

Review Article

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Character Association in French Bean (*Phaseolus vulgaris* L.) and Pea (*Pisum sativum* L.) A Review

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French bean and Pea are an important vegetable crop consumed by human being as green pods and dry seeds due to its high nutritive value as the source of the amino acid, lysine and tryptophan as well as provides valuable dietary protein in the human diet. Considering its use as a vegetable which fits well indifferent cropping systems, there is need for improvement and development of cultivars to specific agro ecological conditions. The knowledge of genetic diversity is an important tool for any breeding programme aimed to exploit hybrid vigour. Moreover, the information related to the nature and extent of association among various yield attributes, direct and indirect influence of each of the component traits on yield could prove helpful in formulating effective breeding strategy. The magnitude of the variability present in a crop species is of utmost importance for the relative improvement of the cultivars, suitable for a particular region. Thus, there is a need to develop varieties having good yield and quality characters. For this, the breeder requires a good knowledge of variability. The subsequent study of interrelations among different characters further helps in bringing effective improvement.

Introduction

Pea (*Pisum sativum* L.) is an important leguminous vegetable crop grown in many parts of the world *i.e.*, temperate and subtropical regions, for fresh green immature pods. Sometimes it is utilized as a pulse crop and also as a green manure crop. It belongs to the family Leguminosae (Fabaceae) having chromosome number $2n=14$, with its origin Central Asia. Pea growing states are Uttar Pradesh, Haryana, Himachal Pradesh, Uttarakhand, Punjab, and Karnataka. However. Uttar Pradesh is the leading state of pea production in India sharing 46.1%. Total

area in India under pea cultivation is about 554-thousand-hectare area and the production is 5524 thousand MT having an annual productivity of 8.9 MT per hectare (NHB, 2018). Pea has a great nutritive value & contains vitamin A, B and C along with minerals, dietary fiber & antioxidant compounds (Urbano *et al.*, 2003). In addition, it also has high nutritive value *i.e.* proteins 7.2g/100g, carbohydrate 14g/100, dietary fiber 5g/100g. Peas are excellence source of protein, help in digestion, protective against some chronic diseases, prevent constipation and reduce bad cholesterol.

French bean (*Phaseolus vulgaris* L.) is an important leguminous vegetable crop grown for its tender green beans and dry beans (Rajmah). It belongs to the family Leguminosae having chromosome number 22. It is known by many names i.e. common bean, haricot bean, marrow bean, bush bean, dry bean, string bean, kidney bean and field bean etc. It is grown in U.S.A., Latin America, Canada, India, Bangladesh, Nepal and almost in all European countries. In India it is cultivated in many states of Maharashtra, Jammu and Kashmir, Himachal Pradesh, Uttar Pradesh hills, Nilgiri (Tamil Nadu), etc. In addition, it is a nutritious vegetable containing 1.7% protein, 0.1% carbohydrate, 4.5% fat, 1.8% fibre and 0.5% mineral matter. The green pods are rich in calcium, potassium and iron.

Basically, India has very low production and productivity of Pea (*Pisum sativum* L.) and French bean (*Phaseolus vulgaris* L.) due to the lack of high yielding hybrid/varieties. Hence it is very important to develop high yielding varieties, hybrids of Pea and French bean having good protein content and resistance to biotic and abiotic stress, which can be released as such for commercial production or can be used in the crop improvement program for improvement of yield and quality traits. For increasing production and productivity, we should examine a genetic improvement factor and the finest and superior way is to study the genetic parameter & character association in French bean and Pea. Considering the significance of above said facts the review paper entitled 'character association & path analysis in various genotypes of French bean and Pea for pod yield & quality traits' has been drafted with the following objectives. This paper mainly reviews genetic variability, heritability, genetic advance, correlation, path coefficient and genetic divergence in Pea and French bean & focuses on potential areas for

further research and development of high yielding varieties and hybrids of Pea and French bean.

