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Morphological, genetic and molecular characterization of garden pea (*Pisum sativum* L.): A review

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Abstract

Pea is a versatile crop that serves multiple agricultural and horticultural purposes. In India, it is grown for both its dry seeds, which are used as pulses, and its green pods, which are consumed as vegetables, especially in the northern regions. Garden pea is grown for its fresh green seeds, tender green pods, dried seeds, and foliage. The green pods and young leaves of peas are consumed as green vegetables, and they can also be dried for utilization as a vegetable and pulse during off-season periods. The most valuable natural resource is germplasm, which offers the qualities needed to create high-yielding inputs that are resilient to diverse biotic and abiotic challenges and sensitive to them. Even though numerous researchers have studied pea germplasm evaluation, variability, correlation, path analysis, and genetic divergence, these studies primarily rely on examining a small number of germplasms in a particular environment.

Keywords: Garden pea, morphology, germplasm, biochemical and molecular studies

Introduction

The diploid pea (*Pisum sativum* L.) belongs to the family Fabaceae and has two sets of genes, one for each chromosome. While it is typically grown for its grazing potential in many regions, it serves other purposes in India beyond just providing protein. The pea is cultivated globally and is a major pulse crop with a diverse range of producing areas. In 2020-21, India's pea crop area was 0.64 million hectares, yielding 0.88 million tons with a productivity of 1,375 kg/ha (Anonymous, 2021) ^[1]. Uttar Pradesh is the country's leading producer, with Bihar, Haryana, Punjab, etc. following closely after. This crop contains all the essential amino acids required for regular living creature function and has a high protein level of 20%. The fractional composition also has other benefits. In addition to a plethora of vitamins and minerals, this vegetable is abundant in digestible protein (7.2 g), carbs (15.8 g), fat (0.1 g), vitamin C (9 mg), vitamin A (139 IU), and iron (1.5 mg). Despite peas' enormous potential for productivity, there is a severe shortage of input-responsive, disease-resistant, high-yielding cultivars that can withstand high temperatures during reproduction without suffering from poor average output. Due to their tolerance to adverse conditions, pulses are being pushed deeper to marginal and submarginal levels as the irrigated area expands. Competition from commercial crops, which are more reliable in terms of output, is severe. Germplasm is the most precious resource since it contains the genetic information necessary to make inputs with high yields that can withstand and even thrive in the face of a wide variety of biotic and abiotic stresses. Researchers have looked at genetic divergence, route analysis, correlation, variability, and evaluation of pea germplasm many times, however most of these studies have only looked at a handful of germplasms in one specific setting. Consequently, the optimal utilization of genetic resources for the development of improved varieties is highly dependent on the growing conditions.

A lot of effort has gone into pea breeding to create types that are both nutritious and produce a lot of food. Along with other traits like earliness, tolerance to local conditions, and seed nutritional content, there is still a great deal of room for improvement in output. The degree to which natural variability exists for a given character determines how much of an improvement in that trait can be achieved through breeding. An accurate understanding of diversity would aid in the development of promising pea cultivars, which would in turn raise the pea productivity level.

Origin and Domestication of garden pea

With twelve distinct legume crops grown throughout the nation, legumes are an integral part of India's agricultural system. Grass pea, Lupine, Fenugreek, Chickpea, Lentil, garden pea, Chickpea, *Lupinus albus*, and other highland legume crops are mainly cultivated in the cooler highland regions. The lowland legume crops that are primarily grown in warmer and lowland regions of India include urd, haricot bean, soya bean, cowpea, pigeon pea, and mung bean (*Vigna radiata* L.; *Phaseolus vulgaris* L.; *Glycine max* L.; Abate, 2020). The common garden pea is the ancestor of the vegetable pea, which is a member of the Fabaceae family (sometimes called Leguminosae) and species "hortense" of the genus *Pisum*. However, the 2n=14-chromosome *Pisum sativum* subspecies "arvense" is indigenous to Central Asia, the Mediterranean, and Ethiopia (Das and Kalloo, 1970). Wild species of *Pisum*, such as *P. fulvum* and *P. erarius*, and the cultivated variety, *P. abyssinicum*, are all part of the genus *Pisum*, which is native to the Mediterranean and the Middle East. The exact location of its diversity center is still uncertain, nevertheless, because of substantial shifts in its origin areas and the disappearance of passport data from early accessions.

