MAINTAINING AND IMPROVING PEAS (*Pisum sativum* L.) CV. MASTER PEA (LOCAL CULTIVAR) USING UPOV DESCRIPTORAND MULTIVARIATE ANALYSIS IN THE VEGETABLE SEED PRODUCTIONFIELD

Comment [RL1]: Should be revised to read as " Maintaining and Improving Peas (*Pisum sativum L.*) cv. Master Pea (local Cultival) as Vegetable Seeds for Field Production

ABSTRACT

Although peascv. master peawas registered more than 25 years ago in Egypt,This variety showed a remarkable superiority over the varieties grown in all governorates of Egypt in terms of production, quality, and environmental adaptation to climate changes.This study intends to assess this cultivar's genetic and environmental traits, and to determine the degree of its deterioration over time to develop an appropriate plan for the maintenance, improvement, and conservation of this strategic variety to withstand changes in climatic conditions in Egypt. Many types of research have been conducted on the study and production of new varieties and lines of peas in Egypt; yet there is a dearth of multivariate analysis as a technique that can combine all variances for all examined qualities using statistics that rely on the algebra of matrices and extract statistical markers from which the researcher can make an appropriate selection program within cultivars without causing genetic erosion. The present experiment was conducted to achieve the following objectives: to monitor the performance of growth traits in the Master pea cultivar using multivariate analysis and UPOV descriptor; Evaluation of yield characteristics, seed yield, and quality of Master pea cultivar using multivariate analysis and UPOV descriptor.In this study,one of the most important results obtained was that the phenotypic diversity within the population (measured using the UPOV descriptor) is an important aspect that reflects genetic diversity and the ability of this genetic diversity to withstand changes in the environment. Natural selection - over the many years of the inherited varieties of countries and societies - affects the diversity of phenotypic traits among the individuals of the population.It can be concluded from thisstudythatthe phenotypic traits identified in the UPOV descriptor and data analysis using multivariate analysis can show differences between lines within cultivars. Therefore, we recommend taking advantage of the UPOV descriptor and multivariate analysis as a successful way toobtain differences and relationships between lines in conservation, maintenance, and improvement programs for ancient and promising cultivars in the Arab Republic of Egypt.

Keywords: *Peas, Pisum sativum* l., maintaining, improving, multivariate analysis,UPOV descriptor

INTRODUCTION

Peas (*Pisum Sativum* L.) originate from the Mediterranean to East Asia (Tibet). Annual Egypt production (in 2021) is about 230.48 tons of dry peas and 156245 tons of green peas from 80 and19001 hectares, respectively; while, annual world production is about 12.404 million tons of dry peas and 20.529 million tons of green peas from 7043605 and 2590367 hectares, respectively **(FAOSTAT, 2023).** Peas are one of the most popular vegetables grown in Egypt.According to the previous statistics, Egypt produces 41% more dry yield of peas per unit area than the global average. While Egypt produces 3.62% more green yield of peas per unit area than the global average.

Peas are a superior meal for humanhealth because are good for digestion, and the high fiber content in the pods helps in maintaining a healthy digestive system. Peas are a great source of iron, Anemia occurs most often due to iron deficiency. Peas are among the best meals for boosting immunity as they are rich in Vitamin C., an antioxidant that can prevent H.Pylori, which causes stomach and duodenal ulcers as well as stomach cancer. Lutein, a carotenoid pigment, is abundant in peas. Lutein is known to reduce the incidence of cataracts, and age-related vision loss. Peas contain insoluble fiber, which reduces the risk of heart disease and stroke. Peas also help maintain the body's ability to regulate blood sugar. peas may also help you lose weight quickly. Peas are a great source of vitamin C, which is essential for collagen synthesis. Collagen keeps skin firm and radiant. In addition, vitamin C protects cells from free radical damage. Antioxidants help prevent oxidation caused by free radicals. In addition, the antioxidants in it, including flavonoids, catechin, epicatechin, carotenoids, and alpha-carotene, help delay the onset of aging. Peas can help boost sperm motility and sperm count. Glycodyline, a compound found in snow peas, "may help strengthen sperm and enhance their ability to fertilize an egg."Pea straw is nutritious fodder **(Sengupta, 2020).** Because a sizable amount of peas are processed for off-season consumption, peas are economically significant. In times of scarcity, it is often used in processed forms like canned, frozen, or dried food.

Pea production is affected by several variables. Chief among these variables is the seed, which is a critical component for the eventual development of the crop. They need an adequate supply of high-quality seeds to grow them successfully. Thus, the quantity of peas seed that can be produced will depend on the ability of these seeds to express the characteristics of the variety well **(Vidyalaya, 2014)**. Methods of multivariate

analysis are an effective strategy to aid in the early phases of crop genetic improvement, in part because it enables the simultaneous evaluation of numerous attributes **(Barth et al. 2022)**.

The security of the long-standing practice of cultivating traditional varieties and germplasms, which may have enormous potential for several essential characteristics, is currently in danger due to the conversion to high-yielding types **(Richharia, 1979, Sharma et al., 1987, Patra, 2000)**. To avoid additional gene loss, it is crucial to collect and preserve such valuable genetic resources. The characterization should ultimately lead to a mechanism for classifying and storing crucial data that can be easily retrieved, distributed to others, and applied to assist in planning breeding programs **(Dabas et al. 1994)**. Because they are more stable through generations, qualitative characteristics are more useful for describing differences**(Raut, 2003)**. The Egyptian government issued a law for protecting plant varieties, in 2002 based on distinctiveness, uniformity, stability (DUS), and novelty. Consequently, a requirement is the characterization of a variation. The protection of new plant varieties depends on the identification of well-known plant varieties. A variety is considered unique if it can be easily distinguished from the common varieties in any country at the time the application is submitted by at least one essential characteristic.

Multivariate analysis effectively quantified the genetic variation of the population, yielding sufficient data for selection based on genetic distance. The more families that are chosen in a new selection cycle, the less the genetic variability is or was altered **(Ferreira et al. 2021)**. The effectiveness of choosing doubled-haploid rice lines that are tolerant to salinity improves with the use of a selection index based on multivariate analysis **(Anshori et al. 2019)**. Studying the genetic diversity associated with the use of selection index procedures for quince cultivars is a critical point in the breeding and cultivar selection processes because it enables the rapid identification of individuals with superior traits. Additionally, research on genetic diversity offers useful suggestions for future investigations targeting to improve national quince crop output by getting more potential cultivars in traditional agricultural regions **(Coutinho et al. 2019)**.

Although the master pea variety has been registered for more than 25 years, it cannot be compared in terms of production or quality with pea varieties grown by vegetable growers in all Egyptian governorates. This research aims to evaluate all the properties of this variety and investigate the degree to which it has deteriorated over time to establish a suitable plan for the selection, improvement, maintenance, and preservation of this strategic variety to tolerate the change in climatic conditions in Egypt.

A lot of research work has been conducted on the varietal performance of peas in Egypt but there is a lack of research work on the evaluation of varieties of this crop under multivariate analysis. The present experiment was carried out with the following objectives:

1. To observe the performance of growth attributes in the Master pea variety using multivariate analysis and UPOV descriptor.
2. To evaluate the yield attributes and seed yield and quality in the Master pea variety using multivariate analysis and UPOV descriptor.

MATERIALS ANDMETHODS

This study was carried out at QahaVegetable Research Farm (QaluobiaGovernorate, Egypt) from 2018 to 2020. The soil type of the experimental site is classified as clay soil.

