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Heritability estimates, correlation and path coefficient analysis for fruit yield in walnut (*Juglans regia* L.)

RK Dogra, Samrita Sharma and DP Sharma

Abstract

This study aimed to understand the inherent relationship for fruit yield with various physiological and development traits using heritability estimates, correlation and path coefficient analysis under mid-hill conditions of north-western Himalayas of India. High heritability coupled with high genetic gain was found for the character tree volume, trunk cross sectional area and fruit yield. Whereas, high heritability coupled with moderate genetic gain was obtained for the characters *viz.*, trunk girth, nut weight and kernel weight. A highly significant and positive phenotypic and genotypic correlation of yield were found with flower density, fruit set, trunk girth, trunk cross sectional area and tree spread. Maximum positive direct effect cited towards yield were contributed by flower density, trunk girth, tree height, shoot length, duration of male flowering, nut weight, fruit set, shell thickness, kernel percentage and nut width. The study concluded that the traits trunk cross sectional area, trunk girth and flower density could serve as selection indices for higher yield with good nut and kernel quality cultivars in walnut.

Keywords: walnut, heritability, correlation, path analysis, nut, kernel, yield

Introduction

Walnut (*Juglans regia* L.) is the most widespread tree nut in the world. It belongs to family juglandaceae. The point of origin for the Persian walnut (*Juglans regia* L.) lies in Central Asia, where the tree grows in a wild and semi-cultivated state. In pre-historic times, it spread to western China, the Caucasus, Persia, and Europe. At present, walnut is cultivated commercially throughout southern Europe, Northern Africa, Eastern Asia, USA and Western South America. China is the leading world producer, followed by the Iran, USA, Turkey, Ukraine, Mexico, France, India, Chile, and Romania (FAO, 2016)^[1]. It is cultivated mainly in the Northern hemisphere between 30° to 50° of latitude and at an altitude of 1200-2150 meter above mean sea level. The chilling requirement ranges from 700-1500 hours and well distributed rainfall of about 80-90cm is sufficient for its cultivation. Walnut has been used globally in human nutrition since ancient times. The kernels of this fruit are high in protein and oil contents. Therefore, the walnut is classified as a strategic species for human nutrition and is included in the FAO list of priority plants (Gandev, 2007)^[2]. Nutritional assets and medicinal benefits of the walnut include omega-3 fatty acids, antioxidants, fibre, and numerous vitamins and minerals. Researchers have shown the diverse benefits of the walnut through many clinical studies. Because of the strong evidence of the walnut's potential role in cardiovascular health, the U.S. Food and Drug Administration approved one of the first qualified health claim for a whole food in March 2004: "Supportive but not conclusive research shows that eating 1.5 ounces of walnuts per day, as part of a low saturated fat and low cholesterol diet, and not resulting in increased caloric intake, may reduce the risk of coronary heart disease. In addition to heart health, studies have shown walnut consumption to benefit people with diabetes and cancer, promote bone health, assist with weight management, improve cognitive performance, and counteract some effects of aging. The husk yields valuable oil and a yellow dye when pressed. The wood is heavy and fine-grained and is used mostly for furniture and gum stocks. Genetic variability is the basis of all plant improvement programmes. Sufficient genetic variability if present can be exploited for developing superior cultivars. Vavilov (1951)^[3] was the first to realize that a wider range of variability in any crop provides a better chance of selecting the desirable types. Another important factor, besides genetic variation for characters is their transmission to the next generation. Knowledge of heritability for different traits is essential for any crop improvement programme because the heritable component is the consequence of genotype and is inherited from one generation to the other. Correlation coefficient is a measure of the degree of association between the two traits worked out at the same time (Hayes *et al.*, 1955)^[4]. Yield is a very complex entity which is not only

