International Journal of Agriculture Innovations and Research
Volume 5, Issue 1, ISSN (Online) 2319-1473
Manuscript Processing Details (dd/mm/yyyy) :
Received : 17/07/2016 | Accepted on : 23/07/2016 | Published : 30/07/2016

Assessment of Heritability and Genetic Advancement for Yield and Yield Attributing Traits in Cabbage (*Brassica oleracea var. Capitata* L.)

Abhishek Chura
Defence Institute of Bio Energy Research,
Field Station, Pithoragarh-262501
Uttarakhand (INDIA)
Corresponding Author: abhisboy@gmail.com

Prem Singh Negi
Defence Institute of Bio Energy Research,
Field Station, Pithoragarh-262501
Uttarakhand (INDIA)

Vandana Pandey
Defence Institute of Bio Energy Research,
Field Station, Pithoragarh-262501
Uttarakhand (INDIA)

Abstract **– Study was carried out to analyze heritability (broad sense) and genetic advancement in nine genotypes of cabbage. Data were observed for percent of mean for yield and yield attributing characters, which include Yield (93.70), head width (91.30), days to 50 % maturity (90.30) and polar diameter (89.70) stalk length (77.20), head length (76.40), harvest index (72.50) and biological yield (71.50). A high heritability (h^2) for Genetic advancement (5%) was observed ranging from 16.74 % for harvest index to 0.58 % for net head weight.**

Keywords **– Broad Sense, Cabbage, Genetic Advancement, Heritability.**

I. INTRODUCTION

Cabbage *(Brassica oleracea* var. Capitata L.) (2n=2x=18) is one of the most popular cole crops in many countries of world including India. It is an economically and nutritionally important vegetable crop, which is grown and consumed widely around the globe [3]. Cabbage is consumed by all sections of people as fresh salad, raw and use as culinary dishes. Worldwide popularity of this high nutritional vegetable crop is because of its wider adaptability, less market price and round the year availability [11]. It is grown under temperate to tropical climatic condition for its heads in more than ninety countries world over [10]. Cabbage is a rich source ascorbic acid, carotenes, sulphur containing amino acids, antioxidants, and is reported to have anti-carcinogenic property [5], [9]. It is highly productive and usually finds its place as the poor man's vegetable crop.

The extent of genetic variability is of paramount importance for the improvement of a crop since greater is the genetic variability in the existing germplasm better would be the chances of selecting superior genotype [14]. Improvement in genetics of any vegetable crop depends upon the availability of genetic variability for important quantitative traits and its judicious exploitation through efficient breeding method. Today, Heritability and genetic advancement is utilized as the most successful approach to increase the productivity of plants and hybrid breeding especially in cross-pollinated vegetable crops like cabbage. Information on the magnitude of heritability and genetic advancement is an important prerequisite for developing a good economically viable hybrid cabbage variety.

The present study was carried out at the Defence Institute of Bio Energy Research (DIBER) Pithoragarh, Uttrakhand during the year 2012-2013. The experimental area is geographically situated at 29°58' NL and 80°22' EL at an altitude of 1514 m above mean sea level. It has relatively warmer during summer than cold winter with an average annual temperature of 10.1°C, rainfall of 36.7 centimetres and relative humidity 81.0%.

II. MATERIAL AND METHOD

Pure seeds of nine diverse genotypes of white cabbage namely SEL-1, SEL-7, C-3, C-5, C-7, C-1, DARL-851, DARL-852 and DARL-SEL were selected for the study. The nurseries were raised in beds after sowing of seeds of each of the genotypes keeping row to row distance 10 cm. All the prophylactic measures were taken care of during the growth of seedlings. Prepared seedlings of each genotype were planted in a plots measuring 3.0 x 2.0 m area in randomized block design (RBD) with three replications. 20 plants in each plot were planted keeping plant to plant distance 60 cm and row to row 50 cm. The recommended agronomic practices and plant protection measures were followed uniformly to all the parents during the entire duration of the experiment. The observations were recorded on maturity for five randomly selected genotypes in each the plot of all replications. Data were recorded for ten important characters viz. head length (cm), head width (cm), stalk length (cm), polar diameter (cm), number of non-wrapper leaves (no.), biological yield (kg), net head weight (kg), yield (kg/plot), days to 50 % maturity and Harvest Index (%).

III. STATISTICAL ANALYSIS

The mean value obtained were used to estimating the analysis of variance for testing heritability, genetic advance [4] and genetic advance as percent of mean were calculated.