Genetic variability

It is defined as the presence of genetic differences in individuals differing in genotype. PCV include the genotypic variance with the environmental variance and their interaction. GCV is due to the genetic causes or the occurrence of differences among individuals due to differences in their genetic makeup. It is usually stable and is not influenced by any environmental factor. Many scientists studied about it and observed that for traits days to maturity and pod length maximum variability was recorded in 31 genotypes (Raffi *et al.*, 2004). High variability for pod break length, pod total /plant & yield potential characters and low genetic variability for time of flowering, time of harvest, pod weight, pod diameter, pod length, seed/pod and 100 seed weight were observed in three genotypes (Rachman *et al.*, 2006). Highly significant differences in yield, leaf area, pod length & width, pod number /plant, fresh pod weight, seed number /pod and 100 seed weight were recorded (Dursun, 2007). For days to maturity, 100-seed weight, protein content, seed yield per plant and days to 50% flowering maximum variability recorded in forty-five genotypes (Singh *et al.*, 2007). Among 12 genotypes of Pea, significant differences in all germplasm for days to germination, days to 50% flowering, no. of pods per plant, weight of pods per plant, pod length, no. of seed per pod, 100 seed weight and green pod yield were observed (Nawab *et al.*, 2008). While evaluating genetic variability in 32 genotypes significant differences were observed for all characters except no. of primary branches and grain yield per plant, no. of pods per plant, no. of seeds per pod and 100 grain weight showed high GCV and PCV (Kumar 2008). In 10

indigenous and exotic genotypes of pea significant varietal differences for all characters were recorded. Highest GCV and PCV were exhibited by seeds per plant, shoot height, internodal length, pod yield and pod number (Guleria *et al.*, 2009). Highest GCV and PCV were recorded for No. of pods per plant, seed yield per plant and 100 seed weight in field Pea crosses in F3 generation (Lavanya *et al.*, 2010). Moderate to high level of GCV and PCV for days to 50% flowering, plant height, no. of pods per plant, days to maturity, no. of seeds per pod, pod length, seed weight and grain yield per plant were recorded. Phenotypic variance for all characters was higher than genotypic variance (Jaiswal *et al.*, 2013). Maximum variability in plant height, number of pods /plants, 100 seed weight & seed yield were recorded for fifty-seven genotypes (Ahmed *et al.*, 2013). High variability for marketable pod yield /plant, plant height, no. of pods/plants, no. of inflorescences /plant & 100 seed weight was recorded for forty-four genotypes (Kumar *et al.*, 2014). Maximum variability for plant height after 30 days of sowing, leaf length, leaf width, days to 50% flowering, pod length, pod width, number of marketable pod /plant, pod yield /plant, seed length, seed width, 100 seed weight & green pod yield was recorded in forty four genotypes (Savita *et al.*, 2014). Highest variability for days to flowering, days to first picking, average pod weight, pod length, pods /plant, plant height & pod yield /plant was recorded in seventeen genotypes (Devi *et al.*, 2014). In 12 genotypes of Pea significant analysis of variance was recorded except for plant height. Highest Genotypic coefficient of variation and Phenotypic coefficient of variation was recorded in pod/plant, seed yield/plant & lowest in days to maturity (Ahmad *et al.*, 2014). Among 54 Pea genotypes which includes 4 checks and were grown in RBD with 3 replications maximum variability were recorded in all genotypes for all

