

Original Research Article

<https://doi.org/10.20546/ijcmas.2018.705.015>

Assessment of Genetic Variability among 78 Cucumber (*Cucumis sativus* L.) Germplams

Rahul Kumar^{1*}, A.D. Munshi¹, T.K. Behera¹, A. Talukdar²,
H. Choudhary¹ and P. Dash³

¹Division of Vegetable Science, ICAR-Indian Agricultural Research Institute,
New Delhi-110012, India

²Division of genetics, ICAR-Indian Agricultural Research Institute, New Delhi-110012, India

³ICAR- NRC on Plant Biotechnology, New Delhi-110012, India

*Corresponding author

ABSTRACT

An experiment was undertaken to study the variability in 78 cucumber germplasm collected from India as well as from abroad. Wide variations for different horticultural traits were observed under study. Lowest node number for first female flower was observed for Gy 421 (3.19) followed by RS 1 (3.22) and Gy 14 (3.25) while days taken for first female flower to anthesis as well as for days taken for first fruit harvest was lowest for Gy 421 (35.55, 46.05) followed by Gy 14(35.59, 46.91). Among fruit traits studied, fruit lengths were found maximum in CL 758 (35.29) followed by CL 746 (30.88). DC 21 recorded lowest fruit diameter (3.85 cm). Average fruit weight was highest in CL 758 (487.89g) followed by DARL-106 (410.00g) and EC 636506 (401.44g). High PCV (>20%) and GCV (>20%) were recorded for fruit length (30.72; 30.22), fruit length/diameter (35.84; 33.57) and average fruit weight (52.31; 52.16). The estimates of heritability were found high for the traits fruit length, average fruit weight and for vine length while node number for first female flower (86.66%), days taken for first female flower to anthesis (88.82%) were close to 90 per cent. Higher variability coupled with moderate to low genetic gain was noticed for days to first female flower, vine length, days taken for first fruit harvest, fruit length and average fruit weight.

Keywords

Genetic variability,
GCV, PCV,
cucumber,
quantitative traits

Article Info

Accepted:
04 April 2018
Available Online:
10 May 2018

Introduction

Cucumber, *Cucumis sativus* L. ($2n = 2x = 14$), which belongs to the gourd family Cucurbitaceae, is an economically important vegetable crop worldwide. Cucumber is originated in India (Sebastian, 2010) from its wild progenitor *Cucumis sativus* var. *hardwickii* R., which is still found in southern

foothills of Himalayas. It is well known for its economic importance as food plant, primarily cultivated for tender fruits, which are used as salad, pickles, rayata preparation and even brined on commercial scale in many part of the world. It is an ideal crop for the people suffering from jaundice, constipation and the seed oil of cucumber is highly valuable for development of brain, therefore it is also used

in *Ayurvedic* medicines. India ranks at 28th position producing about 0.17 million tons annually on 26088 hectares of land with a yield of 164 tons/ha (FAO, 2016). It is considered as a model plant for conducting genetic experiment because of its smaller genome size (367 Mb) and short life cycle (Ren *et al.*, 2009). The cultivated cucumber has narrow genetic base with 3-8% polymorphism, and 10-25% between botanical varieties. India being considered the home of cucumber possesses a vast range of genetic variability for different fruit characters, but this variability has not been fully utilised for its genetic improvement. Selection and hybridization are the two basic and most commonly preferred methods for cucumber improvement. The selection of superior genotypes depends on the amount of genetic variability present in the parental lines used in breeding programme. Use of diverse genotypes in hybridization programme creates broad genetic base for cucumber improvement. The information about genetics of fruit quality traits is utmost important for efficient breeding procedure to be used for the development quality rich produce from lines.

Genetic variability in breeding genotypes is important for successful introgression of desired traits specific genes. The genotypic and phenotypic coefficients of variability are helpful in exploring the nature of variability in the breeding populations. Determining variability in quality and quantitative traits of different cucumber genotypes will enable a breeder to know to what extent the environment affects the yield of the crop (Ahmed and Khaliq, 2007; Ullah *et al.*, 2012). The genetic variability among cucumber genotypes have been studied (Veena *et al.*, 2012; Yadav *et al.*, 2012; Kumar *et al.*, 2013 and Ranjan *et al.*, 2015; Pandey *et al.*, 2013). Estimates of heritability provides index of transmissibility of characters. The information on heritability alone may not help in

