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Study of heritability parameter in hybrids of okra (*Abelmoschus esculentus* (L.) Moench)

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Abstract

The current investigation was carried out using ten genotypes of okra and forty-five F₁ hybrids obtained from these ten parent along with one check Radhika. During season 2021-22 the crosses was made among the ten genotypes in 10 X 10 half diallel fashion mating. The crossing resulted in the development 45 hybrid progeny. The effected 45 F₁ hybrids and ten parents along with one checks were planted during summer and *kharif* of season 2022-23 under Randomised Block Design along with two replications. The research conducted at All India Coordinated Research Project on Vegetable Crops, Department of Horticulture, Mahatma Phule Krishi Vidyapeeth, Rahuri. Various characters are used to analysed the progeny and parents by estimating the heritability parameters. It was resulted in all character that are under study shoes the non-additive gene action implies to heterosis breeding and recurrent selection for further improvement of population.

Keywords: Crosses, F₁ hybrids, half diallel, heritability, non-additive

Introduction

Okra (*Abelmoschus esculentus* (L.) Moench) is a warm season and annual vegetable crop belongs to the family Malvaceae, genus - *Abelmoschus* an amphidiploids having 2n=130 chromosomes and propagated by seed. It is commonly known as lady's finger as well as by several vernacular names, including Okra, Bhindi, Gumbo etc. being a native of tropical Africa. It is an often cross pollinated crop has a prominent position in olericulture because of its high nutritive value, wider adaptability and export potential. The entire plant is edible and is used to make several foods (Lim, 2012 and Jain *et al.*, 2012) ^[11, 12]. In Ayurveda, okra is used as an edible infusion and in different preparation for diuretic effect (Maramag, 2013) ^[13]. Immature tender fresh and green pods are consumed as vegetable. Often the extract obtained from the fruit is added to different recipes like soups, stews and sauces to increase the consistency of it (Hadiya *et al.*, 2018) ^[10]. The immature pods are used in making pickle, stem and root mucilage in jaggery preparation and crude fibre from mature fruits and stem in paper industry. The dry seeds of okra are a good source of edible oil along with high unsaturated fats like oleic and linoleic acids (Sidapara *et al.*, 2021) ^[14].

Okra is a cost-effective and economically affordable natural source with ample reservoirs of carbohydrates, proteins, fatty acids, vitamins, fibre and minerals with various other bio-active phytochemicals those are important for human health. It is having specific mechanisms of action against different diseases. (Elkhalifa *et al.*, 2021) ^[6]. The nutritive values of okra have 88% moisture, 7.7% carbohydrates, 2.2% protein, 1.5% iron, 1.1% fibre, 0.7% mineral matter, 0.09% calcium, 0.2% fat, 0.08% phosphorous and of 41 (k. cal) calorific value. The vitamin contents in okra *viz.*, vitamin A- 58 IU, vitamin B- 0.06 mg, Nicotinic acid - 0.6 mg, Riboflavin- 0.06 mg and vitamin C-13 mg (Devi *et al.*, 2017) ^[4]. Okra cortex is one of the potential sources of mucilage (Girase *et al.*, 2003) ^[9].

The cultivated okra is an artificial amphidiploid of *A. tuberculatus* (2n=58) and *A. ficulneus* (2n=72). There is a considerable variation in the chromosome numbers of cultivated okra species. The genus *Abelmoschus* is a poly-species complex of apparently three levels of ploidy the diploids (2x), including *Abelmoschus coccineus* (2n=38), *A. angulosus* (2n=38), *A. tuberculatus* (2n=58), *A. manihot* (2n=60-68), *A. moschatus* (2n=72) and *A. ficulneus* (2n=72); the tetraploids (4x) including *A. esculentus* (2n=120-140), *A. tetraphyllus* (2n=138)

and *A. pungens* (2n=138); and the hexaploids (6x), including *Abelmoschus manihot* and Guinean type (2n=185-198). Okra is an allopolyploid consisting of two genomes each of 29 and 36 chromosomes. According to them, Indian varieties belong to the group of 2n = 130 chromosomes (Joshi and Hardas, 1956) [15].

India ranks first in the world in production of okra with 64.66 lakh metric tonnes of production obtained from an area of 5.31 lakh hectare with productivity of 12.2 metric tonnes per hectare during 2021-22. The area under the crop in Maharashtra during 2021-22 was 15.40 thousand hectares with the production of 1.56 lakh metric tonnes. However, Maharashtra's productivity 10.17 MT/ha is much lower than that of the country 12.02 MT/ha (Anon, 2022). The geographical distribution of cultivated okra and related wild species is overlapping in South- East Asia. The Indian and West African regions are also known as centres of diversity of okra.

Good nutritive value, popularity, medicinal value, good market value and high export potential are the aspects in favour of okra. However, pests such as Jassids, bollworms and diseases like yellow vein mosaic virus, powdery mildew etc. possess problems in okra cultivation by reducing the quality of the produce and increasing the cost of cultivation. Yellow vein mosaic virus is a serious challenge in cultivation of okra. Some good varieties of okra had been evolved in India, but many of them suffer from one or the other drawback. Crop refinement in okra needs to be focused on plant height, more branching, number of fruits per plant, early flowering, fruit length, tenderness, disease pest resistance and high yield.

