

**Studies on genetic variability, correlation and path  
analysis in French bean (*Phaseolus vulgaris* L.)  
under Lucknow conditions**

**Thesis**

SUBMITTED IN FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF

***Doctor of Philosophy***  
***in***  
***Horticulture***

**BABASAHEB  
BHIMRAO  
AMBEDKAR  
UNIVERSITY**



**LUCKNOW**  
**प्रज्ञा शील करुणा**  
**ESTABLISHED 1996**

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**INDIA**  
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# Dedicated



# To My Beloved Parents

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## Certificate

This is to certify that the work recorded in the thesis entitled “**Studies on genetic variability, correlation and path analysis in French bean (*Phaseolus vulgaris* L.) under Lucknow conditions**” submitted for the award of degree of Doctor of Philosophy in Horticulture to the **Babasaheb Bhimrao Ambedkar (A Central University) University, Lucknow (U. P.), India** has been carried out by Mr. Jay Prakash under my guidance and supervision. He fulfills the terms and conditions as laid down in the Ph. D. ordinances of the university. Data forming the basis of thesis is to the best of my knowledge, no part of the thesis has been submitted for the award of any other degree or diploma.

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

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## **Declaration**

I, **Mr. Jay Prakash** Enrollment No.629/11 hereby declare that thesis entitled “**Studies on genetic variability, correlation and path analysis in French bean (*Phaseolus vulgaris* L.) under Lucknow conditions**” submitted the thesis for the fulfillment of the requirements for the award of the degree of Doctor of Philosophy in Horticulture to the Department of Applied Plant Science (Horticulture) under School for Biosciences and Biotechnology, Babasaheb Bhimrao Ambedkar University, (A Central University) Vidya Vihar, Rae Bareli Road, Lucknow- 226025 (U.P.), India was carried out by me during the experimentations period 2012-2013 and 2013-2014 are my own and original work.

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Place- Lucknow

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## List of abbreviations

%	Percent
ANOVA	Analysis of Variance
CM	Centimeter
°C	Degree Centigrade
DAS	Days After Sowing
C. D.	Critical Difference
SE (d)	Standard Error
MSE	Mean Squares Due to Error
MSS	Mean Sum of Squares
<i>et al.</i>	et alii (Co-authors)
PCV	Phenotypic Correlation Coefficient
GCV	Genotypic Correlation Coefficient
ESS	Error Sum of Squares
VP	Phenotypic Variance
VG	Genotypic Variance
TSS	Total Sum of Squares
CV	Coefficient of Variation
SEM	Standard Error of Mean
RH	Relative Humidity
PPE	Pre-plant Emergence

INM	Integrated Nutrient Management
IPM	Integrated Pest Management
IIPR	Indian Institute of Pulse Research
NSC	National Seed Corporation
KG	Kilogram
Q	Quintal
Y	Yield
G	Gram
A	Area
Ha	Hectares
VL	Vivekananda Laboratory
Ph.	Phaseolus

The beans - Indian bean, French bean, Pea and cowpea belong to family Fabaceae are the important leguminous vegetables. The other beans of lesser economic importance include cluster bean, broad bean, lima bean, winged bean etc. Generally, pea, French bean and broad bean are cool season crops, while other beans are warm season crops. All are direct seeded crops. Most of these crops are important sources of carbohydrates and protein. Legumes are rich in protein because of a symbiotic relationship between the roots of legumes and nitrogen fixing bacteria belonging to the genus *Rhizobium*. The *Rhizobium* lives in nodules, which can be found on roots of the legumes. The immature pods of legume vegetables are also high in vitamins A and C. The legumes are also nitrogen fixers, although the major legume vegetables in cultivation do not fix sufficient amount of nitrogen and it must be provided in fertilizers. In Bangladesh it is called *Jhar seem* or *Farashi seem*. Bush bean is becoming popular for its tender pods and shelled beans. It has also high export potentiality. Few years back it was only used for making *daal* (spicy soup) mostly in the east and south-eastern parts of Bangladesh. It is now available in the big supermarkets of the capital Dhaka. The green pods and dry seeds are used in preparations with fish, meat and other vegetables as well. The dry seeds are also used in various curry preparations. Immature pods are mostly marketed as fresh. Canned pods are also imported to sale in the local market. Common bean is an important component of agricultural and food systems throughout most of the world. Nutritionally dry bean is a nearly, perfect and rich food. It is an excellent source of protein, carbohydrates and fairly good source of minerals, vitamins, folic acid and dietary fiber Rehman *et al.* (2001). Common bean has 25.2 million ha sowing area and 19.7 million tonnes total production per year in the world. On the other hand Turkey has 103.255 ha harvest area and 212.758 tonnes total production per year (FAO, 2010). According to (Amare, 1987), most of the area lies in sub humid high land sand semi-arid zone in the rift valley and eastern regions. It's grown aside as well as intercrop with maize, banana, sorghum, cassava and sweet potato due to its short duration and tolerance to shading (Westphal, 1974). Two crops per year are grown with saving time in January to May and June to September. Bean yields are only 20-35% of the genetic potential of improved varieties (Wartmann *et al.* 1998). Beans are grown for local consumption and for export as cash crops. It's consumed as seeds of dry beans or as pods of snap beans. These are significant source of protein dietary fiber, calories,

minerals and vitamins, especially foliate. French bean (*Phaseolus vulgaris* L.),  $2n = 2x = 22$  belongs to family (Fabaceae) is a nutritious vegetable consumed as tender pods, shelled beans and dry beans. It is known by different names, viz., kidney bean, haricot bean, snap bean, navy bean, pole bean, bush bean, etc. (Daisy, 1979). It is annual herb grown for green tender pods and dry seeds (*rajmash*). The pod size of French bean varies from thin, pencil like to about 2 cm in diameter. The pods are round, flat or curved in shape and the colour varies from green to yellow, red and purple. French bean has evolved from wild growing vine distributed in the high lands of Middle-America and Andes (Brucher, 1988). Having short duration and being a nutritious legume vegetable crop, it is becoming popular with the farmers of India. The French Huguenots introduced French bean into England. Portuguese took the crop to Africa and other parts of the old world. Introduction of French bean into India is comparatively recent and the Europeans brought it to India in the 19<sup>th</sup> century. These two domestications, which led to two groups of cultivars with contrasting agronomic characteristics. During this evolution, some marked changes has affected this plant from climbing to dwarf plants has taken place both in the middle American and Andean domestication centres (Schoonhoven and Voices, 1991) . Among major food legumes the common bean is the third most important worldwide, superseded only by Soybean [*Glycine max* (L.) Merr.] and Peanut (*Arachis hypogaea* L.). Among the pulses i.e., annual leguminous food crops that are harvested for dry seeds the common bean is by far the most important (Ram *et al.* 1988). The genus *Phaseolus* is of American origin and comprises 36 species (Mabberley, 1997). Five of them, namely, *P. acutifolious* A. Gray (Tepary bean), *P. coccineus* L. (Scarlet runner bean), *P. lunatus* L. (lima, butter or madagascar bean), *P. polyanthus* green man (year-long bean), and *P. vulgaris* L. (common bean, haricot, navy, French or snap bean) were domesticated (Debouck, 1999). Among these species, the common bean is the most widely distributed and has the broadest range of genetic variation (Singh, 1999). The common bean mostly used as food crop throughout the word, particularly in developing countries as Mesoamerica, Africa, and other countries. The common bean is a highly variable species. It is placed in the tribe Phaseolae, subfamily Papilionoidae in the family Fabaceae (Leguminosae). Cultivated forms are herbaceous annuals, which are determinate or indeterminate in growth habit (Ram *et al.* 1988). On germination, the plant is initially tap-rooted but adventitious roots emerge soon thereafter and dominate the tap root which remains 10-15 cm in length (Duke, 1981 and Gomez, 2004).

### **Nutritional value**

The nutritional composition of French bean pods, raw and ends trimmed (edible proportion 83%) water 90.7 g, energy 99 J (24 kcal), protein 1.9 g, fat 0.5 g, carbohydrate 3.2 g, dietary fibre 3.0 g, Ca 36 mg, Mg 17 mg, P 38 mg, Fe 1.2 mg, Zn 0.2 mg, carotene 330 µg, thiamine 0.05 mg, riboflavin 0.07 mg, niacin 0.9 mg, foliate 80 µg, ascorbic acid 12 mg (Holland, B., Unwin, I.D. and Buss, D.H., 1991).

### **Practical utility**

Considering the nutritive value, 100 g of green pod contains 1.7 g protein, 0.1 g fat, 4.5 g carbohydrate, 1.8 g fibre and is also rich in minerals and vitamins. It also posses medicinal properties which is useful in controlling diabetes and certain cardiac problems and it is a good natural cure for bladder burn. It has both carminative and reparative properties against constipation and diarrhoea, respectively (Duke, 1981). Its dry seed contains 21.1 per cent protein, 69.9 per cent carbohydrates, 1.7 per cent fat, 381 mg calcium, 425 mg phosphorous and 12.4 mg iron per 100 g of edible part (Ali and Kushwaha, 1987). The common bean (*Phaseolus vulgaris* L.) is an herbaceous annual plant species domesticated independently in ancient Mesoamerica and now grown worldwide both for dry beans and as green bean. Common bean is an important component of agricultural and food systems throughout most of the world. Nutritionally dry bean is a nearly, perfect and rich food. It is an excellent source of protein, carbohydrates and fairly good source of minerals, vitamins, folic acid and dietary fiber (Rehman *et al.* 2001). Young pods of French bean are boiled after cutting both ends and carefully removing the strings, if present; they may then be cooked or fried with sliced onion and garlic or used in salads. They can be boiled together with rice. They require a shorter cooking time than dry bean seeds. The full-grown but immature seeds (larger than dry ones) are sometimes also eaten, and sold in their pods on vegetable markets (shell beans). They can be cooked without previous soaking in water and in a shorter time than dry seeds. Leaves are occasionally used as a vegetable, but few cultivars have leaves of sufficient tenderness. Crop residues are often used as fodder. In East and southern Africa, the use of ripe seeds of *Phaseolus vulgaris* as a pulse is more important than the use of unripe pods or seeds as vegetables.

### **Production and international trade**

World production of French bean (combined with yard-long bean) in 2002 was estimated by FAO at 5.8 million tonnes from 855,000 ha. China produced 2.0 million tonnes, Turkey 515,000 tonnes, the European Union 664,000 tonnes, Tropical Africa about 75,000 tonnes and Northern Africa 312,000 tonnes. An important part of the Tropical African production is

exported to Europe: nearly 40,000 tonnes, the most important exporters being Senegal, Burkina Faso, Kenya and Zimbabwe. French bean is the third most important agricultural export product of Kenya, after only tea and pineapple. The production of French bean pods for canning is important in Europe. An important amount of French bean seeds is produced in East African highlands (e.g. Kenya, Tanzania) for European seed companies. Brazil, Mexico, Argentina and United States are the leading common bean producers in the world. In Latin America and Africa, beans are while Argentina exports 99.5% of its production of 0.25 million metric tonnes (*Phaseolus* Crop Germplasm Committee Report, 1996; FAO, 1998). Studies on variation patterns of the seed protein phaseolin, all enzymes and morphological evidences, revealed the existence of a Middle American and Andean gene pools in *Phaseolus vulgaris* (Gepts *et al.* 1986; Singh *et al.* 1991a; Singh *et al.* 1991b). Phaseolin is common among the three *Phaseolus* races in the Middle American gene pool, while Sb, Sd and B phaseolins are less common. On the other hand, phaseolin T, C and H are present in genotypes from the Andean gene pool. Not only the phaseolin patterns but also the size of the seeds differentiates Middle American from Andean gene pools. Mesoamerican landraces have usually smaller seeds than their Andean counterparts (Gepts *et al.* 1986; Singh *et al.* 1990). Biochemical studies have shown that the cultivated bean germplasm presents a low level of genetic diversity as compared to their wild ancestors (Gepts *et al.* 1986; Koenig *et al.* 1990; Sonante *et al.* 1994; Johnson and Gepts, 1998). Progress in bean breeding around the world has been slow, probably because of a limited genetic variability of the parents which have been selected from the same gene pool. Being a short duration crop French bean can be grown under different cropping patterns of hills and plains of India. In India, it is mainly grown in Himachal Pradesh, Punjab, Haryana, Utrakhnad, Uttar Pradesh, Bihar, Gujarat, Madhya Pradesh, Maharashtra, Karnataka, Andhra Pradesh and Tamil Nadu. Annually, it is grown on an area of 1, 50,000 ha with an annual production of 4, 20,000 tonnes with a productivity of 2800 kg/ha (Anonymous, 2002). Moreover, it is commercially in the hilly regions of Utrakhnad. In Karnataka, the crop is grown on an area of 15,699 ha with an annual production of 1, 67,856 tonnes (Anonymous, 2003). Pole type French bean is an important legume vegetable in Meghalaya of North Eastern Hill region has high agro economic and dietary values as compared to other legume vegetables (Shah *et al.* ). The exploitation of variability is a pre-requisite for the effective screening of superior genotypes in all crops including French bean. The progress in breeding for the yield and its contributing characters of any crop is polygenic ally controlled, environmentally influenced and determined by the magnitude and nature of their genetic variability. Hence, it is essential to

partition the overall variability into its heritable and non-heritable components with the help of genetic parameters like genetic coefficient of variation, heritability and genetic advance. Knowledge of correlations among different characters and further, partitioning those direct and indirect effects are a rational approach to understand the nature and extent of such relationship. Therefore, study of genetic variability, characters association and path coefficient are pre-requisite for improvement of any crop. Nepal is one of the world's richest centres of crop genetic diversity because of diverse agro-climatic conditions and socio-economic and cultural variation. About 400 species of food and horticultural crops have been reported in Nepal and about 200 species are in the vegetable category (Pandey *et al.*2000).The genotype performance varies with location, season and management practices. Phenotypic expression of the plant character is mainly controlled by the combined product of genetic constituents of the plant and environment. It is essential to study the variability and heritable components for yield contributing characters in the available genotypes in different dates of sowing during *rabi-summer* seasons. Pelleting is for précised sowing has been a technique of great success and advantages. It enables for packaging of small quantities of insecticides, fungicides, growth regulators, nutrients, chemicals and bioingredients which can influence the micro environment of individual seed. Pelleting facilitates in improving seed ballistic properties, protection from stress, rodents, insects and pathogens. It boosts the field performance besides economizing the cost of input and reducing the vagaries of the environment. The potential of seed pelleting helps in enhancing biological nitrogen function and intern increase in seed yield. It is involved in biosynthesis of plant hormone, IAA and is component of variety of enzymes like, carbonic anhydrase, alcohol dehydrogenase, glutonic dehydrogenase *etc.* Boron plays pivotal role in cell division and is integral part of cell wall. Boron also facilitates the pollen and ovary formation and subsequently complete development of seed. It has a direct effect on membrane and it inhibits IAA oxidase and RNAase activity and improves root development, it has also direct effect on pollen germination and pollen tube growth. The common bean (*Phaseolus vulgaris* L.) is an herbaceous annual plant species domesticated independently in ancient Mesoamerica and now grown worldwide both for dry beans and as green bean. Therefore, a systematic breeding approach for crop improvement of French bean is highly required. Knowledge of genetic variability, heritability and genetic advance of important economic traits and their genotypic and phenotypic correlation coefficient among themselves, play an important role in farming the breeding programme of any crop .The success of breeding programme depends on the genetic variability present in the population. Therefore, partitioning of the phenotypic

variation into genetic and environmental variation is necessary. the extent of transmission of a quantitative character from parent to the offspring depends upon the heritability of the particular character .The heritability value alone does not have much significance as it fails to account for the magnitude of absolute variability. It's, therefore, necessary to utilize heritability along with genetic advance, while advocating for selection. Hence, to identify the promising cultivars which could grow well under agro-climate conditions of Lucknow, Uttar Pradesh, the information on genetic variability is necessary. Phenotypic expression of the plant character is mainly controlled by the joint product of genetic makeup of the plant and environment. Hence, any breeding programme aiming at increasing yield should consider association between yield and its attributes through estimation of genotypic and phenotypic correlation, which help a great deal in formulating selection indices to aid in selection programmes. An understanding of the variability existing in a crop is necessary to formulate and accelerate conventional breeding programme. Collection and evaluation of germplasm, quantification of the magnitude of variability existing for different characters and classification into groups help in identifying, which would yield greater variability. This enables the breeder to operate selection efficiently. Hence, before venturing into a breeding programme, it is essential to study the variability and its heritable components for the yield contributing characters in the available genotypes. Estimation of inter-relationship of yield with other traits would facilitate effective selection for simultaneous improvement for one or many yield contributing characters as it is controlled by large number of characters and their Interactions. Assessing direct or indirect effects of each component towards yield through path analysis would help in identifying reliable characters contributing to yield. The performance of genotypes varies with location, season and management practices. For releasing a potential genotype agronomic practices should be standardized. The fertility status of soil is not that high so as to meet the entire nutrient requirement of the crop. Hence, external supply of nutrients through fertilizers has become the urgent need of the hour. Therefore, the optimum fertilizer dosage for the crop has to be standardized which enables as to meet the entire nutrients requirement of the crop throughout the crop period. Adequate spacing provides good conditions for maximum light interception wider spacing will ultimately decrease the yield per unit area. While, narrow spacing adversely affects the yield per plant. Therefore, maintenance of optimum spacing will define the yield potential of the crop. French bean is most widely cultivated in temperate regions, and widely cultivated in subtropical regions. In Latin America and parts of tropical Africa, they are grown mainly for the dried pulse. In Europe, the United States and other temperate countries, they are grown

for the green immature pods which are eaten as a vegetable and are also canned and frozen (Purse glove, 1974). Its edible pod and ripe seeds contain protein, carbohydrate, fat fiber, thiamine, riboflavin, calcium, and iron. French beans furnish a large portion of the protein needs of low and middle class families of Bangladesh. Because of high nutritive value, good taste and wide range of use, the popularity of French bean is increasing day by day in Bangladesh. French bean can be considered as vegetable crop as it needs smaller area of land and can also be grown without competition with cereals. Compare to other legume crops, very limited information regarding the gene action controlling the expression of characters of French bean has been available in Bangladesh. Generally yield and yield related characters are governed by polygenes and their inheritance system is complex. Therefore, genetic analysis involving inheritance system of seed yield and related traits may provide useful information on various genetic features leading to crop improvement. Hence, the present study was conducted to find out the information on nature and magnitude of gene action for yield and yield related traits. Beans, the “meat of the poor”, contribute essential protein to the undernourished people living in the hills. In Nepal, beans are grown for their green pods as a fresh vegetable and the dried seeds are used as pulse and for seed purposes, while the foliage is consumed as fodder and is used to restore soil fertility. Different ethnic groups have their own ways of preparing beans and there are special occasions and festivals when the products are relished. Red kidney beans are cultivated during the winter season on the plains (below 500 m ASL) and are an integral part of the cuisine as a socio cultural identity in the plains of Nepal. Different Indian rajmash (red kidney bean) genotypes have been introduced in production areas and the predominant cropping pattern is as a mono crop. In the mid hills, fresh green pods are important and widely consumed as a vegetable. Both pole and bush-type French beans are cultivated for green pods in the hills (500–3000 m ASL) during summer to autumn. Most of the genotypes growing in the hills were introduced from India and China. Green stingless French bean (snap bean) is a very popular vegetable crop among the hill people. These beans are grown as a mono crop in the commercialized peri-urban areas using staking for pole beans. Pole beans are also cultivated or inter cropped with maize as a rain-fed crop in the hills. Dried shelling beans are usually produced from summer to autumn in the high hills and mountains (1500–3000 m ASL). These beans are long duration vegetables, which are grown either with maize or in apple orchards. In the high hills, they are the major source of protein for households and are also a cash-generating crop. Dried beans produced in the high hills are considered to be high quality beans and find their way to distant markets and cities. Farmers regard beans as a cash-generating crop in the hills and grow a number of

landraces with varying morphologies (Neupane and Vaidya, 2002). Yield in dry bean like other crops, is a complex characteristic associated with many morphological and physiological characteristics constitute it. Success in crop breeding also depends on the isolation of genetically superior genotypes based on the amount of variability present in the materials. Therefore, information on genetic variability existed in a group of populations of dry bean are essential (Raffi and Nath, 2004). Many breeders were involved in analyzing the path coefficient. Usefulness of information obtained from correlation can be enhanced by partitioning them into direct and indirect effects for a set of prior cause-and-effect interrelationships (Kang *et al.* 1983; Gravois and McNew, 1993). Many studies have been carried out on variability and interrelationships of characteristics on dry bean (Vaid *et al.* 1986; Singh *et al.* 1994; Ribeiro *et al.* 2000; Rai *et al.* 2001). In this study, relationships between yield and yield attributes characters were evaluated to determine the association of seed yield with its components and some traits related to plant developmental by using correlation and path coefficient analysis. The current research was initiated with the objectives of collection, evaluation and characterization of available exotic and indigenous germplasm so that they can be utilized for varietal improvement and commercial cultivation. Keeping in view the above facts in mind the present investigation entitled “Studies on genetic variability, correlation and path analysis in French bean (*Phaseolus vulgaris* L.) under Lucknow conditions” with the following objectives:

1. To find out extent of genetic variability in French bean germplasm.
2. To estimate of mean, range and coefficient of variation for yield and its component traits.
3. To investigate the genotypic and phenotypic coefficient of variation for different yield and yield attributing traits of French bean.
4. To determine heritability (broad sense) and expected genetic advance in percentage of mean.
5. To evaluated genotypes contributing towards yield by correlation and path coefficient analysis

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To achieve significant progress in breeding programs, it is essential to know the relationship between seed yield and its components Assady *et al.* (2005). Path coefficient analysis is used to partition the relative contribution of yield components via standardized partial regression coefficients. Correlation coefficient which measures the simple linear relationship between two traits does not predict the success of selection. However, path analysis determines the relative importance of direct and indirect effects on seed yield (Bhatt, 1973). In addition, it has been used to organize and present the casual relationships between predictor variables and response variables through a path diagram that is based on experimental results or on a priori grounds Board *et al.*(1997). Path coefficient analysis has been widely used in crop breeding to determine the nature of relationships between grain yield and its contributing components and to identify those components with significant effects on yield for potential use as selection criteria Mohammadi *et al.*(2003).Genetic diversity refers to the variation of genes within populations/species, making it possible to develop new breeds of crop plants and domestic animals and allowing species in the wild to adapt to the changing conditions. In crop plants, genetic diversity arises as consequences of interplay of evolutionary forces (mutation, selection and random genetics) and the influence of human through domestication and selection (Bhatt, 1970). Study of genetic diversity is the process by which variation among individuals or groups of individuals or populations is analyzed by a specific method or a combination of methods. The data often involve numerical measurements and in many cases, combinations of different types of variables. Diverse data sets have been used by researchers to analyze genetic diversity in crop plants; most important among such data sets are pedigree data, morphological data and biochemical data obtained by analysis of isozymes and storage proteins and recently, DNA-based marker data. Since, limited availability of high productive varieties with good plant types and lack of short duration varieties with higher resistance to diseases are the major hindrance to increase the production. The collection of information based on these factors will be useful to crop improvement activities. Genetic relationships in crop species is an important component of crop improvement programs, as it serves to provide information about genetic diversity and is a platform for stratified sampling of breeding populations. Accurate assessment of the levels and patterns of genetic diversity

can be invaluable in crop breeding for diverse applications including (i) analysis of genetic variability in cultivars (ii) identifying diverse parental combinations to create segregating progenies with maximum genetic variability for further selection and (iii) introversion desirable genes from diverse germplasm into the available genetic base. An understanding of genetic relationships among inbred lines or pure lines can be particularly useful in planning crosses and in assigning lines to specific heterotic groups. Analysis of genetic diversity in germplasm collections can facilitate reliable classification of accessions and identification of subsets of core accessions with possible utility for specific breeding purposes. In this regard, literature pertaining to the present work “Studies on genetic variability, correlation and path analysis in French bean (*Phaseolus vulgaris* L.) under Lucknow conditions.” In the present study, the relevant literature pertaining to various aspects of horticultural and nutritive parameters of French bean are reviewed under the following heads:

### **2.1. Genetic variability, heritability and genetic advance**

### **2.2. Correlation coefficient**

### **2.3. Path coefficient analysis**

Genetic variability is the raw material on which selection acts to evolve superior genotypes or varieties in plant breeding programme. The genetic variability for various characters available in the breeding populations or materials is systematically subjected to selection to change the genetic architecture of plant characters and consequently of the plant as a whole to develop improved genotype having higher economic yield. The variability exploited in breeding programme is derived from the naturally occurring variants and the wild relative of crop as well as artificially developed strains and genetic stocks by human -efforts. The reservoir of variability for different characters of a plant species resulting from available natural or artificially synthesized variants or strains constitutes its germplasm. Thus, germplasm may include improved strains, primitive cultivars, wild relatives, obsolete cultures, special genetic stocks, seeds and vegetative parts etc. Most of the germplasm collection are inadequately evaluated or screened for assessment of genetic variability.

### **2.1. Genetic variability, heritability and genetic advance**

The knowledge of existing variability with respect to yield and yield attributing traits in the genotypes of a crop is the basic requirement in order to select the desirable types. The variability observed for a character is due to difference in the genetic constitution of the population as well as variation arising due to environmental condition. The coefficient of genetic variability and phenotypic variation are used as an aid in the plant breeding work. The concept of heritability is important to determine whether phenotypic difference observed among various individuals are due to genetic change or due to effect of environmental factors. Heritability indicates the possibility and extent to which improvement can be brought about through selection. The possibility of achieving improvement in any crop depends on the magnitude of genetic variability. The efforts taken by Johnson, 1909 and East, 1916 have led to the partitioning of total variability into genetic and environmental components and both heritable and non-heritable factors contributed somatic variation in segregating populations and that variation in pure line was entirely due to environment (Johnson, 1909).

Heritability is a useful measure for considering the ratio of genetic variance to the total variance and is generally represented in percentage. This is an index of transmissibility of characters from the parents to their offspring and is a measure of genetic relationship between parents and progeny; hence, changing the characteristics of the population through selection can be predicted only from knowledge of the degree of correspondence between phenotypic and breeding values.

Many workers have defined heritability. Lush (1948) defined broad sense heritability as the ratio of genetic variance and narrow sense heritability as the ratio of additive genetic variance to the total phenotypic variance. Since additive genetic variance is the only fixable portion of total variance, narrow sense heritability is of more practical importance than broad sense heritability. Robinson *et al.* (1949) defined heritability in both broad and narrow sense. In broad sense it is “the ratio of the total genotypic variance to the total phenotypic variance” and in narrow sense, “the ratio of additive genetic variance to the total phenotypic variance.”

Genetic advance is most useful estimate as it is the improvement in the phenotypic value in the new population in contrast to base population. According to Comstock and Robinson (1952) expected genetic advance depends upon:

- (I) The amount of genetic variability.
- (II) The magnitude of masking effect of environment and interaction components of variability on genetic diversity.

(III) The intensity of selection.

Expected genetic advance in percentage of mean is the product of:

(I) Selection differential measured in terms of phenotypic standard deviation and

(II) The genetic coefficient of variability and square root of heritability ratio (Johnson *et al.* 1955).

Since the genetic gain in a character is the product of the heritability and the selection differential expressed in unit of standard deviation, the heritability alone does not have much significance.

Hanson *et al.* (1956) according to heritability measures the relative amount of the heritable portion of variability. Sometimes heritable variation is masked by non-heritable components. Hence, it is necessary to classify the total heritability using genetic parameters into broad sense heritability and narrow sense heritability. Broad sense heritability is the ratio of genotypic variance to the total variance in non-segregating population.

Johnson *et al.* (1955a) reported that the heritability value of a trait indicates the effectiveness of selection based on phenotypic expression. Quantitative characters are governed by more number of genes and further influenced by environment, of which a proportion observed value is heritable. Estimate of narrow sense heritability is not possible thus by estimating broad sense heritability along with genetic gain is usually more useful in selecting the best individual.

Motto *et al.* (1978) studied the inheritance of seed size characteristics between a cross of the small-seeded wild bean NI 325676 and the large seeded cultivar Royal Red. Additive gene effects largely controlled length, width, height and weight of seed, with heritability in narrow sense (HNS) values ranging between 0.72 and 0.87. An average of at least 10 effective factors controlled the seed size difference between large-seeded cultivated and small seeded wild forms. Escribano *et al.* (1994) measured the length parallel to the helium and height from the helium to the opposite side of bean seed. They found HBS ranged from 0.87 to 0.93 and 0.78 to 0.95 for seed length and height, respectively. They concluded heritability values for the seed size traits considered as high.

Malik *et al.* (1983) reported that the genotypic and phenotypic variances were high for plant height (61.39 and 66.19) and number of pods per plant (14.15 and 17.31). Heritability

was high for plant height (0.93) and 100-seed weight (0.89) whereas it was lowest for number of seed per pod (0.18). High heritability combined with high genetic advance expressed as percentage of mean for plant height, number of pods per plant and 100-seed weight indicated the additive gene effect on these characters.

Singh (1985) identified the genotypic and phenotypic variability in 30 geographically diverse strains of pea from different countries. He found significant differences in the varieties for all the characters studied. Variability among varieties was low for days to 50% flowering, days to maturity and harvest index, however, grain yield, plant height, number of pods per plant number of primary branches per plant, main root length and nodules per plant showed a wide range of both genotypic and phenotypic variability. Heritability in broad sense (HBS) was very high for days to flowering (98.3%), plant height (95.54%), nodules per plant (98.27%) and days to maturity (86.7%). Genetic gain was maximum for plant height, pods per plant, length of main root and primary branches per plant. However, genetic gain was of low magnitude for days to flowering, days to maturity and harvest index may be expected to be mainly due to non-additive gene action, whereas for those characters having high heritability and high genetic advance was due to additive gene action.

Agrawal (1986) studied genetic variability in populations of chickpea crosses for days to flowering, days to maturity, primary and secondary branches per plant, plant height, pods per plant seeds per plant, seeds per pod, seed yield per plant and 100-seed weight. The seeds per plant and pods per plant showed high variability at both phenotypic and genotypic levels for some crosses. High GCV is an indication of the extent of fixable variation present in the population. The GCV and PCV were almost similar for days to flowering and days to maturity for all crosses; and 100-seed weight, seeds per plant and plant height for some crosses, indicating the major part of variation shared by genetic component. Wide differences between GCV and PCV indicated greater influence of environment on that trait. High genetic advance as percentage of mean coupled with high heritability estimates were found for days to flowering and days to maturity for all the crosses, indicating the major portion of genotypic variation attributable to additive gene action.

Singh *et al.* (1994) reported the genetic variability in 7 French bean cultivars by analyzing five characters. The genotypes showed significant differences for all the five characters. Yield per plant and days to flowering showed the highest and lowest phenotypic and genotypic coefficients of variation, respectively. The narrow difference between phenotypic

coefficients of variation (PCV) and genotypic coefficients of variation (GCV) of the characters show low environmental influence. The low PCV and GCV value for days to flowering indicated less scope to selection for this trait. Yield per plant had high GCV, genetic advance and heritability; pods per plant and pod length had moderately high GCV and genetic advance and high heritability.

Samal *et al.* (1995) examined performance on variability, correlation and co-heritability estimates in rajmash. They found significant differences for traits such as plant height, branches per plant, pod length, seeds per pod, yield per plant, 100-seed weight, and days to 50% flowering. All the traits except branches per plant and pod length exhibited wide range of variability. The phenotypic and genotypic variances were maximum for yield per plant and minimum for branches per plant. The PCV had higher estimate than the corresponding GCV for all the traits. The small difference between PCV and GCV for days to flowering and pod length indicates that the variability was due to genotypic differences. The heritability estimates were higher for days to flowering, pod length and seeds per pod; and low for plant height, branches per plant, 100-seed weight and yield per plant. Genetic advance and expected genetic advance (as percent of mean) was maximum for yield per plant (42.2) and seeds per pod (57.5) and minimum for pod length and plant height.

Deepak *et al.* (1999) to find out the thirty exotic as well as indigenous accessions of French bean (*P. vulgaris* L.) genetic variability and correlation in Chaubattia, Almora, Uttarakhand, India, during 1991. All the eight agro economic traits exhibited a wide range of phenotypic variation. High estimates of heritability were recorded in six agro economic traits. Three traits showed additive gene effects by way of high heritability and genetic advance. Correlation studies revealed that pod yield had positive correlations with plant height, pod length and pods per plant. A generally high genotypic coefficient of correlation was observed in all the agro economic traits.

Chand (2000) carried out an experiment on twenty genotypes of rajmash (*Phaseolus vulgaris* L.) to assess for the presence of genetic variability in during the *rabi* seasons of 1992-93 and 1993-94 in Tamilnadu, India. Genotypic and phenotypic coefficient of variation were maximum for plant height and 100-seed weight, moderate for pods / plant biological yield, seed yield and seeds /pods and low for number of branches, harvest index, days to flowering and days maturity. The estimates for heritability were high for all the characters

ranging from 68.75 to 92.2% indicating that these characters were less influenced by the environment.

Rai *et al.* (2001) reported that the variability and path correlation coefficient analysis for test weight, seed length seed breadth, seed thickness, seed germination, root length, collar diameter, number of leaves per plant and shoot length was conducted on 20 French bean (*Phaseolus vulgaris* L.) cultivars. Seed test weight was positively correlated with seed length, seed breadth, seed thickness, collar diameter, number of leaves per plant, and shoot length at phenotypic and genotypic leaves. At the phenotypic level only, significant positive correlation was recorded between seed length and seed thickness, collar diameter and shoot length, between seed thickness and collar diameter, number of leaves per plant and shoot length and between shoot length and germination percentage, root length collar diameter and number of leaves per plant. Path coefficient analysis revealed that seed length, seed weight, root length, collar diameter, seed thickness and seed breadth had the greatest effect on vigour and growth, indicating that these characters should be considered for selection.

Govanakoppa *et al.* (2002) investigated genetic diversity among 62 French bean (*Phaseolus vulgaris* L.) cultivars was investigated in Dharwad, Karnataka, India, during the *kharif* seasons of 1999/2000 under moisture stress conditions (at the flowering and pod development stages). The cultivars were grouped into 11 clusters based on Tocher's method of  $D^2$  analysis; the genetic classification did not exhibit a clear relationship with geographical distribution. The cultivars with the greatest average pod length and number of seeds were grouped under cluster 1 (25 cultivars). Cluster II consisted of cultivars (13) with the greatest average plant height, number of reproductive branches per plant, number of pods per plant, and green pod yield per plant. Green pods per plant (69.44%), 100 seed weight (32.95%), plant height (4.44%), and number of reproductive branches per plant (1.48%) showed the greatest contribution to genetic divergence.

According to Dahiya *et al.* (2002) the conducted Genetic divergence analysis of 48 genotypes of French bean (*Phaseolus vulgaris* L.) obtained from different eco-geographical regions of India and abroad for 16 quantitative traits was carried out using Mahalanobis's  $D^2$  statistics. The 48 genotypes were grouped into 12 clusters including 6 single genotype clusters. Genotypes of different eco-geographical regions were found to cluster together. Maximum genetic distance was observed between clusters II and V, indicating greater genetic divergence between the genotypes belonging to these clusters. Clusters per

plant, harvest index and 100 seed weight, which had maximum contribution to the total divergence, should form the basis for selection of parents for hybridization among distantly placed clusters.

Kumar *et al.* (2004) reported that highest for number of pods per plant followed 100-green seed weight and green pod yield per plant. Likewise, other characters also had high heritability. Days to flowering with first pod bearing node and days to first picking , plant height with shelling percentage , pod length with green pod yield and 100 -green seed weight , number of pods per plant with green pod yield and protein content of green seeds and 100-green seed weight with green pod yield exhibited significant and positive correlation. The association of plant height with pod length content with total sugar was negative and significant. Path analysis showed that number of pods per plant, pod length, 100-green seed weight and plant height contributed both directly and indirectly via other characters towards green pod yield per plant and thus was the main components for simultaneous selection and improvement of pea crop.

Raffi and Nath (2004) studied on variability; heritability, genetic advance and relationship on yield and yield contributing characters in dry beans (*Phaseolus vulgaris* L.). They found the highest genotypic and phenotypic variance by days to maturity (57.64 and 74.13) whereas pod length showed the lowest (1.84 and 2.30). In case of number of seeds per plant the variation between genotypic and phenotypic variance (29.17 and 48.66) and coefficient of variation (31.43 and 40.60) were found high indicating larger environmental effect. 100-seed weight showed the highest genotypic coefficient of variation and also had small difference in both genotypic and phenotypic variance (3.91 and 4.91) and coefficient of variation (42.19 and 42.29), indicating more or less equal genetic and environmental effect on the trait. Here, the environmental effect is negligible. In case of number of pods/plant, the difference between genotypic and phenotypic variation (1.08 and 1.97) and coefficient of variation (19.81 and 26.75) were found comparatively higher indicating less genotypic but more environmental effect on the trait. Raffi and Nath (2004), through path coefficient analysis, also identified a positive non-significant direct effect of eighteen days to flowering on seed yield. Days to maturity and plant height had negative direct effects. The pod and seed characters had positive and significant direct effect on seed yield, indicating an increase in number of pods per plant, pod length, number of seeds per pod and 100-seed weight may be contributed directly to seed yield.

Raffi *et al.* (2004) reported that significant variations were observed for all the characters in all the genotypes used in the experiment. Highest and genotypic and phenotypic variations were observed for days to maturity and pod length, respectively. All the characters showed high heritability with high genetic advance. Grain yield was found to be positively correlated with number of pods plant ha<sup>-1</sup>, pod length, number of seeds plant ha<sup>-1</sup> and 20 seed weight.

Gupta and Singh (2005) assessed the genetic diversity for 14 yield-related characters by using Mahalanobis's D<sup>2</sup> statistics in 13 genotypes of French bean during 1997/98 at Ghaziabad, Uttar Pradesh, India. Analysis of variance revealed significant differences among genotypes for all characters. D<sup>2</sup> statistics and Tocher's method grouped the 13 genotypes into 4 clusters. Clustering based on geographical origin was inconclusive. Pant Anupam was the most divergent genotype, indicating its potential for obtaining heterotic hybrids and producing wide spectrum of variation in segregating generations.

Singh (2006) studied on genetic divergence for yield and yield components in 22 genotypes of (*P. vulgaris* L.) grown in Srinagar, Jammu and Kashmir, India during the summer of 2001 and 2002. Significant variation among the genotypes was observed for all traits (plant height, number of branches per plant, number of days to 50% flowering, number of pods per plant, pod length, pod width, number of seeds per pod, average seed yield per plot and seed yield per ha). The genotypes were classified into 5 clusters. The system of classification did not correspond to the geographical origin of the genotypes. Cluster 1 had the greatest inter cluster distance followed by cluster II. The highest inter cluster distance was observed between clusters IV and V. The number of pods had the greatest contribution towards the total divergence. Principal component analysis revealed that the average seed yield per plot, seed yield per hectare, number of pods per plant and number of branches per plant were the most important primary causes of divergence.

Rai *et al.* (2006) evaluated fifty-two genotypes of pole type French bean during *rabi* 2002 in Meghalaya, India. Genetic variability, character association and path coefficient study revealed that there was wide range of phenotypic variation along with high heritability in pole type French bean. The characters namely, pod yield/plant, number of pods/plant, seed weight and pod weight showed high GCV and high heritability along with high genetic advance revealing that these characters are controlled by additive gene. Association studies revealed that pod yield/plant exhibited significant positive correlation with pod length, pod weight and

seed weight at both genotypic and phenotypic levels. Maximum direct effect was observed in pod weight followed by seed length, seed thickness and number of pods/plant towards yield indicated that these characters are very important while making selection for high yielding genotypes.

According to Singh *et al.* (2007) determined sixty-six genotypes of French bean for variability, heritability and genetic advance at Vegetable Research Farm, Institute of Agricultural Sciences, B.H.U., Varanasi. Highly significant differences were observed in the genotypes for all the characters under investigations. The genotypes, Contender, EC-94461, VRF-2, Arka Komal, HUR-15, Pusa Parvati, FB-33A, VRF-1, HUF-0 and HUR-4 were found most promising and higher yielder. Both genotypic and phenotypic coefficient of variations were generally high for number of branches plant-1 and moderate for plant height, number of seeds pod-1number of pods plant-1, pod length and average seed yield plot-1. All these characters also exhibited high heritability and genetic gain, hence, simple selection procedure may be followed for the further improvement in these traits. The characters like days to 50% flowering and pod diameter showed low genotypic and phenotypic coefficient of variations with low to moderate heritability and genetic gain thus the selection in these traits would not be effective.

According to Singh *et al.* (2007) carried out an experiment on forty-five varieties of French bean (*Phaseolus vulgaris* L.) originating from different eco geographical regions of the country were grown in Hisar, Haryana, India to study the pattern of genetic variability. There was a wide range of variability for all the traits. Heritability estimates and expected genetic advance were high for 100-seed weight, number of pods and seed yield, suggesting that these are more useful traits for varietal improvement programme.

Nausherwan *et al.* (2008) conducted a trial at Vegetables Research Institute, AARI, Faisalabad, Pakistan during 2005-06. 12 pea genotypes were sown in a randomized complete block design with three replications. The objective was to ascertain genetic variability, correlation and path coefficient of different traits. Analysis of variance revealed highly significant differences among genotypes for days to emergence, days to 50 percent flowering, number of pods per plant, weight of pods per plant (g), pod length (cm), number of seeds per pod, 100-seed weight (g) and green pod yield (kg/plot). Green pod yield per plot, 100-seed weight, number of pods per plant and weight of pods per plant showed high GCV accompanied with high heritability and genetic advance indicating good scope for selection.

The correlation studies revealed that in general, estimates of genotypic correlation coefficient were higher than corresponding phenotypic correlation coefficient. Green pod yield per plot showed positive and significant correlation with number of seeds per pod and weight of pods per plant at genotypic and phenotypic levels. A strong association was observed between pod length and number of seeds per pod. The results suggested that these traits could be considered as major green pod yield contributing characters in garden peas. 100-seed weight, number of pods per plant, number of seeds per pod and days to 50 percent flowering exhibited maximum positive direct effect on green pod yield per plot, respectively. It indicated that these are main contributors towards yield. Based on results expressing character association and path coefficients for yield and its contributing characters, breeders should give attention to the characters like 100-seed weight, number of pods per plant, number of seeds per pod and days to 50 percent flowering, while making selection of high yielding genotypes in garden pea.

