic divergence, with Cluster III exhibiting the most diversity. Seed yield emerged as a significant contributor to divergence among genotypes.

In conclusion, substantial genetic variability exists among Lablab bean genotypes, highlighting the potential for improving yield and nutritional quality through selective breeding. Genotypes DPLW-22-4 and Pavata are recommended for future breeding efforts aimed at enhancing specific traits in Lablab bean. This research underscores the crop's potential role in sustainable agriculture and nutrition enhancement.

Key words : Variability, Correlation, Path analysis, Heritability, Divergence *etc.*



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Study of genetic diversity in lablab bean (*Lablab purpureus* (L.) Sweet) for yield and yield related components

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Abstract
A genetic diversity study of 25 lablab bean genotypes and one check variety using Mahalanobis D² analysis grouped them into six clusters. The highest inter-cluster divergence was between Clusters V and VI (1294.10), while Cluster III showed the highest intra-cluster distance (304.10), making it the most diverse. Key contributors to divergence were seed yield per plant (13.50%), protein content (9.87%), and harvest index (8.50%). Cluster III genotypes excelled in seed yield, protein content, and test weight, while Cluster VI genotypes were superior in plant height, iron, potassium, and ascorbic acid content. Promising genotypes identified were in Cluster III (high yield and protein content) with genotypes such as- DPLW-22-4, Pavata and Cluster VI (nutritional traits) with genotypes such as – DPLW-22-10. These findings highlight the potential for inter-cluster hybridization, especially between V and VI, to develop high-performing lablab bean varieties.

Keywords: Genetic diversity, lablab bean, cluster, randomized block design

Introduction
Pulse crop plays an important role in Indian economy. They are source of high-quality protein and occupy an important place in human's food and nutritional requirements. Among various pulses grown, lablab bean (*Labalab purpureus* (L.) is one of the important pulse crop, belonging to family fabaceae. Lablab bean , also known as hyacinth bean or lablab, is a leguminous crop of significant economic and nutritional importance in tropical and subtropical regions. It is grown primarily for its edible pods, seeds, and leaves, which are used for both human and animal consumption. Apart from being a food source, lablab bean plays a vital role in sustainable agriculture due to its ability to fix atmospheric nitrogen, thus enhancing soil fertility. It is considered a drought-tolerant crop, making it suitable for cultivation in areas with variable rainfall (Sharma *et. al.*, 2018) [10].

Genetic diversity is the cornerstone of crop improvement, as it provides the raw material for developing new varieties with better yield, disease resistance, and nutritional quality. In lablab bean, the genetic variation is crucial for enhancing productivity and adapting the crop to changing climatic conditions. Despite its importance, the genetic diversity of lablab bean remains underexplored compared to other legumes, with only limited studies focusing on the molecular and morphological diversity within the species (Sahoo *et. al.*, 2019) [8]. Understanding the genetic variability among lablab bean genotypes is essential for formulating effective breeding strategies aimed at improving yield, nutritional content, and resistance to pests and diseases.

Divergence analysis using methods such as Mahalanobis D² statistics has proven to be an effective tool in assessing genetic diversity in various crops, including legumes. This method helps in identifying diverse genotypes that can be utilized for hybridization and selection, thus ensuring the development of improved varieties. The genetic differentiation among lablab bean genotypes, based on traits such as seed yield, pod length, protein content, and resistance to environmental stresses, forms the basis for identifying promising genotypes for breeding programs (Patil *et. al.*, 2020) [6]. Therefore, studies on genetic diversity in lablab bean are crucial for

enhancing its productivity and nutritional quality, contributing to food security and sustainable agriculture in many regions

Materials and Methods

The present investigation was carried out at Research and Education Farm, Department of Agril. Botany, College of Agriculture, Dapoli, Dist. Ratnagiri during *rabi* 2023-2024.

1	Crop	:	Lablab bean
2	Spacing (cm)	:	30 x 30
3	Experimental design	:	Randomized Block Design (RBD)
4	No. of genotypes	:	25 + 1 check
5	No. of plants per line	:	10
6	Plot size	:	3.0 x 0.9 m
7	Recommended fertilizer dose	:	25 kg N: 50 kg P_2O_5: 50 kg K_2O / ha
8	Season	:	*Rabi* 2023-24
9	Date of sowing	:	30 October, 2023

The material for the present evaluation comprised of twenty five different genotypes of Wal and one check. The seeds were obtained from different sources with various qualitative and quantitative characteristics. The investigation involved cultivation of 25 genotypes, alongside the check Konkan wal-1.

