



# Genetic Improvement of Yield and Fruit Traits in Snake Cucumber (*Cucumis melo* var. *flexuosus* L.) by Individual Selection

Mohamed Youssef Abed<sup>1\*</sup>

<sup>1</sup>Department of Vegetable Research, Horticulture Research Institute, Agricultural Research Center, Giza, Egypt.

## Author's contribution

The sole author designed, analyzed, interpreted and prepared the manuscript.

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## ABSTRACT

This investigation was undertaken during 2013-2016 to develop new and superior snake cucumber cultivars and to evaluate the efficiency of individual selection to improve yield in traditional snake cucumber populations. Moreover, genetic behaviour of variability was investigated. Three local cultivars were subjected to three cycles of individual plant selection and were ended up with selection of nine populations. These genotypes were evaluated in a field trial to study the behaviour of the tested populations and provide information on the nature of genetic variability and correlation among traits. The means of selected populations signify that there has been a remarkable change in all traits due to individual selection. However, the magnitudes of improvement varied within and between populations according to their genetic constitution and the basic criteria that selection was directed to. It is suggested that individual selection method improved stem length, whereas it did not considerably improve flowering time and the number of branches plant<sup>-1</sup> in most populations. Otherwise, selection procedure resulted in isolation of superior populations with high yield production viz, AS<sub>1</sub>, DK<sub>2</sub>, DK<sub>3</sub> and SG<sub>3</sub>. Some derived populations showed longer fruit length and lesser diameter when compared with their respective base populations.

The estimates of phenotypic coefficient of variation were higher than the estimates of genotypic coefficient of variation for all studied traits. High heritability coupled with high genetic advance was

\*Corresponding author: E-mail: m.abed2018@yahoo.com;

observed for stem length, fruit diameter and moderate estimates were observed for average fruit weight. Total yield was correlated with stem length, total number and weight of fruits and fruit diameter so that selection for any of these characters would result subsequently in an improvement of the total yield production. In the present study, selection procedure resulted in the isolation of superior populations with high yield production viz, AS1, DK2, DK3 and SG3. Fruit character was improved also through individual selection.

**Keywords:** Snake cucumber; individual selection; PCV; GCV; heritability; genetic advance.

## 1. INTRODUCTION

Snake cucumber (*Cucumis melo* var. *flexuosus* L.) is an important crop, especially in the Middle East and North Africa. It is also known as Chinese, Oriental, Armenian, serpent cucumber [1] or snake melon. The Arabic epithet Qitha and Faqqous are used to denote snake cucumber across the Arabic speaking geographical region [2]. Immature fruits are used as an alternative to cucumber in many parts of the world [3,4,5]. Fruits are eaten as a salad vegetable and they have a flavour rather like cucumber and are very refreshing when eaten raw in hot weather. Its origin is thought to be Mediterranean basin, North Africa, Middle East and Anatolia [2,6,7,8]. Egypt is one of the diversification centers of snake cucumber and possesses valuable genetic resources which exhibit a wide variability [9,10]. There is a high variability among snake cucumber landraces for morphological characters, yield and fruit attributes [11,12,13]. Such genetic diversity of snake cucumber gives plant breeders the sustained ability to develop existing varieties. Snake cucumber plants have an outcrossing habit, so in this case landraces and local cultivars are populations of random mating individuals. These populations are composed of heterozygous individuals and usually exhibit considerable genetic variation for traits with economic importance.

Genetic variability studies provide the essential information about the genetic components of the population. The progress in snake cucumber breeding depends mainly on the magnitude of genetic variability present in the population and it is necessary to evaluate the genetic parameters such as genetic coefficient of variation, heritability and genetic advance [11].

