Received: 02 Sep 2023 | Revised: 11 Mar 2024 | Accepted: 14 Mar 2024

Electronic Journal of Plant Breeding

Research Note

Correlation and path coefficient analyses for some yield-related traits in apple (*Malus domestica* Borkh) under mid-hill conditions of Himachal Pradesh, India

Praveen Verma[1]*, Nirmla Chauhan[2] and Suman Bodh[1]

[1]School of Agriculture, Lovely Professional University, Phagwara, Punjab-14411, India
[2]Dr Yashwant Singh Parmar University of Horticulture & Forestry, Nauni, Solan, (HP)173230, India
***E-Mail:** praveenver2014@gmail.com

Abstract

To understand the utility of genotypes in the breeding program in mid-hill environments of the north-western Himalayas of India, apple cultivars were studied during 2019 and 2020 to discover inter-relationships of variables as well as to study genetic variation across yield attribution traits. For fruit set, fruit drop and fruit volume, high heritability and moderate genetic gain was observed. Substantial correlation between fruit yield per plant and pruning weight, tree volume, tree spread and TSS was observed. However, the increments in tree height and trunk girth were strongly and adversely linked with fruit yield per plant. Thus the traits tree spread, tree volume and flowering length may be used as selection indicators for increased production with high-quality apple cultivars.

Keywords: Apple, Correlation, Genetic variability, Heritability, Path analysis

Apple (*Malus domestica* Borkh.) is one of the most popular fruits of temperate zones in the world and is cultivated extensively in both the Northern and Southern hemispheres (Ebrahimi and Alipour, 2020). The states of Jammu & Kashmir, Himachal Pradesh, and Uttarakhand account for 99 per cent of the India's production of apples, with the remaining 4 per cent is contributed by the states of Arunachal Pradesh, Nagaland, Tamil Nadu, and Sikkim. A total of 1,13,154 acres in Himachal Pradesh are planted with apple, producing 3,68,603 MT of fruit annually (Anonymous 2019). The Himachal Pradesh commercial apple sector is about 60 years old and consists mostly of the delicious group, which accounts for 90 per cent of the types farmed. From the middle of the 1960s through the early 1990s, these cultivars made a considerable contribution to apple production. These kinds, however, began to decline under the scenario of a changing environment because of multiple biotic and abiotic pressures (Verma *et al.,* 2018). Low productivity in apple is caused by several production and protection issues (Singh *et al.,* 2016). These types did not do well in lower pockets or valley regions of the state due to the changing climatic circumstances, particularly in terms of colour development. Low chill cultivars and high colour strains are currently gradually replacing these crops. The region of apple production, on the other hand, has moved to higher altitudes, which is supported by a falling tendency in snowfall over time (Das, 2022). Numerous apple colour strains and varieties have recently been introduced in the state, some of which have thrived in various agro climatic environments. There varieties have numerous potential in the breeding program in mid-hill environments of the North-Western Himalayas of India. Therefore, these cultivars were studied with the objectives to discover inter-relationships of variables as well as to study genetic variation across yield attribution traits.

The current study was conducted at the experimental orchard of HRTS and KVK, Kandaghat, Dr. Yashwant Singh Parmar University of Horticulture and Forestry in Nauni, Solan (H.P.) during two consecutive seasons (2019 and 2020). The experimental material comprised of the apple varieties Early Red One, Scarlet Spur II, Oregon Spur II, Golden Delicious, Granny Smith, Gale Gala, and Gibson Golden that were planted in randomized block design (RBD) with four replications. Five typical fruit samples were collected in four replicates each at the peak of ripeness to examine fruit quality attributes. Before pruning, during dormancy, the growth characteristics like average trunk girth (cm), tree height (m), tree spread (m) and annual shoot growth (cm) were noted using standard procedures. Tree volume (m3) of each replication was calculated using the method recommended by Westwood (1993). An Automatic Leaf Area Metre (Licor Model 3100) was used to measure the area of the leaf, and the results were represented in cm^2. The duration of flowering was measured in days, counting from the first flowering date to the last flowering date. Three weeks after petal fall, fruit set was measured and estimated using Westwood's (1993) recommended formula. Fruit drop was computed by subtracting the total number of fruits retained from the total number of fruit set.

