# GENE ACTION, GENETIC COMPONENTS AND GENETIC ADVANCEIN SWEET PEPPER (*Capsicum annuum* L.)

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**ABSTRACT**:

*The present study were conducted at Privet Farm in Sedi-Salim district, Kafr El-Sheikh Governorate, Egypt, during two successive summer seasons of 2016 and 2017,to estimate the combining abilities, genetic components, heritabilities (broad and narrow sense) and genetic advance on sweet pepper (Capsicum annuum L.). Six parental genotypes and their fifteen $F_1$ hybrids in a half diallel cross system were used.*

*The experimental genotypes were grown in randomized complete blocks design (RCBD), with three replicates on greenhouse. The traits were studied i.e., plant height (PH);branches number (BN); leaf area (LA); early and total yield traits as fruits number (FN) and fruit yield (Y); fruit length (FL); fruit diameter (FD);average fruit weight (AFW); locales number (LN);seeds number (SN); pericarp thickness (PT) and total soluble solids (TSS). The results revealed that, the mean squares for general (GCA) and specific (SCA) combining abilities were highly significant for all the studied traits, suggesting the presence of both additive and non-additive gene effects in the inheritance of the various studied characters, except SCA for (BN), suggesting that its only controlled by additive gene effects. Moreover, the ratio of GCA/SCA showed that GCA effects was more important than SCA effects in all traits except LA and FN in early yield, Y in total yield, AFW and TSS since, SCA were greater than GCA. The majority of GCA effects obscure that these traits would positively respond to direct selection. While, the majority of SCA effects implied that these traits would positively respond to hybridization.*

*  **Conclusively,** these results suggested that the hybrid vigour is available for commercial production of sweet pepper hybrid, and that*

*isolation of pure lines from the progenies of heterotic $F_1$'s is a possible way to improve the fruits yield and fruit quality.*
**Key words:** Sweet pepper, combining abilities, GCA, SCA, heritability and genetic advance.

## INTRODUCTION

Sweet pepper (*Capsicum annuum*L.) commonly recognized as Bell pepper or Capsicum. Moreover, Sweet pepper is popular among the vegetables, for its delicate taste and pleasant flavour. However, it is a vegetable crop grown worldwide belonging to the family *Solanaceae*. Furthermore, Capsicum peppers are most common in tropical and subtropical countries with *Capsicum annuum* L., by far most widespread species (Rehm and Espig, 1984). Capsicum pepper is a diploid species, which has 2n = 24 chromosomes (De Candole, 1886) andrecent studies (Tong and Bosland, 1997) who indicated thatthe chromosome number for non-pungent species isn = 13 whereas, it is n = 12 for the pungent species. Pepper is a generally self-pollinated and chasmogamous crop whose flowers open only after pollination takes place. However, 11-64% outcrossing was observed under open pollination (Lemma, 1998).Despite the increase in cultivation and commercialization of pepper in the last few years (Rêgo *et al.*, 2011). Moreover, in recent years, its demand has increased tremendously with the emergence of pizza industry (Sood *et al.,* 2011). Besides, it also has a medicinal properties and hence, recommended for the treatment of dropsy, colic toothache and cholera (Pairce, 1987). Sweet pepper have high nutritional values; contains a various vitamins, biological pigments (lycopene, carotenoids and xanthophy ll), dietary fiber and several essential minerals. Therefore, pepper consumption is increasing and may represent an important source of vitamins for the world populations (Ghasemnezhad *et al.,* 2011). The antioxidant vitamins C (ascorbic acid) and E (alpha-tocopherol) and pro-vitamin A (â-carotene), which are preventive of cancer and cardiovascular human diseases, are present in high concentrations in various pepper types (Palevitch and Craker, 1995). In addition, peppers are rich in flavonoids (Lee *et al*., 1995) and other phytochemicals (Duke, 1992). Peppers are grown in most countries of the world and their annual production has increased substantially over the years since the cultivated area in worldwide was 1,938,788 ha with an average of 17.79 ton/ha (7.475 ton/fed.) with total production 34,497,462 ton in 2016(Anonymous, 2016). Egypt ranked 8[th]global among the pepper-

