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ORIGINAL PAPER

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ESTIMATION OF GENE ACTION FOR FRUIT YIELD AND MORPHOLOGICAL TRAITS IN GREENHOUSE CUCUMBER BY MATING DESIGNS

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ABSTRACT

In this study, gene action, genetic variances (δ^2_A and δ^2_D), and combining abilities were estimated for fruit related traits using North Carolina Design II (NCD II) for ten different parental genotypes of greenhouse cucumber. This experiment was performed over a two-year period from 2014 to 2015. The variance components of male, female, and male × female were found to be significant for all the studied traits in a combined analysis of variance. Genetic component analysis showed that fruit diameter, fruit length, total fruit weight, fruit number in early picking and fruit number per node were predominantly under the additive gene action, but internode length and plant height were under the dominance of gene action. Male × female × environment interaction was significant for total fruit weight. The highest general combining ability (GCA) effect for total fruit yield was observed in Zohal (male parent) and YaldaR2 (female parent) genotypes. GCA estimation revealed that male parent of Adrian 4510 provided good general combiners for total fruit number. Specific combining ability (SCA) estimation determined the suitability of Janeete × Adrian 4510. Salar hybrid exhibited higher positive SCA effects for total fruit yield and total fruit number in early picking.

Key words: additive, gene, GCA, SCA, yield

INTRODUCTION

Cucumber (*Cucumis sativus* L.), the fourth most cultivated vegetable around the world [Plader et al. 2007], is one of the most economically important cucurbit vegetable plants [Robinson and Decker-Walters 1997, Wang et al. 2011]. It is a member of the Cucurbitaceae family, which is grown in a number of different types [Shetty and Wehner 2002].

The vegetable is mainly used in salads or as pickling, but young and ripe fruits are also used as cooked vegetables [Robinson and Decker-Walters 1997]. The greenhouse cucumber is one of its most important types grown in Iran. According to a 2012 Food and Agriculture Organization Report [FAO 2012], Iran with an annual production of 1,600,000 (mt) ranks third in global cucumber production after China and Turkey.

Implication of gene action in plant breeding knowledge is useful in two principal ways: 1) selection of parents for hybridization, and 2) choice of appropriate breeding procedures aimed at genetic improvement of various quantitative characters [Singh and Pawar 2005]. The choice, however, depends on the type of

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gene action involved in the expression of these characters in a genetic population [Singh and Pawar 2005, Acquaah 2012]. Additive genetic variance is a prerequisite to genetic gain under selection since it is the only genetic variance responding to selection while dominance genetic variance is suitable for breeding selection [Kearsey and Pooni 1996].

General combining ability (GCA) is a measure of additive gene action, whereas specific combining ability (SCA) deals with dominance gene action [Kearsey and Pooni 1996]. Combining ability analysis can be exploited to identify good general combining parents [Joshi et al. 2004], which can then be used in hybridization programs of self-pollinated species to obtain superior segregants in segregating generations, or to develop synthetic and composite varieties in cross-pollinated species [Falconer and Mackay 1996]. Combining ability analysis is an important tool for the selection of desirable parents while it also provides useful information regarding the nature and magnitude of gene effects controlling traits of economic importance [Bhateria et al. 2006].

Different mating designs are available for investigating gene action [Falconer and Mackay 1996, Singh and Pawar 2005]. Selective mating designs, which may not only allow inter-mating of the selects in different cycles, but also exploit both additive and non-additive gene effects, are useful for the genetic improvement of crops [Singh and Pawar 2005].

North Carolina Designs (I, II, and III) were first developed by Comstock and Robinson [1948] for estimating the combining ability, genetic components, and heritability at much less cost than the full diallel. In NCD II, each member of a group of parents used as males is mated to each member of another group of parents used as females in a factorial mating scheme [Nduwumuremyi et al. 2013]. Due to its advantages, NCD II design provides two independent estimates of δ^2_A and one independent estimate of δ^2_D [Mather and Jinks 1982]. Also, NCD II, in contrast to diallel, can be performed with fewer crossings in the same number of parents.

