



Research Article

GENE ACTION STUDIES FOR BIOCHEMICAL TRAITS IN PUMPKIN (*Cucurbita moschata* Duch. Ex. Poir)

KUMAR VIMLESH¹, MISHRA D.P.*¹, YADAV G.C.¹ AND BABU UMESH²

¹Department of Vegetable Science, Narendra Dev University of Agriculture and Technology, Kumarganj, Faizabad, 224229, Uttar Pradesh

²ICAR-Krishi Vigyan Kendra, Sant Kabir Nagar, Narendra Dev University of Agriculture and Technology, Kumarganj, Faizabad, 224229, Uttar Pradesh

*Corresponding Author: Email-vimileshkumaryadav@gmail.com

Received: April 03, 2018; Revised: April 06, 2018; Accepted: April 07, 2018; Published: April 15, 2018

Abstract- The present experiment was conducted with aim to know the nature of inheritance of biochemical traits viz., ascorbic acid (mg/100g), reducing sugars (%) non-reducing sugars (%), total sugars (%), dry matter content, total soluble solids, β -carotene (mg/100g). The fifteen F_1 hybrids developed through the diallel mating excluding reciprocals with the using of six parents. Highly significant values of additive $\hat{D}$ and dominance ($\hat{H}_1$ and $\hat{H}_2$) effects of components were observed for most of the traits studied in all three seasons (E_1 , E_2 , E_3) except the values of $\hat{D}$ for total sugars, reducing sugars and ascorbic acid in all three seasons. Average degree of dominance revealed the presence of over dominance for all traits in all three seasons (E_1 , E_2 , E_3). The proportions of genes ($\hat{H}_2 / 4 \hat{H}_1$) in the parents were less than 0.25 for all the traits indicating asymmetrical distribution of alleles at loci showing dominance in all three seasons (E_1 , E_2 , E_3). In general, the proportions of dominant and recessive genes in parents $[(4 \hat{D}, \hat{H}_1)^{1/2} + \hat{F} / (4 \hat{D}, \hat{H}_1)^{1/2} - \hat{F}]$ were more than unity with positive $\hat{F}$ value for all the traits in all three seasons indicating major contribution of dominant genes. The ratio of ($\hat{h}^2 / \hat{H}_2$) which estimates the number of gene groups revealed that atleast one gene group was involved in the inheritance for total soluble solids during all three seasons. While, for dry matter content, total sugars and reducing sugars exhibited similar number of gene group only during E_2 and rest of traits showed involment of less than one gene group.

Key words- Quality Traits, Pumpkin, β -Carotene.

Citation: Kumar Vimlesh., et al., (2018) Gene Action Studies for Biochemical Traits in Pumpkin (*Cucurbita moschata* Duch. ex. Poir). International Journal of Agriculture Sciences, ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 10, Issue 7, pp.-5687-5689.

Copyright: Copyright©2018 Kumar Vimlesh., et al., This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited.

Introduction

The three economically important species, *C. pepo*, *C. moschata*, and *C. maxima* are showed variation for fruit characteristics, during spiring season although much research into their inheritance although most of such studies have been done in *C. pepo* and *C. maxima*. The gene list of *Cucurbita* sp. includes 79 loci for phenotypic /morphological traits and 48 polymorphic allozyme loci along with linkage and gene mapping [1]. In case of *C. moschata* information regarding inheritance of characters documented in the gene list is almost lacking and among the few that have been reported so far are Trifluralin (a herbicide) tolerance controlled by a dominant gene "T" [2], naked kernel (absence of tough seed coat) trait controlled by a pair of recessive genes [3] and mottled light and dark green fruit colour, monogenic dominant ("Mldg") over dark green fruit [19]. A wide range of expression of the trait "silver leaf mottling" was observed in *C. moschata* although all the reports indicated that this trait showed dominance over non-mottled leaf. Latha and Gopalakrishnan,[4]and a single gene "M" [5]. Information on polygenic inheritance of quantitative characters in pumpkin is also meager. for number of seeds/fruit, 100-seed weight and seed size index [6]; over-dominance [7] and dominance [8]. Over-dominance gene action for all the nutritional traits, namely, total soluble solids, carotenoids, ascorbic acid, calcium, and iron content [9] clearly suggested the importance of exploiting heterosis commercially. The color of pumpkin is due to the orange pigments. The main nutrients are lutein and both α and β -carotene, the latter of which generates vitamin A in the body. Pumpkins are very versatile in their uses for cooking. Most parts of the pumpkin are edible, including the fleshy shell, seeds, leaves, and even flowers. In the United States and Canada, pumpkin is a popular Halloween and

Thanks, giving staple. Pumpkin purée is sometimes prepared and frozen for later use. Pumpkin is relatively high in energy and carbohydrates and a good source of vitamins, especially high caretenoid pigments and minerals. It may certainly contribute to improve nutritional status of the people, particularly the vulnerable groups in respect of vitamin A requirement. Night-blindness is a serious problem of South Asian countries. Encouraging the mass people to take more pumpkin can easily be solved the problem.