Individual plants from cross-pollinated crops are heterozygous, and the progeny from such plants would be heterogeneous and usually different from the parent plant due to segregation and recombination [14]. In individual selection, superior plants are selected and their seeds are sown separately, whereas inferior plants are

discarded. This is an intra-population selection method which mainly based on single plants. Selection within a population is effective where the genetic variances are presented for the desired traits. It improves the performance of populations in continuous and progressive steps by increasing the frequency of desirable alleles for the desired trait under selection [15]. Selection is the most efficient method for traits with high heritability. The information on heritability in conjunction with genetic advance are reliable estimations to identify characters for enforcing selection [16]. Heritability provides information on the magnitude of the inheritance of characters from parent to offspring, while genetic advance shows the degree of gain obtained in a character under a particular selection pressure [17,18]. The high heritability associated with high genetic advance for quantitative traits offer a better scope of selection of genotypes in early segregating generations. Broad sense heritability magnitudes in snake cucumber were high for number of fruits plant<sup>-1</sup>, yield plant<sup>-1</sup>, fruit length and fruit shape index [11], so phenotypic selection for these traits would be reasonably effective. Moreover, it has been reported the association of number primary branches with stem length; fruit length with stem length; stem pubescence with both groove width and number of female to male flowers ratio; and fruit thickness with fruit length and fruit colour with stem pubescence; that can be used in selection [12].

Despite the large variation that has been observed among snake cucumber cultivars, the efforts for development of new and superior varieties are still limited. Substantial effort has to be directed towards genetic breeding of existing cultivars. Hence, the objectives of this study are the genetic improvement of local snake cucumber cultivars and the development of new high yielding cultivars with better fruit characters as well as to gather information on the genetic behaviour of some economic traits. The genetical studies were undertaken for snake cucumber as well.

## 2. MATERIALS AND METHODS

This study was conducted during four consecutive summer seasons during 2013- 2016 at a vegetable growing farm at Talkha, Dakahlia Governorate. Three different local cultivars of snake cucumber (*Cucumis melo* var. *flexuosus* L.) were collected from three different regions in Egypt, namely Assiut, Dakahlia and Sohag; which were denoted hereafter AS, DK, and SG, respectively.

### 2.1 Individual Plant Selection Procedures

Seeds of the three diverse genetic populations of AS, DK, SG were separately sown on March, 2013. The best individual plants were selected based on their phenotypic performance. The selection criteria used to select plants were mainly based on the desirable characters, e.g. robust vegetative growth, early flowering, long stem length, medium fruit diameter and weight, non bitterness, adaptation and higher yield. To produce the seeds of the first selfed progenies of the selected plants, some floral buds of the selected plants were selfed then were bagged, by paper bags, till fruits setting. The fruits were left to full ripening and then seeds were extracted manually. Seeds of the selected plants from each population in the first selection cycle were separately sown on March, 2014. Selection, in the same foregoing basis, was practiced within and between the individual plants of each population to maintain the most promising progenies for the next selection cycle. The same selection procedure was practiced in summer season of 2015 to generate the best progenies for each genotype of the third selection cycle. The final selected progenies of each population were declined to the best three genotypes, according to their desirable traits. The selected progenies were designated AS<sub>1</sub>, AS<sub>2</sub>, AS<sub>3</sub>, DK<sub>1</sub>, DK<sub>2</sub>, DK<sub>3</sub>, SG<sub>1</sub>, SG<sub>2</sub>, SG<sub>3</sub>, depending on their initial population from which they were derived from.

Phenotypic evaluation experiment of the original populations, AS<sub>0</sub>, DK<sub>0</sub> and SG<sub>0</sub>, and the derived populations e.g. AS<sub>1</sub>, AS<sub>2</sub>, AS<sub>3</sub>, DK<sub>1</sub>, DK<sub>2</sub>, DK<sub>3</sub>, SG<sub>1</sub>, SG<sub>2</sub>, SG<sub>3</sub>, was conducted on March 23, 2016.

### 2.2 Experimental Design

The experiment was conducted using Randomized Complete Block Design (RCBD) with three replications. Each experimental plot consisted of two rows; 10 m long and 2 m wide,

with a spacing of 0.5 m between plants. All agricultural practices as recommended for snake cucumber production were adopted.

