



## DETERMINING RELATIONSHIPS BETWEEN DIFFERENT HORTICULTURAL TRAITS IN (*Cucumis sativus* L.) GENOTYPES WITH MULTIVARIATE ANALYSIS

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### SUMMARY

The objective of this study was to determine the relationships among fruit yield, fruit yield components and morphological traits using 20 different genotypes of cucumber. Total fruit yield per pickling (TFY)(g), fruit number per pickling (FNP), branch number per plant (BP), plant height (PH) (cm), the length of branch (LB) (cm), shoot diameter (SHD) (cm), leaf length (LL) (cm), leaf width (LW) (cm), fruit diameter (FD) (cm), fruit length (FL) (cm), vigor of plant (VP), fruit number per node (FNN), and distance between node (DN) (cm) were measured on genotypes. Results of correlation analysis was indicative of importance of fruit number for predicting of fruit yield in cucumber and there was a significant correlation between TFY and FNP ( $r = 0.7^{**}$ ). Stepwise linear regression showed that 49% of the total variation in fruit yield could be explained by variation in fruit number per plant. Therefore it could be concluded that fruit number per plant is the most suitable selection indices for improvement of fruit yield in cucumber. Based on factor analysis, four factors related to plant shape, shoot characters, fruit yield and fruit number were recognized. According to path analysis, among considered traits (FNP, LL, DN and BP), FNP had the greatest positive effect on TFY. Overall, highly significant and positive correlation coefficients as well as high direct effects of fruit number on fruit yield indicated that this trait is simultaneously the most reliable component for selecting high fruit yielding cucumber genotypes.

**Keywords:** Cucumber, correlation, fruit yield, path analysis

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### INTRODUCTION

Cucumber (*Cucumis sativus* L.) is one of the most important cucurbits that grown as a salad (Arankumar *et al.*, 2011). Cucumber has originated in India or China. It is a member of the *Cucurbitaceae* family (Harlan, 1975). The crop is grown throughout the world and is the fourth most important vegetable crop after tomato, cabbage, and onion (Tatlioglu, 1993).

Cucumber is grown as a number of different types that used for fresh or processed vegetables (Shetty and Wehner, 2002). The final aim of cucumber breeding is improvement of fruit yield (Wehner *et al.*, 1989).

Multivariate analysis such as principle component analysis (PCA), factor analysis (FA) and stepwise regression could be used to measure genetic diversity in a collected germplasm (Johnson and Wichern, 1988). PCA

is a multivariate technique that analyzes a series of data which observations are described by several inter-correlated quantitative dependent variables (Abdi and Williams, 2010). Factor analysis (FA) is a statistical method used to describe variability among observed, in terms of a potentially lower number of unobserved, uncorrelated variables called factors (Johnson and Wichern, 1988). Factor analysis has been done in cucumber lines to evaluate cold tolerance based on growth, physiological and biochemical indexes at seedling stage (Dan-dan *et al.*, 2009).

Stepwise regression analysis is used to distinguish the percentage of more important traits that had significant association with fruit yield. Path analysis determines the relative importance of direct and indirect effects of fruit yield components on fruit yield (Li, 1975). Correlation and path analysis furnish information regarding the nature and magnitude of various association and help in measurement of direct effect of one variable on other (Chandra *et al.*, 2010). In path analysis, multiple regression analysis is used to calculate the partial regression coefficients (path coefficients) for each yield component and its effect on independent variable such as fruit yield. In most studies involving path analysis, researchers considered the predictor characters as first-order variables to analyze their effects over a dependent or response variable such as yield (Bhagowati and Saikia, 2003; Tunçtürk and Çiftçi, 2005). This approach might result in multicollinearity for variables, particularly when correlations among some of the characters are high. There may also be difficulties in interpretation of the actual contribution of each variable, as the effects are mixed or confounded because of colinearity (Samonte *et al.*, 1998).

Path analysis has been done in cucumber (Cramer and Wehner, 2000; Chandra *et al.*, 2010; Arunkumar *et al.*, 2011). The objective of this study was to determine the relationships between some horticultural traits with fruit yield as selection criteria in some cucumber genotypes with different multivariate analysis.

