

## ORIGINAL ARTICLE

# The Study of Inheritability and Relationship among the Traits Using Multivariate Statistics in Omid Bakhsh Line of White Pea

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### ABSTRACT

Having knowledge regarding the genetic diversity and genetic resource management is considered as an important step in plant breeding projects. Diversity and selection are main two elements of every breeding program. In order to investigate the genetic diversity and the relationship between the effective traits in yield of Omid Bakhsh line of white pea, a study was carried out in completely randomized design with 3 replicates during two years (2014-2015) in Agricultural and Natural resource research center of Zanjan. Treatments of the study consisted of 12 lines of white pea. The results of genotypic and genetic coefficient of variation for grain yield, individual plant yield, 100-seed weight, and plant height were high. General heritability for 100-seed weight, grain yield, day to maturity, single shrub yield and plant height were high too. With regards to high coefficient of these traits, these traits can be used in breeding programs. grain yields had the highest correlation with individual plant yield ( $r=0.9^{**}$ ), 100-seed weight ( $r=0.47^{**}$ ), Number of pod per plant ( $r=0.51^{**}$ ). The results of Principal Component Analysis showed that based on Eigenvalues, three first principal components that captured 86% of the variance was selected. The second component has the biggest positive coefficient for individual plant yield, grain yield, number of pod per plant and days to maturity and this relationship was obtained as significant in the simple correlation table.

**Keywords;** White pea, the Principal Component, Clustering, Genetic diversity, General heritability

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## INTRODUCTION

Food shortages and malnutrition as one of the most important and most disturbing problems of human society and the lack of protein in the diet, cause serious physical and mental harm to humans [1]. Legumes, especially beans contain large amount of protein and play important in treating protein deficiency.

Having knowledge of genetic diversity and genetic resource management is considered as a major step in plant correction projects. Variation and selection are of two essential elements of every breeding program. Selection for specific traits is only feasible when there is appropriate variation in experiment materials. So that the plant genetic diversity is considered as one of the essential component of real crop production system in every ecosystem [2]. A breeding program is successful when the two factors of variation and selection is present. Adopting local varieties and landraces for creating required diversity is useful [3].

Given the importance of studying genetic diversity in plant breeding and the increasing production of white pea, investigating genetic diversity of white pea is very important. Until recently, many studies have been conducted on quantitative and qualitative traits in the world and Iran. Discovering the great genetic diversity asset in plants has been one of the important findings in the field of plant breeding over the past few decades, but only a preliminary step was taken to identify great potential of it. According to studies, about ten percent of species had been evaluated in scientific methods [4]. Since multivariate statistical

methods take into account several measures, have been used extensively in the analysis of genetic variation based on morphological, biochemical and molecular.

General heritability for the number of seeds per pod of beans was reported 24% [5]. Indirect selection in modified early generation through traits that had good correlation with grain and had higher heritability than their yield is one of the important strategies for breeding. Investigation of inheritance of traits in different environmental conditions indicates that by changing the environmental conditions of the plant, gene performance, estimation of genetic parameters and heritability of traits will change. The heritability of yield and number of pods per white pea plant in low water stressed environments was average for number of seeds per pod and was high for 100-seed weight [6].

Plant breeding experts classify the cultivar and varieties of different plant to determine the genetic distance between them and to use the existence diversity for cross classification programs. Using analysis of genetic relationships between modified materials is required [7, 8]. Among the different methods of multivariate analysis, cluster analysis and principal component analysis are the most important methods [9]. In order to study the yield and adaptability of 12 varieties of white chickpea in rainfed conditions of Kurdistan using canonical analysis of variance concluded that in terms studied traits cultivars had genetic diversity and studied cultivars had significant difference in terms of all investigated traits.

There have been many studies on the correlation among traits. Identification and understanding of the relationships between traits with complex and low heritability and traits with simple and higher heritability will result in increased genetic yield of modification of complex traits such as grain yield, because of selection for correlated traits also leads to change in the main traits [11]. According to Falconer [10], the correlation may indicate the degree of genetic relatedness between two or more traits. In other words, the values estimated as a phenotypic correlation are in genetic and environmental sectors.

The goal for using principal components analysis is to reduce the number of variables of interest while the maximum variation in the original data is maintained [12].

