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Yashpal Singh Bisht

Department of Vegetable Science, G. B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India

DK Singh

Department of Vegetable Science, G. B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India

NK Singh

Department of Genetic and Plant Breeding, G. B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India

Dhirendra Singh

Department of Vegetable Science, G. B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India

Shashank Shekhar Singh

Krishi Vigyan Kendra, Nawada, Bihar, India

Corresponding Author: Yashpal Singh Bisht Department of Vegetable Science, G. B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India

Studies of genetic variability in parthenocarpic cucumber (*Cucumis sativus* L.)

Yashpal Singh Bisht, DK Singh, NK Singh, Dhirendra Singh and Shashank Shekhar Singh

Abstract

The aim of present experiment was to study genetic variability in parthenocarpic cucumber (*Cucumis sativus* L.) material consist of 44 genotypes. A sufficient amount of genetic variability was present in all 44 genotypes for 12 characters *viz.*, days to first female flower, node number to first female, days to first harvest, days to last harvest, internodal length (cm), fruit length (cm), fruit diameter (cm), vine length (m), number of fruits/plant, average fruit weight (g), yield/plant (kg) and total yield/hectare (quintal). The GCV and PCV varies from 2.01 to73.84 and 3.30 to 74.78. The difference between PCV and GCV was less which indicate these traits are less influence by the environments. PPCUC-2 was found best performing genotypes for yield per plant and yield per hectare. Hence, these genotypes can be used for further improvement of cucumber germplasm for sound breeding program.

Keywords: Breeding, cucumber, genotypes, parthenocarpic, variability

1. Introduction

Cucurbits are one of the important summer vegetable crops grown in large scale in India. After tomato and watermelon, cucumber and melons are mostly cultivated vegetable. Cucumber (*Cucumis sativus* L.) is a member of the Cucurbitaceae, is one of the oldest cultivated vegetable. Cucumber is mostly cultivated at tropical and sub-tropical region and sensitive to frost, grown best at temperature of 20 °C (Tatlioglu, 1993) ^[16]. Total worldwide production of cucumber is 91.25 million tonnes form an area of 2.261 million hectares with productivity of 4.04 kg/m². China is largest producer of cucumber in the world with production of 72.778 million tonnes accounting for 79.75% world cucumber (FAOstat, 2020) ^[4]. In India, it is cultivated in the area of 109 thousand ha and production of 1664 thousand MT. West Bengal rank first in the production of cucumber in India with production of 326.82 thousand tonnes and share 20.32 percent in total production (NHB, 2020-21)^[9].

To overcome the situation of low production, genetically stable genotypes having high yield potential are urgently needed. It is therefore, necessary to estimate relative amounts of genetic and non-genetic variability exhibited by different characters using suitable parameters like genetic coefficient of variability, heritability estimates and genetic advance. Besides estimating the nature and magnitude of correlation coefficient, path coefficient analysis and genetic association between yield with other traits that contributed to yield and are suitable to identified by variability, correlation and path coefficient analysis between yield and its attributes. The information on their genetic variability and traits association contributes with yield and among itself is of considerable importance in selection for elite genotype as well as exploitation of heterosis breeding programme. A study on genetic variability and correlation alone are not enough to give an exact figure of relative importance of direct and indirect influence of each of the component traits on yield. In such case, path coefficient analysis is an important technique for partitioning the correlation coefficient in to direct and indirect effect of independent variables on dependent variable. It is therefore, genetic variability as well as correlation and path coefficient may be important tools for the breeder to enhancing the production and productivity of the cucumber. The present study was conducted to assess genetic variability, heritability and path coefficient analysis yield and its component characters to provide necessary information that could be useful in cucumber improvement programmes aimed at improving yield.

2. Materials and Methods

Fourteen cucumber advanced breeding lines (10 line, 3 tester and 1 check) crossed in a line × tester mating design to developed 30 F_1 hybrids. 44 (30 F_1 hybrids + 10 line + 3 tester + 1 check) were tested and evaluated during the *Kharif* season of 2021 in the Vegetable Research Centre (V.R.C.), G. B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India. The experiment was arranged in randomized block design with 3 at spacing of 60×90 cm. All the cultural practise are followed till the transplants are ready. Five plants were randomly selected and tagged from each replication from every genotype. Observation was recorded from tagged plants for days to first female flower, node number to first female, days to first harvest, days to last harvest, intermodal length (cm), fruit length (cm), fruit diameter (cm), vine length (m), number of fruits/plant, average fruit weight (g), yield/plant (kg) and total yield/hectare (quintal).