morphological traits. Total soluble solids, total sugar, pod yield/ha and total phenols exhibited highest GCV & PCV (Kumar *et al.*, 2015). Significant variability in green pod yield /plant, plant height, germination percent & protein was observed in twenty-five genotypes (Prakash *et al.*, 2015). The seeds were treated with different concentration of chemical mutagen i.e., gamma ray's high variability was recorded for plant height, length of pod, days to maturity and number of pods per plant (More *et al.*, 2016). Very high variability in plant height, seed yield /plant, pod yield /plant, pod yield /hectare, number of pods /clusters, no. of pods /plant & 100 seed weight was recorded in seventy-four genotypes (Panchbhaiya *et al.*, 2017). For seed weight /pod, plant height, pods /plant, no. of leaves /plants, pod weight & pod yield/plant, maximum variability was found in eighteen different genotypes (Lyngdoh *et al.*, 2017). In nine French bean (*Phaseolus vulgaris* L.) genotypes grown at two different locations highest variability for primary branches, grain yield, hundred seed weight & number of pods /plants was recorded (Wondimu *et al.*, 2017). In 15 genotypes of Pea, significant differences among all genotypes were observed regarding growth yield and yield attributes parameters. Moderate PCV and GCV were exhibited by plant height, no. of branches, no. of leaves, leaf area, days to initiation of first flowering, no. of clusters/plant, pod length, no. of seeds per green pod, green pod yield/plant, pod yield/plot, pod yield/hectare and crop duration (days) (Tambolkar *et al.*, 2017). In 120 genotype of field Pea along with 4 check varieties, analysis of variance showed significant differences in all the genotypes for all traits except no. of primary branches per plant. All the genotypes showed moderate to high level of GCV and PCV. PCV were higher than GCV in magnitude (Lal *et al.*, 2018). High variability in plant height, no. of primary branches, pod length, pod width, pod

flesh thickness, no. of pods per cluster, no. of pods /plant, weight of ten pods, no. of root nodules /plant & dry matter contents of pods & roots were recorded in thirty-six genotypes (Jhanavi *et al.*, 2018). Maximum variability was observed for no. of branches/plant, pod yield/plant & pod yield per plot (Vijayakumar *et al.*, 2019). While estimating genetic variability in quantitative characters in new varieties of field pea using one line & their F₃ & F₄ hybrids, significant differences were recorded for number of pods/plant, number of grains/pod, 1000 seed weight & grain yield (Lakić *et al.*, 2019).

Heritability

It is a statistical tool used in breeding that gives us the degree of variation in phenotypic trait that is mainly due to genetic variation. High broad sense heritability was observed between 92.03% (plant spread) to 99.80% (days to maturity) (Masal, 2000). For traits like first flowering, days to 50% flowering, days to pod initiation, plant height, primary branches per plant and secondary branches per plant high heritability was observed (Dahiya *et al.*, 2000). In 30 different genotypes of Pea (*Pisum sativum* L.) high heritability combined with high genetic advance for traits were recorded for plant height, pod yield per plant, seed yield per plant, no. of primary branches and 100 seed weight (Sureja and Sharma 2000). In 24 different genotypes of field Pea (*Pisum sativum* L.) high heritability coupled with high genetic advance for all traits were observed for seeds per pod, days to 50% flowering etc. (Mahanta *et al.*, 2001). Within the characters, pod yield per plant, number of pods per plant, seed weight and pod weight, high heritability coupled with high genetic advance were recorded for thirty-one genotypes (Raffi *et al.*, 2004). Among 31 different genotype of Pea (*Pisum sativum* L.) high broad sense heritability coupled with

high genetic advance was recorded for all traits excluding days to flowering and pod length (Singh and Singh 2006). Maximum heritability coupled with high genetic advance for pods per plant and pod yield per plant was recorded in 20 genotypes of Pea (*Pisum sativum* L.) (Sharma *et al.*, 2007). Among 40 different genotypes of Pea (*Pisum sativum* L.), high broad sense heritability coupled with high genetic advance for all traits except no. of greens per pod was observed (Singh *et al.*, 2007). High heritability coupled with high genetic advance for green pod yield per plot, 100 seed weight and weight of pods per plant in 12 different germplasm of Pea (*Pisum sativum* L.) were recorded (Nawab *et al.*, 2007). In traits pod width & seed no. per plant, environmental effect on yield, fresh pod weight, pod length, pod number per plant and leaf area heritability was found to be much higher (Dursun, 2007). Very high heritability estimates for 100 seed weight, number of pods and seed yield (Singh *et al.*, 2007). For traits first flower (59%) followed by days to maturity (39%) high heritability was recorded in thirteen genotypes (Msolla *et al.*, 2008). Among 20 genotypes of Pea (*Pisum sativum* L.) moderate to high broad sense heritability coupled with high genetic advance for plant height, pod length and 100 seed weight was recorded indicating role of additive gene action in the expression of these traits (Singh *et al.*, 2011). Heritability was high (60%) for all traits except number of branches per plant and number of seeds per pod in seventy-five genotypes (Mudasir *et al.*, 2012). High heritability for days to 50% flowering and plant height while low heritability coupled with high genetic advance for total soluble solids was recorded which indicate that heritability is basically due to additive gene effect (Sharma and Sharma 2013). High heritability (>80%) for vine length, internodal length, number of nodules per plant, nodule fresh weight, tender pod fresh weight, 100 seeds weight and pod yield were recorded