The simple correlation coefficients of traits in 576 samples of bean showed that number of pods per plant, number of seeds per plant, number of nodes per plant; 100-seed weight and plant height have the greatest effect on seed and grain yield and the study of traits diversification showed that the number of seeds per plant, grain yield, plant height, node number and 100-seed weight are of great diversity. In previous study, principal component analysis showed that the five main components explain 73.19 % percent of the total variation [13]. Aggarwal and Singh [14] reported a study of 35 bean varieties and concluded that yield significantly is associated with the number of days to flowering, days to maturity of pod, number of pods per plant, number of seeds per pod and 100-seed weight. In the previous study, flowering time, number of pods per plant and time of maturity respectively were positively correlated with pod ripening time, number of seeds per pod and the number of seeds per pod, but correlation of pods per plant with 100-seed weight was negative. Escribano *et al* [15] studied 59 varieties of beans and concluded that there was significant diversity in the length and width of pod and thickness and length of the seed. Denis *et al*. [16] studied morphological traits and yield components in determinate, and indeterminate genotypes of beans using compacting the variable by means of Factor analysis introduced 3 factors that respectively explain 31.31%, 31 % and 8.14 % of the total variation of traits. The aim of this study was to evaluate and classify Omidbakhsh lines of white beans based on phenologic-agronomic traits in order to recommend the best lines for use in future breeding programs.

## MATERIALS AND METHODS

To study the genetic diversity and relationship among traits affecting yield of Omidbakhsh genotypes of white pea, a study in Agricultural and Natural Resources Research centre of Zanjan Kheyrahad research station was conducted in a randomized complete block design with three replications for two years (2013 and 2014). The experiment treatments consisted of 12 lines of white pea with various types including: prostrate, semi-upright and upright (Table 1). Each plot consisted of four ridges 6 m and 0.5 m width. In the spring of each year, surface plowing, disk and creating a furrow with a width of 50 cm was carried out. Based on the recommendations of the Soil and Water Research Centre of Zanjan province, 150 kg of superphosphate and 50 Kg of urea fertilizer were added to each hectare of soil. The seeds were planted by hand with distance of 10 cm apart on the lines. In the third trifoliolate stage were thinned. Normal Irrigation according to plant needs was performed. To control weeds Trifluralin was sprayed using 1.5 L/ha before planting and one hand weeding was undertaken during the growing season. During growth and development stage individual experiment in every plot was carried out to measure the traits including the time of 50%-flowering, plant height and during harvesting time 5 plants were selected from every plot to

measure the yield components including: number of seeds per pod, number of pods per plant, 100-seed weight, yields per plant and crop of each plot.

**Table 1- special number of evaluated line of white bean**

Origin	Pedigree of Genotype	Genotype No
Iran	DANESHKADE/G11867	1
Iran	JULES/DANESHKADE	2
Iran	JULES/DANESHKADE	3
Iran	JULES/74EMERSON	4
Iran	11805/DANESHKADEH	5
Iran	74EMERSON /JULES	6
Iran	SEFEN/74EMERSON	7
Iran	KARA/G11867	8
Iran	KARACASIHIRO	9
	GOYONOK98	10
	Dorsa	11
	Pak	12

### Statistical calculations

Genotypic, phenotypic and environmental variance was calculated by following formulas:

$$\delta^2g = \frac{MSg - MSe}{r}$$

$$\delta^2e = MSe$$

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

Coefficients of phenotypic, genotypic, environmental variation and public heritability were calculated by means of HIZER formula and M.S Excel:

$$CVg = \frac{\sqrt{\delta^2g}}{\bar{X}} \times 100$$

$$CVp = \frac{\sqrt{\delta^2p}}{\bar{X}} \times 100$$

$$h^2 = \frac{\delta^2g}{\delta^2p}$$

In this relationship:  $\delta^2g$  is genetic variance,  $\delta^2e$  is environmental variance,  $\delta^2p$ , phenotypic variance,  $CVg$  is coefficient of genetic variation,  $CVp$ , coefficient of phenotypic variation and  $h^2$  is general heritability. To determine the share of each trait in total variation, to reduce data dimension and to better data interpret the relationship, principal components analysis was used (Senath & Sokal, 1973). Genotypes classification and cluster analysis was performed in Ward's method and statistical analysis of data was conducted using SAS software.