Different genetic analyses have been conducted to study the combining ability in cucumber for fruit yield and its components [Munshi et al. 2006, Mule et al. 2011, Sarkar and Sirohi 2011, Singh et al. 2011, Golabadi et al. 2015] using such different genetic designs as diallel and NCD. Studies have been conducted on some economically important traits of cucumber including fruit yield and its components [Lopez-Sese et al. 2002, Dogra and Kanwar 2011, Jagesh et al. 2013, Golabadi et al. 2015]. Gulam-ud-Din et al. [2002] evaluated the combining ability of 12 different traits in cucumber by line × tester analysis. Genetic variances for fruit yield and quality-related traits have been already estimated by NCD II in previous studies [Strefeler and Wehner 1986]. The variance components of NCD II are presented in Table 1 [due to Kearsey and Pooni 1996].

According to Kearsey and Pooni [1996], additive variance (δ^2_A), dominance variance (δ^2_D), and dominance ratio, respectively, are calculated using Relations (1) through (3) below:

$$\hat{\sigma}_m^2 = \hat{\sigma}_f^2 = Cov_{H.S} = \frac{1}{4}\sigma_A^2 \qquad (1)$$

$$\hat{\sigma}_{mf}^2 = Cov_{F.S} - Cov_{H.S\,m} - Cov_{H.S\,f} = \frac{1}{4}\sigma_D^2 \qquad (2)$$

$$\bar{d} = \sqrt{\frac{2\sigma_{mf}^2}{\sigma_f^2}} = \sqrt{\frac{2\sigma_D^2}{\sigma_A^2}} \qquad (3)$$

where, $\hat{\sigma}_m^2$ and $\hat{\sigma}_f^2$ represent male and female variances, respectively. Our literature review showed that the majority of genetic parameters investigated are related to field cucumber genotypes.

The present study was designed to achieve the following objectives: 1) to estimate the genetic components involved in gene action of fruit yield; certain morphological traits involved in the selection of an appropriate breeding method to improve fruit weight and fruit number; and some morphologic traits of greenhouse cucumber; 2) to determine the combining ability of female and male genotypes through NCD II analysis for developing cucumber hybrids. Such information is more reliable when drawn over various environments and genotypes. The present investigation was therefore undertaken to generate information about gene action and combining ability effects of the studied traits during the years from 2013 to 2015.

Table 1. Analysis of variance and its components in North Carolina Design (II)

Source of variation	DF	Expected mean squares	Related covariance
Replication	r-1		
Male	m-1	$\sigma^2+r\sigma^2_{fm}+rf\sigma^2_m$	$\sigma^2+r(CovF.S-CovH.S_f-CovH.S_m)+rfCovH.S$
Female	f-1	$\sigma^2+r\sigma^2_{fm}+rm\sigma^2_f$	$\sigma^2+r(CovF.S-CovH.S_f-CovH.S_m)+rmCovH.S_f$
Female × male	(f-1) × (m-1)	$\sigma^2+r\ \sigma^2_{fm}$	$\sigma^2+r(CovF.S-CovH.S_f-CovH.S_m)$
Error	(mf-1) (r-1)	σ^2	σ^2

DF – degree of freedom; r, f, and m are denoted to replication, female and male, respectively

MATERIAL AND METHODS

This experiment was carried out at the Research Greenhouse of the Department of Agriculture, Islamic Azad University (Isfahan Branch), Isfahan, Iran (longitude 51º36'E and latitude 32º63'N) during the years 2013 to 2015. To prepare the required genetic population, the five cucumber genotypes of Green Majic (Netherland), Janeete (Netherland), Gohar (Netherland), Zohal (Netherland), and Adrian4510 (Netherland), as male parents, and the five cucumber genotypes of Adrian-Salar (Netherland), Sina (USA), Danish (Denmark), KhassibR2 (Netherland), and YaldaR2 (Netherland), as female parents, were selected randomly from a population of 30 different greenhouse cucumber genotypes. The selected genotypes were crossed in 2013, one year before the study period, based on the North Carolina II genetic design. As all the genotypes used were gynoecious, gibberellic acid (Merck) at a concentration of 1500 ppm was used at the 2–4 leaf stage at intervals of one to three weeks on male parents in order to produce enough male flowers. The progeny seeds were planted and evaluated as a factorial based on a completely randomized block design with three replications in the spring of 2014 and 2015. The greenhouse conditions included a relative humidity of 60%, and average day and night temperatures of 27 ±2°C, and 20 ±2°C, respectively. The soil used had equal amounts of peat moss, perlite, and cocopeat (coir) bed with a pH of 7.7. The space between two consecutive rows was 90 cm and a space of 180 cm was left between every other two rows. Seeds were planted at a distance of 50 cm from each other along the rows.