## MATERIALS AND METHODS

This experiment was conducted at Research Greenhouse of Agricultural Department of Islamic Azad University, Khorasgan (Isfahan) Branch, in Iran, (51 ° 36' longitudes and 32°63'). Genotypes were planted in March 2011 for the spring season, in pitmas, perlite, cocopit bed. The experiment was conducted as a randomized complete block design (RCBD) with 4 replications. There were 10 plants in every plot. In this study 20 genotypes from different geographical regions of world were evaluated that their name is presented in Table 1. Studied traits were measured on 10 plants for each genotype in each replication and used from average of them in analysis.

### Cultural practices

The space between and within couple rows were 90 (cm) and 50 (cm), respectively, and 180 (cm) between every couple rows. Irrigation was applied when needed. Dichlorvos, Trigard, Vertimec and Organic neem oil were applied for insect control. The greenhouse air temperature at the growing period was 25-30 °C day / 19-21 °C nights with a relative humidity of about 60%.

Different horticultural traits including: total fruit yield per pickling (TFY; g), fruit number per pickling (FNP), branch number per plant (BP), plant height (PH; cm), the length of branch (LB; cm), shoot diameter (SHD; cm), leaf length (LL; cm), leaf width (LW; cm), fruit diameter (FD; cm), vigor of each plant (VP), fruit number per node (FNN), distance between internode (DN; cm) and fruit length (FL; cm) were measured on 20 different genotypes of cucumber.

Plant height was measured from soil surface to the tip after final harvest. The length of nodes per vine on the main stem was measured from node number 10 to number 20. Number of branch per plant, length of branch and vigor of plant was rated on a 1 to 4 scale at the time of harvesting, based on the least to the most number and vigor in each plant. Length of 15 fruits harvested randomly in 5 days on 3 fruit in each day at edible maturity was recorded from base to the apex of fruit and averaged. Diameter

of the same 15 fruits selected for recording the length, was measured at maximum thickness (cm) with the help of vernier caliper. Length of leaf was measured from dom to tip and width of leaf was recorded at maximum point. The number of fruit per node was recorded based on more than 75% on nodes.

### Statistical analysis

The collected data were subjected to analysis of variance (ANOVA) using general linear model (GLM) of Statistical Analysis System program (SAS, Inc, 1999). Multivariate analysis including stepwise regression, Principle Components Analysis (PCA) and Factor Analysis (FA) were performed using SAS (SAS Inc, 1999). Path coefficient analysis was carried out by path analysis. In this analysis, TFY and FNP used as dependent variables and other traits used as independent variables.

## RESULTS

Results of the analysis of variance (ANOVA), maximum, minimum and means of the studied traits with their coefficient of variation (CV) are summarized in Table 2. According to Table 2, there was significant variation for all of the studied traits, among evaluated genotypes. In this study the CV ranged from 7.3% in LL to 39.3% in FNN.

### Correlation analysis

Correlation coefficient was measured among studied genotypes of cucumber. There was a high significant correlation between TFY and FNP ( $r = 0.7^{**}$ ) (Table 3). A negative and significant correlation ( $r = -0.47^*$ ) was observed between TFY and DN (Table 3). There were no significant correlation between yield and other components of yield. FNP showed a non-significant correlation with other traits (Table 3). However, Serquen *et al.* (1997) reported a positive and significant correlation between FNP and BP. FNN had negative and significant correlation with BP ( $r = -0.45^*$ ) and SHD ( $r = -0.6^*$ ), however a positive correlation with VP ( $r = 0.51^{**}$ ) (Table 3).

Correlation between fruit yield and branch number per plant was weak in this study. Plant height had a positive and significant correlation with FL ( $r = 0.44^*$ ) and LB ( $r = 0.71^{**}$ ) (Table 3). A similar correlation between fruit length and length of branch ( $r = 0.54^{**}$ ) was observed. However there was negative and significant correlation between plant height and FD and VP. BP and LB showed the highest significant and positive correlation ( $r = 0.83^{**}$ ). Therefore selection for an increased branch number per plant would increase the length of branch. The highest negative and significant correlation was observed between SHD and DN ( $r = -0.57^*$ ) (Table 3). The significant positive correlation coefficients of total fruit yield with fruit number resulted from positive indirect effect of fruit number, and other traits did not reveal high indirect effect. Therefore gain from selection of these two traits based on them would be high. Similar position was obtained for fruit number.