### 2.3 Data Collection

Observations were recorded for number of days to flowering, stem length (cm), number of branches plant<sup>-1</sup>, total yield as number (thousand feddan<sup>-1</sup>) and weight of fruits (ton feddan<sup>-1</sup>), average fruit weight (g), fruit length (cm), fruit diameter (cm). Shape index of fruits was calculated as fruit length/fruit diameter ratio.

### 2.4 Statistical Analysis

Data were subjected to statistical analysis according to the standard statistical procedure described by Gomez and Gomez [19]. Significant means of the genotypes were compared using least significant difference (LSD) at P ≤ 0.05. Correlation coefficient among all possible pairs of characters were analyzed following the method outlined by Singh and Chaudhary [20].

### 2.5 Estimation of Variability Parameters

#### 2.5.1 Genetic variance

The phenotypic and genotypic variances were estimated by the formulae suggested by Singh and Chaudhary [20] as follows:

$$\begin{aligned} \text{Phenotypic variance } (\sigma^2_{ph}) &= \sigma^2_g + \sigma^2_e \\ \text{Genotypic variance } (\sigma^2_g) &= (Ms_g - Ms_e)/r \\ \text{Environmental variance } (\sigma^2_e) &= Ms_e \end{aligned}$$

Where:

Ms<sub>g</sub> is the mean square of genotypes, Ms<sub>e</sub> is the mean square of error and r is the number of replications.

Estimates of phenotypic and genotypic coefficients of variation (PCV and GCV) were estimated according to the procedures as outlined by Johnson et al. [16] as follows:

$$\begin{aligned} PCV &= \frac{\sqrt{\sigma^2_{ph}}}{x} \times 100 \\ GCV &= \frac{\sqrt{\sigma^2_g}}{x} \times 100 \end{aligned}$$

Where,

$\bar{x}$  = General mean of the character under study.

### 2.5.2 Estimates of broad sense heritability ( $h^2 b$ ) and genetic advance (GA)

Broad sense heritability and genetic advance were calculated as outlined by Singh and Chaudhary [20] as follows:

$$h^2 b = \frac{\sigma^2 g}{\sigma^2 ph} \times 100$$

Where,

$h^2 b$  = Heritability in broad sense

Expected genetic advance was calculated as follows:

$$GA = h^2 b . K . \sqrt{\sigma^2 ph}$$

Where,

K = Selection differential (constant) i.e. 2.06 at 5% selection intensity.

## 3. RESULTS AND DISCUSSION

### 3.1 Efficiency of Individual Plant Selection

Performance of base populations AS<sub>0</sub>, DK<sub>0</sub> and SG<sub>0</sub> and the nine progenies derived from them, i.e., AS<sub>1</sub>, AS<sub>2</sub>, AS<sub>3</sub>, DK<sub>1</sub>, DK<sub>2</sub>, DK<sub>3</sub>, SG<sub>1</sub>, SG<sub>2</sub>, SG<sub>3</sub> is shown in Table 1. The results revealed the presence of significant differences for all studied traits. The means of selected populations signify that there has been a remarkable change in all traits due to selection procedure.

The mean values for flowering revealed that AS<sub>3</sub>, DK<sub>1</sub> and SG<sub>2</sub> were the most earlier in flowering time than their corresponding base populations. Moreover, the obtained results reflected that selected populations exhibited longer stem length than their corresponding original populations, whereas means of number of branches plant<sup>-1</sup> for AS<sub>2</sub>, DK<sub>1</sub>, DK<sub>2</sub> significantly increased when compared with AS<sub>0</sub> and DK<sub>0</sub>, respectively. The rest of the populations exhibited lesser means or insignificant increment for a number of branches plant<sup>-1</sup>. It is suggested that individual selection method improved stem length, whereas it did not considerably improve flowering time and the number of branches plant<sup>-1</sup> in most populations.

