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Assessment of variability in Broccoli (*Brassica oleracea* var. *italica* L.) genotypes

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Abstract

The present experiment was carried out thirteen broccoli genotypes under Randomized Block Design with three replications to assess the genetic variability, heritability and genetic advance for various horticultural traits. Analysis of variance revealed that there is a considerable variability exists among the genotypes for all the fourteen characters. High genotypic and phenotypic coefficients of variation were recorded for leaf length (23.89 and 24.25), curd weight/plant (35.34 and 35.47) and Curd yield (33.67 and 34.85). High heritability combined with high genetic advance as percent mean were observed for number of leaves (89.60 and 29.08 percent), leaf length (97.00 and 48.47 percent), leaf width (84.60 and 24.74percent), days to curd initiation (91.50 and 20.74 percent), curd length (97.00 and 30.36 percent), curd width (98.10 and 41.07 percent), curd weight/plant (99.20 and 72.52 percent), curd yield (93.40 and 67.02 percent) and Ascorbic acid (96.70 and 24.68 percent).

Keywords: Broccoli, variability, heritability and genetic advance as per cent of mean

Introduction

Broccoli (*Brassica oleracea* L. varitalica) is a member of the Brassicaceae (Cruciferae) family, originated from west Europe has considered as cool-season crops, now been distributed in both tropical and the sub tropical areas. Other members of the family include cauliflower, cabbage and kale (Guo *et al.*, 2001) ^[5]. Its optimum growing temperature is in the range between 16 and 20 ^oC and is a biannual, herbaceous vegetable crop (Karistsapol *et al.*, 2013) ^[11]. Compared to cabbage and cauliflower, broccoli is nutritionally very rich in protein (3.6%), fat (0.3%), carbohydrate (5.9%), vitamin A (9000 I.U.), calcium (2-16%) and iron (684 ppm). This nutritious vegetable also contains a chemical known as indole- 3-carbinol, which is supposed to possess anticancerous properties (Choudhury, 2005) ^[3]. United States of America is a leading producer of broccoli. In India, broccoli has become a commercial crop very recently and is grown in smaller area. The cultivation of sprouting broccoli is now gaining popularity among Indian growers for the last couple of years obviously due to increasing awareness of its high nutritive values and tourist influx.

For any efficient plant improvement programme the existence of sufficient genetic variability in the population is a prerequisite and selection is perhaps the most important activity in all plant breeding programmes which is made on the basis of phenotype. The continuous variation exhibited by a quantitative trait includes the heritable and the non heritable components, while the heritable may be the consequence of genotype, the non heritable part is mostly due to environmental factors (Fisher, 1918)^[4]. The presence of genetic variation in the breeding material determines the success or failure of any breeding programme. Therefore the measurement of genetic variation and understanding the mode of inheritance of qualitative and quantitative traits are the essentials in any crop improvement programme. The present investigation has been conducted to assess the genetic variability, heritability and genetic advance studies in 13 genotypes of broccoli under Ooty condition.

Materials and Methods

An experiment was carried out at Horticultural Research Station, ooty during the period of February to June 2018. The experiment was carried out in thirteen genotypes of broccoli (Punjab broccoli 1, Palamsamridhi, Palam Kanchan, Palamvichithra, CITH 1 and CITH 2, Lucky, Fiesta, Dynasty, SSB06, A1, Green magic, Punjab hybrid. The seeds were sown in nursery on February 27th, 2018 in Horticultural Research Station, Ooty and seedlings were

transplanted with a spacing of 45 x 45 cm under Randomized Block Design (RBD) with three replications. Recommended crop production and protection practices were followed. The performance of different broccoli genotypes was studied and data recorded on plant height (cm), number of leaves (cm), leaf length (cm), leaf width (cm), curd length (cm), curd width (cm), curd weight g plant⁻¹, days to curd initiation, days to curd harvest, curd dry matter (%), leaf dry matter (%), total carotenoids (mg/100g⁻¹), Ascorbic acid (mg/100g⁻¹) and curd yield (ton ha⁻¹) were analysed in this study. The mean over replications for each character was subjected to statistical analysis. The phenotypic and genotypic coefficients of variations (PCV, GCV) were estimated by using the formulae suggested by Burton (1952)^[2]. Heritability in broad sense was estimated by using the formulae suggested by Lush (1940) ^[13] and expected genetic advance was computed by using formulae suggested by Johnson et al., 1955^[7].