In this study, a material comprised of 60 pea lines derived from cv. Master pea;Seeds were obtained from the Vegetable Seed Production Unit, Vegetable ResearchDepartments, Dokki, Giza, Egypt.The maintenance program started withthe Single Seed Descent (SSD) method;this method was proposed for the first **Goulden (1939)** and later modified by **Brim (1966)**. Instead of bulking a whole seed lot of selected plants, a single seed is selected randomly from each selected plant to make bulk. The key elements of this program are raising generations from a bulk of one seed to ensure that each plant is represented equally in the final population, and there are no special efforts for artificial selection or even the possibility of natural selection until thefifth and sixth generation when the population is reasonably homozygous. The single seed-descent strategy is growing in popularity among breeders due to its speed and affordability.This method involves less record-keeping (pedigree method) and works better where the main focus is on the improvement of quantitative traits or characteristics such as yield and earliness, rather than qualitative traits or characteristics such as flesh color and disease resistance.Traits were determined on each line. Quantitative and qualitative traitswere identified from the morphological characterization list determined by UPOV (The International Union for the Protection of New Varieties of Plants) (Table 1).Harvest time was determined consideringthat the plant's stems and leaves have dried and seedshave ripened. Tocharacterize pea genotypes, obtained datawere subjected to Principal Components Analysis (PCA) firstto determinemorphological variability and then toclustering analysis to compose a dendrogram and to seeclassification**(Rencher, 1995)**. Minitab software was used for Clusterand Principal Components Analysis PCA analysis**(Minitab, 2010).**

The acquired data were statistically evaluated using Fisher's analysis of variance (given as a pairwise comparison procedure called the least significant difference (LSD) test). This test should be employed only if the

overall F test rejects the hypothesis that all means are equal. If the overall test is significant, any pair of means is tested using a process similar to a standard Student's t-test. No additional tests are run if the total F ratio is not significant. When it is used, the two treatments are deemed different if the absolute difference between the two sample means is more than 5% using combined ANOVA across years with one-way randomized blocks analysis (Multiple comparisons and trends among treatment means) **(Gomez and Gomez, 1984)**.

The experimental areawas 105 $m^2$and consisted of 60 rows 2.5 m in length with 10 plants in each row. Rows were spaced 70 cm apart and plants within rows were 25 cm apart; where one row contains the seeds of one line.An experimental field is homogeneous for soil fertility. Conventional cultural practices wereapplied regularly during the growing season. in this study, morphological traits and their description are used in principle component analysis and cluster analysis as follows: Plant height (cm); no. of leaves per plant; number of nodes of 1st flowering; number of pod per plant; number of seeds per pod; fresh weight of plant (g); dry weight of plant (g); numberof branches per plant;seed yield per plant (fresh weight)(g); seed yield per plant (number);maximum number of flowers per node;Pod length (g); Podwidth (g); Pod: number of ovules; andseed yield per plant (dry weight)(g). After completing the multivariate analysis, four economic characteristics were identified todetermine the location of the lines resulting from the cluster analysis on the normal curve, especially thetruncation selection area (Figure1), in the breeding of plants;truncation selection is a standard method inselective breeding in choosing the plants to be bred for the next generation. Animals are arranged according to their appearance value through some traits. These characteristics were as follows:The number of pods per plant;theseed yield per plant (g)(fresh weight);the seed yield per plant (number); andtheseed yield per plant (dry weight) (g).

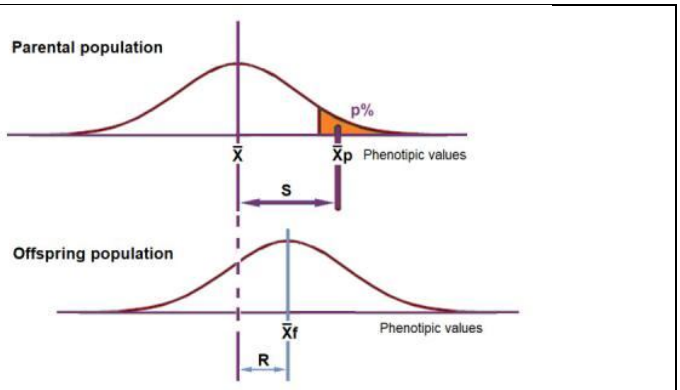


Figure 1. Illustration of a population with the fraction best plants selected (***p* %**) by truncation point (***p***). On the y-axe is the frequency of plants with that phenotype, and on the x-axe is the trait under consideration. **X** –Phenotypic average of traits in population; **p%** = proportion of selected animals (parents of next generation), **p** = truncation point; **XP** = average of phenotypic values of selected plants (average of parents) **(Hutu et al., 2020)**.

RESULTS

The study selected lines of pea cv. Master Pea was evaluated for morphological characterization based on the UPOV descriptor list **(UPOV, 2007)**. A morphological characteristic was assessed and tabulated (Table 1). The tabulated data on the differences in morphological traits among the studied selected lines of pea cv. Master Pea revealed considerable variations.

The diversity between the lines of the pea cv. Master Pea was shown by applying factorial analysis by the method of principal components (PCA – principal component analysis) based on the fifteen studied quality characteristics (Table 2). The analysis of the principal components reduced the initial number of variables from fifteento four artificial, mutually uncorrelated variables, i.e., principal components. To explain the majority of the variability of all tested characteristics, this strategy concentrates the variability on the first and second principal component analysis.When the variance of the principal component is less than one, the eigenvalue is also less than one, which means that an eigenvalue having less than one was considered to be of no effect on the overall variation observed in the total variation for all studied traits. Removing all components with eigenvalues less than one from the analysis is one way to choose the appropriate number of measurable principal components. It is occasionally required to choose as many major components of control as necessary, to satisfactorily explain the variance group's satisfying proportion of variance**(Kovačić, 1994)**. The arithmetic sign of the coefficient is irrelevant since a common rule of thumb for determining the significance of a trait coefficient is to treat a

coefficient (Eigenvectors) greater than 0.3 as having a large enough effect to be considered important **(Raji, 2003)**. Traits having less than 0.2 coefficient valuewere considered to be of no effect on the overall variation observed in the present study. Also from Table 2, the results from the (principle component analysis (PCA) revealed that only four of the principal components had Eigen values greater than 1.0. The first fourvalues with Eigenvalues of 7.47, 2.30, 1.52, and 1.03 respectively, jointly accounted for 82.3% of the total variation among the lines. The first PCA accounted for 49.8% of the variability and was related to the number of leaves per plant(0.306) (Table 3), the number of pods per plant(0.342), the fresh weight of plant(0.337), dry weight of plant(0.345), seed yield per plant (fresh weight)(0.335), seed yield per plant (number)(0.352), andseed yield per plant (dry weight) (0.335). The second principal component accounted for 15.3% of the totalvariation and was dominated by Plant height (0.420), numberof the node of 1st flowering (0.383), Numberof branches per plant (-0.445), and maximum number of flowers per node (0.446). The third principal component accounted for 10.2% of the total variation and was dominated by no. of branches per plant (0.301), Pod length (-0.578), Pod width (-0.371), and Pod: the number of ovules (-0.584). The fourth PCA accounted for an additional 6.9% of the total variation and was dominated by the number of the node of 1st flowering (0.488),the number of seeds per pod (-0.482), andPod width (0.312). A further understanding was obtained by plotting the PCA scores for individual observations concerning the axes of PCA1 and PCA2 (Figure 2). The genotypes are arranged on axes 1 (PCA1) and 2 (PCA2), and the positive direction and lines closest to axes of PCA1 are as follows: L12.L29, L44, L7, L69, L22, L27, L30, L4.L38, L21,and L28.Line 29was the most distinct from the others and they were discriminated by characters related to axis 1 were the most distinct from the others as shown in Figure 2.

Based on the number of pods per plant, seed yield per plant (fresh weight), seed yield per plant (dry weight), and seed yield per plant(number), the genotypes were divided into six groups using cluster analysis (Figure 3 and Table 4).At an average similarity distance of 100.00, all genotypes could be distinguished, however at 0.00, they were no longer distinguishable.Severities of proximity between genotypes were discovered by identifying genotypes included in the main and sub-groups identified in the Cluster Analysis's result.The relationship severities of the L23 and L40 genotypes were found to be greater than those of other genotypes.The genotypes L1, L2, and L21 have the least severe relationships.

