Indian Journal of Agricultural Sciences **93** (1): 19–23, January 2023/Article
https://doi.org/10.56093/ijas.v93i1.127373

Genetic assessments, dominance estimates of economic traits of gynoecious cucumber (*Cucumis sativus*) under Himalayas

NIDHI TYAGI[1]*, H R SHARMA[1], R K DOGRA[1] and MEENU GUPTA[1]

Dr. Y.S. Parmar University of Horticulture and Forestry, Solan, Himachal Pradesh 173 230, India

Received: 25 August 2022; Accepted: 22 November 2022

ABSTRACT

In India generally monoecious and cross-pollinated cucumber (*Cucumis sativus* L.) hybrids/varieties are grown. The use of stable gynoecious cucumber varieties/hybrids would increase the productivity of cucumber in India. In the past, despite improvement in monoecious cucumber varieties/hybrids, little effort has been done into the development of stable gynoecious hybrids. To address this issue 3 genetically diverse gynoecious lines and improvement, and 6 testers were crossed in line × tester fashion to develop 18 crosses during 2017. These 18 crosses along with 9 parents evaluated at the Krishi Vigyan Kendra, Kandaghat, Himachal Pradesh and Dr. YSPUHF, Solan, Himachal Pradesh during pre-*kharif* season 2018–19 to determine the mode of gene action, combining ability, extent heterosis and potence ratio for 12 quantitative traits. Experimental results depicted that the dominant component of variance (σ2S) was found higher than the additive component of variance (σ2S) for all the traits indicating a predominant role of non-additive gene action governing yield and its contributing traits during both the years. Gynoecious inbred lines KTG-40, 2870G and testers K-90, UHF-16 were found most promising general combiners for fruit yield. The cross combination KTG-40 × K-90 and 2870G × K-90 isolated based on heterosis manifested and SCA effects. Further, the performance of top 7 heterotic crosses illustrate the presence of overdominance in most of the crosses for traits under study, suggesting the importance of heterosis breeding for the development of early, high-yielding, disease tolerance stable gynoecious hybrids in cucumber.

Keywords: Combining ability, Dominance estimates, Disease tolerance cucumber, Gene action, Heterobeltiosis

Cucumber (*Cucumis sativus* L. 2n = 2x =14) is high-water content, nutritious summer vegetable crop belongs to Cucurbitaceae family. The cucumber progenitor *Cucumis hardwickii* R. (Alef) is found within the foothills of the Himalayas that's why India is consider as home of cucumber possesses a vast genetic variability for vegetative and fruit characters (De candolle 1882, Sebastian *et al.* 2010).

Cucumber has polymorphic sex expression which provides lots of scope for improvement in earliness, yield, fruit characteristics and resistance to pest and diseases by using heterosis breeding. In India, area covered by monoecious cucumber cultivation is 82.04 thousand hectares with annual production of 1259.94 thousand tonnes and 15.5 t/ha productivity (Anonymous 2018). In India mostly, monoecious cucumbers are produced which have high seeds cost and gives less yield compared to gynoecious cucumber. Only a few gynoecious based hybrid were developed in India, however these are still not commercialized (Jat *et al.* 2017). It is the need of the hour to develop comparatively more yielding stable gynoecious hybrids through heterosis breeding by exploring new gynocious lines of cucumber from different indigenous and exotic sources. But, before the exploitation of gynoecy in heterosis, choice of suitable parents based on their combining ability is utmost important. Such study not only provides necessary information regarding the choice of parents but also provides the knowledge of nature and magnitude of gene action controlling the inheritance of desirable traits. Further, dominance estimates is useful to determine the nature of dominance and its direction. Till date, very scant information is available in the literature pertaining to estimation of combining ability, gene action, heterosis and potence ratio for yield and its contributing traits, using gynoecious lines of cucumber. Therefore, present study was aimed to develop high yielding stable gynoecious hybrids based on the knowledge of combining ability, gene action, heterotic potential and potence ratio in cucumber.