### Multivariate analysis

#### *Stepwise regression*

Based on stepwise regression, 58% of variation in fruit yield could be explained by two traits including FNP (49%) and BP (9%) (Table 4). Therefore, these two traits have a significant effect on fruit yield.

#### *Principle Component Analysis (PCA)*

Principle components analysis (PCA) based on standardized phenotypic means was carried out to analyze the structure of genetic diversity. The results of the PCA of the genotypes are presented in Table 5. With considering eigenvalues of the first four principal components that accounted 79% of the total variability were retained. The first principal component (PC<sub>1</sub>) had an eigenvalue of 4.45 and explained 34% of the total variation (Table 5). BP, LB and PH had the highest positive eigenvectors in PC<sub>1</sub>. The second principal component (PC<sub>2</sub>) had an eigenvalue of 2.66 that accounted for 20% of the total variation. SHD had the highest positive Eigenvectors in PC<sub>2</sub>. Then, DN had the highest negative eigenvector in it. In the third PC, TFY, FNP and LW had the

highest Eigenvectors. This PC had an eigenvalue of 1.88 that accounted for 14% of the total variation. FNP had the highest positive Eigenvector in PC<sub>4</sub>. On the other hand, in this PC, LW and VP showed the highest negative eigenvectors.

In order to investigation of relation between all traits and genotypes, biplot analysis was used. Based on this analysis (Figure 1), the angle between different traits was related to correlation coefficient, as angles less than 90° showed more correlation, and angles more than 90° revealed less correlation between different traits. For example, the correlation between LB and BP was 0.83, and the angle between them was an oblique angle. There are four sections in this diagram that are related to high and low amount of PC<sub>1</sub> and PC<sub>2</sub>. Genotypes number 1, 5, 6, 8 and 9 (based on table 1) showed positive PC<sub>1</sub> and PC<sub>2</sub> and have high amount of BP, FL and SHD. Genotypes number 13, 14, 15 and 17 revealed positive and negative amount of PC<sub>1</sub> and PC<sub>2</sub>, respectively. Therefore these genotypes can be selected for high amount of PH, BP, LB, LL and LW, and low amount of DN. Genotypes number 2, 3, 4, 7 and 10 revealed positive and negative amounts of PC<sub>2</sub> and PC<sub>1</sub>, respectively. Selection of this hybrids redounded to high amount of TFY. Finally, genotypes number 11, 12, 16, 18, 19 and 20 had negative amount of PC<sub>1</sub> and PC<sub>2</sub> and showed low amount of VP, FD and FNN.

### Factor analysis

Variable data were subjected to factor analysis which divided 13 variables in to four factors with overall justifying 79 (%) of the total genetic variation (Table 4). Factor one was strongly associated with BP, LB and PH (Table 6). The positive signs of these traits (0.84, 0.83, and 0.82) indicated the positive direction of the relationship between the factor 1 and these variables. This also shows that these characters could be influenced by the same genes and may be suitable for screening desirable cucumber genotypes. With considering the high magnitude of bush shape in the first factor, this factor could be titled as plant shape factor. Second factor explained 20% of the total genetic variation (Table 6). In this factor, DN (with positive load) and SHD (with negative load) had the highest loads among evaluated traits. This factor could be named as shoot factor. Selection of genotypes based on this factor can select genotypes with high distance between internode and low shoot diameter. In other words, selected genotypes are tall plants. The third factor explained 11% of the total genetic variation. TFY and FNP had the highest positive load in this factor. So, this factor could be titles as fruit yield factor. Selection based on this factor separate genotypes with high number and weight of fruit. In fourth factor, FNP had the highest load. So, this factor could be titled as fruit number factor.