### RESULTS AND DISCUSSION

Analysis of two-year variance showed that the effect of year was significant in 1% level of probability for days to flowering, days to maturity, plant height and was significant in 5% for number of pods per plant, 100-seed weight. But the effect of year was not significant for number of seeds per pod, individual plant yield and yield. Also, all studied traits for genotypes were significant at 1% level. Therefore the genetic materials have necessary diversity.

Results of descriptive statistics such as mean, standard deviation, minimum and maximum of traits have been showed in Table 2. Phenotypic and genetic coefficients of variation and general heritability for all the traits have been shown in Table 2. Genetic and phenotypic coefficients of variation are used for determining the presence or absence of diversity. Comparing these coefficients, demonstrates the effect of environmental factors on the studied traits. Coefficients of genetic variation were larger than phenotypic coefficient of variation for all the traits. Meanwhile, in many cases there is small difference between the coefficients, which indicates the little effect of environmental factors in estimation. According to the theory of Stansfield [17] if the heritability of traits is more than 50%, the trait has high, if it is between 20 and 50% its heritability is moderate and if it is less than 20% the heritability is low.

The difference was little between the days to flowering and days to maturity but days to flowering (59.91%) and days to maturity (87.36%) had high coefficients of heritability that represents the top value of these traits in breeding programs. Coefficients of genetic variation, phenotypic variation and general heritability of plant height, was 20.63%, 22.49% and 84.17 % respectively. Due to the high genetic

diversity of this trait, the trait can be used in breeding programs. The number of pods per plant has a high coefficient of phenotypic variation (26.55%) and lower coefficient of genetic variation (12.19%), which reflects the high impact of the environment on the number of pods per plant. The heritability of this trait was average too (21.08%). Therefore according to the average heritability of this trait, genotype-based selection method should be used [2]. Genetic and phenotypic coefficients of variation for seeds per pod (10.03% and 12.11%) had little difference, but had high heritability (68.51%). Due to the high general heritability, it can be concluded that both environmental and genetic factors are responsible for this trait. Coefficient of variation for genetic and phenotype and heritability for 100-seed weight was 18.55%, 18, 62% and 99.2 respectively. These values indicate that 100-seed weight heavily dependent on the interaction effect of genotype and environment. Higher heritability of this trait in comparison with other traits indicates the importance of 100- seed weight in the breeding program. Marjani [5] reported that general heritability of 100-seed weight was 37%. Singh [18], reported that heritability of 100-seed weight was 61%. General heritability of yield per plant and total yield was 70.57% and 83.24% respectively. The genotypes studied were of great diversity in term of these traits and can be used in breeding programs. Vazei *et al* [2] stated that there is much variation in yield and yield components and this variation can be used for breeding bean cultivars. Dargahi *et al* [19] and Zeven *et al* [20] have reported that there are considerable variations in seed and plant traits.

**Table 2. Quantitative traits statistics in studied traits in beans and phenotypic and genetic coefficients of variation, and heritability**

Trait	Average	SD	Maximum	Minimum	Genetic Coefficient of variation	Phenotypic Coefficient of variation	Heritability coefficient public
Days to flowering	23.57	03.3	62	51	12.2	74.2	91.59
Days to maturity	93.110	74.6	121	97	04.3	25.3	36.87
plant height	47.50	71.17	8.96	8.22	63.20	49.22	17.84
Number of pods per plant	38.13	1.5	44	8	19.12	55.26	08.21
Number of seeds per pod	11.5	72.0	66.7	4	03.10	11.12	51.68
Seed weight	46.33	6.6	43.47	3.18	55.18	62.18	2.99
Yield per plant	24.15	72.4	69.27	58.4	93.20	92.24	57.70
Overall yield	06.3127	17.943	46.5538	33.958	62.22	8.24	24.83

The results of the correlation coefficient table (Table 3) showed that grain yield had positive and significant correlation with yield components traits including: number of pods per plant ( $r = .51^{**}$ ) and number of seeds per pod ( $r = 0.23^*$ ). Grain yield showed positive and significant correlation with 100-seed weight ( $r = -0.47^{**}$ ) and yield per plant ( $r = 0.9^{**}$ ) too. Grain yield showed significant negative correlation with days to flowering ( $r = 0.25^*$ ) and days to maturity ( $r = -0.32^{**}$ ). Number of pods per plant had significant positive correlation with yield per plant ( $r = 0.58^{**}$ ). In accordance with the result, Raffi and Nath [21] and Dargahi *et al* [19] also reported the positive and significant correlation of number of pods per plant with grain yield per plant. Chalyk *et al* [22], reported 72% as the highest correlation of plant yield with number of pods per of plant. 100-Seed weight and number of grain per pod had significant negative correlation ( $r = 0.3^{**}$ ). Plant height showed negative correlated with all traits. According to the results it can be concluded that as the obtained correlation coefficient of the traits suggest, number of pods per plant, number of grain per plant and 100-seed weight had the highest positive role in improving grain yield per plant that is consistent with the results of Beyzaie [23] and Ramalto *et al* [24]. Therefore they can be selected as the most important and prominent selection criteria.