Nutrients dissolved in the irrigation water consisted of N 216, P 58, K 286, Ca 185, Mg 185, S 43, Fe 5.59, Mn 1.97, B 0.7, Zn 0.2, Cu 0.07, and Mo 0.05 mg L^{-1}. Based on soil analysis, the different fertilizers including potassium nitrate, ammonium nitrate, magnesium nitrate, iron, and sulphates were also dissolved in the irrigation water.

Drip irrigation was applied when needed using urban tap water with an electrical conductivity (EC) of 0.4 dS m^{-1} and a pH adjusted to 6.5 with nitric acid. Observations were recorded on ten plants randomly selected per entry and per replication to determine total fruit weight per picking (TFW – the weight (in g) of all the fruits harvested daily in each plot if there was a fruit of marketable size on each plant), fruit number per node (FNN), fruit number per early picking (FNE – similar to TFW for fruit number), fruit length (FL – the lengths (in cm) of 15 fruits at edible maturity and randomly harvested in 5 d, three per day from the base to the apex), fruit diameter (FD – the diameters (in cm) of 15 fruits at maximum thickness measured with a vernier caliper), plant height (in cm) (PH), and internode length (IL – the length (in cm) of nodes per vine on the main stem from node number 15 to node number 20).

The data thus collected were subjected to combined analysis of variance (ANOVA) using the general linear model (GLM) of Statistical Analysis System program (SAS ver. 9). The differences between male and female parents and their interactions were measured on the basis of the Least Significant Difference (LSD) test ($P < 0.05$) according to their importance at the 0.05 confidence level. The GCA and SCA effects were calculated according using the following formulas [King et al. 1961]: $\widehat{g}i = \frac{yi..}{rf} - \overline{y}...$ for the i genotype as male

Table 2. Analysis of variance for the studied traits of greenhouse cucumber genotypes crossed according to NCD II genetic design

Source of variation	Mean square							
	DF	IL	PH	FD	FL	FNE	TFW	FNN
Year	1	34.27	11213.2^{**}	1.84	1.10	13.32	72864.24^{**}	2.34
Replication (year)	4	46.36	374.98	0.28	1.79	9.44	8.64	3.50
Genotype	24							
Male	4	75.23^{**}	8098.57^{**}	2.83^{**}	122.03^{**}	48.21^{**}	13169.16^{**}	6.05^{**}
Female	4	99.67^{**}	8439.47^{**}	3.64^{**}	111.78^{**}	48.66^{**}	15326.34^{**}	7.71^{**}
Male × female	16	13.06^{**}	1966.76^{**}	0.23^{**}	3.90^{**}	3.49^{**}	716.445^{**}	0.14^{*}
Genotype × year	24							
Female × year	4	9.91^{**}	92.05	0.020	2.05^{*}	0.56^{ns}	33.42^{**}	0.049
Male × year	4	7.85^{s}	80.74	0.032	1.51^{*}	1.06^{*}	32.91^{*}	0.024
Female × male × year	16	5.32	70.68	0.014	0.72	0.55	64.50^{*}	0.026
Error	96	5.85	39.11	0.015	0.86	0.79	38.1	0.02
Genetic components								
Additive variance		8.28	817.57	0.34	15.75	5.96	1660.36	0.78
Dominance variance		5.160	1264.05	0.14	2.11	1.95	434.62	0.07
Narrow sense heritability		0.60	0.39	0.70	0.88	0.75	0.79	0.91
Dominance ratio (in male)		1.11	1.75	0.92	0.51	0.81	0.72	0.44

DF – degree of freedom; IL – internode length; PH – plant height; FD – fruit diameter; FL – fruit length; FNE – fruit number in early picking; TFW – total fruit weight per picking; FNN – total fruit number per node. * and ** represent significance at $P < 0.05$ and $P < 0.01$, respectively, ns – non significant

and $\hat{g}j = \frac{yi..}{rm} - \bar{y}...$ for the j genotype as female. The specific combining ability for i and j parents were determined via $\hat{S}ij = \frac{yij.}{r} - \frac{yi..}{rf} - \frac{y.j.}{rm} + \bar{y}...$ Also the standard error (SE) for g_i was calculated based on $SE_{gi} = \sqrt{\frac{\sigma_e^2}{rf}}$, i as the male parent and $SE_{gj} = \sqrt{\frac{\sigma_e^2}{rm}}$, j as the female one. The additive variance for the studied traits was calculated using the mean of two estimates for additive variance including ($\delta^2_{A\ \mathrm{male}}$ and $\delta^2_{D\ \mathrm{female}}$) [Mather and Jinks 1982].