in sixty-five genotypes (Singh *et al.*, 2014). High heritability for pods per plant (88.20%) and lowest for branches per plant (38.50%) was observed in thirty-three genotypes (Devi *et al.*, 2014). Maximum heritability was observed in green pod yield per hectare (99.84%) minimum heritability in pod weight 77.63% was observed in 40 genotypes (Savita *et al.*, 2014). Maximum heritability in 100 seed weight (99.50%) & lowest heritability in green pod breadth (26.80%) in twenty-four genotypes (Prakash *et al.*, 2015). Among 54 different genotypes of Pea (*Pisum sativum* L.) high heritability coupled with high genetic advance for pod yield, no. of pods/plant and total phenols was recorded (Kumar *et al.*, 2015). High genetic advance for traits: plant height, seeds per pot and 100 seed weight were recorded in 12 different genotypes of Pea (*Pisum sativum* L.). This shows that the particular traits can be used as effective selection during any breeding program for yield improvement (Jaberson *et al.*, 2016). High heritability for green pod yield, basal internode diameter, days to 1st green pod picking, plant height, basal internodal length, green pod width, no of pods per plant, days to 50% flowering, no of secondary branches per plant was estimated (Panda *et al.*, 2016). Genotype named Varun was treated with different concentration of chemical mutagen i.e., gamma rays and observed maximum heritability for 100-seed weight, plant height and length of pod (More *et al.*, 2016). At two different locations the heritability varies from 38.9% for primary branch to 86.9% for harvest index at one location & from 30.5% for days to emergence to 95.86% at another location for nine genotypes (Wondimu *et al.*, 2017). Maximum heritability coupled with high genetic advance for pod yield, pod yield per plot and plant height was recorded which indicate presence of additive gene action (Gudadinni *et al.*, 2017). Among two crosses i.e. IM 9214-10x Rachna (C-1) and IM 9214-10x Ambika (C-2) maximum heritability

coupled with high genetic advance was recorded for clusters for plant, pod bearing length and seed yield per plant (Meena *et al.*, 2017). High heritability coupled with genetic advance in 35 different genotypes of Pea (*Pisum sativum* L.) was recorded for plant height, days to 50% flowering & pods/plant (Kumar *et al.*, 2018). High heritability for protein content followed by number of root nodules per plant and lowest heritability was recorded for pod length (cm) in thirty-six genotypes (Jhanavi *et al.*, 2018). High heritability in no. of pods per plant (99.59) accompanied by green pod yield/plant (99.43%) & test weight (99.35%) and lowest heritability for days to germinate (82.94%) was recorded in forty genotypes (Singh *et al.*, 2018). For traits pod width, pod weight, green pod yield high heritability was recorded and for trait days to first picking lowest heritability was recorded (Ramdeep *et al.*, 2018). In 29 genotypes of Pea (*Pisum sativum* L.), high heritability coupled with high genetic advance were recorded for plant height, seed yield per plant, no. of pods/plant & no. of seeds/plant. Thus, these characters can be used in any breeding program for yield increasement (Pathak *et al.*, 2019). Combination of high heritability & high genetic advance in no. of pods per plant, pod length, pod yield/plot, 100 seed weight & TSS was recorded in 20 varieties of Pea (*Pisum sativum* L.) (Kumar *et al.*, 2019).

