



Genetic studies in cucumber involving *Cucumis hardwickii* derived lines and gynomonoecious lines

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ABSTRACT

The present investigation which aims to improve fruit yield and widen the genetic base in cucumber by use of *Cucumis hardwickii* derived lines and gynomonoecious lines was conducted at ICAR-RCER Research Centre, Ranchi during 2002–14. For this purpose crossing was initiated using a *C. hardwickii* line and cultivated cucumber. Simultaneously, gynoeceous condition was transferred to the cultivated cucumber through an exotic collection EC-399587. Five stable lines from each experiment were obtained after continuous selection and selfing was done up to 10 generations. Twenty eight crosses were made using the four gynomonoecious lines, three *C. hardwickii* derived lines and a collection from North East. Combining ability studies revealed predominance of non additive gene effects for number of fruits per plant, yield per plant, yield, node at which first female flower appears and days to 50% flowering. HACGM-3, HAC-158 and HAC-159 showed significant GCA effects for number of fruits per plant, yield per plant and yield. It indicated that the increase in number of pistillate flowers in gynomonoecious lines and sequential fruiting habit of *C. hardwickii* had contributed to the increase in yield and yield components. These genotypes are superior and can be used in cucumber improvement program. Based on SCA effects, hybrid vigour vis-a-vis mean performance and consumer preference, the crosses HACGM-3 × HAC-163 and HAC-160 × HAC-163 were found to be superior and can be directly utilized as promising hybrids. Multivariate analysis of the eight parents based on morphological data grouped them into two main clusters.

Key words: Cucumber, *Cucumis hardwickii*, Gynoeceous, Gynomonoecious, Heterosis, Yield components

Cucumber (*Cucumis sativus* var *sativus*, $2n=2x=14$) is the most widely cultivated crop of the cucurbitaceae family. Previous studies indicated very narrow genetic diversity in cucumber, which emphasizes the creation of new genetic diversity for its improvement. Also fruit yield per plant in cucumber is very low, as fruit yield is suppressed due to inhibition of first pollinated flower on subsequent fruit development.

Cucumber originated in India (Harlan 1975), from north eastern region, eastern Himalaya and its foothills including northern plains (Arora 1991) from a closely related wild species *Cucumis hardwickii* which still exists and is largely unexploited. *C. hardwickii* ($2n=2x=14$), an annual monoecious cucurbit species resembling *C. sativus*, hybridizes readily with *C. sativus*, producing a fertile F_1 with no observed reduction of fertility in the F_2 (Horst and Lower 1978). This wild cucumber offers promise for the breeding of cultivated cucumbers for improved yield (Lower and Nienhuis 1990). It possesses several desirable characters, viz.

sequential multiple fruiting habit, multiple lateral branching and total fruit weight per plant, less internodal length, lack of apical dominance and lack of fruit set inhibition, dark green colour fruits, more number of fruits per plant (Wilde and Duyfjes 2010), early flowering, early maturing, bearing fruit during rainy season and resistance to various diseases. Gynoeceous lines in combination with monoecious lines have enormous potential to breed for earliness, high yield and yield contributing characters (Jat *et al.* 2016). Gynoeceous line when used in crossing successive generations showed very high percentage of pistillate flowers and resulted in high yield potential (Cramer and Wehner 1998).

Keeping this in view, a crossing programme was planned to utilize *C. hardwickii* derived lines and gynomonoecious lines so as to transfer the favourable characters and increase the yield potential of cucumber. Selection of parents for hybridization must be based on the complete genetic information and prepotency of potential parents. Hence, combining ability studies are prerequisite to generate information regarding varietal improvement.