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polygenically controlled but also subjected to the fluctuating environment. For selecting superior genotypes, the breeder has to choose from the material on the basis of their phenotypic expression. Path coefficient analysis proposed by Wright (1921) ^[5] is a standardized partial regression coefficient and permits the partitioning of the correlation coefficients into direct and indirect effects. Dewey and Lu (1959) ^[6] were the first to suggest the use of path coefficient analysis in breeding programmes. This technique determines yield contributing characters and thus is useful in indirect selection. Present day need of precocious and high yielding walnut types with good nut and kernel quality warrants availability of improved cultivars for commercial growing. Therefore, prior to recommendation of new cultivars, they should be tested and extent of variability present must be adequately assessed so that they perform consistently over a long period of time. The present endeavour aims to estimate the genetic variability in respect of various quantitative and qualitative traits and to understand inherent relationship for fruit yield with various physiological and development traits in walnut genotypes so as to bring improvement through future breeding programmes.

Materials and Methods

The present investigation was carried out at Experimental Farm, Department of Fruit Science, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan Himachal Pradesh (India) at 1320 m above mean sea level between 31° N and 77° E witnessing mild temperate climate. The experimental material consisted of 15 years old ten walnut genotypes *viz.*, Hartley, Kainthal selection, Kashmir Budded, Kinnaur selection, Montignac, Perial Lara, Shimla selection, Sirmour selection, Solan selection and Wilson Wonder planted at 8 x 8 m apart. The observations were recorded for two consecutive years 2015-16 and 2016-2017 on three randomly selected plants each in ten walnut genotypes. The plants were selected on the basis of the apparent yield performance and the past history of trees. During the course of study, all the recommended cultural practices were followed. The data recorded for each trait was analysed on mean values from pooled data using standard Randomized Complete Block Design with three replications as described by Gomez and Gomez (1983) ^[7], Each single tree randomly selected in a genotype was considered as one replication. Coefficient of variability at phenotypic, genotypic, environmental levels, Heritability (%) in broad sense, expected genetic advance resulting from selection of five per cent superior individuals and genetic gain expressed as genetic advance per cent of population mean were calculated as per formula suggested by Burton and De Vane (1953) ^[8] and Johanson *et al.*, (1955) ^[9], The genotypic and phenotypic correlation coefficients were calculated as per Al-Jibouri *et al.*, (1958) ^[10] by implying the techniques of statistical analysis in variance-covariance matrix analysis in which total variability had been split into replications, genotypes and errors. The phenotypic and genotypic correlation coefficients were used in finding out their direct and indirect contribution towards yield per tree. To have a deeper insight into, the direct and indirect effects of various yield components (independent variables) on dependent variables (fruit yield), the path coefficient analysis was worked out. Path coefficient analysis splits up the correlation coefficients between each pair of dependent variables and independent variables into a direct effect (path coefficient) and as indirect effects or via effects (path coefficient ×

correlation coefficient). Thus, the correlation coefficients between dependent variables and independent variables, which are of utmost importance, are the summation of direct and indirect effects. Path coefficient analysis was done by the method given by Dewey and Lu (1959) ^[6].

Comprehensive observations on various plant growth traits, flowering, yield, nut and kernel characteristics were recorded as per the IPGRI descriptors (IPGRI, 1994) ^[11].

Tree characteristics

Tree height: The tree height was recorded by staff flag from the base to the terminal most growing point and was expressed in meters (m).

Tree Spread: Tree spread was measured with the help of calibrated staff in two directions (North-South and East-West) and the average was expressed in meters (m).

Tree volume: Tree volume was calculated as per the methodology suggested by Westwood (1978) ^[12].

For the trees which were having height more than mean spread:

$$\text{Tree volume} = \frac{4}{3} \pi a^2 b$$

For the trees which were having height less than mean spread:

$$\text{Tree volume} = \frac{4}{3} \pi a b^2$$

$$a = \frac{1}{2} \text{ of the mean spread}$$

$$b = \frac{1}{2} \text{ of the tree height}$$

$$\pi = 3.1428$$

Trunk girth: The trunk girth (cm) was taken at breast height of nine inch from the grafting point and expressed as per cent increase in trunk girth.

$$\text{Per cent increase} = \frac{\text{Final girth} - \text{Initial girth}}{\text{Initial girth}} \times 100$$

Trunk cross sectional area (TCSA): The trunk cross sectional area was calculated as per method given by Westwood (1993) ^[13]. $TCSA = \pi r^2$ Where, r = radius of the trunk

Shoot length: The character was taken by measuring the length of current season growth and expressed in centimetre.