Genetic advance

Maximum genetic advance was recorded in 100 seed weight accompanied by green pod yield/plant (Nandi *et al.*, 1995). Maximum genetic advance in pod yield/plant, plant height & 100 seed weight were recorded (Masal, 2000). Very high genetic advance for pod yield/plant, no. of pods/plant, seed weight & pod weight (Rai *et al.*, 2000). High heritability for days to maturity and lowest heritability for number of seeds/plants was

recorded (Raffi *et al.*, 2004). For the traits, days to first flowering, days to 50% flowering, days to pod initiation, plant height, primary branches per plant and secondary branches per plant maximum genetic advance was observed (Dahiya *et al.*, 2006). Highest genetic advance was recorded for 100 seed weight, number of pods/plant & seed yield (Singh *et al.*, 2007). Maximum genetic advance was recorded for traits like 100 seed weight, seed yield/plant in 42 different genotypes (Singh *et al.*, 2013). Genetic advance in terms of percentage of mean was maximum for number of pods/plant (58.00%) & minimum for days to 50% maturity (14.95%) in forty genotypes (Savita *et al.*, 2014). Maximum genetic advance for 100-seed weight was recorded in forty-five genotypes (Kumar *et al.*, 2014). For traits plant height and days to 50% flowering maximum genetic advance was recorded (Lad *et al.*, 2017). Maximum genetic advance for plant height and seed yield per plant in seventy-five genotypes was recorded (Panchbhैया *et al.*, 2017). At two different locations the percentage of genetic advance varied from 6.8% (Days to maturity) to 65.47% (stand out at harvest) in nine different genotypes (Wondimu *et al.*, 2017). Highest genetic advance were recorded for yield/plant (72.78%) & pod flesh thickness (0.11%) in seventy-five genotypes (Jhanavi *et al.*, 2018).

Correlation

It is a statistical measure that indicates the extent to which two or more variables fluctuate together. Maximum GCV & PCV in days to flowering, days to 50% flowering, days to pod initiation, plant height, primary branches /plant & cluster /plant were estimated (Dahiya *et al.*, 2000). In seed yield /plant positive correlation was found with days to first flower, days to maturity, plant height, plant spread, no. of branches /plant, no. of pods /branch and no. of seeds /pod

breadth while non-significant negative correlation within pod breadth, pod length & 100 seed weight at phenotypic & genotypic level (Shinde *et al.*, 2001). Highest GCV and PCV for 20 seed weight (42.19% and 42.29%), seed yield /plant (39.35% & 47.64%) and number of seeds per plant (31.43% and 40.60%) and moderate GCV and PCV were recorded for number of pods per plant (19.81% and 26.75%), pod length (17.10% and 19.12%), plant height (15.67% and 17.63%) and lowest GCV and PCV were recorded for days to maturity (7.19% and 8.15%) and days to 50% flowering (6.99% and 8.01) respectively (Raffi *et al.*, 2004). Positive and significant correlation with green pod yield was recorded for no. of green pods per plant, no. of grains per pod; shelling percentage and pod length (Mehta *et al.*, 2005). Significant positive correlation of green yield plant with plant height, pod length and seeds per pod and non-significant negative correlation with days to flowering was recorded and GCV was higher than PCV (Singh and Singh 2005). In 18 different genotypes of Pea (*Pisum sativum* L.) it was recorded that at genotypic and phenotypic level seed yield possess significant positive correlation with no. of seeds per pod, pod length and pod diameter and significant negative correlation of no. of days to 50% flowering with no. of pods per plant and no. of branches per plant (Singh and Yadav (2005). At phenotypic level days to flowering with days to maturity, plant height with no. of pods per plant, pod length with plant height are positively correlated with each other (Sirohi *et al.*, (2006). Pod yield /plant contributed positive correlation with the pod length, pod weight and seed weight in genotypic and phenotypic levels (Rai *et al.*, 2006). Positive and significant correlation between correlation no. of seeds /pod, no. of pods /plant & pod length with grain yield was observed in different genotypes (Salehi *et al.*, 2008). Correlation within pod no. /plant &