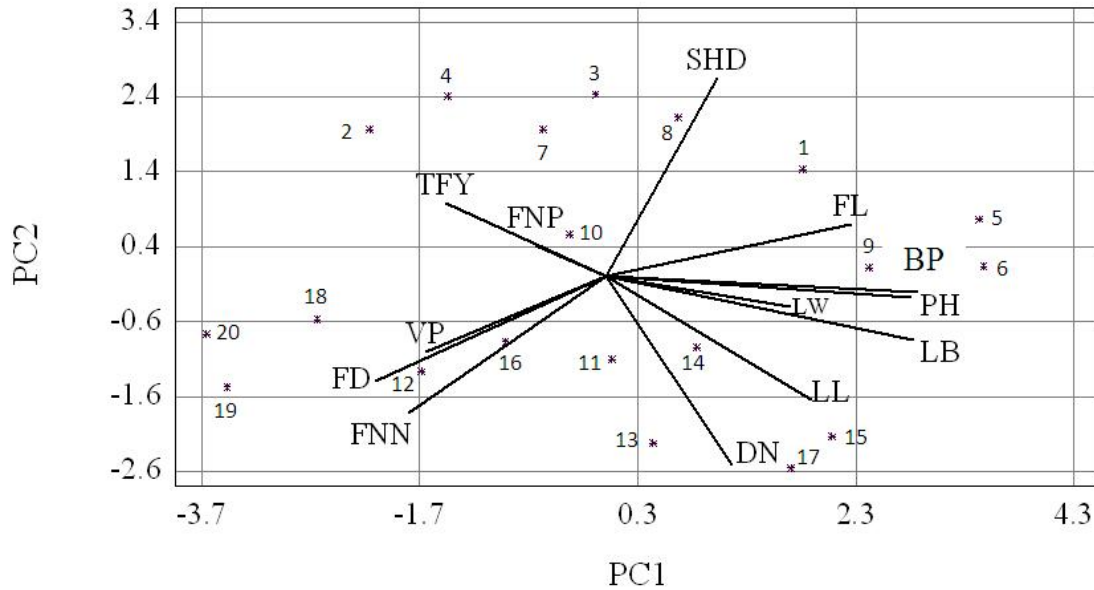
**Table 1.** Plant materials used for evaluation of cucumber genotypes used in this experiment.

Code number	Genotype	Origin	Code number	Genotype	Origin
1	Green majic	Netherland	11	Adrian451	Netherland
2	Nasim	Netherland	12	Adrian salar	Turkey
3	Storm	Netherland	13	Neda	Turkey
4	Janeete	Netherland	14	Sina	USA
5	Karim	Russia	15	Tornado	Spain
6	Atilgan	France	16	Amiral	Spain
7	Vista	France	17	Sco4184	Denmark
8	Raneem	Netherland	18	Danish	Denmark
9	Zohal	Netherland	19	Yaldar2	Netherland
10	Gohar	Netherland	20	Khassibr2	Netherland

**Table 2.** Results of analysis of variance and descriptive statistics of evaluated traits in cucumber genotypes.

		Mean squares												
Source of variation	df	TFY <sup>¥</sup>	FNP	FNN	BP	PH	LL	LW	FL	FD	DN	SHD	LB	VP
Replication	3	15028.6**	2.4	5.2**	0.01	13700.9**	24.02	19.5	2.2	0.09	471.06**	5.43**	1.08	0.3
Genotype	19	7132.5**	3.7**	1.4*	3.9**	4593.7**	15.5**	13.4**	4.1**	0.12*	252.19**	0.73**	3.5**	1.5**
Residual	57	3260.2	1.04	0.6	0.1	449.2	5.54	7.0	1.4	0.07	70.74	0.26	0.8	0.2
CV (%)	-	14.4	22.8	36	13	6.3	7.30	8.5	7.8	10.2	9.16	32.6	35.9	15.1
Max.	-	474.25	6.52	3.41	3.87	381.25	36.37	34.37	17.27	3.07	105.5	2.03	3.87	4
Min.	-	338.31	3.50	1	0.87	267.25	29.12	28.25	12.88	2.46	78.25	1	1.12	1.75
Mean	-	394.68	4.48	2.11	2.6	334.5	32.24	31.17	15.12	2.62	91.78	1.56	2.49	2.96

¥: TFY: Total fruit yield per pickling(g), FNP: Fruit number per pickling, FNN: fruit number per node, BP: branch number per plant, PH: plant height (cm), LL: l (cm), LW: leaf width (cm), FL: fruit length (cm), FD: fruit diameter (cm), DN: distance between internode (cm), SHD: Shoot diameter (cm), LB: length of branch of plant \* and \*\* significant at  $P < 0.05$  and  $P < 0.01$ , respectively.



