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Gene action of yield and quality traits in bottle gourd [*Lagenaria Siceraria* (Mol.) Standl.]

Aastik Jha[1]*, B. Singh[2], S.P. Mishra, Waquar Akhter Ansari[2], P.K. Dwivedi and Moakala Changkiri[1]

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Abstract

In present study, diallel cross analysis was carried out for development of hybrid in bottle gourd [*Lagenaria siceraria* (Mol.) Standl]. The gene effects with respect to its nature and magnitude for yield and quality attributes (10 characters) were studied by involving 66 hybrids obtained by crossing 12 × 12 half diallel pattern during Kharif 2013 and Zaid 2014. Additive as well as dominant component of variance were significant of most of the characters. The estimates of dominance component ($1 and $2) were higher than those of additive () component for all the characters and suggesting major role of dominance component in controlling the expression of character. Average degree of dominance showed over dominance for all characters in both the seasons. The ratio of dominance and recessive alleles suggested that the dominant alleles were distributed frequently than the recessive for all the characters.

Keywords: Gene action, diallel cross, *Lagenaria siceraria,* hybrids

Introduction

Bottle gourd [*Lagenaria siceraria* (Mol.) Standl.] is an important vegetable crop in India. It thrives well in hot humid weather condition but it can be grown in diverse low temperature condition also Maurya et al. 1993, Singh et al. 1996). In India wide range of genetic variability available in this crop but unfortunately very little attention has been paid for its genetic improvement and commercial cultivation. There is thus good scope for improvement in yield and other character of bottle gourd through breeding. Bottle gourd, a cross pollinated crop, exhibit high heterosis in its crosses (Maurya et al. 1993, Singh et al. 1996, Maurya et al. 2003 and Jha et al. 2016). To estimate the average gene action one may construct models involving different types of gene interaction and choose the model which best fits the experimental data. In thus reducing the total gene action entering into the expression of a complex characteristic to that of a simple model, it cannot be assumed that all genes behave in the manner prescribed by the chosen model. In fact, it has been suggested that quantitative genes probably have as diverse types of action as the so called qualitative ones and differ from qualitative genes only in magnitude of effect reported by Dubey and Maurya (2003). However, it has been shown in various quantitative traits that the system of genes involved does have average properties which are measurable. Estimation of these group genetic parameters is the objective of a statistical analysis, and these estimated parameters are associated with a gene model also supported by Askel and Johnson (1963). The principal approach that has developed over the years involves, a description of frequency distributions resulting from segregating populations by use and a partitioning of variances into components Considering the importance of such information, an experiment was conducted to understand the gene effects governing various yield and related traits in bottle gourd. Among the biometrical techniques, diallel analysis has been used extensively for deciphering nature of gene action and selection of large number of parents for hybridization. It seems that information on genetic architecture of parents, their combining ability, transmissibility of characters and expected genetic advance will be of immense value to ascertain the selection of desirable parents in the choice of suitable breeding methodology for the improvement of bottle gourd. Therefore, the present study was undertaken to elucidate the nature and magnitude of gene action involved in inheritance of fruit yield and its component in bottle gourd.

Mahatama Gandhi Chitrakoot Gramoday Vishwavidyalaya, Chitrakoot, Satna, M.P.
[1] Department of Horticulture, School of Agricultural Sciences & Rural Development, Medziphema Campus, Nagaland University, Nagaland
[2] ICAR-Indian Institute of Vegetable Research, Varanasi, UP
*Corresponding author, Email: aastikiivr@gmail.com

