

# Journal of Plant Production

Journal homepage & Available online at: [www.jpp.journals.ekb.eg](http://www.jpp.journals.ekb.eg)

## Breeding of New Dolma Types Capsicum by Selection

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### ABSTRACT

Selection is the first step in a successful pepper breeding program of parents and genetic diversity is one of the criteria for selection of parents in hybrid production. Six successive seasons (2019 early spring and autumn and the winter season of 2020, 2021, 2022 and 2023) field experiments on pepper were carried out at Experimental Farm, Fac. Agric., Zagazig Univ., Egypt to improve superior dolma pepper genotypes that are highly adaptive to the local environment, high-yielding, and high-quality. Results indicated that there were three genotypes showed high coefficient of variation (CV%) for yield/ plant. Fourteen genotypes recorded low CV% (Less than 10%) and showed values nearly similar that of the check hybrid (Control). The mean performance of total yield per plant showing that the new selected genotype (BS-5-2) widely varied in this trait. Estimated genetic parameters of the new selected genotypes showed a noticeable amount of environmental effect for total yield per plant. The heritability in broad sense ( $h^2_{bs}$ ) represents the proportion of genotypic variations that is passed from parent to progeny, it was 0.91, 0.92 and 0.95% for average fruit weight, total yield per plant and fruit diameter, respectively. The genotypes (BS-5-2, M-19-4, TOP-4-2 and 90-17-3) were considered the best genotype for yield per plant and could be used in breeding program to develop new local  $F_1$  hybrids of dolma pepper.

**Keywords:** Pepper, *Capsicum*, selection, total yield.



### INTRODUCTION

In Egypt, sweet pepper (*Capsicum annum* L.) is a valuable vegetable crop. There are species in the *Capsicum* genus with  $n=12$  chromosomes. The fruit has glands next to the veins that contain capsaicin, a strong alkaloid. Most of the species *C. annum*, which is farmed throughout the globe in greatest quantities and is eaten as ground spices or fresh veggies, has a bland flavor (Madoşă *et al.*, 2022). *Capsicum* fruits have high nutritional value and higher export prospects. Bell pepper or so-called dolma type pepper is rich in vitamins (A, C, and E). *Capsicum* fruits also contain antimicrobial and anti-inflammatory substances which have very much health benefits. Although Egypt's cultivated area, productivity, and consumption are rising, the current output of the available types is insufficient to satisfy the rising demand in both the local and foreign markets. Sweet pepper cultivators in Egypt are cultivating varieties that are imported from other countries. The only way to meet the local and international markets' demand is to develop local sweet pepper genotypes that yield more and are of higher quality than the imported genotypes (Erika *et al.*, 1998).

The main classical methods utilized in pepper breeding are; Mass selection, Pedigree method (or Genealogical method), Single Seed Descent - SSD method, Backcross, Recurrent Selection and Hybridization are those more (Henrique and Barbieri, 2016). Pedigree method: Keeping records of matings and their progeny. This includes making single plant selections and self-pollination.

Selection is the first step in a successful plant breeding program of parents and genetic diversity is one of the criteria for selection of parents in hybrid production. One of the ways to evaluate the magnitude and nature of the gene effects controlling a certain quantitative trait is through generation

analysis, which allows for simultaneous evaluation of several generations or populations, including parents, hybrids ( $F_1$ ) and segregating populations like the  $F_2$  and those originating from backcrosses (Said 2014).

Assessing the extent of genetic variability and the relationship between different characteristics is crucial for breeders to plan an effective breeding program. This assessment will assist breeders in successfully planning their breeding program by understanding the nature of character association with respect to various traits. Determining if morphological and genetic variances exist among the population individuals in a breeding program is important. This is figuring out the variables that affect genetic and phenotypic variability. Previous pepper populations have exhibited genetic diversity. It is possible to have genetic and environmental variants that form the total phenotypic variations. It is possible to distinguish between the overall phenotypic variation and genetic variation using the coefficient of heritability. Furthermore, the correlation coefficient analysis is a valuable tool for assessing the relative impact of different factors on yield, but it does not offer a precise indication of the specific importance of each factor in relation to yield. The number of effective factors determining the inheritance of characters can be inferred, at least relatively, from the broad sense heritability estimations. Reports have been made regarding the estimated values of broad sense heritability for several pepper characters (Naves *et al.*, 2022). To explore genetic variability, interrelationships among crucial factors, and their direct and indirect effects on fruit yield, a study was conducted using 20 bell pepper genotypes resulted from the current selection program. Therefore, the objective of this study is to improve superior dol ma pepper genotypes (*Capsicum annum* L.) that are highly adaptive to the local environment, high-yielding, and