**Figure 1.** Biplot analysis of 20 genotypes and 13 different traits. TFY: Total fruit yield per pickling, FNP: Fruit number per pickling, FNN: fruit number per node, BP: branch number per plant, PH: plant height, LL: leaf length, LW: leaf width, FL: fruit length, FD: fruit diameter, DN: distance between internode, SHD: Shoot diameter, LB: length of branches, VP: Vigor of plant. PC1 and PC2: principle component 1 and 2.

**Table 3.** Correlation coefficients between studied traits of 20 genotypes of cucumber.

	TFY	FNP	FNN	BP	PH	LL	LW	FL	FD	DN	SHD	LB	VP
TFY	1												
FNP	0.7**	1											
FNN	0.17	0.19	1										
BP	-0.21	0.12	-0.45*	1									
PH	-0.2	-0.14	-0.32	0.7**	1								
LL	0.21	-0.1	0.02	0.51**	0.4	1							
LW	-0.1	0.11	-0.07	0.33	0.38	0.38	1						
FL	-0.17	-0.21	-0.32	0.44*	0.44**	0.26	0.18	1					
FD	0.19	0.14	0.42	-0.35	-0.47*	-0.15	-0.47*	0.09	1				
DN	-0.4*	-0.27	0.29	0.27	0.38	0.45*	0.17	0.07	0.1	1			
SHD	0.15	0.12	-0.6**	0.09	0.13	-0.2	0.28	0.39	-0.6**	-0.57**	1		
LB	-0.27	0.1	-0.27	0.83**	0.71**	0.54**	0.29	0.54**	-0.22	0.5*	-0.10	1	
VP	0.27	0.12	0.51**	-0.48*	-0.41*	0.21	0.26	-0.3	0.21	-0.13	-0.24	-0.4*	1

\* and \*\* significant at  $P < 0.05$  and  $P < 0.01$ , respectively.

¥: TFY: Total fruit yield per pickling(g), FNP: Fruit number per pickling, FNN: fruit number per node, BP: branch number per plant, PH: plant height (cm), LL: leaf length (cm), LW: leaf width (cm), FL: fruit length (cm), FD: fruit diameter (cm), DN: distance between internode (cm), SHD: Shoot diameter (cm), LB: length of branches, VP: Vigor of plant

**Table 4.** Predicted regression equations for fruit yield per pickling based on other horticultural traits.

Regression equations	Coefficient of partial determination	Cumulative coefficient determination
FY* = 257.6 + 30.57FNP	0.49	0.49
FY = -283.77 - 12.85BP + 32.2FNP	0.09	0.58

\*FY = Fruit yield per pickling, FNP = Fruit number per pickling, BP = Branches per plant

**Table 5.** Eigenvector, Eigen value, total variance and cumulative variance for 20 genotypes.

Variables	PC of genotypes			
	PC <sub>1</sub>	PC <sub>2</sub>	PC <sub>3</sub>	PC <sub>4</sub>
TFY	-0.20	0.21	0.46	0.31
FNN	-0.25	-0.36	0.16	-0.02
BP	0.40	-0.04	0.07	0.30
LB	0.39	-0.16	0.01	0.27
FL	0.31	0.14	-0.03	-0.06
FD	-0.29	-0.27	-0.10	0.32
DN	0.16	-0.51	-0.13	-0.01
PH	0.39	-0.05	0.039	0.14
FNP	-0.09	0.08	0.49	0.49
LL	0.26	-0.33	0.32	-0.15
LW	0.23	-0.08	0.46	-0.37
VP	-0.22	-0.2	0.37	-0.39
SHD	0.14	-0.53	0.11	-0.20
Eigen value	4.45	2.66	1.88	1.53
Partial Variance (%)	34	20	14	11
Cumulative variance (%)	34	54	68	79

¥: TFY: Total fruit yield per pickling, FNP: Fruit number per pickling, FNN: fruit number per node, BP: branch number per plant, PH: plant height, LL: leaf length, LW: leaf width, FL: fruit length, FD: fruit diameter, DN: distance between internode, SHD: Shoot diameter, LB: length of branches, VP: Vigor of plant