Materials and Methods

The experiment was conducted at experimental farm of the ICAR-Indian Institute of Vegetable Research, Varanasi (U.P.) which is geographically located between 25.15 ^{0}N latitude 60.03 ^{0}E latitude. The experimental materials for the present study comprised of twelve diverse inbred differing in horticultural and fruit characters was selected as parents from the genetic stocks maintained at ICAR-Indian Institute of Vegetable Research, Varanasi (U.P.). These inbred *viz*, ABG-1 (P-1), Rajendra Chamatakar (P-2), VRBG-7 (P-3), VRBG-136 (P-4), Narendra Rashmi (P-5), NDBG-619 (P-6), Narendra Dharidar (P-7), Kalyanpur Long Green (P-8), Kashi Ganga (P-9), NDBG-132 (P-10), Pant Lauki-1 (P-11) and VRBG-6 (P-12) were crossed in diallel excluding reciprocals mating design to obtain the crosses during July-September 2013 (E1) and February-May 2014 (E2), the derived 66 F_1's were evaluated in randomized complete block design (RCBD) in three replications. 10 plants were maintained keeping row-to-row and plant-to-plant spacing 4 m and 70 cm, respectively. Observations were recorded from seven random but competitive plants of parent and their F_1 hybrid in each treatment and replication for days to first female flowering, node at which first female flower appears, number of fruits per plant, average fruit weight (g), fruit length (cm), fruit breadth (cm), days of edible maturity, yield per plant (kg), protein (mg/g) and carbohydrate (g/100g). Total protein was estimated as per Lowry method (Lowry et al. 1951) and Total carbohydrate was determined by Anthrone method (Hedge and Hofreiter 1962). The genetic components of variation were calculated according to Griffing's numerical approach and graphical analysis (Wr-Vr graph) given by Jinks and Hayman (1953), Hayman (1954) and Askel and Johnson (1963).

Results and Discussion

The diallel cross analysis was carried out for 10 characters, using analytical method in terms of genetic parameters. The estimates of genetic parameters,, $--1 $2, , %2 and Ê along with their respective standard errors are presented in Table 1. The genetic parameters were used for the estimation of average degree of dominance ($1/) 0.5, proportion of genes with positive and negative effects in the parents ($2/4$1), the proportion of dominant and recessive genes (KD/KR) in the parents [(4$1)0.5+F/(4$1)0.5] and number of group of genes which control the character and exhibit dominance (h2/$2]. The coefficient of correlation (r) between the parental order of dominance (Wr+Vr) and the parental measurement (Yr) were calculated to know the order of dominance, character wise results on genetic parameter are presented in Table 1. For days to first female flowering the t^2 value was non-significant in the population in E1 and significant in E2. Which leading to confirmation of validity of hypothesis for diallel cross analysis in E1 only. The significant values of $1 and $2 in both season (E1 and E2) and were higher and in E1 suggested the major role of dominance components in the expression of this character (table 1). The, %2 and Ê were found non-significant in both seasons (E1 and E2). The average degree of dominance was more than one in both seasons showed over dominance. The values of $2/4$1 in the parents were 0.21 and 0.22 in both seasons (E1 and E2), respectively and indicating the asymmetrical distribution of genes among the parents. The proportion of dominance and recessive alleles among the parents was more than one showed the excess of dominant genes. The number of gene groups (%2/$2) found to 0.08 and 0.03 in E1 and E2, respectively. Positive value of correlation coefficient suggested the excess of receive genes in the population in both the seasons (E1 and E2). Sit and Sirohi (2008) found that the gene distribution among the parents was asymmetry as the proportion of dominant and recessive genes exceeds one for all studied traits except vine length. In all the traits except fruit length, the dominance component of genetic variation (H1) was higher than additive component (D). Heritability in narrow sense (h2) was found highest for fruit length (72%). All the remaining traits had narrow sense heritability less than 50 % which is sign of preponderance of non-additive gene action for most of the traits under study as similar reported by Quamruzzaman and Ahmad (2010). Results pertaining to node at which first female flower appears the t^2 value was non-significant in the population in both seasons indicating the validity of hypothesis for diallel cross analysis. The estimates of $1 and $2 were significant in both season (E1 and E2). The estimate of additive component was non-significant in both seasons (E1 and E2) and smaller than $1 and $2 component. Suggesting the major role of both additive and dominance components in the expression of this character. The estimates of component was positive and non significant in both the seasons indicating excess of recessive genes. The %2 and Ê component were found positive and non significant in both seasons ((E1 and E2). The average degree of dominance (H1/D) 0.05 was more than one in both seasons, which showed over dominance. The ratio of $2/4$1 indicated asymmetrical distribution of genes among the parents. The proportion of dominance and recessive alleles among the parents was more than unity showed the excess of dominant genes. The number of gene groups (%2/$2) indicated one gene group controlling the character and exhibiting dominance. The coefficient of correlation (r) between parental order of dominance (Wr + Vr) and parental measurement (Yr) was negative and non-significant in both the seasons, which showed excess of dominant genes. For days to first harvesting the t^2 value was non-significant in both the seasons indicating the validity of hypothesis for diallel cross analysis. The estimates of \$1 and \$2 were significant in both seasons (E1 and E2). The estimate of additive component () was significant and smaller than (H1 and H2) and suggesting the major role of the dominance component in controlling the expression of this character. The estimate of component was positive and significant in both the seasons. The %2 and Ê component was positive and significant. The estimate of degree of dominance showed over dominance in both the seasons (E1 and E2). The estimate ratio of \$2/4\$1 indicated asymmetrical distribution of genes among the parents. The proportion of KD/KR was more than unity indicating excess of dominant genes in both seasons. The ratio of %2/\$2 indicating that one gene group is controlling the character and exhibiting dominance. The coefficient of correlation (r) between the parental of dominance (Wr + Vr) and parental measurement (Yr) was positive and non-significant in both seasons. The positive values of correlation coefficient indicated preponderance of recessive gene, also reported earlier Kushwaha and Ram (1997). The genetic component variation for number of fruits per plant *viz.* t^2 value was significant for this character in both seasons (E1 and E2). The estimates of , \$1 and \$2 were highly significant for this trait in both the seasons which indicates the