**Table 3. Correlation coefficients of simple agronomic traits**

Trait	Days to flowering	Days to maturity	plan height	Number of pods per plant	The number of seeds per pod	100-Seed weight	Yield per plant	Yield
Days to flowering	1							
Days to maturity	0/79 **	1						
plant height	ns-0/36	-0/4 **	1					
Number of pods per plant	ns0/2	ns0/12	-0/42 **	1				
Number of seeds per pod	ns-0/04	ns-0/16	ns0/12	0/37 **	1			
Seed weight	-0/31 **	ns-0/13	ns-0/15	ns0/05	-0/3 **	1		
Yield per plant	-0/25 *	-0/32 **	ns-0/08	0/58 **	ns0/23	0/41 **	1	
grain yield	-0/32 **	-0/39 **	ns-0/12	0/51 **	0/23 *	0/47 **	0/9 **	1

\*\* , \* and ns: means significant difference at 1%,5% and no significant difference

### PRINCIPAL COMPONENTS ANALYSIS

The results of principal components analysis based on eight measured traits are provided in Table 4. According to the eigenvalues of principal component, the first three principal components were selected that explained 86% of the variation. As seen in Table 5, the first component in determining the total variance had the largest share with 60 percent. The positive coefficients of the first principal component of days to flowering, days to maturity, number of seeds per pod is the number of seeds per pod. This type of analysis would lead to conversion of the primary variables to new variables called principal components and using their variation, more complete idea is obtained [25]. As seen in Table 5, the first component with 60 % had the largest share in determining the total variance. The largest positive coefficients of the first principal component are belongs to days to flowering, days to maturity, number of seeds per pod.

The second component, which accounted for 15 percent of the variance, has the largest positive coefficient in yield per plant, grain yield, and number of pods per plant and negative coefficient in 100-seed weight and days to maturity. This relationship significantly had been obtained in simple traits correlation table. Amini [13] reported that grain yield per plant and yield components such as number of pods per plant and number of seeds per plant with positive effect were in one component.

The third component which accounted for 10%of the total variance has the biggest positive coefficient in plant height, grain yield and total yield.

Kamel and Moradi [26] studied on 36 lines of chickpea and used principal components analysis, four factors were obtained. Based on the eigenvalues, two principal components that explained 77.2% of the variance were selected. The first component accounted for 56.8% of the data variation. Based on coefficients of eigenvalues, days to flowering, plant height, days to maturity and 100-seed weight with positive sign and grain yield with negative sign had important role in the first component. Plant height and grain yield were the most important traits in explaining the second component.

According to the results, it seems that breeding of bean to the second component have a higher priority than the first component that includes consecutive phenological traits: Because this component consists of yield and Related Traits to it. That outcome has been suggested by Azizi *et al* [27] on bean genotypes. Dargahi (2006) using principal components analysis of high correlated traits demonstrated that seven principal components: explained 65.43% of the total variance in the traits and reported that yield had greatest influence on the second component. Amini [13] reported in his study that five principal components, explained 73.19% of the total variation.

**Table 4. Eigenvalues and the share of each component in the principal component analysis based on the all studied traits**

Component No	Eigen value	difference	Variance %	Cumulative variance%
1	85.4	66.3	6.0	6.0
2	19.1	35.0	15.0	75.0
3	84.0	25.0	1.0	86.0
4	58.0	25.0	07.0	93.0
5	33.0	2.0	04.0	97.0
6	12.0	07.0	01.0	99.0
7	05.0	05.0	007.0	999.0
8	001.0		0002.	1