RESULTS AND DISCUSSION

Genetic components for the studied trait

The estimates of genotypes (male, female, male × female) and genetic parameters (δ^2_A and δ^2_D) for the fruit traits of cucumber are presented in Table 2. Based on the combining analysis of variance, male, female, and male × female genotypes were significant for all the studied traits in both years. Mean squares due to female × year were significant for IL, FL, and TFW. Also the male × year interaction was highly significant for FL, FNE, and TFW at $P < 0.01$.

The mean square of male × female × year was significant for TFW at $P < 0.01$ (tab. 2). The additive (δ^2_A) and dominance (δ^2_D) variances were calculated for all the traits in the combining analysis of variance. The additive variance was found to be greater than the dominance one in all the studied traits, except for internode length and plant height. The narrow-sense heritability varied from 0.39 (plant height) to 0.91 (total fruit number). High estimates of heritability (>0.70) demonstrated the predominant role of the additive gene action for the genetic control of the investigated traits. The dominance ratio, as an indicator of gene action, varied from 0.44 (total fruit number) to 1.75 (plant height), which correspond to partial, complete, and over-dominance in different traits.

Internode length

Comparison of the genetic variance of genotypes, dominance ratio, and heritability estimates indicated the relative superiority of dominance gene effects over additive ones in the genetic control of internode length (tab. 2). This finding is similar to those reported by Dogra and Kanwar [2011] but contrary to those of Golabadi et al. [2015] on cucumber. The discrepancies could be related to differences in the materials used and environmental conditions.

Plant height

Plant height is an important agronomic trait for crop management. Reduced plant height in cucumber breeding offers the potential use in once-over mechanical harvest [Liebig et al. 2002]. On the other hand, increased plant height redounds to both more nodes and higher fruit numbers. So, information about the genetic control of this key trait is an important feature in greenhouse cucumber breeding. Based on the variance components and dominance ratios obtained (greater than unity), the predominant role of dominance gene action for the genetic control of plant height may be considered (tab. 2). Similar to our study, Kanobdee et al. [1990] reported that genetic components in plant height were non-additive gene action. In the present study, heritability of plant height was found to be low (0.39); thus, F_1 hybrid production could be useful for its improvement.

Fruit size (fruit length and diameter)

Combining analysis of variance showed that additive variance had greater effects on the genetic control of fruit diameter and fruit length than did dominant variance (tab. 2). A high narrow-sense heritability was also found to be effective in fruit diameter (0.70) and fruit length (0.88).

Genetic variances and deviation of dominance ratio from unity implied the importance of additive gene action for the genetic control of fruit length and fruit diameter across two years. These results are compatible with those reported by Dogra and Kanwar [2011], Sarkar and Sirohi [2011], and Golabadi et al. [2015]. However, the results obtained were inconsistent with those reported by Hormuzdi and More [1989].

Total fruit weight

Fruit yield has been reported as the most important breeding trait in cucumber [Singh et al. 2011]. Comparison of variance components (additive and dominance), narrow-sense heritability (>0.70), and dominance ratio (< unity) implies that additive effects had a predominant role in the genetic control of total fruit weight per picking across two years (tab. 2). This is similar to the results reported by Sarkar and Sirohi [2011], Dogra and Kanwar [2011], and Jagesh et al. [2013]. However, the predominant role of additive gene action in the genetic control of fruit yield per plant yield has also been previously reported [Olfati et al. 2012, Golabadi et al. 2015]. The fact that additive gene action is of prime importance for the genetic control of number of fruits per plant, total fruit weight, fruit number in early picking suggests that cyclic selection should be effective for improving number of fruits per plant and fruit weight in greenhouse cucumber. Based on full-sib family selection, Strefeler and Wehner [1986] reported a fruit yield heritability in the range of 0.03 to 0.25, which is inconsistent with the finding in the present study (0.79).