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DOI: 10.21608/jpp.2024.306410.1357

high-quality. Furthermore, determines the genetic traits that affect pepper yield and its components. Gene-environment interactions, genetic variance, heritability, and expected genetic advancement were all assessed using the combined analysis of variance over years technique. These parameters are essential for selecting superior genotypes that are highly adaptive to the local environment and can serve as parents for hybridization, resulting in the production of superior hybrids that can compete with imported hybrids.

**MATERIALS AND METHODS**

This experiment was carried out during the six successive seasons 2019 (early spring and autumn), and the winter season of 2020, 2021, 2022 and 2023 on pepper were carried out at Experimental farm, Agriculture Faculty, Zagazig University, Egypt to improve superior sweet pepper genotypes (dolma type) that are highly adaptive to the local environment, high-yielding, and high-quality. The source of these six F<sub>2</sub> hybrids was selected from the best commercial dolma pepper hybrids in the Egyptian market including 9016, Top Star, Al-Kapeer, Madrid, Espirina and Belly Star is presented in Table 1.

The selection program started in early spring season of 2019 with seeds of six F<sub>2</sub> populations of sweet pepper came from F<sub>1</sub> hybrids self-pollinated. Selection criteria depend on visual observation of fruit characters and yield traits from F<sub>2</sub> to F<sub>7</sub>, selection and self-pollination ended by 20 stable populations (F<sub>6</sub>) as final selection program in winter season of 2022 as presented in Table 2. All these 20 populations (F<sub>7</sub>) and Top Star F<sub>1</sub> hybrids as check commercial cultivar evaluated in a randomized complete block design with three replicates during winter season of 2023.

**Table 1. Source and characteristics of the used hybrids in the selection program**

No.	Code	Used hybrid name	Source	Fruit type	Average fruit weight (g)	Fruit length (cm)	Fruit diameter (cm)
1	90	9016	USA	Dolma	54	12	7
2	Top	Top Star	Japan	Dolma	49	10	6
3	AL	Al-Kapeer	USA	Dolma	45	13	6
4	M	Madrid	Spain	Dolma	40	9	6
5	ESP	Espirina	India	Dolma	39	10	5
6	BS	Belly Star	Turkey	Dolma	39	8	5