Flowering characteristics

Time and duration of male flowering: Date of first catkin bud burst and last were recorded, gap between the two was treated as duration of male flowering.

Time and duration of female flowering: Date of female flowering was recorded at the opening of first female flower and last female flower. The difference between the two was taken as duration of female flowering.

Flower density: Four uniform shoot on each tree were randomly marked with tags and the number of flowers were counted on the branch. Flower density was calculated by using the number of flowers divided by Branch Cross Sectional Area (cm²) given by Hassani *et al.*, 2006 ^[14].

$$\text{Flower density (\%)} = \frac{\text{No. of flowers}}{\text{Branch Cross Sectional Area (cm}^2\text{)}}$$

Yield characteristics

Fruit Set: Four shoots were selected in all directions of the

tree and were tagged for counting the flowers. The fruit set was recorded 4-5 weeks after flowering and expressed as per cent fruit set as suggested by Westwood (1978)^[12].

$$\text{Fruit set (\%)} = \frac{\text{Number of fruits set}}{\text{Number of flowers}} \times 100$$

Fruit Yield: The yield of dry nuts was recorded in each genotype in terms of kilograms per plant.

Nut characteristics

Nut weight: The average weight of ten randomly collected sun dried nuts from ten genotypes was recorded on electrical balance and expressed in grams.

Nut length: As per UPOV (1988)^[15] method, ten randomly collected nuts were measured with digital Vernier's Calliper and average was calculated, expressed in millimetres.

Nut width: Average of width of ten nuts was worked out as method suggested by UPOV (1988)^[15] and expressed in millimetres.

Shell thickness: The shell thickness of nuts was measured by taking the average shell thickness of ten nuts with the help of Vernier's Calliper and expressed in millimetres.

Kernel weight: The weight of kernel was recorded on the basis of kernel extracted from ten sun-dried nuts and average was calculated expressed in grams.

Kernel width: Data on the width of ten kernels were used for working out the average kernel width with the help of digital Vernier's Calliper.

Kernel percentage: For recording data on kernel percentage on each of the selected genotypes, first weight of ten nuts was taken and then the weight of its kernel was recorded. The kernel percentage was worked out as under:

$$\text{Kernel percentage} = \frac{10 \text{ kernel weight}}{10 \text{ nut weight}} \times 100$$

Results and Discussions

Variability studies

The estimates of average mean performance and genetic variability parameters for yield and its contributing traits were worked out from analysis of variance and are presented in Table 1. In the present study the phenotypic coefficient of variation indicated higher values than genotypic coefficient of

variation for all the traits studied, though with narrow difference for most of the characters. This indicates that these are less influenced by environmental factors. The highest phenotypic coefficient of variation was observed for the characters trunk cross sectional area (50.75%), fruit yield (44.34%) and tree volume(43.05%) followed by moderate values of flower density (28.77%), trunk girth (26.00%), tree height (23.03%), nut weight (21.18%), kernel weight (20.52%), fruit set (16.56%), duration of male flowering (16.01%), duration of female flowering (15.66%) and tree spread (15.33%) indicating the existence of substantial variability pointing ample scope for their improvement through selection. Greater improvement therefore, could be obtained for these characters. Comparatively, low phenotypic coefficient of variation was shown by the characters like shoot length, nut length, nut width, shell thickness, kernel width and kernel percentage. The low variation indicated the highly stable nature of these characters among different genotypes studied and less scope of improvement in these characters. The variability for genotypes under present study for fruit yield which is reflected by means of nut and kernel size and shape given in the Fig.1 and Fig. 2.