Botanical description of garden pea

The garden pea, or *Pisum sativum*, is a herbaceous plant that can reach a maximum length of around 2 meters, as stated in the third book of the flora by Hedberg and Edwards. The leaflets are smaller and less numerous than the stipules, which can grow to a length of 10 cm. Each raceme, or cluster of flowers, that this plant produces usually has anywhere from one to two blossoms, but can sometimes have as many as three. The flower's petals, or corolla, can be any color from white to purple and range in length from 15 to 35 mm. garden pea pods are long and narrow, ranging in size from 3-9.5 cm in length and 1-1.8 cm in width. In a typical pod, you'll find anywhere from two to nine seeds. The seeds can vary in size, shape, texture (smooth or wrinkled), and even angle, with a diameter ranging from 5 to 8 mm. In contrast to older cultivars, which can reach vine lengths of up to 9 feet, today's garden peas typically only reach vine lengths of about 2 feet. According to Elzebroek and Wind, the plant's stem is hollow, and taller varieties need something to climb. garden pea inflorescences are racemes that contain one to four blooms and emerge in the spaces between the leaves. The flower features five fused sepals of green hue and five petals of white, purple, or pink, varied in size. The "standard" refers to the biggest petal, and the "keel or boat" is the combined appearance of the two lesser petals. According to Elzebroek and Wind (2008), the "wings" are the last two petals that narrow as they approach the base. The keel contains ten stamens, nine of which surround the pistil in a tube and one of which is free-floating. According to Pavék and Pamela (2012), the fruit that develops from an ovary that contains fifteen or more ovules is a closed pod that ranges in length from one to four inches and frequently has a rough inner membrane. Round and colored with a spectrum from green to yellow to beige to brown to red to orange to blue-red to dark violet to nearly black, with or without markings, mature garden pea seeds are a sight to behold. Breeders are able to create true-breeding lines of garden peas because the blossoms mostly self-pollinate.

Morphological characters of garden pea

In order to investigate the kind and level of variability, correlation, and path coefficient analysis, Lal *et al.* (2011) ^[17] examined thirty genotypes of garden pea (*Pisum sativum*) throughout the 2009-2010 rabi growing season for twelve

quantitative variables. The analysis of variance revealed that there were significant variances among the 30 genotypes for all of the traits. Factors such as plant height, harvest index, number of major branches, seed weight per pod, number of clusters, and biological GCV, heritability, and genetic advancement were moderate to high in both the yield per plant and the grain yield per plant. Among all the features, plant height had the highest GCV and PCV values at 38.8 and 38.82, followed by harvest index at 36.88 and 37.1, and biological yield at 38.8 and 38.82.

In 2013, Pal *et al.* assessed twenty-five different pea genotypes. Genotypes showed a great deal of variation, with statistical analysis showing that there were substantial differences across all traits. In their study conducted in Rabi 2016-17 using Augmented Block Design and involving 90 genotypes and 4 control varieties, Prasad *et al.* (2018) found a high degree of variability for all traits except pod length (cm) when comparing the means of the genotypes using least significant differences. Using genetic variability, heritability, and genetic advance for yield, Yumkhaibam *et al.* (2019) ^[34] examined thirty-two garden pea genotypes for twenty-two parameters. The results showed that heritability exerts a high degree for all the plant characters studied, including plant height, days to first flowering, days to first pod harvesting, ascorbic acid, protein content, pod weight, shelling percentage, internodal length, number of primary branches per plant, pod yield per plant, pod yield per hectare, and other yield attributing characters. When it came to genetic advancement, the plant's internodal length, number of main branches, and height were at the top, while the days to first pod harvest were at the bottom. Variation in plant height, internodal length, and primary branch number was highly heritable and associated with significant genetic advancement.

Various yield and yield contributing characteristics were reported by Azam *et al.* (2020) ^[4]. Widespread variations in genotypes for the majority of factors were seen in the strikingly different performance of all cultivars. After Bagha local and Jhikargachha local, BFP 11015 had the greatest pod production. Each character's PCV flowed smoothly from their corresponding GCVs. The presence of a broad genetic base was shown by the high GCV and PCV for pod yield, number of pods per plant, 100 seed weight, powdery mildew severity, and pod number. Except days to maturity, all traits showed significant heritability values and high genetic progress over% mean. In a randomized full block design, Bhardwaj *et al.* (2020) ^[6] examined 41 genotypes, including four controls ('Lincoln', 'Azad P-1', 'Palam Priya', and 'Punjab-89'). In terms of pod yield and associated characteristics, there were noticeable genetic variances. When looking at pod output per plant and PCV per plant, both were quite high. There was a strong correlation between genetic advancement and the number of pods produced per plant, suggesting a high degree of heredity.

Finding the right balance between main and secondary features as a selection criterion to boost productivity is important, according to Bahadur *et al.* (2021) ^[5]. All characteristics were determined to have a very significant analysis of variance. Harvest index, days to 50% flowering, biological yield per plant, and strong heritability and genetic advance percent of mean plant height follow. Variances in both genotype and phenotype were quite high, indicating a well-developed genotype. The phenotypic coefficient of variance (PCV) was marginally larger than the genotypic coefficient of variance (GCV) for all characteristics, suggesting that environmental factors had a little impact on trait expression. The plant's height was the most important factor in determining its GCV, while the number of secondary branches per plant came in second.

All of the variables were statistically significant at the 1% level, according to the research by Bishnoi *et al.* (2021) [7]. Overall, there was a lot of heterogeneity in the phenotypic and genotypic coefficients for plant height, pod count, effective nodes, seeds per plant, harvest index, 100-seed weight, and yield per plant. This proved that there was enough variation among the traits. The characteristics yield/plant, 100-seed weight, number of pods/plants, harvest index, plant height, number of effective nodes, number of seeds/pods, and width of pods showed a high level of heritability and genetic advancement as a percentage of the mean. This suggests that additive gene action is the dominant effect.