Using a digital Vernier Calliper (Model No. CD-6"CS, Mitutoyo Corp. Japan), fruit length, diameter and pedicle length was measured. Five fruits under four replicates of each cultivar were weighed and the average fruit weight was calculated. With the use of an Effigi penetrometer and a 7/16" plunger in kg/cm2, fruit firmness was determined. Using an Erma hand refractometer (0-32 Brix), the total soluble solids content of fruits was calculated. According to the prescribed protocol of AOAC 1980, the total sugars, reducing sugars, non-reducing sugars were measured. The quantification of ascorbic acid was determined using the methodology described in Bassi *et al.* 2018 and AOAC 2005. Utilizing the Folin-Ciocalteu method, the amount of total phenols was estimated by measuring the absorbance at 650 nm in a spectrophotometer (Singleton and Rossi 1965). By dividing the TSS value by the percent titratable acidity, the TSS/acidity ratio was calculated. When the fruits were harvested, the yield of each cultivar was measured by weighing the entire crop on a top pan balance. The yield was recorded as kilograms per plant. The genotypic and phenotypic coefficients of variation were estimated by following method of Burton and De Vane (1953). The pooled data were statistically analyzed using SPAR 2 to find out different genetic variability, correlation and path coefficient characteristics.

Table 1 lists the estimates of heritability, genetic gain and genotypic and phenotypic coefficients of variation. The disparity between the PCV values and the GCV values can be explained by the environmental effect. Genetic variability studies revealed that yield (80.32%), tree volume (68.29%), pruning weight (65.21%), tree spread (41.64%), trunk girth increment (39.98%) and tree height increment (33.26%) were having high genotypic coefficients of variation (GCV) (**Table 1**), while total phenol (19.46%) and fruit drop (26.99%) registered moderate values. The traits acidity (13.36%), leaf area (10.48%), TSS/acidity ratio (9.97%), ascorbic acid (9.43), and non-reducing sugars (8.96%) all showed low GCV. The phenotypic coefficient of variation (PCV) was high for pruning weight (88.98%), tree volume (86.82%), yield (83.58%), trunk girth increment (48.97%), tree spread (47.53%), tree height increment (37.66%) and fruit drop (27.57%); moderate for flowering duration (24.18%), pedicel length (23.24%), fruit set (22.08%), total phenol (20.35%), acidity (17.07%), TSS/acidity ratio (15.82%) and non-reducing sugars ((15.41%). In general, the GCV and PCV were comparable, with the PCV being slightly greater than PCV indicating the influence of the environment on the expression of the traits. This finding is consistent with the findings of Bandale et al. (2006), Chattopadhay *et al.* (2011) and Rasool *et al.* (2019)

Heritability estimates were also calculated for fruit and tree traits in the broad sense. Heritability was observed to range from 30.29 to 98.56%. Fruit set (98.56%), fruit drop (95.86%), yield (92.33%), TSS (91.99%), total phenol (91.49%), leaf area (90.66%), fruit volume (86.11%), flowering duration (85.07%), pedicel length (82.30%), firmness (80.36%), tree height increment (77.98%), tree spread (76.75%), trunk girth increment (66.65%), tree volume (61.86%), fruit weight (61.68%) and acidity (61.26%) showed high heritability. Moderate heritability was observed for L/D ratio (43.69 %) and reducing sugars (55.58%) whereas, low heritability was recorded for traits like fruit length (30.29%) and TSS / acid ratio (39.75%). The traits with high and moderate heritability are less influenced by the environment and could be selection based on these traits could yield better results (Ahandani *et al.,* 2014; Barua and Sharma 2004). Among the traits studied, genetic gain varied from 3.12% to 98.98%. It scored high for yield (98.98%) followed by tree volume (98.64%), pruning weight (98.46%), tree spread (75.15%), trunk girth increment (67.23%) and tree height increment (60.50%). For fruit set (44.83%), flowering time (42.37%), pedicel length (39.39%) and total phenol content (38.35%), it was shown to be moderate. Titratable acidity (21.55%), fruit volume (20.69%), leaf area (20.56%), fruit weight (18.17%), TSS (15.82%), ascorbic acid (13.80%) and fruit diameter (3.12%) all showed low genetic gain. Johanson *et al.* (1955) indicated that estimates of genetic gain were more helpful in forecasting the impact of selection than heritability values alone in predicting the effect of selection. Rasool *et al.* (2019) provided support for the results, reporting significant heritability and high genetic gain for various metrics in apples. High heritability coupled with moderate genetic gain indicate that these traits were under the strong influence of additive gene action and hence simple selection procedure based on phenotypic expression of these characters would be more reliable (Fanizza *et al.,* 2005; Sabesan *et al.,* 2009).