MATERIALS AND METHODS

Experimental site and layout plans: The present study was carried out during pre-*kharif* seasons of 2017, 2018

[1]Dr. Y.S. Parmar University of Horticulture and Forestry, Solan, Himachal Pradesh. *Corresponding author email: nidhityagivs@gmail.com

and 2019 at Krishi Vigyan Kendra, Kandaghat, Himachal Pradesh and Dr. YSPUHF, Solan, Himachal Pradesh (30.59ºN, 77.07ºE and altitude of 1425 meters amsl). Eighteen crosses were developed by crossing 3 gynoecious lines and 6 testers in line × tester design (Kempthrone 1957). All the parents and their 18 F_1's along with the standard checks (KH-1) were planted during 2018 and 2019 in randomised complete bock design (RCBD) with 3 replications for their comparative analysis and evaluation. Three to four seedlings per basin were sown at a spacing of 100 cm × 75 cm in a plot size 2.0 m × 4.5 m, that accommodated 12 plants per plot. The standard cultural practices were followed raising a healthy crop of cucumber.

Data recording and statistical analysis: Data were taken from 5 randomly selected plants in each entry (genotype/hybrid) over the replications for 12 important horticultural traits. Severity of downy mildew and powdery mildew disease was determined at 30 days interval from sowing up to 120 days after sowing. Fifteen leaves were randomly selected from different levels of height (from top to bottom) from 5 vines of each genotype/hybrid and per cent disease index for downy mildew and powdery mildew was recorded by adopting 0–4 scale given by Reuveni (1983) and 0–5 scale agreed by Ransom *et al.* (1991) respectively. Per cent disease index (PDI) was calculated at final harvest (120 DAS) as:

$$\text{PDI} = \frac{\text{Numercal ratings}}{\text{Highest grade of rating} \times \text{total number of plants examined}} \times 100$$

Data were statistically analyzed using line × tester analysis, subjected to analysis as per the model suggested by Kempthorne (1957) through R software version 3.6.1. Further, additive and dominance components of variance were also calculated (Dabholkar 1992, Singh and Chaudhary 1997). The magnitude of heterosis over better-parent (BPH) was calculated as (Singh 1973):

$$\text{BPH} = [(F_1\text{-B.P.}) / \text{B.P.} \times 100]$$

The dominance estimates (D.E.) also referred to as "potence ratio" was computed as (Smith 1952):

$$\text{D.E.} = F_1\text{- MP}/0.5 \times P_2\text{-}P_1$$

Table 1 Estimates of genetic components of variance for yield and yield contributing traits in cucumber

Character	Year	σ^2 GCA (Lines)	σ^2 GCA (Testers)	σ^2 GCA (Average)	σ^2 SCA	σ^2g	σ^2s	σ^2g/σ^2s (Variance ratio)	Predictability ratio
DFFFA	2018	2.87	13.77	1.28	24.18	5.10	9.35	0.55	0.52
	2019	2.16	13.38	1.20	21.00	4.80	6.57	0.73	0.59
NNBFFF	2018	0.05	1.00	0.08	1.48	0.33	0.76	0.43	0.46
	2019	0.06	1.01	0.08	1.52	0.33	0.80	0.41	0.45
DFFH	2018	2.91	15.29	1.40	25.33	5.59	8.45	0.66	0.57
	2019	2.48	14.29	1.30	23.34	5.16	8.14	0.63	0.56
NPBPP	2018	0.10	0.52	0.05	0.90	0.19	0.37	0.51	0.51
	2019	0.10	0.54	0.04	0.92	0.19	0.36	0.53	0.51
VL (m)	2018	0.08	0.16	0.02	0.44	0.07	0.23	0.30	0.38
	2019	0.11	0.15	0.01	0.44	0.07	0.12	0.58	0.54
FL (cm)	2018	1.90	3.82	0.42	8.96	1.70	2.66	0.64	0.56
	2019	1.33	3.65	0.37	7.70	1.50	2.76	0.54	0.52
FB (cm)	2018	0.00	0.13	0.01	0.15	0.04	0.06	0.67	0.57
	2019	-0.01	0.12	0.01	0.16	0.03	0.07	0.43	0.46
NMFPP	2018	1.82	2.87	0.34	8.70	1.37	4.37	0.31	0.39
	2019	1.26	3.46	0.35	7.48	1.42	2.98	0.48	0.49
AFW (g)	2018	-19.85	178.54	12.91	374.04	51.64	470.41	0.11	0.29
	2019	-17.03	139.19	9.96	280.37	39.86	350.52	0.11	0.39
MFYPP (kg)	2018	0.14	0.38	0.04	0.74	0.12	0.26	0.46	0.48
	2019	0.10	0.42	0.04	0.70	0.18	0.37	0.49	0.49
SDMD (%)	2018	2.81	45.18	3.76	64.51	15.05	27.44	0.55	0.52
	2019	2.46	45.34	3.75	63.92	15.02	27.28	0.55	0.52
SPMD (%)	2018	-3.54	23.21	1.62	37.00	6.47	41.74	0.16	0.24
	2019	-3.81	21.37	1.45	36.59	5.81	45.71	0.13	0.20