The cluster 1 included 28 genotypes (L1, L8, L18, L15, L14, L4, L6, L5, L7, L11, L13, L16, L20, L3, L17, L10, L9, L37, L60, L19, L55, L33, L54, L59, L23, L40, L31, and L34). Cluster 2 included 16 genotypes (L2, L43, L57, L12, L24, L42, L25, L26, L45, L48, L32, L58, L47, L50, L56, and L52. Four genotypes (L21, L38, L30, and L46) joined in cluster 3. Cluster 4 included seven genotypes L22, L39, L41, L49, L44, L27, and L28). One genotype (L29) joined in cluster 5. Cluster 6 included 4 genotypes (L35, L36, L53, and L51).

The dendrogram that was created at the end of the clustering analysis revealed a substantial range of variation in both the qualitative and quantitative attributes examined.The extent of this variance suggested that we have genetic material that will provide a solid foundation for future selection and improving programs.

Results in Figure (4) which the normal curve illustrates revealed that the mean and standard deviation values of the 28 genotypes joined in Cluster 1 as based on multivariate analysis concerning the traits of the number of pods per plant(7.357, 2.094),seed yield per plant (fresh weight) (16.37,5.291), seed yield per plant (dry weight)(2.339,0.756), seed yield per plant(number) (48.96,12.69) were less than those of the original population for the same traits ((11.35,5.230),(30.30,19.31),(4.329,2.759), and (88.64,50.49),respectively),the plants joined to the first group on the normal curve is lower than the mean for the plants in the original population,the mean for the plants associated with the first group was not within the truncation selection area, based on these previous results, the plants of this group are excluded from the conservation and improvement program.Note that the standard deviation values always decrease with the curve of the plants joined from cluster analysis.

Results in Figure (5) which the normal curve illustrates revealed that the mean and standard deviation values of the 16 genotypes joined in Cluster 2 as based on multivariate analysis concerning the traits of the number of pods per plant(12.06,2.462),seed yield per plant (fresh weight) (32.33,8.519), seed yield per plant (dry weight)(4.619,1.217), seed yield per plant(number) (95.09,21.27) were higher than those of the original population for the same traits ((11.35,5.230),(30.30,19.31),(4.329,2.759), and (88.64,50.49),respectively),Despite the mean for the plants joined to the second group on the normal curve is higher than the mean for the plants in the original population,the mean for the plants associated with the second group was not within the truncation selection area, based on these previous results, the plants of this group are excluded from the conservation and improvement program.

Results in Figure (6)which the normal curve illustrates revealed that mean and standard deviation values of the four genotypes joined in Cluster 3 as based on multivariate analysis concerning the traits of the number of pods per plant(23.25,1.5),seed yield per plant (fresh weight) (68.17,16.66), seed yield per plant (dry weight)(9.739,2.381), seed yield per plant(number) (198,22.98) were higher than those of the original population for the same traits ((11.35,5.230),(30.30,19.31),(4.329,2.759), and (88.64,50.49),respectively),The mean for the

plants joined to the third group on the normal curve is higher than the mean for the plants in the original population,the mean for the plants associated with the third group waspartly within the truncation selection area, based on these previous results some plants of this group were included in the conservation and Improvement Program.

Results in Figure (7) which the normal curve illustrates revealed that mean and standard deviation values of the seven genotypes joined in Cluster 4 as based on multivariate analysis for the traits ofthe number of pods per plant(16.71,0.951),seed yield per plant (fresh weight) (46.56,9.560), seed yield per plant (dry weight)(6.652,1.366), seed yield per plant(number) (150.6,17.27) were higher than those of the original population for the same traits ((11.35,5.230),(30.30,19.31),(4.329,2.759), and (88.64,50.49),respectively),The mean for the plants joined to the fourth group on the normal curve is higher than the mean for the plants in the original population,the mean for the plants associated with the fourth group waspartly within the truncation selection area, based on these previous results some plants of this group were included in the conservation and Improvement Program.

Results in Figure (8) which the normal curve illustrates revealed that mean and standard deviation values of the one genotype joined in Cluster 5 as based on multivariate analysis for the traits ofthe number of pods per plant,seed yield per plant (fresh weight), seed yield per plant (dry weight, seed yield per plant(number) The mean for the plants joined to the fifth group on the normal curve is higher than the mean for the plants in the original population,the mean for the plants associated with the fifth group waswithin the truncation selection area, based on these previous results this plant of this group were included in the conservation and Improvement Program.

Results in Figure (9) which the normal curve illustrates revealed that mean and standard deviation values of the 4 genotypes joined in Cluster 6 as based on multivariate analysis concerning the traits ofthe number of pods per plant(12, 1.633),seed yield per plant (fresh weight) (34.77,5.754), seed yield per plant (dryweight)(4.967,0.822), seed yield per plant(number) (91,8.246) were less than those of the original population for the same traits ((11.35,5.230),(30.30,19.31),(4.329,2.759), and (88.64,50.49),respectively),Despite the mean for the plants joined to the Sixth group on the normal curve is higher than the mean for the plants in the originalpopulation,the mean for the plants associated with the Sixth group was not within the truncation selection area, based on these previous results, the plants of this group are excluded from the conservation and improvement program.

Based on the previous results, three lines were selected, namely: L29 (cluster 6), L38 (cluster 3), and L39 (cluster 5).Values and grades of phenotypic traits in the stages of plant vegetative growth, flowering, and maturity of the selected pea lines using UPOV measurements and multivariate analysiswere tabulated in Table 5.

Results in Table (6) revealed that mean values of the selected population (L29, L38, and L39) using cluster analysis and the truncation selection area in respect to the traits of the number of pod per plant (22), the, the seed yield per plant (fresh weight) (92.13g/plant), and the Seed yield per plant (dry weight)(13.2g/plant) were significantly higher than those of the original population for same traits (11.35, 30.30g/plant, , and 26.35 g/plant, respectively).

Discussion

Looking at the preceding findings, it is clear that the peas genotypes that were under investigation varied in their vegetative traits.Yet there are several reasons why this can be the case, and those are what we'll talk about in this study.As with other horticultural plants, peas grow through a complex process of progressive development that results in a greater combination of genetic and environmental variation over a number of years. This places a high value on the inherited varieties from the countries that have been improved by researchers and the environmental conditions.The following studies have been organized and presented to evaluate the findings in light of the goals of this study.

Based on morphological and molecular characteristics, the genetic diversity of populations has been quantified using multivariate analysis techniques **(Cabral et al. 2010; Babay et al. 2015; Blind et al. 2020; Araujo et al. 2019).**In small populations, selection pressure can change the genetic diversity of the population by causing the loss of critical alleles **(Reis et al. 2011)**. The discovery and selection of parents that exhibit more genetic dissimilarity with one another for recombination is a potential strategy for conserving genetic diversity. According to **Kurosawa et al. (2017)**, parental selection based on genetic diversity may favor the occurrence of segregation in populations by promoting the growth of the genetic base. Gains from the selection of agronomic features are thus made possible.The success of the genetic improvement program depends critically on the estimation of the genetic diversity of the population subject to recurrent intrapopulation selection.The measurement of genetic variability and the understanding of the genetic makeup of populations through morphological and molecular descriptors **(Cerqueira-Silva et al. 2012a; Fonseca et al. 2017; Paiva et al. 2014)** enable the identification of superior genotypes and the development of strategies to improve selection **(Oliveira et al. 2013)**.The drop in polymorphism, the number of alleles, and the Shannon and Neidiversity indices all reflect

a loss in genetic variability that was facilitated by increased selection strength.These findings are consistent with **Reis et al(2011)** .'s observation that two rounds of recurrent selection in families of complete brothers of fruit resulted in a drop in the diversity indices.In their evaluation of a population of fruit and the open pollination progenies from that population, **Cordeiro et al. (2020)** noted a loss of alleles and a decline in the predicted heterozygosity.There will be less genetic variability in the following selection cycle since the selection of more divergent families was unable to stop the loss of alleles.The selection of 10 to 20 families with greater population dissimilarity resulted in a drop in diversity of less than 40%, according to Shannon and the diversity indices of **Nei**(**1973**).The lowest values of Shannon's diversity index, 0.17, and Nei's diversity index, 0.12, respectively, were validated for the five most divergent families.