identifying characters for enforcing selection therefore, heritability estimates in conjunction with predicted genetic advance is more reliable (Johnson *et al.*, 1955). Heritability gives the information on the magnitude of inheritance of characters from parent to off spring, while genetic advance will be helpful in finding the actual gain expected under selection. The direct selection only for higher yield can give masking effect because many factors interact to determine crop yield (Gatti *et al.*, 2005). Separate yield components are less influenced by the environment than yield itself; hence, selection for such yield components can be useful to acquire genotypes with better yield abilities (Gatti *et al.*, 2005). All these measures are important for the identification of genetically distant parental lines to get superior hybrids and segregants which help in evaluation of the degree of genetic erosion, or extent of the genetic base of cultivated forms to develop heterotic groups. Keeping above facts in view, the present study was carried out to estimate genetic variability, genetic advance of important horticultural traits of cucumber, which will help in its genetic improvement for both yield and quality.

Materials and Methods

In this study, a total of 78 cucumber genotypes were used collected from various states of India as well as from abroad (Table 1). The present investigation was carried out at the Research Farm of Division of Vegetable Science, ICAR-IARI, New Delhi during the *kharif* season of the year 2016. The experiment was laid out in a randomized block design (RBD) having three replications with a row-to-row spacing of 100 cm and plant-to-plant spacing of 60 cm inside net house. Recommended fertilizer dose and standard cultural practices along with plant protection measures were followed. Five plants were randomly chosen and tagged to record data on

8 quantitative traits viz., node number for first female flower, days taken for first female flower to anthesis, days taken for first fruit harvest, fruit length (cm), fruit diameter (cm), fruit length/diameter ratio, average fruit weight (g), and vine length (cm). The data were analyzed using the ANOVA procedure of SAS 9.2 (SAS Institute, Cary, NC, USA) to derive their summary statistics including mean, range, standard deviation, variance, and coefficient of variation. Phenotypic and genotypic components of variance were estimated by using the formula given by Cochran and Cox, (1957). The expected genetic gain or advance for each character was estimated by using the method suggested by Johnson *et al.*, (1955). Genotypic correlation between two characters was determined by using the variance and covariance components as suggested by Al-Jibouri *et al.*, (1958).

Results and Discussion

The mean value of selected 8 horticultural traits of the genotypes studied under net house is given in table 2. Node number for first female flower for genotypes Gy 421 (3.19) followed by RS-1 (3.22), Gy 14 (3.25), GLK-1 (3.67) and DC 22 (3.97) were less than four while overall average was 5.51 days. Genotypes Gy-421(35.55) followed by Gy 14(35.59), GLK-1 (35.91), DC 22(35.98) revealed lowest average for days taken for first female flower to anthesis as well as for days taken for first fruit harvest (46.05, 46.91, 46.98 and 46.98 days respectively). Among fruit traits studied, fruit lengths were found maximum in CL 758 (35.29) followed by CL 746 (30.88) while 15.29 cm was average for all the genotypes. DC 21 recorded lowest fruit diameter (3.85 cm). Average fruit weight was highest in CL 758 (487.89g) followed by DARL-106 (410.00g) and EC 636506 (401.44g) while overall average was 179.90 g. Wide variations for different horticultural traits were also reported by many researchers

for traits such as for number of primary branch per vine, number of nodes bearing first male and female flower, days to first fruit harvest (Munshi *et al.*, 2006; Hanchinamani *et al.*, 2008) fruit length, fruit diameter (Kumar *et al.*, 2010; Jat *et al.*, 2014; Innark *et al.*, 2013) average fruit weight, number of fruit per vine and total fruit yield per vine (Singh *et al.*, 2014; Shah *et al.*, 2017; Veena *et al.*, 2013; Pandey *et al.*, 2013) indicating that simple selection based on phenotypic performance of these traits may be effective to improve.