The results of total yield, as number of fruits feddan<sup>-1</sup>, indicate that AS<sub>1</sub>, DK<sub>1</sub>, DK<sub>2</sub>, DK<sub>3</sub>, SG<sub>2</sub> and SG<sub>3</sub> significantly surpassed their original populations as a result of individual selection, besides that; most of the derived populations produced larger yield, as weight of fruits than their corresponding base populations. The largest improvements in yield within selected progenies in relation to their base populations were recorded for AS<sub>1</sub>, DK<sub>2</sub>, DK<sub>3</sub> and SG<sub>3</sub> with an average yields of 6.69, 5.43, 5.37 and 7.51 ton feddan<sup>-1</sup>, respectively. Overall, SG<sub>3</sub> produced the largest yield with an average yield of 7.51 ton feddan<sup>-1</sup>, followed by AS<sub>1</sub>, SG<sub>2</sub> and SG<sub>1</sub> with an average yields of 6.69, 6.46 and 6.28 ton feddan<sup>-1</sup>, respectively. These progenies could be promising cultivars for snake cucumber production rather than the existed varieties.

The parental cultivars are open pollinated cultivars so that they are subjected to outcrossing. The individual plant selection within these cultivars improved the yield characters through the accumulation of a small gain in each cycle towards the high yielding ability. However, the magnitudes of improvement varied within and between populations according to their genetic constitution and the basic criteria that selection was directed to.

The positive response to selection has been reported for stem length, branches number, fruit weight and fruit number plant<sup>-1</sup> [21].

Selection within the base populations AS<sub>0</sub>, DK<sub>0</sub> and SG<sub>0</sub> generated diverse progenies for fruit traits. The new progenies exhibited lesser or greater mean values of the various fruit traits, according to selection criteria, when compared with their parental populations. The base population AS<sub>0</sub> and the respective progenies AS<sub>1</sub>, AS<sub>2</sub> and AS<sub>3</sub> showed the largest magnitudes of average fruit weight. Otherwise, the base population SG<sub>0</sub> and respective progenies SG<sub>1</sub>, SG<sub>2</sub> and Sg<sub>3</sub> showed the largest means of fruit length and diameter. Ultimately, some of the derived population are characterized by a reduced fruit length and diameter, since the selection was directed towards shorter fruit length and lesser diameter as a desirable form. Apart from the SG<sub>0</sub> population and the respective populations, that revealed insignificant differences, the shape index data illustrated that other selected populations exhibited greater values in relation to their parental populations, indicating that the selected populations are characterized by more attractive and uniform fruits.

**Table 1. Mean performance of the tested populations for vegetative, yield and fruit traits**

<b>Genotypes</b>	<b>Flowering time (Days)</b>	<b>Stem length (cm)</b>	<b>No. of branches</b>	<b>Total yield (No)</b>	<b>Total yield (Wt)</b>	<b>Average fruit weight (g)</b>	<b>Fruit length (cm)</b>	<b>Fruit diameter (cm)</b>	<b>Shape index</b>
AS <sub>0</sub>	36.61	167.12	2.62	10.50	4.62	482.87	31.70	4.23	7.49
AS <sub>1</sub>	35.46	194.43	2.34	12.40	6.69	441.69	34.54	3.37	10.27
AS <sub>2</sub>	36.21	183.67	3.40	10.43	4.75	523.53	35.31	3.20	11.05
AS <sub>3</sub>	33.63	169.87	2.77	9.97	5.39	526.17	28.68	3.83	10.13
DK <sub>0</sub>	41.67	237.57	2.13	11.48	4.40	308.14	29.13	3.40	8.58
DK <sub>1</sub>	38.51	272.31	2.63	13.14	4.63	344.21	32.99	3.47	9.51
DK <sub>2</sub>	42.18	239.40	2.53	15.83	5.43	334.80	28.53	3.43	8.56
DK <sub>3</sub>	40.82	258.07	2.47	17.41	5.37	295.88	29.46	3.13	9.40
SG <sub>0</sub>	38.19	219.38	1.83	14.49	5.82	336.46	35.19	4.53	7.78
SG <sub>1</sub>	39.47	233.73	2.04	15.56	6.28	381.24	31.69	4.27	7.42
SG <sub>2</sub>	36.23	247.21	2.16	17.98	6.46	354.88	36.84	4.43	7.19
SG <sub>3</sub>	37.35	238.81	1.73	19.34	7.51	317.52	32.40	4.27	7.37
LSD 5%	1.86	3.25	0.34	1.11	0.35	13.12	2.14	0.23	0.73