Genetic breeding is based on the use of various traits to investigate phenotypic diversity, exposing the genetic structure and population variance. Natural selection is assumed to have led to phenotypic variation, which reflects both genetic diversity and adaptation to local environmental traits**(Price et al. 2003;Liang et al. 2005; Wang et al. 2009)**,such as genetic drift, characteristic mutation, and meteorological change**(Liu et al. 2004)**.Relevant research has demonstrated that phenotypic plasticity is a key strategy for plants to adapt to the diversity of environmental factors**(Loretta, 2014)**.When enough genetic variety exists, phenotypic plasticity can develop**(Sara and Russell,1987)**due to genetic drift or genetic relationships with other traits that are being selected for**(Via et al. 1995**).

Plant phenotypes thus reflect genetic adaptation to environmental changes and are a product of interactions between genotype and environment. Long-term stress selection produces phenotypes, which are irreversible processes that can be passably inherited by generations. Phenotypic variation is crucial for classification and adaptation because phenotypes show how well plants can adapt to their environment. Diversity Variation within populations is a crucial aspect of species variety, showing population adaptation to various environments. To some extent, the degree of variation reflects the species' capacity to adapt to various situationsand traits**(Kleunen and Fischer,2005)**.Natural selection, which affects the variety of phenotypic traits among individuals in a population, is what drives the evolution of life**(Smith, 2011).**

Multivariate analysis effectively quantified the genetic variation of the population, yielding sufficient data for selection based on genetic distance. The more families that are chosen in a new selection cycle, the less the genetic variability is or was altered **(Ferreira et al. 2021)**. The effectiveness of choosing doubled-haploid rice lines that are tolerant to salinity improves with the use of a selection index based on multivariate analysis **(Anshori et al. 2019)**. Studying the genetic diversity associated with the use of selection index procedures for quince cultivars is a critical point in the breeding and cultivar selection processes because it enables the rapid identification of individuals with superior traits. Additionally, research on genetic diversity offers useful suggestions for future investigations targeting to improve national quince crop output by getting more potential cultivars in traditional agricultural regions **(Coutinho et al. 2019)**.

In this study, we showed diversity within populations is a crucial aspect of species variety, showing population adaptation to various environments. To some extent, the degree of variation reflects the species' capacity to adapt to various situations. Natural selection, which affects the variety of phenotypic traits among individuals of a population, is what drives the evolution of cultivars. The ability of the phenotypic traits specified in the UPOV guide and data analysis using multivariate analysis to show differences between lines within cultivars. We recommend taking advantage of the UPOV descriptor and multivariate analysis and seeking to obtain differences and relationships between lines in conservation, maintenance, and improvement programs for ancient and promising cultivars in the Arab Republic of Egypt.

Table 1. The qualitative and quantitative characteristics tabulated by the UPOVdescriptor of the peas crop.

Stage1 (The stage of vegetative and flowering growth) (40 - 55 days after sowing date)

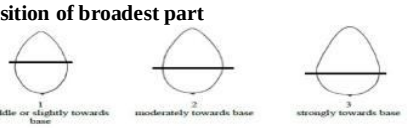
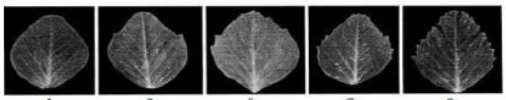
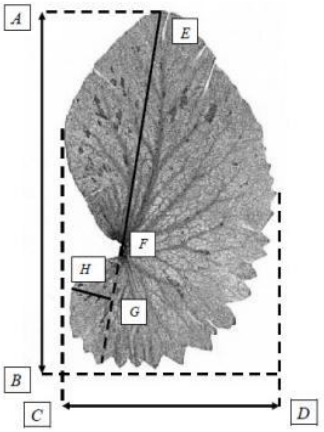
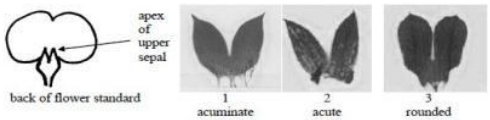
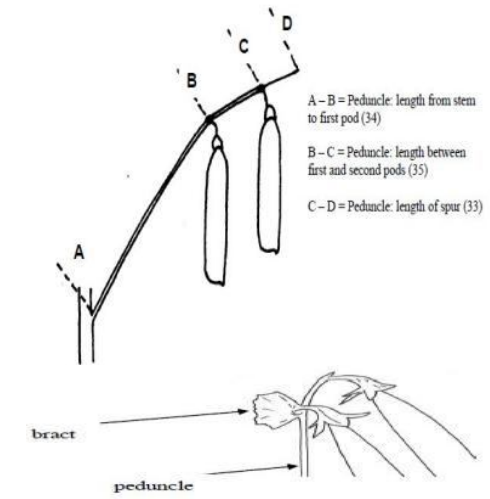
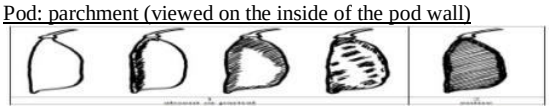
Genotype:	**Pictures**
Sowing date:	
Date:	
Plant No. ( )	**Leaflet: position of broadest part**
Characteristics	
Green area index	
Leaf appearance rate (phyllochrom)	
Thermal time accumulation	**Leaflet: dentation**
Plant: anthocyanin coloration (absent = **1**) (present = **9**)	
Stem: anthocyanin coloration of axil (absent = **1**)(single ring = **2**) (double ring = **3**)	
Stem: fasciation (absent = **1**)(present = **9**)	
Foliage: color (yellow green = **1**)(green =**2**) (blue green = **3**)	**Stipule :**
Foliage: intensity of color: (light = **3**)(medium = **5**) (dark = **7**)	
Leaf: leaflets (absent = **1**)(present = **9**)	
Leaf: maximum number of leaflets	Stipule: length (15) A - B Stipule: width (16) C - D Stipule: length from axil to tip (18) E - F Stipule: length of lobe below axil (19) G - H *(perpendicular to the line E – G)*
Leaflet: size	
Leaflet: length	**Stipule: flecking density of flecking**
Leaflet: width	
Leaflet: position of broadest part (at middle or slightlytowards base=**1**) (moderately towards base = **2**) (strongly towardsbase = **3**)	
Leaflet: dentation (absent or very weak = **1**) (weak = **3**) (medium =**5**) (strong = **7**) (very strong = **9**)	**Petiole: tendril**
Stipule: length	
Stipule: width	
Stipule: size	
Stipule: length from axil to tip	**Flower: shape of base of standard**
Stipule: length of lobe below axil	
Stipule: flecking (absent = **1**)(present = **9**)	
Stipule: density of flecking (very sparse = **1**)(sparse = **3**)(medium = **5**) (dense = **7**)(very dense = **9**)	**shape of apex of upper sepal**
Petiole: length from axil to first leaflet or tendril	
Only varieties with leaflets absent: Petiole: length from axil to last tendril	
Time of flowering	
Flower: color of wing: (white with pink blush =**1**)(pink = **2**) (reddish purple = **3**)	
Flower: shape of apex of upper sepal (acuminate = **1**)(acute = **2**)(rounded = **3**)	
Flower: width of standard	
Flower: shape of base of standard (strongly raised = **1**)(moderately raised = **3**)(level = **5**)(moderately arched = **7**)(strongly arched = **9**)	
Flower: undulation of standard (absent or very weak = **1**)(weak = **3**)(medium = **5**)(strong = **7**) (very strong = **9**)	
Flower: width of upper sepal	
Flower: color of standard: (White = **1**)(whitishcream = **2**)(cream = **3**)	