The selection of variable parents is one of the crucial decision for plant breeder has to make for performing any breeding program. If the genetic combination of the plant is known, then it is helpful in understanding the nature and magnitude of the gene action present in the inheritance of various characters. The purpose of this research to study heritability in okra which will provide valuable information in the selection of parents for further hybridization programs

and also to identify a superior hybrid in okra for cultivation on farmer's field.

Materials and Methods

The present research was conducted at All India Coordinated Research Project on Vegetable Crops, Department of Horticulture, Mahatma Phule Krishi Vidyapeeth, Rahuri during 2021-22. The experimental field has an altitude of 532 m above MSL, latitude of 19°47' to 19°57' N and a longitude of 74°82' to 74°91' E. The parental material consisted of 10 diverse genotypes and seeds of these genotypes were obtained from Senior Vegetable Breeder, All India Coordinated Research Project on Vegetable Crops, Mahatma Phule Krishi Vidyapeeth, Rahuri. The detail lineage about parental materials are depicted in Table 1.

The seeds of ten parental genotypes were sown in the field during summer 2021 to constitute the crossing block. The crosses were made in between ten diverse parents following 10 x 10 diallel without a reciprocal mating design. The field was prepared for sowing by ploughing, harrowing and levelling and 50 kg N, 50 kg P and 50 kg K per ha was applied as a basal dose and the remaining 50 kg N was applied at 30 DAS as per the recommended dose of fertilizer. The seeds were dibbled at a spacing 60 x 30 cm. All other cultural operations like weeding, irrigation and plant protection measures were carried out as per the requirement of crop. The obtained Forty-five crosses along with the ten parents and a standard hybrid check (Radhika) were sown in a Randomized Block Design with two replications in summer 2022 (1st Feb) and *Kharif* 2022 (27th July) respectively. Each genotype was entered as a separate treatment and was represented by a single row of 3.0 m length spaced 30 cm apart in which the seeds were dibbled. The observation on required character says morphological or yield associated parameter was taken with suitable tools and methods within time during trial. The analysis was done by Randomized Block Design (RBD) was carried out by following Panse and Sukhatme (1985) [16] and Heritability in a narrow sense was calculated by Falconer (1960) [8].

Table 1: Okra genotypes with their source of collection, morphological characters and symbol

Sr. No.	Symbol	Genotype	Morphological characters	Source
1.	P ₁	RHOK03	Green colour, medium pubescent and slight seedy fruit with five ridges	AICRP on Vegetable Crops, MPKV, Rahuri (MS)
2.	P ₂	RHOK12	Green in colour, highly pubescent and non-seedy fruit with five ridges	
3.	P ₃	RHOK14	Green in colour, medium pubescent and slight seedy fruit with five ridges	
4.	P ₄	RHOK17	Green in colour, less pubescent and high seedy fruit with five ridges	
5.	P ₅	RHOK22	Dark green in colour, highly pubescent and slight seedy fruit with five ridges	
6.	P ₆	RHOK23	Green in colour, medium pubescent and slight seedy fruit with five ridges	
7.	P ₇	RHOK26	Green in colour, medium pubescent and non-seedy fruit with five ridges	
8.	P ₈	RHOK30	Green in colour, medium pubescent and non-seedy fruit with five ridges	
9.	P ₉	RHOK31	Green in colour, highly pubescent and non-seedy fruit with five ridges	
10.	P ₁₀	Phule Vimukta	Green colour, pubescent and non-seedy fruit with five ridges	

Results and Discussion

Heritability is nothing but the degree of transmission of characters from parents to their offspring. So for the selection of characters for further improvement is depends on its heritability means the characters having high heritability are selected for improvement purpose. Hence forth here are two types of heritability one is Broad sense and second one is narrow sense heritability. Here is the use of narrow sense heritability is appropriate as the materials was segregating population. Variance like Genetic,

Phenotypic, Additive and Environmental are computed to estimate the heritability. The observation was recorded on 45 F₁ hybrids and 10 parents during both and summer and *Kharif* of 2022-23 and depicted in Table 2.

The heritability in narrow sense was observed moderate for all the characters in both the seasons. The non additive gene action observed for plant height was 2.70 and 30.20% in *summer* and *kharif* seasons respectively. As for number of branches per plant it was 11.64% in *summer* and 30.80% in the *kharif* season. The heritability for the number of nodes

per plant was 14.00% in summer and 10.00% in *kharif* and for inter-nodal length, it was 23.00% in summer and 13.00% in *kharif*. Heritability for days to 50% flowering in summer (2.50%) and *kharif* (7.20%) and the days required for first harvest was 23.50 and 5.20% in summer and *kharif* seasons respectively.