Results and Discussion

The presence of genetic diversity offers enormous potential for crop development for character of interest. The primary factor is estimation of genetic distance. The genetic divergence can be assessed using powerful statistical method, Mahalanobis D^2 statistics which provides a detailed picture of genotype diversity. Clusters were formed using Rao's (1952) [7] Tocher technique. Based on the magnitude of D^2 values the 25 genotypes and one check was grouped in six clusters. Cluster I with 16 genotypes was obtained as the cluster having largest genotypes followed by cluster III with 6 genotypes whereas the cluster II, IV, V were solitary.

Table 1: Grouping of Lablab bean genotypes into different clusters by Tocher method

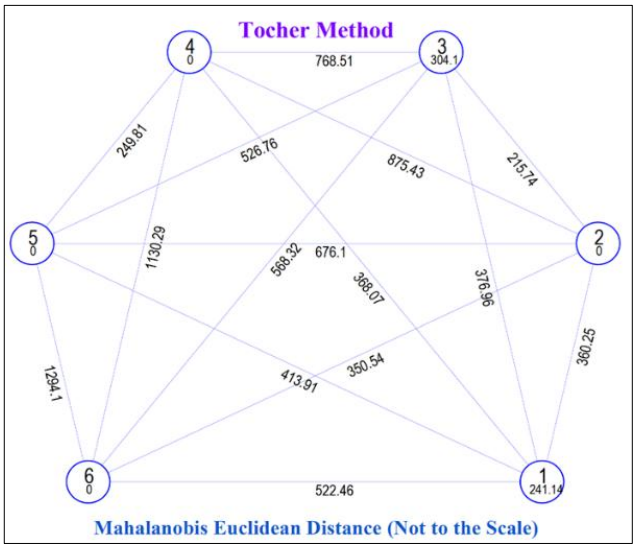
Cluster Group	No. of Genotypes	List of Genotypes
I	16	Local Kadwa, Goda Wal, Konkan Wal-2, DPLW-22-2, DPLW-22-3, DPLW-22-14, DPLW-22-12, Kadwa Wal, DPLW-22-61, DPLW-1, DPLW-22-9, DPLW-22-6, DPLW-22-45, DPLW-22-54, DPLW-22-8 and DPLW-22-5
II	1	DPLW-48
III	6	Local Pen, Kelshi Wal, Local Alibaug, Pavata, DPLW-22-13 and DPLW-22-4
IV	1	DPLW-22-7
V	1	DPLW-22-33
VI	1	DPLW-22-10

The highest divergence was observed between clusters V and VI (1294.10), followed by cluster IV and cluster VI (1130.29), cluster II and cluster IV (875.43), cluster III and cluster IV (768.51), cluster II and cluster V (676.10), cluster III and cluster VI (568.32), cluster III and cluster V (526.76), cluster I and cluster VI (522.46). The minimum divergence was observed between cluster II and cluster III (215.74) followed by cluster IV and cluster V (249.81), cluster II and cluster V (350.54), cluster I and cluster II (360.25), cluster I and cluster IV (368.07), cluster I and cluster III (376.96), cluster I and cluster V (413.91). This suggests that the genotypes in these clusters may have different genomic architecture. Cluster III has the maximum intra cluster distance (304.10), followed by cluster I (241.14). Clusters II, cluster IV, cluster V and cluster VI have the shortest distance (0.00). Cluster III was the most diversified, as it shared the most inter-cluster distance with several other clusters. Chaitanya *et al.* (2013) [2], Nidhin *et al.* (2021) [5], Islam *et al.* (2023) [4] and Subashri *et al.* (2023) [12] reported similar results in lablab bean.

Table 2: Average intra and inter cluster D^2 values in 6 clusters in 25 genotypes and 1 check of Lablab bean

Cluster Distances						
	I	**II**	**III**	**IV**	**V**	**VI**
I	241.14	360.25	376.96	368.07	413.91	522.46
II		0.00	215.74	875.43	676.10	350.54
III			304.10	768.51	526.76	568.32
IV				0.00	249.81	1130.29
V					0.00	1294.10
VI						0.00

In general, more inter cluster distance than intra cluster distance suggested homogeneous and heterogenous nature of the genotypes within and between the clusters, respectively. In the present study more inter cluster distance was observed as compared to the intra cluster distance which suggest the presence of diversity between the genotypes of inter cluster. Therefore, selection of genotypes for hybridization from between clusters possessing maximum genetic divergence is beneficial.