Sharma *et al.* (2009) evaluated thirty three genotypes of pole type French beans obtained from India and abroad were evaluated during *Kharif*, 2006 in Solan, Himachal Pradesh with the objective to genetically evaluate these genotypes for important horticultural traits and to work out the genetic divergence in the genotypes for further breeding studies. Significant differences were observed for all the characters studied. The material was subjected to genetic analysis and further, based on Mahalanobis's  $D^2$  statistics, genotypes were grouped into six clusters, majority of which were accommodated in cluster I followed by cluster VI. Maximum intra cluster distance was in cluster V followed by cluster I and the inter cluster distance was observed maximum between cluster IV and V followed by cluster I and VI. Cluster mean for different characters revealed that cluster V was the best of all from snap bean point of view and should be exploited in breeding programme. Further, hybridization between cluster IV and V could be utilized for getting the superior recombinants or transgress segregates in segregating generations.

Biswas *et al.* (2010) worked on RAPD molecular markers to evaluate the genetic diversity in the fourteen varieties of French bean (*Phaseolus vulgaris* L.) of three eco-geographical regions of Bangladesh. Out of the 20 primers, only 6 yielded polymorphic banding patterns. In total, 40 different DNA bands were reproducibly obtained, out of which 28 (70%) were polymorphic. The polymorphisms were scored and used in band-sharing analysis to identify genetic relationships. Cluster analysis based on Jaccard's similarity coefficient using

UPGMA grouped all the 14 genotypes into two major groups. Pair-wise variety comparison of the varieties showed that inter-variety similarity indices for PV004 versus PV005 (98.51) was higher than all other varieties pairs. On the other hand, inter-cultivar similarity index for BARI 01 versus PV009 (59.58) cultivar was lower than all other cultivar pairs. Therefore, the inherent simplicity and efficiency of RAPD analyses will be to facilitate the construction of RAPD-based genetic linkage maps in French bean.

According to Vipin *et al.* (2010) investigate the genetic diversity of 115 indigenous and exotic common bean (*Phaseolus vulgaris* L.) accessions was studied using morphological traits and molecular tools divergence study of all the 115 accessions revealed that genetic material have sufficient diversity on morphological and molecular basis which can be exploited for better recombinant selection and hybrid vigour. The study of natural genetic diversity in important pulses crop viz., common bean on morphological and molecular basis is an important and essential activity of the future crop improvement program either through conventional breeding approaches or biochemical tool *i.e.* marker assisted selection (MAS).

Rai *et al.* (2010) reported that wide range of phenotypic variation along with high heritability values observed in 66 pole type French bean genotypes. Number of pods per plant, 100-seed weight, green pods yield per plant showed high heritability along with high genetic advance. Association studies revealed that pod yield per plant exhibited significant positive correlation with number of pods/plant, % fruit set per cluster and 100-seed weight at both genotypic and phenotypic level. Maximum direct effect was observed in number of pods/plant followed by % fruit set/cluster, number of seeds/pod towards yield. Hence, these characters have significant effect on yield, while making selection for high yielding genotypes. Multivariate hierarchical clustering classified 66 genotypes in 2 groups with 23 and 43 genotypes. First group further divided into 2 groups with 1 and 22 genotypes (VRBFB-36 is genetically different from 22 other genotypes), while 43 genotypes divided into 2 clusters with 9 and 34 genotypes, respectively.

Pandey *et al.* (2011) assessed the variability was studied among 18 exotic and indigenous French bean (*Phaseolus vulgaris* L.) genotypes collected from research centres, agro-vets and traditional farming villages of the western hills of Nepal. The collected genotypes were field evaluated at the Agriculture Research Station, Malepatan, Pokhara at 848 m above sea level during the summer season of 2010 with the objectives to assess the variability in the exotic

and indigenous genotypes and their potential for utilization in improvement programmes. The results of the study showed that the variability was higher in adaption, vegetative growth, floral and pod characteristics. The plant survival at harvest was higher in pole-type than in bush-type beans. Bush-type beans were earlier in flowering than pole-type beans ranging from 97.92 to 54.17% with means of 83.71% and 79.80%, respectively. Bush-type beans were earlier in flowering than pole-type beans ranging from 32 to 174.33 d with a mean of 35.76 and 76.61 d, respectively. Pod length and width were higher in pole-type beans than in bush-type beans ranging from 20.45 to 7.67 cm in length and 33.53 to 7.37 mm in width. The variability indicated that the collected genotypes were distinctly different. The results revealed that the French bean genotype in mid hills of Nepal is highly diverse and could be considered as the secondary centre of genetic diversity. The diverse genotypes should be conserved and utilized for varietal improvement.

Praveenkumar *et al.* (2011) assessed the twelve genotypes of French bean for variability, heritability and genetic advance. Highly significant differences were observed in the genotypes for all the characters. Both genotypic and phenotypic coefficient of variations were generally high for number of pods per plant, tenderness of pod, weight of ten pods, pod yield per plant, total yield per hectare and shelf life of pods and moderate for plant height, number of branches, days to 50% flowering, pod length, pod width and leaf miner maggots per leaf. All these characters also exhibited high heritability and genetic advance over mean except number of branches. Hence, simple selection procedure may be followed for the further improvement in these traits. Whereas, stem thickness, chlorophyll content, ovule number per pod, number of seeds per pod exhibited low genotypic and phenotypic coefficient of variation with low to moderate heritability and genetic advance over mean thus the selection in these traits would not be effective.

Kamaluddin and Ahmed (2011) used ten common bean genotypes to study their performance, genetic variability, heritability and genetic advance, correlation and path analysis for yield and yield contributing characters *viz.*, days to 50% flowering, plant height (cm), number of pods/plant, pod length (cm), number of seeds/pod, 100-seed weight (g) and seed yield (q/ha). Significant variations were observed for all the characters in all the genotypes used in the experiment. Highest genotypic and phenotypic variations were observed for plant height followed by number of pods/plant and pod length. Plant height, 100-seed weight and days to 50% flowering showed high heritability with

high genetic advance. Seed yield was found to be positively correlated with days to 50% flowering, plant height and number of seeds/pod. Path coefficient analysis revealed that days to 50% flowering, number of pods/plant, pod length and 100-seed weight showed positive direct effects on seed yield. Hence, selection for these traits for improving seed yield in French bean is suggested.

Junaif *et al.* (2011) evaluated twenty six genotypes of French beans (*Phaseolus vulgaris* L.) during *Kharif* 2008 to estimate the genetic variability parameters. Phenotypic and genotypic coefficients of variation for most of the traits were found moderate to high except for protein content per cent. High heritability along with high genetic gain was observed for green pod yield plot-1 followed by green pod yield plant-1 and number of pods per plant indicating that these traits could be exploited for further improvement through selection procedures.

Bhadru and Navale (2012) estimated genetic variability parameters in  $f_2$  and  $f_3$  population of two crosses viz., Dapoli Safed x GC 10 and Manjarkheda local xG1 of cowpea. In both the crosses magnitude of PCV, GCV, heritability and genetic advance values higher in  $f_3$  as compared to population. Number of pods per plant, biomass at harvest, days to maturity, number of seeds per pod, pod length, 100 -seed weight and seed yield per plant recorded higher GCV, PCV, heritability and genetic advances, indicating the prevalence of additive gene action in the control of these characters and simple selection in development of high yielding cowpea genotypes.

Noubissie *et al.* (2012) worked out on fifteen common bean (*Phaseolus vulgaris* L.) cultivars of the highlands zone of Cameroon to estimate the genetic variability for seed protein content. Heritability values, gene effects and the potential for genetic improvement of crude protein content in bean were investigated using generation's means analysis with selected parents,  $f_1$  and  $f_2$  generations as well as backcross populations (BC) produced in three hybrid combination. The differences among the genotype were significant at  $p \leq 0.01$  for protein concentration measured by Kjeldahl method. The range of variation was from 18.22% DM (Marbre) to 28.32% DM (PB). Only three cultivars, all with white seed coat i.e., 'PB', 'GB' and 'Bamendjou 87' showed high seed protein level. Broad -sense heritability was of a moderate 0.46 to high 0.72 value and material effects were detected in  $f_1$ . Narrow -sense heritability (0.16 to 0.41), heterosis (-1.25 to -4.35%) values and gene effects analysis suggested that the protein content is controlled by additive and non-additive genes.

At 10% level of selection, an increase of only 3.60 to 10.16% is predicated after one cycle of selection. Non-allelic interactions were significant in all crosses and the presence of duplicate dominant epistasis was observed in the expression of this trait. A minimum of 4 to 10 genes affected the protein accumulation in bean seeds. These results suggested that breeding for increased protein content in the seeds of common bean can be quite successful through recurrent selection in later generations.

Babbar *et al.* (2012) conducted trial on forty four promising lines of chickpea grown in RBD with three replications under late sown season. The maximum genotypic coefficient of variation was noticed for damaged pod percentage, total number of seeds per plant and total number of pods per plant. Days to 50% flowering, days to maturity, plant height, 100-seed weight and seed yield per plant showing high heritability coupled with medium genetic advance as percentage of mean, whereas, damage pod percentage, number of seeds per plant and number of pods per plant showing medium heritability and high genetic advance as percentage of mean. Seed yield per plant showed high significant positive correlation with total number of seeds per plant, total number of pods per plant, biological yield, plant height and 100-seeds weight, whereas, significant negative correlation with days to 50% flowering and damaged pod percentage. Based on D<sup>2</sup> cluster analysis, the forty genotypes were grouped into nine clusters, depending upon the genetic constitution of the genotypes. The maximum intra cluster distance was found in cluster IV followed by cluster I, cluster VI and cluster VIII. Intra cluster values varied from 2.75 to 9.02. Total pods per plant, 100-seed weight, days to maturity, biological yield and seed yield per plant considered as selection criteria, while selecting superior genotypes under late condition. High yielding advanced breeding lines viz., JG14, JSC56, AKG, JG9602974, BG3005, PG 03110, Phule G00108 were found suitable under late sown condition.

Magalingam *et al.* (2013) reported that field bean (*Dolichos lablab* L.) is an important vegetable crop throughout India due to its local acceptability by the people. It has wide genetic variability for various traits like plant habit, branching habit, stem pigmentation, pod colour and pod characters etc. In the past, very little attention was given by the scientists on systematic crop improvement in dolichos bean. The present investigation was laid out in a simple randomized complete block design with three replications during *Rabi* 2011-2012 to study the variability present in 23 genotypes of dolichos bean. Analysis of variance revealed that there were significant differences among the genotypes for all the characters studied. The

difference between PCV and GCV was narrow for all characters except percentage of pod set. Hence, these characters were less influenced by environment. High GCV and heritability estimates were associated with greater genetic advance for the nine traits viz., percentage of pod set, number pods per cluster, number pods per plant, green pod length, green pod width, individual green pod weight, pod yield, crude protein and crude fibre indicating that these characters had additive gene effect and were more reliable for effective selection in the improvement of dolichos bean. It is inferred from correlation and path analysis that the individual green pod weight, percentage of pod set, number of flowers per cluster and number of pods per plant exhibited significant positive correlation and direct positive effect on yield. Hence, these traits may be used as selection indices for yield improvement of dolichos bean.

According to Alemu *et al.* (2013) snap bean is an important crop in Ethiopia and its production has been steadily increasing. It occupies the highest share (94%) of export potential among all vegetables. Despite its importance, limited research effort was made to improve yield, pod quality to export market standard and tolerance to diseases. Thus, the present study was conducted to estimate the extent and pattern of genetic variability, heritability and genetic advance expected under selection to be used in the future breeding programs. Thirty six snap bean (*Phaseolus vulgaris* L.) genotypes were tested in 6H6 simple lattice designs at Melkassa Agricultural Research Center in 2010 in the off-season using furrow irrigation. Data on yield and yield contributing traits were collected. Significant difference among the genotypes for most of the characters was observed. High phenotypic coefficient of variation was recorded for green pod yield and other yield contributing traits. Similarly, green pod yield per plant depicted high genotypic coefficient of variation while pod number per plant, single green pod weight and green pod width showed medium genotypic coefficient of variation. High to medium heritability coupled with high expected genetic advance as percent of mean was observed for green pod yield and pod number per plant indicating the opportunity to improve these characters through selection. Generally, the present study entails the presence of genetic variability among the test genotypes with respect to the traits under investigation. This implies the opportunity to bring about green pod yield improvements in snap bean either through direct selection or hybridization.

Pal and Singh (2013) carried out an experiment at Department of Horticulture, Janta P.G. College, Bakewar, Etawah during the year 2007-08 to evaluate twenty five diverse genotypes of pea. Analysis of variance indicated highly significant difference among the genotypes for

all the characters indicating the presence of wide range of variability in the genotypes. Among the entries evaluated, the genotype VRP-345 recorded maximum plant height (173.50 cm). Days to 1st flower emergence (36.90 days), days to 50% flower emergence (41.70 days), days to 1st pod set (41.80 days) and days to maturity of green pod (63.30 days) was recorded minimum in the genotype VRP-5. The number of primary branches/plant ranged from 1.20 (VRP-301) to 3.10 (VRP-38). The maximum pod length (9.29 cm) and diameter (1.38 cm) was recorded in genotype VRP-7 and VRP-8, respectively. The maximum number of pods/plant was recorded in genotype VRP-190 (47.0). The number of seeds/pod was observed in genotype VRP-10 (8.70) and it's ranged from 5.60 to 8.70. The 10-seed weight varied from 19.98 g to 28.20 g and maximum in VRP-2. Maximum shelling percentage was recorded in genotype VRP-86 (5.84 %). The maximum green pods yield/plant was recorded in genotype VRP-38 (240.72 g) and it ranged from 74.48 to 240.72 g. VRP-5 was found the earliest flowering and fruiting genotype among all the genotypes under study. The phenotypic variance and PCV were higher as compared to genotypic variance and GCV for all the characters. Maximum GCV and PCV were recorded for plant height followed by number of pods/plant and green pod yield/ plant. The highest heritability was recorded for green pod yield/plant and days to 50 per cent flower emergence and its higher value may be attributed to additive gene action. The estimate of genetic advance showed a wide range from 0.07 to 73.38 and it was highest for green pod yield/plant. High heritability coupled with genetic advance indicated that importance of the considerable additive (heritable) gene effects.

Alom *et al.* (2014) an experiment was conducted at the Regional Agricultural Research Station (RARS), BARI, Rahmatpur, and Barisal during the period from January, 2013 to April, 2013 to studied on the variability, heritability, genetic advance and interrelationship via correlation coefficient and path coefficient analysis among the important eight characters in relation to seed yield. Significant variation was observed among the studied 54 mungbean genotypes for all characters. Different genotypes were found superior for different characters. Among the genotypes, ACC-12810002 for plant height (71.80 cm), TPK-2558-97 for days to 50% flowering (48.67 days as minimum), BC-6960-88 and VO-1558 (B-G) for days to pod maturity (89.00 days as minimum), VC-6149 (B-12) for pod length (17.30 cm), ACC-12810006 for pods plant-1 (31.73), ACC-12890073 for seeds pod-1 (17.60), VC-6960-88 for 100- seed weight (5.63 g) and GK-40 for seed yield (1846.00 kg ha<sup>-1</sup>) were found to be the superior genotypes. Including seed yield, all the characters, except seeds pod-1 exhibited high

heritability accompanied by medium to high genetic advance as percent of mean. These characters also showed medium to high GCV and PCV. However seeds pod-1 showed moderate heritability and genetic advance as present of mean. In all these case significant genotypic correlation coefficient were found to be higher than their corresponding phenotypic ones. The character 100-seed weight showed significant positive relationship with seed yield. Path coefficient analysis suggested that pods plant-1 contributed maximum direct effects having positive on seed yield. Plant height, pod length and 100-seed weight had also positive direct effect on seed yield. Thus selection based on pods plant-1, days to first flowering, plant height and 100-seed weight might be effective for improving seed yield in mungbean.

Kulkarni *et al.* (2014) studied on genetic variability, heritability; genetic advance and correlation for different yield contributing characters were studied in 20 genotypes of French bean. Significant differences were observed among the genotypes for all the traits. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits. Traits thickness of pods, green pod yield per plant, number of seeds per pod, weight of 100- seeds and plant height reported high heritability. Highest heritability coupled with high genetic advance was obtained in plant height (98.91), total leaf area (97.73) and green pod yield per plant (95.30). Green pod yield per plant exhibited highly significant positive correlation at genotypic as well as phenotypic levels with length of pod, weight of 100 -seeds and dry seed yield per plant.

Kulkarni and Musmade (2014) also worked on genetic variability, heritability, genetic advance and correlation for different yield contributing characters in 20 genotypes of French bean. Significant differences were observed among the genotypes for all the traits. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits. Traits thickness of pods, green pod yield per plant, number of seeds per pod, weight of 100 seeds and plant height reported high heritability. Highest heritability coupled with high genetic advance was obtained in plant height (98.91), total leaf area (97.73) and green pod yield per plant (95.30). Green pod yield per plant exhibited highly significant positive correlation at genotypic as well as phenotypic levels with length of pod, weight of 100 seeds and dry seed yield per plant. Number of leaves per plant (0.86108) recorded magnitudinally the highest positive direct effect on green pod yield followed by stem fly infestation (0.63142) and number of seeds per pod (0.50453). Weight of 100-seed

had positive indirect effects via days for first flowering, pod set percentage, breadth of pod, number of leaves per plant, mean leaf area, duration of harvest for green pod, number of seeds per pod, seed maturity, height of plant, dry seed yield per plant and leaf minor incidence. It had negative indirect effects through remaining all other characters.

Bendangkumzuk and Chaturvedi (2014) an experiment was carried out on genetic variability, correlation and path coefficient analysis was studied in twenty French bean (*Phaseolus vulgaris* L.) genotypes of Nagaland for grain yield and its attributing characters. The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating a high degree of variability in the material. The highest PCV and GCV were recorded for plant height at maturity, 100- seed weight, yield per plant, protein content, pods per plant and seeds per pod indicating the presence of ample variation for these traits in the present material. In the present study high estimates of heritability and genetic advance as percent of mean were obtained for plant height at maturity, 100- seed weight, yield per plant, protein content, pods per plant, seeds per pod and pod length. Thus, selection of these traits is likely to accumulate more additive genes leading to further improvement of their performance and these traits may be used as selection criteria in French bean breeding program. The grain yield exhibited significant positive correlation with 100- seed weight indicating relative utility of this trait for selection. 100-seed weight exerted maximum positive direct effect and exhibited significant positive correlation with yield indicating a true relationship among the traits.

Pandey *et al.* (2014) an experiment was carried out on 43 diverse genotypes of cowpea to studied the genetic variability, heritability, genetic advance, correlations and path coefficient for different traits and to identify diverse genotypes of cowpea belonging to different multi-groups through multivariate analysis. A fairly high degree of variability was observed for most of the traits. Higher estimated of heritability coupled with the higher genetic advance for plant height, number of peduncles per plant, number of pods per plant and pod yield per plant indicated that these traits are under the control of additive genes. Correlation analysis pointed out the importance of number of branches/plant, peduncles/plant, pods/plant, pod length, pod weight and number of seeds/pod towards pod yield. Forty three genotypes were mainly divided into 2 clusters with 38 and 5 genotypes at the first node. The representatives of distant clusters would be more useful for choosing the parents in cowpea breeding programme.

Savita *et al.* (2014) an experiment was carried out on genetic variability, heritability, genetic advance and path analysis was studied in forty French bean (*Phaseolus vulgaris* L.) genotypes for pod yield and yield related characters viz., plant height at 30 days after sowing (cm), leaf length (cm), leaf width (cm), days to 50 per cent flowering, pod length (cm), pod width (mm), number of marketable pod per plant, pod yield per plant (g), number of pods per plant, weight of marketable pods per plant (g), days to 50 per cent maturity, seed length (mm), seed width (mm), number of seeds per pod, 100-seed weight (g) and green pod yield (q/ha). Significant differences were observed for all the characters in all the genotypes used in the experiment. Highest heritability 99.84% was recorded for green pod yield per hectare and pod weight (77.63%) had lowest heritability among all the characters studied and genetic advance as per cent of mean was highest for number of pods per plant (58.00%) and lowest for days to 50 per cent maturity (14.95%). A critical perusal of path coefficient analysis, at the level of phenotypic correlation coefficient, revealed that green pod yield per plant (0.657) had the highest direct effect on pod yield per hectare.

Sharma *et al.* (2014) an experiment was carried out on 23 genotypes and 2 commercial varieties of Dolichos bean to find out the magnitude of the genetic variability, correlation and path coefficient analysis. A large variation was found for all the characters studied under the experiment. Genotype 10/DOLPVAR-6 exhibited maximum spikes/plant, number of pods/cluster, number of seeds/pod, 25 pods weight, pod length, pod width, 1000 seed weight, pod yield/plant, pod yield/plot and pod yield/ha. High level of phenotypic coefficient of variation, genotypic coefficient of variation, heritability with genetic advance for number of flowers/cluster, pod yield/plant, pod yield/plot and pod yield/ha could be improved through direct selection. The correlation studied indicates chances for upgrading Dolichos bean genotypes by simultaneous selection through spikes/plant, days taken to first flowering, days taken to 50% flowering, days taken to first pod harvest, 25 pods weight, pod length, pod width, pod girth and 1000-seed weight. Path coefficient analysis revealed that there is ample scope for the improvement of pod yield by selecting a genotype having higher pod weight, early flowering and pod harvesting, more pods/cluster, spikes/plant, long pod with more width and girth and having bold seed size.

Singh *et al.* (2014) worked on French bean (*Phaseolus vulgaris* L.), especially pole-type, is one of the most widely cultivated and popular vegetables in Mizoram due to its wide adaptability, round the year availability and better tender pod quality (slender, fleshy, soft with fewer parchment strings). However, there is little information on genetic variability,

heritability and interrelationships of economic traits in pole-type French bean. Therefore, sixty-five genotypes (Indian and exotic collections) were evaluated. A significant genotypic mean square for the traits studied indicated sufficient variation among genotypes. Ten genotypes showed better pod yield potential (>13.5 t/ha) which were collected from Mizoram (IC593590, IC593591, IC593594, MZFB-48, IC595238, MZFB-32, IC593593, MZFB-29, MZFB-51 and MZFB-47). Vine length, inter-nodal length, number of nodules/plant, nodule fresh weight, tender pod fresh weight, 100- seeds weight and pod yield showed additive gene action, i.e., high heritability (>80 %) and high genetic advance (>40 %) which could be improved by selection and hybridization. While non-additive genes were responsible for days to 50 % maturity (earliness) that could be exploited through heterosis breeding. However, both additive and non-additive genes are accountable for pod length, number of seeds/pod and number of pods/plant and could be improved through reciprocal recurrent selection. Pod weight and number of pods/plant could be reliable tools for selection indices to identify the productive genotypes and to realize maximum genetic gain. Viewing the genetic potential, it is convincing to include genotypes from Mizoram regions in the genetic enhancement as well as varietal improvement of French bean for tender pod yield.

## **2.2. Correlation coefficient**

Correlations measures mutual association with regard to causation between to attributes. Knowledge of the nature and magnitude of interrelationship among yield and its components is of great interest in plant breeding. The statistics which measure the relationship and its extents, between two or more variable is known as Correlation coefficient. Correlation studies provides information that selection for one character will results in progress for all positively correlated characters. Many of the characters are correlated, because of association positive or negative with other characters. As more variables are considered in correlation table, their indirect correlation becomes more complex. The original concept of correlation was presented by Galton (1989), which was elaborated later by Fisher (1918) and Wright (1921).

Johnson *et al.* (1955) observed that a moderately close relationship between phenotypic coefficient of variation (PCV) and genotypic coefficient variation for the entire trait except plant height, pod length and pod breadth suggested greater success through phenotypic selection. High heritability estimates (71.13 to 92.99 %) for harvest index, seeds per pod, pod

per plants, 100-seed weight and green pod yield per revealed scope transferring such performance to the progenies.

Coyne (1968) examined high correlations between total seed yield and each seed yield component in spaced plant studies. Each component contributed about equally to total seed yield. Heritability of total seed yield and of each of the three yield components were evaluated and some yield components are found more heritable than total seed yield.

Sakrajitjana and Das (1983) reported that yield was positively and significantly associated with number of pods per plant. Number of pods per plant was also positively and significantly correlated with number of primary branches. The number of primary branches was negatively associated with days to flower and pod length but positively correlated with vegetable pod yield per plant in 11 varieties of cluster bean.

Shah *et al.* (1986) found that the genotypic and phenotypic variance were pod length showed positive and significant correlation with plant height (0.179), 100-seeds weight (0.165), seed yield per plant (0.371), whereas, positive but non-significant correlation with days maturity (0.101) and pod length (0.656).

Patil *et al.* (1989) reported that the grain yield was highly correlated with pods per plant, 100- seed weight, clusters per plant, pod length and days to 50 % flowering based on diallele cross involving ten diverse indigenous lines and varieties of cowpea.

Saha *et al.* (1990) observed that the estimates of correlation coefficients of economic traits with plant yield and among themselves provide the basis for identifying the traits for ideal plant type and indirect selection. The phenotypic and genotypic correlation coefficient between pairs of characters are presented. Green pod yield / plant was found to be positively associated with plant height, seed yield /plant and seeds / pod and negatively with 100- seed weight. Such a correlation between plant height and green pod yield.

Siddique and Gupta (1991b) observed a significant correlation of seed yield per plant with days to 50 % flowering, days to maturity, number of clusters per plant and number pods per plant. In 1992, Oseni, *et al.*, revealed that there is a positive correlation between seed yield and pods per plant, between days to flowering and 100- seed weight. While, negative correlations were observed between days flowering and seed yield and between 100- seed weight, seed yield, days to flowering, 100 -seed weight, days, days to pod filling and pod length were the major components contributing to yield. Altinbas and Sepetoglu (1993)

concluded that correlated with pods per plant, seeds per pod and number of branches per plant. Both days to flowering and maturity had no influence on seed yield, 100- seed weight was negatively and significantly associated with pods per plant and seeds per pod. Sawant (1994) found that the seed yield was significantly and positively correlated with branches per plant, inflorescence per plant, pods per plant, pod length, seeds per pod, 100- seed weight and harvest index.

Singh (1993) studied on genetic variability, heritability estimates and correlation coefficient were studies in diallel crosses ( $f_1$ ) of French bean. High heritability estimates associated with high genetic advance were found for green pod yield per plant and 100-seed weight, green pod yield per plant showed positive and significant association with plant height, seed yield and seeds per pod. Hence selection could effectively be made on the basis of these said characters.

Tamilselvan and Das (1994) reported that the number of clusters, number of pods per plant and 100- seed weight should be used as a selection criterion in the development of high yielding genotypes of cowpea. In a study involving three  $F_2$  populations Birader, *et al.*(1996) reported that strong correlation between pod weight per plant and seed yield, pod length and number of seeds per pod, number of clusters and number of pods per plant and pod weight per plant. Gowda (1996) revealed that a positive and significant association of seed yield with number of pods per plant, number of seeds per pod and 100- seed weight and also found a significant and negative association with 100- seed weight and number of seeds per plant. In 1997, Singh and Singh revealed that number of clusters per plant, number of seeds per pod and total biomass made greatest direct contribution to seed yield in 45 cowpea genotypes.

Vasic *et al.* (1997) found correlations of plant height and productive height with yield, which were established, via the number of pods per plant and the number of seeds per plant. These results give a clear indication that the yield components are mutually very closely associated. Thus, they concluded that productivity was more dependent on the number of pods per plant than on the number of seeds per pod because the latter characteristic was quite stable in the climatic region. The authors exhibited a positive direct correlation between seed size and yield, which was masked by the negative correlation between seed size and the number of pods per plant.

Vardhan and Savithamma (1998) reported that a very high positive association of green pod yield with pods per plant. Rangaiah *et al.* (1999) reported that total seed weight

was positively and significantly associated with all the traits except plant height and pod weight made the greatest contribution towards yield per plant in both crosses. Plant height, number of pods per plant and number of seeds per pod showed significant and positive association with hundred seed weight indicating that more number of pods gives more number of seeds and also observed a positive association of pod length with plant height, number of branches per plant and number of pods per plant.

Dahiya *et al.* (2000) information on correlation coefficient is derived from data on 16 quantitative traits in 48 germplasm lines of French bean (*Phaseolus vulgaris*) grown at Hisar, Haryana, India during *rabi* 1998-99. In general, the values for genotypic correlation coefficient were slightly than corresponding phenotypic values. Seed yield exhibited significant positive association with primary branches per plant, pods per plant, clusters per plant and biological yield. There was a negative association between seed yield and seed weight.

Seed yield was significantly correlated with number of branches, number of pods per plant, pod weight and number of seeds per pod in cowpea (Mallikarjun *et al.* 1993). Tyagi *et al.* (2000) carried out correlation study with twenty-four genotypes in cowpea. They reported seed yield per plant had high significant and positive correlation with days to 50 per cent flowering, plant height, pod length, number of pods per plant, seed weight per pod and hundred seed weight at both phenotypic and genotypic levels. The path coefficient analysis indicated that, higher seed weight per pod, number of pods per plant and hundred seed weight are important for effective selection.

Shinde and Dumbre (2001) evaluated fifty genotypes of French bean (*Phaseolus vulgaris* L.) for 11 characters, in Pune, Maharashtra, India, during *kharif* 1998. Seed yield per plant was positively and significantly correlated with days to first flower, days to maturity, plant height, plant spread, number of branches per plant, number of pods per branch and number of seeds per pod. It showed positive but non-significant correlation with pod breadth, while negative non-significant correlation with pod breadth, pod length and 100-seed weight both at genotypic and phenotypic levels. The characters 100-seed weight and number of seeds per pod showed strong positive direct effects, while number of pods per plant and number of branches per plant showed moderate direct effects. The direct negative effects on yield were observed for pod length and days to first flower.

Nath and Korla (2004) studied on twenty–eight dwarf French bean (*Phaseolus vulgaris*) genotypes for correlation and path coefficient analysis during 1998 at Solan, Himachal Pradesh, India. Eight quantitative characters were analyzed for their path coefficient in relation to pod yield. Number of pods per plant, pod length and harvest index had significant positive association with pod yield. Number of pods per plant had the highest direct effect, while harvest index and pod length had the highest indirect effects through pod numbers.

Mohammadali and Madalageri (2004) worked on correlation and path analysis studies of twenty green pod yield and yield attribute traits in thirty six accessions of winged bean revealed that green yield per plant had highly significant and positive association with the number of early and late pods per plant, total green pods number plant, early and late pod yield per plant, total dry weight of plant indicating the possibility of improvement in these traits through simultaneous selection. Path analysis green pod yield revealed that traits like late pod yield, early pod yield and number of late pods per plant exhibited high positive direct effects on green pod yield. Late pod yield being chief contributing character for green pod yield with indirect effects through early pod yield and number of early pods per plant.

Singh *et al.* (2005) carried out correlation studies in twenty-four advanced cluster bean genotypes. High estimates of the phenotypic and genotypic coefficients of variation were obtained for pod yield per plant, seed yield per plant, pods per plant, clusters per plant, days to flowering and branches per plant. High heritability (broad sense) accompanied by high genetic advance was observed for seed yield, pod yield, pods per plant, clusters per plant, days to flowering, branches per plant, plant height and days to maturity. The path analysis revealed that pod yield per plant had direct positive effect on seed yield per plant followed by days to maturity, pod length, pods per plant, 100-seed weight and plant height.

Bhushan *et al.* (2007) observed on simple correlation coefficient for seven characters in 441 exotic genotype of French bean (*Phaseolus vulgaris* L.). Seed yield per plant showed positive and significant correlation with number of pods per plant, pod length and 100-seed weight. However, number of pods per plant exhibited positive and significant correlation with pod length, days to maturity and plant height.

Bhushan *et al.* (2008) observed on simple correlation coefficient and path analysis for seven characters with 441 exotic French bean germplasm lines during 2005. Seed yield per plant showed positive and significant correlation with number of pods per plant, pod length

and seed index (100- seed weight). However, number of pods per plant exhibited positive and significant correlations with pod length, days to maturity and plant height. Path coefficient analysis revealed that number of pods per plant, pod length and seed index was most important traits contributing towards seed yield. It could, therefore, be suggested that these characters were dependable for selection of yield in French bean.

Karasu and M. (2010) carried out to determine simple correlations between seed yield and certain important agronomical characters and direct and indirect effects of these characters on seed yield in field bean. The research was conducted with 30 bean cultivars or lines under Isparta ecological conditions in 1996 and 1997. Seed yield, number of branches per plant, number of pods per plant, number of seeds per pod, number of seeds per plant, number of immature pods per plant, biomass yield, seed yield per plant, 1000- seed weight, pod length, pod width, plant height and first pod height were observed in the study. According to the results, simple correlation coefficients were positively significant in all pairs of the characters except correlations between seed yield per hectare and pod length, pod width and first pod height. The highest positive correlations were observed between seed yield per plant with biomass yield ( $r = +0.974^{**}$ ), number of pods per plant ( $r = 0.860^{**}$ ) and number of branches per plant ( $r = +0.790^{**}$ ). Path coefficient analysis indicated that seed yield per plant had the greatest direct effect (+0.668) on seed yield per hectare, followed by 1000- seed weight (+0.185) and plant height (+0.301). Percentages of direct effects on seed yield per hectare were 63.1%, 51.7% and 48.9%, respectively, for seed yield per plant, 1000- seed weight and plant height. In the study, characters such as number of pods per plant, biomass yield, number of branches per plant, number of seeds per plant, number of immature pods per plant, number of seeds per pod and plant height gave the highest indirect effects on seed yield per hectare through seed yield per plant (with contributions 63.6%, 63.0%, 62.8%, 58.1%, 47.8%, 42.3%, and 33.6% respectively).

Kumar *et al.* (2014) studied on correlation and path analysis on 18 marketable pod yield pod and yield attributing traits in 44 accessions of French bean revealed that marketable pod yield per plant had highly significant and positive association with length of inflorescence, number of inflorescence per plant, number of flowers per inflorescence, pod length, pod weight, number of pods per plant pod width and number of seeds per pod indicating the possibility of improvement in these traits through simultaneous selection. Path analysis for green pod yield per plant revealed that traits like number of pods per plant and pod weight exhibited high positive direct effects on green pod yield per plant. Number of pods per plant

being chief contributing character for green pod yield with indirect effects through number of inflorescences per plant, number of seeds per pod, number of pods per inflorescence and length of inflorescence. Keeping in view the direct and indirect contribution of component traits towards total green pod yield per plant, the indirect selection on number of pods per plant number of inflorescences per plant, number of seeds per pod, number of pods per inflorescence and length of inflorescence in French bean is suggesting rewarding.

### **2.3. Path coefficient analysis**

The path coefficient analysis technique of path coefficient was originally developed by Wright (1921). He defined the path coefficient as the ratio of the standard deviation of the effect to the total standard deviation when all the causes are constant, except the one in question. The variability of which is kept unchanged. Dewey and Lu (1959) employed the path coefficient technique in crested wheat grass to establish the relative importance of seed size, fertility and plant size as the determinates of seed yield. In any crop, grain yield has been associated with a number of yield contributing characters and these characters themselves are interrelated. Path coefficient analysis permits the separation of direct and indirect effect through the other related characters by apportioning the correlation coefficients. The available literature on path analysis on seed yield with their component traits in French bean is being briefly reviewed.

Choudhary and Lodhi (1980) reported that the characters like branches per plant, leaves per plant, leaf weight and stem weight were positively and significantly correlated with green fodder and dry matter yield per plant in cluster bean genotypes. Path analysis revealed that number of leaves, leaf weight and stem weight were the major component characters for both green fodder yield and dry matter in guar. Number of clusters per plant number of pods per plant were positively correlated with themselves and also seed yield per plant. In cluster bean Path coefficient analysis revealed that number of pods per plant was the most important character of the seed yield. However, number of branches per plant and number of clusters per plant affected seed yield indirectly via pods per plant (Ramnath and Saini, 1980).

Singh *et al.* (1985) conducted path coefficient study in pea for ten quantitative traits. They concluded number of pods per plant, number of seeds per pod, 100-seed weight and harvest index are the main yield components affecting yield directly. High indirect effects were contributed by number of branches, plant height and flowering via number of pods per plant;

by pod length via 100-seed weight and by maturity via both the component traits. Protein content had negligible effect on seed yield.

Vijay *et al.*(1988) studied correlation and path coefficient analysis for seed yield and its components in seventeen cultivars of winged bean. Their studies revealed that, seed yield per plant showed positive and significant correlation with number of dry pods per plant, hundred seed weight and days to flowering. Path analysis revealed that, the number of dry pods per plant, weight of dry pods per plant and hundred seed weight exhibited positive and direct effect on seed yield, while the pod length showed negative direct effect. Days to flowering had negative direct effect on seed yield. Motior *et al.*(1997) reported significant and positive correlation of seed yield with pods per plant and hundred seed weight in winged bean.

Patil *et al.*(1989) reported that pods per plant, 100- seed weight and seeds per pod had greatest positive direct effect on yield.

Shiddique and Gupta (1991a) reported that pods per plant, 100- seed weight and seeds per pod as the most important yield attributing characters.

Oseni *et al.*(1992) concluded through path analysis that the major components contributing to seed yield were days flowering, 100- seed weight, days to pod filling and pod length.

Sepetoglu (1993) revealed by path analysis study that the most important yield component was number of pods per plant affecting the yield through path analysis.

Sawant (1994) also revealed by the path analysis that pods per plant had the highest positive direct effect on seed yield followed by 100- seed weight, seeds per pods, days to flowering, inflorescence per plant, harvest index per plant and pod length.

Vardhan and Savithamma (1998) studied path coefficient analysis for green pod yield per plant in 29 accessions of cowpea and concluded that green pods per plant, pod length, pods per plant, pod length, pod width and number of primary branches were major traits contributing to yield. Amanakapoor *et al.* (2000) revealed that the number of seeds per pod and 100- seed weight were the main contributing characters towards the seed yield. Pod length contributed indirectly towards seed yield via the number of seeds per pod and 100- seed weight in the study involved I60 genotypes of cowpea.

Neema and Palanisamy (2001) reported that the direct effect of pod yields on grain yield and genotypic correlation between pod yield and grain yield were almost equal and they also

reported that the highest positive direct effect on grain yield was recorded by pod yield and the lowest by pod length. The indirect effect was maximum for pod length via pod yield.

Singh *et al.* (2002) conducted a study to determine the direct and indirect effects of various grain yield components on 43 genotypes of cluster bean (*C. tetragonoloba*). Positive and significant correlations of grain yield were observed with the number of branches per plant, number of clusters per plant and number of pods per plant. Pods per plant had a significant and positive association with days to 50% flowering, plant height, number of branches per plant and number of clusters per plant. The number of clusters per plant was positively and significantly correlated with plant height and number of branches per plant. Days to 50% flowering had a positive significant association with plant height and a negative significant association with 100-seed weight. Days to 50% flowering, followed by the number of clusters per plant, 100-seed weight (g) and number of pods per plant exhibited the maximum positive direct effect to seed yield, but plant height had a negative direct effect on yield. The maximum indirect effects were observed in plant height through days to 50% flowering. Pods per plant, through days to 50% flowering, and the number of clusters per plant exerted good indirect effects on grain yield. The indirect effects of the number of branches per plant through the number of clusters per plant, and the number of clusters per plant through the number of pods per plant were moderate, whereas 100-seed weight had negative indirect effects on grain yield via days to 50% flowering.

Kumar *et al.* (2002) studied five cowpea cultivars and showed that dry fodder yield had the highest direct positive contribution towards green fodder yield followed by number of days to 50% flowering, leaf: stem ratio, number of branches, plant height, leaf breadth and leaf length respectively.

Makhdoomi *et al.* (2002) worked on correlation and path coefficient analysis for different morphological and parameters in 35 germplasm lines of 'Rasmash' French bean (*Phaseolus vulgaris*) under two cropping systems viz. monoculture and intercrop. Seed yield plant-1 had highly significant and positive association with seed pod-1, pods plant -1, days to 50% flowering and days to maturity under both the cropping system. The number of pods plant-1 had highest direct effect and high negative indirect effect via 100-seed weight on seed yield. Selection on the basis of seed pod-1 and number of pods plant-1 may lead to improvement of seed yield in "rajmash" bean cultivars in Jammu and Kashmir.

Nimbalkar *et al.* (2002) conducted an experiment during 1998, 1999 and 2000 rainy season in Pune, Maharashtra, India, to study the stability in seed yield and yield contributing

characters of 16 French bean (*Phaseolus vulgaris*) genotypes. Analysis of variance for individual and pooled environments revealed that the mean difference between genotypes (G) and environmental (E) were highly significant for yield and yield attributes, indicating the presence of genetic variability among the G and E for majority, of the characters studied. The (G x E) interaction was also significant for days to maturity, plant height and seed yield, while the mean square due to E+ (G x E) interaction was highly significant for all the characters studied. Based on individual parameters of stability, the genotypes Red Cloud and PDR 5 for days to maturity; PDR 5 for plant height ; ACPR 11, ACPR 94037, and HPR 35 for primary braches; ACPR 94035 for pods per plant ; ACPR 94038 for 100-seed weight; and ACPR 94040 for seed yield were the most responsive and stable.

Belhekar *et al.* (2003) revealed that plant height and number of branches per plant showed a strong positive direct effect, the number of pods per peduncle and seed index showed a strong negative direct effect and leaf area per plant and number of peduncles per plant showed a moderate negative effect. The number of seeds per pod and pods per peduncle showed a strong positive direct effect. The seed index and number of branches per plant showed a moderate positive direct effect at the genotypic level. The direct negative effect was observed for 100 seed weight, complete maturity and leaf area per plant.

Yadav *et al.*(2003) studied on 28 F<sub>1</sub>s and 28 F<sub>2</sub>s, green pod yield per plant had positive and significant association with plant height, pods per cluster, pod length, seed per pod and pod dry matter in all the three generations. Path analysis revealed that dry matter in pod, pods per plant, and a seed per pod and plant height was the main components of green pod yield in the early generation of cowpea.