**Table 2. Pedigree of the selected lines**

2019Early spring season (6 F <sub>2</sub> )	2019Autumn season (33 F <sub>3</sub> )	2020Winter season (26 F <sub>4</sub> )	2021Winter season (21 F <sub>5</sub> )	2022Winter season (20 F <sub>6</sub> )	2023Winter season (20 F <sub>7</sub> )
90	90-1 90-10 90-11 90-12 90-17 90-19 90-21 90-22	90-1-20 90-10-8 ----- 90-12-2 90-17-3 ----- 90-21-4 90-22-10	90-1-20-5 90-10-8-4 ----- 90-12-2-9 90-17-3-6 ----- ----- 90-22-10-1	90-1-20-5-3 90-10-8-4-4 ----- 90-12-2-9-3 90-17-3-6-2 ----- ----- 90-22-10-1-4	90-1-20-5-3-10 90-10-8-4-4-2 ----- 90-12-2-9-3-3 90-17-3-6-2-9 ----- ----- 90-22-10-1-4-8
Top	Top-4 Top-6 Top-7 Top-9 Top-14 Top-16 Top-20	Top-4-2 Top-6-17 Top-7-19 Top-9-12 Top-14-11 ----- Top-20-4	Top-4-2-1 Top-6-17-6 ----- Top-9-12-8 Top-14-11-5 ----- Top-20-4-7	Top-4-2-1-2 Top-6-17-6-4 ----- Top-9-12-8-7 Top-14-11-5-3 ----- Top-20-4-7-4	Top-4-2-1-2-6 Top-6-17-6-4 ----- Top-9-12-8-7-3 Top-14-11-5-3-2 ----- Top-20-4-7-4-2
AL	AL-1 AL-6 AL-9 AL-15 AL-19	AL-1-5 AL-6-9 AL-9-15 AL-15-4 -----	AL-1-5-6 AL-6-9-4 AL-9-15-3 ----- -----	AL-1-5-6-2 AL-6-9-4-3 AL-9-15-3-9 ----- -----	AL-1-5-6-2-1 AL-6-9-4-3-2 AL-9-15-3-9-1 ----- -----
M	M-5 M-7 M-13 M-18 M-19	M-5-7 M-7-3 M-13-9 M-18-6 M-19-4	M-5-7-4 M-7-3-2 ----- ----- M-19-4-1	M-5-7-4-8 ----- ----- ----- M-19-4-1-8	M-5-7-4-8-3 ----- ----- ----- M-19-4-1-8-2
ESP	ESP-4 ESP-8 ESP-14	----- ESP-8-3 ESP-14-2	----- ESP-8-3-8 ESP-14-2-6	----- ESP-8-3-8-2 ESP-14-2-6-4	----- ESP-8-3-8-2 ESP-14-2-6-4-3
BS	BS-5 BS-8 BS-12 BS-17 BS-19	BS-5-2 ----- ----- BS-17-1 BS-19-7	BS-5-2-5 ----- ----- BS-17-1-6 BS-19-7-3	BS-5-2-5-3 ----- ----- BS-17-1-6-7 BS-19-7-3-4	BS-5-2-5-3-1 ----- ----- BS-17-1-6-7-2 BS-19-7-3-4-2

The plot area was 7.5 m<sup>2</sup> (7.5 m long × 1.0 m width). Drip irrigation system was used with a distance of 1 m between each two dripper lines and 25 cm between plants in the same line. Routine agricultural practices for pepper

production were done according to the ministry of agriculture recommendations.

**Data recorded:**

Phenotypic selection based on the morphological characters was used in the best plants growing in winter

conditions were labeled from each population. The best plants from the labeled ones in each population was selected to obtain seeds of the next generation during the successive seasons of 2019-2022. At the winter season of 2023, F<sub>7</sub> populations, the following parameters were determined.

The selected F<sub>7</sub> genotypes with the controls were evaluated concerning some traits including total yield per plant (g), total yield per fed. (ton), early yield per plant (g) (calculated as the first harvest), early yield to total yield ratio (%), total number of fruits per plant, average fruit weight (g), fruit length (cm), and fruit diameter (cm).

**Degree of homogeneity:**

In the F<sub>7</sub> season coefficient of variation (CV%) as an indicator of homogeneity was calculated for all populations as individual plants for each genotype related to each character studied as following:

$$C.V. \% = \frac{\sqrt{S^2}}{\bar{x}} \times 100$$

Where,  
S<sup>2</sup> is the variance

$$S^2 = \frac{(\sum x^2 - (\sum x)^2/n)}{n-1}$$

$\sum x^2$  is total square of values  
 $\sum x^2 = \sum (x_1^2 + x_2^2 + x_3^2 + \dots + x_n^2)$   
 $(\sum x)^2$  is square of total values  
 $(\sum x)^2 = (x_1 + x_2 + x_3 + \dots + x_n)^2$

n is number of observations, and  $\bar{x}$  is the grand mean

Coefficient variation (C.V.%) was classified as suggested by Sivasubramanian and Menon (1973) as follows: Low; 0-10%, Moderate; 10-20% and High; above or equal to 20%.