The estimates of phenotypic and genotypic coefficients of variation gave a clear picture on the magnitude of variations presents in the available germplasm (Table 3). High PCV (>20%) and GCV (>20%) were recorded for fruit length (30.72; 30.22), fruit length/diameter (35.84; 33.57) and average fruit weight (52.31; 52.16). The PCV and GCV were lower for days taken for first female flower to anthesis (8.36; 7.88), days taken for first fruit harvest (7.32; 6.50), fruit diameter (12.74; 8.39) as well as for vine length (9.00; 8.79). However there is very less variation between phenotypic coefficient of variation and genotypic coefficient of variation for all the characters under study which reflects that the variability existing in them was mainly due to their genetic makeup. Thus, selection on the basis of phenotype will be effective. The values of range reflects the amount of phenotypic variability which is not very reliable since it includes genotypic, environmental and genotype X environmental interaction components and does not reveal as to which character is showing higher degree of genetic variability. Further, the phenotype of crop is influenced by additive gene effect (heritable), dominance (non-heritable) and epistatic (non-allelic interaction). Therefore, it becomes necessary to split the observed variability into phenotypic variation (PV) and genotypic variation (GV) which indicates the extent of variability existing for various traits.

Table.1 List of genotypes used under study along with their source of origin

Sl. No.	Germplasm	Origin	Sl. No.	Germplasm	Origin
1.	702-6-B76	China	40	GS-2	Western Uttar Pradesh
2.	AS -1	Karnataka	41	GS-3	Western Uttar Pradesh
3.	Baropata Sasha	West Bengal	42	Gy 14	USA
4.	Barsha Magal	West Bengal	43	Gy 421	USA
5.	BC 1	Karnataka	44	HS-1	Haryana
6.	CCUH-3	Uttarakhand	45	HS3	Haryana
7.	CCUH-5	Uttarakhand	46	HS4	Haryana
8.	CL 746	China	47	HS-5	Haryana
9.	CL 758	China	48	HS-9	Haryana
10.	CL 773	China	49	Kalyanpur Green	Eastern Uttar Pradesh
11.	DARL-106	Uttarakhand	50	KP/PKS 1325	Meghalaya
12.	DC 21	Western Uttar Pradesh	51	KP/PKS 1330	Meghalaya
13.	DC 22	Western Uttar Pradesh	52	KP/PKS 748	Meghalaya
14.	DC-102	Western Uttar Pradesh	53	Mirpur Selection	West Bengal
15.	DC-103	Western Uttar Pradesh	54	Pa-5	Eastern Uttar Pradesh
16.	DC106	Western Uttar Pradesh	55	Pahari 77	Western Uttar Pradesh
17.	DC-27	Western Uttar Pradesh	56	Pahari Barsati	Western Uttar Pradesh
18.	DC-505	Western Uttar Pradesh	57	Panipat Local	Haryana
19.	DC92-1	Western Uttar Pradesh	58	PCUC-8	Uttarakhand
20.	DG-4	Karnataka	59	Poinsett	USA
21.	Dharwad Green	Karnataka	60	Pusa Sanyog	IARI, New Delhi
22.	Dofasli	Western Uttar Pradesh	61	Pusa Uday	IARI, New Delhi
23.	EC 636504	USA	62	Ragini	West Bengal
24.	EC 636505	USA	63	RK-100	Eastern Uttar Pradesh
25.	EC 636506	USA	64	RS 1	China
26.	EC 636509	USA	65	SN-25	Eastern Uttar Pradesh
27.	EC 636510	USA	66	Swarna Ageti	Jharkhand
28.	EC 636511	USA	67	Swarna Sheetal	Jharkhand
29.	EC 636512	USA	68	WBC-1-1	West Bengal
30.	EC 636513	USA	69	WBC-13	West Bengal
31.	EC 636514	USA	70	WBC-21	West Bengal
32.	EC 636517	USA	71	WBC-2-1	West Bengal
33.	EC 757855	USA	72	WBC-27-1	West Bengal
34.	EC 757857	USA	73	WBC-37-2	West Bengal
35.	EC 757858	USA	74	WBC-39-2	West Bengal
36.	EC757856	USA	75	WBC-5	West Bengal
37.	Faizabad Nutan	Eastern Uttar Pradesh	76	WBC-55	West Bengal
38.	GLK 1	IARI, New Delhi	77	WBC-6	West Bengal
39.	GS 4	Western Uttar Pradesh	78	WBC-9	West Bengal