Kumari *et al.*(2003) reported that the number of clusters, pods, seeds per pod, and 100 - seed weight showed the greatest positive direct effects on seed yield.

Singh *et al.*(2004) conducted an experiment to study the relationship between seed yield and its components in 176 cluster bean lines. Seed yield per plant was positively and significantly correlated with plant height, branches per plant, clusters per plant and pods per plant. Plant height exhibited significant correlation with branches per plant, clusters per plant and pods per plant. Branches per plant exhibited positive correlation with clusters per plant and pods per plant. The number of clusters per plant was significantly correlated with pods per plant. Seeds per pod had negative direct effect on seed yield. Clusters per plant had appreciable positive direct effects and highly significant positive correlation with seed yield.

Subhadeep and Korla (2004) carried out on twenty-eight dwarf French bean (*Phaseolus vulgaris* L.) genotypes for correlation and path coefficient analysis during 1998 at Solan, Himachal Pradesh, India. Eight quantitative characters were analyzed for their path coefficients in relation to pod yield. Number of pods per plant, pod length and harvest index had significant positive association with pod yield. Number of pods per plant had the highest direct effect, while harvest index and pod length had the highest indirect effects through pod numbers.

Pan *et al.* (2006) conducted an experiment to study the stability parameters, viz., regression coefficient ( $b_i$ ) and mean square deviations ( $S^2_{di}$ ) from linear regression, along with per-se performance of 13 varieties of bush type French bean for 9 yield related characters. Highly significant pooled deviation for green pod yield/plant, number of branches/plant, number of pods/plant and pod weight and highly significant/significant G x E (linear) interaction for days to 50% flowering, plant height and pod length indicated the preponderance of non-linear components of G x E interaction. The linear and non-linear components of G x E interactions were high and low, respectively, for pod width. The roundish and stringless podded line EC 350949 was better performing, stable and suitable for favourable environment for green pod yield (23.74 t/ha) and number of pods/plant (20.18) and suitable for unfavourable environment for number of branches/plant (5.14). EC 398564 was also better performing, stable and suitable for favourable environment for green pod yield (16.32 t/ha), pod length (17.63 cm), pod width (1.20 cm), pod girth (0.86 cm) and pod weight (10.68 g.). EC 398570 was better performing, stable and suitable for favourable environment for pod girth (0.88 cm) and suitable for unfavourable environment for pod length (19.42 cm) and pod width (1.97 cm). EC 350955 was better performing, stable and suitable for favourable environment for number of branches per plant (5.14) and number of pods/plant (18.10) and suitable for unfavourable environment for pod girth (0.90 cm).

Dahiya *et al.* (2006) conducted a trial to determine the direct and indirect effects of the different yield attributing characters on seed yield of 48 French bean genotypes during the *rabi* season of 1998-99 in Haryana, India. Observations were recorded on five competitive plants for 16 quantitative traits (days to first flowering, days to 50% flowering, days to pod initiation, days to maturity, plant height, primary branches per plant, secondary branches per plant, cluster per plant, pods per cluster, pod length, pods per plant, seeds per pod, biological yield, harvest index, 100-seed weight, and genotypic correlations with seed yield). Five pods

per plant were selected to study po characters. Path coefficient analysis of yield attributes and seed yield in 48 French bean genotypes representing wide agro climatic regions of the world revealed that in selection programmes, maximum weight should be given to biological yield, days to pod initiation, number of clusters per plant, seeds per pod and secondary branches per plant since their direct influence on seed yield was highly significant, while their indirect influence via most of the other component characters was negligible.

Roy *et al.* (2006) studied on the relationship between yield and its component characters of twenty seven bush bean (*Phaseolus vulgaris* L.) genotypes were studied during November 2002 to February 2003. Ten characters were studied to identify suitable traits for yield improvement of this crop. Significant variation in seed yield per plant was noticed among the genotypes and the yield difference was attributed mainly due to variation in yield components. The number of pods per plant was the highest in BB 15 followed by BB 3. The highest number of seeds per pod was found in BB 3, while BB 22 had the least. Based on the seed yield per plant, the 27 genotypes were grouped as high yielder (BB 3, BB 9 and BB 15), medium yielder (BB 10, BB 11, BB 12, BB 13, BB 14, BB 16 and BB 18) and low yielder (BB 1, BB 2, BB 4, BB 5, BB 6, BB 7, BB 8, BB 17, BB 19, BB 20, BB 21, BB 22, BB 23, BB 24, BB 25, BB 26 and BARI Bush bean-1). The differences between genotypic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV) were low for all the characters, indicated a low environmental influence over genetic factors on the characters. The GCV and PCV were generally high for pods/plant, 100-seed weight, duration of flowering, seeds/pod and seed yield/plant. High heritability coupled with high genetic advance was observed for duration of flowering, pods/plant, 100-seed weight, seed yield/plant and protein content. Days to 50% flowering, duration of flowering, plant height, pods/plant and seeds/pod had high degree of significant positive correlation with seed yield/plant. Path analysis indicated that pods/plant, days to 50% flowering, 100-seed weight, seeds/pod, plant height and pod length had positive direct effect on seed yield/plant. Those traits could, therefore, be of useful for yield improvement program of bush bean.

Mishra *et al.* (2008) used thirty three genotypes (including check variety "Lakshmi") of pole type French bean (*Phaseolus vulgaris* L.) to find out the relationship among different yield contributing characters by using various statistical parameters like genetic variability, heritability, correlation and path coefficient analysis. A wide range of variability was observed for all the traits. However, maximum variability was observed for number of pods

per plant. Further number of flowers per cluster, pod yield per plant and 100- seed weight reported high heritability coupled with high genetic gain. A positive correlation of green pod yield per plant was observed with days to first flowering, number of pods per plant, pod length and days to first marketable maturity. Among all the characters studied, days to first flowering, number of pods per plant and pod length showed maximum direct effect on pod yield. Hence, these characters should be given more emphasis while making selection for high yielding genotypes in pole beans.

Junaif *et al.* (2009) evaluated twenty-six genotypes of bush type French beans determined the relationship among yield and its component using correlation and path coefficient analysis, were evaluated during 2008. Studied on genotypic and phenotypic correlations revealed positive and significant correlation of green pod yield with number of pods per plant, pod length and average pod weight. Maximum direct contribution came from number of pods per plant, average pod weight, green pod yield per plot and plant spread indicating that these traits are the strongest forces influencing pod yield in French beans.

Singh *et al.* (2009) carried out a trial for green pod yield per plant showed positive and significant association with number of pods per plant, pod length, number of seeds per pod and 10- pod weights in all the three environments studied. The magnitude of the genotypic correlation was higher than the phenotypic correlation but both genotypic and phenotypic correlations followed the same direction, indicating that the selection based on phenotypic correlation could be effective. Path coefficient analysis revealed that selection would be based on both direct and indirect factors simultaneously to make the selection more effective. However, in  $E_1$  and  $E_2$ , selection could be based on 10- pod weight and green pod yield per plant, because these traits had value almost equal to correlation.

Saini *et al.* (2010) evaluated one hundred genotypes of cluster bean and found that the seed yield per plant was positively associated with pods per plant, clusters per plant, biological yield per plant, primary branches per plant and pods per cluster. Non significant positive association of seed yield per plant with days to flowering, maturity and plant height were also shown desirable association in cluster bean and indicated that early and dwarf genotypes were more desirable for cluster bean. It was observed on the basis of desirable direct effects of each character on seed yield per plot obtained through path analysis that pods per plant followed by clusters per plant, test weight, biological yield per plant, seeds per pod harvest index and branches per plant had positive direct effects and low or negative direct effects of

days to maturity, days to 50% flowering, reproductive period, pod length and plant height on seed yield.

Devi *et al.* (2012) conducted trial on bush bean breed new and better cultivars, the breeder requires a comprehensive knowledge on variability existing in the germplasms. The investigation was performed using thirty three genotypes (including two standard checks 'Contender' and 'Arka Komal') of bush type French beans (*Phaseolus vulgaris* L.) to evaluate the genotypes for seed yield and related traits. The experiments were laid out in Randomized Complete Block Design with three replications for two seasons (summer-rainy season, 2008 and 2009). Quality analyses of these genotypes were also done for ascorbic acid, protein, total sugar and total soluble solids for one year. Based on crop characters genotype DPDFB-2(M) was the most superior line for seed yield among all the genotypes followed by MFB-2, DPDFB-1(M), MFB-3 and HAFB-1 which was attributed due to high 100 seed weight. Quality analysis showed that ascorbic acid content was highest in genotype JFB-97-1. Similarly, lines DPDFB-1 for protein, IVFB-2 for total sugar and KPV-2 for total soluble solids content were found to be superior.

Pandey *et al.* (2013) evaluated twenty genotypes including few released cultivars of French bean to determine genetic variability, heritability, genetic advance as per cent of mean, correlations among yield and economically important traits and direct and indirect effects of these traits on overall yield. Field trial was conducted during *Rabi* 2011-12. A high phenotypic (34.20) and genotypic (34.03) coefficients of variations were recorded for number of pod per plant followed by green pod yield, pod weight and pedicel length. Phenotypic coefficients were higher than their respective genotypic correlations in most of the cases indicating that genotypic correlations are stronger, reliable and free from environmental effects. A significant positive correlation between green pod yield and economic traits like number of pods per plant, pod length, individual pod weight and number of seed per pod was estimated which indicates that improvement in these traits could lead to increase in pod yield. Path analysis revealed that number of pods per plant had maximum direct effects on green pod yield followed by pod weight, pod thickness and seed length thus, in improvement programmes, emphasis should be given on these traits to improve green pod yield. The traits like plant height, number of pods per plant, pod length and individual pod weight are important dependable yield contributing traits and need due weight age while formulating selection strategies for genetic improvement of French bean.

Sharma and Devi (2013) reported the characterization of genetic resources allowed the identification of sources of genetic variability, which is important to select potential genotypes for use in future breeding programs. An attempt was made to determine the degree of divergence by using 33 genotypes of bush-type French bean, which were evaluated in randomized complete block design at Vegetable Research Farm, CSK HPKV, Palampur for two consecutive seasons during summer 2008 and 2009. Based on Mahalanobis's  $D^2$  statistics, genotypes were classified into 6 groups each during 2008 and pooled over the years and 4 during 2009. Cluster I was found to be the largest. Intra cluster distances were found to be highest for cluster II for both years and for those pooled over the years. The clustering pattern indicated the absence of any relationship between genetic divergence and geographical distribution. Critical studies of cluster means for different characters indicated that genotypes Palam Mridula, DWDFB-53, HAFB-1, Aparna, JFB-97-1, Chandini, Surya, Falguni and IVRFB-1 showed greater potential for fresh pod yield and seed yield based on maximum inter cluster distances for horticultural desirable traits. It was concluded that the line JFB-97-1 was the most divergent, followed by KPV-2 and Palam Mridula. Superior lines may be obtained from segregating populations by using these in hybridization-e.g., Contender x JFB-97-1/Palam Mridula, JFB-97-1x Palam Mridula, Palam Mridula x KPV-2 and JFB-97-1x KPV-2.

Sarker *et al.* (2014) evaluated eight chickpea varieties to determine the relationship among yield and its components using correlation and path-coefficient analysis. Correlation studies revealed that seed weight per plant expressed positive significant correlation with number of primary branches at maximum flower, number of secondary branches at maximum flower, number of pods per plant, pod weight per plant and number of seeds per plant at genotypic level. In phenotypic level, seed yield showed positive significant correlation with number of pods per plant, pod weight per plant and number of seeds per plant. Path-coefficient analysis expressed that the highest positive direct effect was observed for number of seeds per plant followed by pod weight per plant and 1000-seed weight at genotypic level and at phenotypic level number of seeds per plant followed by 1000-seed weight and number of secondary branches per plant on seed yield. These traits could be used for the improvement of seed yield.

Singh and Anand (2014) carried out an experiment on 42 genotypes/accessions of French bean which were evaluated for eleven economically important characters. The studied

showed considerable variability for these characters. Heritability in broad sense was high for all the characters studied except for number of primary branches/plant. High genetic advance as percentage of mean coupled with high heritability was observed for characters namely, plant height at 60 days after seed sowing, number of pods/cluster, pod length and pod yield/plant. Number of pod/cluster, diameter of pod, pod length and number of pod cluster/plant had a significant positive association with pod yield/plant. Whereas, in genotypic level, maximum positive direct effect on number of pod clusters per plant, followed by pod length, seed yield per plant, days to 50% maturity, number of primary branches per plant, and diameter of pod. Hence selection on these traits could be improving pod yield in French bean.

Verma *et al.* (2014) evaluated thirty four pole type French bean (*Phaseolus vulgaris* L.) genotypes to assess for the presence of genetic variability to identify desirable ones for yield and quality traits. The genotypic variance was moderate to high for the all the 14 traits studied, which resulted in high heritability and moderate to high genetic advance values. Pod yield/plant was positively correlated with all traits except days to 50% flowering, pod diameter and vitamin C content. High heritability and genetic advance of leaf width, first flowering node, number of seeds/pod, number of pods per plant, average pod weight and dry matter content vis-a-vis their positive association and direct positive effect on pod yield per plant suggested for their improvement through simple selection method. All the French bean genotypes were grouped into five distinct clusters. An analysis of the percentage contribution of individual characters towards genetic diversity revealed that vitamin C content, number of pods/plant and dry matter content were the major characters contributing to genetic diversity in French bean. Based on the finding it can concluded that French bean genotypes exhibited a wide range of variability for most of the traits. Some genotypes possessed desirable genes for more than one characters, hence may be utilized directly or included in hybridization programme.

Bala *et al.* (2015) studied on the nature and extent of genetic variability as well as direct and indirect effects of yield related traits on seed yield in 25 chickpea genotypes. The pooled analysis of variance over the environments indicated significant genotypes effect compared to genotype (g) x environment (e) interactions for all the characters. The mean values of the characters studied showed a wide spectrum of genetic variation. The genotypes ICCV 96904 and Himachal Chana-1 were found to be promising for seed yield and biological

yield per plant in pooled over the environments. The phenotypic correlation coefficient revealed significant positive associations of pods per plant, harvest index, biological yield per plant and primary branches per plant with seed yield per plant. The path coefficient analysis revealed that biological yield per plant and harvest index exhibited positive and high direct effects on seed yield per plant. Therefore, these characters could be considered as the best selection parameters for the improvement of seed yield per plant.

Mahbub *et al.* (2015) determined twenty eight soybean genotypes were evaluated for eleven morphological characters during *Rabi* season, 2011 at Sher-e-Bangla Agricultural University, Dhaka, Bangladesh. Analysis of variance revealed significant differences among the genotypes for all the traits. Plant height, seed yield per plant, branches per plant, number of seeds per pod, number of pods per plant and hundred seed weight exhibited that they were controlled by additive gene action and selection for the improvement of these traits would be rewarding. The phenotypic variance was higher than the corresponding genotypic variance for all the characters. All the characters showed moderate to low phenotypic and genotypic coefficient of variation. Genotypic coefficient of variation was the highest for seed yield per plant (31.45%) followed by number of branches per plant (29.9%) and plant height (27.42%). Days to maturity (99.93%) had the highest heritability. Plant height, pod length, number of seeds per pod, number of pods per plant, hundred seed weight, branches per plant and number of seeds per pod showed significant positive genotypic and phenotypic correlation with seed yield. In path analysis, seeds per pod, hundred seed weight, pod length, days to maturity and plant height showed positive direct effect on yield. Considering genetic variability, correlation and path analysis, emphasis should be given on plant height, pod length, seeds per pod and hundred seed weight during breeding program to improve seed yield of soybean.

The present research work entitled “**Studies on genetic variability, correlation and path analysis in French bean (*Phaseolus vulgaris* L.) under Lucknow conditions**” was undertaken to study the morphological, yield and quality components performance; the coefficient of variability of traits under studied; magnitude of heritability, path analysis, genetic advance of traits studied; correlation coefficients among traits, genetic divergence of genotypes incorporated in the studied, identification of source (s) of field resistance from among the genotypes. The experiment was carried out at Horticultural Research Farm first of the Department of Applied Plant Science, (Horticulture), Babasaheb Bhimrao Ambedkar University, (A Central University), Vidya Vihar, Rae Bareli Road, Lucknow, (U. P.), India during the year 2012- 2013 and 2013-2014, respectively. The details methodology adopted in this investigations has been presented under the following headings:

### **3.1- Location and weather conditions**

Geographical, Babasaheb Bhimrao Ambedkar University, (A Central University), Vidya Vihar, Rae Bareli Road, Lucknow (U. P.), India at 80°52; East longitude and 26°56; North latitude and 111 meter above MSL (mean sea level). It is located approximate five km away from Chaudhary Charan Singh International Air-Port and 10 km away from the Lucknow near ( Charbagh) railway junction, towards South – East on Lucknow - Rae Bareli Road, Lucknow- Bijnor- Kanpur Road also connects it. The climate of Lucknow is characterized by Sub- tropical with hot, dry summer and cool winters. This region received an averages annual rainfall of 650-750mm, which is distributed over a period of more than 100 days with peak period during July- August. It also received scattered showers during winter months. In general, the temperature ranges from 5.5° to 25°. The coldest month is January, while the maximum temperature is observed during May- June. The averages relative humidity is 50-70% in different seasons of the year. The monthly weather conditions prevailing during experimental period is given in Table (3.1 and 3. 2) and also shown in Fig. (3.1 and 3.2). The soil of the experiment site was a saline - alkaline, low in organic matter, nitrogen, phosphorus and potash, respectively.

**Table-3.1 Monthly average meteorological (weekly data) during the experimentation under Lucknow conditions during the period 2012-2013:**

Period		Temperature ( °C)		Total Rainfall (mm)	Relative Humidity (%)	Wind Velocity (Km/hr)
Month	Date	Max.	Min.			
Oct. 2012	01-07	34.8	21.7	0.0	57.00	2.4
	08-14	32.8	19.1	0.0	67.00	2.2
	15-21	32.9	15.0	0.0	65.00	1.7
	22-28	30.6	14.8	0.0	66.00	1.9
Nov.20 12	29-04	29.6	12.2	0.0	66.50	1.0
	05-11	28.6	13.4	0.0	68.00	0.9
	12-18	28.5	11.1	0.0	64.50	1.1
	19-25	27.2	10.4	0.0	65.50	1.6
Dec. 2012	26-02	25.8	10.8	0.0	63.50	2.0
	03-09	25.6	9.0	0.0	60.00	2.9
	10-16	26.3	10.1	0.0	66.50	1.0
	17-23	21.3	9.1	0.0	73.00	4.3
Jan.20 13	24-31	15.7	6.3	0.0	81.00	0.9
	01-07	15.6	4.9	0.0	79.50	1.6
	08-14	18.3	3.3	0.0	71.50	1.7
	15-21	23.2	10.2	0.0	75.65	2.5
Feb. 2013	22-28	18.3	4.9	0.0	77.50	2.1
	29-04	23.2	6.6	0.0	68.00	1.2
	05-11	22.3.	11.2	0.0	74.00	3.0
	12-18	22.5	12.7	0.0	76.00	3.1
Mar.2013	19-25	24.4	12.7	0.0	76.50	3.0
	26-04	26.8	13.3	0.0	64.50	5.4
	05-11	30.4	13.9	0.0	64.50	3.6
	12-18	31.5	16.1	0.0	59.00	3.6
	19-25	39.9	17.7	0.0	56.50	5.8
	26-01	32.3	16.87	0.0	57.00	5.8

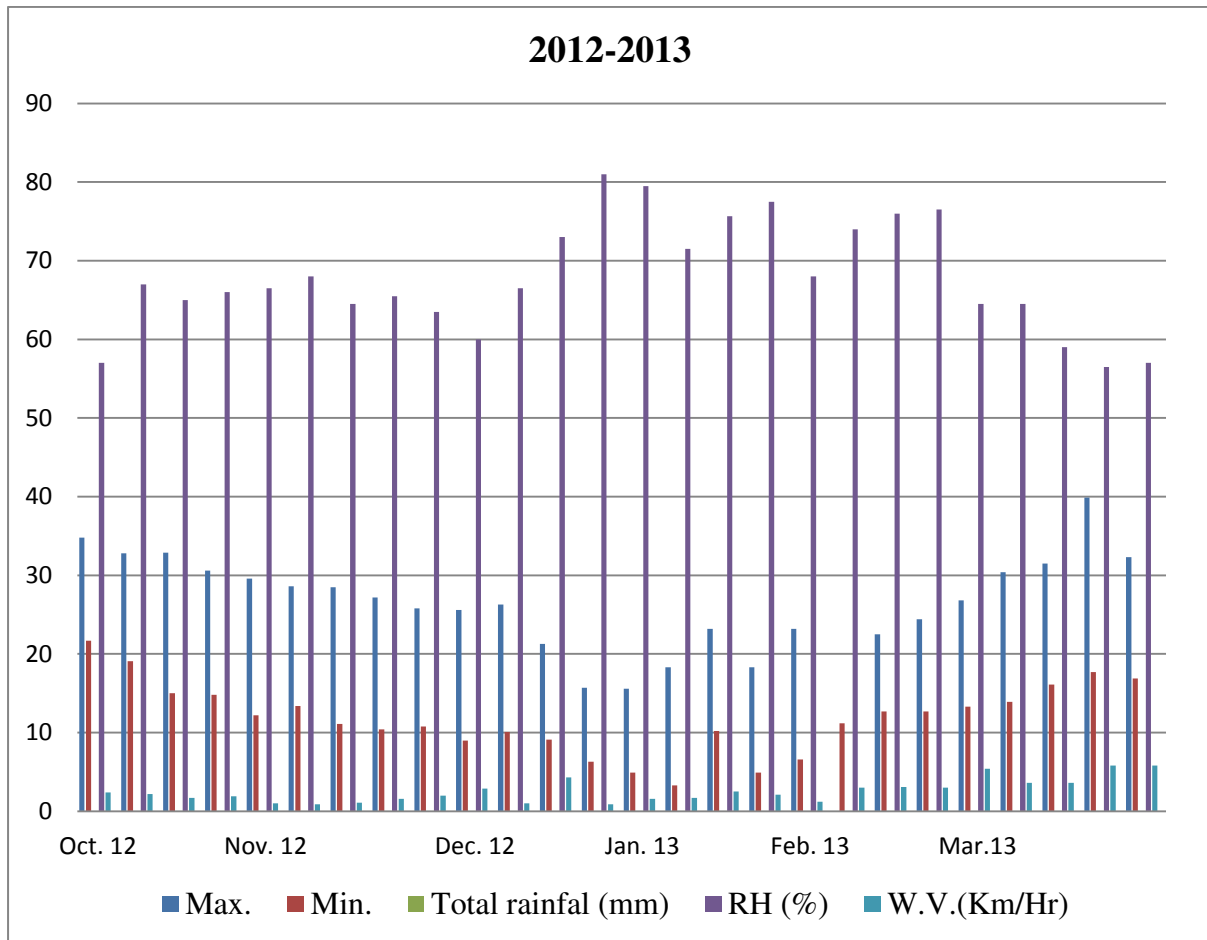
**Source. Indian Institute of Sugarcane Research (IISR), Lucknow, Uttar Pradesh**

**Table-3.2 Monthly average meteorological (weekly data) during the experimentation under Lucknow conditions during the period 2013-2014:**

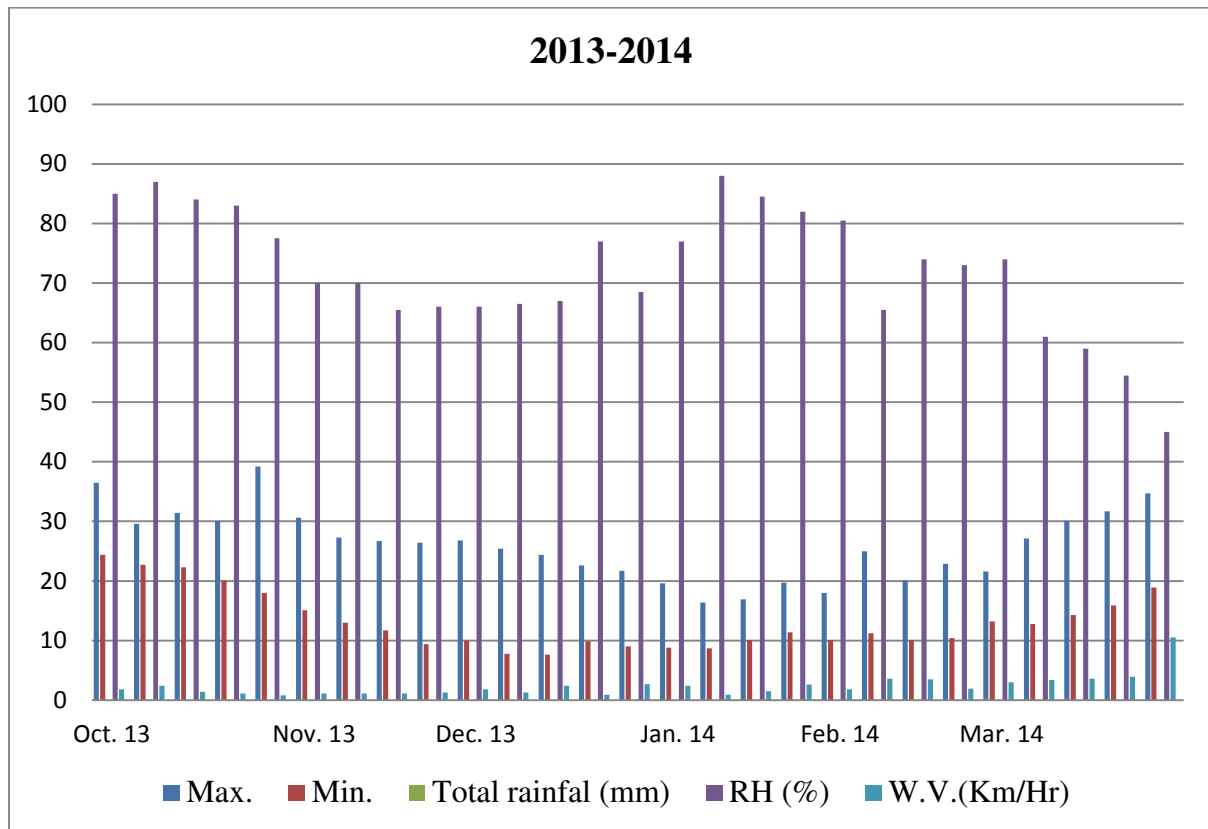
Period		Temperature ( °C)		Total Rainfall (mm)	Relative Humidity (%)	Wind Velocity (Km/hr)
Month	Date	Max.	Min.			
Oct.20 13	25-01	36.5	24.4	0.0	85.00	1.8
	02-08	29.6	22.7	0.0	87.00	2.4
	09-15	31.4	22.3	0.0	84.00	1.4
	15-21	30.1	20.1	0.0	83.00	1.1
Nov.2013	22-28	39.2	18.0	0.0	77.50	0.8
	29-04	30.6	15.1	0.0	70.00	1.1
	05-11	27.3	13.0	0.0	70.00	1.1
	12-18	26.7	11.7	0.0	65.50	1.1
Dec. 2013	19-25	26.4	9.4	0.0	66.00	1.3
	26-02	26.8	9.98	0.0	66.00	1.8
	03-09	25.4	7.8	0.0	66.50	1.3
	10-16	24.4	7.6	0.0	67.00	2.4
Jan. 2014	17-23	22.6	9.9	0.0	77.00	0.9
	24-31	21.7	9.0	0.0	68.50	2.7
	01-07	19.6	8.8	0.0	77.00	2.4
	08-14	16.4	8.7	0.0	88.00	0.9
Feb. 2014	15-21	16.9	10.1	0.0	84.50	1.5
	22-28	19.7	11.4	0.0	82.00	2.6
	29-04	18.0	10.1	0.0	80.50	1.8
	05-11	24.98	11.2	0.0	65.50	3.6
Mar.2014	12-18	20.1	10.1	0.0	74.00	3.5
	19-25	22.9	10.4	0.0	73.00	1.9
	26-04	21.6	13.2	0.0	74.00	3.0
	05-11	27.1	12.8	0.0	61.00	3.4
	12-18	30.06	14.3	0.0	59.00	3.6
	19-25	31.7	15.9	0.0	54.50	3.9
	26-01	34.7	18.9	0.0	45.00	10.5

Source. Indian Institute of Sugarcane Research (IISR), Lucknow, Uttar Pradesh

**Fig-3.1- Monthly average meteorological (weekly data) during the experimentation under Lucknow conditions 2012-2013.**



**Fig-3.2-Monthly average meteorological (weekly data) during the experimentation under Lucknow conditions 2013-2014.**



### **3.2- Materials and methods**

The experimental materials of the present investigations were comprised 25 French bean genotypes (lines) of tropical and subtropical origin. The list of the genotypes (breeding lines) is given in Table (3.3), which were received from Indian Institute of Pulse Research (IIPR), Kanpur, (U.P.) and Vivekananda Parvatiya Krishi Anusandhan Sansthan (VPKAS), Almora, Uttarakhand, India and evaluated at the Horticulture Research Farm first of the Department of Applied Plant Science (Horticulture), Babasaheb Bhimrao Ambedkar University, Vidya Vihar, Rae Bareli Road, Lucknow, (U.P.). Experimental field was laid out in randomized block design with 25 genotypes/lines and replicated thrice, each block into 25 unit plots. The twenty five genotypes were allotted to the 25 unit plots of each block. This, experimental were total 75 plots having to size of each plot 1.80m X 1.00m, and the row-row and plant – plant spacing were 30cm and 20cm, respectively. The plots were raised by 15cm from the ground level to avoid water-logging, if occurred. The plot to plot (1.00m) and block to block (1.80m) distances were 30cm and 1.0m, continue. The each plot divide into six rows and each row contained five plants this, each plot accommodates 30 plants and total plants maintained in cultivated area 2250. Farm yard manure (FYM) 200 q/ha and nitrogen, phosphorus and potash were applied @ 55 kg, 80 kg and 36 kg per hectare, respectively. Nitrogen was applied in to split doses; half at the time of sowing and remaining half at the time of vegetative growth and pod formation of French bean genotypes. Metasystocs was sprayed @ 2g per liter to save the crop from the attake of common mosaic virus. All necessary cultural operations were done as and when required during the experimentation trial.

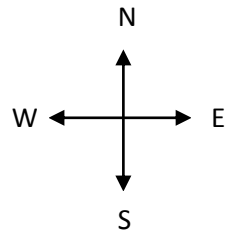
**Table- 3.3 The name of the genotypes, symbols and their source are follows:**

<b>S. No.</b>	<b>Genotypes/ Accessions</b>	<b>Symbol</b>	<b>Source</b>
1	LD-2-1	G1	IIPR, Kanpur
2	EC-400400	G2	IIPR, Kanpur
3	IL-25537	G3	IIPR, Kanpur
4	HURG-15	G4	IIPR, Kanpur
5	EC-400445	G5	IIPR, Kanpur
6	NO. -3127	G6	IIPR, Kanpur
7	IC-14351	G7	IIPR, Kanpur
8	EC-400401	G8	IIPR, Kanpur
9	ET-8415	G9	IIPR, Kanpur
10	PLB-438	G10	IIPR, Kanpur
11	EC-400407	G11	IIPR, Kanpur
12	BSRR-2	G12	IIPR, Kanpur
13	EC-400414	G13	IIPR, Kanpur
14	ET-8435	G14	IIPR, Kanpur
15	ET-8490	G15	IIPR, Kanpur
16	IPR-98-3-1	G16	IIPR, Kanpur
17	EC-400409	G17	IIPR, Kanpur
18	ET-3409	G18	IIPR, Kanpur
19	BLF-101	G19	IIPR, Kanpur
20	PDR-14	G20	IIPR, Kanpur
21	IL-25337	G21	IIPR, Kanpur
22	BD-19162	G22	IIPR, Kanpur
23	GPR-203	G23	IIPR, Kanpur
24	VL Bauni-1	G24	VPKAS, Almora
25	VL Bean-2	G25	VPKAS, Almora

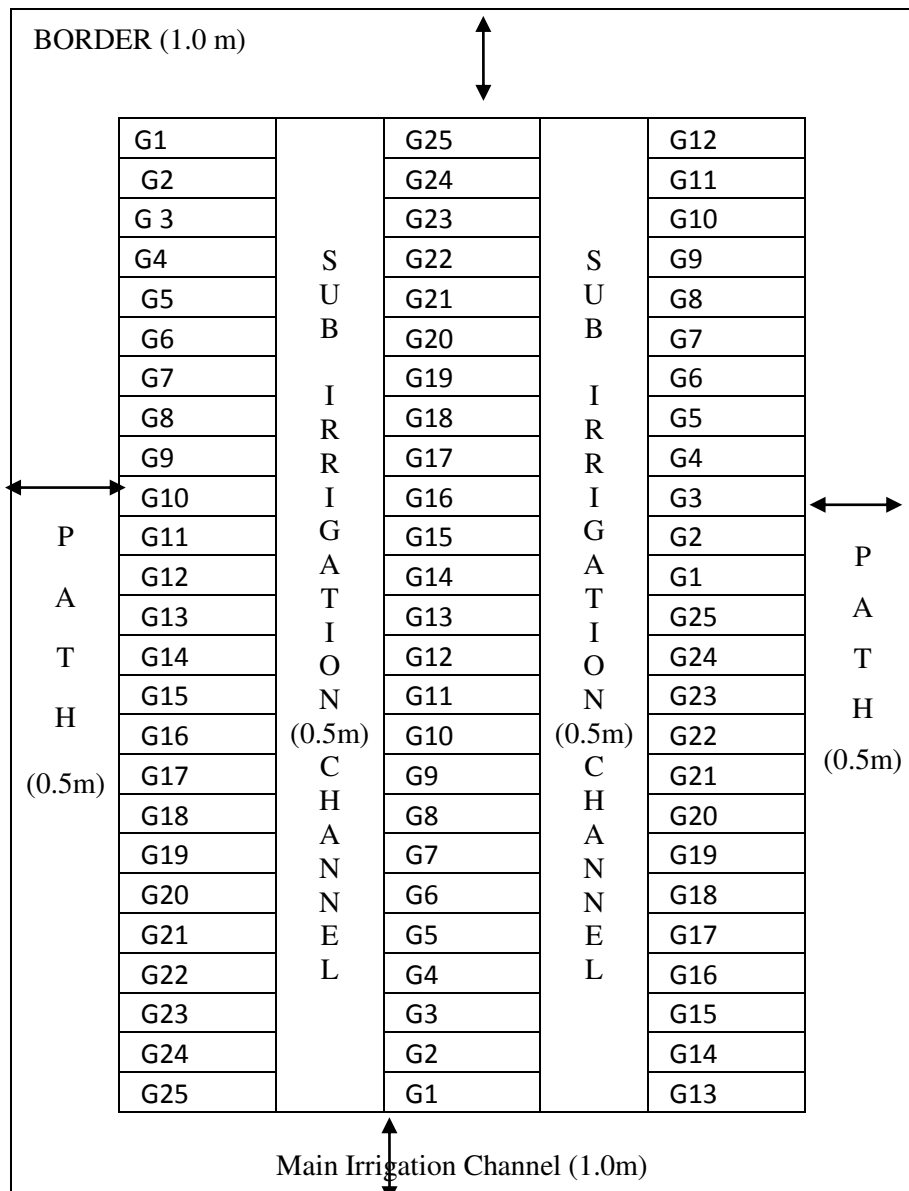
**Table-3. 4 The details of layout plan of the experimental field.**

		-	1. R.B.D.
		-	2. Number of replications-3
(I)	Design	-	3. Number of genotypes-25
		-	4. Number of plots-75
5.	Spacing	-	30 x 20 cm (row to row and plant to plant)
6.	Number of plant /row	-	5
7.	Number of row/plot	-	6
8.	Number of plants/plot	-	30
9.	Number of plants in 75 plots	-	2250
10.	Net plot area	-	1.80m X 1.00 m <sup>2</sup>
11.	Gross plot area	-	2.10m X1.20 m <sup>2</sup>
12.	Block border	-	1.0 m
13.	Field border	-	0.5 m
14.	Width main channel	-	1.0 m
15.	Width of sub-channel	-	0.5 m
16.	Width of bund	-	0.3 m
17.	Total length of block	-	34.80 m
18.	Total width of block	-	9.80 m
19.	Total area of experimental field	-	341.04 m <sup>2</sup>
20.	Date of showing	-	21.10.2012 and 2013
21.	R. D. F.	-	F.Y.M.200q/ha and fertilizers 55 kg N <sub>2</sub> , 80 kg P <sub>2</sub> O <sub>5</sub> and 36 kg K <sub>2</sub> O ha <sup>-1</sup>

The experiment was conducted under randomized block design with three replications. Each genotype was treated as a treatment. Thus, all together 75 plots were prepared to accommodate twenty five genotypes.



### Layout of experiment field



### **3.3-Soil analysis**

Soil sampling on yearly basis before application of fertilizers were done. Analysis of soil samples were taken plot wise for soil texture, PH, electrical conductivity, organic carbon and cation exchange capacity, available N, P, K, Ca, Mg, S and Zn. Before Start of the experiment, the representative soil samples were taken randomly a depth of 15 cm from experimented field and brought to laboratory for physical and chemical analysis. The results of soil analysis have been presented in the soil of field way texturally classified and sandy loam and slightly alkaline soil having organic matter (0.45%) in the soil content. The PH 8.82 and electrical conductivity (0.294) the available N<sub>2</sub>O (kg/ha), 150.23, P<sub>2</sub>O<sub>5</sub> -22.50 and K<sub>2</sub>O 285.60 (Kg/ha). The available secondary fertilizers in ppm/ha in the soil as well as Ca, 15.160, Sulphur, 11.270, Mg, 3.140, Zn, 0.690 in medium form and high form Copper,0.170 and low form Iron, 3.690 in quantity ppm/ha available in the soil.

### **3.4.-Intercultural and irrigation**

A light irrigation was given immediately after germination. As sowing was done in *Rabi* seasons so, there was no need of frequent irrigation. However, irrigation, weeding and hoeing were done as and whenever, required.

### **3.5-Observations recorded:**

Observations were recorded for the following quantitative and qualitative traits on ten plants basis and averages were computed.

#### **Phenotypic characters**

##### **I - Growth attributes**

**3.5.1-Germination (%)** -Ninety seeds in three replications were drawn at random from each treatment and the germination test was conducted using between paper methods as per ISTA procedure (Anon., 1999). The rolled paper towels were placed in a cabinet and seed germination maintained at a constant temperature of at  $25 \pm 10^{\circ}\text{C}$  and 95 per cent relative humidity. The number of normal seedling were counted at end of ninth day and expressed in percentage.

**3.5.2-Plant height (cm)** -The length of the plant from ten randomly selected from tagged plants were manually counted main stem from ground level to the tip of the growing point at 90th day was measured by scale in centimetres (cm).

**3.5.3-Number of leaves/plant-** The total number of leaves from ten randomly selected from tagged plants were manually counted. The mean per plant per leaves were calculated.

**3.5.4-Leaf length (cm)-**The length of ten plants leaves from individual plants measured from basal end to proximal end was averaged and expressed in centimetres (cm).

**3.5.5-Leaf width (cm)-**The width of ten plants leaves from individual plants measured from basal end to proximal end was averaged and expressed in centimetres (cm).

**3.5.6-Primary branches/ plant -**The primary branches of individual ten plants at pod development stage were counted.

**3.5.7-Secondary branches/ plant -**Total number of secondary branches of individual ten plants per plant at pod development stage was taken.

**3.5.8-Days to first flowering-** The number of days taken from the days of germination to opening of first flower.

**3.5.9- Days to 50 per cent flowering-** The number of days taken from the day of germination to opening of 50 per cent flowering.

## **II – Yield and yield attributing traits**

**3.5.10-Number of pods per plant-** The total number of pods from ten randomly selected from tagged plants were manually removed and counted. The mean per plant per pod were calculated.

**3.5.11-Number of seeds/ pod-** The total number of seeds from ten randomly selected pods from tagged plants were manually removed and counted. The mean seeds per pod were calculated.

**3.5.12-Green pod length (cm)-**The length of ten pods from individual plants measured from basal end to proximal end was averaged and expressed by vernier callipers in centimetres (cm).

**3.5.13-Green pod width (cm) -** The maximum width *i.e.* suture to suture end of pods measured using vernier calliper for ten pods was averaged and recorded in centimetres (cm).

**3.5.14-Green pod breadth (cm) -** The maximum breadth of pods measured using vernier calliper for ten pods was averaged and recorded in centimetres (cm).

**3.5.15-Flower colour-** Petal colour of the all the twenty ten genotypes was observed at flowering under natural day light and grouped as pink, purple and white.

**3.5.16- Single green pod weight (g) -** Pod weight were taken for ten pods and averaged and recorded in grams (g).

**3.5.17-Green pod yield per plant (g)** - Total green pod yield of individual ten plant recorded over the successive harvests was summed up and expressed in grams (g) .

$$\text{Average green pod yield/plant} = \frac{\text{Total yield (no. or wt.) of selected plants}}{\text{Number of selected plants}}$$

**3.5.18-Green pod yield per plot (kg.)**-The pods separated from plants each plot were weighed and pod yield per plot is expressed in kilograms by using electronic balance.

$$\text{Green pod yield /plot} = \text{average yield of plant X number of plants in the plot}$$

**3.5.19-Green pod yield (q/ ha)** - Total vegetable pod yield was expressed in per hectare basis from the harvestable pod yield using the following formula.

$$\text{Yield per hectare (q/ha)} = \frac{\text{Yield per plot (kg) X 10,000 (m}^2\text{)}}{\text{Net area of the plot (m}^2\text{)}}$$

**3.5.20-100- Seed weight (g.)**- One hundred seeds in three replications from each treatment were counted and weighed by using electronic balance as per ISTA procedure (Anon., 1999). The average weight was expressed in grammes.