The improvement of fruit characters could be ascribed to a small gain in each selection cycle and accumulation of the gene frequencies of favourable alleles in the offspring. The obtained results reflected a relatively high improvement, with different magnitudes, in vegetative characters, yield, average fruit weight and dimensions, as a response to individual plant selection. Such relatively high improvement of quantitative traits signifies that the individual plant selection led to increasing the frequency of desirable alleles in the selected populations rather than their corresponding original populations. The role of selection in genetic improvement by raising the gene frequencies of the desirable alleles for various economical characters of cucurbits has been reported by Mitiady et al. [22], Hazara et al. [23] and Gwanana et al. [24].

### 3.2 Genetic Variance

Improvement of snake cucumber depends on the nature and magnitude of genetic variability in the population. Genetic variability studies provide basic information regarding the genetic properties of the population. The extent of variability presented in snake cucumber cultivars was measured in terms of phenotypic variance ( $\sigma^2_{ph}$ ), genotypic variance ( $\sigma^2_g$ ), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ( $h^2_b$ ) and genetic advance (GA) as shown in Table 2.

Estimates of phenotypic variance ( $\sigma^2_{ph}$ ) were larger than the corresponding genotypic variance ( $\sigma^2_g$ ) for all examined traits. Moreover, close estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were noted in all characters, which imply the contribution to phenotypic expression of these characters are mostly due to genetic

factors, while the environmental ones were not great importance. Characters having a high genotypic coefficient of variation indicate a high potential for effective selection. These findings are in agreement with those reported by Rakhi and Rajamony [25], Mehta et al. [26], Ibrahim [27], Potekar et al. [28] and Janghel et al. [29].

Although genotypic coefficient of variation revealed the extent of genetic variability present in the genotypes for various traits, it does not provide full scope to assess the heritable variation. Burton [30] suggested that GCV together with heritability estimates would give the best insight into the extent of the advance to be expected by selection. Highly estimates of heritability ( $h^2 > 80\%$ ) were obtained for most studied characters, with the exception of moderate estimations for fruit length (77.19%) and fruit diameter (60.42%). High heritability estimates indicate that high proportion of variation is inherited in the selected progenies so that phenotypic selection for characters that showed high heritability would be highly efficient.

Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone [16]. High heritability coupled with high genetic advance were observed for stem length (99.42% and 72.17, respectively), average fruit weight (92.24 and 18.27, respectively) and fruit diameter, (60.42% and 86.23, respectively). Genetic advance shows the degree of gain obtained in a character under a particular selection pressure.

Since high heritability coupled with high genetic advance estimates offers the most suitable condition for selection, therefore good improvement could be made if some of these traits are considered as selection criteria in the future breeding program.

**Table 2. Genetic parameters for the studied characters of the evaluated populations**

Characters	$\sigma^2_{ph}$	$\sigma^2_g$	PCV %	GCV %	$h^2_b$ %	GA
Flowering time	6.63	5.42	6.83	6.17	81.75	4.34
Stem length	1234.71	1231.04	15.87	15.85	99.42	72.17
No. of branches	0.25	0.21	21.24	19.42	84.00	0.86
Total yield (No)	10.42	9.99	23.02	22.45	95.87	6.37
Total yield (Wt)	1.01	0.97	17.92	17.52	96.04	1.98
Average fruit weight	7928.89	7988.92	23.60	23.51	99.24	18.27
Fruit length	7.06	5.45	8.38	7.36	77.19	4.23
Fruit diameter	0.48	0.29	16.27	15.85	60.42	86.23
Shape index	1.87	1.67	15.65	14.83	89.30	2.50

High heritability and high genetic advance, as recorded in the present investigation, were also reported by several researchers such as Rakhi and Rajamony [25]; Torkadi et al. [31]; Tomar et al. [32]; Reddy et al. [33] and Mishra et al. [34].