producing countries with about 650,554 tons with cultivated area 98,301 fed. with an average of 15.44 ton/ha (6.488 ton/fed.) with total production 637,760 ton in 2016. While, China ranked the $1^{st}$ one with total production 17,435,376 with an average 23.220 ton/ha (9.756 ton/fed.), which coming from 750,893ha. (Anonymous, 2016). Statistical records illustrated that (Egypt) average productivity from cultivated unit (fed.) is low, therefore, greatly courtesy must be given to increase the productivity by rising new cultivars or hybrids through breeding programs. The popularity of $F_1$ hybrid cultivars are high yielding, uniformity, disease resistance, stress tolerance and good horticultural behaviors including earliness and long shelf life and therefore giving constant stable high yielding (Sood and Kumar, 2010). Moreover, Betlach (1967) testified that, to develop a good looking hybrid, it is important to have a good balance between length and width of the fruit, pericarp thickness is a desirable trait as it imparts fruit firmness and also prolongs harvest shelf life. Also, medium sized fruit was preferred over large size fruits.

The knowledge of general combining ability (GCA) and specific combining ability (SCA) helps to select the parents as well as crosses and to find out gene action to formulate an effective breeding practice. Regarding the combining ability effects, Griffing (1956) stated that, analysis of combining ability is an one of the possible tools for identifying productive parents to develop commercial $F_1$ hybrids. The information on the relative importance of GCA and SCA are of great values in the breeding programs for the species which are amenable to the development of $F_1$ hybrid cultivars, as sweet pepper. In broad-spectrum, when a specific line reflects high estimate of GCA, it means that it is a good combiner parent and possesses a good genes; whereas, high SCA of a particular combination means that the parents of this cross can combine well to produce a hybrid with a superior general performance, which reflects a clear heterotic effect. Moreover, when the additive gene action is the major component of the total genetic variation, GCA parameter would be high and a maximum progress to expected in a selection program. While, a hybrid breeding program may be the appropriate choice, as reflected with SCA estimate.

Accordingly, the present investigation was conducted to estimate some important genetic parameters, *i.e.,* general and specific combining abilities (GCA and SCA), genetic parameters and genetic advance in some important traits of sweet pepper.

## MATERIALS AND METHODS

The experiment was conducted at the a privet greenhouse of Sedi Salem district, Kafr El-Sheikh Governorate, Egypt, during two successive summer seasons of 2016 and 2017 to estimation combining abilities (general and specific) for some traits in Sweet pepper (*Capsicum annuum* L.). Six parental genotypes namely: California Wonder, Maor *cvs.* and four lines, *i.e.,* $L_1$, $L_2$, $L_6$ and $L_8$ which obtained from Dr. Gendy, Hort. Res. Inst., Agric. Res. Center, Egypt; and their fifteen $F_1$ hybrids that obtained from a diallel cross system, without reciprocals, were used in the present study. These lines were produced by pedigree selection method with high degree of homozygosity. The *cvs.* California Wonder and Maor were self-pollinated for two generations to be sure a pure.

The parental genotypes had a widely differed on most characters (Table A). Crossing was made in the first season of 2016 between the parental genotypes, without reciprocals, to produce $F_1$ genotypes (15 ones). All genotypes in the second season of 2017 (parents and $F_1$'s crosses) were assessed in a greenhouse. A randomized complete blocks design (RBCD) with three replications was used, each replicate contains 10 plants in every genotype (parents or crosses). The seeds were sown on nursery in seedling trays at $15^{th}$ of March and the plants were transplanted in the greenhouse on the first week of May to hybridization and evaluation in the two growing seasons. The plants of each genotypes (parents and $F_1$'s crosses) were scattered in ridges 5.0 meters long and 80 cm in width, the space between plants was 50 cm.

Agricultural practices for pepper production, *i.e.,* irrigation, fertilization, plant protected against weeds, and pests control were practiced as recommended. The studied characters were i.e.*,* plant height (PH), cm; branches number (BN); leaf area, $cm^2$ (LA); early and total yield as (fruit number (FN) and yield, (Y) (kg $plant^{-1}$); fruit length, cm (FL) and diameter, cm (FD); average fruit weight, g (AFW); locales number (LN); pericarp thickness, mm (PT) and total soluble solids (TSS), which was determined by a hand refractometers.