Table 1. Variability parameters of tree, flowering and fruit characteristics of different apple cultivars

Parameters	Coefficient of variation (%)		Heritability (%)	Genetic advance	Genetic gain (%)
	Genotypic	Phenotypic			
Tree height increment	33.26	37.66	77.98	8.30	60.50
Tree spread	41.64	47.53	76.75	0.85	75.15
Tree volume	68.29	86.82	61.86	2.76	98.64
Trunk girth increment	39.98	48.97	66.65	3.18	67.23
Pruning weight	65.21	88.98	53.72	0.89	98.46
Leaf area	10.48	11.01	90.66	7.55	20.56
Flowering duration	22.30	24.18	85.07	6.23	42.37
Fruit set	21.92	22.08	98.56	33.14	44.83
Fruit drop	26.99	27.57	95.86	25.37	54.44
Fruit length	3.53	6.41	30.29	2.41	4.00
Fruit diameter	2.04	2.75	55.09	2.09	3.12
L/D ratio	3.02	4.57	43.69	0.04	4.11
Fruit weight	11.23	14.30	61.68	24.20	18.17
Fruit volume	10.82	11.66	86.11	30.68	20.69
Pedicel length	21.08	23.24	82.30	0.73	39.39
Firmness	3.75	4.19	80.36	0.97	6.93
TSS	8.01	8.35	91.99	1.63	15.82
Acidity	13.36	17.07	61.26	0.16	21.55
TSS/acidity ratio	9.97	15.82	39.75	1.80	12.95
Total sugars	2.75	4.45	38.34	0.32	3.51
Reducing sugars	4.99	6.69	55.58	0.45	7.66
Non reducing sugars	8.96	15.41	33.86	0.34	10.75
Ascorbic acid	9.43	13.27	50.51	0.97	13.80
Total phenol	19.46	20.35	91.49	21.40	38.35
Yield	80.32	83.58	92.33	6.58	98.98

The estimates of genotypic and phenotypic correlation among different traits are furnished in **Table 2**. Generally, genotypic correlation coefficients were stronger than phenotypic correlation coefficients in terms of magnitude. According to the genotypic correlation coefficients for the studied traits, yield exhibited the most positive link with pruning weight (0.99), tree volume (0.96), tree spread (0.84), leaf area (0.69) and TSS (0.60), which is consistent with earlier findings (Bayazit, 2012). This strong correlation suggests that yield can be improved by improving these attributes (Barua and Sharma, 2004). In a study on walnuts, Dogra *et al.* (2018) also found a positive correlation between fruit weight and fruit length (0.98); fruit diameter (0.87) and leaf area (0.52). Fruit length (0.82) was observed to have a positive and significant association with leaf area (0.62), and fruit set showed a positive and significant correlation with flowering duration (0.70). Fruit length and fruit diameter had a positive and substantial association. This indicates that yield can be enhanced by selecting trees with fruit with higher dimensions and weight. Typically, genotypic correlations had a higher significance than phenotypic correlations (**Table 2**). This suggests that there are innate correlations between many qualities and that the environment did not significantly alter these correlations. At the genotypic level, there were strong and favourable associations between fruit weight and length. Additionally, at both the phenotypic and genotypic levels, there was a positive and highly significant association between fruit diameter and weight. There is evidence to suggest that fruit length and weight were positively correlated. Therefore, choosing germplasm with characteristics likes fruit length, fruit diameter and leaf area would be useful for achieving increased fruit weight. A strong correlation between yield and the fruit's weight and dimensions reported by various workers supported the current findings (Bayazit, 2012; Gopinath and Vethamoni 2017).

Correlation studies may not always adequately portray correlations since they evaluate reciprocal associations without accounting for reasons. The link becomes complex when multiple interconnected features influence a particular variable. A path coefficient analysis in this situation enables a revaluation of the direct impact of one

https://doi.org/10.37992/2024.1501.029

Table 2. Genotypic and Phenotypic coefficients of correlation among different traits in apple cultivars

