Study of Genetic Parameters of Pecan Plant (*Peganum harmala*) in Some Regions of Western Iran

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ARTICLE INFO	ABSTRACT
	Pecan (*Peganum harmala* L.) has many characteristics, such as antibacterial, antioxidant, antifungal, anticancer drugs, etc. In different genetic analyses, the calculation of the genotype correlation coefficient is more important than the phenotype correlation coefficient. Similarly, the use of other genetic parameters (such as heritability, etc.) is very useful in plant breeding projects. Therefore, it is not correct to choose the ecotype (genotype) with the help of other traits without considering the relationship and calculating the correlation between the traits, it strongly affects the desired results. For this research, First, pecan plant samples were identified and collected simultaneously. In this study, the pecan ecotypes identified in habitats (Three habitats in Asadabad-Hamedan including Mousi-Abad Village 1, Mousi-Abad Village 2 and Najaf-Abad Village, and the fourth habitat in Kangavar –Kermanshah include Karkhaneh Village (located in the west of Iran) traits related to the morphology of the pecan plant were evaluated. In order to calculate the genetic correlation and other genetic parameters, the form of random complete block design is designed and implemented with three replications. The genetic correlation coefficients calculated in this study indicated that there is a genetic correlation between traits associated with yield. In addition, the maximum percentage of heritability was assigned to the traits of number of branches per plant (0.99%) and stem diameter (0.99%), and the minimum percentage of heritability was assigned to the traits of number of nodes (0.24%) and fresh weight of a single stem (0.0009%), respectively. The stem diameter trait had the maximal heritability value and also had the maximal genetic advance rate. Also, the traits of number of nodes, fresh weight of whole plant and fresh weight of single stem, in addition to having the lowest heritability, had the lowest genetic advances.

1. Introduction

Plants with medicinal value have been considered for a long time as medicine for human and animal diseases, they contain many medicinal chemical compounds with appropriate activity such as antifungal, antibacterial, antifungal agents, etc. (Shah *et al*., 2012; Moharrami fard *et al.*, 2015). Pecan (*Peganum harmala*) belongs to the Zagophyllaceae family and is one of the most famous medicinal plants in the traditional medicine of Iran and European countries (Darabpour *et al.*, 2011). The height of this plant is about 30 and 50 cm, its appearance is like a bush, and it has green leaves with long, irregular and narrow divisions. The pecan plant has large flowers, thin sepals and large greenish-white petals, its fruit has many black seeds and it has a wide range of medicinal properties (Shah *et al.,* 2012; Moharrami fard *et al*., 2015). Pecan has been used as an antiseptic in Iran in the past (Sabbagh *et al*., 2015), so this plant is used to treat back pain, asthma, jaundice and colic (Sabbagh *et al*., 2015). Among its important alkaloids, harmine alkaloid, harmaline, harmalol and quinazoline can be mentioned (Akbary *et al*., 2015). Among other medicinal properties of pecan in the field of veterinary medicine, we can mention its antibacterial effects (Shahverdi *et al*., 2008; Akbary *et al*., 2015).

Studying and paying attention to genetic diversity in plants is evaluated from two perspectives: A, genetic diversity is a necessary condition for obtaining the product and the consistency and stability of the

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product, and B, genetic diversity identifies favorable genetic resources for breeding plans (Gepts and Papa, 2003; Kakaei and Mazaheri Laghab, 2014). Plant genetics scientists want to identify characteristics beyond yield until they are able to use them for the selection of parents or in the selection of a single plant in the separating generations. Based on the research done in the past, selection based on yield trait components has a higher genetic advance, compared to the selection based on the yield trait itself in increasing yield. If the breeder selects the parents based on their phenotypic characteristics, its success in changing population characteristics can be estimated only when the degree of correspondence between phenotypic values and breeding values is known. The degree of adaptation is calculated with the help of heritability. The predictive role of heritability is its most prominent role in traits. The phenotypic value of individuals can be calculated directly but the value of reproducing people determines the effect of phenotypic values in future generations (Siahpoush *et al*., 2003; Falconer, 1989). In fact, the concept of heritability is the quantitative calculation of the chance of passing a biological trait from parents to progeny. According to geneticists, the rules of inheritance of discrete traits from one generation to another are owed to Mendelian genetics (Kalirad, 2022). For each trait in the plant breeding project, the most significant issue is the response to selection among the necessary factors for an appropriate response, the existence of a source of primary variation, which is the phenotypic variance, is necessary (Falconer, 1989). In fact, broad heritability cannot determine the genetic contribution of diversity as accurately as narrow sense heritability however, the high numerical rate of general heritability indicates the relative transmission of traits from parents to progeny.