Materials and Methods

The experimental materials for the present study comprised of six promising and diverse inbreds and varieties of pumpkin selected on the basis of genetic variability from the germplasm stock maintained in the Department of Vegetable Science, N.D. University of Agriculture & Technology, Kumarganj, Faizabad (U.P.) India. The selected parental lines i.e. Narendra Upkar (P_1), NDPK-120 (P_2), Narendra Agrim (P_3), NDPK-39-2 (P_4), Kashi Harit (P_5) and NDPK-11-3 (P_6) were raised and crossed in the all possible combinations, excluding reciprocals, during Zaid, 2015 to get 15 F_1 hybrid seeds for the study of character association for fourteen quantitative traits. The experiments were conducted in Randomized Block Design (RBD) with three replications to assess the performance of 15 F_1 hybrids and 6 parents. The treatments were planted in rows spaced at 3.0 meters apart with a plant to plant spacing of 0.5 meter. The seeds were sown on 23th July, 2015 and 7th November 2015, 26th March, 2016 for Kharif, Rabi and Zaid crops, respectively. All the recommended agronomic package of practices and plant protection measures were followed to raise good crop.

Biochemical/quality traits analysis

The Ascorbic acid content in fruit was estimated at marketable green fruit stage by '2, 6- dichlorophenol-indophenol Visual Titration Method' as described by [10]. Reducing sugars were estimated by Fehling 'A' and 'B' solution method given by Ranganna [18]. Non-reducing sugars was calculated by deducting the quantity of reducing sugars from total invert sugars and multiplied by factor 0.95. The results were expressed as per cent non-reducing sugars.

Total sugars (%)

Total sugars were calculated by adding the quantity of reducing and non-reducing sugars. The results were expressed as total sugars in per cent.

$$\text{Total sugars (\%)} = \text{Reducing sugars (\%)} + \text{Non-reducing sugars (\%)}$$

Dry matter content in fruit

The dry matter content in fruit was determined on the fresh weight basis. A quantity of 100 g of fresh fruit was taken, cut into small pieces in oven at $60 \pm 2^\circ\text{C}$ for 8-10 hours per day till the complete drying to have constant weight and dry matter percentage was calculated as:

$$\text{Dry matter (\%)} = \frac{\text{Dry matter of fruit (g)}}{\text{Fresh weight of fruit (g)}} \times 100$$

Total soluble solids (TSS) (°B)

Total soluble solids of the juice of fresh fruit of each lines and F_1 's was determined with the help of hand refractometer (Erma, Japan) of 0-32 per cent range. The values were collected at 20°C and expressed as per cent TSS of fresh fruit juice.

β -Carotene (mg/100g)

The β - carotene content was determined in mature fruit sample using the method developed [11]. The genetic components of variation were calculated for the analysis of numerical approach followed the method given [12-14].