Fruit number per picking

The magnitudes of additive and dominance ratios and the heritability estimates obtained from combined analysis point out the prime importance of additive gene action for the genetic control of number of fruits per node and number of fruit in early picking (tab. 2). Golabadi et al. [2015] reported the predominant role of additive gene action for the genetic control of fruit number per picking, which agrees well with the present results. Previous studies reported the significance of both additive and dominant gene actions for the genetic control of fruit number per picking [Kanobdee et al. 1990, Lopez-Sese and Staub 2002]. Sarkar and Sirohi [2011] also reported the over-dominance of gene action for the genetic control of fruit number per plant. These results suggest that breeding methods based on selection should be effective for improving number of fruits per plant in cucumber.

GCA effects of parents

The values for general combining ability (GCA) of the studied genotypes across the environments are presented in Table 3. GCA and SCA effects for the selected parents as combined with other genotypes were also estimated in this study over the two-year study period. Estimates of GCA effects for internode length were found to vary from 1.57 (Sina) to -1.97 (KhassibR2). Based on the estimates for combined analysis, the KhassibR2 genotype with the least GCA value for internode length was considered to be an appropriate parent for hybridization as a negative combiner to reduce internode length.

Table 3. General combining ability (GCA) effects for different parents of greenhouse cucumber crossed according to the NCD II genetic design (means of two years)

	Parents	IL	PH	FD	FL	FNE	TFW	FNN
Male parents	Green Majic	-1.45**	10.50**	-0.22**	0.04	-0.43**	-6.95**	-0.168**
	Janeete	-0.03	17.15**	0.14**	-0.65**	-0.69**	-4.07**	-0.010
	Zohal	-0.02	-0.67	0.13**	0.01	0.61**	8.97**	0.042
	Gohar	1.01*	-19.15**	-0.01	-0.28	0.10	-4.66**	0.055*
	Adrian4510	0.50	-7.83**	-0.03	0.88**	0.41*	6.71**	0.081**
Female parents	Adrian-Salar	0.51	7.84**	-0.14**	-0.50**	0.09	0.43	-0.050*
	Sina	1.57**	6.74**	-0.10**	-0.37*	0.24	-4.98**	0.056*
	Danish	-0.18	13.73**	-0.01	1.05**	-0.09	0.89	0.019
	YaldaR2	0.07	-17.99**	0.18**	0.08	0.07	6.76**	0.024
	KhassibR2	-1.97**	-10.31**	0.08**	-0.27	-0.30*	-3.11**	-0.050*

IL – internode length; PH – plant height; FD – fruit diameter; FL – fruit length; FNE – fruit number in early picking; TFW – total fruit weight per picking; FNN – total fruit number per node. * and ** are significant at $P < 0.05$ and $P < 0.01$, respectively

The GCA effects for plant height varying from -19.15 (Gohar) to 17.15 (Janeete) showed variations among the genotypes evaluated (tab. 3). Therefore, the Gohar genotype with the highest negative GCA effect may be recommended for PH reducing in cucumber.

Fruit shape is a marketable feature and fruit size is an indicator of yield improvement [Golabadi et al. 2015]. Greater GCA values for fruit length and fruit diameter indicate the capacity of the parent to produce superior progenies for fruit size in the main stem when combined with another parent [Golabadi et al. 2015]. The GCA effects for fruit diameter showed variations from 0.18 (YaldaR2) to -0.22 (Green Majic) (tab. 3).

The highest (1.05) and lowest (-0.65) GCA effects for fruit length were observed in Danish and Janeete genotypes, respectively (tab. 3). The genotype of YaldaR2 and Danish could be used as appropriate parents in hybridization programs to increase fruit size (length and diameter).

Another trait of great importance for fruit yield is fruit number. The highest GCA effect for fruit number in early picking was found in Zohal (0.61) while the lowest was observed in Janeete (−0.69) (tab. 3).

Parents with significant GCA effects resulting from additive gene effects were found to be good components for enhancing fruit number in early picking. Thus, Zohal exhibited an enhanced effect for FNE in cucumber.

The highest (8.97) and lowest (-6.95) GCA values for total fruit weight were observed in Zohal and Green Majic genotypes, respectively (tab. 3). This implies that Zohal could be selected as the best component in hybrid programs for improving TFW.