Analysis of variance and significant of differences tested according to Cochran and Cox (1957). Differences among means for all traits were tested for significant, according to the least significance differences (L.S.D.) according to Snedecor and Cochran (1990). Combining ability analysis is a powerful tool to identify good combiners and select appropriate parents in hybrid development program according to Kumar *et al.* (2016). For that the general combining ability (GCA) and specific combining ability (SCA) and its effects (*gca* and *sca*) were estimated according to Griffing (1956) method II

Model I diallel analysis. To determine the relative magnitudes of mean squares of GCA and SCA, GCA/SCA ratios were calculated from their respective of GCA and SCA mean squares. Standard errors for differences between means of the measured characters and for combining ability effects were determined and used to calculate the least significant differences (LSD) for $P$ <0.05. The relative contributions of genetic components were determined to obtain estimates of GCA variance ($\sigma^2$gca) and SCA variance ($\sigma^2$sca) for each character. Additive variance ($\sigma^2$ A) and dominance variance ($\sigma^2$ D) were estimated as the formula of $\sigma^2$ A = 2($\sigma^2$gca) and $\sigma^2$ D = ($\sigma^2$sca). Genotypic variance ($\sigma^2$ g) and phenotypic variance ($\sigma^2$ p) were also calculated as:

$$\sigma^2 \text{ g} = \sigma^2 \text{ A} + \sigma^2 \text{ D, and } \sigma^2 \text{ p} = \sigma^2 \text{ g} + \sigma^2 \text{ e.}$$

Heritability in broad sense, it was estimated as the ratio of total genotypic variance to the phenotypic variance according to (Falconer, 1981):

$$\text{Heritability, } h^2 \text{ (bs)} = (\sigma^2 g/\sigma^2 p) \times 100.$$

Moreover, heritability in the narrow ($h^2$n) sense was calculated from the estimated components of variances as:

$$h^2 n = (\sigma^2 A/\sigma^2 \text{ p}) \times 100.$$

The heritability percentage was classified as low (0–30%), moderate (30–60%), and high ≥60% as given by Johnson *et al.,* (1955).

Furthermore, a genetic Advance is the extent of genetic advance expected through selection for the character was calculated as:

Genetic Advance (GA) = H×P×K according to Addissu (2012).

Where *H* is heritability, *P* is phenotypic standard deviation, and *K* is selection deferential (2.06 at 5%). While, genetic gain (%) was calculated as the following equation:

Genetic gain (%) = GA × 100.

It is classified as low (0–10%), moderate (10–20%) and high (20% or higher) as given by (Johnson *et al.,* 1955).

Finally, the average degree of dominance $\sqrt{H/D}$ was estimated as $\sigma^2$sca/$\sigma^2$gca according to Singh and Chaudhary (1979).

## RESULTS AND DISCUSSIONS

Data in Tables (1 and 2) reflected that the analysis of variances due to genotypes and its components (parents, crosses and parents *vs.* crosses) were highly significant for all studied traits, except branches number and early yield (parents *vs.* crosses) were insignificant. These results indicating the wide diversity between the used parental materials in this study.

The success of breeding program mainly depends upon the choice of suitable parents and their utilization by adopting an appropriate breeding methodology (Sprague, 1966). The concept of combining ability was originally developed to identify potential parents either to be used in the development of hybrids or recombinant breeding for getting elite pure lines (Sprague, 1966). This analysis facilitates the partitioning of genotypic variation of crosses into variation due to general combining ability (*gca*) and specific combining ability (*sca*) effects and there variances (GCA and SCA).