Result and discussion

The estimates of variability on the basis of genotypic variance, phenotypic variance, genotypic coefficient of

variation and phenotypic coefficient of variation, heritability and genetic advance as per cent of mean are presented in Table (1). Variability is the most important characteristic feature of any population. Estimation of genetic variability is an important pre-requisite for realizing response to selection as the progress in breeding depends upon its amount, nature and magnitude of genetic variability. The breeder should have the capability of distinguishing the genetic and non-genetic components of variation occurring in a population. In the present investigation, a similar analysis of variability was carried out. An insight into the magnitude of variability present in a crop species and heritability of characters is essential as it provides the basis of effective selection (Anandhi and Oommen, 2007)^[1]. The present study meets out, the extent of variability available in 13 genotypes collected from different sources and the scope of selection through heritability and genetic advance estimates was analysed and the results obtained are discussed here under. The analysis of variance revealed significant differences among the 13 genotypes for all the traits studied.

Genetic parameters	GCV (%)	PCV (%)	Heritability	Genetic Advance as percent mean
Plant height (cm)	10.25	10.86	89.10	19.94
Number of leaves	14.91	15.75	89.60	29.08
Leaf length (cm)	23.89	24.25	97.00	48.47
Leaf width (cm)	13.06	14.20	84.60	24.74
Curd length (cm)	14.96	15.19	97.00	30.36
Curd width (cm)	20.13	20.33	98.10	41.07
Curd weight/plant	35.34	35.47	99.20	72.52
Days to curd initiation	10.53	11.01	91.50	20.74
Days to curd harvest	9.32	9.82	90.20	18.23
Estimated yield t/ha	33.67	34.85	93.40	67.02
Curd dry matter %	11.91	14.68	65.80	19.91
Leaf dry matter %	9.28	10.06	85.10	17.63
Total carotenoids (mg/100g)	11.90	16.04	55.00	18.18
Ascorbic acid (mg/100g)	12.25	12.51	95.70	24.68

Phenotypic and genotypic coefficients of variation

High genotypic and phenotypic coefficients of variation were recorded for leaf length (23.89 and 24.25), curd weight/plant (35.34 and 35.47) and Curd yield (33.67 and 34.85). Moderate genotypic and phenotypic coefficients of variation were recorded for plant height (10.25 and 10.86), number of leaves (14.91 and 15.75), leaf width (13.06 and 14.20), days to curd initiation (10.53 and 11.01), curd length (14.96 and 15.19), curd width (20.13 and 20.33), curd dry matter (11.91 and 14.68), total carotenoids (11.90 and 16.04) and ascorbic acid (12.25 and 12.51). Low genotypic and phenotypic coefficient of variation were recorded for days to curd harvest (9.32 and 9.82) and leaf dry matter (9.28 and 10.06). The result is in accordance with the findings of Hakala et al., (2003) and Singh et al., (2010), Kalia and Shakuntla (2002), Santhosha et al., (2015) [18, 9, 16] in cauliflower, Kumar et al. (2017) [12] in cauliflower and Singh et al., (2013)^[19] in cabbage.

The result from this study indicated that phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters in thirteen genotypes under study. Even though PCV was more than GCV but the difference was very narrow suggesting that, there is less influence of environment on alteration of these characters. Hence, these characters can be relied upon and simple selection can be practiced for further improvement.

Heritability and genetic advance as percent mean

High heritability combined with high genetic advance as percent mean were observed for number of leaves (89.60 and 29.08 percent), leaf length (97.00 and 48.47 percent), leaf width (84.60 and 24.74 percent), days to curd initiation (91.50 and 20.74percent), curd length (97.00 and 30.36 percent), curd width (98.10 and 41.07 percent), curd weight/plant (99.20 and 72.52 percent), curd yield (93.40 and 67.02 percent) and Ascorbic acid (96.70 and 24.68 percent). High heritability coupled with moderate genetic advance as percent mean were noticed for plant height (89.10 and 19.94 percent), days to curd harvest (90.20 and 18.23 percent), curd dry matter (65.80 and 19.91 percent) and Leaf dry matter percentage (85.10 and 17.63 percent). Moderate heritability combined with moderate genetic advance as percent mean were observed for total carotenoids (55.00 and 18.18 percent). High heritability along with high genetic advance results from heritability due to additive gene effect thereby making the selection effective and rewarding whereas high heritability coupled with low genetic advance results in non-additive gene effects, thereby rendering the selection ineffective. The result is in accordance with the findings of Santhi et al. (2015)^[15] in carrot, Nagar *et al.* (2016) ^[14], Singh *et al.* (2017) ^[17] in radish, Singh *et al.*, (2013) ^[19] in cabbage, Kanwar and Korla (2002) ^[10], Jindal and Thakur (2004) ^[8] and Thakur and

Thakur (2002) [20].

From the above result, it is concluded that there is a wide range of variability present among the genotypes for almost all characters indicating that a wide scope for genetic improvement of crop. The narrow difference was retained between GCV and PCV indicating a little effect of environment in the expression of characters. So, selection of these traits on the basis of their phenotypic values becomes effective. High heritability coupled with greater genetic advance was observed for curd length, curd width, curd weight/plant and curd yield and there is possibility for improvement of these traits by selection.

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