IV. RESULT & DISCUSSION

Analysis of variance has revealed that highly significant difference for almost all the characters. The amount of variation in about ten characters of nine genotypes were measured in terms of Mean range, general mean, heritability (h^2), genetic advancement and genetic advancement as percentage of mean (GAM) are presented in table 1. The genotypes exhibited large amount of variation for all the ten characters as 21.13 to 26.13 cm for head length, 51.33 to 60.56 cm for head width, 10.46 to 18.45 cm for stalk length, 38.6 to 51.16 cm for polar diameter, 10.50 to 18.23 for no. of non wrapper leaves, 1.80 to 2.62 kg for biological yield, 1.01 to 1.48 kg for net head weight, 23.520 to 32.436 kg per plot for yield, 76 to 104.93 for days to 50 percent maturity and 45.76 to 67.86 for harvest index. This spacious range of variability for different characters showed the scope for selection of suitable material for breeding in the improvement of cabbage.

The value of heritability in broad sense for all the characters ranged from 71.50 for biological yield to 93.70 for yield (kg/plot). High heritability (>80%) was observed for Yield (93.70 %), head width (91.30 %), Days to 50 % maturity (90.30 %), Polar diameter (89.70 %) and no. of non wrappers leaves (82.90 %) whereas, moderate for net head weight (78.90 %), stalk length (77.20 %), head length (76.40 %), harvest index (72.50 %) and biological yield (71.50 %). Similar finding were also reported by Singh et al [12] and Meena et al [7]. Heritability assessment is an explanatory parameter to the breeder for selecting the varieties for future use with higher magnitude of heritability suggested that major role of genotypic factor in the expression of characters. Therefore, degree of success in selection depends upon the magnitude of heritability value. Allard [1] viewed that characters which have low heritability are dependable because their genotypic expression is superimposed by the environmental influences. Heritable variation can be found out with greater degree of accuracy when heritability is studied in connection with genetic advancement. High heritability does not mean a high genetic advance for a particular quantitative character. Johnson et al. [4] reported that heritability estimates along with genetic gain would be more rewarding than heritability alone in predicting the consequential effect of selection to choose the best individual. High estimate of heritability coupled with high genetic advances were observed for the characters yield (kg/plot) and no. of non-wrapper leaves. The characters those exhibit maximum heritability and high genetic advance as percentage of mean could be used as powerful tool in selection process such characters are controlled by the additive genes and less influenced by the environment [8].

Genetic advance as percentage of mean (>30%) assorted from 16.78 % to 66.96 % for days to 50 % maturity and yield (kg / plot). It was highest for yield (66.96 %) followed by net head weight (53.69 %), biological yield (36.25 %), Harvest index (34.57 %), stalk length (34.47 %) and no. of non wrapper leaves (33.11 %); moderate for head width (20.33 %), polar diameter (19.96 %), head length (19.43 %) and days to 50 percent maturity (16.78 %) respectively. Similar finding were also reported from Atter et al [2], Soni et al [13] and Kumar et al [6] respectively. Heritability estimates provide a measure of the effectiveness with which selection can be exploiting the genetic variability but the effectiveness and potentiality of the traits under selection could be revealed by an assessment of genetic gain. So heritability value across with genetic advance as percent of mean, jointly, are more useful tools for selection than either them alone.

V. CONCLUSION

In the present study, high heritability coupled with a high genetic advance for yield and number of non-wrapper leaves clearly recommended that the role of additive gene action thus, a high genetic gain is expected from selection of these characters. Moderate heritability (h^2) beside with high genetic advance for net head weight, harvest index, stalk length and biological yield suggested that the involvement of both additive and non additive gene action. Whereas, high heritability across with moderate genetic advance reflected the directive role of the aforementioned traits through non additive gene action, which can be utilized for the success in development of cabbage hybrids.

VI. ACKNOWLEDGMENT

Sincerely obliged to the Director, DIBER, Haldwani for providing all facilities to carry out the present work. DG, DRDO is thankfully acknowledged to award Fellowship to Mr. Abhishek Chura.

REFERENCES

[1] Allard R.W. 1960. Principles of plant breeding. John Wiley and Sons Inc., New York.

[2] R.S Atter, K.C Sharma, and A.S. Sundouri. 2009. Genetic variability for head yield and component traits in cabbage (*Brassica oleracea* var. *capitata* L.). Indian J. Ecol., 36(1): 88-90.

[3] M.S Chiang, C. Chong, B.S. Landry and R.Crete. 1993. Cabbage (*Brassica oleracea* var. *Capitata* L.). In: Genetic Improvement of Vegetable Crops. G. Kalloo and B.O. Berg (eds.). Pergamon Press, New York, pp. 113-55.

[4] H.W. Johnson, H.F. Robinso and R.E. Comstock. 1955. Estimates of genetic and environmental variability in soybeans. Agron. J., 47: 314-318.

[5] D.E, Kopsell, D.A. Kopsell, M.G. Lefsrud and C.J. Curran. 2004. Variability in elemental accumulations among leafy *Brassica oleracea* cultivars and selections. Journal of Plant Nutrition 27: 1813-1826.