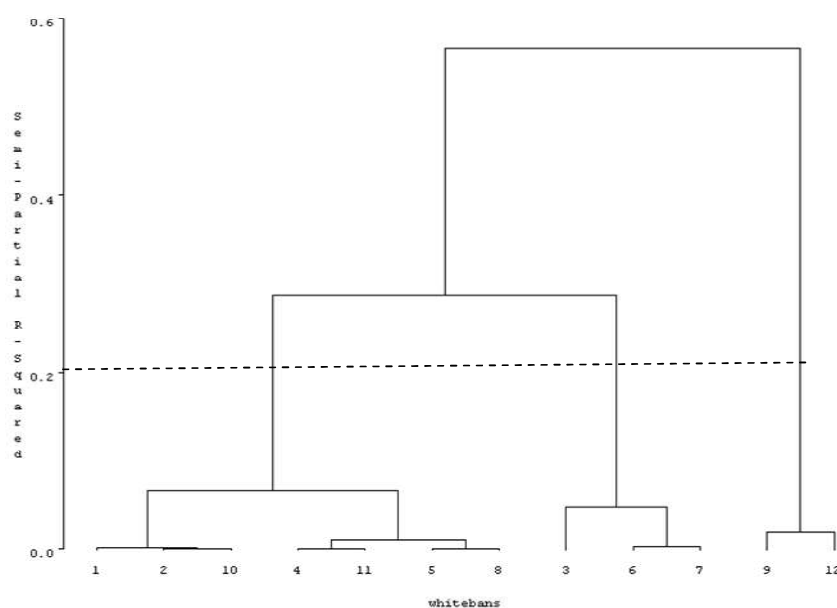
**Table 5. the results of Principal component analysis for yield-related traits in 12 genotypes of white bean**

8th component	7th component	6th component	5th component	4th component	3rd component	2nd component	1st component	Genotype
0.09	0.29	0.74	0.31	0.24	0.17	0.089	0.41	Days to flowering
-0.04	-0.4	0.01	0.46	0.54	0.25	-0.39	0.32	Days to maturity
0.04	-0.17	-0.4	-0.4	-0.2	0.69	0.15	0.31	Bush height
-0.09	0.3	0.12	0.56	-0.63	0.17	-0.12	0.35	Number of pods per plant
0.04	0.47	-0.42	0.23	0.39	-0.14	0.51	-0.33	The number of seeds per pod
0.1	0.63	-0.18	-0.08	0.19	0.32	--0.55	-0.32	Seed weight
0.67	-0.08	0.17	0.35	0.01	0.35	0.35	-0.38	Yield per plant grain performance
-0.71	0.05	0.18	0.16	0.13	0.39	0.33	-0.38	

**CLUSTER ANALYSIS**

According to the Figure 1, grouping of studied samples based on the evaluated traits in 0.2 Euclidean distances resulted in three clusters. The first cluster consists of two subgroups which the first subgroups included 1, 2 and 10 genotypes and the second subgroups included of four genotype 4, 11, 5 and 8. The second cluster also includes two subgroups. In terms of yield, Genotypes of this cluster had average yield. Only genotype 3 was in the first group and the second sub-group the genotypes 6 and 7. The second cluster was the highest yield and high yielding genotypes but the genotypes of this cluster and high performance. Only genotype No 3 was in the first sub-group and genotypes 6 and 7 was in second sub-group. The second cluster had the highest yield and the genotypes of this cluster were belonged to the high yielding genotypes. 9 and 12 genotypes were also in the third cluster. Genotypes of this cluster had the lowest yield and belonged low-yielding genotypes.

This division reflected a great diversity among the masses that it can be used in breeding programs and hybridization. Dargahi [19] grouped samples of white beans into three categories based on climate. The greatest difference was observed between the second and third cluster. The third cluster of was full season than second cluster genotypes and had large differences in terms of yield. Desired samples can be selected in breeding programs based on this grouping.



**Figure 1: Tree Diagram of cluster analysis for 12 Omidbakhsh lines of white bean using morphological traits and yield**

**CONCLUSION**

The results of this study showed that there is considerable genetic variation for agronomic traits such as yield and its components in bean genotypes and some genotypes have large genetic potential for increasing grain yield. However, due to the high genetic variation and high general heritability of all traits, their improvement through selection programs is possible. According to the results of PCA, traits affecting grain yield in the second component has to be considered in future research as major variables.

In terms of selecting superior genotypes, 3 samples of second cluster are important in comparison to commercial cultivars and validity of yield stability in introduction as a cultivars.

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