Table 1: Genetic parameters, , \$$_1$, \$$_2$,%^{2} and Ê and their related statistics in diallel for eighteen characters over two varied season

Genetic Parameters & Related Statistics	Season	Days to first female flowering	Node at which first female flower appears	Number of fruits per plant	Average fruit weight (g)	Fruit length (cm)	Fruit breadth (cm)	Days of edible maturity	Yield per plant (kg)	Protein (mg/g)	Carbohydrate (g/100g)
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
$\hat{D}$	E1	8.297**	6.402	0.262*	5784.385	2.939	0.041	4.338**	0.441	5.746*	0.140**
		±2.002	±3.455	±0.093	±2852.966	±2.366	±0.029	±0.841	±0.203	±1.918	±0.043
	E2	3.49	4.62	0.191	4234.05**	3.580	0.150	4.129**	0.192	5.782*	0.134*
		±1.58	±2.36	±0.237	±819.65	±2.680	±0.073	±1.067	±0.229	±1.906	±0.043
$\hat{F}$	E1	9.055	12.800	0.213	10152.360	-0.269	0.007	8.378**	0.763	6.648	0.248*
		±4.536	±7.830	±0.210	±6466.078	±5.363	±0.067	±1.907	±0.460	±4.347	±0.097
	E2	4.12	7.50	0.175	6142.96**	4.137	0.361	8.248**	0.237	5.920	0.255*
		±3.58	±5.35	±0.537	±1857.69	±6.074	±0.165	±2.419	±0.520	±4.320	±0.098
?$_1$	E1	29.226**	31.872**	1.079**	21583.830**	22.922**	0.203**	11.268**	1.755	19.769**	0.607**
		±4.004	±6.911	±0.186	±5707.456	±4.734	±0.059	±1.683	±0.406	±3.837	±0.085
	E2	19.68**	16.20**	1.819**	11536.63**	27.090**	0.878**	13.338**	1.852**	20.754**	0.549**
		±3.16	±4.72	±0.474	±1639.74	±5.361	±0.146	±2.135	±0.459	±3.813	±0.086
?$_2$	E1	23.384**	23.100**	0.935**	16447.670**	20.056**	0.192**	6.961**	1.289**	17.236**	0.479**
		±3.331	±5.749	±0.154	±4747.623	±3.938	±0.049	±1.400	±0.337	±3.192	±0.071
	E2	16.05**	11.66**	1.620**	8353.27**	23.340**	0.585**	9.029**	1.533**	18.612**	0.411**
		±2.63	±3.93	±0.395	±1363.98	±4.460	±0.121	±1.776	±0.382	±3.172	±0.072
?^{2}	E1	1.838	0.860	0.073	-301.706	2.008	0.002	0.054	0.006	3.573	0.005
		±2.227	±3.844	±0.103	±3174.303	±2.633	±0.033	±0.936	±0.226	±2.134	±0.048
	E2	0.41	0.19	0.390	-42.53	3.572	-0.011	0.303	0.382	4.371	0.004
		±1.76	±2.63	±0.264	±911.97	±2.982	±0.081	±1.187	±0.255	±2.121	±0.048
Ê	E1	0.682	1.082	0.025	1223.214	0.849	0.031**	0.043	0.092	0.022	0.004
		±0.555	±0.958	±0.026	±791.270	±0.656	±0.008	±0.233	±0.056	±0.532	±0.012
	E2	0.38	0.30	0.037	183.62	0.293	0.037	0.036	0.042	0.016	0.000
		±0.44	±0.65	±0.066	±227.33	±0.743	±0.020	±0.296	±0.064	±0.529	±0.012
H$_1$/D$^{0.05}$=F$_1$	E1	1.88	2.23	2.03	1.93	2.79	2.23	1.61	2.00	1.86	2.08
	E2	2.37	1.87	3.09	1.65	2.75	2.42	1.80	3.10	1.90	2.02
?$_{2}$/4?$_1$	E1	0.20	0.18	0.22	0.19	0.22	0.24	0.15	0.18	0.22	0.20
	E2	0.20	0.18	0.22	0.18	0.22	0.17	0.17	0.21	0.22	0.19
KD/KR	E1	1.82	2.62	1.50	2.67	0.97	1.09	3.99	2.53	1.91	2.48
	E2	1.66	2.53	1.35	2.57	1.53	2.97	3.50	1.50	1.74	2.77
h 2/H2	E1	0.08	0.04	0.08	-0.02	0.10	0.01	0.01	0.01	0.21	0.01
	E2	0.03	0.02	0.24	-0.01	0.15	-0.02	0.03	0.25	0.24	0.01
R	E1	0.188	-0.135	0.223	0.082	0.366	0.428	0.107	-0.155	-0.012	-0.020
	E2	0.102	-0.536	0.061	0.007	0.308	0.101	-0.464	-0.111	-0.11	-0.285
t^2	E1	0.00	0.46	9.20**	5.60**	10.22	5.21**	0.72	0.216	6.013**	1.747
	E2	6.51**	0.52	11.62**	1.80	5.54**	0.03	0.72	15.736**	3.135*	6.745**

*,**, Significant at 5 and 1 percent level of probability, respectively; E1= Rainy, E2= Summer