DFFFA, Days to first female flower appearance; NNBFFF, Node number bearing first female flower; DFFH, Days to first fruit harvest; NPBPP, Number of primary branches per plant; VL, Vine length; FL, Fruit length; FB, Fruit breadth; NMFPP, Number of marketable fruits per plant; AFW, Average fruit weight; MFYPP, Marketable fruit yield per plant; SDMD, Severity of downy mildew disease; SPMD, Severity of powdery mildew disease.

Complete dominance (D.E. = ±1); Partial dominance (D.E. is between -1 and +1); Absence of dominance (D.E.= Zero): Over dominance (D.E. exceeds ±1). The '+' and '-' signs indicate the direction of dominance of either parent.

RESULTS AND DISCUSSION

Gene action: The additive and non-additive components of genetic variance are essential for successful crop improvement programme. The estimates of σ^2 SCA value were higher than the σ^2 GCA (average) as well as dominant component of variance (σ^2S) was also higher than the additive component of variance (σ^2S) for all the traits during both the year (Table 1) indicating predominant role of non-additive gene action governing these traits. Baker (1978) had also recommended that progeny performance should be evaluated by estimating the component of variance and expressing them in predictability ratio. These predictability ratios were <0.50, again it confirmed that the inheritance of fruit yield per plant along with yield related component, powdery mildew and downy mildew diseases severity in cucumber apparently controlled by non-additive gene action. It was reported earlier for yield and its contributing traits by Jat *et al.* (2017) and Kumar *et al.* (2017) and severity of downy mildew and powdery mildew diseases by Kumar *et al.* (2018) and Das *et al.* (2019) in cucumber. Here, gene action stated that non-additive gene action governed almost all the traits under study during both the years, hence hybrid breeding could be exploited for these traits in cucumber.

Identification of good general and specific combiners: During both years study revealed that monoecious testers KTG-40, UHF-16 and gynoecious line 2870 G and K-90 exhibited significant GCA effect in desired direction indicating these were found as good general combiner for earliness, fruit yield per plant, severity of downy and powdery mildew disease traits (Kumar *et al.* 2018, Das *et al.* 2019).Therefore, KTG-40, 2870 G, K-90 and UHF-16 could be picked up as potential donors for yield contributing and other important horticultural traits (Table 2).

The significant desirable SCA effect of top 3 cross combinations for different traits under study (Table 2) revealed that the no single cross was adjudged as good specific combiner for all the traits studied. The cross

Table 2 Elite parents (lines and testers) and cross combinations identified on the basis of GCA, SCA effect and heterosis (over better parent) for the year 2018 and 2019