Results and Discussion

The estimates of components of variation provide detailed information of additive and dominant components and allied statistics. The genetic progress in a population largely depends upon the relative values of these components. The diallel cross analysis through analytical method is based on a number of assumptions regarding applicability of this method as advocated by [13] viz., homozygous parents, diploid segregation, no reciprocal differences, no multiple allelism, no epistasis and absence of linkage, absence of epistatic and random mating. The validity of specific assumptions of diploid segregation, lack of reciprocal differences and multiple allelism were presumed. Pumpkin being cross pollinated crop it is tedious to get complete homozygous parents for all the characters. However, if some traits exhibit the partial non-fulfillment of assumption, the estimates of population parameters are still possible [13]. However, the results in such cases are less reliable than would have been if all the assumptions are completed. The estimates of the components of variation and their related statistics for different traits of pumpkin have been presented in [Table-1]. The present study revealed that the highly significant values for additive ($\hat{D}$) and dominance ($\hat{H}_1$ and $\hat{H}_2$) effects of components were observed for most of the quality traits in all three seasons (E_1 , E_2 , E_3) except the values of $\hat{D}$ for total sugars, reducing sugars and ascorbic acid in all three seasons. The significant values of $\hat{D}$, $\hat{H}_1$ and $\hat{H}_2$ indicated the importance of both additive and dominance gene action in the expression of these traits, which is in consonance with the findings of [15]. However, additive ($\hat{D}$) genetic variance components were lower in magnitude than dominant component of genetic variance for all the twenty traits over all three seasons which showed preponderance of dominance components of variance in expression of fruit yield and its attributing traits in all three seasons. Similar findings were also recorded by Sharma, *et al.* [16] in pumpkin. The positive values of $\hat{F}$ were found for all traits in all three seasons, which indicated that there was an excess of dominance gene in the inheritance of these traits among the parents. The average degree of dominance ($\hat{H}_1 / \hat{D}$)^{1/2} revealed the presence of over dominance for all characters in all three seasons (E_1 , E_2 , E_3). This suggested that heterosis breeding might be advantageous for improvement of yield and its

attributing traits in pumpkin. The results are in agreement with the finding of Jha, *et al.* [15] and Sharma, *et al.* [16]. Ratio of ($\hat{H}_2 / 4 \hat{H}_1$) which estimates frequency of alleles with positive and negative effects in the parents were less than 0.25 in all three seasons for all characters which showed asymmetrical distribution of loci showing dominance for all traits [Table-1]. The ratio of ($4 \hat{D}$, $\hat{H}_1$)^{1/2} + $\hat{F}$ / ($4 \hat{D}$, $\hat{H}_1$)^{1/2} - $\hat{F}$ indicated that the dominant alleles were more frequent than recessive alleles for all the traits studied in all the seasons [Table-1]. These findings are similar to that of Sharma, *et al.* [16]. The proportion of $\hat{H}_2 / \hat{H}_1$, which provides information about groups of gene exhibiting little or no dominance. The less than one $\hat{H}_2 / \hat{H}_1$ ratio suggested that atleast one gene group mainly governed the characters under study for most of the quality traits. The positive correlation (r) between parental order of dominance ($W_r + V_r$) and parental measurement (Y_r) were showed for most of the characters in all three seasons, except total sugars in all three seasons, ascorbic acid in E_2 and E_3 , dry matter content and reducing sugars in E_1 . The positive correlation suggesting the preponderance of recessive genes while, positive values suggested preponderance of dominant genes. The results of present investigation suggested preponderance of dominant genes in the expression of most of traits studied. Therefore, heterosis breeding approach could be advantageous to produce superior hybrids for good quality fruit in pumpkin. The above findings are in agreement with that of Singh, *et al.* [17]. Thus, the non-significant values of ' t^2 ' or (1-b/SEb) indicates the validity of assumptions pertaining to diallel analysis, while significant values of ' t^2 ' or (1-b/SEb) showed failure of hypothesis or null hypothesis for diallel cross analysis [Table-1]. The result of present study suggested preponderance of dominance genes in the expression of most of the biochemical traits studied. Therefore, heterosis breeding approach might be advantageous rather than selection to develop superior hybrids having quality fruits in pumpkin.

Applications of research

The present research results would be helpful to making of breeding strategy for improvement of quality traits of pumpkin.

Research Category: Vegetable Science

Acknowledgement / Funding: Author thankful to Narendra Dev University of Agriculture and Technology, Kumarganj, Faizabad, 224229, Uttar Pradesh.

*Research Guide or Chairperson of research: Dr. D. P. Mishra

University: Narendra Dev University of Agriculture and Technology, Kumarganj, Faizabad, 224229, Uttar Pradesh

Research project name or number: Ph.D. Thesis

Author Contributions: All author equally contributed

Author statement: All authors read, reviewed, agree and approved the final manuscript

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

References

- [1] Paris H.S. and Brown R.N. (2005) *HortScience* 40, 1620-1630.
- [2] Adeoye A.A., Coyne D.P. (1981) *Horticultura Brasileira* 13, 170-171.
- [3] Zhou S.K., Qiu Z.H., Li G.X., Li Z. and Li X.R. (1995) *Crop. Genet. Res.*, 2, 13.
- [4] Latha P. and Gopalakrishnan T.R. (1993) *Horticultural Journal* 6, 97-101
- [5] Wessel-Beaver L. and Katzir N. (2000) *Acta Horticulturae*, 510, 289-295
- [6] Doijode S.D., Sulladmath U.V., Kulkarni R.S. (1987) *Inheritance Vegetable Science* 14, 143-146.
- [7] Galka A.I. (1987) *Oveshchevodstvo I Bakhchevodstvo*, 32, 45-46.