		2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
1	G	-0.92*	-0.87*	0.86*	-0.70*	-0.93*	-0.22	0.02	-0.23	-0.54*	-0.35	-0.43	-0.43	-0.50*	-0.87*	0.05	-0.49*	0.36	-0.69*	0.04	0.03	0.00	0.16	-0.07	-0.86*
	P	-0.78*	-0.72*	0.71*	-0.51*	-0.81*	-0.14	0.00	-0.15	-0.32	-0.18	-0.38	-0.35	-0.49*	-0.73*	-0.00	-0.43	0.20	-0.29	0.00	0.00	0.00	0.15	-0.06	-0.73*
2	G		0.95*	-1.00*	0.72*	0.84*	0.28	-0.05	-0.03	0.22	-0.16	0.39	0.12	0.13	0.99*	0.22	0.39	-0.43	0.73*	0.14	-0.21	0.32	-0.57*	0.20	0.84*
	P		0.89*	-0.86*	0.60*	0.72*	0.26	-0.03	-0.04	0.22	-0.08	0.33	0.07	0.15	0.74*	0.20	0.32	-0.33	0.43	-0.02	-0.09	0.06	-0.30	0.14	0.68*
3	G			-0.86*	0.89*	0.82*	0.22	-0.03	0.27	-0.14	-0.19	0.01	-0.01	0.23	0.89*	0.18	0.59*	-0.11	0.46	0.22	0.05	0.14	-0.78*	0.18	0.96*
	P			-0.72*	0.78*	0.62*	0.21	-0.01	0.20	0.06	-0.08	0.10	-0.10	0.24	0.55*	0.13	0.46	-0.03	0.16	0.05	0.06	-0.00	-0.28	0.15	0.68*
4	G				-0.60*	-0.87*	-0.50*	-0.07	0.19	-0.36	0.27	-0.66*	-0.25	0.01	-0.96*	-0.17	-0.09	0.68*	-0.85*	-0.05	0.33	-0.37	0.43	-0.14	-0.75*
	P				-0.48	-0.67*	-0.42	-0.06	0.16	-0.33	0.07	-0.47	-0.11	-0.00	-0.65*	-0.23	-0.16	0.46	-0.49*	0.19	0.09	0.08	0.27	-0.13	-0.63*
5	G					0.58*	0.42	0.42	0.71*	-0.48*	-0.35	-0.30	-0.15	0.18	0.62*	-0.01	0.67*	0.30	-0.01	0.14	0.11	0.01	-0.92*	-0.25	1.06*
	P					0.43	0.34	0.29	0.51*	-0.16	-0.01	-0.17	-0.17	0.20	0.27	0.03	0.52*	0.24	-0.08	0.13	0.21	-0.06	-0.34	-0.19	0.70*
6	G						0.41	-0.07	0.11	0.62*	0.25	0.58*	0.52*	0.48	0.64*	-0.16	0.15	-0.49*	0.63*	-0.20	0.25	-0.41	-0.03	0.35	0.69*
	P						0.38	-0.06	0.09	0.36	0.21	0.46	0.46	0.47	0.55*	-0.14	0.15	-0.38	0.37	-0.13	0.16	-0.23	0.08	0.30	0.62*
7	G							0.70*	0.11	0.16	-0.44	0.52*	0.23	-0.26	0.08	-0.21	-0.39	-0.40	0.19	-0.31	0.06	-0.32	-0.20	-0.26	0.42
	P							0.64*	0.10	0.01	-0.26	0.24	0.10	-0.24	-0.02	-0.22	-0.34	-0.30	0.09	-0.26	0.04	-0.23	-0.11	-0.23	0.36
8	G								0.36	-0.36	-0.45	-0.06	-0.25	-0.41	-0.07	-0.48	0.08	0.04	-0.03	0.24	0.06	0.15	-0.41	-0.72*	0.35
	P								0.35	-0.19	-0.34	-0.01	-0.17	-0.36	-0.04	-0.43	0.08	0.05	-0.04	0.14	0.04	0.08	-0.31	-0.68*	0.34
9	G									-0.41	0.29	-0.63*	0.05	0.54*	-0.17	-0.25	0.56*	0.82*	-0.76*	-0.10	0.41	-0.49*	-0.20	-0.46	0.54*
	P									-0.27	0.23	-0.45	0.03	0.49*	-0.15	-0.19	0.52*	0.63*	-0.45	-0.04	0.32	-0.28	-0.13	-0.42	0.51*
10	G										0.82*	0.94*	1.15*	0.51*	0.32	-0.01	-0.47	-0.89*	0.72*	-0.80*	-0.25	-0.43	1.01*	0.17	-0.05
	P										0.43	0.81*	0.59*	0.36	0.23	0.06	-0.26	-0.40	0.28	-0.29	-0.28	-0.02	0.38	0.13	0.02
11	G											0.29	0.87*	0.98*	-0.03	-0.13	0.11	0.12	-0.16	-0.57*	0.08	-0.57*	0.87*	0.03	-0.02
	P											0.03	0.59*	0.72*	-0.14	-0.00	0.09	0.09	-0.08	-0.27	0.07	-0.28	0.57*	0.04	-0.05
12	G												0.77*	-0.02	0.40	-0.01	-0.60*	-1.10*	0.92*	-0.57*	-0.39	-0.11	0.52*	0.17	0.02
	P												0.50*	0.09	0.40	0.07	-0.39	-0.64*	0.48*	-0.20	-0.26	0.04	0.30	0.11	0.07
13	G													0.69*	0.04	0.04	-0.36	-0.39	0.13	-0.98*	-0.07	-0.76*	0.93*	0.04	0.09
	P													0.64*	0.12	0.05	-0.32	-0.26	0.09	-0.52*	-0.20	-0.26	0.44	-0.01	0.11
14	G														0.04	-0.07	0.32	0.28	-0.24	-0.50*	0.33	-0.74*	0.55*	0.13	0.30
	P														0.09	-0.03	0.25	0.23	-0.19	-0.30	0.15	-0.35	0.36	0.12	0.29
15	G															0.30	0.48	-0.44	0.80*	0.19	-0.46	0.61*	-0.47	0.01	0.70*
	P															0.25	0.38	-0.38	0.56*	0.17	-0.34	0.39	-0.39	0.03	0.66*
16	G																-0.14	0.04	-0.17	-0.56*	-0.87*	0.38	-0.21	-0.03	0.03
	P																-0.11	0.06	-0.09	-0.26	-0.52*	0.19	-0.12	-0.05	0.07
17	G																	0.53*	-0.03	0.72*	0.14	0.48	-0.60*	-0.20	0.60*
	P																	0.42	-0.01	0.34	0.18	0.13	-0.40	-0.20	0.56*
18	G																		-0.87*	0.11	0.35	-0.26	-0.24	-0.34	0.07
	P																		-0.89*	0.08	0.07	0.01	-0.20	-0.30	0.05
19	G																			0.43	-0.34	0.70*	-0.10	0.33	0.19
	P																			0.13	0.02	0.09	0.01	0.25	0.13
20	G																				0.41	0.45	-0.76*	0.10	0.04
	P																				0.18	0.66*	-0.27	0.11	-0.03
21	G																					-0.63*	0.11	0.49*	-0.04
	P																					-0.62*	0.10	0.35	-0.03
22	G																						-0.75*	-0.39	0.07
	P																						-0.30	-0.17	0.00
23	G																							0.24	-0.59*
	P																							0.17	-0.45
24	G																								-0.29
	P																								-0.28