[6] D. Kumar, V. Bahadur, S.B.Rangare and D Singh. 2012. Genetic variability, heritability and correlation studies in chilli (*Capsicum annuum* L.). Hort Flora Res.Spectrum, 1 (3): 248-252.

[7] M.L, Meena, R.B. Ram and R. Lata. 2011. Genetic variability, heritability and genetic advance for yield and its contributing traits in cabbage (B*racica oleraceav* ar. c*apitata* L.). Adv. Plant Sci., 24(2): 661-663.

[8] V. G. Panes and P. V. Sukhatme. 1995. Statistical methods for agricultural workers (3rd ed., p. 58). ICAR, New Delhi.

[9] B.K. Singh, S.R. Sharma and B. Singh. 2009a. Heterosis for antioxidants and horticultural traits in single cross hybrids of cabbage (*Brassica oleracea* var. *capitata*). Indian Journal of Agricultural Sciences 79: 703-708.

[10] B.K. Singh, S.R. Sharma and B. Singh. 2009b. Heterosis for mineral elements in single cross hybrids of cabbage (*Brassica oleracea* L. var. *capitata*). Scientia Horticulturae 122: 32-36.

[11] B. K. Singh, S.R. Sharma and B. Singh. 2010. Heterosis for superoxide dismutase, peroxidase and catalase enzymes in the head of single cross-hybrids of cabbage (Brassica oleracea var. capitata) Journal of Genetics 89(2):217-21

[12] B.K. Singh, S.R. Sharma, P. Kalia and B. Singh. 2011. Genetic variability for antioxidants and horticultural traits in cabbage Indian J. Hort. 68(1)*: 51-55*

[13] S.Soni, S. Kumar, S.Maji and A. Kumar 2013. Heritability and genetic advance in cabbage (Brassica oleracea var. capitata L.) under Lucknow condition. Hort flora Research spectrum, 2(3): 274-276.

[14] N.I. Vavilov 1951. The origin, Variation, Immunity and Breeding of Cultivated Plants. Chronica Botanica. 13: 1-366.

AUTHORS' PROFILES

First AUTHOR

Abhishek Chura is a senior research fellow in Defence Institute of Bio Energy Research (DIBER) DRDO Pithoragarh, when doing the work. Presently senior research fellow at Dr. D.P. Rastogi centeral research institute for Homeopathy, Ministry of AYUSH, Noida. He has completed M.Sc. in Botany in 2010 and M.PHIL in Botany in 2011 from MGSU, Bikaner. He has been working in research field from last 5 years. His research contribution in field of plant genetics and breeding. He is Correspondence author of this paper.

Dr P. S. Negi is presently working as Senior Scientist in Defence Institute of Bio Energy Research, Field Station, Pithoragarh (Uttarakhand) and is having research experience of more than 35 years in various R & D activities in basic and applied Life Sciences. He has done his M. Sc. and Ph. D. in Botany from Kumaun University, Nainital. There are more than 50 research papers in various national and international journals to his credit. His research contribution relates to Plant Tissue Culture, Myco-taxonomy, Cultivation of edible and Medicinal Mushrooms. Dr P. S. Negi has identified more than 60 species of wild edible and poisonous mushroom species (Ascomycotina and Basidiomycotina) from Kumaun Himalayas ranging from 5500 ft to 14000 ft altitude.

Vandna Pandey is Senior Scientist at Defence Institute of Bio Energy Research (DIBER, DRDO). She has more than 15 years of research experience the field of Vegetable Breeding. She has made a significant contribution in developing a number of hybrids and varieties. She has several publications to her credit, which includes chapter in books, research papers, scientific articles and popular articles. She is recipient of national and lab level awards viz: Plasticon Award, National Science Day Award and Technology Group Award.

Table 1: Estimate of mean range, heritability and genetic advancement for 10 characters in cabbage

S. No.	Characters	Mean Range		General mean	Heritability (%)	Genetic advance (5 %)	Genetic advance (1 %)	Genetic advance as % of mean (5 %)	Genetic advance as % of mean (1 %)
		Min.	Max.						
1.	Head length (cm)	21.13	26.13	23.46	76.40	3.56	4.56	15.16	19.43
2.	Head width (cm)	51.33	60.57	57.56	91.30	9.13	11.70	15.86	20.33
3.	Stalk length (cm)	10.46	18.45	12.45	77.20	3.35	4.29	26.90	34.47
4.	Polar diameter (cm)	38.60	51.16	46.68	89.70	7.27	9.32	15.57	19.96
5.	No. of non wrapper leaves	10.5	18.23	13.71	82.90	3.54	4.54	25.83	33.11
6.	Biological yield (kg)	1.80	2.62	2.24	71.50	0.63	0.81	28.29	36.25
7.	Net head weight (kg)	1.01	1.48	1.39	78.90	0.58	0.75	41.89	53.69
8.	Yield (kg/ plot)	23.52	32.43	27.40	93.70	14.32	18.35	52.25	66.96