Kakaei et al. (2015) expressed in the evaluation of yield and indices affecting yield and their heritability in chickpea genotypes, that the maximum and minimum percentages of heritability were assigned to the traits of harvest index and number of seeds per plant, respectively. Also, they announced that due to the presence of desirable diversity in traits, these traits can be used as a suitable source of diversity to increase yield and select more privileged genotypes. They are mentioned in the study, in order to examine the relationships between traits, they used genetic correlation analysis and stepwise regression analysis.

Kakaei and Mazahery Laghab (2015), in the study of alfalfa ecotypes, with the help of correlation and heritability assessment, stated that the phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV), genetic advance (GA), genetic gain (GG) and heritability in the evaluation of cultivated alfalfa populations for future decisions in the alfalfa breeding programs are noteworthy. In another part of their findings, they expressed that the coefficient of genetic diversity of traits indicates that the difference in diverse traits is different because there was high diversity in some traits and very limited diversity in some other traits.

In this regard, Falconer (1989) stated that the higher the diversity in the traits, the more favorable the selection will be in those traits. Therefore, the current research was done to calculate the components of genetic variance, heritability and genetic correlation of yield traits and yield indicators, as well as the selection of the most effective trait that can be used in breeding programs for indirect selection of yield.

2. Materials and methods
2.1. Plant materials
To investigate the characteristics related to the yield of four populations of pecan plants, an experiment was set up based on a randomized complete block design with three replications in 2023. In the present study, the characteristics related to the yield of four ecotypes, including three ecotypes in Asadabad (Mousi-Abad Village 1, Mousi-Abad Village 2 and Najaf-Abad Village) and the fourth population in Kangavar (Karkhaneh Village) located in the west of Iran were checked (Table 1). First, pecan plant samples were collected and identified at the same time (early July 2023) in this study, 12 traits (Table 2) were evaluated. Fig. 1 shows pictures of the place where the pecan samples were collected in the village of Mousi-Abad in Asadabad-Hamadan.

2.2. Statistical calculations
To calculate the heritability percentage of significant traits, the genotypic variance was divided into phenotypic variance. The genotypic diversity coefficient and phenotypic diversity coefficient were calculated using genotypic variance and phenotypic variance, respectively, based on the following Equations or formulas (Equation 1-9). Genotypic

correlation coefficients were calculated with the help of genotypic variance and covariance using the method of Miller et al. (1958) and with the help of the following formulas. In genotypic correlation formulas, the numbers 1 and 2 represent the first and second traits. Statistical calculations were done using SPSS 26 and Excel 2013 software.

Table 1. Location of the population of the studied pecan samples

Row	Habitat name	City	Province	Map coordinates
X1	Mousi-Abad Village 1	Asadabad	Hamedan	Eastern: 48.15051°- Northern: 34.28488°
X2	Mousi-Abad Village 2	Asadabad	Hamedan	Eastern: 48.15051°- Northern: 34.28488°
X3	Najaf-Abad Village	Asadabad	Hamedan	Eastern: 47.56'56"- Northern: 34.39'07"
X4	Karkhaneh Village	Kangavar	Kermanshah	Eastern: 47.9973°- Northern: 34.4957°

Table 2. Traits studied in pecan population

Row	Trait name	Row	Trait name	Row	Trait name
X1	SPAD Chlorophyll index	X5	Number of branches per stem	X9	Dry weight of single stem (gr.)
X2	Stem height (cm)	X6	Number of nodes	X10	Fresh weight of single stem (gr.)
X3	Number of flowers per plant	X7	Number of branches per plant	X11	Dry weight of the whole plant (gr.)
X4	Number of leaves	X8	Fresh weight of the whole plant (gr.)	X12	Stem diameter (cm)