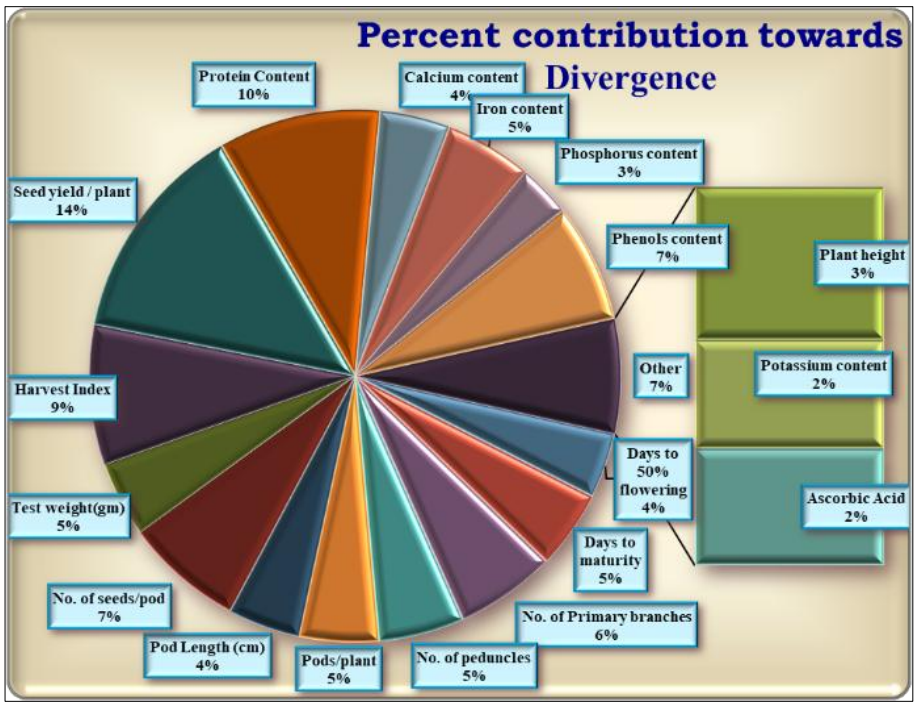
The mean performance of clusters with their contribution towards total divergence is presented in Table 3. For days to 50% flowering the genotypes in Cluster II showed early flowering (66 days), while those in Cluster V flowered late (71.33 days). For, days to maturity Cluster I genotypes matured early (99.94 days), while Cluster IV genotypes matured late (105.33 days).Plant height cluster II genotypes

had the shortest plants (65.38 cm), and Cluster VI genotypes had the tallest (96.54 cm). Cluster I genotypes had the fewest branches per plant (3.28), whereas Cluster V genotypes had the most (3.93). Genotypes in Cluster IV had the fewest peduncles per plant (4.60), while Cluster III had the most (6.42). Cluster IV genotypes had the lowest number of pods (21.47), and Cluster III had the highest (28.26). Shortest pods were in Cluster I (4.40 cm), and longest were in Cluster IV (5.04 cm). Lowest seeds per pod in Clusters I and VI (3.80), and highest in Clusters II and V (4.00). Cluster VI genotypes had the lowest weight (16.00 g), while Cluster III had the highest (19.59 g).Harvest Index was lowest in Cluster V (31.33%) and highest in Cluster VI (34.79%). Seed Yield per Plant was lowest in Cluster IV (10.47 g) and highest in Cluster III (12.55 g). Protein Content was lowest in Cluster II (20.52%) and highest in Cluster III (24.06%). Calcium Content was lowest in Cluster II (94.33 mg/100 g) and highest in Cluster IV (109.67 mg/100 g). Iron Content was lowest in Cluster V (1.66 mg/100 g) and highest in Cluster VI (5.33 mg/100 g). Potassium Content was lowest in Cluster II (621.11 mg/100 g) and highest in Cluster VI (746.89 mg/100 g). Phosphorus Content was lowest in Cluster I (341.73 mg/100 g) and highest in Cluster II (403.33 mg/100 g). Ascorbic Acid Content was lowest in Cluster II (9.19 mg/100 g) and highest in Cluster VI (10.44 mg/100 g). Phenols Content was lowest in Cluster IV (1.67 mg/100 g) and highest in Cluster II (6.27 mg/100 g).

It is suggested that parent selected for hybridization among the genotypes of above said clusters would produce high heterosis and segregant for more than one economic character. The potential genotypes are identified from different clusters and used as parents in hybridization programmes.

Table 3: Mean performance of clusters with their contribution towards total divergence.