Character	Heterosis over better parent	GCA effect	SCA effect	Type of combination
DFFFA	KTG 40 × K-90, KTG 40 × UHF-16 and 2870 G × K-90	KTG 40, K-90 and UHF-16	2870 G × K-90, KTG 40 × K-90 and 2870 G × UHF-16	H × L
NNBFFF	2870 G × UHF-16, KTG 40 × UHF-16 and 1983 G × UHF-16	2870 G and UHF-16	KTG 40 × UHF-16, 1983 G × UHF-16, and 2870 G × UHF-16	L × H
DFFH	2870 G × K-90, KTG 40 × K-90 and KTG 40 × UHF-16	KTG 40, K-90 and UHF-16	1983 G × K-90, KTG 40 × K-90 and KTG 40 × UHF-16	H × H
NPBPP	KTG 40 × K-90, 1983 G × UHF-16 and KTG 40 × UHF-16	2870 G, KTG 40 and UHF-16	2870 G × K-90, 1983 G × UHF-16 and KTG 40 × K-90	H × H
VL(m)	2870 G × K-90 and KTG 40 × K-90	KTG 40, K-90 and UHF-16	KTG 40 × K-90, KTG 40 × UHF-16 and 1983 G × K-90	H × H
FL (cm)	KTG 40 × K-90, 2870 G × UHF-16 and KTG 40 × UHF-16	KTG 40, UHF-16 and K-90	2870 G × K-90, KTG 40 × UHF-16 and KTG 40 × K-90	L × H
FB (cm)	2870 G × UHF-16 and KTG 40 × UHF-16	UHF-16 and K-90	1983 G × UHF-16, 2870 G × UHF-16 and KTG 40 × UHF-16	L × L
NMFPP	KTG 40 × K-90, 2870 G × UHF-16 and 2870 G × K-90	KTG 40, K-90 and UHF-16	KTG 40 × K-90, 2870 G × K-90 and 2870 G × UHF-16	H × H
AFW (g)	KTG 40 × K-90, 2870 G × K-90 and KTG 40 × UHF-16	2870 G, K-90 and UHF-16	2870 G × K-90, KTG 40 × UHF-16 and 2870 G × UHF-16	H × L
MFYPP (kg)	KTG 40 × K-90, KTG 40 × UHF-16 and 2870 G × K-90	KTG 40, K-90 and UHF-16	2870 G × UHF-16, KTG 40 × K-90 and 2870 G × K-90	H × H
SDMD (%)	1983 G × KTC-7, KTG 40 × K-90, 2870 G × K-90, 2870 G × Kohinoor Local and 2870 G × KTC-7	2870 G, K-90, and KTC-7	KTG 40 × K-90, 2870 G × UHF-16 and 1983 G × KTC-7	L × H
SPMD (%)	2870 G × K-90, 1983 G × K-90, 1983 G × Pant Khira, KTG 40 × K-90 and 1983 G × Kohinoor Local	K-90, Kohinoor Local and Pant Khira	KTG 40 × K-90, 1983 G × UHF-16, and 1983 G × K-90	L × H

DFFFA, Days to first female flower appearance; NNBFFF, Node number bearing first female flower; DFFH, Days to first fruit harvest; NPBPP, Number of primary branches per plant; VL, Vine length; FL, Fruit length; FB, Fruit breadth; NMFPP, Number of marketable fruits per plant; AFW, Average fruit weight; MFYPP, Marketable fruit yield per plant; SDMD, Severity of downy mildew disease; SPMD, Severity of powdery mildew disease.

combination 2870 G × K-90 (L × H), KTG 40 × K-90 (H × H) and KTG 40 × UHF-16 (H × L) exhibited significant and negative SCA effects and A × A; D × A type of gene action for days to first female flower appearance, days to first fruit harvest traits related to earliness during both the years in cucumber as also reported by Kumar *et al.* (2017) and Das *et al.* (2019). Significantly high positive SCA effects were exhibited in 2870 G × K-90 (L × H), 2870 G × UHF-16 (L × H) and KTG 40 × UHF-16 (H × L) for fruit length and breadth. Significantly high SCA effects for number of marketable fruits per plant, average fruit weight, marketable fruit yield per plant were found in KTG 40 × K-90 (H × H), 2870 G × K-90 (L × H) and KTG 40 × UHF-16 (H × L) and lowest severity of disease (downy mildew and powdery mildew) observed in cross combination KTG 40 × K-90 (H × H), 2870 G × K-90 (L × H) and 1983 G × KTC-7 (L × L) during both the years. The crosses which involved H × H type parents include positive alleles from both parents and thus repulsion phase linkage is present, whereas crosses which involved L × L type combiners may be used for exploitation of heterosis in F_1 generations. Different crosses expressing high desirable SCA effects with respect to earliness, fruit yield and its components, downy and powdery mildew diseases severity in cucumber had also been reported by Das *et al.* (2019).

Heterosis and dominance estimates (DE): In the present experiment, out of 18 crosses top 7 crosses were revealed desire direction heterobeltiosis for all the studied traits during both years. The cross combination KTG 40 × K-90, KTG 40 × UHF-16 and 2870 G × K-90 showed the highest significant negative value of heterobeltiosis for days to first female flower appearance and days to first fruit harvest (Table 3). It indicated that these cross combinations could be useful for developing early commercial hybrids. The value of dominance estimates in top 7 crosses illustrated that all the hybrid combination exhibited >-1 for earliness traits only 1983 G × UHF-16 showed <1. For node no. bearing first female flower traits four crosses showed >-1 and three were with <1 value. It reflected that during both the years overdominance and partial dominance involved