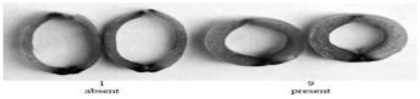
Table 1. Cont.:The qualitative and quantitative characteristics tabulated by the UPOVdescriptor of the peas crop.	
Stage 2 (The Pre-drying stage of seeds) (70 - 80 days after sowing date)	
Genotype:	**pictures**
Sowing date:	**Peduncle:**
Date:	
Plant No. ( )	
Characteristics	
Plant height	
No. of leaves per plant	
Number of node of 1st flowering	
Number of pod per plant	
Number of seed per pod	
Fresh weight of plant	
Dry weight of plant	
Number of branches per plant	
Plant: maximum number of flowers per node	
Peduncle: length of spur	
Peduncle: length from stem to first pod	
Peduncle: length between first and second pods	
Peduncle: number of bracts	
Pod: length	
Pod: width	
Pod: parchment (absent or partial = **1**) (entire = **2**)	
Pod: thickened wall (Absent = **1**) (present = **9**)	
Pod: shape of distal part (pointed = **1**) (blunt = **2**)	
Pod: curvature (absent or very weak = **1**)(weak = **3**)(medium = **5**)(strong = **7**)(very strong = **9**)	
Pod: color (Yellow = **1**) (Green = **2**) (blue green = **3**) (purple = **4**)	
Intensity of green color (light = **3**) (medium = **5**) (dark = **7**)	
Pod: suture strings absent = **1**) (present = **9**)	
Pod: number of ovules	
Immature seed: intensity of green color (light = **3**) (medium = **5**) (dark = **7**)	



Pod: parchment (viewed on the inside of the pod wall)



Pod: thickened wall



Pod: shape of distal part

Pod: curvature

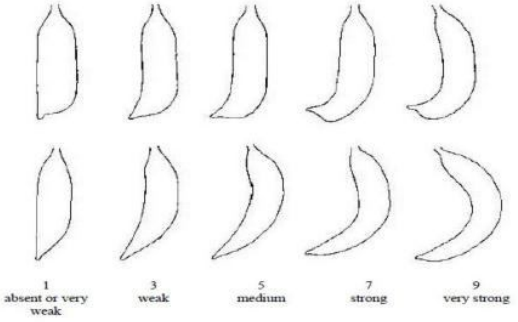
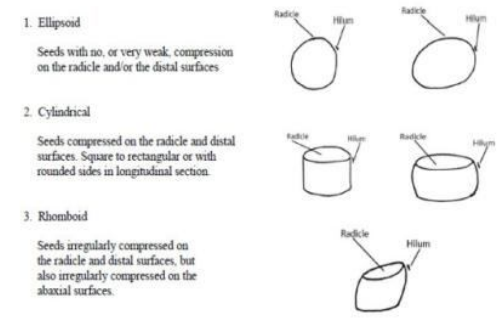


Table 1.Cont.:The qualitative and quantitative characteristics tabulated by the UPOVdescriptor of the peas crop.	
Stage 3 (The drying stage of seeds)	
Genotype:	**pictures**
Sowing date:	**Seed: shape**
Date:	
Plant No. ( )	
Characteristics	
Seed yield per plant (fresh weight)	
Seed yield per plant (number)	
Seed yield per plant (dry weight)	
Seed: shape (ellipsoid = **1**) (cylindrical = **2**) (rhomboid = **3**) (irregular = **4**)	
Seed: type of starch grains (simple = **1**) (compound = **2**)	
Seed: wrinkling of cotyledon (absent = **1**) (present = **9**)	
Seed: intensity of wrinkling of cotyledon (weak = **3**) (medium = **5**) (strong = **7**) (very strong = **9**)	
Seed: color of cotyledon (green = **1**) (yellow = **2**) (orange = **3**)	**Seed: wrinkling of cotyledon**
Seed: marbling of testa (absent = **1**) (present = **9**)	
Seed: violet or pink spots on testa (absent = **1**) (faint = **2**) (intense = **3**)	
Seed: hilum color (same color as testa = **1**)(darker than testa = **2**)	
Seed: color of testa (reddish brown= **1**)(brown = **2**)(brownish green = **3**)	
Resistance to Fusarium oxysporum f. sp. Pisi- Race 1	
Resistance to Fusarium oxysporum f. sp. Pisi-Race 5	
Resistance to Fusarium oxysporum f. sp. Pisi-Race 6	
Resistance to Erysiphe pisi Syd.	
Resistance to Ascochyta pisi, Race C	

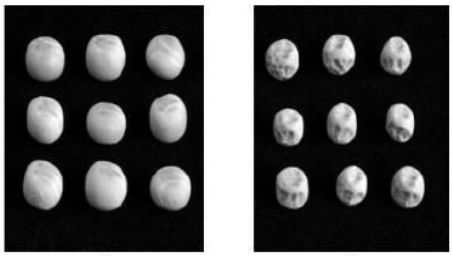


Table 2. Eigen values, percent of total variation of examined traits in the conclusion of principal components.													
	PCA1	**PCA2**	**PCA3**	**PCA4**	**PCA5**	**PCA6**	**PCA7**	**PCA8**	**PCA9**	**PCA10**	**PCA11**	**PCA12**	**PCA13**
Eigen value	7.47	2.30	1.52	1.03	0.69	0.61	0.49	0.24	0.23	0.16	0.12	0.06	0.02
Variance (%)	49.8	15.3	10.2	6.9	4.6	4.1	3.3	1.6	1.6	1.1	0.8	0.4	0.1
Cumulative variance (%)	49.8	65.1	75.3	82.3	86.9	91.0	94.3	95.9	97.5	98.6	99.4	99.8	100

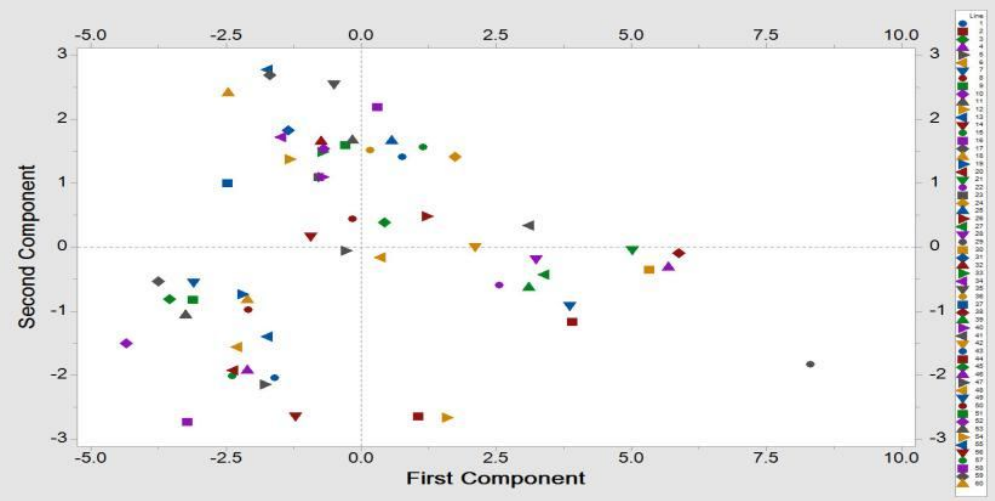


Figure 2. Score plot of the first and second principal components to show the interrelationship of morphological traits of the 60 lines of pea's cv. Master Pea. Based on characteristics ofPlant height; no. of leaves per plant; number of node of 1st flowering; number of pod per plant; number of seed per pod; fresh weight of plant (g); dry weight of plant (g); numberof branches per plant;seed yield per plant (fresh weight)(g); seed yield per plant (number); maximum number of flowers per node; Pod length; Podwidth; Pod: number of ovules; and seed yield per plant (dry weight).