Analysis of variance was done following the method given by Panse and Sukhatme (1967)^[10]. Genotypic and phenotypic

coefficients of variations were calculated by the formula given by Burton and Devane (1953)^[1]. Heritability in broad sense is expressed in percentage was calculated by Falconer (1981)^[3] method. Robinson *et al.* (1949)^[12] gave the formula to calculate genetic advance (GA). Johnson *et al.* (1955)^[6] gave the formula to calculate the estimation of genetic advance as percentage over mean. Statistical analyses were done using SPSS Professional Version 13.0 and SAS 9.3 Professional Version.

3. Results and Discussions

Analysis of variance for various quantitative characters revealed that mean sum of squares were significant for all the characters under study, indicating an existence of sufficient genetic variability for all the characters under studied (Table 1). Thus, these genotypes can be further used for the heterosis breeding program for further improvements. The presence of significant variability were also in accordance with the finding of Shet *et al.* (2018) ^[13]; Singh *et al.* (2018) ^[15]; Mishra *et al.* (2021)^[8] and Singh and Dhillon (2022) ^[14].

S.	Characters	Jf.	Replication	Treatments	Error	
No.	Characters	df	2	43	86	
1	Days to first female flo	ower	63.90	27.86**	4.50	
2	Node number to first femal	e flower	0.54	14.42**	0.81	
3	Days to first harves	t	27.99	27.27**	2.87	
4	Days to last harves	t	26.88	20.47**	7.42	
5	Vine length (m)		0.15	0.22**	0.07	
6	Fruit length (cm)		0.59	21.17**	1.50	
7	Average fruit diameter	(cm)	0.10	0.73**	0.10	
8	Number of fruit per pl	ant	0.48	136.41**	1.15	
9	Average fruit weight	(g)	1771.94	10115.65**	515.21	
10	Fruit yield per plant (kg)	0.09	0.76**	0.05	
11	Internodal length		2.29	3.91**	0.83	
12	Fruit yield (q/ha)		2965.65	22501.13**	1370.16	

Table 1: Analysis of variance (ANOVA) for 12 quantitative characters in cucumber

3.1 Variation observed for mean values

The per se performance of various characters under study was shown in table 2. Days to first female flower range from 33.44 days (PPCUC-5 & PPCUC-11) to 45.11 days (PCUC-8) with general mean value of 39.28 days. Node number to first female flower varies from PPCUC-2 (2.97) to PPCUC-7 \times PCUC-8 (10.50). Days to first harvest varies from PPCUC-10 (41.83 days) to PPCUC-12 \times PCUC-8 (52.25 days). Days to last harvest varies from PPCUC-3 (97.32 days) to PPCUC-12 × PCUC-51 (107.70 days). Vine length range from PPCUC-10 (2.74 m) to PPCUC-6 \times PCUC-8 (3.80 m). Fruit length varies from PPCUC-12 (12.59 cm) to PPCUC-9 \times PCUC-51 (23.74 cm). Fruit diameter varies from PPCUC-12 (3.40 cm) to PPCUC-6 × PCUC-28 (5.25 cm). Number of fruit per plant varies from PPCUC-6 \times PCUC-8 (4.07) to PPCUC-5 (23.08). Average fruit weight varies from PPCUC-5 (120.25 g) to PPCUC-9 × PCUC-51 (291.64 g). Fruit yield per plant varies from PPCUC-6 \times PCUC-8 (1.22 kg) to PCUC-2 (3.03 kg). Internodal length varies from PPCUC-10 (9.15 cm) to PPCUC-12 × PCUC-51 (13.47 cm).Fruit yield per hectare varies from PPCUC-6 \times PCUC-8 (225.76 g/ha) to PCUC-2 (568.33 q/ha).