The progress of breeding programme is conditioned by the magnitude and nature of genotypic and non-genotypic variation in the various characteristics. Since, most of the economic characters like yield are complex in inheritance and are greatly influenced by the various environmental conditions, the study of heritability and genetic gain is very useful in order to estimate the scope for improvement by selection. Heritability magnitude indicates the reliability with which the genotypes will be recognized by its phenotypic expression. The heritability estimates were high for the characters like tree volume (94.60%), yield per tree (93.90%), trunk girth (90.03%), trunk cross sectional area (88.94%), nut weight (86.35%), kernel weight (84.82%) and flower density (81.74%). High heritability estimates indicated that selection for these characters would be effective being less influenced by the environmental effects. Johanson *et al.* (1955)^[9] impressed that heritability values along with estimation of genetic gain were more useful than heritability value alone in predicting the effect of selection. High heritability coupled with high genetic gain was found for the character tree volume, trunk cross sectional area and fruit yield. Whereas, high heritability coupled with moderate genetic gain was obtained for the characters *viz.*, trunk girth, nut weight and kernel weight which indicated that these characters were under the strong influence of additive gene action and hence simple selection procedure based on phenotypic expression of these traits would be more reliable. These results are in line with the findings of earlier workers Singh *et al.*, (2009)^[16], Ahandani *et al.*, (2014)^[17] and Zhao *et al.*, (2014)^[18].

Table1: Genetic Variability analysis of yield and its contributing traits in walnut genotypes

S. No	Character	Range	Mean± SE(m)	Variance		Coefficient of variation (%)		Heritability (%)	Genetic advance	Genetic gain (%)
				Phenotypic	Genotypic	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)			
1.	Tree height (m)	3.60-6.50	5.05±0.46	1.35	1.04	23.03	20.23	77.12	1.85	36.60
2.	Tree spread (m)	2.88-4.72	4.01±0.27	0.38	0.27	15.33	12.86	70.39	0.89	22.22
3.	Tree volume (m ³)	15.95-73.83	45.04±0.91	375.87	355.57	43.05	41.87	94.60	37.78	83.89
4.	Trunk girth (cm)	27.95-71.90	51.14±3.43	176.86	159.24	26.00	24.67	90.03	24.67	48.23
5.	Trunk cross sectional area (m ²)	0.06-0.41	0.22±0.03	0.01	0.01	50.75	47.86	88.94	0.20	93.12
6.	Shoot length (cm)	10.05-14.73	11.99±0.67	2.75	2.09	13.84	12.06	75.90	2.59	21.64
7.	Duration of male flowering (days)	10.50-18.00	15.25±0.82	5.96	4.71	16.01	14.23	78.94	3.97	26.04

8.	Duration of female flowering (days)	12.00-17.50	14.25±0.93	4.98	3.70	15.66	13.49	74.23	3.41	23.95
9.	Flower density	0.20-0.46	0.30±0.03	0.01	0.01	28.77	26.02	81.74	0.15	48.51
10.	Fruit set (%)	50.9-76.1	62.72±4.20	107.94	81.61	16.56	14.40	75.61	16.18	25.80
11.	Nut weight (g)	7.20-13.00	9.82±0.63	4.32	3.73	21.18	19.68	86.35	3.70	37.67
12.	Nut length (mm)	30.71-43.33	35.32±1.68	24.03	17.56	13.88	11.86	73.06	7.38	20.89
13.	Nut width (mm)	27.98-36.33	31.69±0.97	9.56	5.04	9.76	7.09	52.74	3.36	10.60
14.	Shell thickness (mm)	1.50-1.88	1.64±0.06	0.02	0.01	8.57	5.77	45.37	0.13	7.98
15.	Kernel weight (g)	3.38-6.30	4.72±0.18	0.94	0.80	20.52	18.89	84.82	1.69	35.85
16.	Kernel width (mm)	19.14-28.20	23.61±0.93	11.36	8.64	14.28	12.45	76.01	5.28	22.35
17.	Kernel Percentage (%)	40.63-49.87	45.55±2.37	16.78	8.15	8.99	6.27	48.55	4.10	8.99
18.	Fruit Yield (kg/tree)	1.80-6.00	3.22±0.29	2.04	1.92	44.34	42.97	93.90	2.76	85.75