**Genetic parameters:**

Variability in 20 different genotypes was measured in terms of mean, range, genotypic coefficient of variation

(GCV), phenotypic coefficient of variation (PCV), heritability (h<sup>2</sup>), expected genetic advance, and genetic advance as a percentage of the mean (GAM). The genotypic and phenotypic variances were calculated as suggested by Singh and Chuadhary (1995). The genotypic and phenotypic coefficient of variation were calculated by formula suggested by Burton and Devane (1953).

Heritability in broad sense (h<sup>2</sup><sub>bs</sub>) estimates were obtained as described by Burton and Devane (1953), heritability in broad sense was determined as follow:

$$h^2 (b. s.) = \frac{\sigma^2 g}{\sigma^2 ph} \times 100 = \frac{(\sigma^2 A + \sigma^2 D)}{(\sigma^2 A + \sigma^2 D + \sigma^2 e)} \times 100$$

**RESULTS AND DISCUSSION**

**Degree of homogeneity:**

Degree of homogeneity is expressed as the coefficient of variation (CV%). It is very often used to describe variability in a population of study. CV% is classified as suggested by Sivasubramanian and Menon (1973) which indicated high homogeneity when the CV% is lower than 10%, moderate homogeneity when the CV% ranged between 10-20% and low homogeneity when its value more than 20%.

In the current study estimated CV% values for yield per plant and yield ton per fed. (Table 3) ranged from 0.41% (genotype Top-20-4) to 113.03% (ESP-14-2) with a mean of 14.69% in the selected genotypes. Among the 20 selected genotypes, fourteen ones recorded low CV% (Less than 10%) and showed values nearly similar that of the check hybrid (Control) indicating high homogeneity. In addition, three genotypes showed moderate coefficient variance. Meanwhile, there were three genotypes showed high coefficient variance indicating lower homogeneity. The results were consistent with previous studies by Tripodi *et al.* (2020) and Anilkumar *et al.* (2021).

**Table 3. Estimated coefficient of variation (CV%) values for six studied traits in the selected genotypes (season 2023)**

Lines	Yield/ plant (g)	Yield/ fed. (Ton)	Early yield/ plant (g)	Early to total yield ratio	Total number of fruits/plant	Average fruit weight (g)	Fruit length (cm)	Fruit diameter (cm)	Mean
90-1-20-5	3.46 L	3.46 L	5.55 L	5.94 L	2.85 L	2.24 L	2.10 L	3.76 L	3.67
90-10-8	4.05 L	4.05 L	10.50 M	7.12 L	2.44 L	1.89 L	7.03 L	5.06 L	5.27
90-12-2	4.42 L	4.42 L	9.38 L	5.74 L	5.06 L	1.65 L	17.45 M	2.75 L	6.36
90-17-3	5.68 L	5.68 L	18.86 M	18.02 M	4.01 L	1.89 L	7.50 L	8.73 L	8.79
90-22-10	1.60 L	1.60 L	6.98 L	5.44 L	0.70 L	2.21 L	8.90 L	11.58 M	4.88
Top-6-17	23.20 M	23.20 H	9.89 L	27.39 H	6.21 L	17.23 M	3.22 L	39.23 H	18.70
Top-4-2	5.23 L	5.23 L	6.25 L	7.93 L	5.18 L	1.04 L	30.30 H	9.94 L	8.89
Top-9-12	2.11 L	2.11 L	11.97 M	12.74 M	0.82 L	2.14 L	15.97 M	2.39 L	6.28
Top-14-11	3.63 L	3.63 L	4.45 L	3.81 L	2.15 L	3.04 L	2.91 L	8.19 L	3.98
Top-20-4	0.41 L	0.41 L	5.71 L	5.93 L	1.50 L	1.42 L	6.75 L	3.03 L	3.14
AL-1-5	7.41 L	7.41 L	13.90 M	14.89 M	4.30 L	4.36 L	3.68 L	12.06 M	8.50
AL-6-9	16.39 M	16.39 M	15.33 M	5.11 L	5.31 L	11.33 M	7.95 L	10.02 M	10.98
AL-9-15	28.27 H	28.27 H	21.74 H	11.28 M	13.13 M	16.76 M	35.90 H	1.42 L	19.60
M-5-7	34.38 H	34.38 H	32.38 H	5.24 L	14.08 M	22.95 H	4.48 L	5.08 L	19.12
M-19-4	6.12 L	6.12 L	11.66 M	16.18 M	0.88 L	5.95 L	6.54 L	3.56 L	7.12
ESP-14-2	113.03 H	113.03 H	82.91 H	29.53 H	41.61 H	77.60 H	18.87 M	5.25 L	60.23
ESP-8-3	5.84 L	5.84 L	0.23 L	6.08 L	3.69 L	3.66 L	13.17 M	2.64 L	5.14
BS-5-2	16.49 M	16.49 M	5.56 L	15.57 M	8.04 L	8.48 L	7.00 L	18.77 M	12.05
BS-17-1	5.85 L	5.85 L	9.39 L	5.28 L	2.47 L	3.36 L	17.72 M	18.45 M	8.55
BS-19-7	6.31 L	6.31 L	7.71 L	4.19 L	3.52 L	3.36 L	5.49 L	8.23 L	5.64
Mean	14.69	14.69	14.52	10.67	6.40	9.63	11.15	9.01	
Check (Top Star)	5.43 L	5.43 L	12.36 M	8.04 L	4.00 L	1.73 L	4.57 L	11.25 M	6.60