Table 3. Eigen vectors of examined traits in the conclusion of principal components.

Traits	PCA1	PCA2	PCA3	PCA4	PCA5
Plant height	0.216	**0.420**	0.034	0.217	0.282
Number of leaves per plant	**0.306**	-0.207	0.207	0.220	-0.054
Number of node of 1st flowering	0.040	**0.383**	0.041	**0.488**	-0.659
Number of pod per plant	**0.342**	-0.010	0.052	0.029	0.199
Number of seed per pod	0.216	0.029	-0.154	**-0.482**	-0.601
Fresh weight of plant	**0.337**	-0.035	0.088	0.148	0.040
Dry weight of plant	**0.345**	-0.059	0.117	0.093	0.095
Number of branches per plant	0.143	**-0.445**	**0.301**	0.273	-0.146
Seed yield per plant (fresh weight)	**0.335**	-0.023	0.006	-0.278	-0.013
Seed yield per plant (number)	**0.352**	-0.034	0.018	-0.144	-0.021
Maximum number of flowers per node	0.213	**0.446**	0.052	0.096	0.121
Pod length	0.174	-0.004	**-0.578**	0.212	-0.063
Pod width	0.051	-0.473	**-0.371**	**0.312**	-0.037
Pod: number of ovules	0.123	0.065	**-0.584**	0.026	0.172
Seed yield per plant (dry weight)	**0.335**	-0.023	0.006	-0.278	-0.013

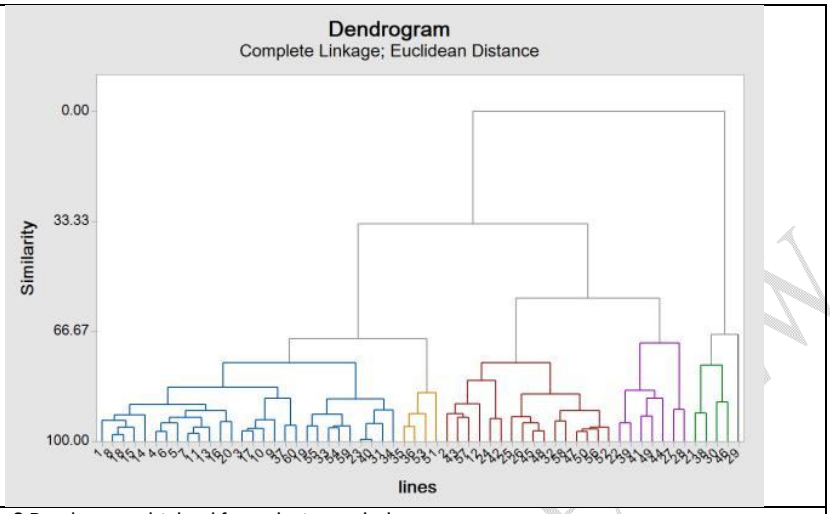


Figure 3. Dendogram obtained from cluster analysis

Table 4. Lines owned by Clusters and sub- clusters as a result of cluster analysis			
Clusters	**Sub-clusters**	**Lines**	**Lines number**
Blue Cluster (Cluster 1)	1	**L1,L8,L18,L15,L14**	**5**
	2	**L4,L6,L5,L7,L11,L13,L16,L20**	**8**
	3	**L3,L17,L10,L9,L37,L60**	**6**
	4	**L19,L55,L33,L54,L59,L23,L40,L31,L34**	**9**
Red Cluster (Cluster 2)	1	**L2,L43,L57,12**	**4**
	2	**L24,L42**	**2**
	3	**L25,L26,L45,48**	**4**
	4	**L32,L58,L47,L50,L56,L52**	**6**
Green Cluster (Cluster 3)	1	**L21,L38**	**2**
	2	**L30,L46**	**2**
Purple Cluster (Cluster 4)	1	**L22,L39**	**2**
	2	**L41,L49,L44**	**3**
	3	**L27,L28**	**2**
Grey Cluster (Cluster 5)	1	**L29**	**1**
Yellow Cluster (Cluster 6)	1	**L35,L36,L53,L51**	**4**

Cluster 1

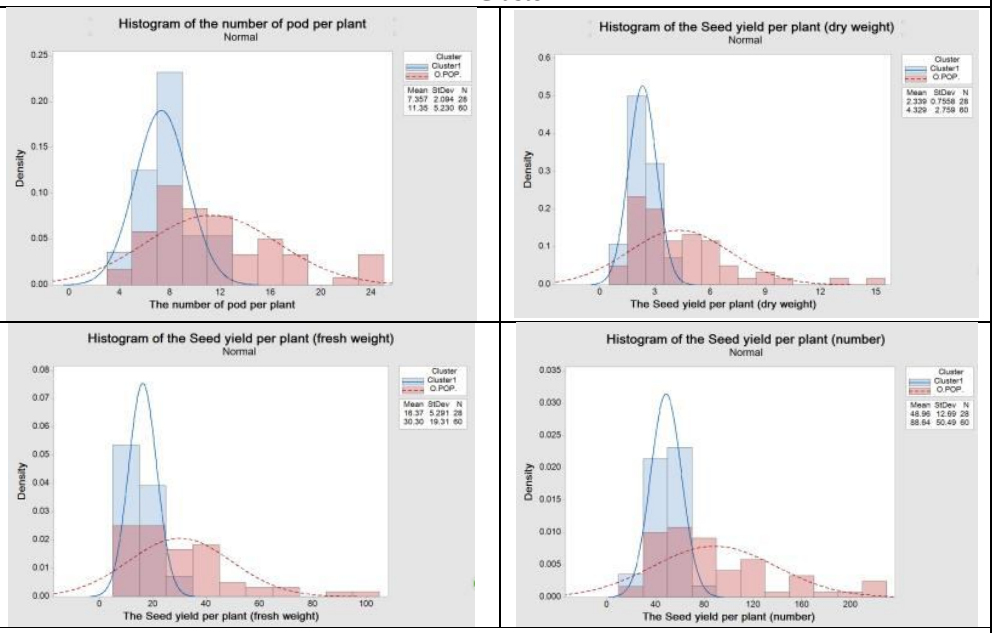


Figure 4. The position of the economic characteristics of the cluster (1) lines is attributed to the normal curve and their proximity to or distance from the truncation selection area.

Cluster 2

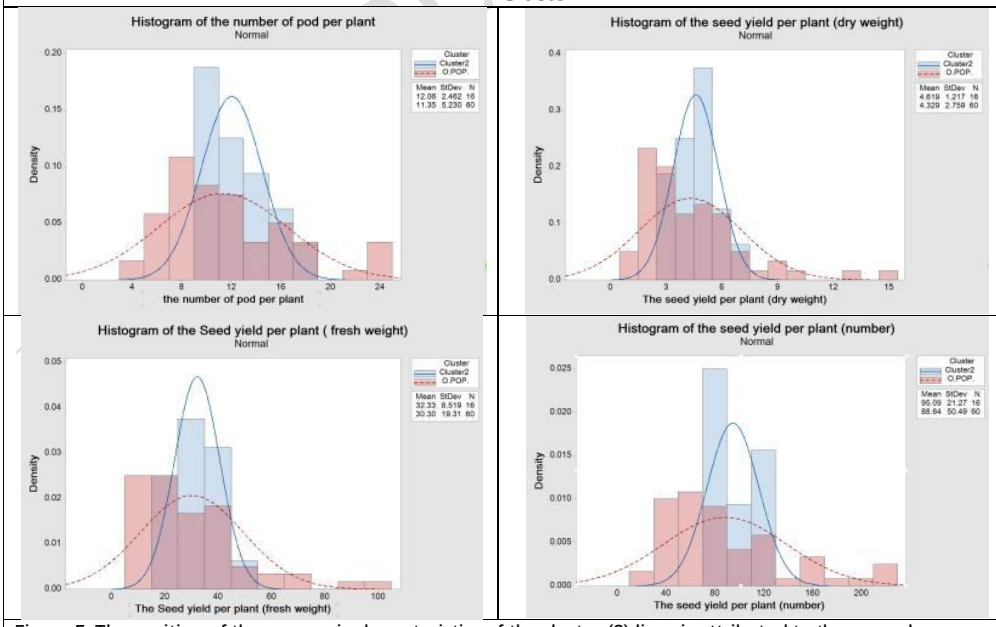


Figure 5. The position of the economic characteristics of the cluster (2) lines is attributed to the normal curve and their proximity to or distance from the truncation selection area.