Fig 1: Variability in nut shape





Fig 2: Variability in kernel shape

Association studies

The variation in correlation coefficient may be due to heterogeneous population having differences in genetic makeup of individual trees. The significant and positive correlation between different pairs can be helpful for genetic improvement of different characters in single step, if the higher or low value of each is required. While the negatively associated characters where increase or decrease in values of both the characters is required cannot be improved in a single step. The characters which had no significant correlation suggest that they are independent of each other. Fruit yield was taken as dependent variable. Genotypic and phenotypic correlation coefficients are presented in Table 2. In general, the genotypic correlation coefficients were higher in magnitude than phenotypic correlation coefficients. The phenotypic correlation coefficients among studied characters showed that yield per tree had positive and significant association with flower density (0.91), fruit set (0.70), trunk girth (0.61), trunk cross sectional area (0.59) and tree spread (0.48), which is in agreement with the results obtained by Bayazit (2012)^[19]. Flower density had positive and significant correlation with fruit set (0.61) and kernel percentage (0.52). These findings are in accordance with the findings of Zhao *et al.*, (2014)^[18], who concluded that walnut growers should

strengthen the tree management so as to expand the tree crown and increase the number of fruiting branches in the cultivation and management practices. Tree height was significantly and positively correlated with tree volume (0.93), tree spread (0.84), and trunk girth (0.60), trunk cross sectional area (0.58), nut length (0.55) and shoot length (0.42). Atefi (1990)^[20] had also reported a positive correlation between

walnut yield and trunk diameter as well as tree height. Zhao *et al.*, (2014)^[18] reported positive correlation of tree height with walnut yield. Tree spread was significantly correlated with tree volume (0.88), trunk girth (0.63), trunk cross sectional area (0.57) and flower density (0.47). Tree volume was significantly correlated with trunk girth (0.66), trunk cross sectional area (0.63) and nut length (0.53). Trunk girth was significantly correlated with trunk cross sectional area (1.00), fruit set (0.56) and flower density (0.47). Trunk cross sectional area was significantly correlated with fruit set (0.55). Shoot length had positive significant correlation with tree height (0.42) and negative significant correlation with duration of male flowering (-0.76). The negative effect of male flowering with shoot length is due to the fact that position of male flowers is at a fixed point, just below the initiation of new growth

Table 2. Phenotypic and genotypic coefficients of correlation among different traits in different walnut genotypes

		X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18
X1	P	0.84*	0.93*	0.60*	0.58*	0.42*	-0.20	-0.11	0.34	0.32	0.27	0.55*	0.30	-0.11	0.42	0.11	-0.04	0.45
	G	0.88*	1.00*	0.71*	0.68*	0.53*	-0.22	0.20	0.36	0.40	0.39	0.67*	0.23	0.03	0.49*	0.14	0.25	0.48*
X2	P		0.88*	0.63*	0.57*	0.20	-0.17	-0.02	0.47*	0.38	0.29	0.46	0.32	0.14	0.32	-0.04	-0.21	0.48*
	G		0.98*	0.81*	0.73*	0.22	0.15	0.12	0.45	0.53*	0.38	0.57*	0.19	0.41	0.35	0.14	-0.36	0.55*
X3	P			0.66*	0.63*	0.37	-0.19	-0.10	0.34	0.35	0.35	0.53*	0.25	-0.01	0.40	0.02	-0.19	0.43
	G			0.71*	0.67*	0.42	-0.22	0.13	0.38	0.44	0.36	0.61*	0.27	0.06	0.44	0.03	-0.27	0.46
X4	P				1.00*	0.09	-0.18	-0.12	0.47*	0.56*	0.01	0.34	-0.10	-0.03	0.07	-0.27	-0.02	0.61*
	G				0.99*	0.15	-0.26	0.15	0.57*	0.70*	-0.02	0.36	0.13	0.06	0.03	-0.31	0.08	0.69*
X5	P					0.12	-0.21	-0.17	0.46	0.55*	-0.04	0.33	-0.16	-0.11	0.04	-0.29	0.04	0.59*
	G					0.18	-0.30	-0.21	0.55*	0.70*	-0.07	0.33	0.22	0.04	0.00	-0.32	0.14	0.68*
X6	P						-0.76*	-0.27	-0.05	-0.24	0.04	0.37	0.15	-0.15	0.06	-0.00	-0.24	0.02
	G						0.82*	0.45	0.10	0.23	0.10	0.46	0.24	0.15	0.13	0.05	0.42	-0.01
X7	P							0.35	-0.18	0.10	0.27	-0.20	0.10	-0.11	0.30	0.37	0.12	-0.15
	G							0.49*	0.13	0.12	0.27	0.20	0.25	0.01	0.36	0.52*	0.32	-0.13