### III- Quality traits (chemical aspects)

**3.5.21-Moisture (%)** – Moisture percent of the harvesting of French bean crop was determined by the method as mentioned by Rangnna (1986). The content of moisture take 2 or 3 gm sample in duplicate in pre-dried and pre-weighed 7cm dia. aluminium dishes. Remove the dish cover and put them in vacuum oven and dry for 6 hours at 70<sup>0</sup>c and 26-28 inch vacuum. During this process, admit to oven a slow current of air (2 bubbleser second) dried by passing H<sub>2</sub>SO<sub>4</sub>. Replace the cover, cool it in dedicator and weigh again.

$$\% \text{ Moisture} = \frac{\text{Loss in weight X100}}{\text{Weight of sample}}$$

**3.5.22-Total sugars (%)** -Total sugars was determined by method as mentioned by Rangnna (1977). Take 10 ml sugar extract and 2ml of HCL (50%) in flask and keep it for 10 minutes at 68<sup>0</sup>c and make volume after hydrolysis of sugars. Neutralized the solution by adding anhydrous Na<sub>2</sub>CO<sub>3</sub> solution. Till the effervescence stops. The method describe under educing sugars should be employed for further estimations.

**Reducing sugars (%)**- Reducing sugars was determined by method as mentioned by Rangnna (1977). Take 5ml/g of juice or pulp or powder (in case of dehydrated product) in a glass tube. Add 5ml of potassium ferricyanide to it. Boil on hot plate for 15 minutes. Then cool under running tape water. Now titrate it against N/100 sodium thiosulphate using starch as indicator. Disappearance of blue colour makes the end point. Simultaneously, run a blank and record the observation.

**Calculation**

mg. sugar/5ml juice or extract = [ ( ml of Na<sub>2</sub> S<sub>2</sub> O<sub>3</sub> used in blank) – ml of Na<sub>2</sub> S<sub>2</sub> O<sub>3</sub> used in sample) + 0.05] X 0.338

**Calculations**

$$\% \text{ Reducing sugars} = \frac{\text{Factor (0.052) X dilution X100}}{\text{Titer X weight of sample}} = \text{X (say)}$$

$$\% \text{ Total sugars} = \frac{\text{Factor X dilution X100}}{\text{Titer X weight of sample}} = \text{Y (say)}$$

$$\begin{aligned} \% \text{ Non- Reducing sugars} &= \text{Total sugars} - \text{Reducing sugars} \\ &= Y - X = Z \end{aligned}$$

**3.5.23-Protein (%)** -The seeds were weighed and powdered. Total nitrogen in powdered sample was determined by employing the method described by Jackson (1973). Percentage of total protein was obtained by multiplying the per cent N by 6.25, the factor.

**Calculation-** calculate percentage of nitrogen (N) as follows:

$$\% N = \frac{\left[ \text{ml HCl used in ml HCl used determination in blank} \right] \times \text{Normality of HCl} \times 14.00 \times 100}{\text{mg sample}}$$

$$\% \text{ Protein} = \% N \times 6.25.$$



**Plate-3.1-General view of experimental field**



**Plate-3.2-An over view of fully germinated genotypes of French bean on the experimental field**

### 3.6 - Statistical analysis:

The experiment data were compiled by taking the mean value for all the 22 characters in all the 25 genotypes in all the three replications. Then it was subjected to the following statistical analysis.

3.6.1 Analysis of variance.

3.6.2 Genetic variability, heritability and genetic advance.

3.6.3 Correlation coefficient.

3.6.4 Path coefficient analysis.

#### 3.6.1- Analysis of variance

The analysis of variance for the design of experiment was done for partitioning the variance into treatments and replications, which was carried out according to the procedure outlined by Panse and Sukhatme (1967). The significance of difference among treatment means was tested by 'F' test. The analysis of variance for Randomized Block Design is given below:

$$Y_{ij} = \mu + t_i + b_j + e_{ij}$$

Where,

$Y_{ij}$  = Yield of  $i^{\text{th}}$  entry in the  $j^{\text{th}}$  replications

$\mu$  = General mean

$t_i$  = Effect of the  $i^{\text{th}}$  entry (  $i=1,2,\dots, v.$ )

$b_j$  = Effect of the  $j^{\text{th}}$  replicate (  $j= 1,2,\dots, r.$ )

$e_{ij}$  = environmental effect

**Table- 3. 5 Analysis of variance**

<b>Source of variation</b>	<b>D. F.</b>	<b>S.S.</b>	<b>M.S.S.</b>	<b>F calculated</b>
Replications	(r-1)	SSr.	MSr	MSr/MSe
Genotypes	(g-1)	SSg	MSg	MSg/MSe
Error	(r-1)(g-1)	SSe	MSe	
Total	(rg-1)	TSS		

Where,

r = Number of replications.

g = Number of genotypes.

MSr = Mean Squares due to replications.

MSg = Mean Squares due to genotypes

MSe = Mean Squares due to error

TSS = Total Sum of Squares

The mean squares due to replication and genotype were divided by corresponding error mean squares and the calculated F value was compared with table value of F at P= 0.05 and P= 0.01, respectively.

$$\text{Grand mean} = \frac{\text{Grand total}}{N}$$

Where,

N = Total number of Treatments x Replications

$$\text{Correction factor} = \frac{(\text{Grand total})^2}{N}$$

Total sum of squares = Sum squares of each treatment-C.F.

$$\text{Treatment sum of squares} = \frac{\text{Sum of treatment squares}}{\text{Replication number}} - \text{C.F.}$$

$$\text{Replication S.S.} = \frac{\text{Sum of replications squares}}{\text{Treatment number (t)}} - \text{C.F.}$$

Error S.S. = Total S.S. – (Treatment S.S. + replication S.S.)

Mean sum of squares were obtained by dividing the sum of squares with the respective degrees of freedom.

$$\text{F. Variance ratio} = \frac{\text{Treatment MS}}{\text{Error MS}}$$

The significance of treatments was tested by 'F' test by comparing the calculated F value with tabulated F value at 5% level of significance for the corresponding degree of freedom. The analysis of variance was set up as follows:

$$\text{Standard Error/plot} = \sqrt{\text{Error MS}}$$

There, F. test was observed to be significant, comparison was further extended by testing difference of any 2 treatments means against critical difference (CD) at 5% level of significance.

The calculation of CD at 5% was carried out with the help of following: formula.

$$\text{CD} = \text{SEd} \pm x \text{ t Value at 5\% error F}$$

Where,

$$\text{CD} = \text{Critical difference.}$$

$$\text{SEd} \pm = \text{Standard error of difference between}$$

two treatment means.

$$\text{S.E. (Treatment means)} = \sqrt{\frac{\text{EMS}}{r}}$$

Coefficient of variation = SED x t values at 5%

$$= \sqrt{\frac{2\text{EMS}}{r}} \times t \text{ 5\% at Error d. f.}$$

### Parameters of variability

#### (i) Mean

The mean value of each character was determined by dividing the total number of corresponding number of observations.

$$\bar{X} = \text{SX}/\text{N}$$

Where,

SX is the summation of the variables

N is the number of observations.

#### (ii) Range

Lowest and highest values for each trait were recorded.

### Estimation of components of variation:

The estimation procedure of variance components requires mating design that result in different types of relatives:

Using appropriate experimental design and Statistical analysis, Variance components calculated, Robinson et al. (1923).

Environmental Variance ( $\sigma^2_e$ )

$$\sigma^2_e = \text{MSe}$$

$$\text{Genotypic Variance } (\sigma^2_g) = \frac{\text{MSg} - \text{MSe}}{r}$$

r

$$\text{Phenotypic Variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

The mean square due to error was subtracted from the mean square due to genotypes and their difference was divided by replications for obtaining the genotypic variance, which was calculated accordingly to the method suggested by Burton (1953).

### Standard error

S.E. of the mean was calculated with the help of error mean square from ANOVA.

$$\begin{aligned} \text{S.E. (Mean)} &= \sqrt{\frac{\sigma_e^2}{r}} \quad \text{or} \\ &= \sqrt{\frac{\text{Variance due to Error}}{\text{Number of replications}}} \end{aligned}$$

### 3.6.2- Phenotypic and genotypic coefficient of variability

Phenotypic and genotypic coefficients of variability were calculated as per the method suggested by Burton and Devane (1953). The same is as follows.

$$\text{Phenotypic coefficient of variation (PCV)} = \sqrt{\frac{\text{Phenotypic variance}}{\bar{X}}} \times 100$$

$$\text{Genotypic coefficient of variation (GCV)} = \sqrt{\frac{\text{Genotypic variance}}{\bar{X}}} \times 100$$

$$\text{ECV} = \sqrt{\frac{\text{Genotypic variance}}{\bar{X}}} \times 100$$

Where  $\bar{X}$  is the mean of character?

### (iii) Heritability

Heritability is the transmissibility of characteristics from parents to offspring. Heritability in a broad sense is the ratio of genotypic variance to total phenotypic variance in percentage.

Heritability in broad sense ( $h^2$ ) was calculated by the following formula suggested by Henson *et al.* (1956).

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2}$$

$$\sigma_p^2$$

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

$$\sigma^2_p$$

Where

$$\sigma^2_g = \text{Genotypic Variance}$$

$$\sigma^2_p = \text{Phenotypic Variance}$$

$$\sigma^2_e = \text{Environmental Variance}$$

**(iv) Genetic advance**

To calculate the expected genetic advances the formula given by Lush (1949) and Johnson *et al.* (1955) was applied.

$$G = \frac{\sigma^2_g}{\sigma^2_{ph}} K \sigma_{ph}$$

$$= h^2 \times K \cdot \sigma_{ph}$$

Where, G = Genetic advance

$h^2$  = heritability in broad

$\sigma_{ph}$  = phenotypic standard deviation

K = Standardized selection differential which is 2.06 at 5% selection intensity (Lush, 1949) in large sample from normally distributed population.

Genetic advance as percent of mean was work out as:

$$GS (\%) = GS$$

Where,

GS = genetic advance

X = grand mean of the character

### 3.6.3 - Estimation of correlation coefficient:

Genotypic and phenotypic correlation coefficients were calculated from variance and covariance components. The calculations were based on the mean values of the characters. The method of computation was given by Panse and Shukhatme (1967).

a) Genotypic correlation coefficient (XY)

$$\frac{\text{Genotypic covariance XY}}{\sqrt{(\text{Genotypic variance X})(\text{Genotypic variance Y})}}$$

$$= \frac{\text{Genotypic covariance XY}}{\sqrt{(\sigma^2_g X)(\sigma^2_g Y)}}$$

b) Phenotypic correlation coefficient XY,  $r = \text{ph}(XY) =$

$$\frac{\text{Phenotypic covariance XY}}{\sqrt{(\sigma^2_{ph X})(\sigma^2_{ph Y})}}$$

the significance of 'r' values was tested at 5% and 1% from 'r' table at (V- 2) degrees of freedom.

Where,

V is number of genotypes on which the observations were recorded.

#### Test of significance of correlation:

For the test the significance of correlation co-efficient the following formula was used:

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

Where,

r = Correlation Coefficient.

n = Number of Observation

The calculated value of 't' was tested against table value of 't' at 5% and 1% level of significance with n-2 degrees of freedom for phenotypic correlation and error d.f.- for environmental correlation.

### 3.6.4 - Path coefficient analysis

Path coefficients were calculated by using the method suggested by Wright (1921) and elaborated by Dewey and Lu (1959) using phenotypic and genotypic correlation coefficient. Different characters were included in the path -coefficient analysis to find out their direct and indirect effects upon French bean yield/ plant. Residual factor was also included in the causal system representing all other factors which might affect the end-products. The correlation 'cause' with effects were calculated by solving the following simultaneous equation.

$$rmp = pmp + rmn pnp + rmo pop \quad (1)$$

$$rnp = rnp pmp + pnp + rno pop \quad (2)$$

$$rop = romp mp + ron pnp + pop \quad (3)$$

Where,

pmp, pnp and pop are direct 'effects' of rmn and on 'cause' p and rmp, pnp, rmo, pop..... are indirect effects on cause. These simultaneous equations were solved by using matrix method and are expressed as:

Here,

A and B vectors are known for calculated C vector, the formula used

$$C = B^{-1} A$$

Here,

$B^{-1}$  is the inverse matrix of B vector.

Residual effect (R) was computed as follows.

$$\text{Residual effect (R)} = 1 - \bar{O}a_2 + b_2 + c_2 + \dots i_2 + 2abr_{12} + 2acr_{13} + \dots$$

The next commencing chapter deals with the findings of the investigation.



**Plate-3.3 View of experimental crop after 20 days of sowing**



**Plate-3.4 View of experiment crop after a month days of germination**

# EXPERIMENTAL FINDINGS Chapter- IV

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The present investigation was carried out with 25 genotypes of French bean (*Phaseolus vulgaris* L.), at Horticulture Research Farm first of the Department of Applied Plant Science (Horticulture), Babasaheb Bhimrao Ambedkar Central University, Vidya Vihar, Rae Bareilly Road Lucknow (U. P.), India during *Rabi* seasons 2012-2013 and 2013-2014, respectively. A view to find out the extent of genetic advance, degree of association, relative importance of various metric traits upon vegetable pod yield. The productivity of French bean is very low due to non-availability of high yielding varieties with good plant types and resistance to diseases also, it is a major hindrance to the breeders for further research. An attempt was made to identify such varieties, having high yields with good plant types and resistance to diseases. The results obtained from the investigations on quantitative and qualitative characters related to yield and yield contributing characters and disease resistance are presented in the following sub headings.

## **4.1 Studies on economic traits:**

4.1.1 Analysis of variance and component of variance

4.1.2 Mean performance of genotypes

4.1.3 Genetic variability, heritability and expected genetic advance in percent of mean

4.1.4 Phenotypic and genotypic correlation coefficient

4.1.5 Path coefficient analysis

### **4.1.1 Analysis of variance and component of variance for the twenty two economic traits:**

The analysis of variance was carried out for 22 traits germination (%), plant height (cm), primary branches/ plant, secondary branches/ plant, number of leaves /Plant, size of leaves length and width (cm), days to first flowering, days to 50 percent flowering, number of pods/ plant, number of seeds/ pod, green pod length (cm), green pod width (cm), green pod breadth (cm), single green pod weight (g), green pod yield per plant (g), green pod yield per plot (kg), green pod yield (q/ ha), 100- seed weight (g), moisture(%), total sugars(%) and protein(%) the analysis of variance is depicted in Table(4. 6 and 4.7). The mean sum of square due to treatment was highly significant for all the characters under study. The data recorded on 180<sup>th</sup> days at the crop harvest stage for different characters from the experiments

carried out of in 2012-2013 and 2013-2014 was subjected to analysis of variance to test the significance of different among 25 genotypes of French bean for different characters is present in Table (4.6 and 4. 7) . The differences due to genotypes were highly significant for all the characters under study. However the differences due to replications were not significant. Mean of yield and its component traits for 25 genotypes has also been given in Table (4.6 and 4. 7).

#### **4.1.2- Mean performance:**

The mean, range, coefficient of variance, standard error and critical difference of variability for 19 morphological and 3 quality characters were discussed in Table (4.8 and 4.9). A wide range of variation was observed for almost all the traits in the material studied. The best lines with respect to morphological and quality attributes have shown in plates.

**4.1.2.1-Germination (%)** - The germination percent with grand mean of  $88.60 \pm 2.76$ , ranged from 70.15 % in VL Bean-2 to 100.00% in ET-3409.

**4.1.2.2- Plant height (cm)** - The treatment mean for plant height range from 34.62 to 129.16 with minimum in genotype IL-25537 and maximum in genotype ET-3409. The grand mean  $50.16 \pm 2.07$ .

**4.1.2.3-Number of leaves/plant**-The treatment mean for the number of leaves/plant ranged from 42.13 to 87.11 with minimum number of leaves/plant in genotype BD-19162 followed by LD-2-1 (45.32), No.- 3127 (45.67), VL Bean-2 (45.95), ET-8435 (46.06) and IPR-98-3-1 (46.48). The genotype ET-3409 (87.11) showed maximum number of leave/plant with grand mean  $53.52 \pm 2.19$ .

**4.1.2.4-Leaf length (cm)**-The maximum leaf length was recorded in genotype PLB-438 (12.86) and minimum in genotype VL Bean-2 (7.38) with grand mean  $10.69 \pm 0.6177$ .

**4.1.2.5-Leaf width (cm)**- the maximum and minimum leaf width was observed in genotypes No. 3127 (12.53) and genotype VL Bauni-1(5.02), respectively with grand mean  $9.86 \pm 0.6610$ .

**4.1.2.6-Primary branches/plant**-The treatment mean for primary branches/plant ranged from 2.57 to 5.11 with minimum primary branches/plant in genotype LD-2-1 (2.57) followed by IL-25537 (2.73), EC-400400 (2.77), EC-400407(3.12) and VL Bean-2 (3.44). The genotype ET-3409 (5.11) showed maximum primary branches/plant with grand mean  $3.86 \pm 0.2793$ .

**4.1.2.7-Secondary branches /plant-**The maximum secondary branches /plant was recorded in genotype ET-8490 (9.58) followed by ET- 3409 (9.56). The genotype LD-2-1 (4.24) showed minimum secondary branches /plant with grand mean  $7.24 \pm 0.3770$ .

**4.1.2.8-Days to first flowering-**The maximum and minimum days to first flowering was observed in genotypes VL Bean-2 (43.50) and ET-8435 (30.33), respectively with grand mean  $36.84 \pm 0.9840$ .

**4.1.2.9-Days to 50% flowering -** The maximum days to 50% flowering was recorded in genotype VL Bean-2 (48.50) and minimum days to 50% flowering ET-8435 (36.00), with grand mean  $41.79 \pm 1.010$ .

**4.1.2.10-Number of pods /plant-**The maximum and minimum number of pods /plant was recorded in genotype ET- 3409 (30.22) and LD-2-1 (10.46), with grand mean  $20.96 \pm 0.7289$  respectively.

**Table-4.6 Analysis of variance for different morphological characters in French bean.**

Source of Variance	D.F	Germination (%)	Plant height (cm)	Number of leaves/plant	Leaf length (cm)	Leaf width (cm)	Primary branches /plant	Secondary branches/plant	Days to first flowering	Days to 50% flowering	Number of pods /plant	Green pod length (cm)
Replication	2	14.875	49.203	3.203	1.032	0.4511	1.144	0.9101	6.445	6.203	10.332	3.311
Treatment	24	340.743**	2495.201**	604.588**	15.390**	18.074**	2.130**	14.511**	91.582**	58.045**	138.91**	16.111**
Error	48	22.975	12.977	14.517	1.144	1.310	0.2340	0.4273	2.909	3.116	1.593	0.6772

\*, \*\* significant at 0.05% and 0.01% level, respectively.

**Table -4.7 Analysis of variance for different yield and quality traits in French bean.**

Source of Variance	D.F	Green pod width (cm)	Green pod breadth (cm)	Single green pod weight (g)	Green pod yield /plant (g)	Green pod yield /plot (kg)	Number of seeds /pod	100-seed weight (g)	Green pod yield (q/ha)	Moisture (%)	Total sugars (%)	Protein (%)
Replication	2	0.00298	0.0184	0.7373	133.312	0.2244	0.7630	3.6562	848.2500	2.4589	0.6230	4.1250
Treatment	24	0.0878**	0.03019**	2.8679**	3885.71**	3.1988**	1.452**	1154.38**	10796.60**	4.8368**	4.4465**	110.433**
Error	48	0.005134	0.007915	0.2646	62.777	0.1214	0.2549	1.0122	156.476	0.5598	0.3409	1.2108

\*, \*\* significant at 0.05% and 0.01% level, respectively.

**4.1.2.11-Green pod length (cm)**-The treatment mean for green pod length ranged from 8.33 to 13.76 with minimum green pod length LD-2-1 (8.33) followed by VL Bean-2 (9.04), BD-19162(9.12), HURG-15(9.30), IL-25337 (9.31) and GPR-203(9.44). The genotype ET-8415 (13.76) showed maximum green pod length with grand mean  $11.14 \pm 0.4751$ .

**4.1.2.12-Green pod width (cm)**-The maximum green pod width was recorded in genotype EC-400401 (0.95) and minimum in genotype VL Bauni-1(0.49) with grand mean  $0.68 \pm 0.0413$ .

**4.1.2.13-Green pod breath (cm)**-The treatment mean for green pod breath ranged from (0.83 to 1.10) with minimum green pod breath in genotype ET-8415 (0.83) followed by VL Bauni -1(0.84), PDR-14 (0.88), EC400401 (0.88), IC-14351 (0.88). The genotype green pod breath (1.10) showed maximum green pod breath with grand mean  $0.96 \pm 0.0513$ .

**4.1.2.14-Single green pod weight (g)**-The maximum and minimum single green pod weight was recorded in genotype PLB-438 (7.94) and genotype VL Bauni-1(4.56), respectively with grand mean  $6.21 \pm 0.2970$ .

**4.1.2.15-Green pod yield/plant (g)**-The maximum green pod yield/plant was recorded in genotype ET-3409 (149.11) and minimum in genotype LD-2-1 (55.06) followed by EC-400445 (62.03) with grand mean  $92.37 \pm 0.457$ .

**4.1.2.16-Green pod yield/plot (kg)**-The maximum green pod yield/plot was recorded in genotype ET-3409 (4.51) followed by ET-8490 (3.95) and minimum in genotype LD-2-1 (1.66) followed by IL-25537 (1.92) and EC-400445(1.92) with grand mean  $2.77 \pm 0.2010$ .

**4.1.2.17-Number of seeds/pod**-The treatment mean for no. of seeds/pod ranged from (3.64 to 5.96) with minimum number of seeds/pod in genotype LD-2-1 (3.64) followed by VL Bean-2(4.09), GPR-203 (4.17) and BD-19162 (4.38). The genotype EC-400401(5.96) showed maximum number of seeds/pod with grand mean  $4.81 \pm 0.2910$ .

**4.1.2.18-100-seed weight (g)**-The maximum and minimum 100-seed weight was recorded in genotype ET-8490(60.28) and genotype ET-8415 (12.49), respectively with grand mean  $32.26 \pm 0.05808$ .

**4.1.2.19-Green pod yield (q/ha)**-The treatment mean for green pod yield ranged from (91.73 to 248.51) with minimum green pod yield LD-2-1 (91.73) followed by EC-400445 (102.99), IL-25537 (103.31), VL Bean-2(107.80), IC-14351 (110.20) and VL Bauni-1(110.23). The genotype ET-3409 (248.51) showed maximum green pod yield with grand mean  $153.69 \pm 7.220$ .

**4.1.2.20-Moisture (%)**-The maximum moisture was recorded in genotype EC-400414 (12.92) followed by HURG-15 (12.73) and minimum in genotype VL Bean-2(9.53) followed by VL Bauni-1 (9.55) with grand mean  $11.08 \pm 0.04320$ .

**4.1.2.21-Total sugars (%)**-The maximum and minimum total sugars was observed in genotype EC-400401(8.99) and genotype LD-2-1 (5.13), respectively with grand mean  $7.02 \pm 0.3370$ .

**4.1.2.22-Protein (%)**-The treatment mean for protein ranged from (17.15 to 30.53) with minimum protein in genotype IL-25537(17.15) followed by EC-400445(18.17), LD-2-1 (18.74) and HURG-15(18.74). the genotype EC-400414 (30.53) showed maximum protein with grand mean  $23.35 \pm 0.6353$ .

### **4.1.3-Genetic variability, heritability and expected genetic advance in percent of mean**

**4.1.3.1- Range**- The material showed wide range of variability for green pod yield per plant (91.73-248.51 q/ha), green pod yield per plant (55.06-149.11g), plant height (34.62-129.16cm), germination percent (70.15-100), number of leaves/plant (42.13-87.11) and 100-seed weight (12.49-60.28).

**4.1.3.2-PCV** –The genotypic and phenotypic coefficient of variation (GCV and PCV) for 19 investigated horticultural traits and 3 quality characters revealed that all the horticultural parameters had significant range of genotypic and phenotypic coefficient of variation Table (4.10). In morphological, yield and quality characters, the highest phenotypic coefficients of variation was observed for 100-seed weight (43.10) followed by plant height (41.21), green pod yield /plot (28.95), green pod yield/plant (28.85), green pod yield (28.77), number of pods/plant (23.72), secondary branches/plant (23.29), leaf width (20.78), green pod width (20.64) and number of leaves/plant (20.05) and lowest for days to 50% flowering (8.54) followed by germination percent (10.03) and moisture percent (10.32).

**4.1.3.3-GCV**- The genotypic coefficient for days to 50% flowering (7.42) followed by germination percent (8.44) were the minimum, while it was observed to be the highest for 100-seed weight (42.99) followed by plant height (40.58), green pod yield (27.60), green pod yield/plant (27.55), green pod yield/plot (26.08) and number of pods/plant (22.94) in morphological and quality characters. It was manifested from the data that the phenotypic

Coefficients of variation for all the traits (morphological, yield and quality characters) was higher than the corresponding genotypic coefficient variation.

#### **4.1.3.4 -Heritability and genetic advance**

Heritability estimates for morphological, yield and quality characters. Heritability estimates give a measure of transmission of characters from one generation to another, thus given an idea of heritable portion of variability and enabling to the plant breeder in isolating the elite selection in the crop. Heritability and genetic advance increase the efficiency of the selection in breeding programme by assessing the influence of environmental factors and additive gene action. Heritability estimates for morphological, yield and quality characters range from (38.50%) for green pod breath (cm) to (99.50%) for 100-seed weight. Heritability estimates for all the characters were high except 100-seed weight (99.50), plant height (97.00), number of pods/plant (93.60), protein percent (93.60), green pod yield (92.00) and green pod yield/plant (91.20) and lowest heritability green pod breath (38.50) followed by number of seeds/pod (47.80) Table 10. The magnitude of heritable variability is the most important aspect of genetic constitution of the genetic material which has close bearing on the response to selection of crop. Heritability along with genetic gain is more useful criterion in predicting the resultant effect for selecting the best individual character. High heritability with high genetic advance was observed for 100-seed weight (g), green pod yield (q/ha), green pod yield/plant (g), plant height (cm) and number of leaves/plant. High heritability with high genetic advance tells that the character is governed by the additive gene action and for this simple selection is advocated. High heritability with medium genetic advance suggests that the character is governed by the dominant and epistatic gene action and for this hybridization is done. Characters like days taken to first flowering and days taken to 50 % flowering were found with high heritability and medium genetic advance. The estimates for heritability in broad sense for different characters are presented in Table (4.10) respectively.

#### **4.1.3.5- Expected genetic advance**

Expected genetic advance and genetic gain for morphological, yield and quality characters. Genetic advance at 5% selection intensity and its estimates as percentage of mean for various morphological, yield and quality characters were calculated and present in Table (4.10). The data recorded revealed maximum genetic advance was observed for green pod yield (83.82 q/ha) with 54.53 percent advance followed by green pod yield/plant, plant height and 100-

seed weight and less the mean and minimum for green pod breath (0.09) with 9.37 percent genetic advance followed by green pod width, primary branches/plant and single green pod weight over the mean Table (4.10) Fig. 4. 23.

#### **4.1.4- Correlation coefficient**

Phenotypic and genotypic correlation between yield and various yield and yield contributing characters as well as correlation among quality characters were estimated and phenotypic morphological and quality results are presented Table (4.12 and 4.16). In general, the results revealed that the estimates of genotypic correlation coefficients are higher than the phenotypic correlation for almost all characters under investigations. The results obtained from the Phenotypic and genotypic correlation are presented characters wise here as under.

#### **Morphological characters**

##### **Phenotypic correlation coefficients**

**4.1.4.1-Germination (%)**-The germination percent had a positive and highly significant association with leaf length (0.358), leaf width (0.379), number of pods/plant (0.383), green pod width (0.462), and single green pod weight (0.360), but non-significant association with plant height (0.288), number of leaves/plant (0.274), primary branches/plant (0.145), secondary branches/plant (0.308), green pod length (0.186), green pod breath (0.184), green pod yield/plant (0.279), green pod yield/plot (0.261), number of seeds/pod (0.277), 100-seed weight (0.192) and green pod yield (0.268) while its association was negative and non-significant with days to first flowering (-0.365) and days to 50% flowering (-0.465).

**4.1.4.2-Plant height (cm)**- Plant height had a positive and highly significant association with germination (0.288), number of leaves/plant (0.720), primary branches/plant (0.368), green pod yield/plant (0.511), secondary branches/plant (0.419), number of pods/plant (0.631), green pod yield/plot (0.538), green pod yield (0.514), but plant height had a negative and non-significant association with days to 50% flowering (-0.030) and number of seeds/pod (-0.102), while its association was positive and non-significant leaf length (0.109), leaf width (0.171), days to first flowering (0.137), green pod length (0.190), green pod width (0.107) and green pod breath (0.102).

**4.1.4.3-Number of leaves/plant-**This trait expressed positive and highly significant association with plant height (0.720), number of pods/plant (0.531) and green pod width (0.308), while its association was positive and non-significant germination (0.274), leaf length (0.229), primary branches/plant (0.353), secondary branches/plant (0.250), green pod length (0.299), green pod yield/plant (0.256) and green pod yield (0.256).

**4.1.4.4-Leaf length (cm)-** This trait expressed positive and highly significant association with leaf width (0.480), number of pods/plant (0.413) and green pod length (0.460), while its association was positive and non-significant germination (0.358), number of leaves/plant (0.229), primary branches/plant (0.257), secondary branches/plant (0.335), green pod width (0.371), single green pod weight (0.337), green pod yield/plant (0.235), green pod yield/plot (0.251), number of seeds/pod (0.327), 100-seed weight (0.224) and green pod yield (0.226).

**4.1.4.5-Leaf width (cm)-** A positive and highly significant association was expressed by leaf width with germination (0.379), leaf length (0.480), secondary branches/plant (0.489), number of pods/plant (0.412), green pod length (0.482), while its association was negative and non-significant with days to first flowering (-0.172) and days to 50% flowering (-0.171).

**4.1.4.6-Primary branches/plant-** This trait expressed positive and highly significant association with plant height (0.386), number of leaves/plant (0.353), leaf length (0.257), number of pods/plant (0.440), green pod yield/plant (0.418), green pod yield/plot (0.388), green pod yield (0.416), while its association was negative and non-significant with green pod breath (-0.028).

**4.1.4.7-Secondary branches /plant-** This trait expressed positive and highly significant association with plant height (0.419), leaf width (0.489), number of pods/plant (0.690), green pod yield/plant (0.642), green pod yield/plot (0.607), 100-seed weight (0.535) and green pod yield (0.641), while its association was positive and non-significant with germination (0.308), leaf length (0.335), primary branches/plant (0.315), green pod length (0.338), green pod width (0.212), green pod breath (0.228), single green pod weight (0.287) and number of seeds/pod (0.232).

**4.1.4.8-Days to first flowering-** This trait exhibited positive and highly significant association with days to 50% flowering (0.849), while its association was negative and non-significant with germination (-0.365), green pod width (-0.307), green pod breath (-0.230),

single green pod weight (-0.208), number of seeds/pod (-0.203) and 100-seed weight (-0.117).

**4.1.4.9-Days to 50% flowering** -- This trait showed negative and non- significant association with all traits., germination (-0.465), leaf length (-0.320), number of pods/plant (-0.134), green pod length (-0.057), green pod width (-0.393), green pod breath (-0.305), single green pod weight (-0.246) green pod yield/plant (-0.263), green pod yield/plot (-0.219), number of seeds/pod (-0.300), 100-seed weight (-0.140) and green pod yield (-0.248). This trait expressed positive and highly significant association with days to first flowering (0.849).

**4.1.4.10-Number of pods /plant-** A positive and highly significant association was expressed by number of pods/plant with germination (0.383), plant height (0.631), number of leaves/plant (0.531), leaf length (0.413), leaf width (0.412), primary branches/plant (0.440), secondary branches/plant 90.690), green pod length (0.515), green pod yield/plant (0.611), green pod yield/plot (0.583) and green pod yield (0.612).

**4.1.4.11-Green pod length (cm)-** A positive and highly significant association was expressed by green pod length with leaf length (0.460), leaf width (0.482), and number of pods/plant (0.515). Green pod length showed positive and non- significant association with all traits, green pod width (0.321), green pod breath (0.055), single green pod weight (0.230), green pod yield/plant (0.110), green pod yield/plot (0.107), number of seeds/pod (0.273), 100-seed weight (0.162) and green pod yield (0.105).

**4.1.4.12-Green pod width (cm)-** Green pod width showed positive and non- significant association with all traits., green pod breath (0.056), green pod yield/plant (0.081), green pod yield/plot (0.069), number of seeds/pod (0.302), 100-seed weight (0.112) and green pod yield (0.101), while its association was positive and significant with germination (0.462), number leaves/plant (0.388), leaf length (0.371), leaf width (0.348), number of pods/plant (0.309), green pod length (0.321) and single green pod weight (0.418).

**4.1.4.13-Green pod breath (cm)-** Green pod breath had a showed negative and non- significant association with days to first flowering (-0.230), days to 50% flowering (-0.305) and number of seeds/pod (-0.029), while its association was positive and significant with single green pod weight (0.153), green pod yield/plant (0.181), green pod yield/plot (0.225), 100-seed weight (0.239) and green pod yield(0.180).

**4.1.4.14-Single green pod weight (g)**- Single green pod weight showed positive and non-significant association with all traits., germination (0.360), leaf length (0.337), leaf width (0.299), secondary branches/plant (0.287), number of pods/plant (0.272), green pod width (0.418), green pod yield/plant (0.079), green pod yield/plot (0.069), number of seeds/pod (0.026), 100-seed weight (0.168) and green pod yield(0.096).

**4.1.4.15-Green pod yield/plant (g)**-Green pod yield/plant showed positive and highly significant association with plant height (0.511), primary branches/plant (0.418), secondary branches/plant (0.642), number of pods/plant (0.611), green pod yield/plot (0.926), 100-seed weight (0.643) and green pod yield(0.976), while its association was positive and non-significant with germination (0.279), number of leaves/plant (0.256), leaf length (0.235), leaf width (0.251) and number of seeds/pod (0.138) respectively.

**4.1.4.16-Green pod yield/plot (kg)**-A positive and highly significant association was observed by 100-seed weight with plant height (0.538), primary branches/plant (0.388), secondary branches/plant (0.607), number of pods/plant (0.583), green pod yield/plant (0.623) and green pod yield/plot (0.927), while its association was positive and non-significant with germination (0.261), number leaves/plant (0.260), leaf length (0.251), leaf width(0.292) and number of seeds/pod (0.087).

**4.1.4.17-Number of seeds/pod**-These trait showed positive and non-significant association was observed by 100-seed weight with germination (0.277), leaf length (0.327), number of pods/plant (0.270), green pod length (0.273), green pod width (0.302), green pod yield/plant (0.097) and (0.134).

**4.1.4.18-100-seed weight (g)** -This trait indicated positive and highly significant association with leaf width (0.336), secondary branches/plant (0.535), number of pods/plant (0.387), green pod yield/plant (0.643), green pod yield/plot (0.623) and green pod yield (0.644).

**4.1.4.19-Green pod yield (q/ha)** - This trait indicated positive and highly significant association with germination (0.268), plant height (0.514), number of leaves/plant (0.256), leaf length (0.226), primary branches/plant (0.416), secondary branches/plant (0.641), number of pods/plant (0.612), green pod yield/plant (0.976), green pod yield/plot (0.927) and 100- seed weight (0.644).

## **Biochemical aspects**

**4.1.4.1-Moisture (%)**-This trait exhibited positive and non- significant association with total sugars (0.100), Protein (0.298) and green pod yield (0.208).

**4.1.4.2-Total sugars (%)**-This trait showed that the total sugars revealed it negative and non-significant association with Protein (-0.060), while its association was positive and non-significant with moisture (0.100) and green pod yield (0.270).

**4.1.4.3-Protein (%)**-This trait highly significant and positive association with moisture (0.298) and green pod yield (0.477). This trait showed that the total sugars revealed it negative and non- significant association with total sugars (-0.060).

### **4.4.2.1 -Genotypic correlation coefficient**

Genotypic correlation coefficient for morphological and quality characters:

A perusal of data on morphological genotypic correlation coefficient result presented in Table (4.11) and quality genotypic correlation coefficient result given in Table (4.15). Exhibited highest positive genotypic correlation between green pod yield and green pod yield/plot (1.002). yield manifested a highly significant and positive association with germination percent (0.313), plant height (0.544), number of leaves/plant (0.290), leaf length (0.277), leaf width (0.334), primary branches/plant (0.561), secondary branches/plant (0.747), number of pods/plant (0.661) and green pod yield/plant(1.000). 100-seed weight had a highly significant and positive correlation secondary branches/plant (0.586), number of pods/plant (0.401), green pod breath (0.403), green pod yield/plant (0.674) and green pod yield/plot (0.688), while its association was negative and non-significant with number of leaves/plant (-0.195), no. of seeds/pod had strong association with germination percent (0.401), leaf length (0.501), leaf width (0.353), secondary branches/plant (0.381), number of pods/plant (0.410), green pod length(0.463 )and green pod width (0.524). Number of seeds/pod had strong positive significant association with germination percent (0.401), leaf length (0.510), leaf width (0.353), secondary branches/plant (0.381), number of pods/plant (0.410), green pod length (0.463) and green pod width (0.524). Green pod yield/plot had strong positive significant association with plant height (0.593), leaf width (0.367), primary branches/plant (0.591), secondary branches/plant (0.747), number of pods/plant (0.675) and Green pod yield/plant (1.001). Green pod yield/plant had a highly strong positive significant association with plant

height (0.543), primary branches/plant (0.560), secondary branches/plant (0.747), and number of pods/plant (0.661). A positive and significant association was observed for single green pod weight with germination percent (0.417), leaf length (0.587), leaf width (0.424), and green pod width (0.610). A positive and significant association was observed for green pod width with germination percent (0.586), number of leaves/plant (0.486), leaf length (0.587), leaf width (0.502), and green pod length (0.447). A positive and significant association was observed for green pod length with number of leaves/plant (0.397), leaf length (0.608), leaf width (0.595), secondary branches/plant (0.408), and number of pods/plant (0.594). A positive and significant association was observed for no. of pods/plant with germination percent (0.433), plant height (0.658), number of leaves/plant (0.589), leaf length (0.496) leaf width (0.519), primary branches/plant (0.593) and secondary branches/plant (0.810), A positive and significant association was observed for secondary branches/plant with germination percent (0.434), plant height (0.461), leaf length(0.498) leaf width (0.633) and primary branches/plant (0.467). A positive and significant association was observed for primary branches/plant with plant height (0.482), number of leaves/plant (0.437) and leaf length (0.447). A positive and significant association was observed for leaf width with germination percent (0.581) and leaf length (0.660). A positive and significant association was observed for leaf length with germination percent (0.574) and number of leaves/plant (0.326). A positive and significant association was observed for number of leaves/plant with germination percent (0.367) and plant height (0.778).

**4.4.2.2- Quality traits:** A positive and significant association with green pod yield with moisture percent (0.286), total sugars (0.309) and protein (0.505). A positive and significant association with protein with moisture (0.392).A positive and significant association with total sugars with moisture (0.242).

#### **4.1.5.-Path analysis**

In case of path coefficient analysis, green pod yield were considered as the dependent variables for morphological and quality characters, respectively while remaining 19 morphological and three quality characters were considered as independent varieties. For morphological characters, the phenotypic and genotypic path analysis representing the direct and indirect effects of different characters has been presented in Table (4.13and 4.14) and quality characters Table (4.17and 4.18) respectively.

## **Morphological characters**

### **Phenotypic path coefficient**

**4.1.5.1-Germination (%)** -Germination percent showed negative direct effect (-0.015) upon yield and indirect negative effects through number of leaves/plant (-0.007), leaf length (-0.022), days to 50% flowering (-0.031) and green pod length (-0.001). Phenotypic correlation of this traits with green pod yield was positive and high (0.268).

**4.1.5.2-Plant height (cm)**-This characters expressed allow positive direct upon yield (0.017) and indirect negative effects were positive through primary branches/plant (0.003) and secondary branches/plant (0.013). This character exhibited low indirect effects via number of leaves/plant (-0.017). Phenotypic correlation of this trait with green pod yield was positive and high significant (0.514).

**4.1.5.3-Number of leaves/plant-** The direct contribution of number of leaves/plant on yield was negative and low (-0.024) together with positive indirect effects through secondary branches/plant (0.008), primary branches/plant (0.003), number of pods/plant (0.013), green pod width (0.019), single green pod weight (0.002), green pod yield/plant (0.201) and green pod yield/plot (0.049). The positive direct effect resulting in positive phenotypic correlation with yield (0.256). While it exhibited allow negative indirect effects through leaf length (-0.001), leaf width (-0.008), days to first flowering (-0.005), days to 50% flowering (-0.005), green pod length (-0.001) and 100-seed weight (-0.001).

**4.1.5.4-Leaf length (cm)** - The leaf length showed negative direct effects (-0.005) upon yield and indirect negative effects through number of leaves/plant (-0.005), days to 50% flowering (-0.021), leaf width (-0.028), green pod length (-0.002) and germination percent (-0.005). Phenotypic correlation of this trait with green pod yield was positive and significant (0.226).

**4.1.5.5-Leaf width (cm)** – The leaf width showed negative direct effects (-0.057) upon yield and indirect negative effects through germination percent (-0.006), number of leaves/plant (-0.003), days to 50% flowering (-0.011) and green pod length (-0.002). Phenotypic correlation of this trait with green pod yield was positive and significant (0.223).

**4.1.5.6-Primary branches/plant-** Primary branches/plant showed positive direct effects (0.008) upon yield and indirect negative effects through germination percent (-0.002), number of leaves/plant (-0.008), leaf length (-0.001), leaf width (-0.001), days to 50% flowering (-0.006) and green pod length (-0.001). Phenotypic correlation of this trait with green pod yield was positive and significant (0.416).

**4.1.5.7-Secondary branches /plant-** Secondary branches/plant showed positive direct effects (0.032) upon yield and indirect positive highly significant effects through green pod yield/plant (0.504). Phenotypic correlation of this trait with green pod yield was positive and highly significant (0.641).

**4.1.5.8-Days to first flowering-** Days to first flowering showed negative direct effects (-0.062) upon yield and indirect negative effects through number of leaves/plant (-0.002), secondary branches/plant (-0.003), green pod yield/plant (-0.008) and 100-seed weight (-0.001). Phenotypic correlation of this trait with green pod yield was negative (-0.080).