Genetic variation and associations among agronomic traits of pea (*Pisum sativum* L.) genotypes were investigated by Kumar *et al.* (2021) [13]. Ten different genotypes were used in the field experiment. Based on the data we have, genotype G6 has the optimal mean squares for 50% blooming, days to maturity (122.08), and fresh pod shelling percentage (65.29%). It is possible to incorporate genotypes G6, G2, G9, and G5 into future breeding programs due to their superior performance among the evaluated genotypes. These qualities are the most important in order to increase the crop's production in the future, breeders emphasize yield variety. The study of genetic variability and the agronomic traits associated with it can be used to successfully increase pea output. Using 21 different garden pea genotypes, Pujari *et al.* (2021) [23] determined the genetic factors for eleven different features. Results from the analysis of variance reveal that the genotypes under consideration exhibit a great deal of variation. Plant height, number of pods per plant, and number of major branches per plant are qualities with moderate to high GCV and PCV estimates. Using 42 unique genotypes and two sets of checks for quantitative and qualitative features, Yadav *et al.* (2021) [33] investigated the various genotypes. Analysis of variance predicted that the genotypes used in this study would be genetically varied and of high breeding value, and the results were indeed accurate. A yield that was noticeably higher than the best check PC-521 was achieved by eighteen of the forty-four genotypes.

Research conducted by Temesgen Abo Ertiro (2022) at Bekoji in 2020 used a basic lattice design to assess 49 different genotypes of garden peas. Data acquired from morpho-agronomic studies were subjected to analyses of variance. Except pod length, seed per pod, and pod per plant, most traits showed a significant difference among genotypes. garden pea genotypes display reasonable genetic variation, according to the study. This information might be utilized to create breeding programs.

Genetic divergence

The concept of selecting parents from diverse backgrounds originates from the work of Lu (1939), who discovered that inbred lines selected from a cross resulted in offspring with a single parent. consistently yielded less than those of single crossings made from inbred lines of diverse genetic origins. The selection of parents for the hybridization program is influenced by the level of genetic variation in the population. Because it raises the odds of achieving beneficial gene recombination to generate substantial heterotic effects, Mahalanobis' D2 statistic is a useful tool for evaluating genetic divergence in biological populations. To classify a group of people according to their average position in a three-dimensional space—representing the characters scored on each individual field—with each point serving as the diversity's center—the concept of generalized distance was first proposed by Mahalanobis in 1936. The

clusters belonging to different normal populations were fully described by:

Character mean

(b) The dispersion and correlation at that specific yield point; from this, he deduced a generalization about the dispersion of normal populations (Rao, 1952). Because of its roots and original usage in anthropometry, Mahalanobis's generalized distance has found usefulness in assessing genetic divergence in a number of agricultural species.

Zeng *et al.* (2012) [35] used ISSR markers to document genetic diversity in seventy-three *Pisum sativum* samples collected domestically and internationally. Out of one hundred primers with clear and polymorphic bands, eleven were chosen. Seventy-three materials yielded 91 bands, with 78 of those bands being polymorphisms. The polymorphism percentage was 86.4% and each primer amplification site averaged 8.2. With an average Shannon's index of 0.4202 and 1.4518 effective alleles, a genetic similarity coefficient ranging from 0.4065 to 0.9340, and a wealth of genetic diversity, this sample is quite remarkable. The 73 materials were categorized into five categories using UPGMA cluster analysis, which used a genetic similarity coefficient of 0.52 for borders. The materials were clustered based on their geographical origin, and each class had a certain distribution pattern.

To evaluate genetic divergence for use in a breeding program to increase garden pea production potential, Saxena *et al.* (2013) [25] examined twenty-one advanced breeding lines and two varieties (HUDP 15 and IPFD 1-10) as controls. making use of the Mahalanobis D2 statistic. Results showing significant divergence between the advanced breeding lines were obtained when the intra-cluster D2 values varied between 0.00 and 65.10 and the inter-cluster D2 values varied between 101.389 and 763.200. Clusters IV and V had no intra-cluster distance values, indicating that the genotypes within them were not homogeneous, whereas cluster I had the largest intra-cluster distance of 65.109. The inter-cluster distance score (763.200) indicates that clusters II and V contain more genetically distinct advanced breeding lines.

Based on their research, Selvi *et al.* (2014) [28] identified eight distinct clusters, including twenty-six genotypes. Cluster I had the most genotypes (10) out of the eight clusters, whereas cluster VIII had the second-most (4) genotypes. Cluster VII had the highest mean values for the 23 characters, followed by clusters VIII and II. The best cultivars for yield-related features were identified as Azad P-3, Arka Sampoorana, PSM-4, and Arka Karthik genotypes.