X8	P								0.03	0.23	-0.13	-0.31	0.20	-0.33	-0.16	0.11	0.31	-0.08
	G								0.02	0.31	0.11	0.45	0.27	0.42	0.12	0.06	0.37	-0.12
X9	P									0.61*	-0.17	0.28	-0.15	0.04	-0.08	-0.15	0.52*	0.91*
	G									0.84*	0.15	0.30	0.21	0.11	0.09	0.29	0.65*	0.98*
X10	P										0.14	0.27	0.12	-0.14	0.16	0.01	0.43	0.70*
	G										0.19	0.35	0.14	0.26	0.27	0.08	0.62*	0.79*
X11	P											0.52*	0.73*	0.17	0.88*	0.70*	-0.42	-0.04
	G											0.65*	0.93*	0.20	1.00*	0.80*	0.41	-0.01
X12	P												0.45	0.21	0.50*	0.21	-0.10	0.40
	G												0.68*	0.39	0.70*	0.28	0.24	0.51*
X13	P													0.09	0.64*	0.56*	-0.32	-0.06
	G													0.15	0.85*	0.72*	-0.38	-0.08
X14	P														-0.00	-0.13	-0.38	0.08
	G														-0.02	-0.45	-0.68*	0.17
X15	P															0.74*	-0.26	0.04
	G															0.91*	-0.21	0.08
X16	P																-0.01	-0.11
	G																0.03	-0.15
X17	P																	0.44
	G																	0.54*

X1 = Tree height

X2 = Tree spread

X3 = Tree volume

X4 = Trunk girth

X5 = Trunk cross sectional area

X6 = Shoot length

X7 = Duration of male flowering

X8 = Duration of female flowering

X9 = Flower density

X10 = Fruit set

X11 = Nut weight

X12 = Nut length

X13 = Nut width

X14 = Shell thickness

X15 = Kernel weight

X16 = Kernel width

X17 = Kernel Percentage

X18 = Fruit yield

G = Genotypic correlation values

P = Phenotypic correlation values

(* Significant at 0.05 level)

Nut weight had positive and significant correlation with kernel weight (0.88), nut width (0.73), and kernel width (0.70) and nut length (0.52). Nut length showed positive and significant correlation with kernel weight (0.50), whereas, nut width showed positive and significant correlation with kernel weight (0.64) and kernel width (0.56). Abedi and Parvaneh (2016) [21] also reported positive correlation between kernel weight and fruit weight. Kernel weight showed positive and significant correlation with kernel width (0.74). Sharma and Sharma (2001) [22] observed that the nut weight was significantly and positively correlated with nut width, nut length, kernel weight and kernel width, whereas, nut width with kernel weight and kernel width. Eskandari *et al.*, (2006) [23] found positive correlation between kernel weight and nut weight. Significant correlations between nut weight and nut length, nut width, and kernel weight have also been reported by Arzani *et al.*, (2008) [24].