Figure 1. Collected pecan samples studied in the village of Mousi-Abad, Asadabad-Hamedan

(1) $\quad H^2(\%) = \dfrac{\sigma^2 g}{\sigma^2 p} \times 100$

(2) $\quad GCV(\%) = \dfrac{\sqrt{\sigma^2 g}}{X} \times 100$

(3) $\quad GA = \dfrac{K \times \sigma^2 g}{\sqrt{\sigma^2 p}}$

(4) $\quad \sigma^2 g = \dfrac{\sigma^2 t - \sigma^2 e}{r}$

(5) $\quad PCV(\%) = \dfrac{\sqrt{\sigma^2 p}}{X} \times 100$

(6) $\quad GG = \dfrac{GA}{\overline{X}}$

(7) $\quad \sigma^2 p = \sigma^2 g + \sigma^2 e$

(8) $\quad r_g = \dfrac{\sigma_{g\,1,2}}{\sqrt{(\sigma^2 g1)(\sigma^2 g2)}}$

(9) $\quad r_{ph} = \dfrac{\sigma_{ph1,2}}{\sqrt{(\sigma^2 ph1)(\sigma^2 ph2)}}$

GCV, Genotypic Coefficient of Variation (Equation 2); PCV, Phenotypic Coefficient of Variation (Equation 5); H2, Heritability (Equation 1); GA, Genetic Advance (Equation 3); GG, Genetic Gain (Equation 6).

3. Results and discussion

3.1. Estimation of variance components

Estimation of variance components according to Table 3, the number of branches per plant (%0.99) and stem diameter (%0.99) have the maximum amount of heritability, and correspondingly, the stem diameter also has the maximal amount of genetic gain (GG), and the stem diameter trait has the maximal amount of genetic advanced (GA). The lowest rate of heritability belonged to the traits number of nodes, fresh weight of the whole plant and fresh weight of a single stem, and these traits had a minimal amount of genetic advance. These traits (number of nodes, fresh weight of the whole plant and fresh weight of a single stem) were less than the genetic advance. In most of the traits, the phenotypic variance accounts for more than the genotypic variance.

The trait of stem diameter had maximum heritability and it has equal phenotypic variance and genetic variance and a small environmental variance and in other words, the role of environmental factors in it is very small. The trait number of branches in each plant also has a very small environmental variance, in which the effects of the environment are very small, although it has equal genetic and phenotypic variance values. The traits of the number of branches per plant, fresh weight of a single stem, and stem diameter have higher genetic coefficient variation and phenotypic coefficient variation than other traits. When two traits have maximal heritability, phenotypic correlation is usually determined by genotypic correlation, but if both traits have low heritability, then the correlation will be largely due to environmental correlation (Bernardo, 2002). Kahrizi et al. (2010) in the study of durum wheat agronomic traits, announced that a maximum genetic gain has been observed between the studied traits.

3.2. Genetic correlation analysis

According to the genetic correlation table (Table 4), The SPAD chlorophyll index has a negative correlation and is significant at the 5% probability level (P≤%5), with the fresh weight of one stem (-0.386[*]), With the dry weight of the entire plant (-0.076[*]) and the stem diameter (-0.637[*]) traits. The stem height trait was negatively and significantly correlated with the whole stem fresh weight trait, with a value of (0.44[**]). Also, the number of branches per plant trait had a positive and significant correlation of (0.467) at the probability level of 5% (P≤%5), That is, with the increase in the plant's height, Also, the number of branches in the plant increases. Also, with the increase of plant height trait, the plant diameter increases to the extent (0.426). As the plant grows taller, its stem diameter must become stronger to ensure its stability and strength. The number of flowers in a plant trait and the dry weight of a single plant trait have a significant correlation of (0.796[*]) at a probability level of (P≤%5). As the plant grows larger and has more stems, there is also an increase in the number of flowers it produces. The number of leaves in a plant trait has a negative and significant correlation with the fresh weight of a single stem trait, known as the amount (-0.056[*]).