yield, fresh pod weight & yield, seed number /pod & yield were found significantly positive (Dursun, 2007). In 12 different types of Pea (*Pisum sativum* L.) it was recorded that at genotypic and phenotypic level green pod yield per plot have significantly positive correlation with no. of seeds per pod and pod weight per plant. This indicates that these characters could be considered as a major green pod yield contributing characters in garden Pea (Nawab *et al.*, 2008). In 10 different indigenous and exotic germplasm of Pea (*Pisum sativum* L.) it was observed that traits like no. of flowers, no. of pods and no. of seeds per pod have strong positive correlation with yield (Guleria *et al.*, 2009). Significant correlation of seed yield per plant was recorded for plant height, biological yield, harvest index, no. of pods per plant and days to maturity (Lavanya *et al.*, 2010). Significantly positive correlation with seed yield /plant was recorded with no. of branches per plant, no. of pods per plant, pod length, no. of seeds per pod & 100-seed weight at GCV & PCV level and significantly negative correlation in days to 50% flowering & days to maturity was observed and GCV was higher as compared to PCV (Mudasir *et al.*, 2012). Low level of differences was observed within PCV and GCV for days to 50% flowering, plant height, 100 seed weight & seed yield in fifty-seven genotypes (Ahmed *et al.*, 2013). High GCV and PCV for length of inflorescence (52.94% & 51.17%), no. of pods /plant (43.22% & 42.25%) & marketable pod yield /plant (42.81% & 41.71%) & moderate GCV & PCV were recorded for no. of inflorescence /plant (35.04% & 34.16%), number of flowers per inflorescence (33.85% and 30.64%) and pod weight (31.15% and 30.71%) and lowest GCV and PCV were recorded for days to last pod harvest (9.33% and 8.98%) respectively in forty four genotypes (Kumar *et al.*, 2014). Positively significant correlation of pod yield with days to flowering, average pod weight, branches

per plant, pods per plant and plant height were recorded in seventeen genotypes (Devi *et al.*, 2014). Marketable pod yield per plant was found significantly positively correlated at GCV & PCV levels within length of inflorescence, no. of pods /inflorescence, no. of flowers /inflorescence and no. of inflorescences /plant in forty-five genotypes (Kumar *et al.*, 2014). High genotypic coefficient variation & phenotypic coefficient variation for traits 100-seed weight, plant height, green pod yield /plot, green pod yield /plant and green pod yield (q/ha) in twenty-five genotypes (Prakash *et al.*, 2015). In 28 different genotypes of Pea (*Pisum sativum* L.) it was recorded that seed weight per plant have significant positive correlation with no. of pods per plant, weight of pods per plant and harvest index (Tofiq *et al.*, 2015). In 5 germplasm of forage Pea (*Pisum sativum* L.) it was concluded that seed yield possesses positive significant correlation with pod stem and 1000 seed weight (Georgieva *et al.*, 2016). There was a positive significant correlation of pod yield with pod length, pod width and no. of grains per pod in 15 different genotypes of Pea (*Pisum sativum* L.) (Thakur *et al.*, 2016). For traits like no. of seeds /plant (70.93% & 73.83%), plant height (52.16% and 59.13%) and no. of pods (50.09% & 51.99%) highest GCV and PCV were recorded in forty-two genotypes (Topwal *et al.*, 2016). Highly significant & positive association with germination percentage, plant height, no. of primary branches /plant, number of secondary branches /plant, no. of clusters /plant, no. of pods /cluster, no. of pods per plant, pod length, pod circumference, harvest index both at genotypic and phenotypic level in twelve genotypes (Heena *et al.*, 2016). High GCV and PCV in plant height, seed yield /plant, pod yield /plant, pod yield /hectare, no. of pods /cluster, no. of pods /plant & 100 seed weight in seventy-four genotypes (Panchbhैया *et al.*, 2017). At genotypic