**Table 6.** Loading of four important principal factor (PF) from a factor analysis of 13 traits in cucumber.

Variables	Factor (matrix of factor coefficients)			
	1	2	3	4
TFY	-0.43	-0.35	0.63	0.38
FNN	-0.53	0.59	0.22	-0.02
BP	0.84	0.06	0.10	0.37
LB	0.83	0.27	0.02	0.34
FL	0.66	-0.22	-0.04	-0.07
FD	-0.62	0.45	-0.13	0.39
DN	0.34	0.81	-0.17	-0.01
PH	0.82	0.09	0.05	0.17
FNP	0.18	-0.13	0.68	0.61
LL	0.55	0.53	0.45	-0.18
LW	0.50	0.12	0.63	-0.46
VP	-0.48	0.32	0.51	-0.49
SHD	0.30	-0.86	0.16	-0.25
Variance (%)	34	20	14	11
Cumulative variance (%)	34	54	68	79

¥: TFY: Total fruit yield per pickling, FNP: Fruit number per pickling, FNN: fruit number per node, BP: branch number per plant, PH: plant height, LL: leaf length, LW: leaf width, FL: fruit length, FD: fruit diameter, DN: distance between internode, SHD: Shoot diameter, LB: length of branches, VP: Vigor of plant,

**Table 7.** Results of path analysis for total fruit yield and fruit number per pickling with other traits

A						B						
TFY	Traits					FNP	Traits					
	FNP	LL	DN	BP	Total		TFY	FL	DN	FNN	Total	
	FNP	<b>0.65</b>	0.06	.01	-0.06	0.65	TFY	<b>0.62</b>	0.02	0.01	0.01	0.66
	LL	0.1	<b>0.4</b>	-0.16	-0.24	0.1	FL	-0.1	<b>-0.05</b>	-0.01	-	0.18-
	DN	-0.16	.25	<b>0.32-</b>	-0.13	-0.36	DN	-0.24	-0.01	-	0.02	-0.24
	BP	.07	0.28	-0.1	<b>-0.41</b>	-0.16	FNN	0.11	0.02	-	<b>0.05</b>	0.16
										0.01		
Residual effect: 0.46						Residual effect: 0.66						

TFY: Total fruit yield per pickling, FNP: Fruit number per pickling, FNN: fruit number per node, BP: branch number per plant, LL: leaf length, FL: fruit length, DN: distance between internodes, Direct effects of TFY and FNP with other traits are on diameter. Indirect effects are upper and lower of diameter.

### Path analysis

Path analysis for TFY and some of the horticultural traits is shown in Table 7; section A. Among considered traits (FNP, LL, DN and BP), FNP had the greatest positive effect on TFY. Similar position was obtained for fruit number (Table 7, section B) and TFY had the highest positive direct effect on FNP. This result was similar with the reports of Rao *et al.* (2004) and Arunkumar *et al.* (2011). The most negative direct effect on total fruit yield was belonged to BP and DN. According to Table 7, section B, the most positive and negative direct effects were belonged to TFY and FL, respectively. Total correlation between TFY and other traits was highest with FNP. Similarly, the greatest total correlation in section B of Table 7 belong to TFY.

Different genotypes showed wide range of variation for the majority of traits, especially total fruit yield per pickling, fruit number, plant height, fruit length and length of branch. Therefore, fruit yield or number of fruit per pickling, plant height and the other traits might be improved by using the high performing genotypes in this study.

Negative correlation between fruit yield and distance between internodes showed that in tall plants, the number of node decreases and fruit yield reduces. On the other hand, there were no significant correlation between yield and other components of yield. Cramer and Wehner (1998) reported that most correlations between yield components and between yield

components and fruit yield were weak, and strong correlations varied between populations, seasons, and yield components. Selection weakened many strong correlations between yield components and between yield and components. Wehner and Shetty (2000) studied 761 gynocious hybrids and tested them for early, total, and marketable yield under two locations. In general, correlations between locations for the yield traits were low. Shetty and Wehner (2002) reported a positive and significant correlation ( $r = 0.7^*$ ) between number of branches per plant with total yield. Correlations between fruit number per node and branch per plant and shoot diameter revealed that an increase in fruit number per node result in a decrease in branch number per plant and shoot diameter and an increase in vigor of plant. Although correlation between fruit yield and branch number per plant was weak in this study, however Wehner and Guner (2004) showed that among vegetative traits, number of nodes/branch and branches/plant were correlated with early yield, indicating that early yield was higher when the plants were able to grow longer branches having more nodes.