**4.1.5.9-Days to 50% flowering-** Days to 50% flowering showed positive direct effects (0.066) upon yield and indirect positive highly significant effects through germination percent (0.007), number of leaves/plant (0.002), leaf length (0.002), leaf width (0.010), green pod breath (0.001). While it showed a negative indirect effect via plant height (-0.001), secondary branches/plant (-0.008), days to first flowering (-0.052), number of pods/plant (-0.003), green pod width (-0.019), single green pod weight (-0.003), green pod yield/plant (-0.207), green pod yield/plot (-0.041) and 100-seed weight (-0.001). Phenotypic correlation of this trait with green pod yield was negative and significant (-0.248).

**4.1.5.10-Number of pods /plant-** The number of pods/plant exhibited a low positive direct effect on yield (0.024) coupled with green pod width (0.015), plant height (0.011), primary branches/plant (0.003), secondary branches/plant (0.022) and highly significant green pod yield/plant (0.479). While it showed a negative indirect effect via germination percent (-0.006), number of leaves/plant (-0.013), leaf length (-0.002), days to first flowering (-0.004), days to 50% flowering (-0.009) and green pod length (-0.002). Phenotypic correlation of this trait with green pod yield was positive and highly significant (0.612).

**4.1.5.11-Green pod length (cm)-** The green pod length showed negative direct effects (-0.004) upon yield and indirect negative effects through germination percent (-0.003), number of leaves/plant (-0.007), leaf length (-0.002), leaf width (-0.028), days to first flowering (-0.002), days to 50% flowering (-0.004). Phenotypic correlation of this trait with green pod yield was positive (0.105).

**4.1.5.12-Green pod width (cm)-** The green pod width showed positive direct effects (0.048) upon yield and indirect negative effects through germination percent (-0.007), number of leaves/plant (-0.009), leaf length (-0.002), leaf width (-0.020), days to 50% flowering (-0.026) and green pod width(-0.001). Phenotypic correlation of this trait with green pod yield was positive (0.101).

**4.1.5.13-Green pod breath (cm)-** The green pod breath showed negative direct effects (-0.002) upon yield and indirect negative effects through germination percent (-0.003), leaf length (-0.001), leaf width (-0.009) and days to 50% flowering (-0.020). Phenotypic correlation of this trait with green pod yield was positive (0.180).

**4.1.5.14-Single green pod weight (g)-** The single green pod weight showed positive direct effects (0.013) upon yield and indirect negative effects through germination percent (-0.005), number of leaves/plant (-0.003), leaf length (-0.002), leaf width (-0.017), days to 50% flowering (-0.016) and green pod length (-0.001). Phenotypic correlation of this trait with green pod yield was positive (0.096).

**4.1.5.15-Green pod yield/plant (g)-**The green pod yield/plant showed highly positive significant direct effects (0.784) upon yield and indirect negative effects through germination percent (-0.004), number of leaves/plant (-0.006), leaf length (-0.001), leaf width (-0.014) and days to 50% flowering (-0.017). ). Phenotypic correlation of this trait with green pod yield was highly positive significant (0.976).

**4.1.5.16-Green pod yield/plot (g)-** The green pod yield/plot showed positive direct effects (0.187) upon yield coupled with plant height (0.009), primary branches/plant (0.003), secondary branches/plant (0.020), days to first flowering (0.003), number of pods/plant (0.014), green pod width (0.003), single green pod weight (0.001), green pod yield/plant (0.726) and 100-seed weight (0.005). Phenotypic correlation of this trait with green pod yield was highly positive significant (0.927).

**4.1.5.17-Number of seeds/pod-** The number of seeds/pod showed positive direct effects (0.001) upon yield and indirect negative effects through germination percent (-0.004), plant height (-0.002), number of leaves/plant (-0.002), leaf length (-0.002), leaf width (-0.004) and days to 50% flowering (-0.020) and green pod length (-0.001). Phenotypic correlation of this trait with green pod yield was positive (0.134).

**4.1.5.18-100-seed weight (g)-** The 100-seed weight showed positive direct effects (0.007) upon yield coupled with positive indirect effect via., plant height (0.002), number of leaves/plant (0.004), primary branches/plant (0.001), secondary branches/plant (0.017), days to first flowering (0.007), number of pods/plant (0.009), green pod width (0.005), single green pod weight (0.002), green pod yield/plant (0.504) and green pod yield/plant (0.116). Phenotypic correlation of this trait with green pod yield was highly positive significant (0.644).

## **Quality traits:**

**4.1.5.19- Moisture (%)** -This trait showed positive direct effects on moisture percent (0.034) along with positive indirect effect through total sugars (0.029) and protein (0.145). Phenotypic correlation of this trait with green pod yield was highly positive significant (0.208).

**4.1.5.20-Total sugars (%)** -The direct effect of this trait on total sugars was positive (0.296), whereas the indirect effect through protein (-0.029) was negative. Positive indirect effect through moisture (0.029). Phenotypic correlation of this trait with green pod yield was highly positive significant (0.270).

**4.1.5.21-Protein (%)**-The direct effect of this trait on protein was highly positive significant (0.485). the negative indirect effect through total sugars (-0.018). Positive indirect effect through moisture (0.010). Phenotypic correlation of this trait with green pod yield was highly positive significant (0.477).

## **4.5.2-Genotypic path coefficient**

A critical review of path coefficient analysis at genotypic level representing direct and indirect effect of morphological, yield and quality characters as given in Table (4.17 and 4.18 ) respectively. Exhibited that green pod yield/plant (0.996) had the highest genotypic positive direct effect on yield. The lowest positive direct effect on yield was showed by plant height (0.008), days to 50% flowering (0.005), green pod yield/plot (0.005), leaf length (0.004), secondary branches/plant (0.004), green pod width(0.004) and green pod length (0.001). The indirect negative effect through with germination percent (-0.002), number of leaves/plant (-0.011), leaf width (-0.004), days to first flowering (-0.005), single green pod weight (-0.011), number of seeds/pod (-0.002) and 100-seed weight (-0.007).

For quality parameters, genotypic path coefficient analysis which is presented in Table (4.18) showed that protein (0.518) had the highest genotypic positive direct effect on green pod yield content followed by total sugars (0.296), moisture percent (0.002) exhibited a positive direct effect on green pod yield, but these positive direct effects was neutralized due to positive indirect effect through moisture content (0.001) and (0.001).The data celerity revealed that in both morphological and quality characters, the residual effect at genotypic level was less compared to the effect of phenotypic level.

**Table- 4.8 Mean performance of twenty five genotypes of French bean for horticultural traits.**

Characters	1	2	3	4	5	6	7	8	9	10	11
<b>Genotypes</b>											
LD-2-1	83.97	44.02	45.32	7.65	7.32	2.57	4.24	33.33	40.83	10.46	8.33
EC-400400	84.10	37.53	48.43	9.25	9.45	2.77	5.24	33.83	40.83	12.16	9.40
IL-25537	94.37	34.62	52.17	10.32	10.46	2.73	5.55	34.33	40.50	16.36	11.40
HURG-15	97.67	38.61	45.11	11.07	10.71	3.94	7.11	32.67	38.83	16.37	9.30
EC-400445	98.40	49.24	59.33	11.96	9.09	4.33	5.02	35.00	40.67	19.32	12.27
NO.3127	84.03	42.31	45.67	13.30	12.53	3.71	7.19	38.33	45.67	22.71	13.68
IC-14351	96.40	52.99	56.81	11.77	9.72	3.96	7.41	40.50	43.17	23.70	12.06
EC-400401	85.22	39.79	65.16	10.65	10.78	3.64	7.08	36.00	41.00	24.27	12.40
ET-8415	87.35	36.82	57.29	12.14	11.91	4.14	7.33	39.00	43.17	22.08	13.76
PLB-438	94.21	47.28	61.35	12.86	9.13	4.43	6.92	31.50	37.50	21.60	11.67
EC-400407	92.31	46.56	48.95	10.32	11.47	3.12	9.09	30.83	38.33	24.25	12.81
BSRR-2	92.06	50.96	59.38	12.67	11.50	3.99	8.24	39.83	42.83	20.11	11.72
EC-400414	82.68	49.02	47.33	11.36	10.44	4.31	8.80	39.67	44.00	21.60	13.36
ET-8435	87.29	40.71	46.06	12.42	9.38	4.44	7.73	30.33	36.00	20.70	9.40
ET-8490	97.81	39.90	47.12	11.70	10.17	3.80	9.58	33.83	37.50	25.23	11.27
IPR-98-3-1	93.54	51.11	46.48	9.73	10.52	4.54	7.56	33.83	40.17	22.61	12.39
EC-400409	91.57	82.87	53.93	9.69	10.83	4.00	8.21	40.50	43.67	29.08	11.01
ET-3409	100.00	129.16	87.11	11.21	10.98	5.11	9.56	39.17	42.00	30.22	11.60
BLF-101	86.23	78.77	67.43	11.30	10.48	3.69	8.01	34.00	38.50	25.02	12.58
PDR-14	84.55	61.35	63.73	10.53	8.65	4.37	8.45	41.17	43.00	25.57	11.78
IL-25337	89.67	47.67	51.29	11.26	10.18	3.70	9.00	36.67	42.00	23.17	9.31
BD-19162	86.99	38.62	42.13	9.41	11.45	3.95	8.06	38.50	43.00	18.50	9.12
GPR-203	82.20	38.37	47.59	9.73	8.17	4.01	5.30	42.33	46.50	17.74	9.44
VL Bauni -1	72.30	38.46	47.01	7.75	5.02	3.93	5.14	42.50	46.67	15.62	9.52
VL Bean-2	70.15	37.31	45.95	7.38	6.41	3.44	5.21	43.50	48.50	15.73	9.04
F-value	**	**	**	*	*	*	*	**	**	**	*
<b>Mean</b>	88.60	50.16	53.52	10.69	9.86	3.86	7.24	36.84	41.79	20.96	11.14
<b>Range</b>	70.15-100.00	34.62-129.16	42.13-87.11	7.38-12.86	5.02-12.53	2.57-5.11	4.24-9.58	30.33-43.50	36.00-48.50	10.46-30.22	8.33-13.76
<b>CV</b>	5.40	7.18	7.11	10.00	11.60	12.51	9.02	4.62	4.22	6.02	7.38
<b>SEm±</b>	2.76	2.07	2.19	0.6177	0.6610	0.2793	0.3774	0.9847	1.01	0.7289	0.4751
<b>CD (P= 0.05)</b>	5.556	4.174	4.415	1.240	1.327	0.5608	0.7578	1.977	2.046	1.463	0.954

**\*Significance at 0.05% level; \*\* significance at 0.01% level**

1 = Germination percentage      2 = Plant height (cm)      3 = Number of leaves/plant      4 = Leaf length (cm)      5 = Leaf width (cm)      6 = Primary branches /plant  
 7 = Secondary branches/plant      8 = Days to first flowering      9 = Days to 50% flowering      10 = Number of pods /plant      11 = Green pod length (cm)

**Table- 4.9 Mean performance of twenty five genotypes of French bean for horticultural traits.**

Characters	12	13	14	15	16	17	18	19	20	21	22	23
<b>Genotypes</b>												
LD-2-1	0.59	0.95	5.56	55.06	1.66	3.64	16.33	91.73	11.14	5.13	18.74	white
EC-400400	0.58	0.92	5.37	80.23	2.42	4.66	20.69	133.14	11.41	6.92	19.07	purple
IL-25537	0.66	0.94	5.73	62.21	1.92	5.27	13.02	103.31	11.13	7.80	17.15	white
HURG-15	0.77	1.02	6.89	67.18	2.06	4.61	26.56	111.78	12.73	7.35	18.74	white
EC-400445	0.79	1.02	6.05	62.03	1.92	5.14	23.87	102.99	10.73	7.42	18.17	white
NO.3127	0.72	0.92	6.17	83.59	2.72	4.57	49.47	139.25	10.19	7.08	20.83	purple
IC-14351	0.65	0.88	7.02	66.48	2.01	5.23	19.72	110.20	10.41	6.64	20.01	Purple
EC-400401	0.95	0.88	6.00	80.87	2.20	5.96	19.82	134.09	10.66	8.99	23.83	Purple
ET-8415	0.67	0.83	6.51	72.62	2.21	4.80	12.49	120.98	10.81	6.10	26.85	White
PLB-438	0.88	0.98	7.94	93.27	2.83	4.87	21.73	155.22	10.93	6.02	26.74	White
EC-400407	0.74	1.03	6.54	90.68	2.76	5.08	55.32	150.77	10.91	6.44	26.64	Purple
BSRR-2	0.91	1.05	7.10	92.75	2.82	4.92	47.09	154.38	11.74	7.43	29.71	white
EC-400414	0.51	1.10	5.25	106.96	3.19	4.85	35.33	178.35	12.92	7.03	30.53	White
ET-8435	0.59	1.02	6.42	119.98	3.49	5.21	36.82	200.04	11.28	7.08	28.65	White
ET-8490	0.75	0.98	6.43	143.24	3.95	5.69	60.28	238.14	12.71	7.64	26.95	white
IPR-98-3-1	0.70	0.95	6.42	125.54	3.79	4.90	54.47	208.77	10.92	6.47	24.31	Purple
EC-400409	0.62	0.91	6.45	108.56	3.30	4.57	34.11	181.19	9.97	7.18	19.33	Purple
ET-3409	0.73	0.98	5.72	149.11	4.51	4.34	32.56	248.51	10.38	7.47	23.26	Purple
BLF-101	0.71	1.07	6.92	108.19	3.28	4.74	35.47	179.95	11.10	8.29	24.58	White
PDR-14	0.71	0.88	6.42	100.81	3.04	4.87	28.58	167.64	10.83	7.15	28.03	Purple
IL-25337	0.65	0.98	5.80	104.74	3.08	5.05	38.54	174.30	12.27	6.70	30.44	Purple
BD-19162	0.60	1.03	6.19	102.47	3.10	4.38	39.18	170.32	11.67	7.55	19.30	White
GPR-203	0.55	0.89	6.17	101.94	3.08	4.17	45.27	169.36	11.25	7.80	19.79	Purple
VL Bauni -1	0.49	0.84	4.56	66.16	2.00	4.68	19.31	110.23	9.55	6.81	20.39	Pink
VL Bean-2	0.50	0.96	5.84	64.71	1.98	4.09	20.65	107.80	9.53	5.18	21.98	Purple
F-value	*	*	*	**	*	*	**	**	*	*	**	
<b>Mean</b>	0.68	0.96	6.21	92.37	2.77	4.81	32.26	153.69	11.08	7.02	23.35	
<b>Range</b>	0.49-0.95	0.83-1.10	4.56-7.94	55.06-149.11	1.66-4.51	3.64-5.96	12.49-60.28	91.73-248.51	9.53-12.92	5.13-8.99	17.15-30.53	
<b>CV</b>	10.51	9.25	8.27	8.57	12.56	10.49	3.11	8.13	6.74	8.30	4.71	
<b>SEm±</b>	0.04137	0.05136	0.2970	4.57	0.2011	0.2915	0.5808	7.222	0.4320	0.3370	0.6353	
<b>CD (P=0 .05)</b>	0.0834	0.1038	0.596	9.184	0.403	0.585	1.166	14.501	0.867	0.676	1.275	

**\* Significance at 0.05% level; \*\* significance at 0.01% level**

12 = Green pod width (cm) 13 = Green pod breadth (cm) 14 = Single green pod weight (g) 15 = Green pod yield /plant (g) 16 = Green pod yield /plot (kg)  
 17 = Number of seeds /pod 18 =100-seed weight (g) 19= Green pod yield (q/ha) 20= % Moisture 21= % Total sugars 22= % Protein 23= Flower colour

**Table-4.10 Estimates of genetic constants for different morphological, yield and quality characters in French bean.**

S. No.	Characters	Range		General Mean	Co-efficient of variation		Heritability in broad sense (%)	Genetic advance (GA)	Genetic advance in % of mean
		Minimum	Maximum		PCV (%)	GCV (%)			
1	X1	70.15	100.00	88.60	10.03	8.44	70.90	12.97	14.63
2	X2	34.62	129.16	50.16	41.21	40.58	97.00	41.29	82.31
3	X3	42.13	87.11	53.52	20.05	18.75	87.40	19.33	36.11
4	X4	7.38	12.86	10.69	17.99	14.95	69.10	2.74	25.63
5	X5	5.02	12.53	9.86	20.78	17.24	68.80	2.91	29.51
6	X6	2.57	5.11	3.86	19.85	15.40	60.20	0.95	24.61
7	X7	4.24	9.58	7.24	23.29	21.47	85.00	2.95	40.74
8	X8	30.33	43.50	36.84	11.51	10.54	83.80	7.32	19.86
9	X9	36.00	48.50	41.79	8.54	7.42	75.50	5.55	13.28
10	X10	10.46	30.22	20.96	23.72	22.94	93.60	9.58	45.70
11	X11	8.33	13.76	11.14	16.42	14.67	79.80	3.01	27.01
12	X12	0.49	0.95	0.68	20.64	17.76	74.00	0.21	30.88
13	X13	0.83	1.10	0.96	11.80	7.33	38.50	0.09	9.37
14	X14	4.56	7.94	6.21	13.86	11.12	64.40	1.14	18.35
15	X15	55.06	149.11	92.37	28.85	27.55	91.20	50.05	54.18
16	X16	1.66	4.51	2.77	28.95	26.08	81.20	1.34	48.37
17	X17	3.64	5.96	4.81	14.53	10.05	47.80	0.69	14.34
18	X18	12.49	60.28	32.26	43.10	42.99	99.50	28.50	88.34
19	X19	91.73	248.51	153.69	28.77	27.60	92.00	83.82	54.53
20	X20	9.53	12.92	11.08	10.32	7.81	57.30	1.35	12.18
21	X21	5.13	8.99	7.02	14.69	12.12	68.00	1.45	20.65
22	X22	17.15	30.53	23.35	18.65	18.05	93.60	8.40	35.97

1 = Germination percentage

6 = Primary branches /plant

11 = Green pod length (cm)

16 = Green pod yield /plot (kg)

21= % Total sugars

2 = Plant height (cm)

7= Secondary branches/plant

12 = Green pod width (cm)

17 = Number of seeds /pod

22= % Protein

3= Number of leaves/plant

8= Days to first flowering

13= Green pod breadth (cm)

18=100-seed weight (g)

4 = Leaf length (cm)

9 = Days to 50% flowering

14 = Single green pod weight (g)

19 = Green pod yield (q/ha)

5 = Leaf width (cm)

10 = Number of pods /plant

15 = Green pod yield /plant (g)