1-Tree height increment 2- Tree spread 3- Tree volume 4- Trunk girth increment 5- Pruning weight 6- Leaf area 7- Flowering duration 8- Fruit set 9- Fruit drop 10- Fruit length 11- Fruit diameter. 12- L/D ratio 13- Fruit weight 14- Fruit volume 15-Pedicel length 16- Firmness 17- TSS 18- Acidity 19- TSS/acidity ratio 20- Total sugars 21- Reducing sugars 22- Non-reducing sugars . 23- Ascorbic acid 24- Total phenol 25-Yield

** Significant at 0.05 %

Table 3. Estimates of direct and indirect effects of different traits on yield of apple cultivars

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
1	**0.06**	0.11	0.08	-0.29	0.04	-0.19	-0.10	0.00	-0.05	-0.15	0.14	0.20	-0.09	-0.02	-0.62	0.01	-0.10	0.12	-0.05	0.42	-0.38	-0.02	0.03	0.01	-0.86
2	-0.05	**-0.12**	-0.09	0.33	-0.04	0.17	0.13	0.00	-0.01	0.06	0.06	-0.18	0.03	0.00	0.72	0.04	0.08	-0.15	0.05	0.36	0.35	-0.77	-0.10	-0.04	0.84
3	-0.05	-0.11	**-0.09**	0.29	-0.05	0.17	0.10	0.00	0.06	-0.04	0.08	0.00	0.00	0.01	0.64	0.03	0.12	-0.04	0.03	0.70	-0.52	-0.20	-0.13	-0.03	0.96
4	0.05	0.12	0.08	**-0.33**	0.03	-0.18	-0.23	0.00	0.04	-0.10	-0.11	0.30	-0.05	0.00	-0.69	-0.03	-0.02	0.23	-0.06	-0.54	-0.30	0.95	0.07	0.03	-0.75
5	-0.04	-0.08	-0.08	0.20	**-0.05**	0.12	0.19	-0.02	0.15	-0.14	0.14	0.14	-0.03	0.01	0.45	0.00	0.14	0.10	0.00	0.43	-0.26	-0.17	-0.16	0.05	1.06
6	-0.05	-0.10	-0.08	0.29	-0.03	**0.21**	0.19	0.00	0.02	0.17	-0.10	-0.27	0.11	0.02	0.46	-0.03	0.03	-0.17	0.04	-0.41	-0.35	0.79	0.00	-0.07	0.69
7	-0.01	-0.03	-0.02	0.17	-0.02	0.09	**0.46**	-0.04	0.02	0.05	0.17	-0.24	0.05	-0.01	0.06	-0.04	-0.08	-0.14	0.01	-0.14	-0.73	0.83	-0.04	0.05	0.43
8	0.00	0.01	0.00	0.02	-0.02	-0.01	0.32	**-0.06**	0.08	-0.10	0.18	0.03	-0.05	-0.02	-0.05	-0.09	0.02	0.02	0.00	0.89	-0.64	-0.23	-0.07	0.13	0.35
9	-0.01	0.00	-0.03	-0.07	-0.04	0.02	0.05	-0.02	**0.21**	-0.12	-0.12	0.29	0.01	0.02	-0.12	-0.04	0.11	0.28	-0.05	-0.02	-0.62	0.73	-0.03	0.09	0.55
10	-0.03	-0.03	0.01	0.12	0.02	0.13	0.07	0.02	-0.09	**0.28**	-0.32	-0.43	0.25	0.02	0.23	0.00	-0.10	-0.31	0.05	-0.79	0.32	0.38	0.17	-0.03	-0.05