level, seed yield per plant have significant positive correlation with protein was recorded in 29 different genotypes of Pea (*Pisum sativum* L.) (Toppo *et al.*, 2017). Highest GCV and PCV were recorded for seed weight /pod (145.12% & 144.87%, respectively (Lyngdoh *et al.*, 2017). Significantly positive GCV were recorded in green pod yield with no. of pod /plant, single green pod weight, pod dry weight, pod length & leaf area /plant and significantly negative GCV were recorded in green pod yield & days to 50% flowering & days to first picking in thirty four genotypes (Alemu *et al.*, 2017). Highest GCV and PCV was recorded for plant height (41.30% and 42.16%) and lowest GCV and PCV for pod length (9.21% and 11.87) respectively (Lad *et al.*, 2017). Significantly positive correlation at PCV and GCV levels in seed yield /plant with no. of pods /plant, pod length, no. of seeds /pod & 100 seed weight and significantly negative correlation within days to 50% flowering & days to maturity were recorded in thirteen genotypes (Razvi *et al.*, 2017). Among 120 different genotypes of Pea (*Pisum sativum* L.), positive correlation of seed yield per plant with plant height, no. of seeds per pod, no. of primary branches per plant, no. of pods per plant and 100 seed weight was observed (Kumar *et al.*, 2017). In 40 indigenous and 10 exotic germplasm of Pea (*Pisum sativum* L.) it was recorded that there was a positive significant relation of seed yield per plant with biological yield per plant, plant height, no. of pods per plant and 100 seed weight and negative correlation with days to maturity (Singh *et al.*, 2017). Genotypic and phenotypic coefficient of variability was recorded in the plant height, no. of primary branches, pod length, pod width, pod flesh thickness, no. of pods /cluster, no. of pods /plant, weight of ten pods, no. of root nodules /plant & dry matter contents of pods & roots in seventy four genotypes (Jhanavi *et al.*, 2018). At genotypic and phenotypic level, pod yield/ha is

positively correlated with primary branches/plant, cluster /plant, pods /cluster, pods /plant, yield /plant, root nodule and dry matter content in pod & negative correlation was observed for days to flowering & 50% flowering in twelve genotypes (Muthal *et al.*, 2018). In 113 diverse germplasm of Pea (*Pisum sativum* L.), positive correlation of seed yield/plant with 100 seed weight, no. of pods/plant, harvest index and biological yield was recorded (Srivastava *et al.*, 2018). Positive significant correlation of harvest index, seeds/pod, pod length & 100 seed weight with seed yield/plant was observed in 120 genotypes of field Pea (*Pisum sativum* var. *arvense*) (Lal *et al.*, 2018).

Path coefficient analysis

It indicates the fact that which character has most positive direct effect on yield. It has been reported that no. of pods /plant has a direct positive effect on yield per plant, pod width has high positive direct and pod length has negative direct effect on yield /plant (Nandi *et al.*, 1997). It has been observed that no. of primary branches, is the only trait that influence pod yield (Mohamad., 1996). It has been reported that pod yield/plant exhibit direct effect on no. of grains/pod, pod length and 1000 seed weight (Choudhary and Sharma 2003). At genotypic level, it was recorded that seeds/pod possess direct effect with seed yield (Sirohi *et al.*, 2006). Among 31 germplasm of Pea (*Pisum sativum* L.) it was recorded that seed yield/plant exhibit positive direct effect with plant height and grains/pod (Singh and Singh 2006). In 20 different genotypes of Pea (*Pisum sativum* L.) it was concluded that pod/plant, plant height & pod length have positive direct effect with green pod yield (Sharma *et al.*, 2007). Path coefficient analysis in 33 diverse germplasm of Pea (*Pisum sativum* L.) concluded that 100 seed weight & primary branches are important element of yield which can be used