presence of both additive as well as dominance gene effects. The estimate of component was positive value in both seasons suggesting frequency of dominant alleles in the parents. The estimate of %2 and Ê were positive and non-significant in both seasons ((E1 and E2). The estimate of degree of dominance in both the seasons, suggested over dominance for this trait. The estimate of ratio $2/4$1 indicated symmetrical distribution of positive and negative genes among the parent. The proportion of KD/KR was more than unity indicating excess of dominant genes in both the seasons. The ratio of %2/$2 was found 0.08 and 0.24 in both seasons (E1 and E2), respectively. The coefficient of correlation (r) between the parental order of dominance (Wr + Vr) and parental measurement (Yr) was non-significant and positive in both seasons (E1 and E2). For average fruit weight the value of t^2 for this character was found non-significant in E1 and significant in E2, which leading to confirmation of validity of hypothesis for diallel cross analysis in E1 only. The estimates of $1 and $2 (dominance component) were higher and significant than those of the estimates of additive components () suggesting the major role of the additive and dominance component in the expression of this character in both the seasons (E1 and E2). The estimate of component was positive in both the seasons, indicating that dominant alleles were more frequent than recessive. The %2 and Ê component was positive and non-significant in both the seasons (E1 and E2). The estimate of degree of dominance, suggested over dominance in E1 and E2. The estimate of ratio $2/4$1 indicated asymmetrical distribution of positive and negative genes among the parent. The proportion of KD/KR was more than unity indicating excess of dominant genes in both seasons. The ratio of %2/$2 indicated that one gene group controlling the character and exhibiting dominance in E1 and E2. The coefficient of correlation (r) between the parental order of dominance (Wr + Vr) and parental measurement (Yr) was positive and non-significant in E2 only. The correlation coefficient value was positive which indicated direction for recessive gene (Karthik et al. 2013). Result pertaining to fruit length the t^2 value was significant for this character in both the seasons. The estimate of $1 and $2 were significant in both seasons. The additive component () was non-significant and smaller than dominance component ($--1 and $2) suggesting the major role of dominance component in expression of this character. The estimate of was negative and non-significant in E1 and positive and non-significant in E2. The %2 and Ê component was positive and non-significant in both the seasons. The average degree of dominance was more than one in both seasons showed over dominance. The frequency of positive and negative alleles ($2/4$1) showed the less than 0.25 in both seasons suggested asymmetrical distribution of genes among the parents. The proportion of dominance and recessive alleles among the parents was more than one in E2 and less than one in E2. The number of gene groups (%2/$2) controlling the character and exhibiting dominance. The coefficient of correlation (r) between parental order of dominance (Wr + Vr) and parental measurement (Yr) was positive and non-significant in both the seasons. The proportion of genes with positive and negative effect in the parents (H2/4H1) was found to be less than 0.25 for all the traits under study indicating asymmetry distribution of dominant genes with positive and negative alleles at loci as similar reported by Dubey and Ram (2006). The estimates of genetic parameters for fruit breath the t^2 value was significant in E1 and non-significant in E2, leading the confirmation of validity of the hypothesis for diallel cross analysis in E2 only. The estimates of $1 and $2 were significant and higher than that of additive component (). The additive component () was significant, suggesting the major role of the dominance component. Positive and non-significant estimate of component indicated that dominance alleles were more frequent than recessive. The component of %2 was found positive and non-significant in both season (E1 and E2). The estimate of Ê component was positive and significant in E1, while non-significant in E2. The average degree of dominance was more than unity suggested over dominance for this character in E1 and E2. The ratio of $2/4$1 indicated