11	-0.02	0.02	0.02	-0.09	0.02	0.05	-0.20	0.03	0.06	0.23	**-0.40**	-0.14	0.19	0.04	-0.02	-0.02	0.02	0.04	-0.01	-0.34	-0.35	0.71	0.15	-0.01	-0.02
12	-0.02	-0.05	0.00	0.22	0.02	0.12	0.24	0.00	-0.14	0.27	-0.12	**-0.46**	0.17	0.00	0.29	0.00	-0.12	-0.38	0.06	-0.27	0.10	0.22	0.09	-0.03	0.02
13	-0.02	-0.01	0.00	0.08	0.01	0.11	0.11	0.01	0.01	0.33	-0.34	-0.35	**0.22**	0.03	0.03	0.01	-0.07	-0.13	0.01	-0.88	0.40	0.46	0.16	-0.01	0.09
14	-0.03	-0.01	-0.02	0.00	-0.01	0.10	-0.12	0.02	0.12	0.14	-0.39	0.01	0.15	**0.04**	0.03	-0.01	0.07	0.10	-0.02	-0.02	-0.70	0.78	0.09	-0.02	0.30
15	-0.05	-0.12	-0.08	0.32	-0.03	0.13	0.04	0.00	-0.04	0.09	0.01	-0.18	0.01	0.00	**0.72**	0.05	0.10	-0.15	0.06	0.33	0.40	-7.83	-0.08	0.00	0.70
16	0.00	-0.03	-0.02	0.06	0.00	-0.03	-0.10	0.03	-0.05	0.00	0.05	0.01	0.01	0.00	0.21	**0.18**	-0.03	0.01	-0.01	-0.57	0.79	-0.45	-0.04	0.01	0.03
17	-0.03	-0.05	-0.05	0.03	-0.03	0.03	-0.18	0.00	0.12	-0.13	-0.04	0.28	-0.08	0.01	0.34	-0.03	**0.20**	0.18	0.00	0.76	-0.54	-0.14	-0.10	0.04	0.60
18	0.02	0.05	0.01	-0.23	-0.02	-0.10	-0.18	0.00	0.18	-0.25	-0.05	0.51	-0.08	0.01	-0.32	0.01	0.11	**0.34**	-0.06	0.26	-0.67	0.52	-0.04	0.06	0.07
19	-0.04	-0.09	-0.04	0.28	0.00	0.13	0.09	0.00	-0.16	0.20	0.06	-0.42	0.03	-0.01	0.58	-0.03	-0.01	-0.30	**0.07**	0.31	0.49	-0.87	-0.02	-0.06	0.20
20	0.00	-0.02	-0.02	0.02	-0.01	-0.04	-0.14	-0.01	-0.02	-0.23	0.23	0.26	-0.21	-0.02	0.14	-0.10	0.15	0.04	0.03	**0.74**	-0.59	-0.30	-0.13	-0.02	0.04
21	0.00	0.02	0.00	-0.11	-0.01	0.05	0.03	0.00	0.09	-0.07	-0.03	0.18	-0.02	0.01	-0.33	-0.16	0.03	0.12	-0.02	0.09	**-0.29**	0.46	0.02	-0.09	-0.04
22	0.00	-0.04	-0.01	0.12	0.00	-0.08	-0.15	-0.01	-0.10	-0.12	0.22	0.05	-0.16	-0.03	0.44	0.07	0.10	-0.09	0.05	0.52	0.14	**-0.79**	-0.13	0.07	0.07
23	0.01	0.07	0.07	-0.14	0.05	-0.01	-0.09	0.02	-0.04	0.28	-0.34	-0.24	0.20	0.02	-0.34	-0.04	-0.12	-0.08	-0.01	-0.64	-0.22	0.86	**0.17**	-0.05	-0.60
24	0.00	-0.02	-0.02	0.05	0.01	0.07	-0.12	0.04	-0.10	0.05	-0.01	-0.08	0.01	0.01	0.01	-0.01	-0.04	-0.12	0.02	0.98	-0.63	0.65	0.04	**-0.19**	-0.29