Notice to relationship between plant height and other traits shows that there are long fruits in tall plants. Fan *et al.* (2006) reported that there is negative correlation between fruit length/diameter and number of fruit in cucumber. It is likely that the negative correlation between these traits precluded genetic gain for one of these traits during phenotypic selection in their population. Another



result was that in tall plants shoot diameter would be decrease. These correlations could give sufficient information for indirect selection to improve fruit yield in cucumber.

Stepwise regression showed that improvement of fruit number per pickling and branch number per plant as a fruit yield components could be a good breeding way for increasing of fruit yield. The lowest  $R^2$  value measured was 0.09 for early fruit weight estimated from total fruit number; the highest  $R^2$  was 0.96 for early fruit weight estimated from early fruit number, total fruit number, and total fruit weight. They reported that most of the fruit yield variation was explained by fruit number. They observed that there is high correlation between fruit weight and fruit number within each grade (early, marketable and cull). An efficient method for estimating fruit weight per hectare of early, marketable, and cull grades is to count total, early, and cull fruit, then measure total fruit weight. Based on regression analysis, if one had to choose just one trait for predicting fruit grade weights due to lack of resources, he or she could be used of total fruit weight with fruit number for estimating the weights of fruit.

The PCA was carried out for 20 genotypes of cucumber to identify the traits that were the main source of the variability. Based on this analysis, traits related to vegetative growth such as number and length of branches, height and vigor of plants, and traits related to fruit yield and fruit number could explained high amount of phenotypic variations. The results of biplot were similar to correlation coefficient and factor analysis, and uphold each other. This analysis could group genotypes based on traits and provided opportunity for selecting different genotypes for different traits.

Existence of some traits with high load in same factors in factor analysis shows that these characters could be influenced by the same genes and may be suitable for screening desirable cucumber genotypes. Four factors were related to plant shape, shoot factor, fruit yield and fruit number. Selection of genotypes based on these four factors could separate genotypes with high amount of traits with high load. For example selection of genotypes based on the second factor can select genotypes with high distance between internode and low shoot

diameter. Selection based on the third factor separate genotypes with high number and weight of fruit. According to factor analysis, selection based on TFY and FNP; LB and BP could be considered as the suitable criteria for selection of superior

In previous analysis such as coefficient of correlations, principle components, factor analysis and stepwise regression, we could recognize relationship between different traits and the effects of them on fruit yield, however these relationships may be direct or indirect from other traits. Path coefficients divided the correlation coefficient into a series of direct and indirect effects of different traits on the fruit yield and fruit number. Genotypic correlation coefficient was portioned into direct and indirect effects through various fruit yield contributing traits using path analysis.

Notice to high direct effects of TFY and FNP with another traits revealed that the significant positive correlation coefficients of total fruit yield with fruit number resulted from positive indirect effect of fruit number, and other traits did not reveal high indirect effect. Therefore gain from selection of these two traits would be high. On the other hand these results imply that FNP could be used as a selection index to improve fruit yield in cucumber, specially, when measurement of fruit yield based on weight is time consuming. Conversely, the significant negative total correlation between total fruit yield and distance between nodes resulted from the negative indirect effects of fruit number and branch number per plant, although leaf length had a strong positive indirect effect on fruit yield (Table 7, section A). Therefore use of distance between nodes as selection criteria of fruit yield is complex. The most negative direct effect on total fruit yield was belonged to BP and DN. This negative direct effect between TFY and BP decreased by high positive indirect effect of leaf length and finally the correlation between TFY and BP was low ( $r = -0.16$ ). According to Table 7, section B, the most positive and negative direct effects were belonged to TFY and DN, respectively. Although total correlation between DN and fruit number was moderate, but direct effect of DN on fruit number was very low that is related to high indirect effect of distance between nodes

via total fruit yield. Therefore the indirect effects of other traits via DN were negative, suggesting the ability of fruit yield components to compensate each other.

Overall, highly significant and positive correlation coefficients as well as high direct effects of fruit number on fruit yield, high variation explanation based on stepwise regression and grouping to each other based on factor analysis and principle components, indicated that this trait is simultaneously the most reliable component for selecting high fruit yielding cucumber genotypes. Other traits having high positive correlation with fruit yield are not the most reliable components for selection.

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