3.2 Analysis of genetic variability, heritability and genetic advance as % mean

The phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance

and genetic advance as per cent of mean was shown in table 3. The range of GCV varied from 2.01% for days to last harvest to 73.84% for number of fruits per plant. High genotypic coefficient (GCV) (> 20%) was found in node number to first female flower (28.55), number of fruit per plant (73.84), average fruit weight (26.09), fruit yield per plant (25.92) and fruit yield per hectare (24.81). Moderate genotypic coefficient of variation (10-20%) was found in fruit length (14.25) and average fruit diameter (10.44). Low genotypic coefficient of variation (<10%) was found in days to first female flower (7.10), days to first harvest (5.91), days to last harvest (2.88), vine length (6.70) and internodal length (8.65). The range of PCV also varied from 3.30% for days to last harvest to 74.78% for number of fruits per plant. High phenotypic coefficient (PCV) (> 20%) was found in node number to first female flower (30.98), number of fruit per plant (74.78), average fruit weight (28.11), fruit yield per plant (28.78) and fruit yield per hectare (27.11). Moderate genotypic coefficient of variation (10-20%) was found in vine length (10.39), fruit length (15.80), average fruit diameter (12.74) and internodal length (11.64). Low genotypic coefficient of variation (<10%) was found in days to first female flower (8.92), days to first harvest (6.87) and days to last harvest (3.30). The estimate of broad sense heritability ranged from 37.00% (days to last harvest) to 97.50% (number of fruits per plant). High heritability (>75%) was found in node number to first female flower (84.90), fruit length

(81.40), number of fruit per plant (97.50), average fruit weight (86.10), fruit yield per plant (81.10) and fruit yield per hectare (83.70). Moderate heritability (50-75%) was found in days to first female flower (63.40), days to first harvest (73.90), average diameter (67.10) and internodal length (55.20). Low genotypic coefficient of variation (<10%) was found in days to last harvest (37.00) and vine length (42.50). Genetic advance ranged from 0.77 (fruit diameter) to 158.19 (fruit yield per plant). High value of genetic advance was observed for average fruit weight (108.16) and fruit yield per hectare (158.19). Moderate value of genetic advance was found in number of fruit per plant (13.66). Low value of genetic advance was found in days to first female flower (4.58), node number to first female flower (4.04), days to first harvest (5.05), days to last harvest (2.61), vine length (0.30), fruit length (4.76), average fruit diameter (0.77), fruit vield per plant (0.90) and internodal length (1.55). Genetic advance ranged from 2.52 (days to last harvest) to 150.21 (number of

fruit per plant). High value of genetic advance as per cent of mean (>20%) was observed node number of female flower (54.18), fruit length (26.48), number of fruit per plant (150.21), average fruit weight (49.88), fruit yield per plant (48.07) and fruit yield per hectare (46.76). Moderate genetic advance as per cent of mean (10-20%) was found in days to first female flower (11.65), days to first harvest (10.46), average fruit diameter (17.61) and internodal length (13.23). Low genetic advance as per cent of mean (<10%) was found in days to last harvest (2.52) and vine length (8.89). Significant variability, heritability, genetic advance and advance as per cent of mean for days to first female flower, node number to first female flower, days to first harvest, vine length, fruit length, average fruit diameter, number of fruit per plant, average fruit weight, intermodal length and yield per plant was observed by Gaikwad et al. (2011)^[5], Kumar et al. (2013)^[7], Ene et al. (2016)^[2], Pushpalatha et al. (2016)^[11] and Tripathi *et al.* (2021)^[17].