Correlation study measures the mutual association without regard to causation, so, correlation may not always provide a true picture of association. The association becomes complex when many correlated characters are affecting the particular variable. In such situation, a path coefficient analysis enables to reevaluate the direct effect of one cause on an effect and its indirect effect through other causes. In the present study for path analysis fruit yield per plant was taken as dependent character and other component traits were considered as independent variables. The direct and indirect effects of various traits were worked out from pooled correlation matrix and are presented in Table 3. The direct positive effects towards fruit yield was recorded by the following traits *viz.* flower density (0.85), trunk girth (0.76), tree height (0.61), shoot length (0.42), duration of male flowering (0.41), nut weight (0.22), fruit set (0.21), shell thickness

Table 3: Estimates of direct and indirect effects of different traits on yield of walnut genotypes

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18
X1	<u>0.61</u>	-0.27	-0.56	0.54	-0.34	0.22	-0.09	0.03	0.31	0.08	0.09	-0.08	0.00	0.00	-0.03	-0.03	-0.01	0.48*
X2	0.53	<u>-0.31</u>	-0.55	0.61	-0.36	0.09	-0.06	0.02	0.38	0.11	0.08	-0.07	0.00	0.06	-0.02	0.03	-0.01	0.55*
X3	0.61	-0.30	<u>-0.56</u>	0.53	-0.33	0.17	-0.09	0.02	0.32	0.09	0.08	-0.07	0.00	0.01	-0.02	-0.01	-0.01	0.46
X4	0.43	-0.25	-0.39	<u>0.76</u>	-0.49	0.06	-0.10	0.02	0.48	0.15	0.00	-0.04	0.00	0.01	0.00	0.06	0.00	0.69*
X5	0.41	-0.22	-0.37	0.75	<u>-0.50</u>	0.07	-0.12	0.03	0.47	0.15	-0.02	-0.04	0.00	-0.01	0.00	0.06	0.00	0.68*
X6	0.32	-0.07	-0.23	0.11	-0.09	<u>0.42</u>	-0.33	0.07	-0.09	-0.05	0.02	-0.05	0.00	-0.02	-0.01	-0.01	-0.01	-0.01
X7	-0.13	0.04	0.12	-0.19	0.15	-0.34	<u>0.41</u>	-0.08	-0.11	0.03	0.06	0.02	0.00	0.00	-0.02	-0.10	0.01	-0.13
X8	-0.12	0.04	0.07	-0.11	0.10	-0.19	0.20	<u>-0.16</u>	0.02	0.06	-0.02	0.05	0.00	-0.07	0.01	-0.01	0.01	-0.12
X9	0.22	-0.14	-0.21	0.43	-0.27	-0.04	-0.05	0.00	<u>0.85</u>	0.18	-0.03	-0.03	0.00	0.02	0.01	0.06	0.02	0.98*
X10	0.24	-0.16	-0.25	0.53	-0.34	-0.10	0.05	-0.05	0.71	<u>0.21</u>	0.04	-0.04	0.00	-0.04	-0.02	-0.01	0.02	0.79*
X11	0.24	-0.12	-0.20	-0.01	0.04	0.04	0.11	0.02	-0.13	0.04	<u>0.22</u>	-0.07	0.02	0.03	-0.06	-0.16	-0.01	-0.01
X12	0.41	-0.18	-0.34	0.27	-0.17	0.19	-0.08	0.07	0.26	0.07	0.14	<u>-0.11</u>	0.01	0.06	-0.04	-0.05	-0.01	0.51*
X13	0.14	-0.06	-0.15	-0.10	0.11	0.10	0.10	-0.04	-0.18	0.03	0.20	-0.08	<u>0.02</u>	0.02	-0.05	-0.14	-0.01	-0.08
X14	-0.02	-0.12	-0.03	0.04	0.02	-0.06	0.00	0.07	0.09	-0.06	0.04	-0.04	0.00	<u>0.16</u>	0.00	0.09	-0.02	0.16
X15	0.30	-0.11	-0.24	0.02	0.00	0.06	0.15	0.02	-0.08	0.06	0.22	-0.08	0.01	0.00	<u>-0.06</u>	-0.18	-0.01	0.08
X16	0.08	0.04	-0.02	-0.24	0.16	0.02	0.21	-0.01	-0.25	0.02	0.17	-0.03	0.01	-0.07	-0.05	<u>-0.20</u>	0.00	-0.15
X17	-0.15	0.11	0.15	0.06	-0.07	-0.17	0.13	-0.06	0.56	0.13	-0.09	0.03	-0.01	-0.11	0.01	-0.01	<u>0.03</u>	0.54*