L; low coefficient of variation (>10%), M; medium coefficient of variation (10-20%), H; high coefficient of variation (>20%)

For early yield for the selected populations, a number of eleven genotypes showed high homogeneity and lower CV%. A number of six genotypes showed moderate

homogeneity with percent ranged from 10-20% CV. On the other hand, a number of three genotypes including (AL-9-15, M-57 and ESP-14-2). According to Table 3 there are twelve

genotypes out of the selected twenty showed high homogeneity with low CV% for early to total yield ratio. Meanwhile, there were six genotypes showed moderate homogeneity and two genotypes showed lower homogeneity (TOP-6-17 and ESP-14-2) as compared to control.

For total number of fruits per plant the degree of homogeneity was high for 17 genotypes. In addition, there were two genotypes showed moderate homogeneity (AL-9-15 and M-5-7) and one genotype showed low homogeneity (ESP-14-2). A number of fifteen genotypes showed high homogeneity for average fruit weight character. While, three genotypes with moderate homogeneity and two with low homogeneity.

Concerning fruit length and diameter, there were thirteen and fourteen genotypes showed lower CV%, respectively indicating high homogeneity. In addition, five genotypes showed moderate homogeneity with CV% ranged between 10-20% in both traits. Meanwhile, there were two genotypes (TOP-6-17 and AL-9-15) and one genotype (TOP-6-17) showed CV% higher than 20% indicating low homogeneity for fruit length and diameter characters, respectively.

In the current results, out of the selected genotypes, ESP-14-2 genotype showed high coefficient of variation among all traits, except for fruit length and fruit diameter. Furthermore, the high genetic variance for all traits in this genotype indicates high heterogeneity. In addition, there were

two other genotypes (AL-9-15 and M-5-7) showed high coefficient of variation in three different characters including yield per plant, yield per fed. and early yield per plant while in the other characters their coefficient of variation ranged between moderate to low which indicates heterogeneity among these three characters for these two genotypes. For these three genotypes, the variance analysis showed significant variations between the genotypes in particular characteristics, demonstrating a wide range of diversity in these genotypes that can be utilized through selection. These results are consistent with previous findings reported by Suwor *et al.* (2017).

**Mean Performance:**

The mean performance of total yield per plant and per feddan is presented in Table 4, showing that the new selected genotype widely varied in this trait. The best genotypes for yield amount included BS-5-2, M-19-4, TOP-4-2 and 90-17-3 with values ranged between 2032 and 2342 g per plant. These superior lines produced total yield with a percentage (78-90%) out of the control yield amount (Top Star). However, it is very good that some of the new selected lines produced about 80-90% of total yield out of the total yield of the commercial F<sub>1</sub> hybrid (Top Star). For early yield trait a number of four of selected genotypes showed early yield higher than the control (TOP-4-2, 90-12-2, M-19-4 and TOP-9-12) which considered as a good indicator for highly improving this trait in the selected populations.