Table 2: Mean performance of cucumber genotype for different quantitative traits

	DFFF	NFFF	DFH	DLH	VL	FL	AFD	NFP	AFW	FYP	IL	FYH
PPCUC-2 \times PCUC-8	42.11	6.75	51.42	104.26	3.63	17.96	5.17	6.17	266.74	1.43	11.75	265.04
$PPCUC-2 \times PCUC-28$	36.09	6.55	47.24	104.92	3.56	16.95	4.60	6.16	211.88	1.53	12.05	275.86
PPCUC-2 \times PCUC-51	38.89	6.71	48.50	107.66	3.79	16.71	4.32	6.57	161.11	1.62	12.59	275.85
PPCUC-3 \times PCUC-8	40.83	6.73	49.59	104.30	3.46	22.94	4.83	6.26	269.44	1.89	12.43	348.17
PPCUC-3 \times PCUC-28	38.22	7.64	49.35	104.60	3.40	21.22	5.09	8.14	288.34	2.18	10.80	359.88
PPCUC-3 × PCUC-51	39.11	9.39	48.97	103.65	3.08	21.36	4.58	6.12	257.59	2.06	12.25	367.07
PPCUC-4 \times PCUC-8	41.89	9.08	51.06	105.92	3.54	20.55	4.30	6.85	237.79	1.55	12.37	286.54
PPCUC-4 \times PCUC-28	42.83	9.97	50.92	102.87	3.73	18.87	4.57	6.33	229.27	2.03	12.82	374.87
PPCUC-4 \times PCUC-51	41.28	9.74	51.57	104.39	3.72	19.44	4.44	5.90	265.38	1.69	12.45	311.48
PPCUC-5 \times PCUC-8	37.17	7.85	47.62	104.55	3.72	18.43	4.47	5.76	231.94	1.75	12.39	323.41
PPCUC-5 \times PCUC-28	36.62	7.03	47.61	103.69	3.33	18.09	4.86	5.09	252.01	1.49	11.78	275.53
PPCUC-5 \times PCUC-51	37.34	8.06	46.86	105.25	3.46	18.23	4.32	5.87	259.02	1.52	12.38	281.58
PPCUC-6 \times PCUC-8	41.88	8.75	50.39	103.25	3.80	19.07	4.79	4.07	258.32	1.22	11.49	225.76
PPCUC-6 \times PCUC-28	41.22	7.17	50.25	106.61	3.07	18.37	5.25	5.62	273.46	1.48	11.25	274.48
PPCUC-6 × PCUC-51	40.52	8.86	50.08	103.63	3.06	16.49	4.64	5.66	243.60	1.39	12.84	257.09
PPCUC-7 \times PCUC-8	41.22	10.50	50.32	103.46	3.03	20.91	4.54	5.61	255.22	1.75	13.16	323.54
PPCUC-7 \times PCUC-28	40.68	8.55	50.48	105.77	3.12	21.70	4.71	4.75	255.99	1.47	12.05	271.92
PPCUC-7 × PCUC-51	41.33	9.62	50.84	104.98	2.97	20.64	4.77	5.79	231.12	1.57	12.03	289.75
$PPCUC-9 \times PCUC-8$	39.28	7.22	48.46	103.84	3.45	19.09	4.58	6.09	265.50	1.57	10.57	291.66
$PPCUC-9 \times PCUC-28$	36.97	6.22	47.25	105.30	3.14	20.32	4.49	4.52	252.59	1.62	10.89	299.76
PPCUC-9 × PCUC-51	38.11	8.61	47.26	105.32	3.20	23.74	5.20	5.10	291.64	1.51	12.28	278.26
PPCUC-10 × PCUC-8	38.91	7.78	49.06	104.49	3.12	16.75	4.30	5.02	203.09	1.85	12.51	342.59
PPCUC-10 \times PCUC-28	42.11	7.75	51.45	106.52	3.15	16.91	4.66	4.37	234.79	1.71	13.25	316.11
PPCUC-10 \times PCUC-51	40.10	7.97	50.70	107.55	3.32	20.49	4.82	4.63	269.17	1.47	12.25	270.72
PPCUC-11 \times PCUC-8	42.42	9.17	49.16	106.76	3.74	21.15	4.37	4.93	284.24	1.86	11.46	344.08
PPCUC-11 \times PCUC-28	40.40	8.25	49.28	106.04	3.26	16.80	4.41	5.03	159.56	1.94	12.25	357.95
PPCUC-11 × PCUC-51	41.40	9.69	50.73	104.80	3.28	20.78	4.80	4.23	268.97	2.06	13.16	380.13
PPCUC-12 \times PCUC-8	43.82	9.14	52.25	103.43	3.33	15.35	3.87	5.63	222.60	1.63	12.71	300.63
PPCUC-12 \times PCUC-28	39.75	8.95	48.63	106.26	3.67	18.19	4.87	4.52	272.87	1.56	12.68	288.51
PPCUC-12 \times PCUC-51	41.31	9.94	49.94	107.70	3.45	18.57	4.32	4.71	255.06	1.37	13.47	252.43
PPCUC-2	33.89	2.97	42.06	97.99	3.25	15.60	4.26	21.45	128.14	3.03	9.85	568.33
PPCUC-3	35.97	3.78	43.71	97.32	3.05	16.23	3.75	18.53	136.90	2.52	10.40	479.00
PPCUC-4	36.70	4.64	43.71	99.75	2.98	15.25	3.46	20.26	140.84	2.71	10.10	489.29
PPCUC-5	33.44	4.11	42.27	99.39	3.56	14.05	3.50	23.08	120.25	2.79	11.58	476.92
PPCUC-6	34.01	3.84	43.28	99.03	2.94	13.29	4.32	21.46	122.53	2.55	10.39	455.25
PPCUC-7	36.42	4.34	43.61	99.26	3.11	13.51	3.49	20.50	125.20	2.51	11.50	459.58
PPCUC-9	35.75	4.55	44.49	101.77	3.07	15.46	3.72	20.82	122.06	2.84	9.95	480.28
PPCUC-10	34.11	3.86	41.83	101.11	2.74	14.66	3.87	22.91	128.61	2.66	9.15	476.15
PPCUC-11	33.44	3.75	43.28	103.26	2.98	14.50	3.55	21.09	128.52	2.39	10.16	409.33
PPCUC-12	38.72	3.95	45.92	101.09	3.14	12.59	3.40	22.47	125.12	2.83	9.61	480.20
PCUC-8	45.11	9.78	50.94	103.98	3.50	16.26	3.79	5.79	137.92	1.44	13.12	266.46
PCUC-28	44.01	9.85	51.28	105.33	3.40	17.03	4.73	5.11	216.69	1.38	9.72	255.28
PCUC-51	42.89	9.82	50.98	107.00	3.46	17.96	4.29	5.79	250.26	1.39	12.64	256.90
Poinsetta	40.25	9.41	49.92	101.56	3.42	18.10	4.00	5.34	228.63	1.32	10.92	221.61