20 = % Moisture

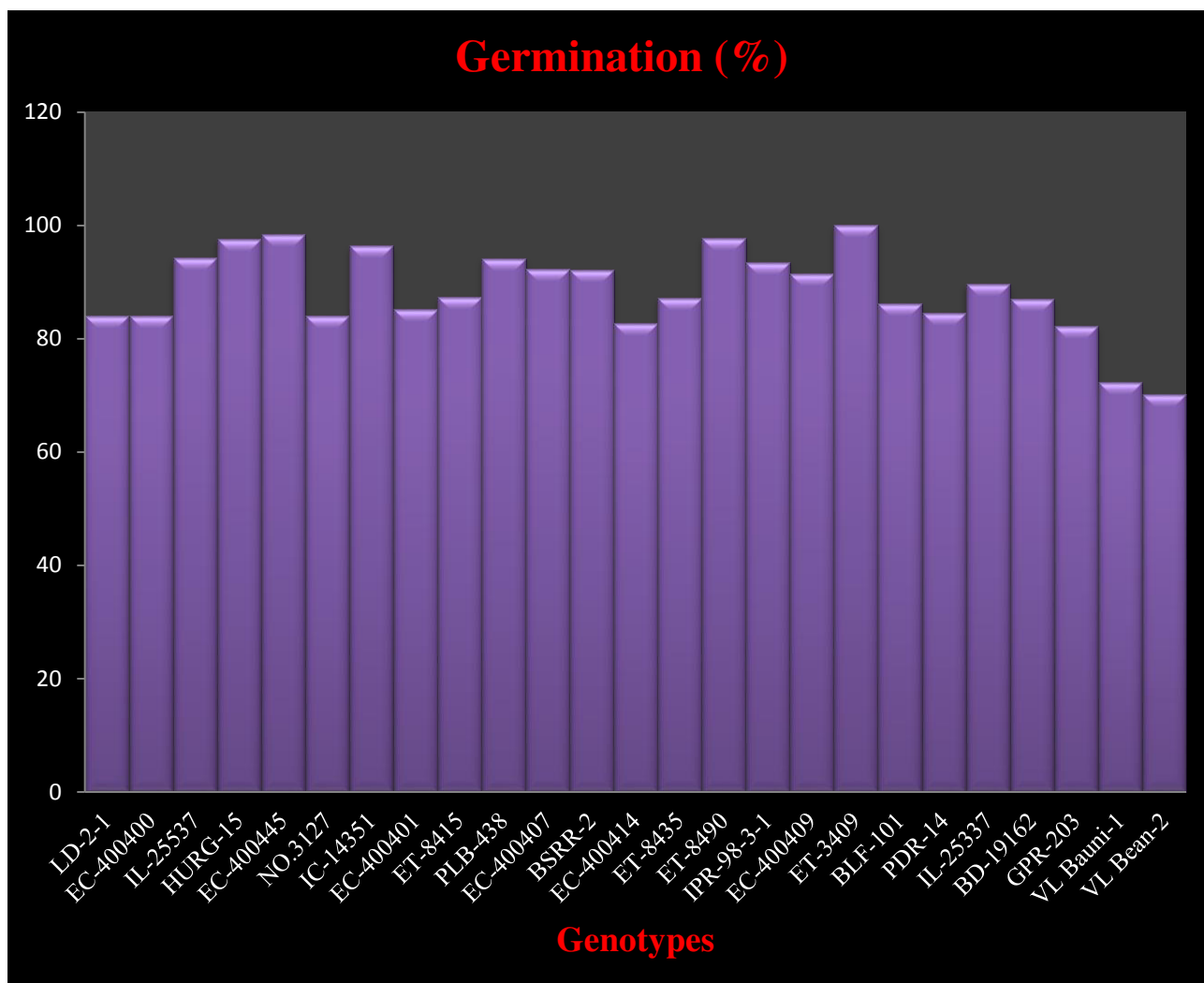


Fig-4.3:-Justified germination percent of the French bean genotypes

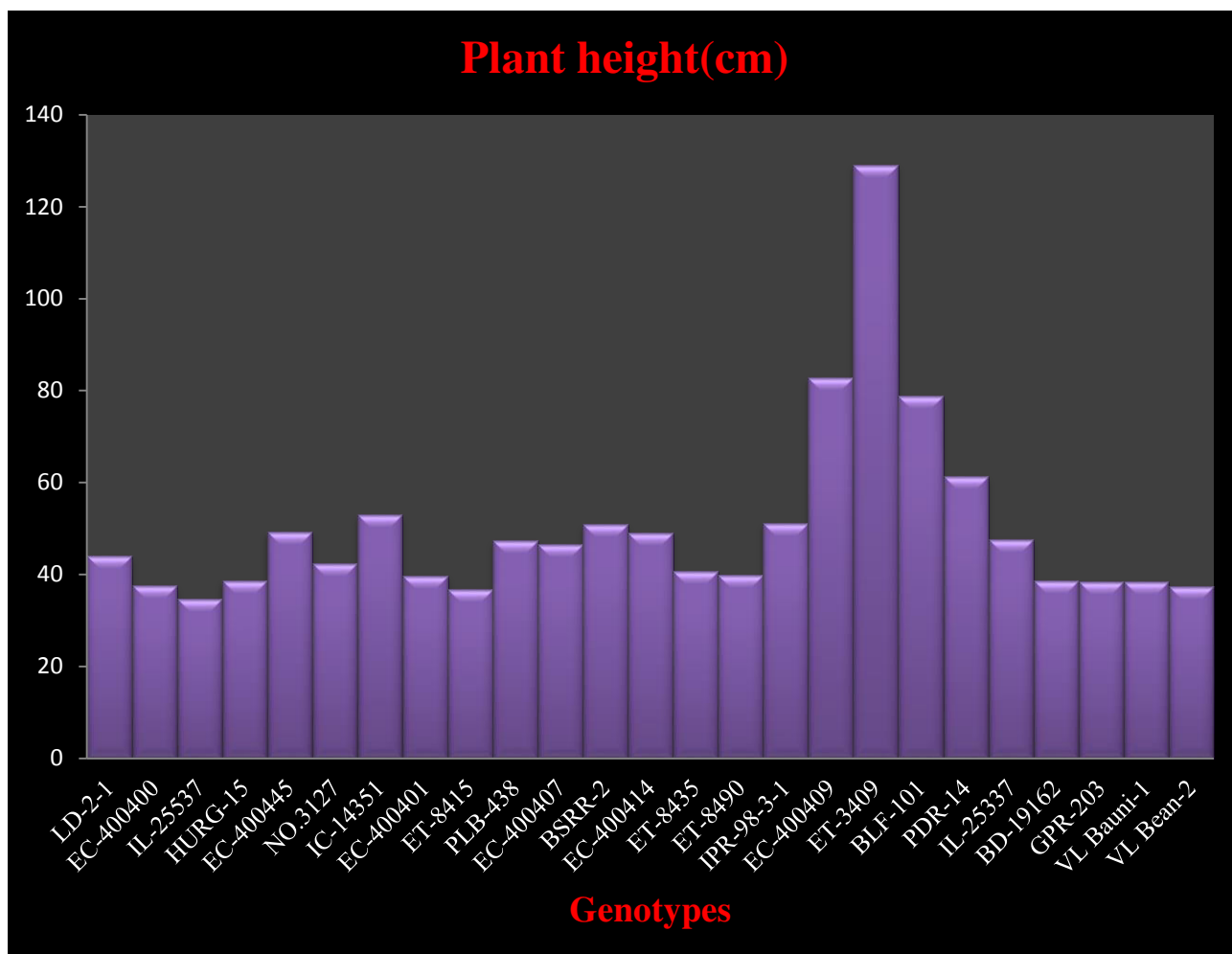


Fig-4.4:-Justified plant height (cm) of the French bean genotypes

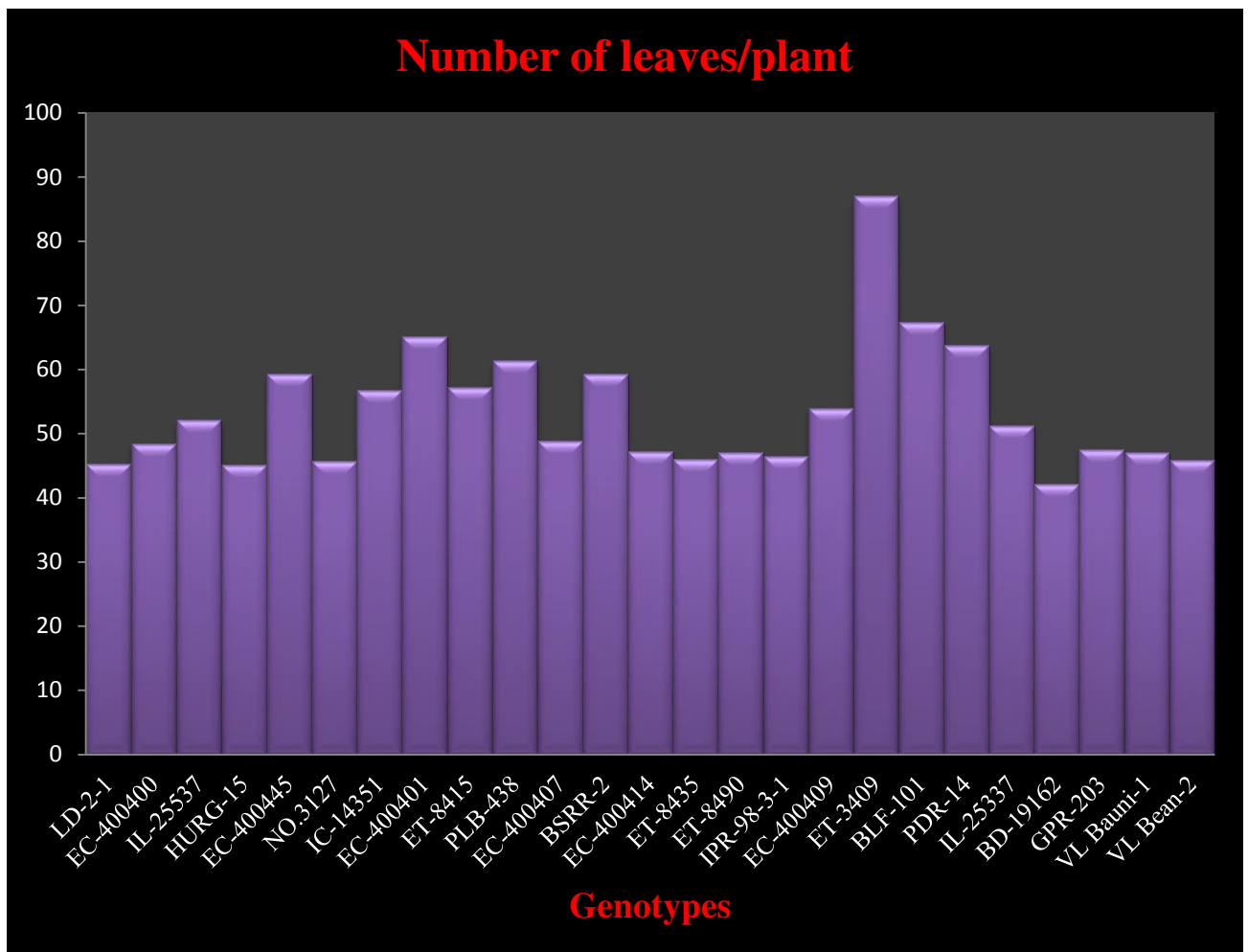


Fig-4.5:-Justified number of leaves/plant of the French bean genotypes

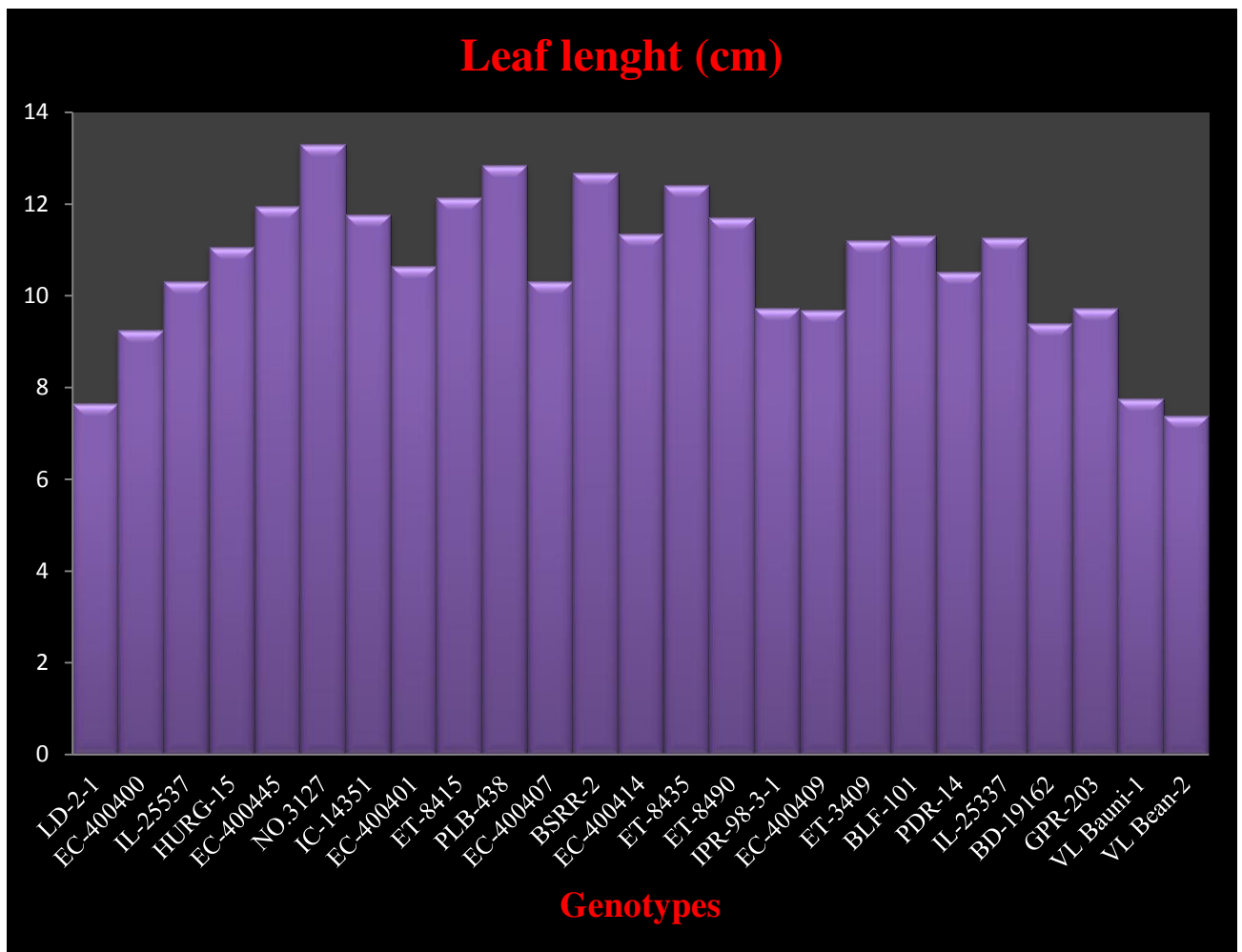


Fig-4.6:-Justified leaf length (cm) of the French bean genotypes

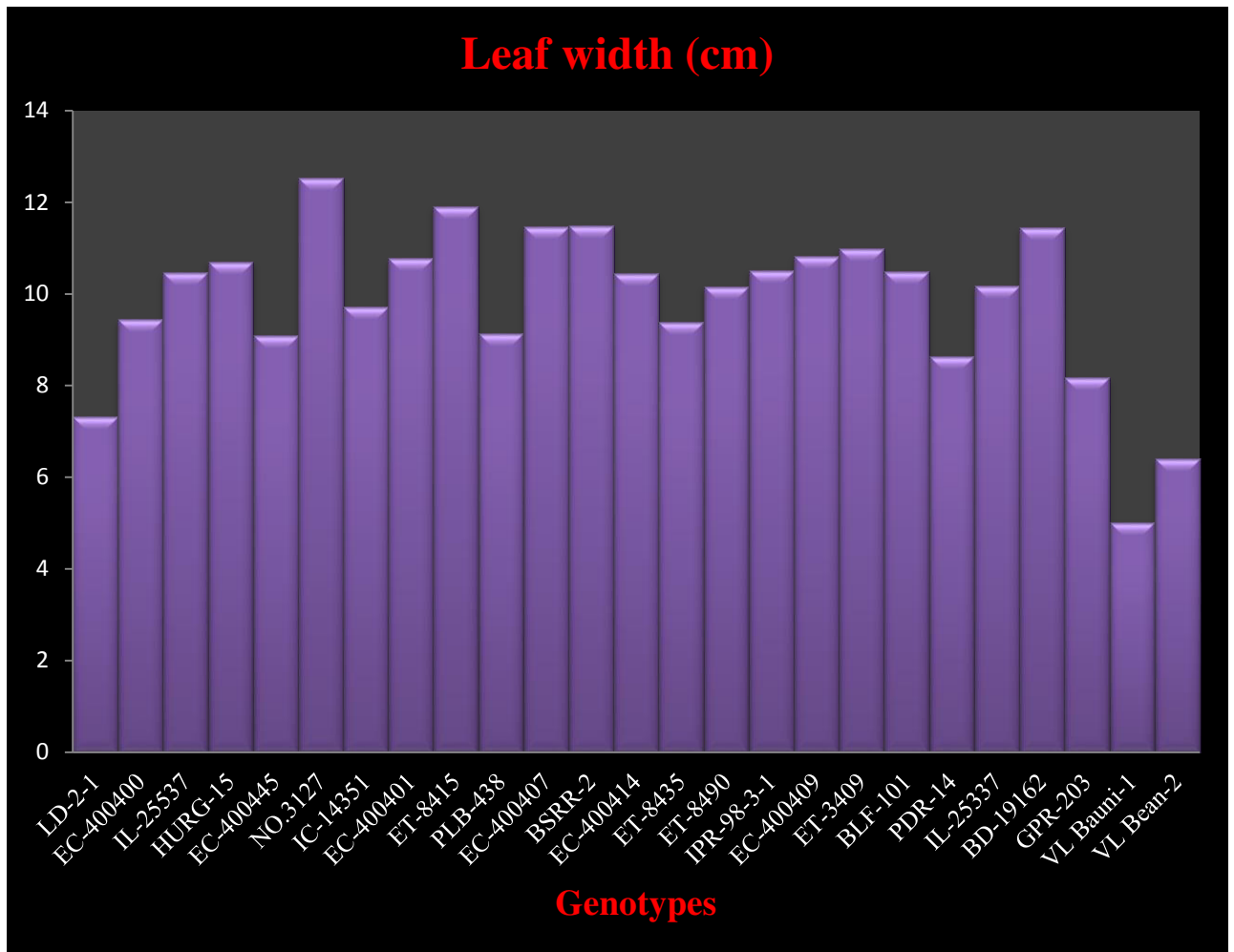


Fig-4.7:-Justified leaf width (cm) of the French bean genotypes

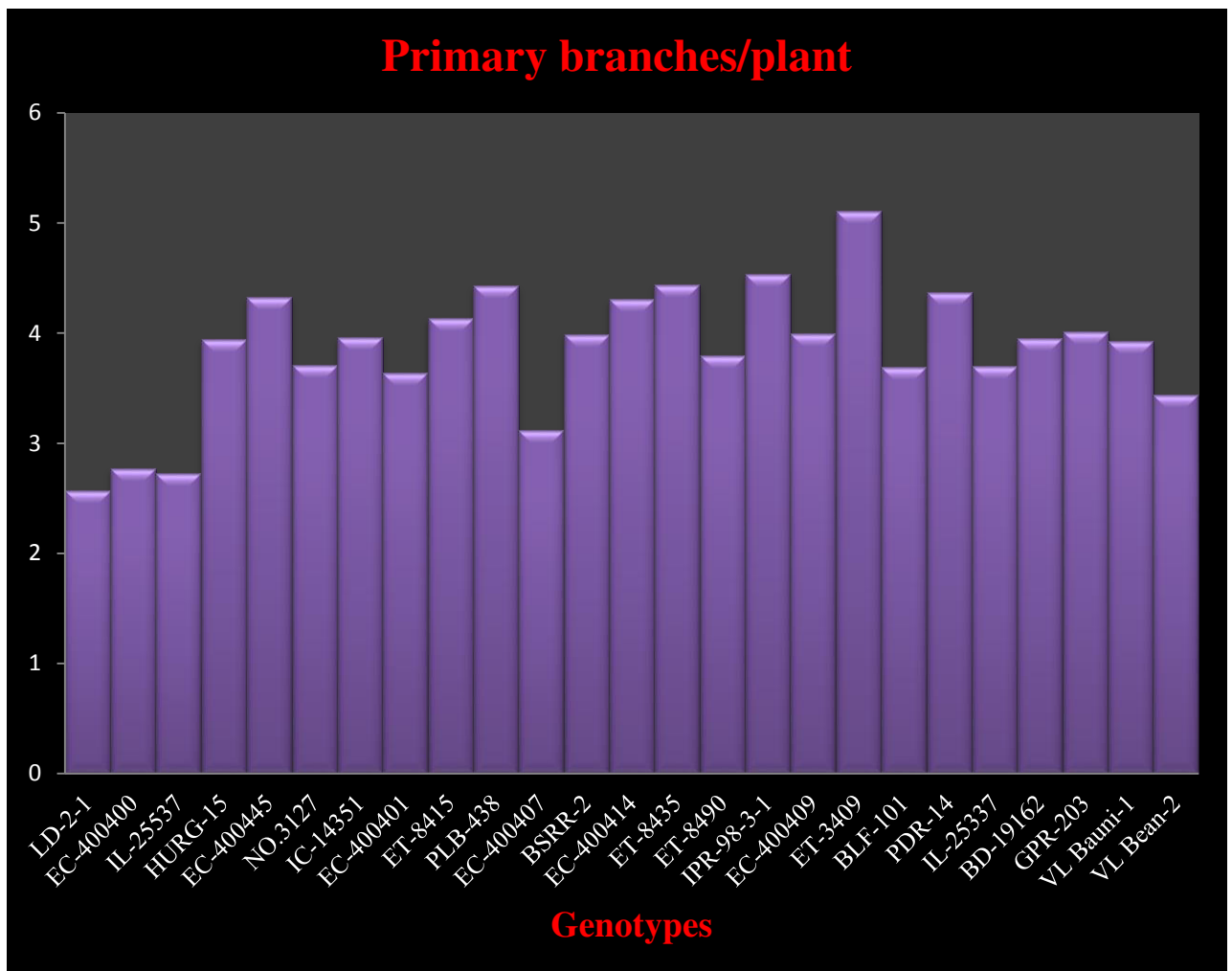


Fig-4.8:-Justified primary branches/plant of the French bean genotypes

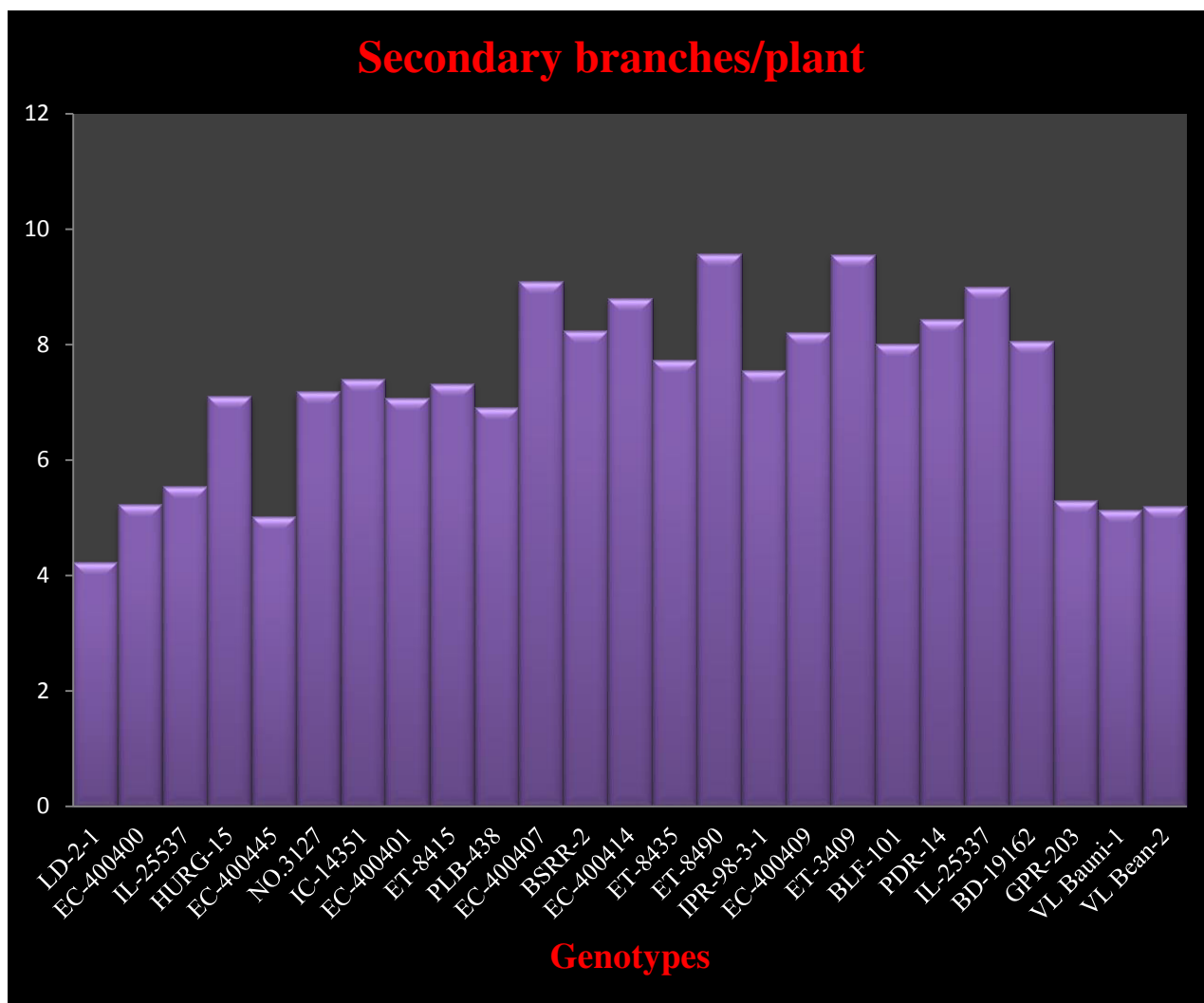


Fig-4.9:-Justified secondary branches/plant of the French bean genotypes

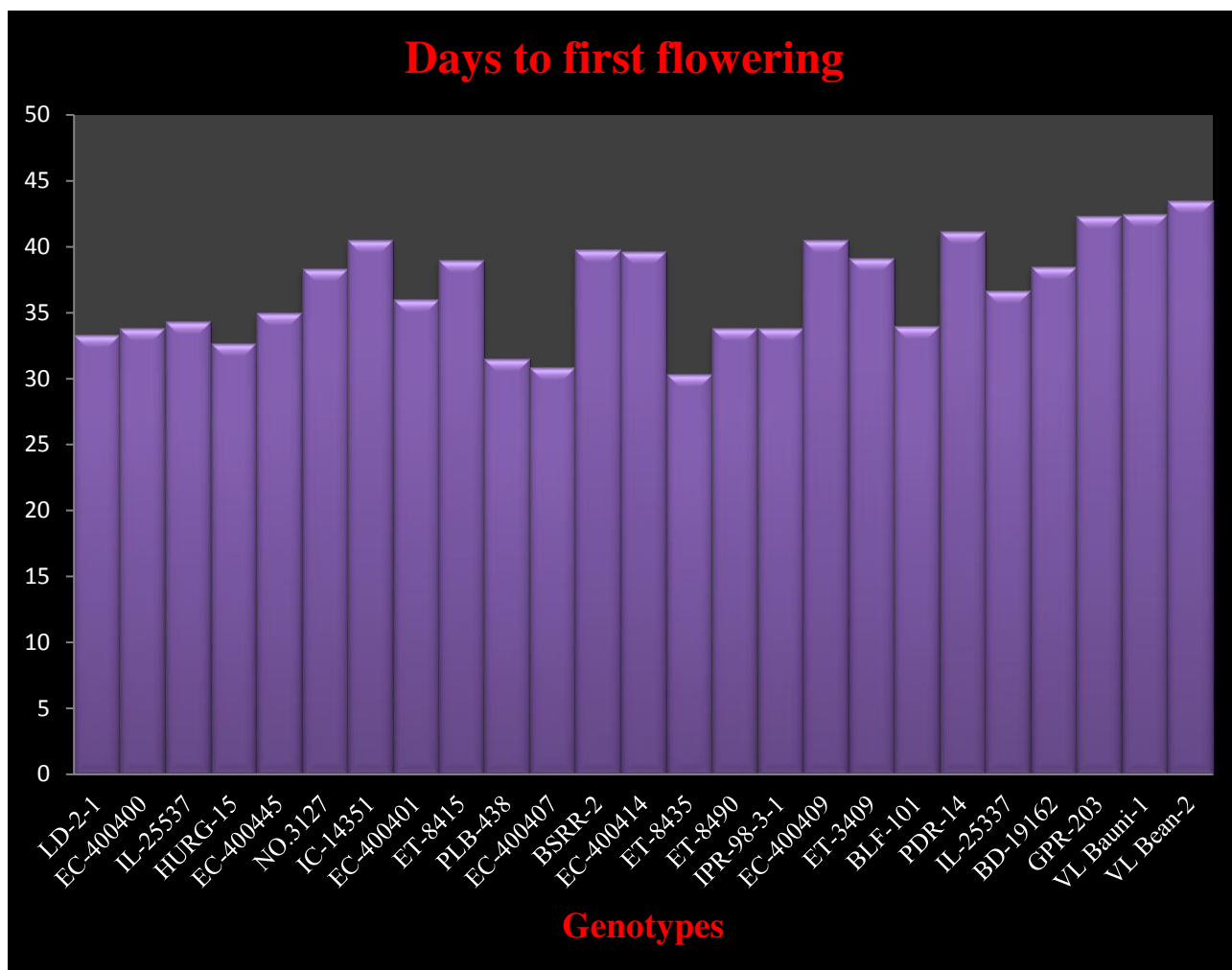


Fig-4.10:-Justified days to first flowering of the French bean genotypes

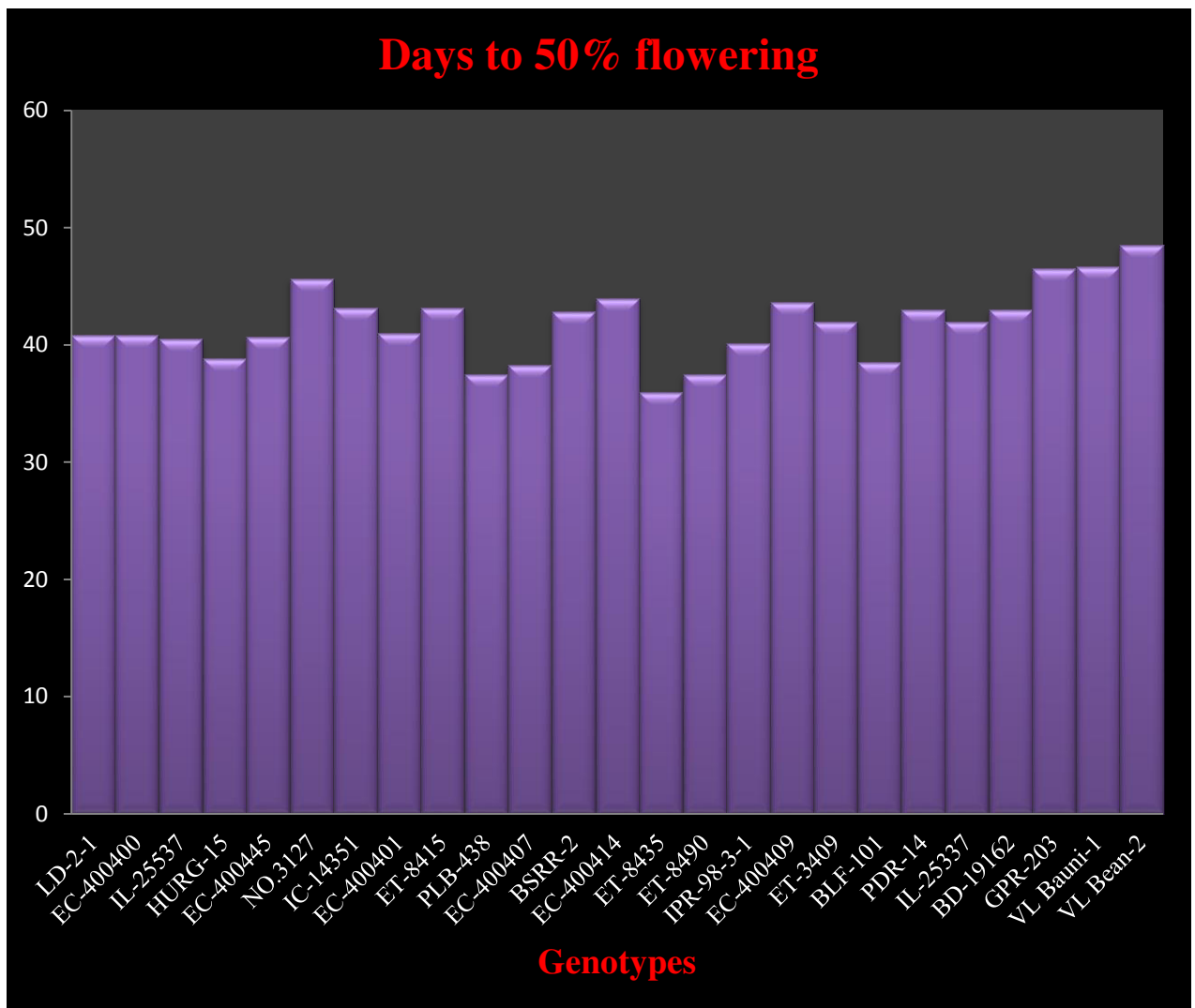


Fig-4.11:-Justified days to 50% flowering of the French bean genotypes

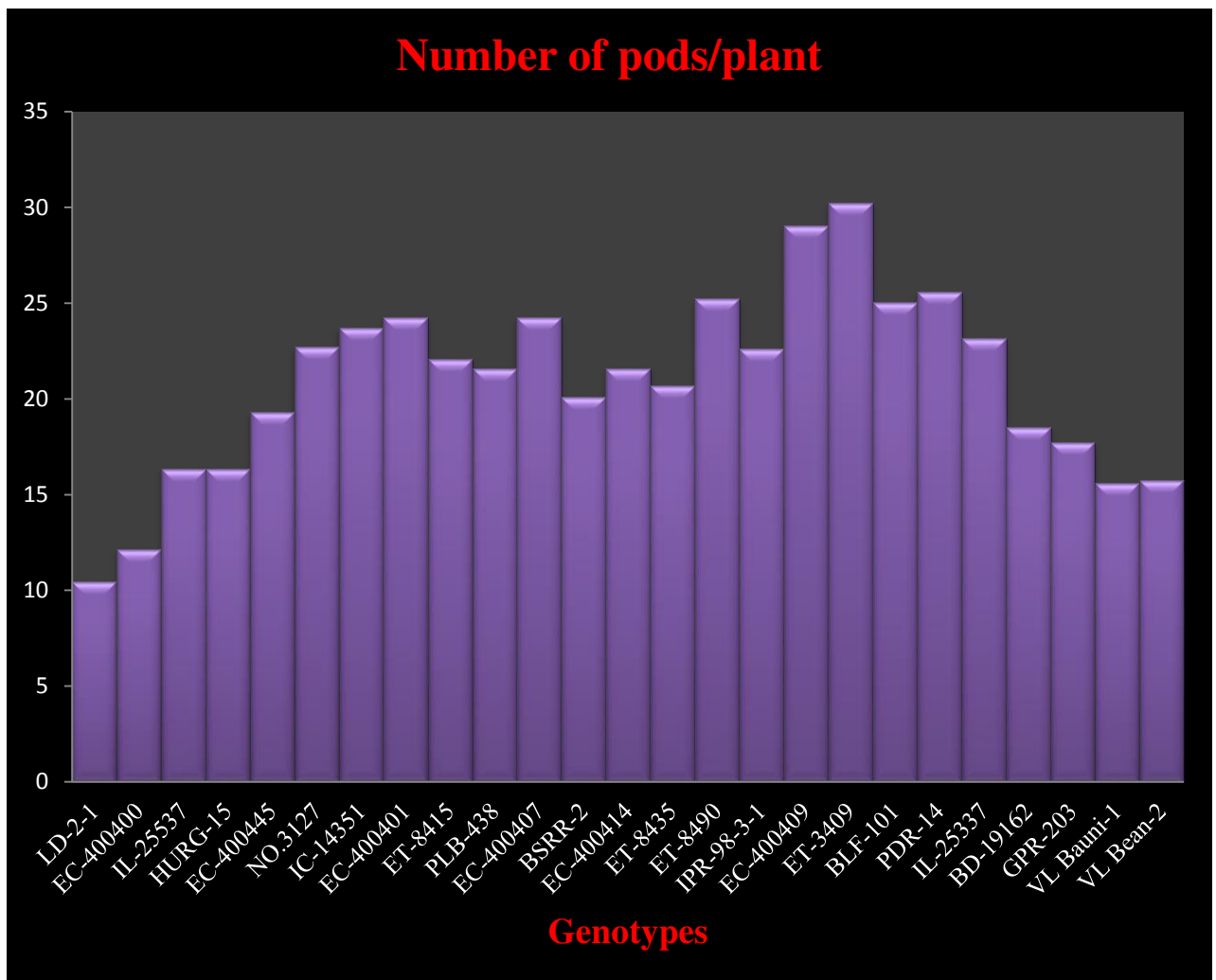


Fig-4.12:-Justified number of pods/plant of the French bean genotypes

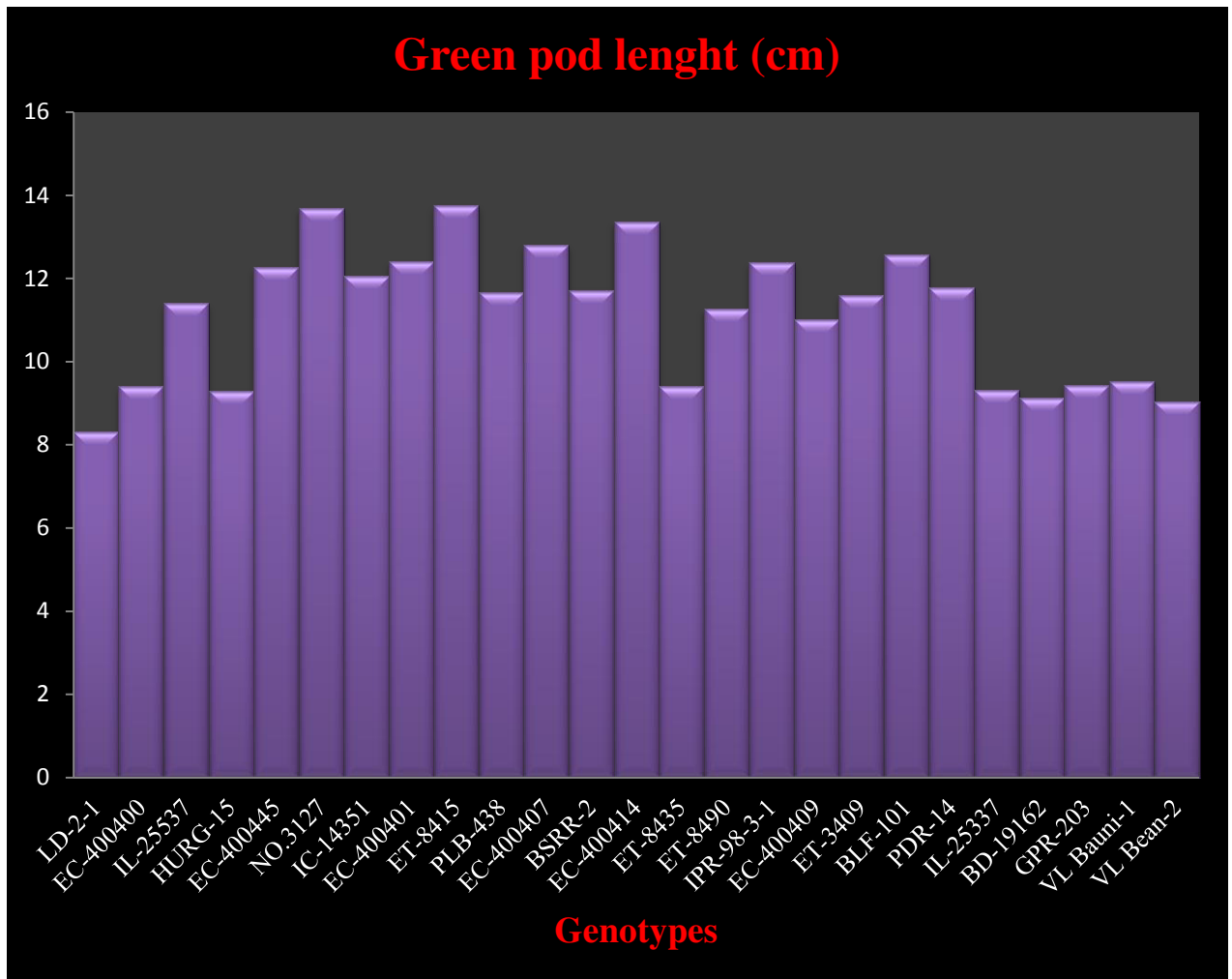


Fig-4.13:-Justified green pod length (cm) of the French bean genotypes

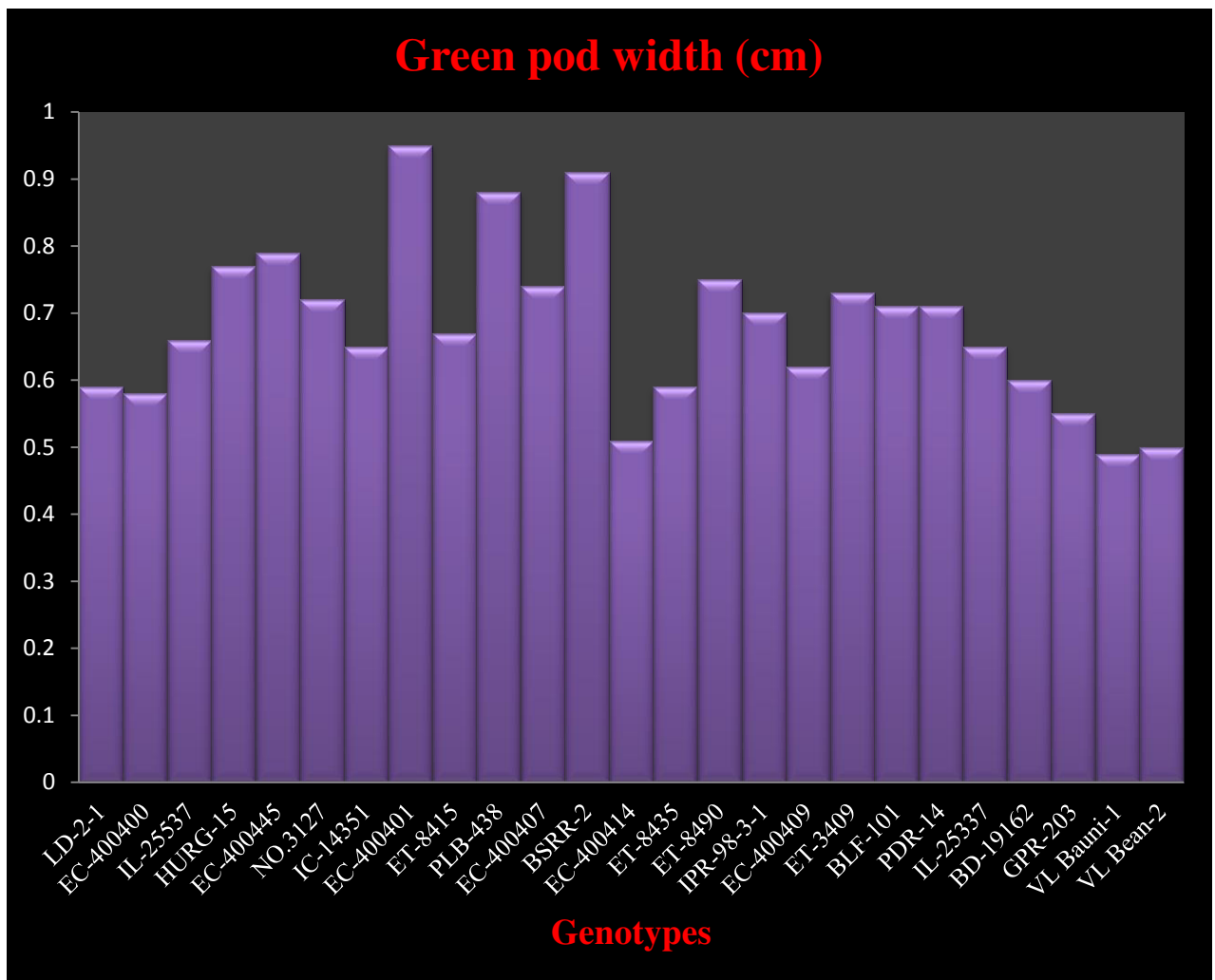


Fig-4.14:-Justified green pod width (cm) of the French bean genotypes

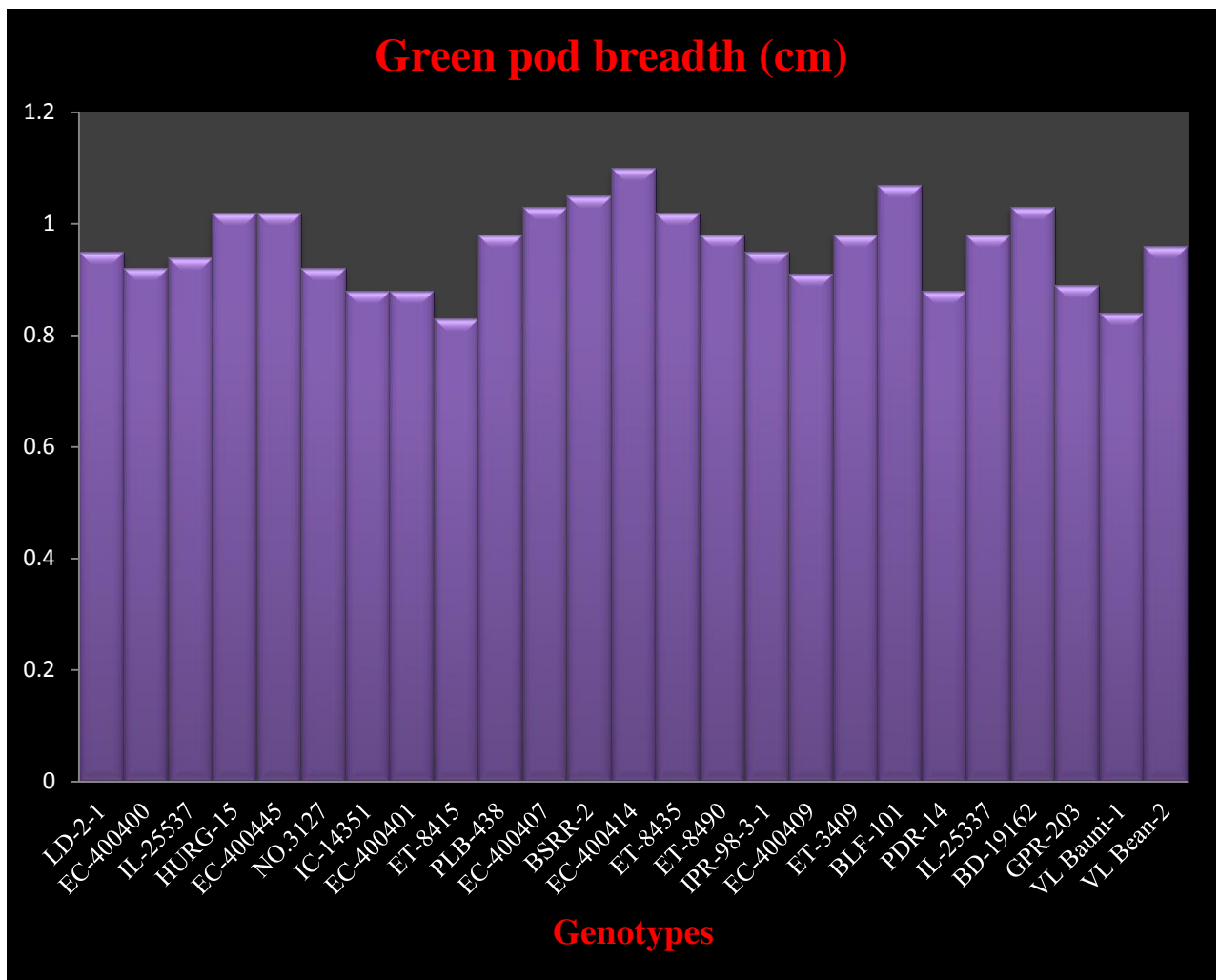


Fig-4.15:-Justified green pod breadth (cm) of the French bean genotypes

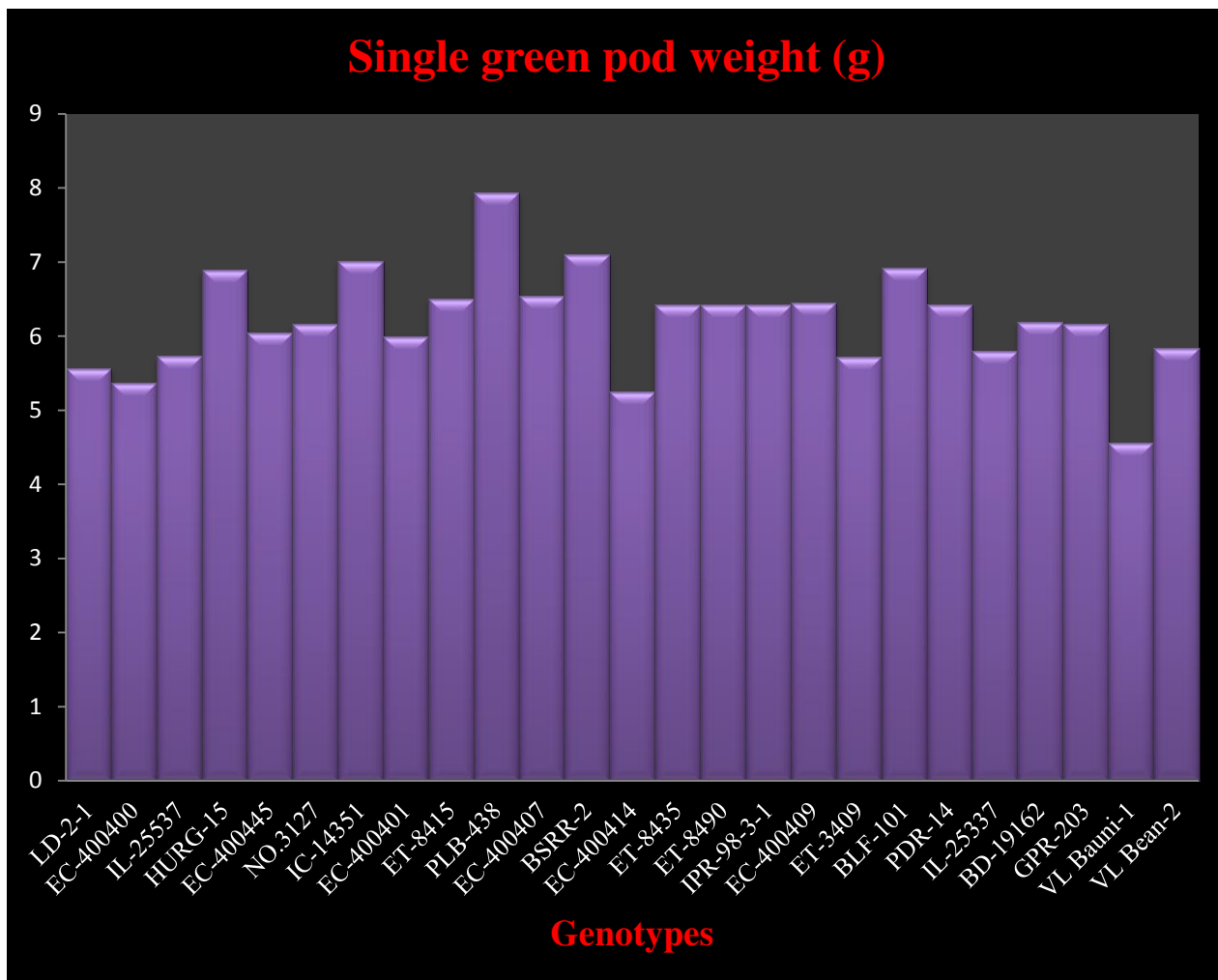


Fig-4.16:-Justified single green pod weight (g) of the French bean genotypes

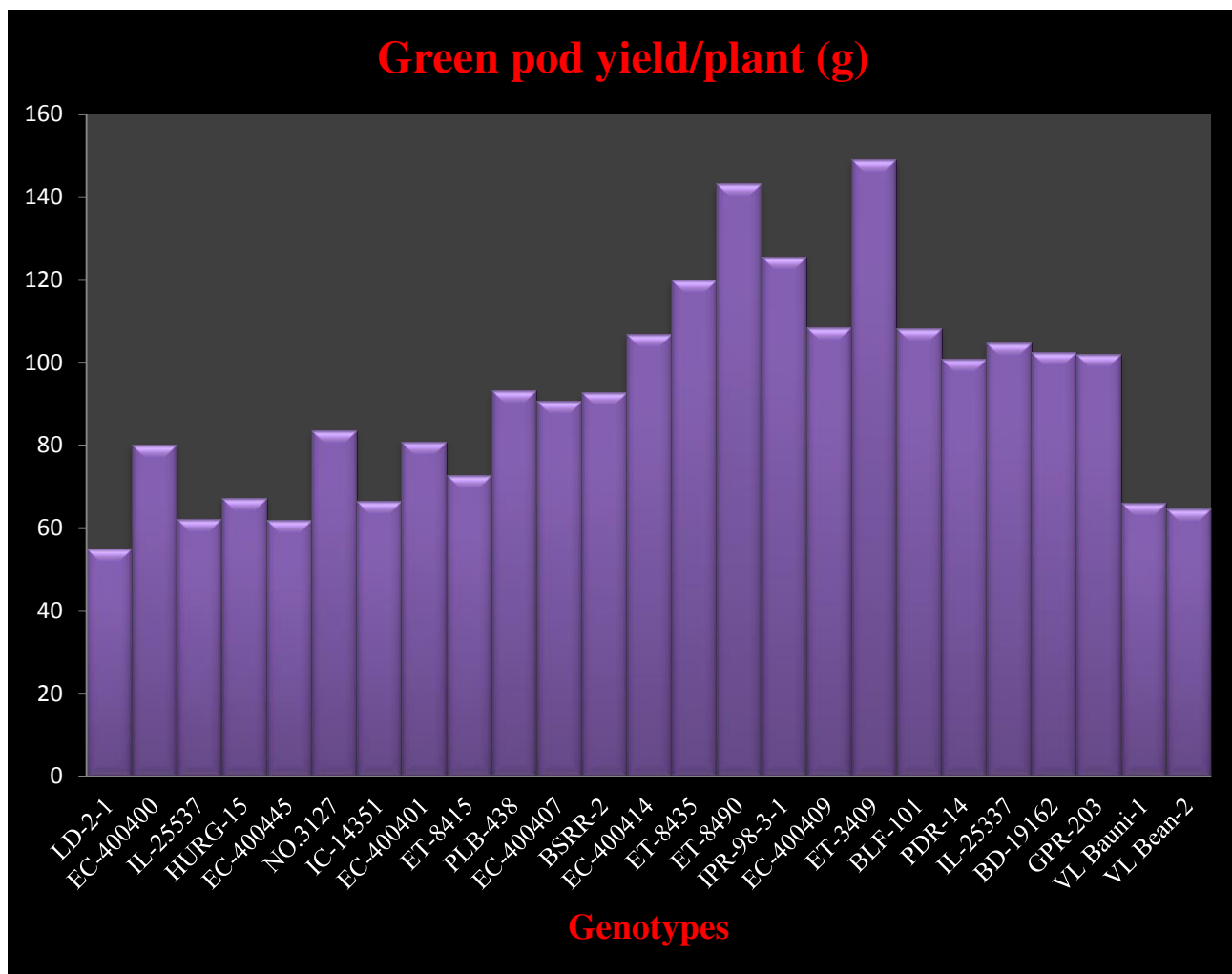


Fig-4.17:-Justified green pod yield/plant (g) of the French bean genotypes

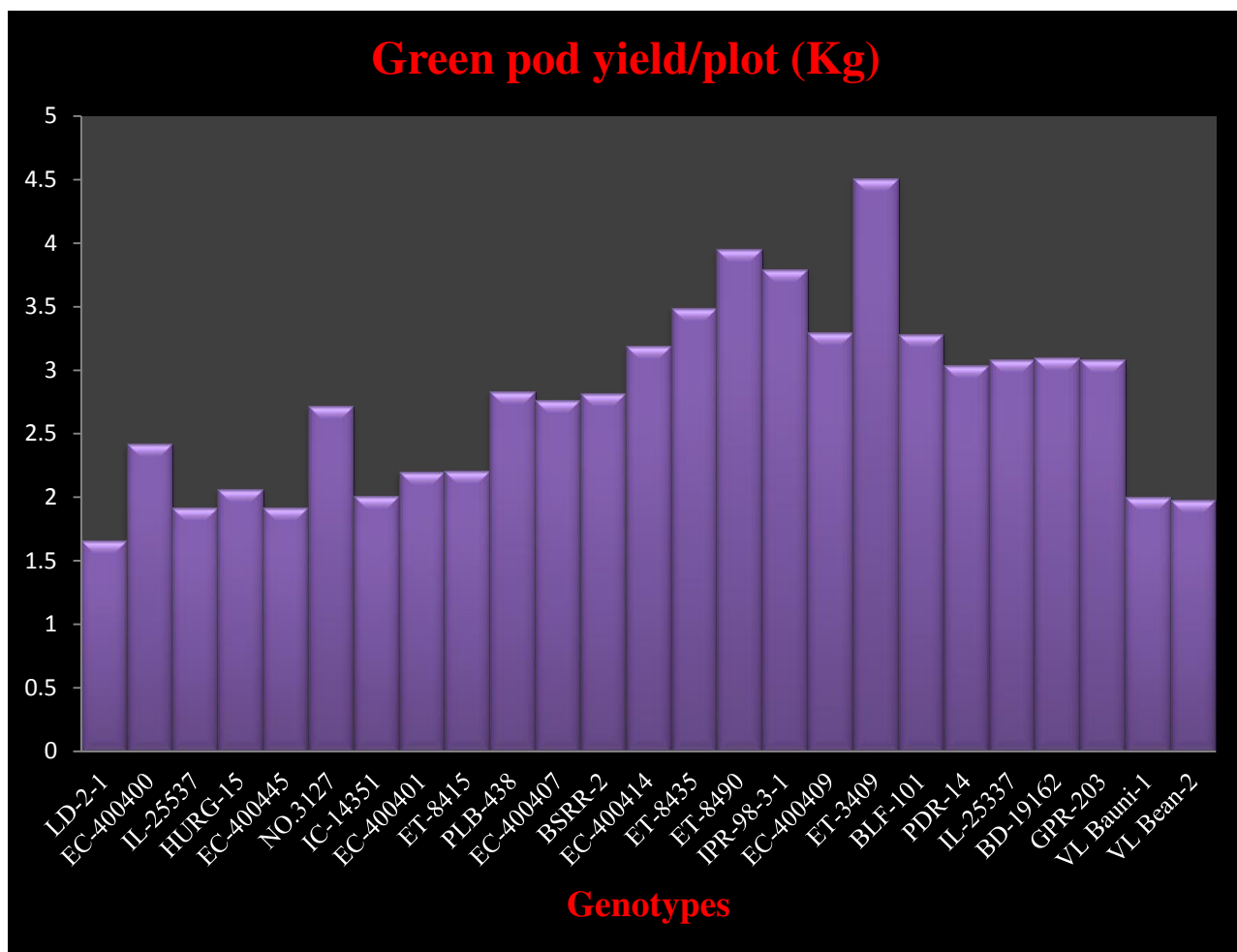


Fig-4.18:-Justified green pod yield/plot (kg) of the French bean genotypes

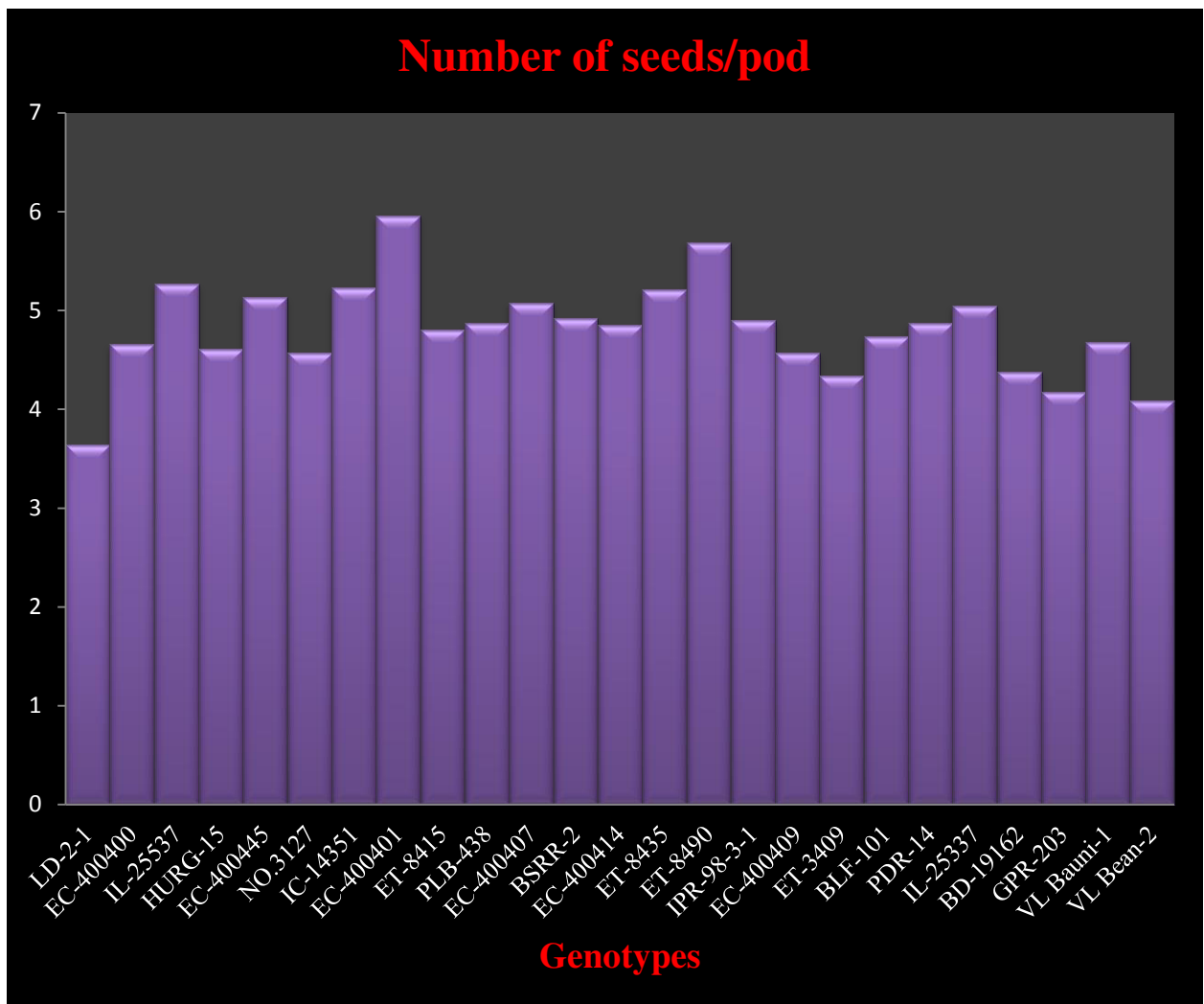


Fig-4.19:-Justified number of seeds/pod of the French bean genotypes

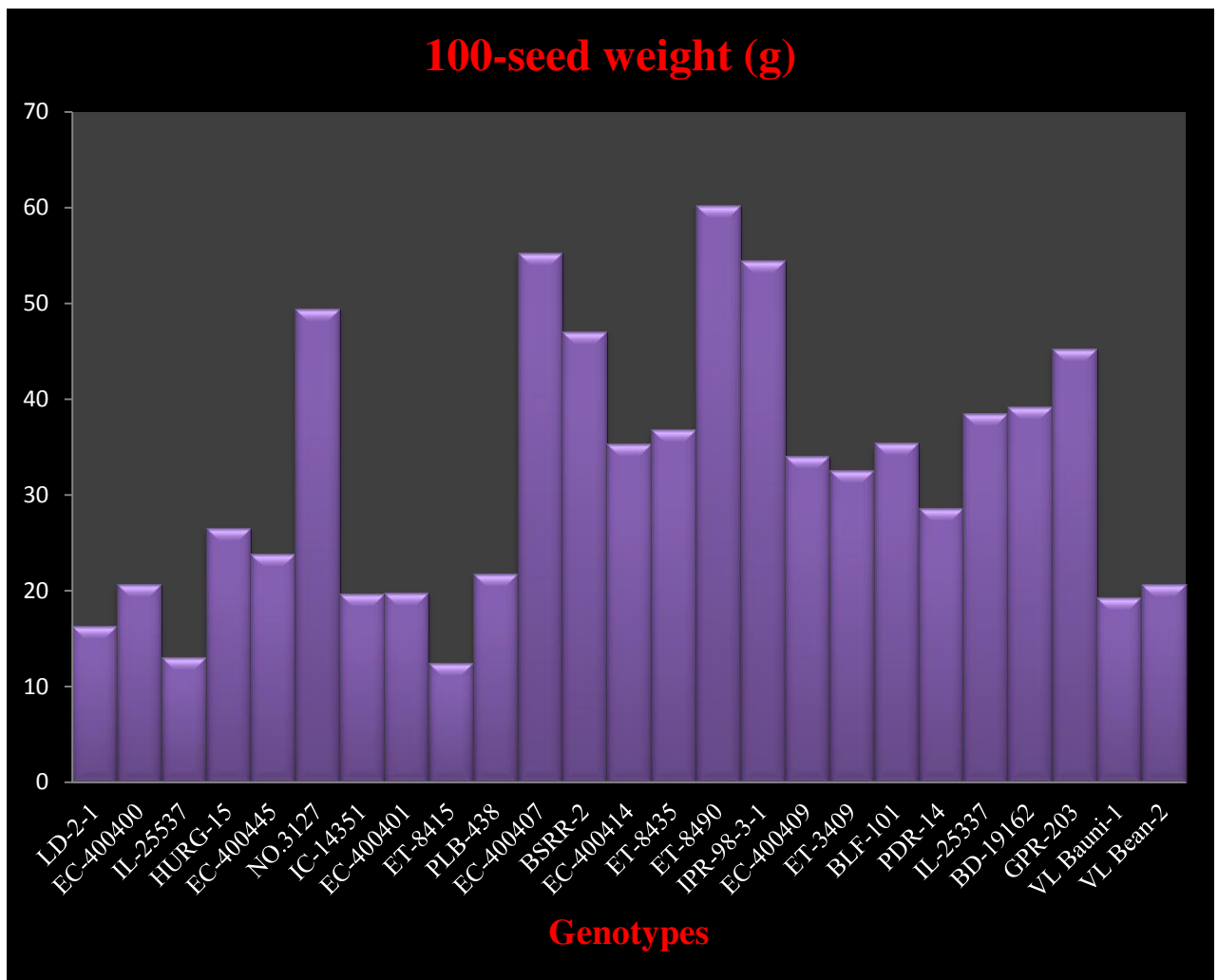


Fig-4.20:-Justified 100-seed weight (g) of the French bean genotypes

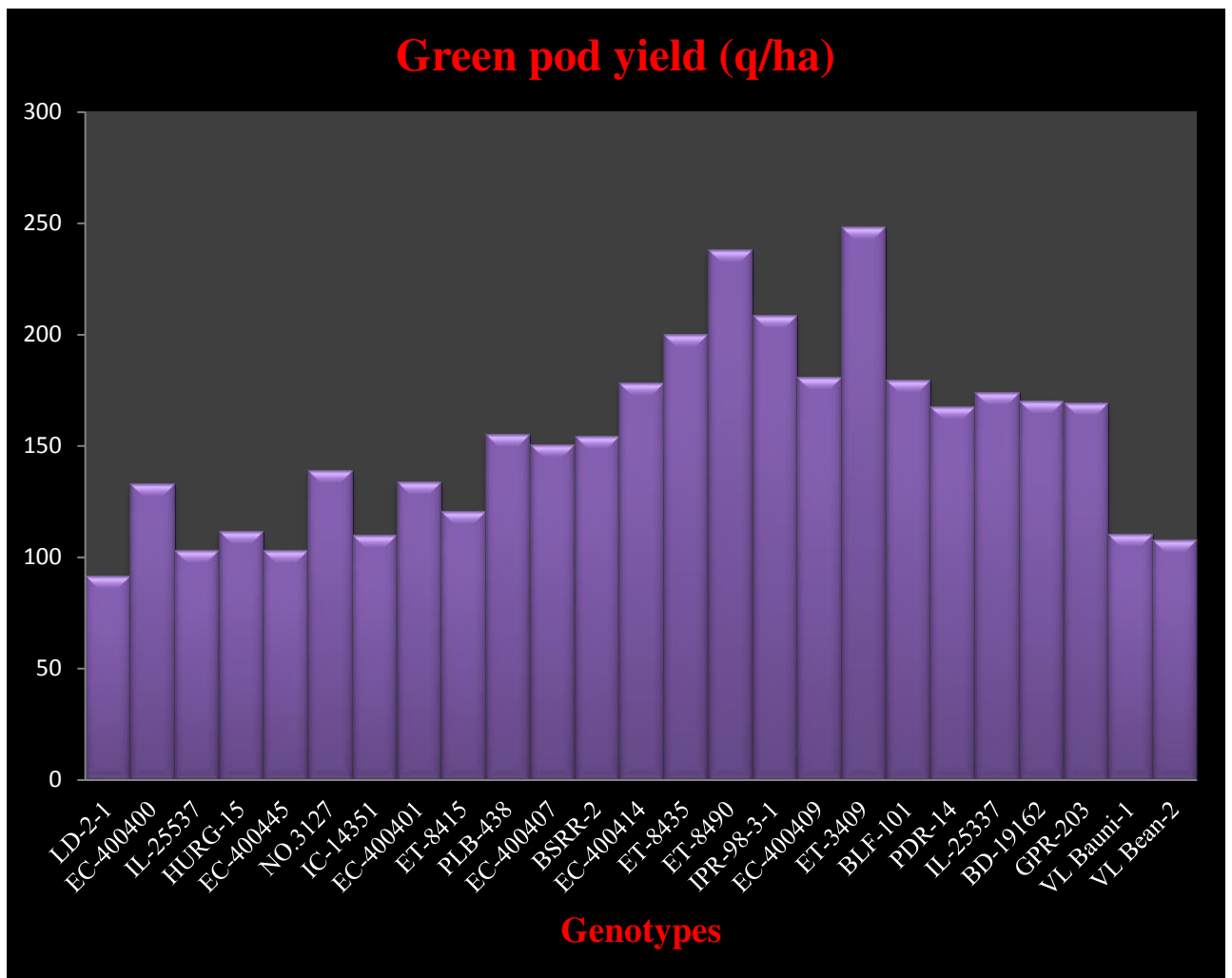


Fig-4.21:-Justified green pod yield (q/ha) of the French bean genotypes

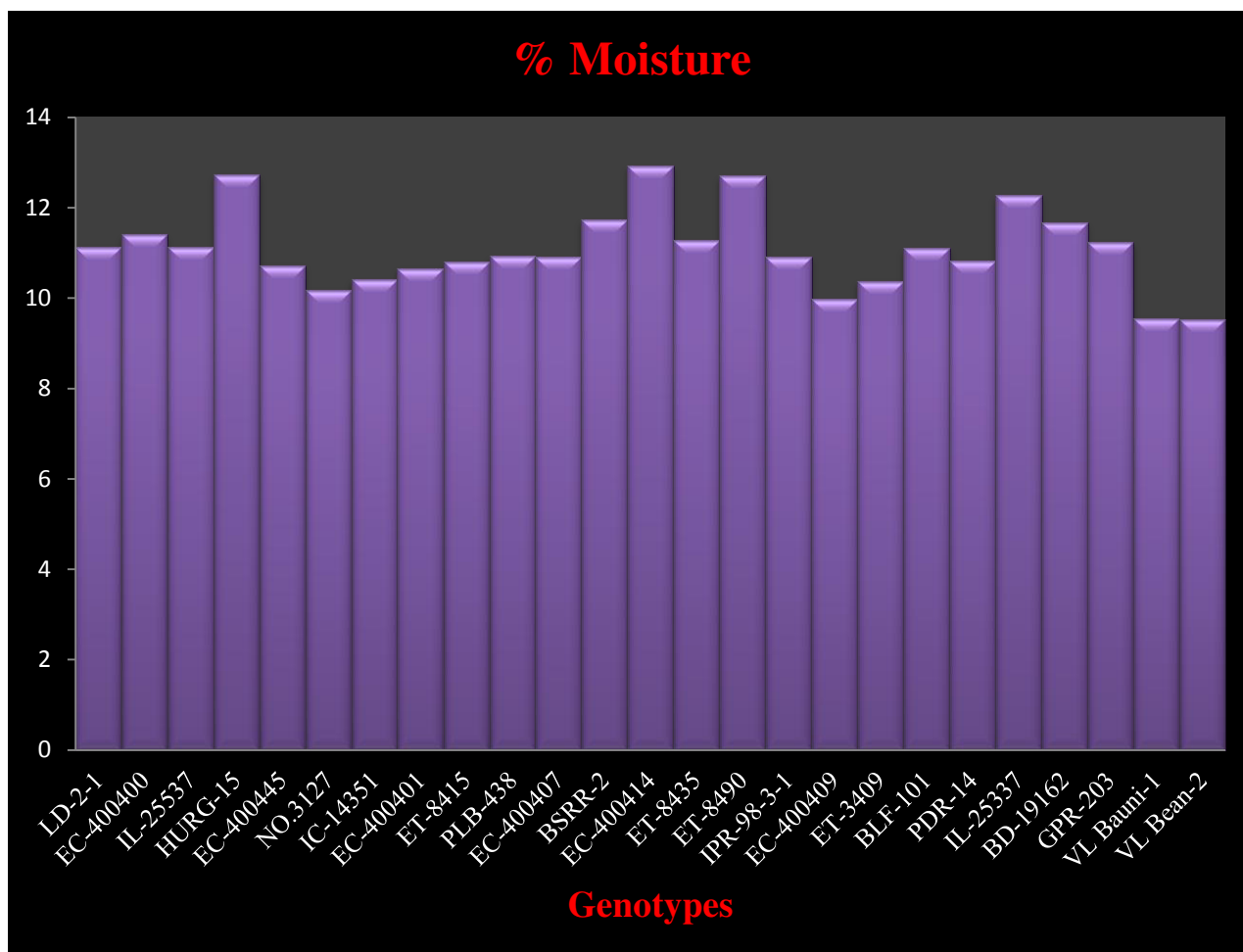


Fig-4.22:-Justified moisture (%) of the French bean genotypes

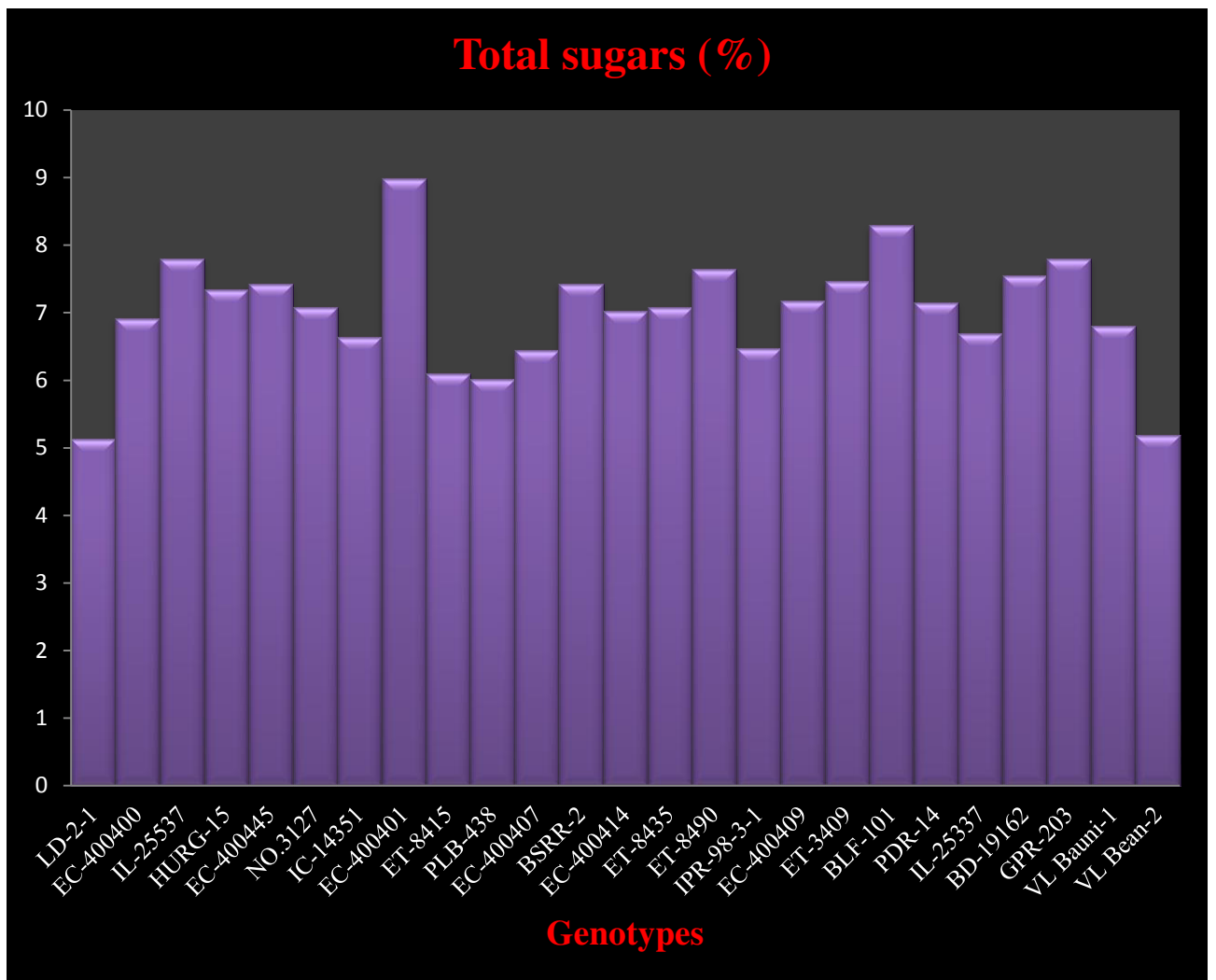


Fig-4.23:-Justified total sugars (%) of the French bean genotypes

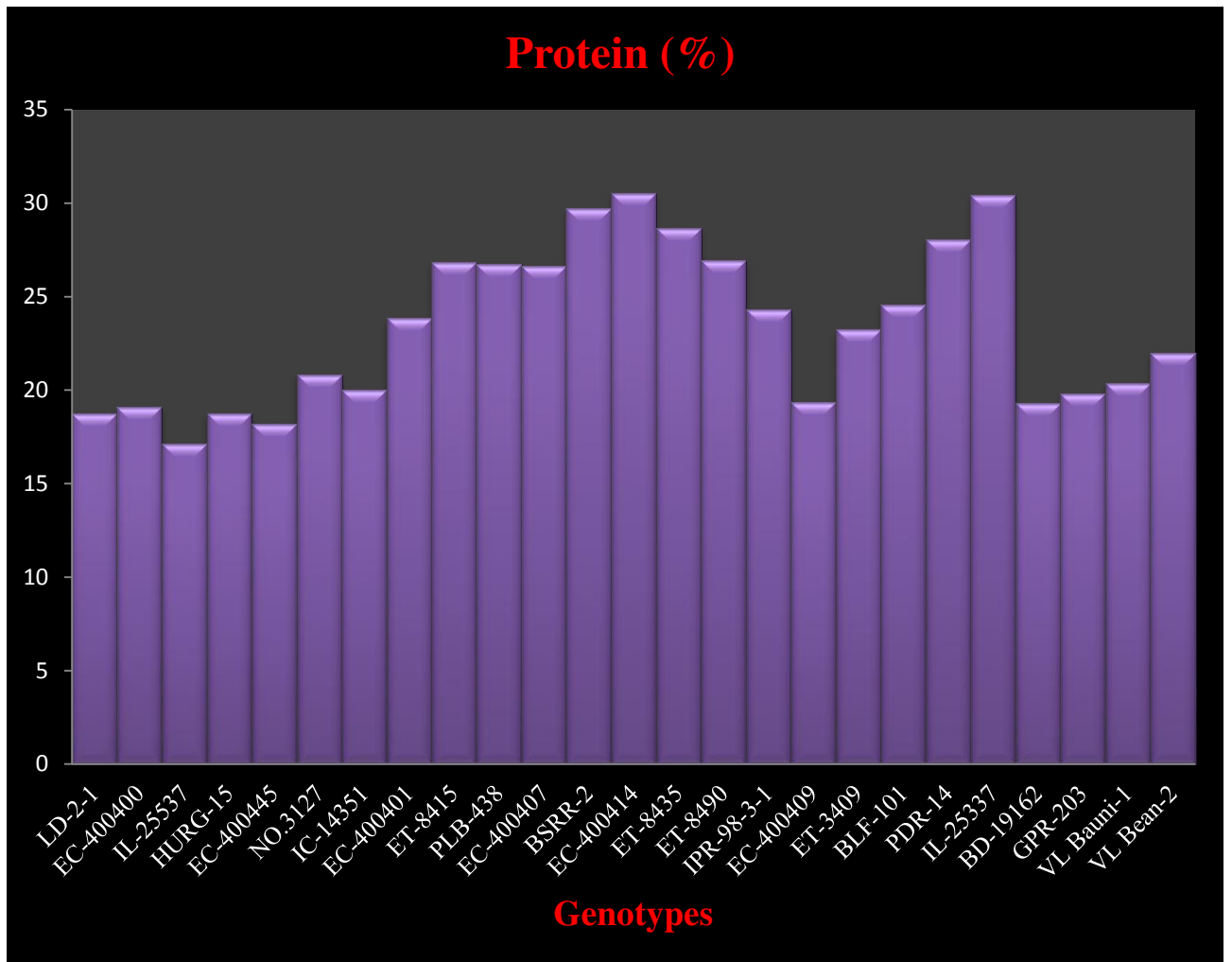


Fig-4.24:-Justified protein (%) of the French bean genotypes

## Phenotypic Coefficient Variability Genotypic Coefficient Variability

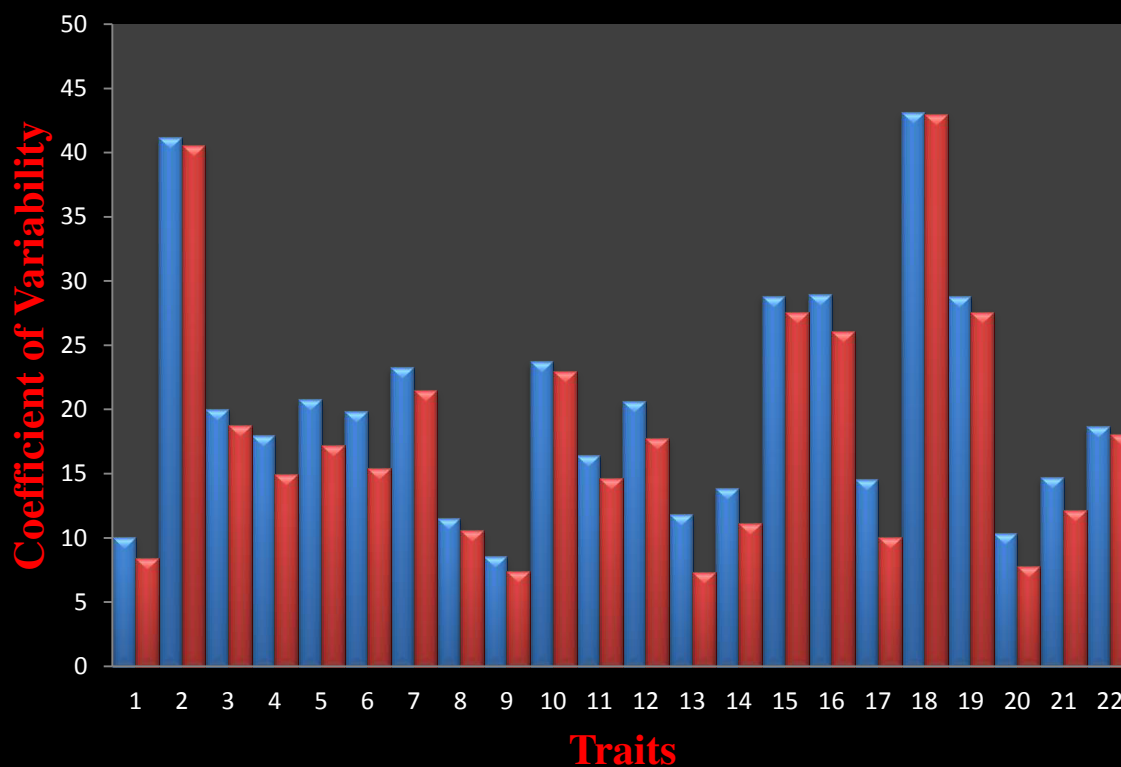


Fig.4.25-Phenotypic and genotypic coefficients of variability for 22 quantitative and qualitative traits in French bean.

- |                            |                                 |                                |                                |
|----------------------------|---------------------------------|--------------------------------|--------------------------------|
| 1= Germination (%)         | 2= Plant height (cm)            | 3= Number of leaves/plant      | 4= Leaf length (cm)            |
| 5= Leaf width (cm)         | 6= Primary branches /plant      | 7= Secondary branches/plant    | 8= Days to first flowering     |
| 9= Days to 50% flowering   | 10= Number of pods /plant       | 11= Green pod length (cm)      | 12= Green pod width (cm)       |
| 13= Green pod breadth (cm) | 14= Single green pod weight (g) | 15= Green pod yield /plant (g) | 16= Green pod yield /plot (kg) |
| 17= Number of seeds /pod   | 18=100-seed weight (g)          | 19= Green pod yield (q/ha)     | 20= Moisture (%)               |
| 21=Total sugars (%)        | 22= Protein (%)                 |                                |                                |

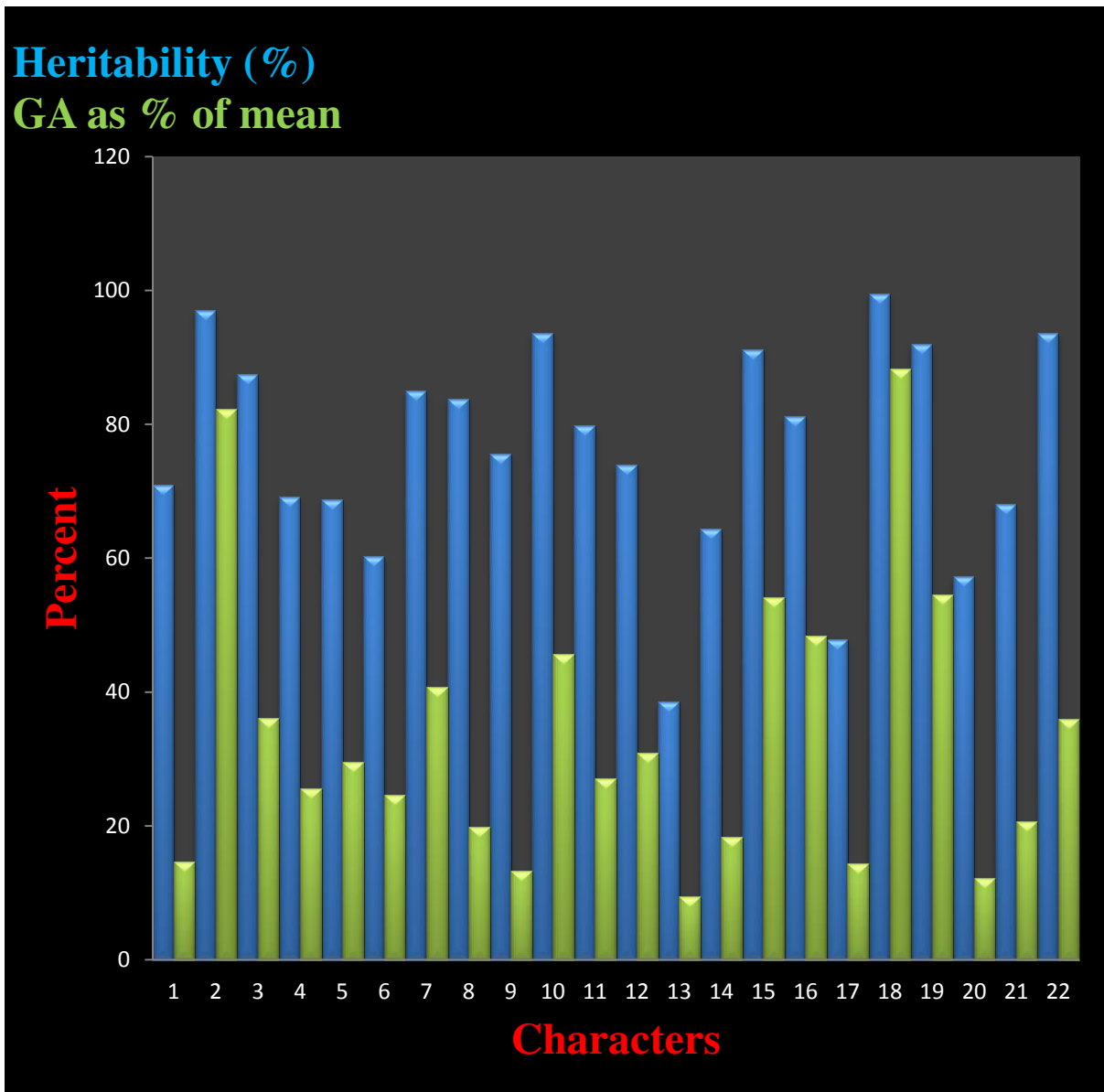


Fig.4.26-Heritability estimate and genetic advance as percent of mean for 22 quantitative and qualitative characters in French bean.

- |                            |                                 |                                |                                |
|----------------------------|---------------------------------|--------------------------------|--------------------------------|
| 1= Germination (%)         | 2= Plant height (cm)            | 3= Number of leaves/plant      | 4= Leaf length (cm)            |
| 5= Leaf width (cm)         | 6= Primary branches /plant      | 7= Secondary branches/plant    | 8= Days to first flowering     |
| 9= Days to 50% flowering   | 10= Number of pods /plant       | 11= Green pod length (cm)      | 12= Green pod width (cm)       |
| 13= Green pod breadth (cm) | 14= Single green pod weight (g) | 15= Green pod yield /plant (g) | 16= Green pod yield /plot (kg) |
| 17= Number of seeds /pod   | 18=100-seed weight (g)          | 19= Green pod yield (q/ha)     | 20= Moisture (%)               |
| 21=Total sugars (%)        | 22= Protein (%)                 |                                |                                |

## 1<sup>st</sup> Set Vegetative Growth and Yield and Yield Attributing Traits:

**Table-4.11 Estimates of genotypic correlation coefficients morphological and yield characters in French bean.**

Character s	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1 G	1.000	0.355*	0.367*	0.574**	0.581**	0.282*	0.434**	-0.486	-0.639*	0.433**	0.304*	0.586**	0.281*	0.517**	0.315*	0.315*	0.401**	0.219*	0.313*
2 G	0.355**	1.000	0.778**	0.120	0.204*	0.482**	0.461**	0.153	-0.039	0.658**	0.214	0.127	0.147	0.072	0.543**	0.593**	-0.178	0.099	0.544**
3 G	0.367**	0.778**	1.000	0.326*	0.197	0.437**	0.314*	0.098	-0.121	0.589**	0.397*	0.486**	-0.028	0.209*	0.291*	0.307*	0.159	-0.195	0.290*
4 G	0.574**	0.120	0.326*	1.000	0.660**	0.447**	0.498**	-0.275	-0.403*	0.496**	0.608**	0.587**	0.261	0.587**	0.277*	0.292*	0.510**	0.257*	0.277*
5 G	0.581**	0.204*	0.197	0.660**	1.000	0.145	0.633**	-0.271	-0.319*	0.519**	0.595**	0.502**	0.295*	0.424**	0.335*	0.367*	0.353*	0.398*	0.334*
6 G	0.282*	0.482**	0.437**	0.447**	0.145	1.000	0.467**	0.277*	0.004	0.593**	0.301*	0.175	0.093	0.270	0.560**	0.591**	0.110	0.222*	0.561**
7 G	0.434**	0.461**	0.314*	0.498**	0.633**	0.467**	1.000	-0.068	-0.296*	0.810**	0.408**	0.288*	0.357*	0.329*	0.747**	0.747**	0.381*	0.586**	0.747**
8 G	-0.486**	0.153	0.098	-0.275*	-0.271*	0.227*	-0.068	1.000	0.928**	0.093	-0.018	-0.380*	-0.397*	-0.312	-0.086	-0.053	-0.315	-0.132	-0.085
9 G	-0.639**	-0.039	-0.121	-0.403*	-0.319*	0.004	-0.296*	0.928**	1.000	-0.149	-0.083	-0.474*	-0.418*	-0.449	-0.287	-0.248	-0.464	-0.162	-0.286
10 G	0.433**	0.658**	0.589**	0.496**	0.519**	0.593**	0.810**	0.093	-0.149	1.000	0.594**	0.370*	0.043	0.360*	0.661**	0.675**	0.410**	0.401	0.661**
11 G	0.304*	0.214*	0.397*	0.608**	0.595**	0.301*	0.408**	-0.018	-0.083	0.594**	1.000	0.447**	0.023	0.291	0.142	0.167	0.463**	0.179	0.141
12 G	0.586**	0.127	0.486**	0.587**	0.502**	0.175	0.288	-0.380*	-0.474*	0.370*	0.447**	1.000	0.132	0.610**	0.077	0.058	0.524**	0.133	0.075
13 G	0.281**	0.147	-0.028	0.261*	0.295*	0.093	0.357*	-0.397*	-0.418*	0.043	0.023	0.132	1.000	0.202	0.300*	0.305*	-0.006	0.403**	0.300*
14 G	0.517**	0.072	0.209*	0.587**	0.424**	0.270*	0.329*	-0.312*	-0.449*	0.360*	0.291*	0.610**	0.202	1.000	0.144	0.157	0.209	0.209	0.143
15 G	0.315*	0.543**	0.291*	0.277*	0.335*	0.560**	0.747**	-0.086	-0.287	0.661**	0.142	0.077	0.300*	0.144	1.000	1.001**	0.164	0.674**	1.000**
16 G	0.315*	0.593**	0.307*	0.292*	0.367*	0.591**	0.747**	-0.053	-0.248	0.675**	0.167	0.058	0.305*	0.157	1.001**	1.000	0.090	0.688**	1.002**
17 G	0.401**	-0.178	0.159	0.510**	0.353*	0.110	0.381*	-0.315*	-0.464*	0.410**	0.463**	0.524**	-0.006	0.209*	0.164	0.090	1.000	0.134	0.161
