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Genetic analysis in okra under *tarai* region of Uttarakhand

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Abstract

The crop improvement depends upon the magnitude of genetic variability present in the available germplasm. Therefore, an effort was made to create and assess the variability through hybridization using parameters like PCV, GCV, heritability, genetic advance for different yield and its contributing traits in okra. The present investigation was carried out during summer season of 2018 in *Tarai* region of Uttarakhand. The experimental material utilized for this study consisted of 59 genotypes including 15 parents (11 lines, 4 testers) and 44 crosses of okra. The analysis of variance showed that significant genetic differences were present among genotypes for all the characters studied. This suggested that there was adequate amount of genetic variability among the experimental material and hence, a greater scope for the improvement of concerned characters through selection. The values of PCV were higher than that of GCV for all the thirteen characters indicating influence of environmental effects in the expression of these characters. Moderate to high GCV together with moderate to high heritability and genetic advance as per cent of mean was reported for majority of the characters under study except days to 50% flowering and fruit length, which indicated predominant additive gene action. Thus these traits have ample scope for the improvement of concerned traits through selection.

Keywords: Genetic variability, heritability and genetic advance

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] commonly known as bhendi or lady's finger is a fast growing warm and rainy season annual herb whose immature green pods are used as a common vegetable. It belongs to the family Malvaceae and is believed to be native of tropical Africa. It is an important vegetable crop throughout the tropics and subtropics (Hammon and Van Stoles, 1989) [11] and is also well distributed in the Indian subcontinent and East Asia (Kochhar, 1986) [13]. The fruits are fairly good in nutritive value and 100 g edible fruit contains dry matter (10.4 g), water (89 g), protein (2-4 g), fat (0.3 g), carbohydrate (7.6 g), calcium (92 mg), phosphorus (51 mg), iron (0.6 mg) and potassium (249 mg). Green fruits are also rich source of iron and vitamin A, B and C (Aykroyd, 1963) [3]. Fruits of okra are useful for the control of goiter disease due to high iodine content (Chaudhary, 1979) [8]. Yields of present cultivars of okra per unit area of land and per unit of time are very low because of their very low yield potential (Balakrishnan and Balakrishnan, 1988) [5]. Genetic variability is a very important component of plant breeding which is a major tool being used to increase yield in crop plants to cope with the ever-increasing pressure of an expanding world population on food production (Ariyo, 1990) [2]. Yield is a complex character influenced by a great extent of environment. Therefore, selection for yield alone is not effective and it is imperative to depend on traits which are highly heritable and contribute greatly for yield. Hence the study of heritability and genetic advance is very important.

Material and Methods

The experimental material utilized for this study consisted of 59 genotypes (11 lines, 4 testers and their 44 F_1 hybrids). The parents were collected from N.B.P.G.R., New Delhi and I.I.V.R., Varanasi. During *Kharif* season of 2017 all the breeding lines and tester were raised in a breeding block and prepared 44 crosses in line × tester mating design. In summer season of

2018, these 44 crosses along with 15 parents were evaluated in RBD design at Vegetable Research Centre, Pantnagar. Observations were recorded from five competitive plants were randomly selected from each entry in three replications. All the 13 quantitative characters studied were days to 50 per cent flowering, first fruit producing node, fruit length (cm), fruit diameter (mm), average fruit weight (g), number of fruits per plant, number of primary branches per plant, stem diameter (mm), inter-nodal length (cm), plant height (cm), fruit yield per plant (g), total yield (q/ha) and number of seeds per fruit. The genotypic and phenotypic coefficients of variance were estimated according to Burton and Devane (1953) [7], while heritability in broad sense and expected genetic advance were estimated by Weber and Moorthy (1952) [19] and Johanson *et al*., (1955).

Result and Discussion

Analysis of variance showed that genotypes differed significantly among themselves for all the traits studied in the present investigation. The mean, genotypic and phenotypic coefficient of variations, heritability and genetic advance as percentage of mean for all traits are presented in Table-1.