Table.2 Means of 8 horticultural traits studied for 78 cucumber genotypes

Germplasms	Node number for first female flower	Days taken for first female flower to anthesis	Days taken for first fruit harvest	Fruit length (cm)	Fruit diameter (cm)	Fruit length/diameter ratio	Average fruit weight (g)	Vine length (cm)
BC 1	6.017	59.057	61.95	15.653	4.923	3.203	180.813	158.867
Pusa Uday	5.39	51.47	57.363	16.397	5.407	3.093	195.71	143.17
Kalyanpur Green	4.933	50.147	57.81	19.92	5.043	3.963	245.697	150.077
Faizabad Nutan	4.85	41.943	56.043	12.27	4.933	2.517	150.56	132.887
Russian	3.22	42.2	54.13	15.84	4.877	3.273	300.073	125.277
EC757856	5.117	47.737	53.61	11.403	4.717	2.433	83.437	142.28
CL 758	5.297	47.303	57.003	35.287	4.953	7.247	487.89	162.627
EC 636510	4.987	45.617	57.153	19.303	5.01	3.857	201.047	135.017
Pusa Sanyog	5.487	46.913	55.633	16.717	4.797	3.583	114.39	125.813
Pahari Barsati	6.193	47.473	63.227	23.963	5.687	4.247	330.31	163.877
Swarna Ageti	4.547	45.32	60.54	11.44	5.21	2.23	152.87	154.563
Pahari 77	7.223	46.813	56.803	12.493	5.737	2.18	59.373	140.293
Dharwad Green	5.613	45.58	59.08	14.187	4.72	3.05	105.043	113.183
EC 636512	7.597	50.87	61.87	12.333	5.25	2.363	150.87	153.677
EC 636513	7.29	50.12	61.03	11.31	5.263	2.163	151.45	157.36
Mirpur Selection	5.56	47.187	61.287	13.963	5.103	2.753	315.217	148.463
EC 636514	7.52	52.353	61.04	11.723	4.73	2.513	149.05	153.663
Poinsett	7.293	47.413	61.76	12.653	4.973	2.547	149.58	154.98
KP/PKS 748	5.323	46.207	58.43	14.793	5.15	2.877	120.263	142.78
SwarnaSheetal	4.593	45.87	60.34	12.273	5.057	2.453	121.553	143.28
Baropata Sasha	4.547	43.52	55.197	15.817	4.643	3.41	298.003	123.7
Ragini	6.657	49.627	56.36	12.537	5.053	2.493	129.5	130.47
Panipat Local	5.593	49.303	59.553	22.793	5.013	4.543	223.08	139.077
EC 636517	6.813	49.81	60.65	27.33	6.007	4.55	396.827	157.357
KP/PKS 1330	4.917	48.187	64.49	26.187	6.11	4.287	122.8	134.867
WBC-6	5.59	44.637	60.577	15.333	4.963	3.09	169.333	155.6
WBC-5	5.96	49.783	60.857	15.483	5.65	2.74	237.933	145.65
WBC-9	7.45	50.673	61.72	12.97	5.18	2.53	150.91	153.64
WBC-13	6.623	47.563	60.827	14.333	6.887	2.083	132.487	147.117

WBC-27-1	6.793	45.91	60.56	14.8	6.143	2.433	152.34	160.447
WBC-1-1	4.77	48.393	57.813	15.113	5.933	2.553	211.89	153.083
SN-25	4.543	42.807	50.407	13.613	4.357	3.14	85.553	123.4
Gy 421	3.187	35.55	46.907	9.727	5.567	1.75	90.33	111.24
GLK 1	3.667	35.91	46.98	12.883	4.337	3.003	95.19	125.953
CL 746	4.377	42.57	57.673	30.88	4.03	7.713	300.267	158.44
GS 4	5.41	49.227	60.843	11.837	5.277	2.26	205.573	157.363
Dofasli	5.9	43.953	61.163	11.003	5.543	1.993	156.313	161.027
WBC-55	5.237	46.763	58.143	14.46	5.183	2.8	171.927	149.803
WBC-2-1	5.33	44.603	61.72	14.507	5.81	2.513	150.76	153.42
WBC-37-2	6.013	46.39	55.03	14.817	5.743	2.59	159.357	154.71
WBC-21	6.38	46.137	60.827	14.543	5.707	2.563	173.22	150.667
WBC-39-2	5.597	48.533	59.86	14.753	5.983	2.467	162.117	154.54
RK-100	5.747	45.097	58.207	16.177	5.607	2.9	397.073	146.337
Pa-5	5.657	49.247	60.87	13.663	4.513	3.063	201.11	141.397
Gy 14	3.253	35.593	46.05	10.343	5.477	1.893	91.63	111.907
EC 636504	4.15	45.71	60.82	13.98	4.833	2.9	156.303	160.483
KP/PKS 1325	5.347	52.34	59.383	13.83	4.893	2.84	122.42	158.22
702-6-B76	4.52	48.273	60.12	13.51	5.683	2.393	120.637	148.54
DARL-106	6.96	49.627	61.93	21.693	5.77	3.83	410.003	164.297
CCUH-3	5.15	47.717	57.563	12.663	4.96	2.553	120.07	146
GS-3	4.773	45.887	60.43	12.98	5.5	2.383	156.78	154.297
HS3	5.663	48.607	57.747	13.853	5.513	2.53	113.48	140.047
HS4	4.733	47.45	60.263	13.437	5.953	2.26	85.03	142.563
EC 636506	7.597	48.46	56.56	16.34	5.207	3.147	401.443	155.82
EC 757857	4.89	46.377	56.85	19.35	4.52	4.33	145.33	164.467
EC 757855	6.367	49.44	61.147	26.91	4.883	5.513	398.76	154.76
GS-2	5.48	47.317	60.933	15.15	5.453	2.793	109.997	154.523
CCUH-5	5.373	46.627	57.643	16.987	6.007	2.83	380.447	150.18
DC 22	3.97	35.98	46.98	11.91	5.643	2.133	96.87	158.067
DC 21	5.313	46.2	56.093	12.557	3.847	3.337	83.14	137.683
Barsha Magal	5.16	44.45	56.597	11.83	5.113	2.357	65.343	117.457
DC106	4.51	47.083	59.577	15.263	5.347	2.883	150.14	161.63
EC 636505	5.067	45.517	56.927	12.42	5.063	2.453	133.81	160.41