Sanwal *et al.* (2015) [24] used multivariate analysis to examine 160 genotypes of garden pea (*Pisum sativum* L.) for nine morphological features. Based on their morphological similarities, the genotypes were sorted into 14 groups using principal component analysis. The majority of the genotypes, 113 (or 70%), were found to be genetically closely related and clustered in 3 groups. On the other hand, 47 genotypes (30%), spread out throughout 11 groups, mostly contributed to the noticeable variety. Distances between clusters III and XIV (61.49), III and VII (51.33), and III and XII (53.27) were the largest observed. The cluster mean suggests that genotypes from cluster III could be good candidates for a future hybridization effort. Results showed that 10-pod weight (58.29), days to 50% flowering (23.83), plant height (11.31), and shelling percent (4.95%) were the most important characteristics in expressing genetic diversity.

According to Negisho *et al.* (2017), 142 different garden pea

germplasm samples from Ethiopia were studied for genetic diversity using SSR markers. The materials were classified into seven separate groups using the Euclidean Distance Matrix. Group I had twenty collections, Group II had eleven, Group III had five, Group IV had forty-one, Group V had seventeen, Group VI had eighteen, and Group VII had thirty. The first main component explained 76.85% of the variance, the second 6.89%, and the third 6.06%. It was unclear whether there was a connection between the pattern of genetic variation and genomic hotspots, shedding information on the germplasm's exceptionally high levels of intra- and inter-genetic variability. Using SSRs with a polymorphic information content (PIC) of 0.33 to 0.95, this study found a comparatively higher PIC.

Crosses between entries with high cluster mean values for one or more improved characteristics and entries with substantial inter-cluster distances are likely to be more beneficial, according to Singh *et al.* (2017) [31]. Plant height was the most important factor in the expression of total genetic variation (76%), followed by days to maturity (9%). Days to 50% blooming and 100-seed weight are the bare minimum that contribute 1% and 1% respectively to genetic divergence. When it came to the total genetic divergence in the germplasms that were available, the middle range was exhibited by the number of pods/plant (2%), biological yield/plant (6%), and harvest index (5%). Using the Mahalanobis D2 statistic, Bijalwan *et al.* (2018) assessed the genetic diversity of 23 pea genotypes. These genotypes were categorized into five groups according to their genetic distance. Out of all the clusters, Cluster IV had the most genotypes at eight, followed by Cluster I at seven, Cluster III at four, Cluster II at three, and finally Cluster V at one. In order to determine the kind and extent of genetic variation among 52 genotypes defined by phenotypic features, Jaiswal *et al.* (2021) [9] used multivariate analysis. The genotypes clustered into three distinct groups according to the cluster analysis. In cluster I, there were 50 genotypes at the maximum level, while in cluster II, there was one, and in cluster III, there was one, respectively. Cluster I displayed the greatest intra-cluster distance ($D2=5.07$), suggesting the most significant difference among the genotypes inside the cluster, whereas clusters II and III displayed the smallest values. Clusters I and III had the largest inter-cluster distance ($D2=16.76$), indicating that their genotypes were very different from those of other clusters and hence suitable as divergent parents for hybridization and selection.

The study by Priyanka *et al.* (2021) [22] found 41 genotypes that were organized into 8 clusters. There were 25 genotypes in cluster I, 8 in cluster II, and 3 in cluster VIII out of 8 clusters. Cluster VIII had the largest intra-cluster distance at 10.26, followed by cluster II at 8.59, and cluster I at 7.72. Cluster I and cluster VI had the greatest inter-cluster distance (24.07), while cluster I and clusters I, III, and IV (22.25), and 21.41. Genetic material from these clusters could thus serve as a foundation for the transgressive segregants. With a significantly higher cluster mean for seed output per plant, cluster IV (12.57) stood out. A plant's harvest index (21.95%), biological yield (19.39%), and seed output (19.15%) were the traits that contributed most to genetic divergence, followed by the number of major branches per plant (25.12%). Six groups best accounted for the genotypes in the study by Singh *et al.* (2021) [30]. Cluster IV had the fewest genotypes (4) and Cluster III had the most (14) correspondingly. Cluster II had the smallest intra-cluster distance ($D2=1.827$), whereas cluster I had the largest ($D2=2.543$), showing the most diversity among the genotypes inside. The inter-cluster distance ($D2=6.471$) was greatest between clusters I and IV, indicating that their genotypes were very different from each other and