**Table 4. Mean performance of evaluated the selected new lines for some plant and fruit characters (season 2023)**

Lines	Yield/ plant (g)	Yield/ fed. (Ton)	Early yield/ plant (g)	Early to total yield ratio (%)	Total number of fruits/plant	Average fruit weight (g)	Fruit length (cm)	Fruit diameter (cm)
90-1-20-5	1006.89	16.11	13.46	1.34	28.51	35.32	8.06	3.58
90-10-8	1250.10	20.00	18.10	1.45	30.83	40.54	10.85	4.37
90-12-2	1659.70	26.56	31.54	1.90	36.20	45.87	12.22	3.47
90-17-3	2032.81	32.53	27.76	1.36	37.42	54.30	10.96	4.61
90-22-10	1091.54	17.46	20.47	1.87	30.15	36.21	10.30	4.52
Top-6-17	692.05	11.07	15.53	2.34	25.50	26.96	6.49	4.15
Top-4-2	2257.12	36.11	32.88	1.46	39.71	56.84	7.94	5.28
Top-9-12	1857.24	29.72	31.09	1.68	36.57	50.79	10.98	9.14
Top-14-11	1237.83	19.81	13.04	1.05	29.99	41.28	10.25	4.52
Top-20-4	714.69	11.44	15.86	2.22	25.69	27.83	10.58	7.19
AL-1-5	915.70	14.65	16.72	1.83	27.91	32.79	9.39	3.63
AL-6-9	1671.82	26.75	28.32	1.70	34.40	48.41	9.56	5.36
AL-9-15	1143.54	18.30	19.49	1.73	28.11	40.10	9.95	4.61
M-5-7	682.85	10.93	13.62	2.01	24.37	27.44	8.90	3.36
M-19-4	2263.30	36.21	31.18	1.39	38.81	58.32	9.06	4.41
ESP-14-2	907.61	14.52	16.54	2.34	26.38	28.34	12.92	2.41
ESP-8-3	656.00	10.50	15.05	2.30	24.60	26.66	3.44	4.56
BS-5-2	2342.35	37.48	28.80	1.25	38.88	59.98	9.69	5.03
BS-17-1	1484.85	23.76	26.18	1.76	32.57	45.57	10.54	5.78
BS-19-7	1871.78	29.95	27.83	1.49	36.26	51.59	9.94	5.55
Check (Top Star)	2598.50	41.58	30.48	1.17	40.62	35.32	9.02	2.38
LSD (0.05)	469.85	7.52	6.95	0.43	5.03	9.82	16.74	0.95
LSD (0.01)	629.34	10.07	9.31	0.58	6.74	13.15	22.42	1.27

Furthermore, for early to total yield ratio the genotypes (ESP-14-2, TOP-6-17, ESP-8-3, TOP-20-4 and M-5-7) recorded higher values 2.34, 2.34, 2.30, 2.22 and 2.01 % as compared to control which gave 1.17%.

For total number of fruits per plant, the control (F<sub>1</sub> Top Star hybrid) was the superior followed by seven genotypes having 90-95% out of the control in this trait. The control recorded 40.62 fruits per plant followed by the seven superior genotypes giving a number of 36 - 39 fruits per plant. However, the control showed higher number of fruits it showed lower average fruit weight. On the other hand, the same seven genotypes showed higher average fruit weight with lower number of fruits per plant as compared to control.

In concern to fruit length, there were two genotypes showed 12 cm fruit length which is not desired for the Egyptian customers. The desired fruit length should be ranged between 8-10 cm similar to control. In this connection, all of the selected lines were at this range of fruit length, except for three genotypes (ESP-14-2, 90-12-2 and ESP-8-3). The selected genotypes showed a great variation in fruit diameter which consume in having a wide range of genotypes that can

be used for hybridization for producing different shape of pepper hybrid fruit.