18 G	0.219*	0.099	-0.195	0.257*	0.398**	0.222*	0.586**	-0.132	-0.162	0.401**	0.179	0.133	0.403*	0.209*	0.674**	0.688**	0.134	1.000	0.673**
19 G	0.313*	0.544**	0.290*	0.277*	0.334*	0.561**	0.747**	-0.085	-0.286*	0.661**	0.141	0.075	0.300*	0.143	1.000**	1.002**	0.161	0.673**	1.000

\*and\*\* indicate significant of values at P=0.05 and 0.01, respectively

G= Genotypic

1 = Germination percentage  
6 = Primary branches /plant  
11 = Green pod length (cm)  
16 = Green pod yield /plot (kg)

2 = Plant height (cm)  
7 = Secondary branches/plant  
12 = Green pod width (cm)  
17 = Number of seeds /pod

3 = Number of leaves/plant  
8 = Days to first flowering  
13 = Green pod breadth (cm)  
18 = 100-seed weight (g)

4 = Leaf length (cm)  
9 = Days to 50% flowering  
14 = Single green pod weight (g)  
19 = Green pod yield (q/ha)

5 = Leaf width (cm)  
10 = Number of pods /plant  
15 = Green pod yield /plant (g)

**Table-4.12 Estimates of phenotypic correlation coefficients morphological and yield characters in French bean.**

Character	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1 p	1.000	0.288*	0.274	0.358*	0.379*	0.145	0.308*	-0.365*	-0.465*	0.383*	0.186	0.462**	0.184	0.360*	0.279*	0.261*	0.277*	0.192	0.268*
2 p	0.288*	1.000	0.720**	0.109	0.171	0.386*	0.419**	0.137	-0.030	0.631**	0.190	0.107	0.102	0.061	0.511**	0.538**	-0.102	0.098	0.514**
3 p	0.274*	0.720**	1.000	0.229	0.144	0.353*	0.250*	0.080	-0.078	0.531**	0.299*	0.388*	-0.026	0.134	0.256*	0.260*	0.068	-0.186	0.256*
4 p	0.358*	0.109	0.229*	1.000	0.480**	0.257*	0.335*	-0.196	-0.320	0.413**	0.460**	0.371*	0.165	0.337*	0.235*	0.251*	0.327*	0.224*	0.226*
5 p	0.379*	0.171	0.144	0.480**	1.000	0.169	0.489**	-0.172	-0.171	0.412**	0.482**	0.348*	0.161	0.299*	0.251*	0.292*	0.073	0.336*	0.233*
6 p	0.145	0.386*	0.353*	0.257*	0.169	1.000	0.315*	0.101	0.048	0.440**	0.229	0.042	-0.028	0.192	0.418**	0.388*	0.031	0.171	0.416**
7 p	0.308*	0.419**	0.250*	0.335*	0.489**	0.315*	1.000	-0.082	-0.244*	0.690**	0.338*	0.212	0.228	0.287*	0.642**	0.607**	0.232*	0.535**	0.641**
8 p	-0.365*	0.137	0.080	-0.196	-0.172	0.101	-0.082	1.000	0.849**	0.070	0.039	-0.307*	-0.230*	-0.208	-0.082	-0.045	-0.203	-0.117	-0.080
9 p	-0.465*	-0.030	-0.078	-0.320*	-0.171	0.048	-0.244	0.849**	1.000	-0.134	-0.057	-0.393*	-0.305*	-0.246*	-0.263*	-0.219	-0.300*	-0.140	-0.248
10 p	0.383*	0.631**	0.531*	0.413**	0.412**	0.440**	0.690**	0.070	-0.134	1.000	0.515**	0.309*	0.039	0.272*	0.611**	0.583**	0.270*	0.387*	0.612**
11 p	0.186	0.190	0.299*	0.460**	0.482**	0.229*	0.338*	0.039	-0.057	0.515**	1.000	0.321*	0.055	0.230*	0.110	0.107	0.273*	0.162	0.105
12 p	0.462*	0.107	0.388*	0.371*	0.348*	0.042	0.212	-0.307*	-0.393*	0.309*	0.321*	1.000	0.056	0.418**	0.081	0.069	0.302*	0.112	0.101
13 p	0.184	0.102	-0.026	0.165	0.161	-0.028	0.228	-0.230*	-0.305*	0.039	0.055	0.056	1.000	0.153	0.181	0.225*	-0.029	0.239*	0.180
14 p	0.360*	0.061	0.134	0.337*	0.299*	0.192	0.287*	-0.208	-0.246*	0.272*	0.230	0.418**	0.153	1.000	0.079	0.069	0.026	0.168	0.096
15 p	0.279*	0.511**	0.256*	0.235*	0.251*	0.418**	0.642**	-0.082	-0.263*	0.611**	0.110	0.081	0.181	0.079	1.000	0.926**	0.138	0.643**	0.976**
16 p	0.261*	0.538**	0.260*	0.251*	0.292*	0.388*	0.607**	-0.045	-0.219	0.583**	0.107	0.069	0.225	0.069	0.926**	1.000	0.087	0.623**	0.927**
17 p	0.277*	-0.102	0.068	0.327*	0.073	0.031	0.232*	-0.203	-0.300*	0.270*	0.273*	0.302*	-0.029	0.026	0.138	0.087	1.000	0.097	0.134
18 p	0.192	0.098	-0.186	0.224*	0.336*	0.171	0.535**	-0.117	-0.140	0.387*	0.162	0.112	0.239*	0.168	0.643**	0.623**	0.097	1.000	0.644**
19 p	0.268*	0.514**	0.256*	0.226*	0.233*	0.416**	0.641**	-0.080	-0.248*	0.612**	0.105	0.101	0.180	0.096	0.976**	0.927**	0.134	0.644**	1.000

**\*and\*\* indicate significant of values at P=0.05 and 0.01, respectively**

**P= Phenotypic**

1 = Germination percentage  
6 = Primary branches /plant  
11 = Green pod length (cm)  
16 = Green pod yield /plot (kg)

2 = Plant height (cm)  
7= Secondary branches/plant  
12 = Green pod width (cm)  
17 = Number of seeds /pod

3= Number of leaves/plant  
8= Days to first flowering  
13= Green pod breadth (cm)  
18=100-seed weight (g)

4 = Leaf length (cm)  
9 = Days to 50% flowering  
14 = Single green pod weight (g)  
19 = Green pod yield (q/ha)

5 = Leaf width (cm)  
10 = Number of pods /plant  
15 = Green pod yield /plant (g)

**Table-4.13 Genotypic path coefficient analysis (direct and indirect effects) for morphological and yield characters in French bean.**

Character s		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	G	<b>-0.002</b>	0.003	-0.004	0.002	-0.002	0.000	0.002	0.002	-0.003	0.000	0.000	0.002	0.000	-0.001	0.313	0.002	-0.001	-0.001	0.313
2	G	-0.001	<b>0.008</b>	-0.008	0.001	-0.001	0.000	0.002	-0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.541	0.003	0.000	-0.001	0.544
3	G	-0.001	0.007	<b>-0.011</b>	0.001	-0.001	0.000	0.001	0.000	-0.001	0.000	0.000	0.002	0.000	0.000	0.290	0.002	0.000	0.001	0.290
4	G	-0.001	0.001	-0.003	<b>0.004</b>	-0.003	0.000	0.002	0.001	-0.002	0.000	0.001	0.002	0.000	-0.001	0.276	0.002	-0.001	-0.002	0.277
5	G	-0.001	0.002	-0.002	0.003	<b>-0.004</b>	0.000	0.002	0.001	-0.002	0.000	0.001	0.002	0.000	0.000	0.334	0.002	-0.001	-0.003	0.334
6	G	-0.001	0.004	-0.005	0.002	-0.001	<b>0.000</b>	0.002	0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.558	0.003	0.000	-0.001	0.561
7	G	-0.001	0.004	-0.003	0.002	-0.002	0.000	<b>0.004</b>	0.000	-0.002	0.000	0.000	0.001	0.000	0.000	0.744	0.004	-0.001	-0.004	0.747
8	G	0.001	0.001	-0.001	-0.001	0.001	0.000	0.000	<b>-0.005</b>	0.005	0.000	0.000	-0.002	0.002	0.000	-0.086	0.000	0.000	0.001	-0.085
9	G	0.001	0.000	0.001	-0.002	0.001	0.000	-0.001	-0.004	<b>0.005</b>	0.000	0.000	-0.002	0.000	0.000	-0.286	-0.001	0.001	0.001	-0.286
10	G	-0.001	0.006	-0.006	0.002	-0.002	0.000	0.003	0.000	-0.001	<b>0.000</b>	0.001	0.002	0.000	0.000	0.659	0.004	-0.001	-0.003	0.661
11	G	-0.001	0.002	-0.004	0.003	-0.002	0.000	0.002	0.000	0.000	0.000	<b>0.001</b>	0.002	0.000	0.000	0.141	0.001	-0.001	-0.001	0.141
12	G	-0.001	0.001	-0.005	0.003	-0.002	0.000	0.001	0.002	-0.003	0.000	0.000	<b>0.004</b>	0.000	-0.001	0.076	0.000	-0.001	-0.001	0.075
13	G	-0.001	0.001	0.000	0.001	-0.001	0.000	0.001	0.002	-0.002	0.000	0.000	0.001	<b>0.000</b>	0.000	0.229	0.002	0.000	-0.003	0.300
14	G	-0.001	0.001	-0.002	0.003	-0.002	0.000	0.001	0.001	-0.002	0.000	0.000	0.002	0.000	<b>-0.001</b>	0.143	0.001	0.000	-0.001	0.143
15	G	-0.001	0.005	-0.003	0.001	-0.001	0.000	0.003	0.000	-0.002	0.000	0.000	0.000	0.000	0.000	<b>0.996</b>	0.005	0.000	-0.004	1.000
16	G	-0.001	0.005	-0.003	0.001	-0.001	0.000	0.003	0.000	-0.001	0.000	0.000	0.000	0.000	0.000	0.998	<b>0.005</b>	0.000	-0.005	1.002
17	G	-0.001	-0.001	-0.002	0.002	-0.001	0.000	0.001	0.002	-0.003	0.000	0.000	0.002	0.000	0.000	0.163	0.000	<b>-0.002</b>	-0.001	0.161
18	G	0.000	0.001	0.002	0.001	-0.002	0.000	0.002	0.001	-0.001	0.000	0.000	0.001	0.000	0.000	0.672	0.004	0.000	<b>-0.007</b>	0.673

**\*and\*\* indicate significant of values at P=0.05 and 0.01, respectively G= Genotypic Residual value: (Genotypic = 0.0000) Bold figures indicate direct effects.**

1 = Germination percentage  
6 = Primary branches /plant  
11 = Green pod length (cm)  
16 = Green pod yield /plot (kg)

2 = Plant height (cm)  
7= Secondary branches/plant  
12 = Green pod width (cm)  
17 = Number of seeds /pod

3= Number of leaves/plant  
8= Days to first flowering  
13= Green pod breadth (cm)  
18=100-seed weight (g)

4 = Leaf length (cm)  
9 = Days to 50% flowering  
14 = Single green pod weight (g)  
19 = Correlated with green pod yield (q/ha)

5 = Leaf width (cm)  
10 = Number of pods /plant  
15 = Green pod yield /plant (g)

**Table-4.14 Phenotypic path coefficient analysis (direct and indirect effects) for morphological and yield characters in French bean.**