The highest value for GCA effect on total fruit number per picking was recorded for the Adrian4510 genotype (tab. 3) while the lowest (-0.168) belonged to Green Majic. Adrian4510 was thus found to be a good new combiner containing positive alleles for enhancing FNN. Parents with significant GCA effects resulting from additive gene effects were found to be good combiners for enhancing fruit yield and number of fruit per plant. Based on GCA effects, the parental genotype of Zohal and Adrian4510 were found to be the best combiners containing positive alleles for improving fruit number per plant and total fruit weight in cucumber.

Comparison of studied traits

The mean crosses for the different traits studied across two years are presented in Table 4. Comparison of means showed a significant variation among the genotypes. The mean value for internode length varied from 51.16 (Adrian-Salar) to (47.89 cm) (Green Majic) among the genotypes evaluated. Plant height varied between 99.51 cm (YaldaR2) to 148.76 cm (Janeete). Fruit diameter varied from 2.31 (Adrian-Salar) to 2.69 cm (Janeete). The highest (16.27 cm) and lowest (13.21 cm) values of fruit length were denoted to Danish and Sina, respectively. The highest mean value for FNE (6.02) was obtained for YaldaR2 but the least was denoted to Janeete (4.61). The highest and lowest mean values for TFW were obtained for Zohal (151.13 g) and Adrian-Salar (115.20 g), respectively. Finally, the highest (2.01) and lowest (1.76) mean for FNN belonged to Adrian4510 and Green Majic, respectively.

Table 4. Performance of parental components of greenhouse cucumber

	Parents	IL (cm)	PH (cm)	FD (cm)	FL (cm)	FNE (no.)	TFW (g)	FNN (no.)
Male parents	Green Majic	47.89	142.11	2.33	14.00	4.86	135.21	1.76
	Janeete	49.30	148.76	2.69	13.31	4.61	138.09	1.92
	Zohal	49.31	130.93	2.68	13.97	5.91	151.13	1.97
	Gohar	50.34	112.45	2.54	13.68	5.40	137.51	1.99
	Adrian4510	49.84	123.78	2.52	14.84	5.71	148.87	2.01
Female parents	Adrian-Salar	51.16	134.71	2.31	12.88	4.93	115.20	1.71
	Sina	49.96	138.55	2.38	13.21	5.46	118.58	1.86
	Danish	47.91	133.65	2.33	16.27	5.85	119.72	1.84
	YaldaR2	51.09	99.51	2.63	14.10	6.02	129.86	1.85
	KhassibR2	48.96	108.4	2.52	13.80	5.58	117.24	1.77
	LSD (5%)	1.22	3.16	0.062	0.47	0.45	3.12	0.072
	LSD (1%)	1.61	4.17	0.082	0.62	0.59	4.11	0.094

IL – internode length; PH – plant height; FD – fruit diameter; FL – fruit length; FNE – fruit number in early picking; TFW – total fruit weight per picking; FNN – total fruit number per node

Specific combining ability (SCA)

The lowest SCA values for IL were measured for Green Majic × Danish (-4.97) (tab. 5). The results show that the cross of Green Majic × Danish is a good combination for reducing internode length in cucumber. The highest (38.66) and least (-26.66) SCA effects for plant height were observed with Janeete × Sina and Zohal × Adrian-Salar crosses, respectively. Thus, the former cross could be used for increasing plant height while the latter could be exploited for reducing it, depending on the special purpose of the breeding program. The highest SCA effects for fruit length (4.89) and fruit diameter (0.30) were recorded for Adrian4510 × Danish and Janeete × Sina crosses, respectively. Therefore, these superior crosses could be selected as valuable genotypes in breeding programs aimed at fruit size enhancement. The highest SCA values for fruit number in early picking (1.37) and total fruit weight (28.19) were recorded for the Janeete × Adrian-Salar cross. Also, the highest SCA for total fruit number (0.25) was observed in Zohal × Adrian–Salar.