Cluster 3

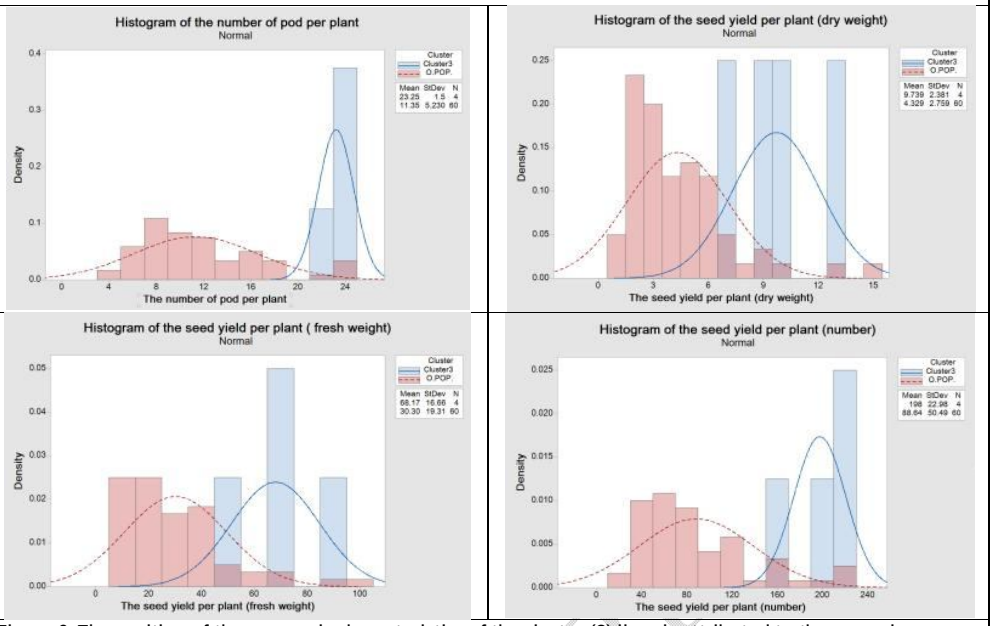


Figure 6. The position of the economic characteristics of the cluster (3) lines is attributed to the normal curve and their proximity to or distance from the truncation selection area.

Cluster 4

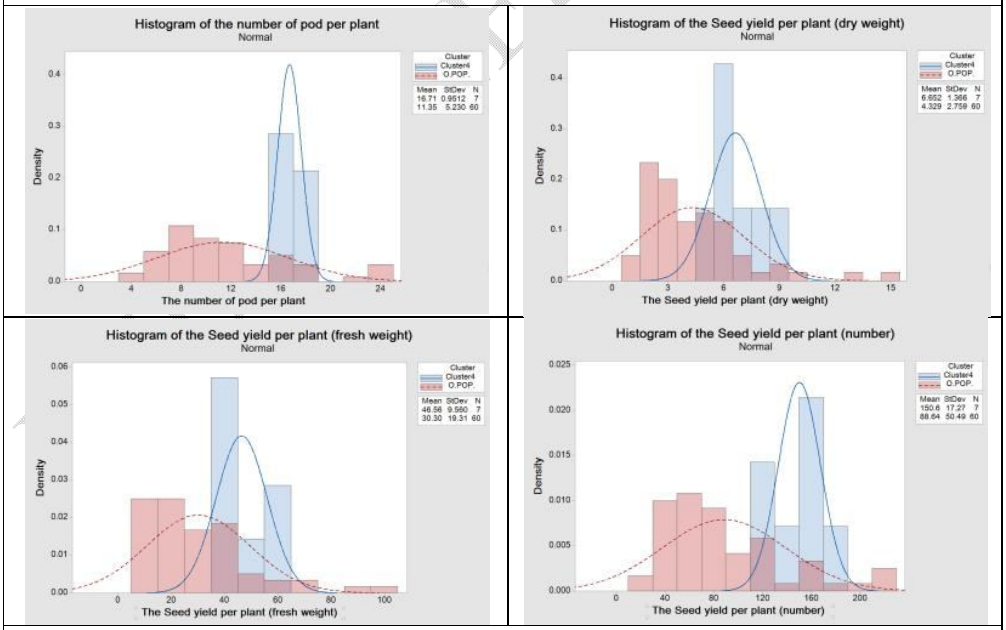


Figure 7. The position of the economic characteristics of the cluster (4) lines is attributed to the normal curve and their proximity to or distance from the truncation selection area.

Cluster 5

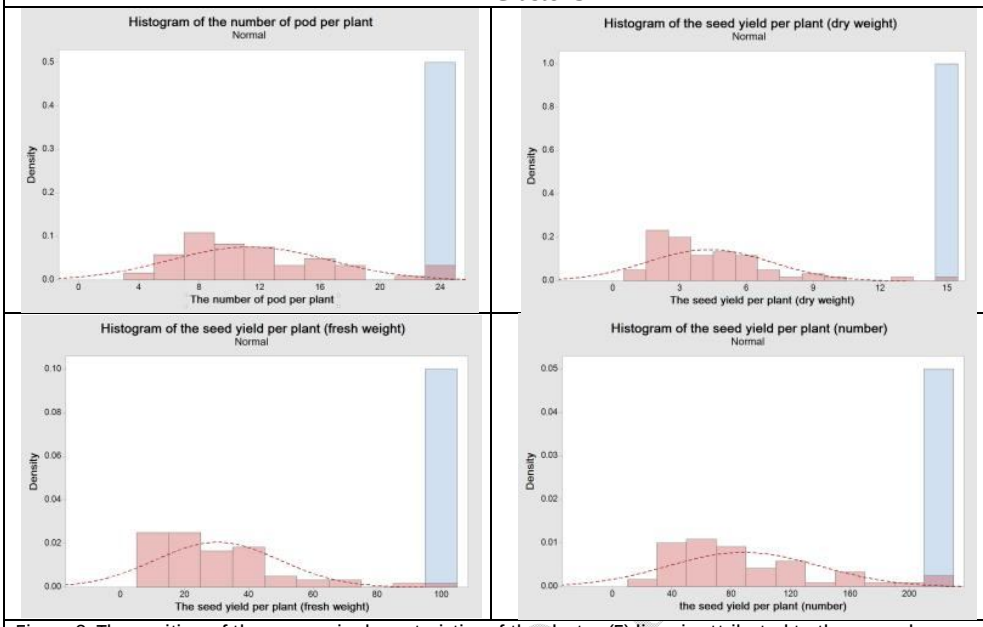


Figure 8. The position of the economic characteristics of the cluster (5) lines is attributed to the normal curve and their proximity to or distance from the truncation selection area.