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Mean	39.28	7.46	48.28	103.86	3.32	17.97	4.39	9.09	216.82	1.87	11.71	338.30
C.V.	5.40	12.05	3.51	2.62	7.94	6.82	7.31	11.79	10.47	12.52	7.79	10.94
F ratio	6.19	17.84	9.51	2.76	3.13	14.10	7.11	118.64	19.63	13.84	4.69	16.42
F Prob.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
S.E.	1.23	0.52	0.98	1.57	0.15	0.71	0.19	0.62	13.10	0.14	0.53	21.37
C.D. 5%	3.44	1.46	2.75	4.42	0.43	1.99	0.52	1.74	36.84	0.38	1.48	60.08
C.D. 1%	4.56	1.93	3.64	5.86	0.57	2.64	0.69	2.31	48.82	0.50	1.96	79.61

*DFFF= Days to first female flower, NFFF= Node number to first female flower, DFH= Days to first harvest, DLH= Days to last harvest, VL= Vine length (m), FL= Fruit length (cm), FD= Fruit diameter (cm), NFP= Number of fruit per plant, AFW= Average fruit weight (g), FYP= Fruit yield per plant (kg), IL=Internodal length (cm), FYH= Fruit yield per hectare (q/ha)

Table 3: Estimation of different genetic parameter for different quantitative characters

	GCV	PCV	h ² (Broad Sense)	Genetic Advance (5%)	GAM (5%)
DFFF	7.10	8.92	63.40	4.58	11.65
NFFF	28.55	30.98	84.90	4.04	54.18
DFH	5.91	6.87	73.90	5.05	10.46
DLH	2.01	3.30	37.00	2.61	2.52
VL	6.70	10.39	41.50	0.30	8.89
FL	14.25	15.80	81.40	4.76	26.48
AFD	10.44	12.74	67.10	0.77	17.61
NFP	73.84	74.78	97.50	13.66	150.21
AFW	26.09	28.11	86.10	108.15	49.88
FYP	25.92	28.78	81.10	0.90	48.07
IL	8.65	11.64	55.20	1.55	13.23
FYH	24.81	27.11	83.70	158.19	46.76

*DFFF= Days to first female flower, NFFF= Node number to first female flower, DFH= Days to first harvest, DLH= Days to last harvest, VL= Vine length (m), FL= Fruit length (cm), FD= Fruit diameter (cm), NFP= Number of fruit per plant, AFW= Average fruit weight (g), FYP= Fruit yield per plant (kg), IL=Internodal length (cm), FYH= Fruit yield per hectare (q/ha), GAM= Genetic advance as per cent of mean

4. Conclusions

The knowledge of genetic variability is pre-requisite for improvement in any breeding programme. For development of superior genotype, more diverse breeding population are needed hence selection of superior and advance genotypes become pre-requisite. Form present study, it was concluded that sufficient amount of genetic variability was present in 44 genotypes. PPCUC-2 was best genotypes for yield per plant and yield per hectare. Hence, these genotypes can be further used for improvements in cucumber germplasms through heterosis breeding.

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