DC92-1	5.45	46.69	57.357	11.297	5.223	2.167	142.437	156.967
HS-9	4.9	46.633	60.72	12.907	5.1	2.547	155.65	141.143
HS-1	5.307	45.663	56.023	13.377	5.997	2.23	130.303	132.777
HS-5	4.763	45.83	60.42	12.98	5.64	2.323	156.587	156.317
DC-103	5.69	44.96	54.483	14.15	5.137	2.757	222.173	135.143
AS 1	5.58	47.313	55.63	12.913	5.35	2.413	176.51	144.03
DC-27	5.007	46.947	59.01	12.847	5.38	2.417	82.82	154.947
EC 636509	5.31	48.553	57.42	12.64	4.667	2.777	90.387	145.303
DC-505	6.183	50.373	60.557	15.297	4.827	3.173	298.15	157.143
EC 757858	6.513	52.03	63.01	17.587	5.253	3.373	182.267	141.807
EC 636511	7.74	50.65	62.82	15.98	5.747	2.8	150.887	156.573
DC-102	4.663	41.357	50.653	12.87	5.277	2.443	118.74	133.613
DG-4	4.54	43.963	51.517	11.923	5.303	2.25	131.653	140.943
CL 773	5.39	44.683	55.37	11.013	6.31	1.757	126.61	140.227
PCUC-8	5.877	46.633	52.4	15.953	4.587	3.51	161.333	147.7

Table.3 Summary statistics of 8 horticultural traits evaluated in 78 cucumber genotypes

Traits	Overall Means	Standard Error of differences	Heritability %	Genotypic Coefficient of Variations	Phenotypic Coefficient of Variations	Genetic Advance	Genetic Advance value % means
Node number for first female flower	5.49	0.32	86.66	18.22	19.57	1.92	34.93
Days taken for first female flower to anthesis	46.70	1.07	88.82	7.88	8.36	7.15	15.30
Days taken for first fruit harvest	58.00	1.60	78.84	6.50	7.32	6.90	11.89
Fruit length (cm)	15.23	0.69	96.75	30.22	30.72	9.33	61.23
Fruit diameter (cm)	45.26	0.41	43.37	8.39	12.74	0.60	11.38
Fruit length/diameter ratio	2.95	0.30	87.70	33.57	35.84	1.91	64.75
Average fruit weight (g)	179.58	5.79	99.43	52.16	52.31	192.40	107.14
Vine length (cm)	146.38	2.30	95.43	8.79	9.00	25.90	17.69

However, these GV and PV estimates are influenced by the units of measurements of the various traits and even these estimates do not always give a correct picture. But, the estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) will indicate the extent of variability existing for various traits irrespective of their units of measurements. High estimates of CV were reported for traits such as fruit length/diameter ratio, average fruit weight (g), yield per plant (g). Such observations are accordance with the findings of Yogesh *et al.*, (2009) for fruit length and fruit length/diameter ratio. Bisht *et al.*, (2010) reported the same finding for average fruit weight and yield per plant in cucumber. It is interesting to note that, the difference between PCV and GCV is very less for all the characters under study. This low difference reflects about the variability existing in these germplasm is due to genetic architecture of cucumber germplasms. Therefore selection on the basis of phenotypic traits will be more effective to identify superior lines of cucumber.