Sr. No.	Characters	Clusters						Mean population	Contribution towards divergence (%)	Times ranked first
		I	II	III	IV	V	VI			
1	Days to 50% flowering	67.40	66.00	67.39	70.67	71.33	65.33	68.02	4.00	13
2	Days to maturity	99.94	98.00	104.50	105.33	102.00	101.67	101.90	4.76	15
3	Plant height (cm)	78.06	65.38	78.95	84.44	88.49	96.54	81.98	2.80	9
4	No. of Primary branches	3.28	3.40	3.29	3.33	3.93	3.73	3.49	6.11	19
5	No. of peduncles	5.68	6.13	6.42	4.60	5.00	5.13	5.49	5.21	16
6	No. of pods/plant	26.00	27.27	28.26	21.47	21.87	24.13	24.83	4.83	15
7	Pod Length (cm)	4.40	4.63	4.58	5.04	4.64	4.44	4.62	4.40	14
8	No. of seeds/pod	3.80	4.00	3.99	3.93	4.00	3.80	3.92	7.21	23
9	Test weight (g)	16.53	18.50	19.59	17.62	18.62	16.00	17.81	4.62	15
10	Harvest Index (%)	32.42	32.55	31.73	33.83	31.33	34.79	32.78	8.50	27
11	Seed yield / plant(g)	11.82	11.30	12.55	10.47	10.84	11.87	11.48	13.50	44
12	Protein Content (%)	21.09	20.52	24.06	22.69	22.65	21.47	22.06	9.87	32
13	Calcium content (mg/100 g)	102.75	94.33	108.78	109.67	106.00	100.33	103.64	4.30	14
14	Iron content (mg/100 g)	3.32	3.48	3.17	3.12	1.66	5.33	3.34	5.32	17
15	Potassium content (mg/100 g)	652.53	612.11	699.91	676.11	719.78	746.89	684.55	2.00	6
16	Phosphorus content (mg/100 g)	341.73	403.33	368.81	374.89	375.56	355.89	370.04	3.21	10
17	Ascorbic Acid (mg/100 g)	9.55	9.19	9.35	9.52	9.32	10.44	9.56	2.15	7
18	Phenols content (mg/100 g)	3.73	6.27	5.60	1.67	2.98	5.53	4.30	7.21	23



Character contribution towards divergence

Table 3 represents how different characters contributed to total deviation. Seed yield per plant (13.50%, 44) had the greatest contribution to divergence, with its respective times placed first, followed by protein content (9.87%, 32), harvest index (8.50%, 27), number of seeds per pod (7.21%, 23), phenols content (7.21%, 23), number of primary branches (6.11%, 19), iron content (5.32, 17), number of peduncles (5.21%, 16), number of pods per plant (4.83%, 15), days to maturity (4.76%, 15), test weight (4.62%, 15), pod length (4.40%, 14), calcium content (4.30%, 14), days to 50 per cent flowering (4.00%, 13), phosphorus content (3.21%, 10), plant height (2.80%, 9), ascorbic acid content (2.15%, 7) and potassium content (2.00%, 6).

The success of the breeding program, which entails selecting the best genotypes, is influenced by its variability and diversity. Selection based on a wide range of genetic variation has its own relevance. As a result, the diversity of 25 distinct genotypes and 1 check of lablab bean were evaluated in the current study. This study provided significant information that might be used to select effective genotypes for introduction as a variety.

The high variability in quantitative character appears to be driving the wide range of genetic variation among biological genotypes. As a result, D^2 analysis was performed using Mahalanobis statistics to quantify the magnitude of divergence among the genotypes, taking into account the relative contribution of different components to overall divergence at the intra and inter cluster levels. (Mahalonobis, 1936) [4].

The similar results were reported by Ananya *et al.* (2015) [1], Shulee *et al.* (2021) [11] in lablab bean revealed that seed yield per plant had the greatest contribution to divergence, with its respective times placed first, followed by harvest index, number of seeds per pod, number of primary branches number of peduncles, number of pods per plant days to maturity, test weight, pod length, days to 50 per cent flowering and plant height.

Conclusion

The analysis of genetic diversity among lablab bean genotypes using Mahalanobis D^2 statistics reveals significant potential for crop improvement. Thus, the 25 genotypes and 1 check were divided into six clusters with a large range of variance. The clustering pattern of 25 genotypes and 1 check of lablab bean followed no definite pattern and was completely random. Cluster I was most prominent one with 16 genotypes in it. The diversity present between the lablab bean genotypes measured by inter-cluster distances was adequate for the improvement of lablab bean by selection. The genotypes clustered in these six clusters may be used to develop a promising variety. Seed yield per plant had the greatest contribution to divergence, with its respective times placed first, followed by harvest index, number of seeds per pod, number of primary branches number of peduncles, number of pods per plant days to maturity, test weight, pod length, days to 50 per cent flowering and plant height. The elite genotypes identified – such as DPLW-22-4 and Pavata- demonstrate exceptional desirable traits, making them valuable candidates foe future breeding programmes.

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