**Genetic parameters:**

Estimated genetic parameters of the new selected genotypes for some yield and fruit characters are shown in Table 5. The current results showed a noticeable amount of environmental effect for total yield per plant and total yield per fed. Low difference between genotypic and phenotypic variance value (0.97 and 1.05) was observed for total yield per plant. Since the phenotypic variance ( $\sigma^2P$ ) due to genotypic variance ( $\sigma^2g$ ) by 92.34%, while 7.7% due to environmental effect ( $\sigma^2e$ ). The estimate broad sense heritability ( $h^2b$ ) was high (0.92); while, expected genetic advance as a percent of mean (GAM%) was high (143.19%). Furthermore, total yield per plant and per fed. under this study showed high GCV and PCV% values. Moderate genotypic and phenotypic coefficient of variance was observed for early yield per plant and early to total yield ratio. Furthermore, the phenotypic

variance ( $\sigma^2P$ ) due to genotypic variance ( $\sigma^2g$ ) by 89.57%, while 10.5% due to environmental effect ( $\sigma^2e$ ) for early yield trait. For early yield GCV%, PCV%,  $h^2bs$  and GAM% recorded values of 56.30, 59.49, 0.90 and 109.77, respectively. For early to total yield ratio, high ratio values were observed of  $\sigma^2g/\sigma^2p$  (86.08%), GCV (37.65%), PCV (40.58%) and  $h^2bs$  (0.86) which suggested low environmental effect for this trait.

The heritability represents the proportion of phenotypic variation that is passed from parent to progeny. The greater the heritable variation, the higher the potential for fixing the traits through selection (Jang *et al.*, 2017). The current results indicating the role of additive and non-additive gene action in the expression of these characters and further improvement of these characters would be easier through mass selection, progeny selection or any modified selection procedure aiming to exploit the additive gene effects rather than simple selection.

**Table 5. Estimated genetic parameters of the evaluation of the selected new lines for some yield and fruit characters**

Genetic Parameters	Yield/ plant (g)	Yield/ fed. (Ton)	Early yield/plant (g)	Early to total yield ratio (%)	Total number of fruits/plant	Average fruit weight (g)	Fruit length (cm)	Fruit diameter (cm)
CV%	20.84 H	20.88 H	19.21 M	15.14 M	9.70 L	14.40 M	13.17 M	12.02 M
$\sigma^2e$	0.08	20.68	17.66	0.07	9.28	35.28	2.18	0.33
$\sigma^2g$	0.97	248.14	151.70	0.43	80.22	375.92	6.12	5.87
$\sigma^2p$	1.05	268.83	169.37	0.50	89.49	411.20	8.31	6.20
$\sigma^2g/\sigma^2p$	92.34	92.31	89.57	86.08	89.64	91.42	73.74	94.67
GCV%	72.34 H	72.31 H	56.30 H	37.65 H	28.52 H	47.02 H	22.07 H	50.65 H
PCV%	75.28 H	75.27 H	59.49 H	40.58 H	30.13 H	49.17 H	25.70 H	52.06 H
GCV/PCV	93.75	5.86	7.27	131.70	10.01	4.72	29.80	39.06
$h^2bs$	0.92 H	0.92 H	0.90 H	0.86 H	0.90 H	0.91 H	0.74 H	0.95 H
GA	1.95	31.18	24.01	1.25	17.47	38.19	4.38	4.86
GAM%	143.19 H	143.12 H	109.77 H	71.96 H	55.63 H	92.60 H	39.05 H	101.53 H

H, High; M, Moderate; and L, Low

The heritability in broad sense, which refers to the ratio of genotypic variance to total variance, was described by Yunandra *et al.*, (2018). Characteristics with high heritability in broad sense demonstrate that a significant portion of the phenotypic variance is attributable to genotypic variance and is less affected by the environment. Consequently, selection can lead to substantial improvements in those characteristics (Xiao *et al.*, 2016). While heritability estimates may not offer precise predictability of the breeding value, genetic advance is considered to be more beneficial measure. As a result, the estimation of heritability along with genetic advance is typically more practical than heritability alone in projecting the resulting impact when selecting the best individuals (Hasanuzzaman and Golam, 2011).