asymmetrical distribution of positive and negative alleles. The proportion of dominance and recessive alleles among the parents was more than one in both seasons (E1 and E2) showed the excess of dominant genes. The number of group of genes that control the character (%2/$2) and exhibited dominance was 0.01 in E1 only. The coefficient of correlation (r) between parental order of dominance (Wr + Vr) and parental measurement (Yr) was negative and non-significant. For yield per plant the t2 value is non-significant in E1 and highly significant in E2, leading the confirmation of validity of the hypothesis for diallel cross analysis in E1 only. The estimates of $1 component were non-significant in E1 and significant in E2. The $2 component was significant in both the seasons (E1 and E2). The additive component () was non-significant and smaller than dominance component ($1 and $-2) in both the seasons (E1 and E2), suggesting the major role of the dominance component in the expression of this character. Positive and non-significant estimate of component indicated that dominance alleles were more frequent than recessive. The component of %2 and Ê component were found positive and non-significant in both season (E1 and E2).The average degree of dominance was more than unity suggested over dominance for this character in both the seasons (E1 and E2). The ratio of $2/4$1 indicated asymmetrical distribution of positive and negative alleles in both seasons. The proportion of dominance and recessive alleles among the parents express more than one in both seasons (E1 and E2) showed the excess of dominant genes. The ratio of %2/$2 indicated that only one gene controlling the character. The coefficient of correlation (r) between parental order of dominance (Wr + Vr) and parental measurement (Yr) was negative and non-significant in both the seasons (E1 and E2). The estimates of genetic parameters for fruit breath the protein The t^2 value was significant for this character in both the seasons (E1 and E2). The estimates of $1 and $-2 were significant in both seasons. The estimates of additive component () was significant and lower than the dominance component ($1 and $2) in both the seasons, suggesting the major role of dominance component in controlling the expression of this charcter. The estimate of component was positive and non-significant in E1 and E2. The %2 and Ê component was positive and non-significant in both the seasons. The estimate of degree of dominance, suggested over dominance. The estimate of ratio $2/4$1 indicated asymmetrical distribution of positive and negative genes among the parent in the E1 and E2. The proportion of KD/KR was more than unity indicating excess of dominant genes. The ratio of %2/$2 indicates that one gene group controlling the charcter in both the seasons (E1 and E2). The coefficient of correlation (r) between the parental order of dominance (Wr + Vr) and parental measurement (Yr) was negative and non-significant in E1 and E2. The higher proportions of dominant genes observed in most of the traits are in agreement with the findings of Pandey et al. (2004) and Dey et al. (2012). For carbohydrate the t^2 value was found non-significant in both the seasons, leading the confirmation of validity of the hypothesis for diallel cross analysis. The estimates of $1, $-2, and were significant in both seasons (E1 and E2), indicated the presence of dominance gene effects for this trait. The %2 and Ê component were found positive and non-significant in both the seasons. The estimate of degree of dominance, suggested over dominance. The estimate of ratio $2/4$1 indicated asymmetrical distribution of positive and negative genes among the parent in the E1 and E2. The proportion of KD/KR was more than unity indicating excess of dominant genes in both the seasons. The ratio of %2/$2 indicates that one gene group controlling the charcter in both the seasons (E1 and E2). The coefficient of correlation (r) between the parental order of dominance (Wr + Vr) and parental measurement (Yr) was negative and non-significant in E1 and E2. The result of present investigation revealed over dominance and dominance gene action for the entire yield and yield related traits. The predominance of non-additive gene action and low narrow sense heritability for most of the important yield and qualitative characters which suggested the heterosis breeding would be advantageous to get higher gain in bottle gourd.