hence suitable as hybridization and selection parents. Using multivariate analysis, Kumar *et al.* (2022) [14] investigated 20 pea (*Pisum sativum* L.) genotypes to determine the kind and degree of genetic variation among genotypes as it pertains to phenotypic traits. D2 analysis showed that there was a lot of variance among genotypes, grouping all 20 variants into five groups. Cluster analysis showed that there were a total of five genotypes in clusters I and II, four in cluster III, three in cluster IV, and one in cluster V. Cluster V had the smallest intra-cluster distance ($D2=1.481$), Cluster II and IV had the largest inter-cluster distance ($D2=5.211$), and Cluster III and V had the smallest ($D2=2.373$), all of which indicate that there was the greatest variation among the genotypes within cluster I ($D2=2.264$). Based on the goals of the breeding program, cluster IV was determined to be the optimal cluster for a variety of characteristics, including plant height, pod yield, days to maturity, pod length, and number of pods per plant. A genetic divergence analysis utilizing Mahalanobis's D2 analysis was performed on those 47 lines, and Kumar *et al.* (2022) [15] found that they clustered into seventeen distinct groups. The average inter-cluster distance was 43.62 between clusters XII and XIII, and the intra-cluster distance was 12.66 inside cluster VII. The characteristics that contribute the most to divergence as a percentage first, the amount of major branches per plant, and then the biological yield per plant. The means of clusters XV and XVII were higher for the majority of genotypes. There is a great deal of genetic variation among the 5 different clusters of genotypes that Kaur *et al.* (2022) [11] found. Clusters I possessed the most genotypes, but clusters IV, V, and III were monogenotypic. Pod yield was the most diverse of the examined characteristics, accounting for 31.16 percent. The results of the cluster mean analysis demonstrated that the germplasm collection was quite diverse, with intra-cluster distances ranging from 0 to 168.79. The greatest distance between clusters, measuring 1430.70, was found between clusters III (Anmol) and V (Shilpa-10).

Biochemical and Molecular Characterization

We must prioritize the enhancement of commercial cultivars' protein quality and quantity as legumes are our country's primary source of protein. It is essential to assess the genetic and biochemical variability of before beginning any initiative to improve crops cultivated varieties at this time in order to choose suitable genotypes to serve as breeding program parents. It is feasible to pick fresh material with suitable qualities for certain uses due to the significant genetic variety in peas about the seed retained starch and protein. Furthermore, there are good indications of quick pea crop production, and the crop satisfies most parameters for sustainable crop production. This research aims to identify intergenotypic variability in ten different *Pisum sativum* L. cultivars' total protein, albumin, globulin, prolamin, glutelin, sugar, starch, and mineral content. Additionally, research on gel electrophoretic banding has been conducted. Researchers also looked at the biochemical changes that occurred in pea plants at various growth and development phases in order to determine their potential as a feed source.

Proteins

Structure, function and classification

Amino acid linkages make proteins extremely complicated compounds. The basic building blocks of proteins, amino acids, include carbon, hydrogen, oxygen, nitrogen, and sometimes sulfur. Amino acids are protein building blocks that are present in most plants and animals.

Proteins known as peptides are formed when amino acids join together. It is not uncommon for proteins to have 500 amino acids or more. Protein structure and function are defined by the specific number and order of amino acids found in each protein. During digestion, proteins are reduced to their amino acid components. The body then absorbs these building blocks and uses them to synthesize new proteins. Some amino acids are bioavailable to humans. Essential amino acids, on the other hand, can't be produced in the body and instead need to be consumed through food. Lysine, phenylalanine, valine, threonine, methionine, and isoleucine are the eight amino acids that humans need. Another amino acid that is deemed necessary for youngsters is histidine. As a result of the accumulation of essential amino acids in the cotyledons as storage proteins, seed proteins are nutritionally significant (Munty, 1982; Mandal and Mandal, 2000) [18]. Along with carbohydrates and oils, they make up an essential class of plant proteins that are produced when seeds are forming, and this fact has led to a great deal of research on these proteins. Proteins are put down at varying rates throughout seed development. There are two phases to the development of cotyledons in legumes: cell division and cell expansion. The majority of the storage proteins are produced in the later stage. At the same time, there is an influx of proteins into membrane-bound vesicles known as protein bodies (Briarty *et al.*, 1970; Graham and Grimming 1970). The nitrogen for the many nitrogenous compounds produced by the growing seedling comes from these protein bodies, which are broken down during germination (Boulter and Barber, 1963). Proteins that are set down at one point of the life cycle to be used later on when the metabolism is more active are called storage proteins. The structure of seed storage proteins in several legumes has been studied with the development of analytical tools like as electrophoresis, chromatography, *in vitro* and *in vivo* protein synthesis, gene cloning, etc. Protein storage has been the subject of much study in terms of its biosynthesis, regulation, and characterisation (Boulter and Croy, 1997; Mandal and Mandal, 2000) [18]. Variety, species, and genera all have a role in the protein spectrum. The seed proteins are subjected to a cascade of modifications prior to their incorporation into the protein bodies. These modifications encompass signal peptide removal, glycosylation, posttranslational cleavage, and more. Proteins play a crucial role in development and maintenance. Almost every biological process in the body relies on them. The metabolic processes in the body rely on enzymes, which are proteins. Proteins are essential for many bodily functions, including helping the immune system do its job, transmitting nerve impulses, and contracting muscles. The structural support is provided by the proteins found in skin and bone. A lot of hormones are proteins. Protein is a potential energy source as well.