Table 3 Dominance estimates for yield and its contributing traits in cucumber

Character	Years	1983 G × K-90	1983 G × UHF-16	2870 G × K-90	2870 G × UHF-16	KTG 40 × K-90	KTG 40 × UHF-16	KTG 40 × Kohinoor Local
DFFFA	2018	-1.29	-1.94	-1.48	-3.37	-1.50	-2.95	-1.39
	2019	-1.37	-2.89	-1.46	-3.78	-1.40	-2.81	-1.34
NNBFFF	2018	0.63	-2.31	0.07	-8.06	0.58	-7.00	1.84
	2019	0.67	-1.90	0.09	-7.75	0.60	-6.89	1.81
DFFH	2018	-1.54	-0.50	-1.76	-7.48	-1.69	-5.29	-1.75
	2019	-1.66	-0.70	-1.72	-5.81	-1.67	-4.86	-1.47
NPBPP	2018	-0.31	6.28	1.95	1.35	6.11	6.73	-0.06
	2019	-0.33	9.53	1.82	1.17	5.27	7.62	-0.24
VL (m)	2018	5.77	2.86	2.31	3.14	1.46	0.05	-0.36
	2019	4.67	4.52	2.37	2.45	1.51	0.05	-0.52
FL (cm)	2018	12.14	1.52	2.48	9.69	3.28	1.54	0.12
	2019	14.53	1.26	6.01	6.36	3.23	1.49	0.18
FB (cm)	2018	2.89	10.69	13.89	5.39	6.68	6.50	1.68
	2019	2.76	11.91	12.82	3.71	5.35	13.50	1.75
NMFPP	2018	5.10	2.20	1.85	9.30	1.86	1.87	0.61
	2019	4.61	3.97	2.00	9.79	1.80	1.99	0.51
AFW (g)	2018	2.83	2.44	3.73	3.70	5.05	2.72	6.59
	2019	2.99	2.17	3.41	2.49	6.98	3.63	7.97
MFYPP (kg)	2018	6.96	2.31	2.17	6.66	2.51	5.81	1.26
	2019	7.02	3.75	2.53	5.36	3.41	7.76	2.26
SDMD (%)	2018	-4.49	2.58	-4.97	-0.14	-9.45	-1.33	1.33
	2019	-6.29	2.17	-4.02	-0.11	-12.01	-1.45	1.82
SPMD (%)	2018	-9.54	0.93	-5.24	-0.13	-1.73	-0.28	9.90
	2019	-11.11	0.92	-5.89	-0.14	-1.83	-0.35	10.52

DFFFA, Days to first female flower appearance; NNBFFF, Node number bearing first female flower; DFFH, Days to first fruit harvest; NPBPP, Number of primary branches per plant; VL, Vine length; FL, Fruit length; FB, Fruit breadth; NMFPP, Number of marketable fruits per plant; AFW, Average fruit weight; MFYPP, Marketable fruit yield per plant; SDMD, Severity of downy mildew disease; SPMD, Severity of powdery mildew disease.

in inheritance of traits related to earliness in cucumber (Table 3). Earlier El-Tahaway *et al.* (2015) and Kumar *et al.* (2017) also reported similar results in pumpkin and cucumber respectively. Top 7 cross combination revealed a significant positive heterobeltiosis for fruit length and breadth, no of fruit per plant, average fruit weight and no. of marketable fruit per plant (Supplementary Table 1). The cross combinations, KTG 40 × K-90, KTG 40 × UHF-16, 2870 G × K-90 and 2870 G × UHF-16 were found to be the best heterotic crosses for fruit yield and its contributing traits which recorded significant positive value for heterobeltiosis during both years. Significant positive heterosis for fruit yield and its contributing traits have already been reported by Kumar *et al.* (2017) and Nimitha *et al.* (2018). Further, D.E. of top 7 heterotic hybrids for yield and its component traits were found > +1 during both years indicating over dominance of this traits towards the better parents. Among top 7 crosses, 3 cross combination KTG 40 × K-90, 2870 G × K-90 and 1983 G × K-90 were showing significant heterobeltiosis for severity of downy and powdery mildew disease in cucumber is in consonance with result of Kumar *et al.* (2018) and Das *et al.* (2019). For severity of downy mildew diseases six crosses exhibited more than one potence ratio and one cross 2870 G × UHF-16 show less than one which indicating over dominance in 6 crosses and partial dominance in 1 cross for this trait. Further, On the basis of overall performance of heterobeltiosis and dominance degree it can be concluded that KTG 40 × K-90, 2870 G × K-90 and 2870 G × UHF-16 had the significant high heterotic, over dominance for fruit yield and found tolerance to fungal diseases in cucumber during the both years under study. Hence, hybrid vigour may be exploited commercially for improvement in cucumber.