The general combining ability variances are the measure of additive gene action which represent the fixable components of genetic variance and are used to classifying parents for the breeding behavior in hybrid combinations. On the other hand, specific combining ability variances are the measure of non-additive gene action which are related to non-fixable component of genetic variance (Sprague, 1966). Moreover, the analysis of variance along with GCA and SCA variances were also revealed highly significant differences amongst the parents and crosses ($F_1$'s) for all characters, indicating contribution of both additive and non-additive gene effects to total genetic variation, except SCA variance for branches number was insignificant indicated that it was under the control of additive gene action and it could well be improved by resorting to simple selection. Therefore, further analysis is appropriate. The results are in collaboration with the findings of Todorov (1995), and Kamble *et al.* (2009), those are reported both of additive and dominance gene action which were involved in the inheritance of vegetative traits. However, the additive component was higher than non-additive one that reported by Doshi (2003); Singh and Choudhary (2005); Sood and Kaul (2006); Ibrahim (2007); Devi (2014) and Amer (2018). While, non-additive gene action was more important than additive gene action (Ahmed *et al.*, 2003; Chaudhary *et al.*, 2013; Adday, 2016; Gandadhara*et al.*, 2016; Herath*et al.*, 2017). Furthermore, the epistasis gene effects played the important role in the control of plant height (Joshi, 1990),and inter-allelic interactions in branches number (Rohini *et al.,*2017).

Regarding the inheritance of early and total yield traits, some studies revealed that both of additive and non-additive effects were important for early and total yield traits which revealed that the additive gene effects were more important than non-additive ones in the inheritance of this trait (Metwally *et al.*, 2003; Khalil *et al.*, 2004; Patel *et al.*, 2004; Chaudhary *et al.*, 2013; Khalil and Hatem, 2014, and Mahmoud, 2014 in number of fruits[-1], and Amer, 2018). On contrary, many researchers reported that non-additive effects were important in the inheritance of this trait (Ahmed *et al.*, 2003;

Nandadevi, 2003a; Ibrahim, 2007; Devi, 2014; Nascimento *et al.*, 2014; Jindal *et al.*, 2015; Adday, 2016; Gandadhara *et al.*, 2016 and Herath *et al.*, 2017). Moreover, Hasanuzzaman and Golam (2011) found that the additive, dominance and epistasis were more important for fruit number and total yieldplant$^{-1}$.

For fruit quality traits many researchers studied and cited that the additive gene effect was involved in the inheritance of such traits (Doshi, 2003; Farag, 2003; Khalil *et al.*, 2004; Metwally *et al.*, 2005; Ibrahim, 2007; Fekadu *et al.*, 2009; Amer, 2018). Moreover, (Ahmed *et al.*, 2003; Nandadevi, 2003a and Geleta and Labuschagne, 2006) reported that both of additive and non-additive are important in inheritance in such traits. While, the non-additive effect was involved in the inheritance of fruit length (Patel *et al.*, 2004, Singh and Choudhary, 2005; Chaudhary *et al.*, 2013; Khalil and Hatem, 2014; Devi, 2014; Nascimento *et al.*, 2014; Jindal *et al.*, 2015; Adday, 2016; Herath *et al.* 2017), fruit diameter (Farag, 2003, Adday, 2016 and Herath *et al.* 2017), pericarp thickness and locales number (Gandadhara *et al.*, 2016; Herath *et al.* 2017 and Amer, 2018), total soluble solids (Geleta and Labuschagne, 2006 and Ibrahim, 2007); locales number, average fruit weight and pericarp thickness(Gandadhara *et al.*, 2016 and Herath *et al.* 2017).

Meanwhile, Joshi (1990) found that epistasis gene action revealed the important role in the control of fruit length, Khereba *et al.* (1995) found that dominance gene effect and non-allelic interactions were important in the inheritance of fruit length and Khalil *et al.* (1989) reported that the additive and epistasis effects were important and played the main role in the inheritance of this trait. Moreover, the additive and non-allelic interactions were important for inheritance of fruit diameter (Khereba *et al.*, 1995), and inter-allelic interactions for total soluble solids (Rohini *et al.,* 2017).