MATERIALS AND METHODS

All the experiments were conducted at experimental Farm of ICAR- RCER Research Centre, Ranchi (23.35° N and 85.33° E at 629 m altitude) during 2002–14. Total annual

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rainfall was 1430 mm with 1100 mm during June–September and the average maximum and minimum temperatures were 37°C and 4°C respectively. Six diverse *Cucumis sativus* line, viz HAC-81-5-1, HAC-81-3-5, HAC-75, HAC-39, HAC-50, HAC-5KR were crossed to *Cucumis hardwickii* line HAC-438-PS-AD/26 (HAC-26) or HAC-438-PS-AD/28 (HAC-28) in all possible combinations in diallel fashion without reciprocals, and fertile F_1 s were obtained (Prasad *et al.* 2004). But the fruits obtained were bitter and spiny. Hence, continuous selection for non bitterness and non spiny was done and selfing of selected lines was carried up to F_{10} generation for stabilization of the selected characters.

In another experiment, EC-399587, a gynoeocious line was crossed with Swarna Ageti, a popular released variety of cucumber for development of gynomonoecious lines. Individual plant selection was made upto F_{10} generation on the basis of desirable phenotypic characteristics, i.e. 2-12% male flower, fruit quality, earliness and yield.

Twenty eight F_1 s were developed with eight parents, viz. HACGM-2, HACGM-3, HACGM-4, HACGM-5, HAC-158, HAC-159, HAC-160 and HAC-163 (NEH region, fruiting only in rainy season) using gynomonoecious and *C. hardwickii* derived lines in half diallel fashion. Evaluation of all the half diallel crosses along with parents had been carried out with two replications in randomized complete block design. Means of observations were subjected to combining ability analysis according to Griffing (1956) method II model I using SPAR3.0. Eight parents were subjected to multivariate analysis using paired group method (UPGMA) and euclidean similarity indices. Mean morphological data of the parents were statistically analysed using PAST v3.12 (Hammer *et al.* 2001)

All the crosses were hand pollinated and seed collected. Gynoeocious lines were maintained by using gibberellic acid (GA_3) (Chaudhary *et al.* 2001). Selfed seeds of the parents were maintained. Seeds were sown in prostrays and seedlings were transplanted after one month keeping row to row and plant to plant spacing 4 m × 2 m, respectively, under trellis system. Standard agronomic practices were followed to maintain healthy crop throughout the growing season. Observations were recorded on all the plants in each parent and F_1 s for each treatment in each replication for days to 50%

flowering, node at which first female flower appears, fruit breadth (cm), fruit length (cm), number of fruits per plant, fruit weight (g), flesh thickness (cm), placental thickness (cm), yield per plant (kg) and yield (t/ha).

RESULTS AND DISCUSSION

Mean performance of C. hardwickii × C. sativus segregating generations: Six stable lines among *Cucumis hardwickii* × *C. sativus* crosses were identified on the basis of yield, quality, earliness and plant type in F_9 generation. Highest yield was recorded in HAC-75 × HAC-26-2 (55.13 t/ha) with green fruit and absence of placental cavity. Among them, five stable lines were identified in F_{10} generation (Table 1). Highest yield was recorded in HAC-159 (42.5 t/ha, dark green fruit with absence of placental cavity) followed by HAC-158 (41.0 t/ha, whitish green with absence of placental cavity). Also F_{10} was photo-insensitive i.e. can be cultivated in both summer and rainy seasons, early flowering, less internode length and downy mildew resistant, but the fruit size was medium. Finally three lines were selected, viz. HAC-158, HAC-159 and HAC-160. HAC-159 was promising and this pure line was further developed as a variety for release. Bisht *et al.* (2004) suggested the use of *C. hardwickii* for improving yield in commercial cucumber.

Mean performance of segregating generations of gynoeocious line as one of the parents: Simultaneously in another experiment five individual plant progeny obtained from the cross of Swarna Ageti × EC-399587 (gynoeocious line) were evaluated in F_{10} generation (Table 2). Out of which highest yield was recorded in HACGM-2 (27.45 t/ha) followed by HACGM-5 (24.75 t/ha) which can be used in the yield improvement programme of cucumber. Gynoeocious based cucumber hybrids were early in flowering and produced concentrated fruit set (Dijkhuizen and Staub 2002).