Variability

An assessment of variability parameters revealed that there is lot of variation among genotypes studied. In general, the value of phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters, indicating the considerable influence of environmental factors on the performance of genotypes for different characters. Similar results were also reported in okra by Singh *et al*. (2006) [17] and Binepal *et al.* (2019) [6]. Moderate to high PCV and GCV estimates were observed for many traits *viz*. first fruit producing node, average fruit weight, number of primary branches per plant, stem diameter, inter-nodal length, plant height, number of seeds per fruit, number of fruits per plant and fruit yield per plant. Moderate to high PCV and GCV for these traits clearly indicate ample scope for yield improvement in okra through selection due to the presence of sufficient variability among genotypes of okra under studied. The PCV and GCV were low for days to 50% flowering, fruit length and fruit diameter. The high PCV accompanied with moderate GCV was observed for number of primary branches per plant and plant height. The first fruit producing node, number of primary branches per plant, fruit length and fruit diameter and plant height were highly influenced by environmental factors as the difference between PCV and GCV value was higher. The result of the present study agreed with the finding of Kumar *et al.* (2016) [15] and *Singh et al.* (2017).

Heritability and Genetic advance as per cent of Mean

Heritability of a character is important in determining its response to selection. Genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an effective breeding program. The broad sense heritability is the relative magnitude of genotypic and phenotypic variance for the traits and it gives an idea of the total variation accounted to genotypic effect (Allard, 1960) [1]. It is generally expressed in percentage. The heritability is the heritable portion of phenotypic variance. It is a good index of transmission of characters from parents to their offspring. Broad sense heritability estimates ranged from 31.10 (Fruit length) to 88.50 (Fruit yield per plant) (Table 1). Fruit yield per plant recorded maximum heritability (> 75%) followed by number of fruits per plant, inter-nodal length, days to 50% flowering and number of seeds per fruit. The heritability estimates for these traits indicate that these characters are least influenced by the environment. Since the estimates of broad sense heritability are based on total genetic variance which include both fixable (additive and additive × additive type of epistasis) and non-fixable (dominance, additive × dominance and dominance × dominance type of epistasis) variance. Hence, the selection for improvement of these characters may not be useful. Stem diameter, average fruit weight, plant height, first fruit producing node and number of primary branches per plant exhibited moderate level of heritability (50 - 75%). However, low heritability was observed for fruit length and fruit diameter (<50%). Low to moderate estimates of broad sense heritability indicates that these characters are highly influenced by environmental effects and the genetic improvement through selection in these traits is difficult due to masking effect of environment on the genotypic effects. High estimates of genetic advance as percentage of mean (> 20%) was observed for most of the characters under study *viz*, plant height, fruit yield per plant and number of seeds per fruit. High estimates of genetic advance as percentage of mean indicated that the preponderance of additive genetic effects in expression of these characters. Therefore, selection for these characters in segregating generations based on phenotypic performance would likely be more effective. Low estimates of genetic advance as percent of mean (< 10%) were observed for first fruit producing node, fruit length, fruit diameter, days to 50% flowering, average fruit weight, number of primary branches per plant, inter-nodal length and stem diameter, whereas, number of fruits per plant exhibited moderate level of genetic advance as per cent of mean (10-20%). Low value of genetic advance suggested that non-additive gene action was involved in controlling the characters. High heritability does not always mean high genetic advance. For yield improvement, selection of superior parents possessing better heritability and genetic advance for yield contributing traits is an essential prerequisite. Heritability in conjunction with genetic advance determines the best picture of the amount of progress to be expected from selection and also the selection method to improve a character (Johnson et al. 1955) [12]. For efficient selection we cannot solely rely on heritability. The combination of high heritability along with high genetic advance will provide a clear base on the reliability of that particular trait in the selection of variable entries.