X1= Tree height X2 = Tree spread X3= Tree volume X4=Trunk girth X5 = Trunk cross sectional area X6 = Shoot length X7= Duration of male flowering X8=Duration of female flowering X9 = Flower density X10 = Fruit set X11= Nut weight X12 = Nut length X13 = Nut width X14= Shell thickness X15=Kernel weight X16 = Kernel width X17 = Kernel Percentage X18 = Fruit yield Residual effect =-0.01934Underline figures are direct effect (*Significant at 0.05 level)

(0.16), kernel percentage (0.03) and nut width (0.02). Present results are in agreement with Amiri *et al.* (2010)^[25] and Zhao *et al.* (2014)^[18]. Thus the biggest yield influencing trait is flower density, It illustrates that when flower density add a standard unit the yield can add 0.85 standard units directly. Flower density showed positive indirect effect via trunk girth (0.43), tree height (0.22) fruit set (0.18) and kernel width (0.06), it clarifies that the effect of flower density is more via trunk girth and tree height. Fruit set is the trait that corresponds with dependent character fruit yield had positive indirect effect via flower density (0.71), trunk girth (0.53) and tree height (0.24). Fruit yield in walnut is determined by nut weight which is the edible part, showed indirect effect via tree height (0.24), duration of male flowering (0.11). Further, nut weight depends on nut length and nut width, Nut length depicted positive indirect effect via tree height (0.41), trunk girth (0.27), flower density (0.26), shoot length (0.19), nut weight (0.14), duration of female flowering (0.07), fruit set (0.07) and shell thickness (0.06). Nut width showed positive indirect effect via nut weight (0.20), tree height (0.14), and trunk cross sectional area (0.11), shoot length (0.10) and duration of male flowering (0.10). In some walnut cultivars, there is a problem of empty /blank nuts; in such a situation kernel percentage decides the fruit yield. In the present study kernel percentage depicted positive indirect effect via flower density (0.56), tree volume (0.15), duration of male flowering (0.13), fruit set (0.13), tree spread (0.11). The findings for kernel characters are confirmed in the studies of Bayazit S (2012)^[19], Zhao *et al.*, (2014)^[18] and Abedi and Parvaneh (2016)^[21].

Unexplained effects are treated as residual effects. Low magnitude of residual effect at genotypic level indicated that the traits included in the present investigation accounted for most of the variation present in the dependent variable that is fruit yield per plant. The studies on path coefficient analysis suggested that selection for traits such as flower density, trunk girth, tree height, shoot length, duration of male flowering, nut weight, fruit set, shell thickness, kernel percentage and nut width could be used as selection indices for genetic improvement in walnut.

Conclusions

The present study indicated sufficient genetic variability among genotypes for all the traits studied. The traits trunk cross sectional area, trunk girth, and flower density showed high heritability along with high to moderate genetic gain, thereby, indicating the additive gene action for these traits and hence simple selection procedure based on phenotypic expression of these traits would be more reliable. Beside this, these traits had shown significant and positive phenotypic and genotypic correlation with fruit yield which revealed the inherent relationship among them. Further, the path analysis studies which has allowed the portioning of the correlations between yield and its components into direct and indirect effects confirms the positive direct effect of these physiological and development traits on fruit yield, hence they could serve as selection indices for development of ideotype cultivar in walnut.

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