Heritability estimate is an informative parameter to the breeder for selecting the desired genotypes for further use (Table 3). The estimates of heritability were found high (>90%) for the traits fruit length, average fruit weight and for vine length while node number for first female flower (86.66%), days taken for first female flower to anthesis (88.82%) were close to 90 per cent. Fruit diameter (45.26%) and days taken for first fruit harvest (78.84%) recorded least heritability. Selection can be exercised on the basis of phenotypic performance for highly heritable characters. Heritable variation can be found out with greater degree of accuracy when heritability is studied in conjunction with genetic advance. The genetic gain measured in terms of GA as % of mean, was found high (>50%) for fruit length (61.23), fruit length/diameter (64.75)

and average fruit weight (107.14). Heritability of yield and quality characters enables the plant breeder to decide the extent of selection pressure to be applied under a particular environment, which separates out the environmental influence from the total variability. However, its use would be limited as this could be changed with different set of environments as well as breeding material. The estimation of heritability has a greater role to play in determining the effectiveness of selection for a character provided it is considered in conjunction with the predicted genetic advance as suggested by Johnson *et al.*, (1955) as the heritability is influenced by biometrical method, generation of hybrid, sample size of experimental material and environment.

The estimate of heritability in both the environments were found more than 90% for days taken for first fruit harvest, fruit length, average fruit weight, yield per plant and vine length. Whereas, node number for first female flower, days taken for first female flower to anthesis, number of fruits per plant and fruit length/diameter ratio recorded moderate heritability (80-90%). It was found that low heritability for fruit diameter in the both the environments. High heritability estimates for number of fruits/plant was also reported by Munshi *et al.*, 2006; Bisht *et al.*, 2010. Yogesh *et al.*, 2009; Arunkumar *et al.*, 2011 reported high heritability for fruit length but found moderate heritability for node number for first female flower. Ranjan *et al.*, (2015) also found high heritability estimates coupled with high genetic gain for node number bearing first female flower whereas high heritability along with moderate genetic gain were observed for fruit length. Result observed by following observations showed that traits are under non-additive gene effect and selection for such traits will be of less important because these traits are under influence of environment. Similar findings

were reported by Yogesh *et al.*, (2009); Bisht *et al.*, (2010) and Kumar *et al.*, (2013).