In addition, the ratio of GCA/SCA showed that GCA effects was more important than SCA effects in all traits (more than unity), except (leaf area, fruits number in early yield, yield in total yield, average fruit weight and total soluble solids), since, SCA were greater than GCA (less than unity). The majority of GCA effects obscure that these traits would positively respond to direct selection. While, the majority of SCA effects implied that these traits would positively respond to hybridization. These results confirmed with (Doshi, 2003, Farag, 2003; Metwally *et al.,* 2003; Khalil *et al.*, 2004; Patel *et al.*, 2004; Metwally *et al.*, 2005; Singh and Choudhary, 2005; Sood and Kaul, 2006; Ibrahim, 2007; Fekadu*et al.*, 2009; Chaudhary *et al.*, 2013; Khalil and Hatem, 2014, and Amer, 2018). While, disconfirmed with (Ahmed *et al.*, 2003; Farag, 2003; Metwally *et al.*, 2003; Nandadevi, 2003a; Ibrahim, 2007;

Chaudhary *et al.*, 2013; Adday, 2016;Gandadhara*et al.*, 2016, and Herath *et al.*, 2017). Indicating there is a huge variability in pepper germ plasma were worked on in these several studying's.

The estimates of *gca* effects of six parental genotypes in fourteen traits Tables (3 and 4) indicated that the parent $P_1$ was the good combiner for yield in total yield, fruit length and average fruit weight in fruit quality traits. Moreover, $P_2$ was the good combiner for plant height, branches number and fruit diameter. However, $P_3$ was the good one in fruits number in early yield, seeds number and pericarp thickness. While, $P_4$ for leaf area and total soluble solids. Furthermore, $P_5$ for locales number. Finally, $P_6$ for yield in early yield and fruits number in total yield. Similar results were observed by Doshi (2003), Mahmoud (2014) and Amer (2018).

The results for *sca* effects in Tables (5 and 6) reflected that, the cross 1×2 had a desirable SCA effect in plant height, 1×3 forfruit numbers in early yield, 1×5 in (branches number, average fruit weightand seeds number) 1×6 for yield in early yield, 2×3 for fruit length, 2×4 for pericarp thickness, 2×5 for fruit numbers in early yield, (fruit numbers and yield) in total yield and total soluble solids, 4×5 for fruit diameter, average fruit weight and locales number, and 4×6 for leaf area. Similar results reported by Huang *et al.*,(2009); Rêgo *et al.* (2009); Khalil and Hatem (2014); Devi (2014); Nascimento *et al.*, (2014); Adday (2016); Amer (2018). Generally, no relationships were observed between GCA effects for parental lines and the SCA of the $F_1$ combinations. Since most types of combinations; i.e., poor × poor, poor × medium, poor × high, medium ×medium and medium ×high, GCA parents, showed a significant SCA effects. These findings were similar to those obtained by Huang *et al.*(2009); Rêgo *et al.*(2010); Khalil and Hatem (2014).

Dominance component was higher than additive one in all studied traits except in branches number the additive one was more important (Tables 7 and 8). This results confirmed with the result obtained from Table (1) since SCA was insignificant and only GCA was highly significant. Also, the degree of dominance ($\sqrt{H/D}$) confirmed the previous result was more than one in all the studied traits except for branches number.

The effective selection depends on the heritable components of genetic variation, which can be measured by heritability. Heritability is the portion of genetic variation which is transmitted from generation to generation. Lush (1940) classified heritability into broad sense and narrow sense. Heritability

in broad sense is the portion of genetic variance to the total variance and therefore, it gives the broad perspective, whereas, narrow sense heritability is the portion of additive genetic variance to the total variance and gives precise estimate of genetic variability. Consequently, the knowledge of heritability is essential for crop improvement. Chang (1977) evaluated according to Burton and De Vane (1953), heritability is a measure of heritable variation and is helpful in prediction of the expected amount of improvement to be achieved through selection.

For the amount of dominance effects, it can be seen from the value of $\sqrt{H/D}$. The value $\sqrt{H/D}$ was less than one (0.158) only for branches number, indicating partial dominance, similar results recorded by (Mahmoud, 2014). while it was more than one for the other traits, indicating over dominance. Similar results recorded by (Mahmoud, 2014 and Amer, 2018).