Character s	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1 p	<b>-0.015</b>	0.005	-0.007	-0.002	-0.022	0.001	0.010	0.023	-0.031	0.009	-0.001	0.022	0.000	0.005	0.219	0.049	0.000	0.001	0.268
2 p	-0.004	<b>0.017</b>	-0.017	-0.001	-0.010	0.003	0.013	-0.008	-0.002	0.015	-0.001	0.005	0.000	0.001	0.400	0.100	0.000	0.001	0.514
3 p	-0.004	0.013	<b>-0.024</b>	-0.001	-0.008	0.003	0.008	-0.005	-0.005	0.013	-0.001	0.019	0.000	0.002	0.201	0.049	0.000	-0.001	0.256
4 p	-0.005	0.002	-0.005	<b>-0.005</b>	-0.028	0.002	0.011	0.012	-0.021	0.010	-0.002	0.018	0.000	0.004	0.184	0.047	0.000	0.002	0.226
5 p	-0.006	0.003	-0.003	-0.002	<b>-0.057</b>	0.001	0.016	0.011	-0.011	0.010	-0.002	0.017	0.000	0.004	0.197	0.055	0.000	0.002	0.233
6 p	-0.002	0.007	-0.008	-0.001	-0.010	<b>0.008</b>	0.010	-0.006	0.003	0.011	-0.001	0.002	0.000	0.002	0.328	0.073	0.000	0.001	0.416
7 p	-0.004	0.007	-0.006	-0.002	-0.028	0.002	<b>0.032</b>	0.005	-0.016	0.017	-0.001	0.010	-0.001	0.004	0.504	0.113	0.000	0.004	0.641
8 p	0.005	0.002	-0.002	0.001	0.010	0.001	-0.003	<b>-0.062</b>	0.056	0.002	0.000	0.015	0.001	0.003	0.064	-0.008	0.000	-0.001	-0.080
9 p	0.007	-0.001	0.002	0.002	0.010	0.000	-0.008	-0.052	<b>0.066</b>	-0.003	0.000	-0.019	0.001	-0.003	-0.207	-0.041	0.000	-0.001	-0.248
10 p	-0.006	0.011	-0.013	-0.002	-0.024	0.003	0.022	-0.004	-0.009	<b>0.024</b>	-0.002	0.015	0.000	0.004	0.479	0.109	0.000	0.003	0.612
11 p	-0.003	0.003	-0.007	-0.002	-0.028	0.002	0.011	-0.002	-0.004	0.013	<b>-0.004</b>	0.015	0.000	0.003	0.086	0.020	0.000	0.001	0.105
12 p	-0.007	0.002	-0.009	-0.002	-0.020	0.000	0.007	0.019	-0.026	0.008	-0.001	<b>0.048</b>	0.000	0.005	0.063	0.013	0.000	0.001	0.101
13 p	-0.003	0.002	0.001	-0.001	-0.009	0.000	0.007	0.014	-0.020	0.001	0.000	0.003	<b>-0.002</b>	0.002	0.142	0.042	0.000	0.002	0.180
14 p	-0.005	0.001	-0.003	-0.002	-0.017	0.001	0.009	0.013	-0.016	0.007	-0.001	0.020	0.000	<b>0.013</b>	0.062	0.013	0.000	0.001	0.096
15 p	-0.004	0.009	-0.006	-0.001	-0.014	0.003	0.021	0.005	-0.017	0.015	0.000	0.004	0.000	0.001	<b>0.784</b>	0.173	0.000	0.005	0.976
16 p	-0.004	0.009	-0.006	-0.001	-0.017	0.003	0.020	0.003	-0.014	0.014	0.000	0.003	-0.001	0.001	0.726	<b>0.187</b>	0.000	0.005	0.927
17 p	-0.004	-0.002	-0.002	-0.002	-0.004	0.000	0.007	0.013	-0.020	0.007	-0.001	0.014	0.000	0.000	0.108	0.016	<b>0.001</b>	0.001	0.134
18 p	-0.003	0.002	0.004	-0.001	-0.019	0.001	0.017	0.007	-0.009	0.009	-0.001	0.005	-0.001	0.002	0.504	0.116	0.000	<b>0.007</b>	0.644

**\*and\*\* indicate significant of values at P=0.05 and 0.01, respectively P= Phenotypic Residual value: (Phenotypic = 0.0393) Bold figures indicate direct effects.**

1 = Germination percentage  
6 = Primary branches /plant  
11 = Green pod length (cm)  
16 = Green pod yield /plot (kg)

2 = Plant height (cm)  
7= Secondary branches/plant  
12 = Green pod width (cm)  
17 = Number of seeds /pod

3= Number of leaves/plant  
8= Days to first flowering  
13= Green pod breadth (cm)  
18=100-seed weight (g)

4 = Leaf length (cm)  
9 = Days to 50% flowering  
14 = Single green pod weight (g)  
19 = Correlated with green pod yield (q/ha)

5 = Leaf width (cm)  
10 = Number of pods /plant  
15 = Green pod yield /plant (g)

## 2<sup>nd</sup> Set Biochemical Aspects

**Table-4.15 Estimates of genotypic correlation coefficients quality characters in French bean.**

Characters		Moisture (%)	Total sugars (%)	Protein (%)	Green pod yield (q/ha)
<b>1</b>	G	1.000	0.242*	0.392*	0.286*
<b>2</b>	G	0.242*	1.000	-0.042	0.309*
<b>3</b>	G	0.392**	-0.042	1.000	0.505**

\*and\*\* indicate significant of values at P=0.05 and 0.01, respectively

G= Genotypic

**Table-4.16 Estimates of phenotypic correlation coefficients quality characters in French bean.**

Characters		Moisture (%)	Total sugars (%)	Protein (%)	Green pod yield (q/ha)
<b>1</b>	P	1.000	0.100	0.298*	0.208*
<b>2</b>	P	0.100	1.000	-0.060	0.270*
<b>3</b>	P	0.298*	-0.060	1.000	0.477**

\*and\*\* indicate significant of values at P=0.05 and 0.01, respectively

P= Phenotypic

**Table -4.17 Genotypic path coefficient analysis (direct and indirect effects) for quality characters in French bean.**

Characters		Moisture (%)	Total sugars (%)	Protein (%)	Correlated with green pod yield (q/ha)
1	G	<b>0.002</b>	0.080	0.203	0.286
2	G	0.001	<b>0.331</b>	-0.022	0.309
3	G	0.001	-0.014	<b>0.518</b>	0.505

**\*and\*\*** indicate significant of values at P=0.05 and 0.01, respectively G= Genotypic

**Residual value: (Genotypic=0.6351)**

**Bold figures indicate direct effects.**

**Table -4.18 Phenotypic path coefficient analysis (direct and indirect effects) for quality characters in French bean.**

Characters		Moisture (%)	Total sugars (%)	Protein (%)	Correlated with green pod yield (q/ha)
1	P	<b>0.034</b>	0.029	0.145	0.208
2	P	0.003	<b>0.296</b>	-0.029	0.270
3	P	0.010	-0.018	<b>0.485</b>	0.477

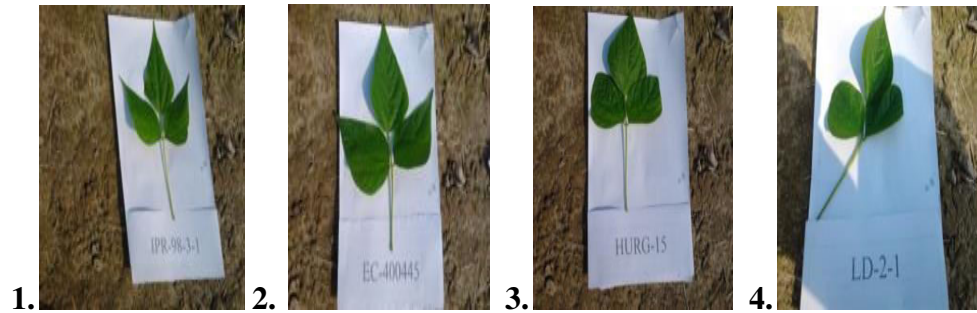
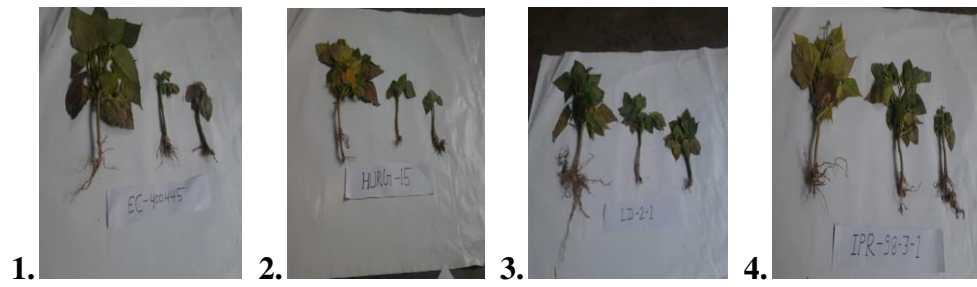
**\*and\*\*** indicate significant of values at P=0.05 and 0.01, respectively P= Phenotypic

**Residual value: (Phenotypic = 0.6819)**

**Bold figures indicate direct effects.**



**Plate-4.5 Yielding plants of French bean genotypes**



**Plate -4.6 Variability in promising genotypes with respect to plant height, leaf shape, floral morphology and pod characters**



**Plate -4.7 Sticks showing the pole type French bean genotypes**

Pulses are consumed as dal, which is a cheap source of plant protein. These are consumed because of body building properties due to presence of various amino acids. These also have medicinal properties. By products of pulses like leaves, pod coats and bran are fed to animals in the form of dry fodder. Some pulse crops like French bean, Gram, Lobia, Urd bean and Mung bean are fed to animals as green fodder. Mung bean plants are also used as green manure which improve soil health and adds nutrient into the soil. French bean is popular legume and vegetable crop of tropical and temperate regions of the global. It is a variously used in different part of the world. Apart from its main use as cooked or fired with sliced onion and garlic or used in salads. They can be boiled together with rice. Leaves are occasionally used as vegetables but few cultivars have leaves of sufficient tenderness. Crop of residue are often used as a fodder. In East and Southern Africa the use of ripe seeds of (*Phaseolus vulgaris* L.) as a pulse is more important than the use of unripe pods or seeds as vegetables. French bean is also rich in minerals and vitamins. Common bean is an important component of agricultural and food systems throughout most of the world. Nutritionally dry bean is a nearly, perfect and rich food. It is an excellent source of protein, carbohydrates and fairly good source of minerals, vitamins, folic acid and dietary fiber (Rehman *et al.* 2001).The tender green pods and dry bean are used in canned, frozen foods, salads, pastas and purees. French bean (*Phaseolus vulgaris* L.) is an extensively cultivated pulse and vegetable crop in India. It is important pulse and vegetable around the world and respect of area, production and productivity, availability and utility. In improvement program, the breeding objectives: 1. To find out the extent of genetic variability in French bean germplasm. 2. To estimate of mean, range and coefficient of variation for yield and its component traits. 3. To investigate the genotypic and phenotypic coefficient of variation for different yield and yield attributing traits of French bean. 4. To determine heritability (broad sense) and expected genetic advance in percentage of mean and 5. To evaluated genotypes contributing towards yield by correlation and path coefficient analysis should be clear so, as to apply appropriate methodology for achieving the desired target. Before initiating any improvement programme one must wild up a germplasm pool that will serve as a gene complex reservoir for different characters and cons equality provide better source of variability, which forms the base for improvement. Since limited information is available on genetic diversity in French bean with respect to morphological and quality characters.

Therefore, an attempt has been made in the present investigation to study the genetic variability in the available French bean germplasm. Possibility of achieving improvement in any crop plants leans heavily on the magnitude of genetic variability. In French bean, pod yield a complex character is not only influenced by their associated characters which are governed by number of genes, but also by environment. So to make selection effective, it is necessary to separate genetic variability from total variability. Since yield is associated with its component characters, it is essential to know the degrees of mutual association as well as to expose the direct and indirect contribution of each component. Being a self pollinated crop, the variability available in French bean needs evaluation which is helpful for breeders to adopt suitable breeding programme for further improvement. Leguminous vegetables have been cultivated for more than 6000 years in different parts of the world. Legumes for human consumption constitute about 5 % of cultivated crops (Shanmugasundaram, 1990). Leguminous vegetable serves as a major source of protein in a diet. To meet the situation of increasing rate of population there is a need to identify and popularize new crop species yielding multiple useful products having food, industrial, forage and nutritional value. Tender pods of French bean are rich in minerals like calcium, phosphorus, iron, vitamin A and C. Immature pods are dried and fried like potato chips and can be cooked like French bean. Because of its highly drought tolerating property, much of its area is concentrated in states like Rajasthan, Gujarat and Haryana. In Karnataka, though large extent of area is under arid and semi-arid experiencing frequent drought, French bean cultivation is revised in high especially for dry seed Ram *et al.* (1988) and has not been rather for vegetable purpose. The present investigations were carried out with twenty five genotypes of French bean. These genotypes were evaluated for some important characters viz., germination (%), plant height (cm), primary branches/ plant, secondary branches/ plant, number of leaves /Plant, size of leaves (length and width cm), days to first flowering, days to 50 percent flowering, flower colour, number of pods/ plant, number of seeds/ pod, green pod length (cm), green pod width (cm), green pod breadth (cm), single green pod weight (g), green pod yield per plant (g), green pod yield per plot (kg), green pod yield (q/ ha), 100- seed weight (g), moisture(%), total sugars(%)and protein(%). The parameters of variability such as coefficient of variation, heritability, correlation, path, genetic advance and genetic gain were computed so, as to help breeders to select desirable genotypes for different characters. Genotypic and phenotypic correlation were work out the degree of association of different component characters with green pod yield (q/ha) and path coefficient analysis was done to provide information on the case of this association (Wright, 1921; Dewey and Lu, 1959). The quantification of available

variability was therefore, carried out for morphological and quality characters in order to identify desirable genotypes based on performance , and to select promising donors for various characters that may be used for hybridization programme to obtain useful recombination and to create additional genetic variability. Success of crop improvement programmes depends largely on the extent of variability present in the germplasm stock for the traits for which the improvement is aimed at. The knowledge of genetic variability and association of various characters are essential in planning the breeding programmes. With this perspective, in the present investigation, 25 accessions of French bean were evaluated for green vegetable pod yield along with its contributing characters. The proportion of variability, broad sense heritability, and genetic advance over mean was estimated. The association among the characters and their direct and indirect effect on yield and genetic divergence were studied. To estimates of different statistical parameters such as variability, correlation coefficient, path analysis helps in deciding the best possible breeding approach to be employed for the improvement for yield and quality of French bean. The experiments results obtained on various attributes and these investigations are discussed under the following heads:

#### 5.1 Evaluation of French bean genotypes

##### 5.1.1 Variability

##### 5.1.2 Heritability and genetic advance

##### 5.1.3 Correlation coefficient

##### 5.1.4 Path analysis

#### **5.1.1 -Variability**

In the present studies, analysis of variance indicated highly significant differences for all characters studied. Although breeding programme depends up on variability present, but absolute variability in different characters cannot be the decisive factor for deciding as to which characters is showing the highest degree of variability. The relative values of phenotypic variance, genotypic variance and coefficient of variance (PCV and GCV), give an idea about the magnitude of variability present in a population, among morphological characters, maximum variation was observed for 100-seed weight followed by plant height for both phenotypic variance and genotypic variance. The variance was very low for characters like days to 50% flowering, germination percent, days to first flowering and green pod yield/plot. The results get support from the findings of Johnson *et al.*(1955) and Vikas and Singh(1999). In the present studies the information obtained shows that the estimates of

PCV were higher than the GCV meaning there by that the apparent variation was not only due to genotypes but also environment influenced. These mentioned characters having higher range of variation like that, green pod yield (q/ha), green pod yield/plant, germination percent, plant height, and number of leaves/plant have better scope of improvement through selection characters such as green pod yield/plant, green pod yield/plot and green pod yield(q/ha). The results are in accordance with findings of Joshi and Mehra (1983), Shah *et al.* (1986), Saha *et al.* (1990), Singh *et al.*(1994), Korla *et al.* (1998), Singh *et al.* (2000) and Govanakoppa (2001). Results showed the moderate value of GCV and PCV, which is considered sufficient to make an effective selection. In the present studies the GCV and PCV estimates revealed that appreciable variation for characters like 100-seed weight, green pod yield (q/ha), plant height, green pod yield/plant and green pod yield/plot which suggest important of these characters in the improvement programme were reported by Sharma *et al.* (1977) and Shah *et al.* (1999). With the help of GCV alone, it is a possible to determine the amount of variation that is heritable.

### **5.1.2- Heritability and genetic advance**

The relative degree to which a characters is transmitted from parent to offspring is indicated by the estimates of heritability, if character showed high heritability value, it indicates that there is has influence for environment in its expression. Accordingly, such traits have an option to be improved by adopting simple selection methods. Heritability estimates along with genetic advance are normally help full in predicting the gain under selection than heritability estimate alone. Hence, both heritability and genetic advance were determined to get a clear picture of the scope for improvement in various characters though selection. The coefficient of variation indicates only the extent of variability present in different characters and does not indicate the heritable portion. This could be ascertained from the heritability estimates, which in broad sense includes both additive and non-additive gene effects Hanson *et al.*(1956), while narrow sense heterosis includes only additive components (Lush, 1940) in animals and Johnson *et al.* (1955) in plants. Knowledge about heritability of a trait is helpful and enables the plant breeder to decide about selection to be followed for the improvement of traits under a given situation. It is known that heritability estimates are useful while making selection based on phenotype. Nevertheless, genetic advance helps to measure the amount of progress that could be expected with selection in a character. So the estimates of heritability have a role to play in determining the effectiveness of selection for characters coupled with

genetic advance as suggested by (Panse, 1957), Johnson *et al.* (1955). The present study estimated both heritability and genetic advance. The discussion of the results is given. In the present investigations characters like 100-seed weight, plant height, moisture percent, number of pods/plant, green pod yield/plant and protein percent all quality characters showed very high heritability estimates, while number of leaves/plant, secondary branches/plant, days to first flowering and green pod yield/plot exhibited medium heritability estimates. The results is in consonance with the research of Liang and Waltre (1969), Joshi and Mehra (1983) for green pod yield per plant and number of secondary branches per plant; Saha *et al.* (1990) for green pod width; Govanakoppa (2001) for number of primary branches per plant and green pod yield per plant and Nimbalkar *et al.* (2002) for plant height, green pod length and number of green pods per plant. Its suggests the highly heritable nature of variability for these characters and effectiveness of selection. Broad sense heritability the portion of genetic advance to the phenotypic variance is improvement parameters in breeding and genetics. The heritability estimates together with expected genetic gain is usually more reliable than either these of two parameters alone in predicting the resultant effects of selecting the best individuals Johnson *et al.* (1955). High heritability accompanied with high genetic advance indicates that most likely the heritability is due to additive gene effects and selection may be effective, from this point of view 100-seed weight, plant height, number of seeds/pod, green pod yield/plant, green pod yield/plot and secondary branches/plant possessed greater estimates of genetic advance as percent of mean coupled with high amount of heritability indicating these traits are governed by additive gene action and continued selection would be help in modifying the mean performance of the population. Johnson *et al.* (1955) reported similar observations. High heritability coupled with moderate genetic advance were expressed by the traits like 100-seed weight, secondary branches/plant, green pod width, single green pod weight, total sugars and protein. It indicates equal contribution of additive and non-additive gene for these traits. The characters, green pod width, no. of seeds/pod, moisture, primary branches/ plant single green pod weight and total sugars, showed low heritability accompanied with low genetic advance medicating non-additive gene action for expression of these traits. Similar results were observed with the findings of Joshi and Mehra (1983) for number of secondary branches per plant, green pod length and number of green pods per plant; Shah *et al.* (1986) for number of primary branches per plant, green pod length, green pod width, number of green pods per plant and green pod yield per plant and Saha *et al.* (1990) for single green pod weight and green pod yield per plant. Moderate genetic advance over mean was recorded for plant height. Similar result was recorded by

Govanakoppa (2001). These confirm the findings of Burton (1952), that GCV together with heritability estimates would give a better picture of genetic advance under selection. It is also clear from the present study (Table- 3) that traits like 100-seed weight, plant height, pods/plant, protein (%) and green pod yield (q/ha) possessing high GCV, heritability and genetic advance could be effectively used in selection, as it has been suggested that characters with high heritability coupled with high genetic advance would respond to selection better than with high heritability and low genetic advance Johnson *et al.* (1955).

The variability and high heritability along with high genetic advance expressed by the above mentioned traits indicated that genotypes could be evaluated in multi location trials and selected as donors for these characters or used as parents in hybridization programme traits.

### **5.1.3- Correlation coefficient**

Yield is the ultimate product in which breeder is interested. It is highly complex quantitative character, governed by polygenes. Its expression depends largely on the environment as polygenes are highly sensitive to the environment. Hence, the selection of superior genotypes based on yield may not be effective. For rational approach towards the improvement of yield, selection has to be operated through associated characters. Study of association of yield component with yield assumes special importance and forms basis for selecting desired strain. In the present investigation, the estimates of genotypic correlation were in general higher than phenotypic correlation showing masking by environmental effects was little and indicating the presence of inherent association between various characters. Correlation studying provides better understanding of yield component that helps the plant breeder during selection. A positive correlation between desirable characters is favourable to the plant breeder because it helps in simultaneously improvement in both the characters. A negative correlation, on other hands, will under the simultaneously expression of both characters with high values. In such situations, some economic compromise has to be made. The correlation studies showed higher estimates of genotypes correlation coefficient than the corresponding PCV similar such findings were also reported by Saha *et al.*(1990) and Kumar Swamy (1990), which showed that the apparent due to favourable influence of improvement. In the present investigation, yield exhibited positive and significant association with all the characters viz., germination percent, plant height, number of leaves/plant, leaf length, leaf width, primary branches/plant, secondary branches/plant, number of pods/plant, green pod breath, green pod yield/plant, green pod yield/plot and 100- seed weight. Thus it may be

deduced that the selection based on these traits either in combination or alone would be beneficial to identify the genotypes having better yield potential. This is in agreement with findings of Rai *et al.* (2001) and Kumar Swamy (1990). It had a also non-significant positive correlation with green pod length, single green pod weight and number of seeds/pod as reported by Shah *et al.*(1986) and Singh *et al.* (2000), and negative significant correlation coefficient with number of leaves/plant. Green pod yield (q/ha) showed positive significant correlation with leaf length, leaf width, primary branches/plant, secondary branches/plant, number of pods/plant, green pod length, green pod width, single green pod weight, green pod yield/plant, green pod yield/plot and green pod yield(q/ha). Hence, 100-seed weight showed positive and highly significant association with green pod yield breeder can rely upon all these twenty character in selecting plant with high yield in French bean. Similar type of association were reported by Natarajan and Arumugam (1980) for number of secondary branches per plant, green pod length and number of pods per plant; Saha *et al.* (1990) for single green pod weight; Kumar (1993) for number of primary branches per plant and number of high green pods per plant and Singh (1993) for plant height. Days to 50% flowering showed non-significant negative correlation with all the morphological traits at both the level. Non-significant negative correlation with yield and most of the yield contributing traits, suggest that days to 50% flowering is a undesirable characters and for improvement in yield attention should be give for selecting of genotypes having green pod yield/plant. Corroborated the findings by Kumar Swamy (1990). Green pod yield had significant and positive correlation with number of pods/plant and green pod yield/plant this is consonance with the results of Natarajan and Arumugam (1980) and Nimbalkar *et al.* (2002) for quality characters also, the correlation studies showed higher estimates of GCV than corresponding PCV in the present investigation green pod yield exhibited significant and positive correlation coefficient with all quality characters, viz., moisture, total sugars and protein. So, for no relevant literature was available concerning the association among total sugars and protein quality characters. Hence, further, investigations on this aspect are suggested. The significantly positive associations suggest that selection should be oriented towards higher content of moisture, total sugars, protein and thus ultimately resulting in higher green pod yield content. The highly significant and positive association among the three quality parameters indicated immense scope for improvement of these characters. Similar results were obtained by Natarajan and Arumugam (1980) and Nimbalkar *et al.* (2002). It is obvious that the increase in number of primary branches and secondary branches per plant will increase in number of green pods per plant ultimately it resulted in higher green pod yield.

#### 5.1.4- Path analysis

Though correlation indicates the association pattern of component trait with green pod yield (q/ha), they simply represent the overall influence of a particular trait on green pod yield (q/ha) without revealing the cause and effect relationship. The path analysis as suggested by Wright (1921) helps to resolve these correlations further and throws more light on the way in which component trait interact to influence green pod yield (q/ha) which enable the breeders to specifically identify component traits of green pod yield (q/ha). Path analysis there is helpful in elucidating patterns of association through direct and indirect effects. Present investigation revealed that out of 22 characters studied. Correlation studies alone are not sufficient to ascertain a clear association among the characters as more variables are considered in the correlation. Path coefficient has been therefore, suggested by Wright (1921) various characters and helps in understanding the direct and indirect contribution of various independent variables towards dependent variables (yield for morphological and quality characters). The results of the path coefficient analysis indicated the direct and indirect effects of the 19 morphological and 3 quality contributing characters on the green pod yield (q/ha). The highest direct effect on green pod yield was contributed green pod yield/plant followed by leaf width. Further, the green pod yield/plot and number of leaves/plant indirectly influenced the green pod yield through leaf width, primary branches/plant, secondary branches/plant, days to 50% flowering, number of pods/plant, green pod width, single green pod weight, green pod yield/plot, number of seeds/pod and 100-seed weight also showed considerable direct effects on the green pod yield (q/ha) indicated that these characters are important in the section program. path coefficient analysis for morphological traits were also studied by Baswana *et al.* (1980) and Biju *et al.* (2001) in Indian bean, Rai *et al.* (2001) in French bean and Patil *et al.* (1989) in cowpea. Among the quality parameters, the highest direct effect on green pod yield (q/ha) was contributed by protein content followed by total sugars and moisture content indirectly influenced by the green pod yield through total sugars content and protein content. This is in consonance with the results of Baswana *et al.* (1980), Biju *et al.* (2001) and Rai *et al.* (2001) in French bean and Patil *et al.* (1989) in cowpea.

## **5.2 Future line of work**

**5.2.1.** Creation of genetic pools with better pod and seed yield.

**5.2.2.** Germplasm characterization of presently available genotypes for traits other than the characters used for study.

**5.2.3.** As an expansion of genetic variability studies, marker assisted analysis can also be carried out to study the variation present among the genotypes.

**5.2.4.** The 100-seed weight (g), green pod yield (q/ha), green pod yield/plant (g), plant height (cm), number of leaves/plant, primary branches/ plant, secondary branches/ plant, number of leaves /Plant, size of leaves (length and width cm), number of pods/ plant, number of grains/ pod, green pod length (cm), green pod width (cm), green pod breadth (cm), single green pod weight (g), green pod yield per plot (kg), recorded high heritability, genetic advance along with significant positive correlation and high direct positive effect on yield. Hence, these characters should be given prime importance in future breeding programme.

**5.2.5.** The genotype 'ET-3409' recorded the highest green pod yield mean values for yield components (plant height, primary branches/plant, secondary branches/plan, single green pod weight, number green pods per plant, green pod yield/plot and green pod yield per plant), which can be used as a donor for the above traits.

**5.2.6.** Integrated nutrient management by using inorganic and biological sources on pod yield, seed yield and quality of French bean needs to be investigated.

**5.2.7.** French bean which is also used as pulse crop (grains), there is an urgent need to study genetic variability for French bean genotypes.

**5.2.8.** Modelling aspects with respect to French bean cultivation should also gain prime importance.

**5.2.9.** Improvement of genotypes can be made through mutation breeding.



**Plate-5.8 Genetic variability in French bean genotypes**

### 6.1-SUMMARY

The principle objective of the present investigations was to study and highlight genetic variability and diversity present in the French bean germplasm collection, to know the association between different morphological, yield and quantitative traits. The present investigations entitled “Studies on genetic variability, correlation and path analysis in French bean (*Phaseolus vulgaris* L.) under Lucknow conditions” were conducted at the Horticulture Research Farm first of the Department of Applied Plant Science (Horticulture), Babasaheb Bhimrao Ambedkar Central University, Vidya Vihar, Rae Bareli Road, Lucknow (U. P.), India during *Rabi* seasons 2012-2013 and 2013-2014, respectively. The data obtained for 22 characters were subjected to statistical analysis for elucidating the information on genetic variation existing for different component characters of vegetable pod yield. The genetic variation was assessed using parameters like genotypic (GCV) and phenotypic (PCV) coefficient of variation, heritability and genetic advance over mean (GAM). The inter character correlation and path analysis were also carried out to know the relationship of different characters with vegetable pod yield. The objectives of present investigations were to study variability in the morphological and quality characters. The present investigations were focused on the following objectives:

1. To find out extent of genetic variability in French bean germplasm.
2. To estimate of mean, range and coefficient of variation for yield and its component traits.
3. To investigate the genotypic and phenotypic coefficient of variation for different yield and yield attributing traits of French bean.
4. To determine heritability (broad sense) and expected genetic advance in percentage of mean.
5. To evaluated genotypes contributing towards yield by correlation and path coefficient analysis.

To determined direct and indirect effect for this study, twenty five genotypes were grown with recommended cultural practices in RBD with three replications. The observations

recorded on twenty three characters viz., germination (%), plant height (cm), primary branches/ plant, secondary branches/ plant, number of leaves /Plant, size of leaves (length and width cm), days to first flowering, days to 50 percent flowering, flower colour, number of pods/ plant, number of seeds/ pod, green pod length (cm), green pod width (cm), green pod breadth (cm), single green pod weight (g), green pod yield per plant (g), green pod yield per plot (kg), green pod yield (q/ ha), 100- seed weight (g), moisture(%), total sugars(%) and protein(%). The data were statistically analyzed for different variability parameters.

The study was carried out during 2012- 2013 and 2013- 2014 at the Horticultural Research Farm first of the Department of Applied Plant Science (Horticulture), Babasaheb Bhimrao Ambedkar Central University, Vidya Vihar, Rae Bareli Road, Lucknow (U. P.), India.

The salient experimental findings of the present investigation are summarized below:

### **6.1.1-Morphological characterization**

- The analysis variance revealed that sufficient variation existed among genotypes for all the characters under investigations.
- The considerable range of variation was observed in germplasm for different characters.
- High magnitude PCV and GCV was observed for 100-seed weight followed by plant height, green pod yield/plot, green pod yield/plant, green pod yield(q/ha), number of pods/plant and secondary branches/plant.
- Highest estimates of heritability in broad sense along with genetic advance as percent of means were recorded for 100-seed weight and plant height. High heritability along with moderate genetic advance were shown by number of pods/plant, protein, green pod yield/plant, green pod yield (q/ha) and number of leaves/plant.
- The characters green pod breath, green pod width, number seeds/pod, primary branches/plant, single green pod weight, green pod yield /plot, moisture and total sugars.
- Correlation analysis revealed that yield exhibited positive and significant associated with green pod yield/plot, green pod yield/plant, secondary

branches/plant, 100-seed weight, number of pods/plant, primary branches/plant and plant height.

- The genotype ET-3409 produced highest yield followed by ET-8490, IPR-98-3-1, EC-400409, and ET-8435 in both the years of investigation.
- Path analysis identified characters such as green pod yield/plant, green pod yield/plot, days to 50% flowering, green pod width, secondary branches/plant, number of pods/plant, plant height, primary branches/plant, 100-seed weight, number of seeds/pod, single green pod weight or having and positive influence on yield.

### **6.1.2-Quality characterization**

- For quality characters green pod yield showed significant and positive correlation coefficient with all three quality characters protein, total sugars and moisture percent, respectively.
- In case of quality characters viz., protein, total sugars and moisture percent content exhibited highest direct effect on green pod yield(q/ha).

## **6.2-Conclusion**

Finally, based on the number of pods/plant, green pod yield/plant, green pod yield/plot, number of seeds/pod, 100-seed weight and green pod yield(q/ha), for Higher yielder genotypes ET-3409, ET-8490 and IPR-98-3-1 were identified to be superior. Whereas, EC-400414, EC-400401 and ET-8490 showed superiority in quality attributes. Coefficient of variability, estimates of heritability and genetic advance as percent of mean, as well as correlation coefficients among yield attributes of French bean recorded in the present investigations substantially revealed the great scope for improvement in many of the desirable economic traits of the crop. However, this trial needs to be repeated time and again to reach the final conclusion.

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# APPENDICES

## Appendix-I Analysis of variance for germination (%).

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	14.875	0.6474		
2.	Treatments	24	340.743	14.831**	1.71	2.60
3.	Error	48	22.975	1.000		
4.	Total	74				

SE (d) = 2.76

CD= 5.556

Result: - \*\* Significant at 0.01% level of significance

**Appendix-II Analysis of variance for plant height (cm).**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	49.203	3.791		
2.	Treatments	24	2495.201	192.38**	1.71	2.60
3.	Error	48	12.977	1.000		
4.	Total	74				

SE (d) = 2.07

CD= 4.174

Result: - \*\*Significant at 0.01% level of significance

**Appendix-III Analysis of variance for number of leaves/plant.**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	3.203	0.220		
2.	Treatments	24	604.588	41.646**	1.71	2.60
3.	Error	48	14.517	1.000		
4.	Total	74				

SE (d) = 2.19

CD= 4.415

Result: - \*\* Significant at 0.01% level of significance

**Appendix-IV Analysis of variance for leaf length (cm).**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	1.032	0.902		
2.	Treatments	24	15.390	13.452**	1.71	2.60
3.	Error	48	1.144	1.000		
4.	Total	74				

SE (d) =0.6177

CD= 1.240

Result: - \*\* Significant at 0.01% level of significance

**Appendix-V Analysis of variance for leaf width (cm).**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	0.4511	0.3443		
2.	Treatments	24	18.074	13.796**	1.71	2.60
3.	Error	48	1.310	1.000		
4.	Total	74				

SE (d) = 0.6610

CD= 1.327

Result: - \*\*Significant at 0.01% level of significance

**Appendix-VI Analysis of variance for primary branches/plant.**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	1.144	4.888		
2.	Treatments	24	2.130	9.102**	1.71	2.60
3.	Error	48	0.2340	1.000		
4.	Total	74				

SE (d) = 0.2793

CD= 0.5608

Result: - \*\*Significant at 0.01% level of significance

**Appendix-VII Analysis of variance for secondary branches/plant.**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	0.9101	2.129		
2.	Treatments	24	14.511	33.959**	1.71	2.60
3.	Error	48	0.4273	1.000		
4.	Total	74				

SE (d) = 0.3774

CD= 0.7578

Result: - \*\* Significant at 0.01% level of significance

**Appendix-VIII Analysis of variance for days to first flowering.**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	6.445	2.215		
2.	Treatments	24	91.582	31.482**	1.71	2.60
3.	Error	48	2.909	1.000		
4.	Total	74				

SE (d) =0.9847

CD= 1.977

Result: - \*\*Significant at 0.01% level of significance

**Appendix-IX Analysis of variance for germination days to 50% flowering.**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	6.203	1.9906		
2.	Treatments	24	58.045	18.6280**	1.71	2.60
3.	Error	48	3.116	1.000		
4.	Total	74				

SE (d) = 1.01

CD= 2.046

Result: - \*\*Significant at 0.01% level of significance

**Appendix-X Analysis of variance for number of pods/plant.**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	10.332	6.4858		
2.	Treatments	24	138.91	87.200**	1.71	2.60
3.	Error	48	1.593	1.000		
4.	Total	74				

SE (d) = 0.7289

CD= 1.463

Result: - \*\*Significant at 0.01% level of significance

**Appendix-XI Analysis of variance for green pod length (cm).**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	3.311	4.889		
2.	Treatments	24	16.111	23.790**	1.71	2.60
3.	Error	48	0.6772	1.000		
4.	Total	74				

SE (d) = 0.4751

CD= 0.954

Result: - \*\* Significant at 0.01% level of significance

**Appendix-XII Analysis of variance for green pod width (cm).**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	0.00298	0.5809		
2.	Treatments	24	0.0878	17.115**	1.71	2.60
3.	Error	48	0.00513	1.000		
4.	Total	74				

SE (d) = 0.04137

CD= 0.083

Result: - \*\* Significant at 0.01% level of significance

**Appendix-XIII Analysis of variance for green pod breadth (cm).**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	0.0184	2.324		
2.	Treatments	24	0.03019	3.8142**	1.71	2.60
3.	Error	48	0.007915	1.000		
4.	Total	74				

SE (d) = 0.05136

CD= 0.103

Result: - \*\*Significant at 0.01% level of significance

**Appendix-XIV Analysis of variance for single green pod weight (g).**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	0.7373	2.7864		
2.	Treatments	24	2.8679	10.8386**	1.71	2.60
3.	Error	48	0.2646	1.000		
4.	Total	74				

SE (d) = 0.2970

CD= 0.596

Result: - \*\* Significant at 0.01% level of significance

**Appendix-XV Analysis of variance for green pod yield/plant (g).**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	133.312	2.123		
2.	Treatments	24	3885.71	61.9039**	1.71	2.60
3.	Error	48	62.777	1.000		
4.	Total	74				

SE (d) = 4.57

CD= 9.184

Result: - \*\*Significant at 0.01% level of significance

**Appendix-XVI Analysis of variance for green pod yield/plot (kg).**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	0.2244	1.8484		
2.	Treatments	24	3.1988	26.3492**	1.71	2.60
3.	Error	48	0.1214	1.000		
4.	Total	74				

SE (d) = 0.2011

CD= 0.403

Result: - \*\*Significant at 0.01% level of significance

**Appendix-XVII Analysis of variance for number of seeds/pod.**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	0.7630	2.9933		
2.	Treatments	24	1.452	5.6963**	1.71	2.60
3.	Error	48	0.2549	1.000		
4.	Total	74				

SE (d) = 0.2915

CD= 0.585

Result: - \*\*Significant at 0.01% level of significance

**Appendix-XVIII Analysis of variance for 100- seed weight (g).**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	3.6562	3.6121		
2.	Treatments	24	1154.38	1140.4663**	1.71	2.60
3.	Error	48	1.0122	1.000		
4.	Total	74				

SE (d) = 0.5808

CD= 1.166

Result: - \*\* Significant at 0.01% level of significance

**Appendix-XIX Analysis of variance for green pod yield (q/ha).**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	848.250	5.4209		
2.	Treatments	24	10796.60	68.998**	1.71	2.60
3.	Error	48	156.476	1.000		
4.	Total	74				

SE (d) = 7.222

CD=14.501

Result: - \*\* Significant at 0.01% level of significance

**Appendix-XX Analysis of variance for moisture (%).**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	2.4589	4.3926		
2.	Treatments	24	4.8368	8.640**	1.71	2.60
3.	Error	48	0.5598	1.000		
4.	Total	74				

SE (d) = 0.4320

CD= 0.867

Result: - \*\* Significant at 0.01% level of significance

**Appendix-XXI Analysis of variance for total sugars (%).**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	0.6230	1.8275		
2.	Treatments	24	4.4465	13.043**	1.71	2.60
3.	Error	48	0.3409	1.000		
4.	Total	74				

SE (d) = 0.3370

CD= 0.676

Result: - \*\* Significant at 0.01% level of significance

**Appendix-XXII Analysis of variance for protein (%).**

S. No.	Source of variation	D.F.	M.S.S.	F (Calculated)	F (Tabulated)	
					0.05%	0.01%
1.	Replications	2	4.1250	3.4068		
2.	Treatments	24	110.433	91.2066**	1.71	2.60
3.	Error	48	1.2108	1.000		
4.	Total	74				

SE (d) = 0.6353

CD= 1.275

Result: - \*\* Significant at 0.01% level of significance

## Abstract

The present investigation entitled “**Studies on genetic variability, correlation and path analysis in French bean (*Phaseolus vulgaris* L.) under Lucknow conditions.**” The experiment consisting of twenty five genotypes for twenty two characters was laid out in Randomized Block Design with three replications grown at Horticulture Research Farm first of the Department of Applied Plant Science, (Horticulture), Babasaheb Bhimrao Ambedkar University, (A central university), Vidya Vihar, Rae Bareilly Road, Lucknow (U. P.), India during the year 2012- 2013 and 2013- 2014 to assess the variability, heritability, genetic advance, correlation, path and to identify/isolate desirable genotypes for different horticultural traits. The observations were recorded on twenty morphological and three quality traits. The studies revealed that there was wide variability in French bean for various characters studied. Analysis of variance for the design of experiment showed that the genotypes were highly sufficient for all the characters under study. The high magnitude of phenotypic and genotypic coefficient of variation were observed for 100-seed weight (g) followed by plant height (cm), green pod yield (q/ha), green pod yield/plant, green pod yield /plot and number of pods/plant. GCV is helpful in the assessment of inherent variability. GCV and PCV detect the amount of variability in the available genotypes. Heritability estimates give a measure of transmission of characters from one generation to another thus, given an idea of heritable portion of variability and enabling to the plant breeder in isolating the elite selection in the crop. Heritability and genetic advance increase the efficiency of the selection in breeding programme by assessing the influence of environmental factors and additive gene action. Heritability estimates for all the characters were high except 100-seed weight (g), plant height (cm), moisture (%), number of pods/plant, green pod yield (q/ha) and green pod yield/ plant (g). Suggesting the role of additive gene action and thus a high genetic gain and heritability along with genetic gain is more useful criterion in predicting the resultant effect for selecting the best individual. High heritability with high genetic advance was observed for 100-seed weight (g), green pod yield (q/ha), green pod yield/plant (g), plant height (cm) and number of leaves/plant. High heritability with high genetic advance tells that the character is governed by the additive gene action and for this simple selection is advocated. High heritability with medium genetic advance suggests that the character is governed by the dominant and epistatic gene action and for this hybridization is done. In all the studies, characters like days taken to first flowering and days taken to 50 % flowering were found with high heritability and medium genetic advance. In the present investigation,

primary branches/ plant, secondary branches/ plant, number of leaves /Plant, size of leaves (length and width cm), number of pods/ plant, number of grains/ pod, green pod length (cm), green pod width (cm), green pod breadth (cm), single green pod weight (g), green pod yield per plant (g), green pod yield per plot (kg), green pod yield (q/ ha) and 100- seed weight (g) are governed with non additive gene action. Suggesting the role of genotypic was generally similar nature than the corresponding phenotypic once. A very strong positive correlation of green pod yield/plot, at genotypic and phenotypic level was observed in green pod yield /plant, secondary branches/plant, 100-seed weight, number of pods/plant, primary branches/plant and plant height. A path coefficient analysis carried out at genotypic as well as phenotypic level revealed green pod yield/plant followed by green pod yield /plant, number of pods/plant, secondary branches/plant, primary branches/plant and plant height had positive direct effect on yield.

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