सारांश

लौकी में संकर के विकास के लिए डाइएलिल क्रॉस का विश्लेषण वर्तमान अध्ययन में किया गया। बारह विभिन्न संकरों से हाफ डाइएलिल पद्धति द्वारा प्राप्त 66 संकरों में उपज एवं उसके गुणवत्ता घटकों के 10 गुणों की प्रकृति एवं परिणाम के संबंध में जीन प्रभाव का अध्ययन खरीफ 2013 एवं जायद 2014 में किया गया। संयोगी घटक के साथ–साथ प्रभावी घटक विविधता भी सभी गुणों में प्रभावशाली मिले। इन सभी लक्षणों प्रभाविता घटक (एच–1 व एच–2) योज्य घटक (डी) के सापेक्ष सभी गुणों हेतु ज्यादा था जो यौगिक घटक की भूमिका का सलाह देता है। औसत प्रभाविता दोनों ऋतुओं में सभी लक्षणों के लिए प्रभुत्व से अधिक दिखाई दिया। प्रभावी एवं अप्रभावी युग्मविकल्पों का अनुपात से प्रदर्शित होता है कि प्रभावी युग्मविकल्पी अप्रभावी युग्मविकल्पी की अपेक्षा सभी लक्षणों में बहुधा वितरित होता है।

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