References

- Ahmed, N.C.B., and I.M.W. Khaliq., 2007, The inheritance of yield and yield components of five wheat hybrid populations under drought conditions. *Indonesian Journal of Agricultural Science*, 8(2): 53-59.
- Al-Jibouri, H.A., Miller, P.A. and Robinson, H.F., 1958, Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin. *Agron. J.*, 50: 633-36.
- Arunkumar, K. H., M. G. Patil, C. N. Hanchinamani, I. S. Goud and S. V. Hiremath., 2011, Genetic relationship of growth and development traits with fruit yield in F2 population of BGD L x Hot season of cucumber (*Cucumis sativus* L.). *Kar. J. Agri. Sci.*, 24(4): 497-500.
- Cochran, W.G. and Cox, G.M., 1957, *Experimental Designs*, John Wiley and Sons, Inc. New York, 611 p.
- FAO, Statistical Database (2016) <http://www.fao.org/faostat/en/#data/QC>. Accessed 12 Dec 2017.
- Gatti, I., F.L. Anido, C. Vanina, P. Asprelli. and E. Country., 2005, Heritability and expected selection response for yield traits in blanched asparagus. *Genetics and Molecular Research*, 4(1):67-73.
- Hanchinamani, C. N., Patil, M. G., Dharmatti, P. R. and Mokashi, A. N., 2011, Studies on heritability and genetic advance in cucumber (*Cucumis sativus* L.). *Crop Res.*, 41(1, 2 &3): 160-163.
- Innarka, P., Khanobdeeb, C., Samipaka, S. and Jantasuriyarata, C., 2013, Evaluation of genetic diversity in cucumber (*Cucumis sativus* L.) germplasm using agro-economic traits and microsatellite markers. *Scientia Horticulturae.*, 162: 278–284.
- Jat, G. S., Munshi, A. D., Behera, T. K. and Tomar, B. S., 2016, Combining ability estimation of gynocious and monoecious hybrids for yield and earliness in cucumber (*Cucumis sativus* L.). *Indian Journal of Agricultural Sciences.*, 86 (3):399–403.
- Johnson, H. W., Robinson, H. F. and Comstock, R. E., 1955, Estimates of genetic and environmental variability in soybean. *Agronomy J.*, 47: 314-318.
- Kumar, A., Kumar, S. and Pal, A. K., 2008, Genetic variability and characters association for fruit yield and yield traits in cucumber. *Indian Journal of Horticulture.*, 65(4): 423–8.
- Kumar, S., Kumar, D., Kumar, R., Thakur, K. S., Dogra, B. S., 2013, Estimation of genetic variability and divergence for fruit yield and quality traits in cucumber (*Cucumis sativus* L.) in North- Western Himalays. *Universal Journal of Plant Science.*, 1(2):27–36.
- Munshi, A. D., Panda, B., Behera, T. K., Kumar, R., Bisht, I. S. and Behera, T. K., 2006, Genetic variability in *Cucumis sativus* var. *hardwickii* R. germplasm. *Cucurbit Genetics Cooperative Report.*, 30: 5-10.
- Pandey, S., Ansari, W. A., Mishra, V. K., Singh, A. K., Singh, M., 2013, Genetic diversity in Indian cucumber based on microsatellite and morphological markers. *Biochem Syst Ecol.*, 51:19–27.
- Ranjan, P., Gangopadhyay, K. K., Bag, M. K., Roy, A., Srivastava, R., Bhardwaj, R. and Dutta, M. 2015. Evaluation of cucumber (*Cucumis sativus* L.) germplasm for agronomic traits and disease resistance and estimation of genetic variability. *Indian J. Agril. Sci.* 85(2): 234-239.
- Ranjan, P., Gangopadhyay, K. K., Bag, M. K., Roy, A., Srivastava, R., Bhardwaj, R.

- and Dutta, M., 2015, Evaluation of cucumber (*Cucumis sativus* L.) germplasm for agronomic traits and disease resistance and estimation of genetic variability. *Indian J. Agril. Sci.*, 85(2): 234-239.
- Ren, Y., Zhang, Z., Liu, J., Staub, J. E., Han, Y., 2009, An integrated genetic and cytogenetic map of the cucumber genome. *PLoS One*, 4 e5795
- SAS Institute. 2007, SAS/STAT user guide: Statistics, version 9.2 SAS Inst., Cary, NC.
- Sebastian, P., Schaefer, H., Telford, I. R. H. and Renner, S. S., 2010, Cucumber (*Cucumis sativus*) and melon (*Cucumis melo*) have numerous wild relatives in Asia and Australia, and the sister species of melon is from Australia. *Proc. Natl. Acad. Sci., U S A* 107, 14269–14273.
- Shah, K. N., Rana, D. K. and Singh, V., 2016, Evaluation of different cucumber strain for various horticultural traits under valley condition of Garhwal Himalaya. *J Plant Dev Sci.*, 8(12):599-603.
- Ullah, M. Z., Hasan, M. J., Chowdhury, A. Z. K. M. A., Saki, A. I. and Rahman, A. H. M. A., 2012, Genetic variability and correlation in exotic cucumber (*Cucumis sativus* L.) varieties. *Bangladesh J. Pl. Breed. Genet.*, 25(1): 17-23.
- Veena, R., Sidhu, A. S., Pitchaimuthu, M. and Souravi, K., 2012, Genetic evaluation of Cucumber (*Cucumis sativus* L.) genotypes for some yield and related traits. *Elec J Pl Bre* 3(3): 945-948.
- Yogesh, C., Yadav, S. K., Brijpal, B. and Dixit, S. K., 2009, Genetic variability, heritability and genetic advance for some traits in cucumber. *Indian Journal of Horticulture.*, 66(4): 488–491.

How to cite this article:

Rahul Kumar, A.D. Munshi, T.K. Behera, A. Talukdar, H. Choudhary and Dash, P. 2018. Assessment of Genetic Variability among 78 Cucumber (*Cucumis sativus* L.) Germplams. *Int.J.Curr.Microbiol.App.Sci.* 7(05): 117-126. doi: <https://doi.org/10.20546/ijcmas.2018.705.015>