- [8] Sirohi P.S., Kumar T.S. and Choudhury B. (1986) *Indian Journal of Agricultural Science*, 56, 171-173.
- [9] Sirohi P.S. and Yayasani S.R. (2001). *Vegetable Science*, 28, 127-129.
- [10] Ranganna S. (1979) Tata McGraw Hill Book Company, New Delhi.
- [11] Ranganna S.C. (1997) Tata Mc Graw Hill Publishing Co., Calcutta, 269-299.
- [12] Jinks J.L. and Hayman B.I. (1953) *Maize Genetics Newsletter*, 27, 48-54.
- [13] Hayman B.I. (1954) *Genetics*, 39, 789-809.
- [14] Askel R. and Johnson L.P.V. (1963) *Analysis. Advancing Frontiers Pl. Sci.*, 2, 37-54.
- [15] Jha A., Pandey S., Rai M., Yadav D.S. and Singh T.B. (2009) *Vegetable Science*, 36, 332-335.
- [16] Sharma N., Sharma N.K. and Malik Y.S. (2010) Abstract book of National Seminar on Recent Trends in Hort. Crops Issues and Strategies for Res. Development, March 22-24, CCS HAU, Hissar, p. 26.
- [17] Singh A., Singh S.P., Singh V. and Singh N.K. (2005) Genetic Abstracts of National Seminar on Cucurbits held in between 22-23 September at Govind Ballabh Pant University of Agriculture & Technology. Pantnagar pp 125.
- [18] Ranganna S.C. (1991) Tata Mc Graw Hill Publishing Co., Calcutta, 279-309.
- [19] Cardoso All, Silva N. and Della-Vecchia P.T. (1995) *Vegetable Science*, 14, 143-146.

Table-1 Estimates of components of variation and their related statistics in 6 x 6 diallel crosses of pumpkin over three seasons (E_1, E_2, E_3)