The total number of fruits per plant showed lower coefficient of variance with values of  $\sigma^2g$  and  $\sigma^2p$  80.22, 89.49%, respectively. Furthermore, it showed high GCV %, PCV%,  $h^2bs$  and GAM% with values 28.52, 30.13, 0.90 and 55.63%, respectively. The average fruit weight, fruit length and fruit diameter all followed the same trend for genetic parameters giving moderate coefficient of variance and high GCV%, PCV%,  $h^2bs$  and GAM% values.

The broad sense heritability shows how effectively genotypes can be selected based on their phenotypic performance (Belay *et al.*, 2020). In the current results, all of the characters showed high heritability estimates. The high heritability estimates suggest that the population could undergo mass selection or a modified selection process to take advantage of any additive effect (Solomon *et al.*, 2019).

Moreira *et al.* (2018) demonstrated that using heritability estimates in conjunction with genetic advance and genetic advance in percent of mean is more effective in predicting the outcome of selecting the best individuals within a population compared to relying solely on heritability estimates. Additionally, Sewore and Abe (2024) stated that when heritability is predominantly attributed to additive gene effects, the expected genetic advance will be high.

Kadium and Svyantek (2023) suggested that broad sense heritability estimates should be considered together for effective selection purposes. Traits such as yield per plant, early yield per plant, average fruit weight and number of fruits per plant, which have high heritability estimates and genetic gain, could be improved through selection.

**CONCLUSION**

Selection is the first step in a successful plant breeding program of parents and genetic diversity. In the current study, six F<sub>2</sub> hybrids was selected from the best commercial dolma pepper hybrids in the Egyptian market including 9016, Top Star, Al-Kapeer, Madrid, Espirina and Belly Star. Out of the selected genotypes, the best genotypes for yield amount were BS-5-2, M-19-4, TOP-4-2 and 90-17-3. These superior lines produced higher total yield. So, this study recommends these genotypes can be used as a superior parent for a hybridization program. In addition, the genotypes BS-5-2, M-19-4, TOP-4-2 and 90-17-3 can be used as good material or genotypes after conducting stability and disease resistance.

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## تربية طرز جديدة من الفلفل الحلو بالانتخاب

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## الملخص

يُعد الانتقاء الخطوة الأولى في برنامج تربية الفلفل الناجح للأباء ويعتبر التنوع الوراثي أحد معايير اختيار الأباء في إنتاج الهجين. أجريت تجربة حقلية خلال ستة أعوام (ربيع وخريف 2019، وشتاء 2020، 2021، 2022 و2023) بالمزرعة التجريبية، كلية الزراعة، جامعة الزقازيق، مصر بهدف انتقاء تراكيب وراثية متفوقة من الفلفل تتميز بالأقلية العالية للظروف البيئية المحلية وذات إنتاجية وجودة عالية. أوضحت النتائج بوجود ثلاث تراكيب وراثية من الفلفل أظهرت قيمة عالية لمعامل الاختلاف (CV%) لصفة المحصول / نبات، سجل 14 تركيب وراثي قيمة منخفضة لمعامل الاختلاف (أقل من 10%) وكانت مشابهة تقريباً لهجين المقارنة (الكنترول). أظهر متوسط الأداء لصفة المحصول الكلي/ نبات أن التركيب الوراثي الجديد (BS-5-2) المنتخبة كان مختلف في هذه الصفة. تقدير المدلولات الوراثية للتركيب الوراثية الجديدة المنتخبة أظهرت قيمة ملحوظة لتأثير البيئة لصفة المحصول الكلي لكل نبات. تقيس درجة التوريث بالمعنى الواسع نسبة الاختلافات الوراثية التي وُرثت من الأب إلى النسل وكانت 0,91، 0,92، و0,95 لصفات متوسط وزن الثمرة، والمحصول الكلي لكل نبات، وقطر الثمرة على الترتيب. تعتبر السلالات (BS-5-2، M-19-4، TOP-4-2 and 90-17-3) أفضل السلالات في كمية المحصول ويمكن استخدامها في برامج تربية الفلفل الحلو.