High heritability coupled with low genetic advance exhibited by traits viz., number of days to flowering, number of branches, total yield as weight, fruit length and shape index. Heritability for these traits could be explained by the non-additive gene effects. This indicates that hybridization followed by selection will be effective for genetic improvement of these traits because direct selection for these traits will not be effective.

The obtained results of heritability and genetic advance are in the same trend as those obtained by previous investigations [35-40].

### 3.3 Association between Characters

To investigate the association between characters, the correlation coefficient among all possible pairs of characters were analyzed. Data of the correlation among all characters are presented in Table 3.

Improvement for a target character can be achieved by indirect selection using other characters that are more heritable and easy to select. This selection strategy requests understanding of the interrelationship of the characters among themselves and with the target.

Flowering time showed a positive and significant correlation with stem length (0.59\*\*) and insignificant positive correlation with total yield, measured as a number of fruits.

Total yield, measured as a number of fruits, exhibited a positive significant correlation with stem length (0.69\*\*), total yield as weight (0.67\*\*) and fruit diameter (0.45\*\*). Furthermore, total yield as weight showed a positive significant correlation with fruit diameter (0.46\*\*). Otherwise, negative and significant correlations were detected between number of branches with both total yield as number (-0.57\*\*) or weight (-0.69\*\*).

It can be deduced that yield is a complex trait associated with stem length, total number of fruits, total weight of fruits and fruit diameter. It is the prime concern of the plant breeder and is the ultimate goal of the breeding program. Hence, selection for any of the aforementioned positively associated characters would result subsequently in an improvement of the total yield. These findings are in agreement with the earlier findings reported by Pandey et al. [41] Ibrahim and Ramadan [42] and Naroui Rad et al. [43], that selection for more yields was accomplished by considering useful traits as indirect selection criteria. Selection for more yields by considering useful traits as indirect selection criteria is an alternative breeding approach.

However, an attention should be given in the breeding program to undesirable correlation with number of branches.

**Table 3. Estimates of correlation coefficients among the different pairs of the studied traits of snake cucumber**

Characters	Stem length	No. of branches	Total yield (No)	Total yield (Wt)	Average fruit weight	Fruit length	Fruit diameter	Shape index
Flowering time	0.59**	-0.10	0.29	-0.21	-0.59**	-0.28	-0.02	-0.19
Stem length		-0.37	0.69**	0.12	-0.56**	-0.16	0.15	-0.28
No. of branches			-0.57**	-0.69**	0.19	0.06	-0.61**	0.68**
Total yield (No)				0.67**	-0.44**	-0.09	0.45**	-0.52**
Total yield (Wt)					-0.07	0.11	0.46**	-0.39*
Average fruit weight						0.06	-0.02	0.28
Fruit length							0.33*	0.22
Fruit diameter								-0.84**

#### 4. CONCLUSION

Individual plant selection could be used to improve quantitatively inherited characters and isolate of superior populations from landraces or native snake cucumber cultivars. The magnitudes of improvement vary within and between populations and the improvement of selection is based substantially on genetic factors for the studied characters. Improving total yield per plant of snake cucumber can be accomplished by selecting plants for more number of fruits, weight of fruits, stem length and fruit diameter. In the present study, selection procedure resulted in the isolation of superior populations with high yield production viz, AS1, DK2, DK3 and SG3. Fruit character was improved also through individual selection.

#### COMPETING INTERESTS

Author has declared that no competing interests exist.

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