Components of variation and related statistics	Seasons	Dry matter content	Total soluble solids	Total sugars	Reducing sugars	Non-reducing sugars	Ascorbic acid	β -carotene
$\hat{D}$ (Additive effect)	E_1	1.07** ± 0.38	0.24** ± 0.05	0.16 ± 0.21	0.05 ± 0.18	0.15** ± 0.02	0.38 ± 0.29	1.21** ± 0.67
	E_2	0.42** ± 0.51	0.15** ± 0.35	0.15 ± 0.35	0.04 ± 0.11	0.14* ± 0.05	0.22 ± 0.92	1.04** ± 0.60
	E_3	1.06** ± 0.37	0.22** ± 0.10	0.16 ± 0.18	0.05 ± 0.16	0.15** ± 0.05	0.36 ± 0.47	1.23** ± 0.56
$\hat{H}_1$ (Dominance effect)	E_1	2.73** ± 0.98	1.68** ± 0.14	2.00** ± 0.55	1.28** ± 0.47	0.47** ± 0.05	6.08** ± 0.58	6.89** ± 1.71
	E_2	4.25** ± 1.31	3.63** ± 0.89	3.50** ± 0.90	1.69** ± 0.29	0.70** ± 0.13	8.67** ± 2.33	8.04** ± 2.02
	E_3	2.60** ± 0.94	1.80** ± 0.26	2.07** ± 0.46	1.24** ± 0.41	0.64** ± 0.14	5.35** ± 1.19	6.84** ± 1.43
$\hat{H}_2$ (Dominance indicating asymmetry of +/- effect of genes)	E_1	2.09** ± 0.88	1.64** ± 0.12	1.68** ± 0.49	1.16** ± 0.42	0.43** ± 0.04	4.53** ± 0.51	5.62** ± 1.58
	E_2	3.71** ± 1.17	3.33** ± 0.79	3.21** ± 0.80	1.65** ± 0.25	0.52** ± 0.11	6.95** ± 2.08	7.02** ± 1.37
	E_3	2.06** ± 0.84	1.67** ± 0.23	1.26** ± 0.41	0.98** ± 0.36	0.43** ± 0.12	4.98** ± 1.06	6.01** ± 1.27
$\hat{F}$ (Mean Fr over arrays)	E_1	1.40 ± 0.94	0.12 ± 0.13	0.24 ± 0.53	0.02 ± 0.45	0.06 ± 0.05	1.37 ± 0.55	1.38 ± 1.64
	E_2	0.70 ± 1.26	0.31 ± 0.85	0.32 ± 0.86	0.04 ± 0.27	0.28 ± 0.12	1.15 ± 2.24	1.52 ± 1.48
	E_3	1.06 ± 0.37	0.23 ± 0.25	0.52 ± 0.44	0.07 ± 0.39	0.20 ± 0.13	0.41 ± 1.15	1.13 ± 1.36
$\hat{H}^2$	E_1	21.80 ± 11.20	14.90 ± 0.97	20.80 ± 5.66	19.90 ± 8.86	32.10 ± 1.20	19.60 ± 1.22	28.30 ± 3.82
	E_2	12.00 ± 17.03	7.80 ± 15.14	7.10 ± 18.12	5.70 ± 9.14	15.30 ± 6.64	18.20 ± 9.31	13.20 ± 6.09
	E_3	22.30 ± 9.79	11.70 ± 2.75	39.30 ± 2.35	31.40 ± 4.74	39.30 ± 2.11	11.30 ± 7.94	23.30 ± 3.19
$\hat{E}$ (Environmental component)	E_1	0.03 ± 0.14	0.02 ± 0.02	0.03 ± 0.08	0.02 ± 0.07	0.01 ± 0.01	0.01 ± 0.08	0.01 ± 0.25
	E_2	0.01 ± 0.19	0.01 ± 0.13	0.01 ± 0.13	0.00 ± 0.00	0.01 ± 0.01	0.01 ± 0.34	0.01 ± 0.23
	E_3	0.03 ± 0.14	0.03 ± 0.04	0.03 ± 0.06	0.02 ± 0.06	0.01 ± 0.02	0.02 ± 0.17	0.01 ± 0.21
$(\hat{H}_1 / \hat{D})^{1/2}$ (Mean degree of dominance)	E_1	1.59	2.64	3.47	4.64	1.74	3.96	2.36
	E_2	3.15	4.82	4.75	6.04	2.25	6.25	2.77
	E_3	1.56	2.81	3.53	4.56	2.06	3.81	2.35
$\hat{H}_2 / 4 \hat{H}_1$ (Proportion of genes with +/- effects in parents)	E_1	0.19	0.24	0.21	0.22	0.23	0.18	0.20
	E_2	0.21	0.22	0.22	0.24	0.18	0.20	
	E_3	0.20	0.23	0.15	0.20	0.17	0.23	0.22
$(4 \hat{D}, \hat{H}_1)^{1/2} + \hat{F} / (4 \hat{D}, \hat{H}_1)^{1/2} - \hat{F}$ (Proportion of dominant and recessive genes in parents)	E_1	2.38	1.22	1.54	1.09	1.29	2.69	1.64
	E_2	1.72	1.52	1.55	1.17	2.61	2.43	1.71
	E_3	2.26	1.45	2.63	1.30	1.93	1.34	1.48
$\hat{H}^2 / \hat{H}_2$ (Number of gene groups)	E_1	0.81	3.16	0.06	0.40	0.22	0.48	0.09
	E_2	1.33	1.40	1.40	1.51	0.61	1.97	0.18
	E_3	0.82	3.09	0.08	0.47	0.23	0.44	0.08
r (Correlation coefficient)	E_1	-0.27	0.89	-0.22	-0.19	0.96	0.54	0.19
	E_2	0.10	-0.17	-0.20	0.49	0.41	-0.22	-0.03
	E_3	0.03	0.82	-0.10	0.16	-0.11	-2.46	-0.02
t^2	E_1	1.27	1.52	0.52	10.12	0.97	0.09	1.79
	E_2	4.12	10.71	11.67	1.90	0.03	10.52	0.35
	E_3	1.49	3.59	0.01	13.28	0.01	2.10	0.74
(1-b/Seb)	E_1	4.06	1.88	3.35	7.35	1.31	1.41	0.71
	E_2	4.67	7.48	7.81	2.92	1.47	7.53	2.76
	E_3	3.49	2.99	2.32	7.47	2.14	4.48	3.08

*, ** Significant at 5 per cent and 1 per cent probability levels, respectively.