Mean performance and combining ability analysis of the parents and their crosses involving hardwickii derived lines and gynomonoecious lines: Twenty eight F_1 s obtained by crossing eight parents involving *C. hardwickii* derived lines and gynomonoecious lines were analysed for combining ability. Based on node at which first female flower appears, gynomonoecious line HACGM-2 was found to be earliest

Table 1 Evaluation of promising lines developed through interspecific hybridization (F_{10})

Acc. No.	Pedigree	No. of fruits/ plant	Yield/plant (kg)	Yield (t/ha)	Fruit weight (g)	Fruit length (cm)	Fruit breadth (cm)	Fruit colour
HAC-158	HAC-50 × HAC-26-3	12.0	3.0	41.0	250.0	16.0	5.0	Whitish green
HAC-159	HAC-50 × HAC-26-3	15.0	3.15	42.5	184.0	13.2	5.0	Dark green
HAC-160	HAC-5kr × HAC-26-1	14.0	2.80	35.0	214.0	16.0	4.7	Whitish green
HAC-161	HAC-75 × HAC-26-2	20.0	2.0	32.5	100.0	10.2	3.8	Whitish green
HAC-162	HAC-75 × HAC-26-3	16.0	2.5	36.0	133.0	14.0	4.0	Green

Table 2 Evaluation of Gynomonoecious lines developed from gynoeceous line of cucumber

Acc. No.	Yield in t/ha	Days to 50% Flowering	Fruit weight (g)	Fruit length (cm)	Fruit breadth (cm)	Flesh Thickness (cm)	Placental thickness (cm)
HACGM-1	21.29	38.25	112.12	16.20	3.75	0.52	1.05
HACGM-2	27.45	36.50	163.25	19.97	4.25	0.60	1.35
HACGM-3	24.50	39.25	153.62	17.42	3.92	0.45	1.02
HACGM-4	24.04	38.50	158.81	16.85	3.97	0.55	1.07
HACGM-5	24.75	39.50	129.68	16.52	3.47	0.55	1.02
SEM	13.44	0.78	5.16	0.57	0.13	0.06	0.05
CV %	11.03	4.09	7.20	6.87	7.08	23.64	10.73
CD (P=0.05)	-	-	15.87	-	0.42	-	0.18
CD (P=0.01)	-	-	22.26	-	0.59	-	0.25

(i.e. 4.50th node), followed by HACGM-4 (5.50th node) and *hardwickii* derived line HAC-158 (i.e., 5.50th node) and HAC-159 (i.e. 6.00th node). HAC-158 and HACGM-3 were earliest parents with 44.50 and 45.00 days to 50% flowering. Parents HAC-158, HACGM-4, HACGM-3 and HAC-159 showed highest *per se* mean for number of fruits per plant, yield per plant and yield (t/ha). Analysis of variance showed significant difference for all the traits under study except for fruit weight, fruit breadth, flesh thickness and placental thickness. ANOVA for combining ability showed significant GCA effects for fruit length and placental thickness indicating additive gene action. Number of fruits per plant, yield per plant, yield (t/ha), node at which first female flower appears and days to 50% flowering showed significant SCA effects. Hence, these characters may be improved through hybridization (heterosis) indicating predominance of non additive gene effects. Sharma (2010) and Sandeep *et al.* (2016) reported similar results in combining ability studies using gynoeceous lines.