Cluster 6

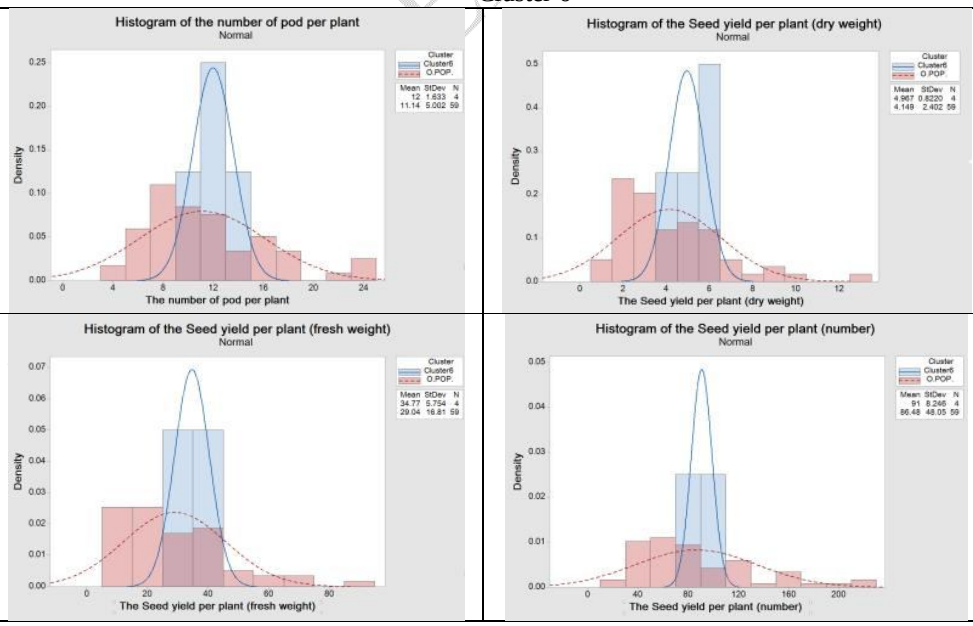


Figure 9. The position of the economic characteristics of the cluster (6) lines is attributed to the normal curve and their proximity to or distance from the truncation selection area.

Table 5. Values and grades of phenotypic traits in the stages of plant vegetative growth, flowering and maturity of the selected pea lines using UPOV measurementsand multivariate analysis.

Characteristics	Selected lines			Characteristics	Selected lines		
	L29	L38	L39		L29	L38	L39
Plant: anthocyanin coloration (absent = **1**) (present = **9**)	1	1	1	Number of seed per pod	9	9	9
Stem: anthocyanin coloration of axil (absent = **1**) (single ring = **2**) (double ring = **3**)	1	1	1	Fresh weight of plant (g)	216.4	183.5	201.5
Stem: fasciation (absent = **1**)(present = **9**)	1	1	1	Dry weight of plant (g)	38.2	30.2	33.4
Foliage: color (yellow green = **1**) (green =**2**) (blue green = **3**)	2	2	2	Number of branches per plant	3	3	3
Foliage: intensity of color: (light = **3**) (medium = **5**) (dark = **7**)	5	5	5	Plant: maximum number of flowers per node	2	2	2
Leaf: leaflets (absent = **1**) (present = **9**)	9	9	9	Peduncle: length of spur	-	-	-
Leaf: maximum number of leaflets	6	6	6	Peduncle: length from stem to first pod	8	8.4	8.1
Leaflet: size	-	-	-	Peduncle: length between first and second pods	-	-	-
Leaflet: length	-	-	-	Peduncle: number of bracts	1	1	1
Leaflet: width	-	-	-	Pod: length (cm)	10	9.4	10.2
Leaflet: position of broadest part (at middle or slightly towards base =**1**) (moderately towards base = **2**) (strongly towards base = **3**)	2	2	2	Pod: width (cm)	1.4	1.2	1.4
Leaflet: dentation (absent or very weak = **1**) (weak = **3**) (medium =**5**) (strong = **7**) (very strong = **9**)	1	1	1	Pod: parchment (absent or partial = 1) (entire = 2)	1	1	1
Stipule: length (cm)	5.5	5.1	5.6	Pod: thickened wall (Absent = 1) (present = 9)	1	1	1
Stipule: width (cm)	3.5	3.1	3.5	Pod: shape of distal part (pointed = 1) (blunt = 2)	2	1	1
Stipule: size	-	-	-	Pod: curvature (absent or very weak = 1)(weak = 3)(medium = 5)(strong = 7)(very strong = 9)	1	1	1
Stipule: length from axil to tip (cm)	6.7	6.4	6.3	Pod: color (Yellow = 1) (Green = 2) (blue green = 3) (purple = 4)	2	2	2
Stipule: length of lobe below axil	-	-	-	Intensity of green color (light = 3) (medium = 5) (dark = 7)	5	5	5
Stipule: flecking (absent = **1**) (present = **9**)	9	9	9	Pod: suture strings absent = 1) (present = 9)	9	9	9
Stipule: density of flecking (very sparse = **1**)(sparse = **3**)(medium = **5**) (dense = **7**)(very dense = **9**)	7	7	7	Pod: number of ovules	10	9	10
Petiole: length from axil to first leaflet or tendril	5.3 cm	5.1 cm	5.1 cm	Immature seed: intensity of green color (light = 3) (medium = 5) (dark = 7)	5	5	5
Only varieties with leaflets absent: Petiole: length from axil to last tendril	-	-	-	Seed yield per plant (fresh weight) (g)	104.5	89.6	82.3
Time of flowering (day)	45	43	46	Seed yield per plant (number)	216	216	192
Flower: color of wing: (white with pink blush =**1**)(pink = **2**) (reddish purple = **3**)	1	1	1	Seed yield per plant (dry weight) (g)	14.9	12.8	11.9
Flower: shape of apex of upper sepal (acuminate = **1**)(acute = **2**)(rounded = **3**)	1	1	1	Seed: shape (ellipsoid = 1) (cylindrical = 2) (rhomboid = 3) (irregular = 4)	2	2	2
Flower: width of standard (cm)	2.7	2.5	2.5	Seed: type of starch grains (simple = 1) (compound = 2)	1	1	1
Flower: shape of base of standard (strongly raised = **1**)(moderately raised = **3**)(level = **5**) (moderately arched = **7**)(strongly arched = **9**)	5	5	5	Seed: wrinkling of cotyledon (absent = 1) (present = 9)	9	9	9
Flower: undulation of standard (absent or very weak = **1**)(weak = **3**)(medium = **5**)(strong = **7**) (very strong = **9**)	5	5	5	Seed: intensity of wrinkling of cotyledon (weak = 3) (medium = 5) (strong = 7) (very strong = 9)	7	7	7
Flower: width of upper sepal				Seed: color of cotyledon (green = 1) (yellow = 2) (orange = 3)	1	1	1
Flower: color of standard: (White = 1) (whitish cream = 2) (cream = 3)				Seed: marbling of testa (absent = 1) (present = 9)	1	1	1
Plant height (cm)	83	91	79.5	Seed: violet or pink spots on testa (absent = 1) (faint = 2) (intense = 3)	1	1	1
No. of leaves per plant	45	37	44	Seed: hilum color (same color as testa = 1) (darker than testa = 2)	1	1	1
Number of node of 1st flowering	12	11	12	Seed: color of testa (reddish brown = 1) (brown = 2) (brownish green = 3)	3	3	3
Number of pod per plant	24	24	18				

Table 6: Yield components characteristics evaluated in the two populations (original population and selected population) of Peas cv. Master pea.		
characteristics	Original population	Selected population (L29, L38, and L39)
Number of pod per plant	11.35[b]	22[a]
Seed yield per plant (fresh weight) (g)	30.30[b]	92.13[a]
Seed yield per plant (dry weight) (g)	4.32[b]	13.2[a]
The means within rows followed by the same letter are not statistically different at 5% level (Unpaired two-tailed Student's t-test.).		

Comment [RL2]: *Should have a section on* ***Summary and Conclusions****, and possible Study* ***Recommendations***

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