For heritability in broad sense, it were more than 90% in all the studied traits indicated that all the traits is none effected by the environment conditions. Moreover, in narrow sense, it was high ($\geq 60\%$) in branches number, moderate (30–60%) in plant height, yield in early yield, locales number and pericarp thickness. In these traits, it well be favorable in enhancement by selection in advanced generations. While, it was low (0–30%) in other traits (plant height, leaf area, fruits number in total yield, fruit length, fruit diameter, average fruit weight and locales number) well be enhancement through hybridization. Similar finding were high in vegetative traits (Marame *et al.,* 2009; Hasanuzzaman *et al.*, 2012; Chaudhary *et al.*, 2013; Devi, 2014; Adday, 2016; Rohini *et al.*, 2017, and Amer, 2018). Moreover, narrow sense heritability found to be high by (Sood*et al.*, 2007; Marame*et al.*, 2009; Hasanuzzaman *et al.*, 2012, and Amer, 2018) for plant height and leaf area. While, others researchers found it were low (Adday, 2016; Rohini *et al*. 2017, and Amer, 2018) for branches number.

For yield traits, many studies revealed heritability in broad sense were moderate to high estimates (Metwally *et al*., 2003; Marame *et al*, 2009; Hasanuzzaman *et al*., 2012; Devi, 2014; Adday, 2016; Rohini *et al.,* 2017, andAmer, 2018). Moreover, narrow sense heritability found to be high by(Hasanuzzaman *et al*., 2012 and Amer, 2018) for fruits number in early yield. While, (Hasanuzzaman *et al.,* 2012; Adday, 2016;  Rohini *et al.*, 2017, and Amer, 2018)for yield in early yield, fruits number and yield in total yield cited that heritability in narrow sense was low.

For fruit quality traits, heritability in broad sense, some studies conducted that it these traits were high (Marame *et al.*, 2009; Hasanuzzaman *et al.*, 2012; Chaudhary *et al.*, 2013; Devi, 2014; Adday, 2016; Rohini *et al.*, 2017, and Amer, 2018). While, Metwally *et al.* (2005) in fruit length; Devi (2014) in fruit diameter revealed that it was low. Moreover, narrow sense heritability found to be high (Metwally *et al.*, 2005; Marame *et al.*, 2009; Hasanuzzaman *et al.*, 2012; Adday, 2016; Rohini *et al.*, 2017, and Amer, 2018 for seeds number, fruit diameter and average fruit weight).And others cited that it was low (Metwally *et al.,*2005) in fruit length, Hasanuzzaman *et al.* (2012) in seeds number, Devi (2014) in fruit diameter, Adday (2016) in fruit length, and Amer (2018) for fruit length, locales number, pericarp thickness and total soluble solids.

For expected genetic advance, the results revealed that it was high and more than 20% in (yield in early yield, pericarp thickness, yield in total yield, fruits number in early yield, seeds number, branches number, leaf area, fruit numbers in total yield and plant height), moderate in other traits since it was above 10% and less than 20% and low in total soluble solids. Similar results found a high estimates of genetic advance observed for marketable fruit yield per plant, number of fruits per plant were in consonance with the finding of earlier researchers (Shrestha (2003), Nazir*et al.* (2005), Sood *et al.* (2007), Naik *et al.* (2010), Sharma *et al.* (2010 a and b), Kumari (2013) and Devi (2014) yield traits.

High heritability coupled with high genetic advance (GA) were observed in $h^2$ and GA in branches number, moderate $h^2$ and high GA in plant height, yield in early yield and pericarp thickness ; moderate $h^2$ and GA in locales number ; low $h^2$ and high GA in Y in total yield, fruits number in early and total yield, seeds number, leaf area; low $h^2$ and moderate GA in fruit length, fruit diameter and average fruit weight; low $h^2$ and low GA intotal soluble solids. This results agreed with Magaji *et al.* (2014) who cited that a high heritability together with high genetic advance was observed in fruit weight, and fruit length traits. However, moderate heritability with high genetic advance was observed in number of fruits and yield per plant.