Protein is utilized for energy instead of carbohydrates and fats, which happens when there is an excess of protein in the diet or when the amounts of fat and carbohydrates are insufficient. It is also possible to accumulate excess protein as fat. Because their biological function was not known, scientists attempted to categorize proteins based on their chemical and physical properties after two German chemists, Franz Hofmeister and Emil Fischer, separately stated in 1902 that proteins are basically polypeptides made up of many amino acids. The main criterion for protein classification was their solubility in various solvents. However, this categorization is now inadequate due to the fact that proteins with substantially different structural and functional properties can exhibit comparable solubilities, while proteins with identical structural and functional properties can

exhibit distinct solubilities. Nonetheless, many people continue to use the words that were used for the previous categorization. Proteins known as albumins dissolve in both water and water that is half-saturated with ammonium sulfate. In contrast, globulins are extracted by half-saturating them with ammonium sulfate, a process known as precipitation. The term "pseudoglobulin" describes globulins that dissolve in salt-free water, while "euglobulin" describes globulins that do not. Some plant proteins, including prolamins and glutelins, are insoluble in water. Others, like glutelins, dissolve in acidified or alkaline solutions, whereas prolamins dissolve in 50 to 80 percent ethanol. Many proteins in fish sperm are known as protamines; these proteins are very alkaline because they contain about 80% arginine. It would appear that histones, which are less acidic, are coupled to nucleic acids and exclusively found in cell nuclei. Animal organ insoluble proteins are known as scleroproteins. Proteins like collagen, found in connective tissues, and keratin, found in some epithelial tissues like hair and skin, are examples of these. Conjugated proteins are a group of proteins that share the property of being complex molecules with both protein and nonprotein components. The prosthetic group refers to the part that is not protein. Nucleoproteins contain nucleic acid, chromoproteins contain pigments like iron-porphyrins, carotenoids, bile pigments, and melanin, and phosphoproteins contain phosphate. Mucoproteins contain carbohydrates in addition to protein. Lipoproteins contain lipids. Phosphoproteins contain phosphorus. There is no clear boundary between globulins and mucoproteins, which is a drawback of the previous categorization because most globulins contain some carbohydrate. In addition, phosphoproteins do not include an isolated prosthetic group; rather, they are proteins with phosphate attached to part of the serine hydroxyl groups. Enzymes, antibodies, fibrous proteins, and contractile proteins are all part of the globulins, which contain proteins with diverse functions.

Pea Proteins

Vegetable proteins are those that originate from plants. These days, it's possible to fortify vegetable proteins with limiting amino acids or combine them with proteins from other sources to create a combination whose biological worth is on par with, or even higher than, that of animal proteins, which there are plenty of. Additionally, the cholesterol level is quite high in animal proteins. Peas are one of the most important grain legumes for treating protein deficiency, both internationally and in India. Although it lacks sulfur-containing amino acids, pea protein makes a great cereal supplement due to its comparatively high lysine content (McPhee, 2003). Pea seeds' protein level and composition determine their nutritional and functional properties. According to Turner *et al.* (1990), there are morphological and genotypic elements that contribute to the variability in the composition of pea seeds. There are a lot of genes that encode pea storage proteins, which causes a lot of polymorphisms, according to many studies (Casey *et al.*, 1982; Higgins, 1984; Boulter *et al.*, 1987). The synthesis of many polypeptides is facilitated by post-translational modifications, such as cleavage and glycosylation, which enhance the heterogeneity of protein molecules (Matta and Gaitehouse, 1982; Muntz, 1989). Similarly, storage proteins are influenced in a pleiotropic manner by the genes located at the *rb* & *r* loci on the third and seventh chromosomes, which determine whether peas are wrinkled or smooth (Kooistra, 1962; Turner *et al.*, 1990; Perez *et al.*, 1992). Matthews and Arthur (1985), Bertholdsson (1990), and Cousin (1992) found that the protein

content and composition of seeds can be influenced by morphological parameters, such as the pea's position within the pod or the pod's placement on the plant. According to Naik *et al.* (2000)^[19] and Sathe (2002)^[26], the majority of research on pea seed proteins has focused on the storage protein fraction, also known as globulin. This portion is of direct quantitative importance in pea nutrition breeding since it comprises 75-80% of the total seed protein. It has long been believed that the albumin fraction, which can range from fourteen percent to forty-two percent of the total seed protein depending on the genetic line and the method used to separate the albumin, is the metabolic and enzymatic component of seeds. Despite its nutritional importance, it has few proteins that are big enough to be easily separated (Murray, 1979). There is a structural protein reserve in the globulin fraction of pea protein, which is also the principal fraction. Based on their sedimentation coefficient, the globulins have been classified into two main groups: the 11S fraction (legumin) and the 7S fraction (vicilin, convicilin). Multimeric globulins, hexamers of mature legumins, and trimers of vicilins and convicilins all build up in the seed. It has also been found that pea globulins go through post-translational modification. A disulfide bridge connects the two processed subunits of legume. Proteolytic cleavage of vicilins can occur at many sites. According to Derbyshire *et al.* (1976), pea legumes, which contain mostly legumin, have a sedimentation coefficient ranging from 11 to 13 S. Legumin is composed of six subunit pairs, with each pair being made up of a 'acidic' subunit (mol. wt. about 40,000) and a 'basic' subunit (mol. wt. about 20,000) connected by one or more disulfide connections. According to Matatte *et al.* (1981), there are three distinct kinds of subunit pairs found in legumes. The first type, with a range of 53,000 to 54,000 mM, is the conventional subunit pair found in the model proposed by Wright and Boulter (1974). The other two types, with lower abundances, are called big (with a range of 55,000 to 58,000 mM) and small (with a range of 35,000 mM). The initial step in synthesizing legumin is the formation of a precursor, which consists of a single polypeptide chain that is later cleaved (Croy *et al.*, 1980).