1-Tree height increment 2- Tree spread 3- Tree volume 4- Trunk girth increment 5- Pruning weight 6- Leaf area 7- Flowering duration 8- Fruit set 9- Fruit drop 10- Fruit length 11- Fruit diameter. 12- L/D ratio 13- Fruit weight 14- Fruit volume 15-Pedicel length 16- Firmness 17- TSS 18- Acidity 19- TSS/acidity ratio 20- Total sugars 21- Reducing sugars 22- Non-reducing sugars . 23- Ascorbic acid 24- Total phenol 25-Yield. Residual effect =0.07

factor as well as the indirect impact of that factor through additional variables. Fruit yield per plant was used as a dependent variable for path analysis in the current study and other component features were taken into account as independent variables. From a pooled correlation matrix, the direct and indirect impacts of various attributes were calculated and are furnished in **Table 3**. Total sugars (0.98), pedicel length (0.72), flowering duration (0.46), acidity (0.34), fruit length (0.28), fruit weight (0.22), leaf area (0.21), fruit drop (0.21), firmness (0.18) and total phenol (0.17) all had direct favourable influence on fruit production. Fruit weight (0.33), total phenols (0.28), L/D ratio (0.27), fruit diameter (0.23) and leaf area (0.17) revealed a positive indirect influence of flowering time, indicating that fruit weight is the main factor in the effect of flowering length. Tree volume (0.96), pruning weight (0.99), tree spread (0.84), fruit set (0.35), fruit drop (0.55), flowering length (0.43) and leaf area (0.69) all had an indirect impact on fruit production. Numerous investigations have supported the conclusions regarding fruit characteristics (Abedi and Parvaneh 2016; Kumar and Shekhawat 2013). The genetic makeup of the studied cultivars, the site, and the various agro climatic conditions may have contributed to the varied positive and negative correlations found in this study. Orchard management techniques may have had an individual or collective impact on the performance of the cultivar and the resulting correlations (Rasool *et al.,* 2019).

Unexplained effects are treated as residual effects. Given the modest magnitude of residual impact at the genotypic level, the characteristics taken into consideration in this study accounted for most of the variance in the dependent variable, which is fruit yield per plant. Studies on path coefficient analysis revealed flowering time, tree volume, fruit weight, fruit set, leaf area, L/D ratio and fruit length could be used as selection indices for genetic improvement in apples.

The present investigation revealed that genotypes exhibit sufficient genetic diversity to explain every trait studied. A simple selection strategy based on phenotypic expression of these attributes would be more accurate because high heritability and high to moderate genetic gain for the parameters like flowering duration, fruit set, and yield showed additive gene action for these traits. Additionally, research has demonstrated the inherent association between these characteristics and fruit yield, showing strong and positive phenotypic and genotypic correlation. The positive direct effect of these physiological and growth traits on fruit yield is further confirmed by path analysis, which allowed the portioning of correlations between yield and its components into direct and indirect effects. As a result, they could serve as selection indices for the development of apple cultivars.

ACKNOWLEDGEMENT

The Dr. YS Parmar University of Horticulture and Forestry, Solan (HP) is highly acknowledged for providing all the assistance to conduct this research trial.

REFERENCES

A.O.A.C. 1980. Association of Official Analytical Chemists. In *Official Methods of Analysis* (ed. Hortwitz, W.), 13th ed. Washington, D.C. 1015 p.

A.O.A.C. 2005. Vitamin C in Juices and Vitamin Preparations. In *Proceedings of the 18th AOAC Official Methods of Analysis* (Gaithersburg, MD: Association of Official Analytical Chemists.

Abedi, B. and Parvaneh, T. 2016. Study of correlations between horticultural traits and variables affecting kernel percentage of walnut (*Juglans regia* L.). *Journal of Nuts*, **7**: 35-44.

Ahandani, E.A., Ramandi, A.D., Sarmad, J., Samani, M.A., Yavari, A. and Ahandani, R.A. 2014. Evaluation of morphological diversity among some Persian walnut accessions (*Juglans regia* L.) in Guilan, Northern Iran. *International Journal of Plant Biology and Research*, **2**: 10-15.