The fresh weight trait of the whole plant has a negative and significant correlation at the 1% probability level (P≤%1) with the stem diameter, with a correlation of (-0.6[**]). The trait of single stem dry weight the amount (0.872[*]) has a positive and significant correlation at the 5% probability level (P≤%5), The trait of single stem dry weight, with the amount (0.872[*]) has a positive and significant correlation at the 5% probability level (P≤%5), With the dry weight of the entire plant in the plant.

The greater the dry weight of a single stem, the greater the dry weight of the whole plant. The study of different genotypes of Camelina was conducted by Fallah et al. (2023), they used the statistical method of genetic correlation analysis and also used other genetic parameters to evaluate the relationships between traits. In another study, Hamzeh et al. (2009) evaluated the genetic parameters of bread wheat cultivars, It was expressed that grain yield has a positive correlation with the number of spikes and the number of seeds contained in the spike, and biomass, in both of these characteristics, the additive component of the total genetic variance has been allocated to itself and caused moderate heritability for them, As a result of this result, Under conditions of irrigation limitation, indirect selection can be recommended for both of the traits mentioned above to increase the grain yield of the genotype in question.

Ale Omrani Nejad et al. (2018), in the study of heritability and genetic diversity of different populations of medicinal plants (*Oliveria decumbens* Vent.), we will use morpho-physiological traits and the amount of essential oil to help identify the genetic diversity of different populations, They announced that

the functional traits of *Oliveria decumbens* are highly heritable for their characteristics, including essential oil content, The number of stipules per plant and the dry weight of 100 stipules were 0.91, 0.5, and 0.77, respectively. In general, based on the findings of this investigation, it was found that most of the variety of traits related to yield were evaluated in the evaluation of traits among pecan populations, it was genetic.

Table 3. Estimation of variance components and other genetic parameters in pecan populations under study

Traits	CV%	ECV%	GCV%	PCV%	G. a.	G. g. %	H2	Var. G.	Var. P.	Var. E.
SPAD Chlorophyll index	65	0.65	3.141	1.89	38.49	3.432	0.8817	396.19	449.334	53.144
Stem height (cm)	22	0.22	1.1	1.122	16.07	2.22	0.9616	63.333	65.861	2.528
Number of flowers per plant	69	0.69	3.786	2.427	29.419	4.189	0.838	243.481	290.425	23.472
Number of leaves	45	0.45	3.513	2.061	36.65	4.04	0.952	332.639	349.278	16.639
Number of branches per stem	20	0.2	0.56	0.36	1.7	0.52	0.699	0.972	1.389	0.417
Number of nodes	10	0.1	0.139	0.114	0.6	0.05	0.24	0.361	1.5	1.139
Number of branches per plant	4	0.04	9.4	9.41	15.3	19.35	0.999	55.33	55.334	0.001
Fresh weight of the whole plant (gr)	19	0.19	0.452	0.303	0.98	0.37	0.608	0.389	0.639	0.25
Dry weight of single stem (gr)	21	0.21	0.902	0.548	11.3	0.01	0.85	35.585	41.7	6.115
Fresh weight of single stem (gr)	18	0.18	24.35	14.06	0.06	0.0003	0.0009	976.58	976.742	0.16
Dry weight of the whole plant (gr)	77	0.77	3.4	2.06	6.04	3.65	0.86	10.01	11.628	1.618
Stem diameter (cm)	35	0.35	1815.6	1048.23	61.07	2137.55	0.99	896.89	896.893	0.0001

Table 4. Genotypic correlation coefficients of studied traits in different pecan populations