Compared to vicilin, legumes are less soluble and heat-insoluble in diluted salt solutions. Throughout pea development, legumes build up. Research on the breakdown of legumin and vicilin during seed germination has shown that sulphhydryl proteinases play a role in the mobilization of storage proteins (Schlereth *et al.*, 2000; Muntz *et al.*, 2001)^[27,1]. In most cases, vicilin is a very small and heterogeneous proportion. Its main components are polypeptides with a molecular weight of around 50,000 Mr. During seed development, there are quantitative and qualitative changes in the subunit polypeptide composition of vicilin. The third storage protein, convicilin, can be isolated from either legumin or vicilin. Despite its antigenically distinct nature from legumin, it elicits an identification reaction with vicilin. However, according to Croy *et al.* (1980), convicilin does not include any subunits of vicilin.

Conclusion

The comprehensive exploration of *Pisum sativum* L. presented in this review underscores the crop's immense agronomic, nutritional, and genetic significance. Despite being a well-established pulse with high protein content and a rich composition of essential nutrients, there exists substantial untapped potential in improving its yield, adaptability, and resilience. The genetic variability and morphological diversity observed across numerous studies reveal promising avenues for selection and hybridization aimed at breeding climate-resilient,

high-yielding, and nutritionally enriched cultivars.

Moreover, the insights into genetic divergence and biochemical profiling—especially concerning storage proteins such as globulins—emphasize the scope of using both traditional and molecular breeding approaches. The application of tools like Mahalanobis' D² statistics and ISSR markers has proven invaluable in characterizing diversity and guiding parent selection for crop improvement.

To ensure sustainable production and meet nutritional demands, it is crucial to utilize diverse germplasm resources and integrate genetic, morphological, and biochemical data. Such a multidisciplinary approach will accelerate the development of elite pea cultivars tailored to diverse agro-climatic regions and consumer needs, thereby enhancing the role of peas as a key crop in food security and agricultural sustainability.

References

1. Anonymous. Project Coordinators Reports (Rabi crops). AICRP on MULLaRP, IIPR, Kanpur. 2021;4(4):30-53.
2. Asha AB, Srinivasa V, Hanumantappa M, Aghora TS, Ganapathi M, Chithra K. Correlation and path analysis in garden pea (*Pisum sativum* L.). J Pharmacognosy Phytochem. 2020;9(5):1728-1731.
3. Assen KY. Trait associations in prostrate and semi-leaf less type garden pea (*Pisum sativum* L.) gene pools. Am J Environ Sci Eng. 2020;4(4):54-60.
4. Azam MG, Iqbal MS, Hossain MA, Hossain J, Hossain MF. Evaluation of garden pea (*Pisum sativum* L.) genotypes based on genetic variation and association among yield and yield-related traits under high Ganges River Floodplain. Int J Plant Biol Res. 2020;8(2):1120.
5. Bahadur L, Devi B. Estimation of correlation and path analysis coefficient among yield and yield attribution trails of garden pea (*Pisum sativum* L.). J Pharmacognosy Phytochem. 2021;10(1):1696-1699.
6. Bhardwaj A, Sharma A, Lata H. Genetic variability for pod yield and related traits in garden pea (*Pisum sativum* L.). Electron J Plant Breed. 2020;11(4):1233-1238.
7. Bishnoi R, Marker S, Kumar KY, Taranum SA. Genetic variability parameters for quantitative traits in farmers' pea (*Pisum sativum* var. arvense L.) varieties. Biol Forum Int J. 2021;13:320-325.
8. Gautam KK, Syamal MM, Singh AK, Gupta N. Variability, character association, and path coefficient analysis of green pod yield and its related traits in pea (*Pisum sativum* L.). Legume Res Int J. 2017;40(5):818-823.
9. Jaiswal RP, Pandey BR, Pandey SK, Kumar V. Genetic divergence of pea genotypes (*Pisum sativum* L.) based on multivariate analysis. Int J Curr Microbiol Appl Sci. 2021;7:3491-3495.
10. Jeberson MS, Shashidhar KS, Iyanar K. Estimation of genetic variability, expected genetic advance, correlation, and path analysis in garden pea (*Pisum sativum* L.). Electron J Plant Breed. 2016;7(4):1074-1078.
11. Kaur N, Dhangra VK, Singh YP. Studies on genetic diversity of garden pea (*Pisum sativum* L.). J Pharmacognosy Phytochem. 2022;10(1):1053-1055.
12. Khan MRA, Mahmud F, Reza MA, Mahbub MM, Shirazy BJ, Rahman MM. Genetic diversity, correlation, and path analysis for yield and yield components of pea (*Pisum sativum* L.). World J Agric Sci. 2017;13(1):11-16.
13. Kumar MS, Singh NB, Jeberson MS, Ramaiah KS, Singh LN, Singh NG. Correlation and path coefficient analysis for yield and its contributing characters in advanced breeding