Anonymous. 2019. Horticulture development in Himachal Pradesh at a glance. www.hpagrisnet.gov.in

Bandale, V.W., Palsuledesai, M.R., Bhave, S.G., Sawant, S.S. and Desai, S. 2006. Genetic evaluation of some economical traits in chilli (*Capsicum annuum* L.) in Konkan region of Maharashtra. *Crop Research Hissar,* 31: 401-403.

Barua, U. and Sharma, R.K. 2004. Correlation and path analysis studies in apple. *Indian Journal of Horticulture,* **61** (1): 18-23.

Bassi, M., Lubes, G., Bianchi, F., Agnolet, S., Ciesa, F. and Brunner, K. 2018. Ascorbic acid content in apple pulp, peel, and monovarietal cloudy juices of 64 different cultivars. *International Journal of Food Properties,* **20**, S2626–S2634. [Cross Ref]

Bayazit, S. 2012. Determination of relationships among kernel percentage and yield characteristics in some Turkish walnut genotypes by correlation and path analysis. *Journal of Animal and Plant Sciences*, **22**: 513-517.

Burton, G.W. and De Vane, E.H. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, **54**: 478-481. [Cross Ref]

Chattopadhyay, A., Sharangi, A.B., Dai, N.S. and Dutta, S. 2011. Diversity of genetic resources and genetic association analysis of green and dry chillies of eastern India. *Chilean Journal of Agricultural Research,* 71: 350-356. [Cross Ref]

Das, P.V. 2022. People's climate knowledge versus scientists' climate knowledge: a study of apple farming communities in Western Himalayas, India. *GeoJournal,* **87**: 2227–2238. [Cross Ref]

Dogra, R.K., Sharma, S. and Sharma, D.P. 2018. Heritability estimates, correlation and path coefficient analysis for fruit yield in walnut (*Juglans regia* L.). *Journal of Pharmacognosy and Phytochemistry,* **7**(2): 3707-3714.

Ebrahimi, A. and Alipour, H. 2020. Screening of wild superior apple genotypes in north and northeast of Iran using multivariate analysis. *Euphytica,* **216**, 136. [Cross Ref]

Fanizza, G., Lamaj, F. and Costantini, L. 2005. QTL analysis for fruit yield components in table grapes (*Vitis vinifera*). *Theorotical and Applied Genetics,* **111**: 658–664. [Cross Ref]

Gopinath, P. and Vethamoni, P.I. 2017. Genetic variability, correlation and path coefficient analysis in F_2 segregating populationin tomato (*Solanum lycopersicum* L.). *Madras Agricultural Journal*, **04**: 76-80. [Cross Ref]

Johanson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimates of genetic and environment variability in soyabean. *Agroomy Journal,* **47**: 314-318. [Cross Ref]

Kumar, M. and Shekhawat, S.S. 2013. Correlation and path coefficient studies in barley Hordeum vulgare L. under dual purpose condition. *Electronic Journal of Plant Breeding*, **44**: 1313-1318.

Mratinic, E., Rakonjac, V. and Milatović, D. 2007. Genetic parameters of yield and morphological fruit and stone properties in apricot. *Genetika,* 39: 315-324. [Cross Ref]

Rasool, M.A., Bhat, K.M., Rehman, H.U., Mir, M.A., Shikari, A. and Pandit, A.H. Genetic variability, heritability and correlation studies in apple (*Malus* × *domestica* Borkh) cultivars of Kashmir valley. *Journal of Experimental Biology and Agricultural Sciences*, 7(2):148-155.

Sabesan, T., Suresh, R. and Saravanan, K. 2009. Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline low land of Tamilnadu. *Electronic Journal of Plant Breeding*, **1**: 56-59.

Singh, N., Sharma, D.P. and Chand, H. 2016. Impact of Climate Change on Apple Production in India: A Review. *Current World Environment*, **11**(1):251-259. [Cross Ref]

Singleton, V.L. and Rossi, J.A. 1965. Colorimetry of total phenolics with phosphomolybedic phosphotungstic acid reagents. *American Journal of Enology and Viticulture,* **16**: 144-158. [Cross Ref]

Verma, P., Thakur, B.S. and Chauhan, N. 2018. Performance of Some Apple (*Malus* × *domestica* Borkh.) Cultivars for Fruit Quality Traits under Mid Hill Conditions of Himachal Pradesh, India. *International Journal of Current Microbiology and Applied Sciences*, 7: 788-793. [Cross Ref]

Westwood, M.N. 1993. Plant efficiency: growth and yield measurements. In: Temperate Zone Pomology. WH Freeman and company (San Francisco). pp.275-282.