The present study illustrated the preponderance of non-additive gene effects in governing all study traits in cucumber. Among the parents, gynoecious inbred lines KTG-40, 2870G and testers K-90, UHF-16 were the most promising general combiners for fruit yield along with good horticultural characters, and they could be used further in gynoecious cucumber hybridization programme. The crosses KTG-40 × K-90 and 2870G × K-90 ranked top in respect of earliness, yield and level of field tolerance against downy and powdery mildew diseases and found promising for commercial exploitation after their critical evaluation. The present finding also suggested partial to over dominance reaction for the inheritance of fruit yield and other economic important traits.

ACKNOWLEDGEMENT

Author is grateful to the Indian Council of Agricultural Research (ICAR) for awarding ICAR-PG Fellowship during the entire period of this experiment.

REFERENCES

Anonymous. 2018. Horticultural statistics at a Glance. Horticulture Statistics Division, Department of Agriculture Corporation and Farmers Welfare, Ministry of Agriculture & Farmers Welfare, Government of India.

Baker R J. 1978. Issues in diallel analysis. *Crop Science* **18**: 533–36.

Dabholkar A R. 1992. *Elements of Biometrical Genetics*. Concept Publishing Company, New Delhi.

Das S P, Mandal A R, Maurya P K, Bhattacharjee T, Banerjee S, Mandal A S and Chattopadhyay A. 2019. Genetic control of economic traits and evidence of economic heterosis in crosses involving monoecious cucumber genotypes. *International Journal of Vegetable Science*. https://doi.org/10.1080/19315260.2019.1639873

De Candolle A. 1882. *Origin of Cultivated Plant*. John Wiley and Sons, New York, London.

El-Tahawey M A F A, Kandeel A M, Youssef S M S and Abd El-Salam M M M. 2015. Heterosis, potence ratio, combining ability and correlation of some economic traits in diallel crosses of pumpkins. *Egypt Journal of Plant Breeding* **19**: 419–39.

Jat G S, Munshi A D, Behera T K, Singh A K and Kumari S. 2017. Genetic analysis for earliness and yield components using gynoecious and monoecious lines in cucumber (*Cucumis sativus* L.). *Chemical Science Review and Letters* **6**: 1075–79.

Kempthorne O. 1957. *An Introduction to Genetic Statistics,* pp. 468–71. John Wiley and Sons, Inc. New York.

Kumar S, Kumar R, Kumar D, Gautam N, Singh N, Parkash C, Dhiman M R and Shukla Y R. 2017. Heterotic potential, potence ratio, combining ability and genetic control of yield and its contributing traits in cucumber (*Cucumis sativus* L.). *New Zealand Journal of Crop and Horticulture Science* DOI: 10.1080/01140671.2016.1270336

Kumar R, Kumar S, Kumar D and Kansal S. 2018. Heterosis, combining ability and gene action studies for insect-pest and disease resistance in cucumber. *Electronic Journal of Plant Breeding* **9**: 815–28.

Nimitha K, Acharya R R and Parmar D J. 2018. Exploitation of hybrid vigour through diallel analysis in cucumber (*Cucumis sativus* L.). *Electronic Journal of Plant Breeding* **9**: 60–65.

Ransom L M, Briens R G O and Glass R J. 1991. Chemical control of powdery mildew in green peas. *Australian Plant Pathology* **20**: 16–20.

Reuveni R. 1983. Resistance of *Cucumis melo* for *Pseudoperonospora cubensis*. *Annals of Applied Biology* **102**: 533–37.

Sebastian P, Schaefer H, Telford I R H and Renner S. 2010. Cucumber (*Cucumis sativus*) and melon (*C. melon*) have numerous wild relatives in Asia and Australia, and the sister species of melon is from Australia. *Proceedings of the National Academy of Sciences of the United States of America* **107**: 14269–73.

Singh D. 1973. Diallel analysis over environments-I. *Indian Journal of Genetics and Plant Breeding* **33**: 127–36.

Singh R K and Chaudhary B D. 1997. *Biometrical Methods in Quantitative Genetic Analysis*, pp. 342. Kalyani Publishers, Ludhiana, Punjab.

Smith H H. 1952. Fixing transgressive vigour in *Nicotiana rustica* L. *Heterosis*. Iowa State College Press, Ames, IA, United States.