Traits	1	2	3	4	5	6	7	8	9	10	11	12
SPAD chlorophyll index	1											
Stem height (cm)	-0.397	1										
Number of flowers per plant	-0.207	0.212	1									
Number of leaves	0.098	-0.024	0.582	1								
Number of branches per stem	-0.726	0.467*	0.559	0.1	1							
Number of nodes	0.447	-0.296	1	0.907	-0.234	1						
Number of branches per plant	-0.457	0.067	0.145	0.28	0.147	-0.037	1					
Fresh weight of the whole plant (gr)	0.266	-0.44**	-0.427	-0.064	-0.858	0.963	0.341	1				
Dry weight of single stem (gr)	-0.136	0.124	0.796*	0.693	0.524	1	0.227	-0.283	1			
Fresh weight of single stem (gr)	-0.386*	0.392	0.41	-0.056**	0.702	-0.119	-0.216	-0.806	0.251	1		
Dry weight of the whole plant (gr)	-0.072*	0.060	0.754	0.729	0.419	1	0.275	-0.138	0.872*	0.138	1	
Stem diameter (cm)	-0.637*	0.426*	0.214	-0.248	0.676	-0.561	0.041	-0.6**	0.046	0.014	-0.055	1

*, ** significant at 1% and 5% probability levels, respectively. Numbers 1 to 12 indicate the names of attributes based on Table 2.

4. Conclusion

Using genetic correlation coefficients instead of phenotypic correlation coefficients is more advantageous in various genetic analyses because the effects of external factors involved in creating unrealistic relationships between studied traits reach their minimal value in genetic correlation. The use of other genetic parameters such as heritability etc. is very useful in plant breeding programs. Therefore, selection with the help of traits is not correct regardless of the way of communication and calculation of correlation, and it strongly affects the certainty of the desired results. Based on the results of this research, the maximum percentage of heritability was assigned to the traits of number of branches per plant and stem diameter, and the minimum percentage of heritability was assigned to the traits of the number of nodes and fresh weight of a stem, respectively. These traits can be used to improve the pecan plant. Based on this, according to the environmental conditions and their changes, agronomic and breeding studies of these valuable plants seem necessary. The results of the calculation of genotypic correlation coefficients showed that there is a high genetic correlation between the traits of the number of flowers per plant, the number of leaves, the number of nodes, the fresh weight of the whole plant, and the dry weight of the whole plant. The results obtained can be used in future research.

Conflict of interests

The author has stated that there is no conflict of interest.

Ethics approval and consent to participate

No humans or animals were used in the present research.

Consent for publications

The final article has been approved by the author.

Availability of data and material

All the data are embedded in the manuscript.

Authors' contributions

The first draft of this manuscript was written by the researcher and has been revised and modified.

Informed consent

The author declares not to use any patients in this research.

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References

Akbary P., Ghareghani Poor M., Fereidouni M.S. 2015. Effect of the seed extract of P*eganum harmala* L supplemented diet on several of non-specific immunity parameters in rainbow trout (*Oncorhynchus mykiss* Walbaum). Animal Research Journal (Iranian Biology Journal) 28(1): 1-8. (In Farsi). https://dorl.net/dor/20.1001.1.23832614.1394.28.1.1.6

Ale Omrani Nejad S.M.H., Naghdi Badi H., Mehrafarin A., Abdousi V., Khalighi Sigaroodi F. 2018. Diversity and heritability of morphophysiological traits and essential oil of *Oliveria decumbens* Vent. in Iran. Eco-phytochemical Journal of Medicinal plants 6(3): 32-46. (In Farsi). https://doi.org/10.30495/ejmp.2018.694523

Bernardo R. 2002. Breeding for quantitative traits in plants. Stemma Press. Minnesota, USA.

Darabpour E., Poshtkouhian Bavi A., Motamedi H., Seyyed Nejad S.M. 2011. Antibacterial activity of different parts of *Peganum harmala* L. growing in Iran against multi-drug resistant bacteria. EXCLI Journal 10: 252-263.

Falconer D.S. 1989. Introduction to quantitative genetics. (3rd edition) Longman, New York. 415 p.