Combining ability analysis indicated that significant GCA effects were recorded for HACGM-3 and HAC-158 for number of fruits per plant (Table 3). Crosses HACGM-3 × HAC-163 and HAC-160 × HAC-163 recorded significant SCA effects (Table 4). HAC-159 showed significant positive

GCA effects and crosses HACGM-5 × HAC-159 showed significant SCA effects for yield per plant. HAC-159 and HACGM-3 × HAC-163, HAC-160 × HAC-163 recorded significant positive combining ability effects for yield (t/ha). HACGM-3 × HAC-158 recorded significant SCA effects for fruit weight. For fruit length, HACGM-2 and HACGM-5 showed significant GCA effects. HACGM-3 × HAC-158 showed significant SCA effects. Cross HACGM-2 × HAC-163, HACGM-5 × HAC-160 and HAC-158 × HAC-160 recorded significant positive SCA effects for flesh thickness. HACGM-3 showed significant positive GCA effects for placental thickness. For node at which first female flower appears, significant negative GCA effects were recorded for HACGM-4 and HAC-159. HACGM-2 × HAC-160 and HAC-158 × HAC-163 showed negative SCA effects. HACGM-2 and HAC-159 × HAC-160 recorded significant negative combining ability effects for days to 50% flowering. These crosses with higher specific combining ability effects are useful to derive high performing hybrids. These crosses (Table 4) involved parents with high × high, high × low and low × low general combining ability effects indicating presence of additive, dominance and epistatic gene actions for controlling these characters. Similar results were reported by Verma *et al.* (2000), Gulam-ud-Din and Ahmed (2002) and Munshi *et al.* (2006). High × low general combining

Table 3 General Combining Ability effects of parents for yield and yield components

Parents	No. of fruits/ Plant	Yield per Plant (kg)	Yield in (t/ ha)	Fruit weight (g)	Fruit Length (cm)	Fruit Breadth (cm)	Flesh Thickness (cm)	Placental Thickness (cm)	Node 1 st female flower appears	Days to 50% flowering
HACGM-2	-0.07	0.10	2.25	6.47	0.78*	0.05	0.05	-0.01	-0.57	-1.33*
HACGM-3	1.02**	0.06	1.60	6.20	-0.41	0.16	0.00	0.11*	0.28	-1.02
HACGM-4	-0.31	-0.16*	-3.11	-8.85	0.32	-0.27	-0.05	-0.05	-0.68*	0.38
HACGM-5	-0.27	-0.05	-0.64	15.15	1.03**	0.02	0.04	0.01	-0.38	0.62
HAC-158	1.19**	0.11	2.40	-9.40	-0.72*	0.04	-0.02	0.03	0.08	-0.98
HAC-159	0.25	0.19*	4.03*	-7.22	-0.94**	-0.23*	0.00	-0.08	-0.68*	-1.17
HAC-160	-1.09**	-0.14	-2.67	0.77	-0.12	0.13	-0.03	-0.03	1.12**	1.67**
HAC-163	-0.73*	-0.11	-3.85*	-3.12	0.05	0.09	0.01	0.02	0.82*	1.83**
SE	0.37	0.08	1.67	10.87	0.32	0.12	0.03	0.04	0.34	0.69

*Significant at 1% **significant at 5%

Table 4 GCA status of crosses with significant SCA effects

Character	Crosses with significant SCA effects	GCA status
No. of fruits per plant	HACGM-3 × HAC-163 (3.24**), HAC-160 × HAC-163 (3.37**)	H × L L × H
Yield per plant (kg)	HACGM-5 × HAC-159 (0.50*)	L × H
Yield (t/ha)	HACGM-3 × HAC-163 (11.09**), HAC-160 × HAC-163 (12.81**)	L × H L × H
Fruit weight (g)	HACGM-3 × HAC-158 (98.34**)	L × L
Fruit length (cm)	HACGM-3 × HAC-158 (2.83**)	L × L
Flesh thickness (cm)	HACGM-2 × HAC-163 (0.19*), HACGM-5 × HAC-160 (0.19*), HAC-158 × HAC-160 (0.20*)	L × L L × L L × L
Node 1 st female flower	HACGM-2 × HAC-160 (-2.19*), HAC-158 × HAC-163 (-3.04*)	L × L L × L
Days to 50% flowering	HAC-159 × HAC-160 (-4.03*)	L × L

ability combinations are suitable for heterosis breeding. High × high general combining ability combinations can be considered for developing superior variants through pedigree method.