The GCV along with heritability provides a reliable estimate of the amount of genetic advance expected through phenotypic selection (Burton and Devane, 1953) [7]. Based on the underlying facts, the traits under study were categorized into three different groups as per the analysis: First group included majority of the characters under study *viz.* first fruit producing node, number of fruits per plant, number of primary branches per plant, stem diameter, inter-nodal length, plant height and fruit yield per plant recorded moderate to high estimates of broad sense heritability and high estimates of genetic advance as percentage of mean. High heritability estimates along with high genetic advance indicated that most likely heritability is due to additive gene effects and the selection may be effective. High heritability and low difference between PCV and GCV estimates for these characters indicated that these traits were less affected by environmental factors. This strongly indicated the preponderance of additive gene action involved in the expression of these characters, and hence, there exists an ample scope for the improvement of concerned traits through direct selection. For different characters, similar results were also observed by various researchers like Bagwale *et al.* (2016) [4] and Kumar *et al.* (2019) [14].

The second group of traits included average fruit weight, fruit diameter and number of seeds per fruits which had moderate to high heritability estimates coupled with moderate genetic advance as per cent of mean. It revealed that average fruit weight, fruit diameter and number of seeds per fruits were governed with additive gene effects and selection will be effective for these traits. Similar results were also reported by Osekita and Akinyele (2008) [16] and Kumar *et al.* (2019) [14].

The third group included only few characters i.e. days to 50% flowering and fruit length which had moderate to low heritability coupled with low genetic advance. Moderate heritability coupled with low genetic advance was indicative of non-additive gene action. The high or moderate heritability is exhibited due to favorable influence of environment rather than genotype as GCV estimates were also low and direct selection for such traits may not be rewarding. So, progeny testing or heterosis breeding could be employed for the improvement of these characters in okra. Such results were also reported by Chaurasiya *et al.* (2010) [9] and Das *et al.* (2012) [10].

Table 1: Genetic parameters of variability for yield and its component traits

Genetic Parameters / Characters	Mean ± S.E	Range	GCV	PCV	h^2 bs (%)	GA	GA% of Mean
Days to 50% flowering	48.08 ± 0.58	46.67 - 52.67	4.24	4.76	79.20	3.58	7.77
First fruit producing node	5.90 ± 0.27	4.67 - 7.44	13.73	17.54	61.30	0.93	22.14
Fruit length (cm)	13.38 ± 0.55	11.73 - 15.91	6.76	12.14	31.10	0.73	7.76
Fruit diameter (mm)	14.79 ± 0.71	12.41 - 16.81	8.82	12.83	47.30	1.65	12.50
Average fruit weight (g)	11.95 ± 0.53	9.29 - 14.23	11.31	13.74	67.70	2.24	19.16
No. of fruit/plant	16.99 ± 0.95	13.11 - 20.67	29.29	32.04	83.60	6.97	55.16
No. of primary branches/plant	2.06 ± 0.21	1.78 - 2.56	15.52	21.74	50.90	0.55	22.81
Stem diameter (mm)	17.91 ± 0.80	15.19 - 20.29	13.24	15.83	70.00	3.66	22.82
Inter-nodal length (cm)	6.34 ± 0.22	5.16 - 7.11	14.27	15.87	80.90	1.44	26.43
Plant height (cm)	92.32 ± 4.75	75.60 - 113.62	17.80	21.69	67.40	19.97	30.09
Fruit yield/plant (g)	204.55 ± 11.91	128.76 - 278.18	38.15	40.55	88.50	111.01	73.94
Total yield q/ha	113.64 ± 7.94	71.53 - 154.54	38.15	40.55	88.50	74.01	73.94
No. seeds/fruit	54.90 ± 1.81	39.40 - 74.59	10.47	11.90	77.40	10.50	18.98

S.E. = Standard Error
GCV = Genotypic coefficient of variation
PCV = Phenotypic coefficient of variation
h^2 bs = Heritability in broad sense
GA = Genetic Advance

Conclusion

Moderate to wide range of mean values among the genotypes for different characters were observed. The value of PCV estimates was higher than the corresponding GCV estimates for all the characters, indicating the considerable influence of environmental factors on the performance of genotypes for different characters. Moderate to high GCV together with moderate to high heritability and genetic advance as per cent of mean was reported for majority of the characters under study except days to 50% flowering and fruit length which indicated predominant additive gene action thus these traits has ample scope for the improvement of concerned traits through selection.

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