- lines of garden pea (*Pisum sativum* L.). J Food Legumes. 2021;34(3):199-204.
14. Kumar MS, Singh NB, Jeberson MS, Ramaiah KS, Singh LN, Singh NG. Genetic analysis in advanced breeding lines of garden pea (*Pisum sativum* L.). Electron J Plant Breed. 2022;13(1):34-40.
 15. Kumar R, Singh B, Tomar H, Singh S. Assessment of genetic divergence in pea (*Pisum sativum* L.) genotypes in Western UP. Int J Environ Clim Change. 2022;12(11):1738-1744.
 16. Kumar S, Ali B, Ahmed W, *et al.* Assessment of the genetic variability for various agronomic traits of pea (*Pisum sativum* L.) genotypes. Plant Arch. 2022;22(1):87-94.
 17. Lal GM, Meena ML, Chandra KUNJ, Singh CM. Assessment of genetic variability and interrelation between yield and its contributing components in garden pea (*Pisum sativum* L.). Environ Ecol. 2011;29(3A):1235-1239.
 18. Mandal S, Mandal RK. Seed storage proteins and approaches for improvement of their nutritional quality by genetic engineering. Curr Sci. 2000;79:576-589.
 19. Mallesh PHC. Variability, heritability and genetic advance for quantitative traits in pigeonpea (*Cajanus cajan* L. Millsp.). Int J Pure Appl Biosci. 2017:25-28.
 20. Naik BS, Pattanayak SK, Kole C. Selection of protein rich genotypes in mungbean. Indian J Genet. 2000;60:321-326.
 21. Pal AK, Shivendra S. Correlation and path analysis in garden pea (*Pisum sativum* L. var. hortense). Asian J Hortic. 2012;7(2):569-573.
 22. Priyanka R, Lal GM. Genetic diversity studies in garden pea (*Pisum sativum* var. arvense L.) germplasm. Int J Plant Soil Sci. 2021;33(19):163-169.
 23. Pujari PK, Salam JL, Sao A, Mandavi NC, Singh DP. Study of genetic variability in garden pea (*Pisum sativum* L.). J Pharmacognosy Phytochem. 2021;10(1):1053-1055.
 24. Sanwal SK, Singh B, Singh V, Mann A. Multivariate analysis and its implications in breeding of desired plant type in garden pea (*Pisum sativum*). Genet Pol. 2015;28:89-99.
 25. Saxena RR, Lal GM, Yadav PS, Vishwakarma MK. Diversity analysis and identification of promising lines for hybridization in garden pea (*Pisum sativum* L.). Bioscan. 2013;8(4):1437-1440.
 26. Sathe SK. Dry bean protein functionality. Crit Rev Biotechnol. 2002;22:175-223.
 27. Schlereth A, Becker C, Horstmann C, Tiedemann J, Muntz K. Comparison of globulin mobilization and cysteine proteinase in embryonic axes and cotyledons during germination and seedling growth of vetch (*Vicia sativa* L.). J Exp Bot. 2000;51:1423-1433.
 28. Selvi BS, Rajangam J, Muthuselvi R. Genetic divergence in pea (*Pisum sativum* L.). Plant Arch. 2014;14(2):887-891.
 29. Singh BK, Sutradhar M, Singh AK, Singh SK. Evaluation of genetic variability, correlation and path coefficients analysis for yield attributing traits in 61 garden pea (*Pisum sativum* L. var. arvense). Res Crops. 2017;18(2):316-321.
 30. Singh S, Sharma VR, Nannuru VKR, Singh B, Kumar M. Phenotypic diversity of pea genotypes (*Pisum sativum* L.) based on multivariate analysis. Legume Res Int J. 2021;44(8):875-881.
 31. Singh SK, Maseed A, Singh VP, *et al.* Evaluation of seed yield and genetic divergence in the germplasms of (*Pisum sativum* L. var. arvense). J Pharmacognosy Phytochem. 2017;6(6S):1016-1021.
 32. Tasnim S, Ivy NA, Raihan MS, *et al.* Evaluation of genetic variation in the segregating population of pea (*Pisum sativum* L.): Genetic variation in pea. SAARC J Agric. 2022;20(1):29-39.
 33. Yadav P, Ram CN, Yadav GC, Nath S, Kumar S. Studies on genetic variability, heritability and genetic advance in garden pea (*Pisum sativum* L. var hortense). J Biochem. 2021;57:508-514.
 34. Yumkhaibam T, Deo C, Ramjan M, Chanu NB, Semba S. Estimation of genetic variability, heritability, and genetic advance for yield and its component traits of garden pea (*Pisum sativum* L.) in North East India. J Pharmacognosy Phytochem. 2019;8(3):4034-4039.
 35. Zeng L, Li M, Yang X. Genetic diversity of (*Pisum sativum*) germplasm resources by ISSR. Acta Pratacult Sin. 2012;21(3):125-131.