In respect of first fruiting node, heritability was 37.60% in summer and 37.00% in *kharif*. The heritability for number of fruits per plant was 13.40% in summer and 6.80% *kharif*. The heritability was observed for average weight of fruit was 29.10% in summer and 23.20% in *kharif*, for fruit length in summer (13.40%) and in *kharif* (4.90%), for fruit diameter it was 12.00% in summer and 13.90% in *kharif*,

heritability for the duration of harvest in summer was 7.40 and 11.40% in *kharif*. In respect of yield per plot and yield per hector it was 13.50% in summer and 4.60% in *kharif*.

The result indicated that moderate to low heritability, so that it is suggested that the inheritance of character is governed by non - additive gene action except first fruiting node. Here in current study results also evident that low heritability which means the high influence of environment on it. Similar results found by Khanorkar and Kathiria (2010) [17], Rai *et al.* (2011) [18], El-Gendy *et al.* (2012) [5], Akotkar *et al.* (2014) [1], Hamada *et al.* (2015) [19], Annapurna and Singh (2018) [2], El-Sherbeny *et al.* (2018) [7], Mundhe *et al.* (2023) [20].

Table 2: Estimation of genetic variance component and heritability for different characters in 10x10 half diallel Okra

Sr. No.	Source	Plant height (cm)		Number of Branch/Plant		Number of Nodes/Plants		Inter-nodal Length		Days to 50% flowering	
		Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif
1.	σ^2 GCA	3.395	27.233	0.005	0.024	1.291	0.394	0.05	0.027	0.016	0.032
2.	σ^2 SCA	221.376	105.134	0.057	0.089	9.967	4.797	0.261	0.174	1.125	1.544
3.	σ^2 A	6.791	54.466	0.009	0.049	2.583	0.788	0.10	0.053	0.033	0.064
4.	σ^2 D	221.376	105.134	0.057	0.089	9.967	4.797	0.261	0.174	1.125	1.544
5.	h^2 (ns)%	2.70	30.20	11.64	30.80	14.00	10.00	23.00	13.00	2.50	7.20
6.	σ^2 GCA/ σ^2 SCA	0.01	0.02	0.87	0.26	0.12	0.082	0.19	0.15	0.014	0.020
7.	A: D	0.03	0.51	0.15	0.55	0.25	0.16	0.38	0.30	0.029	0.041

Table 2: Continued

Sr. No.	Source	Days required to 1 st harvest		1 st fruiting node		Number of fruits/plant		Average fruit wt. (g)		Fruit length (cm)	
		Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif
1.	σ^2 GCA	0.449	0.103	0.016	0.016	0.905	0.246	0.066	0.03	0.028	0.006
2.	σ^2 SCA	2.292	2.052	0.022	0.024	7.809	4.242	0.199	0.087	0.338	0.134
3.	σ^2 A	0.897	0.207	0.033	0.031	1.81	0.491	0.132	0.06	0.055	0.012
4.	σ^2 D	2.292	2.052	0.022	0.024	7.809	4.242	0.199	0.087	0.338	0.134
5.	h^2 (ns)%	23.50	5.20	37.60	37.00	13.40	6.80	29.10	23.20	13.40	4.90
6.	σ^2 GCA/ σ^2 SCA	0.195	0.050	0.727	0.66	0.11	0.057	0.33	0.34	0.08	0.044
7.	A: D	0.391	0.100	1.50	1.29	0.23	0.115	0.66	0.68	0.16	0.089

Table 2: Continued

Sr. No.	Source	Fruit diameter (cm)		Duration of harvest		Yield/plot (kg)		Yield/ha (q)		Incidence of fruit borer (%)		Incidence of powdery mildew (%)
		Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Kharif
1.	σ^2 GCA	0.001	0.001	0.267	0.651	0.046	0.006	35.524	4.68	0.743	0.501	2.828
2.	σ^2 SCA	0.004	0.007	6.352	9.717	0.451	0.209	347.765	161.578	3.531	3.476	25.175
3.	σ^2 A	0.001	0.001	0.535	1.303	0.092	0.012	71.048	9.361	1.487	1.002	5.657
4.	σ^2 D	0.004	0.007	6.352	9.717	0.451	0.209	347.765	161.578	3.531	3.476	25.175
5.	h^2 (ns)%	12.00	13.90	7.40	11.40	13.50	4.60	13.40	4.60	28.50	21.00	13.90
6.	σ^2 GCA/ σ^2 SCA	0.00	0.142	0.042	0.066	0.101	0.028	0.102	0.028	0.21	0.14	0.110
7.	A: D	0.25	0.142	0.084	0.134	0.20	0.057	0.20	0.057	0.42	0.28	0.22

Conclusion

The all characters studied displayed heritability were low in narrow sense, it showed that there is preponderance of non-additive (dominance) gene action. most of the characters like earliness, yield attributing characters shown medium narrow sense heritability in both the seasons. So due to the non-additive gene action character are improved by heterosis breeding or recurrent selection.

Conflict of interest: All authors declare that there is no any conflict of interest.

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