Fallah F., Kahrizi D., Rezaeizad A., Zebarjadi A., Zarei L., Dogan H. 2023. Assessment of genetic variability and genetic parameters of morphological and agro-physiological traits in *Camelina sativa* (L.). Turkish Journal of Agriculture and Forestry 47: 242-251. https://doi.org/10.55730/1300-011X.3082

Gepts P., Papa R. 2003. Possible effects of (trans) gene flow from crops on the genetic diversity from landraces and wild relatives. Environmental Biosafety Research 2(2): 89-103. https://doi.org/10.1051/ebr:2003009

Hamzeh H., Saba J., Jabari F., Nassiri J., Alavi Hosseini S.M. 2009. Estimation of components variation, genotypic and phenotypic correlation coefficients of grain yield and its component in bread wheat (*Tritium aestivum* L.) under rainfed conditions. Environmental Stresses in Crop Sciences 2(1): 29-38. (In Farsi). https://doi.org/10.22077/escs.2009.50

Kahrizi D., Cheghamirza K., Kakaei M., Mohamadi R., Ebadi A. 2010. Heritability and genetic gain of some morpho-physiological variables of durum wheat (*Triticum aestivum* turgidum var. durum). African Journal of Biotechnology 9(30): 4687-4691.

Kakaei M., Mazahery-Laghab H. 2014. Evaluation of alfalfa (*Medicago Sativa* L.) germplasm using multivariat statistical analysis. Iranian Journal of Rangelands and Forests Plant Breeding and Genetic Research 22(1): 125-132. (In Farsi). https://doi.org/10.22092/ijrfpbgr.2014.7689

Kakaei M., Mazahery-Laghab H. 2015. Study of genetic diversity, heritability and the correlation of different traits in alfalfa (*Medicago sativa* L.) related to alfalfa weevil (*Hypera postica* Gyll.) damage in alfalfa germplasm. Plant Genetic Researches 2(1): 63-76. (In Farsi). http://dx.doi.org/10.29252/pgr.2.1.63

Kakaei M., Moosavi S.S., Abdollahi M.R., Farshadfar E. 2015. Grain yield, its components, genetic diversity and heritability in chickpea (*Cicer arietinum* L.). Journal of Crop Production and Processing 5(16): 271-281. (In Farsi). http://dx.doi.org/10.18869/acadpub.jcpp.5.16.271

Kalirad A. 2022. Heritability. Iranian Journal of Biology 5(10): 33-47. (In Farsi). https://dorl.net/dor/20.1001.1.20089406.1400.5.10.5.3

Miller P.A., Williams J.C., Robinson H.F., Comstock R.E. 1958. Estimates of genotypic and environmental variances and covarianes in upland cotton and their implications in selection. Agronomy Journal 50(3): 126-131. https://doi.org/10.2134/AGRONJ1958.00021962005000030004X

Moharrami fard M., Mohammad eini A., Vahidi N., Ahmadifar M., Kalhor N., Gholambabaeian M.M. 2015. Evaluation of methanolic extract of *Peganum harmala* on pituitary-thyroid hormones and histopathological effect on female rats. Journal of Shahid Sadoughi University of Medical Sciences 23(3): 1987-1993. (In Farsi). http://jssu.ssu.ac.ir/article-1-2965-fa.html

Sabbagh S.K., Saeedi S., Dehbashi Z. Mazaheri Naeeini M. 2015. Antimicrobial activity of ethanolic extract of black pepper (*Piper nigrum*) and march (*Peganum harmala*) against antibiotic-resistant of *Staphylococcus aureus* strains. Bimonthly Journal of Sabzevar University of Medical Sciences 22(5): 854-861.

Shah A., Rasapalli S., Mello C., Singh B.R., Cai S. 2012. Antibacterial activity of commonly used traditional Chinese medicines as cold and flu remedies. Journal of Medicinal Plants Research 6(2): 234-242. https://doi.org/10.5897/JMPR11.1165

Shahverdi A.R., Ostad S.N., Khodaee S., Bitarafan L., Monsef-Esfahani H.R., Jamalifar H., Nikavar B., Mohseni M. 2008. Antimicrobial and cytotoxicity potential of *Peganum harmala* smoke. Pathology Magazine 4(15): 236-240. https://phcog.com/article/assets/v4/i15/PhcogMag-4-15-236.pdf

Siahpoosh M.S., Emam Y., Saidi A. 2003. Genotypic variation, heritability, genotypic and phenotypic correlation coefficients of grain yield, its components and some morpho-physiological characters in bread wheat (*Triticum aestivum* L.). Iranian

Journal of Crop Sciences 5(2): 86-102. (In Farsi).
http://dorl.net/dor/20.1001.1.15625540.1382.5.2.2.2