Among parents, HACGM-3 (gynomonoecious line) and HAC-158 (*C. hardwickii* derived line) showed significant GCA effects for number of fruits per plant and HAC-159 (*C. hardwickii* derived line) for yield per plant and yield (t/ha) and mean values were also highest. It indicates that the increase in number of pistillate flowers in gynomonoecious lines and sequential fruiting habit of *C. hardwickii* had contributed to the increase in yield and yield components. Hence these genotypes are superior and can be used in crossing programmes. Jat *et al.* (2016) identified two gynoeious (GPC-1 and PPC-2) parents that were good general combiners for earliness, yield and other yield related traits and could be used in cucumber breeding programmes to improve these traits for the accumulation of favourable genes present in them. Choudhary and Singh (2010) identified three *C. hardwickii* genotypes as good general combiners for number of fruits per plant and fruit yield per plant and showed that Indian germplasm of *C. hardwickii* has great potential for their utilization in future cucumber improvement program. Among the crosses HACGM-3 × HAC-163 and HAC-160 × HAC-163 were superior. Gynoecious as one of parent in cucumber hybrid development holds immense potentiality for exploitation of hybrid vigour with respect to earliness, yield and other yield related traits. These results were very much similar to the findings of Shushir *et al.* (2005) and Sreevani (2005).

Diversity analysis: All the eight parents were grouped into two main clusters based on the multivariate analysis of the morphological data (Fig 1). HACGM-5 grouped separately into a single cluster i.e. Cluster I and the remaining seven genotypes grouped into another cluster i.e. Cluster II. Cluster II is subdivided into two subcluster: Cluster IIA comprising HAC-158 and Cluster IIB comprising

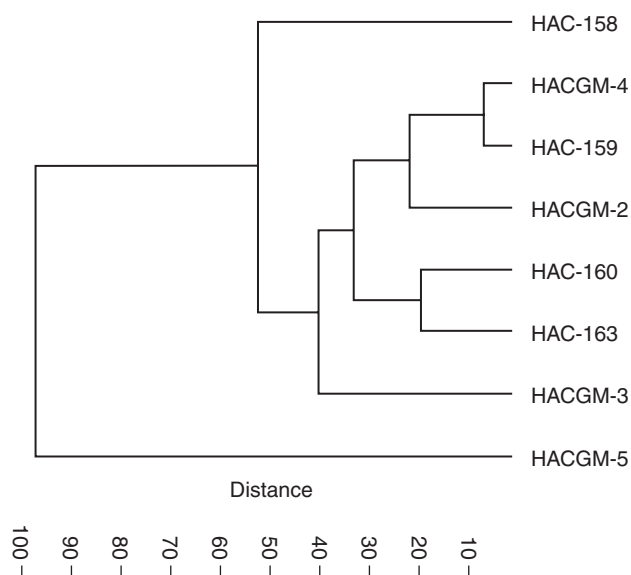


Fig 1 Dendrogram showing genetic variation among the cucumber genotypes for morphological characters.

the remaining six genotypes. In cluster II B, HACGM-3 grouped separately, whereas HAC-160 and HAC-163 formed another subcluster and HACGM-2, HACGM-4 and HAC-159 formed another sub cluster. Crossing program can be designed keeping in view the genetic diversity based clustering pattern. The best combining parents based on GCA i.e. HACGM-3 and HAC-158 are widely placed in different clusters.

The genotypes HACGM-3, HAC-158 and HAC-159 and the crosses HACGM-3 × HAC-163 and HAC-160 × HAC-163 were found to be superior and can be used in cucumber improvement breeding program. Thus the genetic diversity present in *C. hardwickii* species and fruit yield improvement of gynoeious lines of cucumber can be utilized for the improvement of cultivated cucumber.

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