***Generally,*** the characters exhibiting high heritability with high genetic advance are controlled by additive genes and can be improved upon through simple selection procedures. However, the characters with moderate heritability estimates coupled with moderate or low genetic advance can be improved upon by inter-mating the superior genotypes of the segregating population developed from multiple crosses and the desirable genes can be

accumulated in the genotypes (Liang and Walter, 1968). Since, the heritability gives only an idea about proportion of total variability that is due to genetic causes, the more confirmative decision for opting any breeding procedure for the improvement of any trait can only be taken up after ascertaining the type of gene action involved in the inheritance of particular trait. Moreover, Johnson *et al.* (1955) showed that effectiveness of selection depends not only on heritability, but also on genetic advance. Furthermore, Shabanimofrad (2013) conducted that high genotypic coefficient of variation(GCV) together with high heritability and genetic advance provide more information than other parameters alone.

*Conclusively,* these results suggested that the hybrid vigour is available for commercial production of sweet pepper hybrid, and that isolation of pure lines from the progenies of heterotic $F_1$'s is a possible way to improve the fruits yield and fruit quality.

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# الفعل الجيني والمكونات الوراثية والتقدم الوراثي
# في الفلفل الحلو

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أُجريت هذه الدراسة في مزرعة خَاصة بم نطقة سيدي سالم، مُحافظة كفر الشيخ ، مصر خِلال موسمين صيفيين ناجحين لِعامَي 2016 و 2017. بهدف تقدير القُدرة علي التآلف، المُكونات الوراثية، درجة التوريث بمع اننيه الواسع والضيق، والتقدم الوراثي في الفلفل الحلو. واستخدم في هَذه الدراسة ستة آباء وخمسةَ عشر هجيناً الناتجة من نظام التهجين نصف الدائري. زرعت التراكيب الوراثية في تجربة مُصَمَّمَه بطريقة القِطاعات الكاملة العَشوائية في ثلاث مُكررات داخل صوبة زراعية. وكانت الصِفات التي تناولتها الدراسة ه ي: إرتِفاع النبات، وعدد الأفرع، ومساحة الورقة، والمحصول المبكروالكلي ( عدد الثمار ومحصول النبات) ،وطول وقطر الثمرة، و متوسط وزن الثمرة، وعدد حجرات الثمرة، وعدد البذور بالثمرة ،وسمك لحم الثمرة، والمواد الصلبة الذائبة الكلية.

أظهرت النتائج أن متوسط مربعات القدرة العامة والخاصة علي التآلف كانت عالية المعنوية في جميع الصفات تحت الدراسة، مقترحةً بذلك أن وجود الفعل الجيني الإضافي وغير الإضافي يؤثرا في وراثة الصفات المدروسة السابقة، عدا القدرة الخاصة علي التآلف لصفة عدد الأ فرع للنبات مقترحة بذلك أن الإضافة وحدها هي التي تتحكم في هذه الصفة. بالإضافة إلي ذلك أظهرت النسبة بين القدرة العامة علي التآلف والقدرة الخاصة أن تأثيرات القدرة العامة علي التآلف كانت أكثر أهمية من تأثيرات القدرة الخاصة علي التآلف في كل الصفات فيما عدا صفات مساحة الورقة، وعدد الثمار بالمحصول المبكر، والمحصول الكلي، ومتوسط وزن الثمرة ومحتوي الثمرة من المواد الصلبة الكلية ، حيث كان تأثيرات القدرة الخاصة علي التآلف أكبر من تأثيرات القدرة العامة علي التآلف. وترجع أهمية تأثير القدرة العامة علي التآلف في أنها تكشف أن هذه الصفات يمكن أن تستجيب بإيجابية للإنتخاب المباشر، بينما ترجع أهمية تأثير القدرة الخاصة علي التآلف في أنها تكشف أن هذه الصفات يمكن أن تستجيب بإيجابية للتهجين.

**التوصية:** من هذه النتائج تقترح أن قوة الهجين متاحة للإنتاج التجاري في هجن الفلفل الحلو، وأن عزل سلالات نقية من التراكيب الوراثية تظهر قوة الهجين بالجيل الأول هي طريقة لزيادة وتحسين محصول وجودة الثمار.