Table 5. Specific combining ability (SCA) effects for different parent components of greenhouse cucumber crossed according to the NCD II genetic design

Crosses	IL	PH	FD	FL	FNE	FNN	TFW
Green Majic × Adrian-Salar	4.69	34.44	0.00	0.35	-0.94	-0.06	-30.41
Green Majic × Sina	-0.74	-14.76	-0.07	0.14	0.12	0.06	19.46
Green Majic × Danish	-4.97	-15.01	0.02	-1.13	-0.86	-0.13	1.85
Green Majic × YaldaR2	0.91	1.26	-0.08	0.19	0.40	0.03	-3.00
Green Majic × KhassibR2	0.10	-5.93	0.14	0.45	1.28	0.09	12.10
Janeete × Adrian-Salar	0.91	-20.98	-0.11	0.27	1.37	0.04	28.19
Janeete × Sina	0.70	38.66	0.30	0.00	0.07	-0.14	-1.92
Janeete × Danish	0.40	9.80	-0.08	-0.72	-0.32	-0.01	-8.97
Janeete × YaldaR2	0.10	-9.26	-0.22	0.19	-0.73	-0.05	-14.96
Janeete × KhassibR2	-2.11	-18.21	0.11	0.26	-0.39	0.15	-2.34
Zohal × Adrian-Salar	-0.54	-26.66	-0.10	1.25	-0.04	0.25	25.33
Zohal × Sina	0.29	-17.03	-0.13	-0.19	-0.25	-0.15	-19.40
Zohal × Danish	-0.61	26.92	0.25	-1.53	0.21	-0.07	-24.54
Zohal × YaldaR2	0.27	5.44	0.22	-0.73	1.15	0.12	19.24
Zohal × KhassibR2	0.58	11.33	-0.24	1.20	-1.07	-0.15	-0.64
Gohar × Adrian-Salar	-4.25	-6.82	0.19	0.15	0.67	-0.01	-7.29
Gohar × Sina	1.40	3.30	-0.06	0.96	0.10	0.19	11.11
Gohar × Danish	1.42	-8.58	-0.01	-1.51	0.83	0.13	9.22
Gohar × YaldaR2	-0.83	3.22	-0.04	0.53	-1.49	-0.20	-10.59
Gohar × KhassibR2	2.26	8.88	-0.08	-0.13	-0.10	-0.12	-2.45
Adrian4510 × Adrian-Salar	-0.81	20.02	0.02	-2.02	-1.06	-0.22	-15.82
Adrian4510 × Sina	-1.64	-10.17	-0.04	-0.91	-0.05	0.03	-9.25
Adrian4510 × Danish	3.76	-13.13	-0.19	4.89	0.15	0.07	22.43
Adrian4510 × YaldaR2	-0.46	-0.67	0.13	-0.18	0.67	0.09	9.31
Adrian4510 × KhassibR2	-0.84	3.94	0.08	-1.78	0.28	0.03	-6.67
LSD (5%)	2.74	7.08	0.14	1.05	1.01	0.16	6.98

IL – internode length; PH – plant height; FD – fruit diameter; FL – fruit length; FNE – fruit number in early picking; FNN – total fruit number per node; TFW – total fruit weight per picking

CONCLUSION

Greenhouse cucumber cultivation has been considered as the main objective in producing off-season products in arid and semi-arid regions of Iran. The superior genotype of greenhouse cucumber seems to be accompanied with high number of fruits per plant, short internodes, long plant height, and high fruit length and diameter. The prerequisite to the development of superior genotypes includes knowledge about the genetic control of the traits. Comparison of genetic components (additive and dominance variance), narrow-sense heritability, and dominance ratio revealed the predominant role of dominance gene action for internode length and plant height while the additive gene action was found significant for fruit size (length and diameter), fruit number, and fruit weight. Thus, improving the dominant and additive gene action traits calls for the development of hybrid cultivars and selection of segregating generations.

The genotypes with superior GCA could be selected for improving the investigated traits through accumulation of desirable alleles using breeding methods based on selection such as the pedigree method. Crosses with high levels of SCA could, however, be used in cucumber hybrid seed production programs. It may be concluded that major improvements in different traits in cucumber requires heterotic hybrids which could be achieved by tapping combining ability of F_1 hybrids developed from the crossing of two genetically diverse female lines with male testers. Since genetic improvement of fruit yield and its marketable traits are the major goals of greenhouse cucumber breeding in Iran, the new superior genotypes identified in this study could be used in recombination breeding programs to accumulate suitable genes that are responsible for improving cucumber yield in Iran. Based on the results obtained, the Zohal genotype could be considered as a good parent for improving TFW and FNE, while KhassibR2 and Gohar could be adopted for reducing IL and PH. Finally, Adrian4510 could be proposed for enhancement of fruit size (fruit length) and total fruit number in every picking.

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