in selection of improvement in germplasm (Sardana *et al.*, 2007). Among 20 diverse germplasm of Pea (*Pisum sativum* L.) it was recorded that green pod yield/plant possess positive direct effect on 100 seed weight, no. of pods/plant, no. of seeds/pod & days to 50% flowering (Nawab *et al.*, 2008). Among 30 diverse genotypes of Pea (*Pisum sativum* L.) it was concluded that in every environmental condition no. of pods per plant possess a positive direct effect with pod yield per plant (Dhama *et al.*, 2010). At genotypic level green pod yield possess positive direct effect on no. of pods per plant, 100 pod weight (Sharma and Sharma (2012). Path coefficient analysis at genotypic level revealed that seed yield has positive direct effect on harvest index and biomass yield (Million 2012). Among 26 diverse germplasm of Pea (*Pisum sativum* L.) it was recorded that seed yield/plant possess positive direct effect days to 50 % flowering, days to 50% harvesting, no. of branches/plant, pods/plant & 100 seed weight (Siddika *et al.*, 2013). Among 42 different genotypes days to first picking, 100 seed weight, pod length & seed yield/plant contributed positively towards pod yield/ha (Singh *et al.*, 2013). It has been observed that at phenotypic level green pod yield /plant, has the maximum direct effect on pod yield/hectare in 40 different types of French bean (*Phaseolus vulgaris* L.) (Savita *et al.*, 2014). Among 7 diverse germplasm of Pea (*Pisum sativum* L.), there is a positive direct relation of seed weight/plant with biological weight/plant & harvest index whereas positive indirect relation with no. of pods/plant (Tofiq *et al.*, 2015). Path coefficient analysis for seed yield and various components revealed that protein content has very less direct positive effect on seed yield (Toppo *et al.*, 2017). In 120 different genotypes of Pea (*Pisum sativum* L.), positive direct effect of seed yield/plant with days to maturity & 100 seed weight was observed (Singh *et al.*, 2017). Among 113 genotypes of Pea (*Pisum sativum*

L.) path coefficient analysis revealed that seed yield per plant possess the positive direct effect on harvest index, biological yield, 100 seed weight and no. of pods per plant (Srivastava *et al.*, 2018). Among 35 different germplasm of Pea (*Pisum sativum* L.) it was recorded that green pod yield/plant exhibit positive direct effect on plant height and pod length but internodal length exhibit negative direct effect on green pod yield/plant (Vijaya Kumar *et al.*, 2019)

Genetic divergence

Genetic divergence is usually referring to that population having same ancestors and these populations accumulate independent genetic changes after sometimes. In 62 different genotypes of French beans (*Phaseolus vulgaris* L.) grouped into 11 clusters and observed that no. green pod /plant, 100 seed weight, plant height & reproductive branches contributed towards total divergence (Govamakoppa *et al.*, 2002). Among 100 different germplasm of Pea (*Pisum sativum* L.) when classified into 8 clusters. Cluster 1 possess highest genotype accompanied by cluster 2. Highest intra-cluster distance is of cluster 8 and highest inter cluster distance is of cluster 5 and 7 (Kumar *et al.*, 2006). From 20 Characters, total divergence is contributed by no. of pods per plant followed by no. of racemes/plant & 100 seed weight, contributed least (0.19%) (Hossain *et al.*, 2013). It has been revealed that 100 seed weight has the most no. of contribution (38.33%) towards total divergence accompanied by pod weight (17.02%) and protein content (11.52%) in forty-four genotypes (Kumar *et al.*, 2014). Among 66 different germplasm of French bean (*Phaseolus vulgaris* L.), the maximum genetic divergence was reported for days to 50% flowering accompanied by 1000 seed weight, green pod yield, pd weight and pod length (Gangadhara *et al.*, 2014). When 34 germplasm of French bean (*Phaseolus*

vulgaris L.), grouped into 5 clusters and observed that vitamin C content, no. of pods/plant & dry matter content has maximum contribution in total divergence (Verma *et al.*, 2014). Among 20 germplasm of Pea (*Pisum sativum* L.) when grouped in 4 clusters, cluster 3 possess largest no. of genotype accompanied by cluster 2. Cluster 2nd possess highest intra-cluster distances whereas cluster 3rd and 1st possess highest inter-cluster distance (Gupta *et al.*, 2017). Among different genotypes of Pea (*Pisum sativum* L.) cluster 5th possess maximum mean values for root length, no. of pods/plant and days to 50% flowering. Maximum value of inter-cluster distance was exhibited by cluster 5 followed by cluster 2 and cluster 1 (Bijalwan *et al.*, 2018).

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