

## Research Article

# Comparison of north carolina designs for the study of genetic variances in okra (*Abelmoschus esculentus* (L.) Moench)

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### Abstract

The progenies developed through North Carolina Designs (NCD I, II and III) in  $F_2$  populations of okra viz., HRB-55 x Kamini (cross 1) and BO-13 x Parbhani Kranti (cross 2) were used to study the genetic variances. The results indicated that none of the additive variances was found significant in NCD I in both the crosses. Additive gene action was observed for plant height, number of nodes/plant, inter-nodal length, fruit length, number of fruits/plant and average fruit weight in NCD II for both the crosses, and fruit length and average fruit weight for cross 1 in NCD III. None of the dominance variances was significant in NCD I and NCD III in both the crosses. Dominance gene action was important for fruit girth in both the crosses, for fruit yield in cross 1 and for fruit length in cross 2 in NCD II. Considering the significance, signs and SE of genetic variances, NCD II was found to be the most reliable matting design for the study of genetic variances among NC Designs.

### Key words

NCD I, NCD II, NCD III and Okra

### Introduction

Among experimental designs proposed for estimation of genetic variances, North Carolina mating designs are commonly used for characterizing genetic parameters in improvement of cross pollinated crops. Limited critical information regarding the comparison of the estimates of genetical parameters from various designs is available. Similarly, the work on comparison of mating designs from reliability point of view based on field experiments is scanty in okra. Therefore, the present study on comparison of NC designs was planned to select proper design for the study of genetic variance in okra.

### Materials and methods

The  $F_2$  population of two crosses of okra viz., HRB-55 x Kamini (cross1) and BO-13 x Parbhani Kranti (cross 2) were raised at Vegetable Research Station, Junagadh Agricultural University, Junagadh during the *kharif* season. The progenies of two  $F_2$  populations of the above crosses were utilized for generating the experimental materials for NCD I, II and III during summer season. For NCD I,  $F_2$  plants were selected at random as male and female. Each male was mated to five different randomly selected plants as females. Thus, 25 crosses were obtained for each population. From each  $F_2$  base population five plants each as male and female were selected at random and were mated in all possible combinations. Thus, 25 crosses were made in each base population and were evaluated in NCD II. The experimental material for NCD III was generated using the parents of each base population i.e. HRB-55 and Kamini for cross 1 and BO-13 and Parbhani Kranti

for cross 2 as females and were crossed with five randomly selected plants as male from their respective  $F_2$ . Thus, 10 crosses were made from each base population and were evaluated in NCD III. The experimental progenies developed in NCD I, II and III were evaluated in a compact family block design with two replications for NCD I & II and three replications for NCD III. Each entry was sown in a single row having 20 plants, with a spacing of 60 x 30 cm. Thus, the plot size was 6.0 x 0.6 m. All the recommended agronomic practices were followed to raise the good crop.

The observations were recorded for days to flowering, number of nodes per plant, internodal length (cm), plant height (cm), fruit length (cm), fruit girth (cm), number of fruits per plant, yield per plant (g) and average fruit weight (g) from 10 randomly selected plants from each progeny. The estimates of additive and dominance variances (Comstock and Robinson, 1948, 1952) and the standard error for variance components were estimated (Moll *et al.*, 1960 and Anderson and Bancroft, 1952).

### Results and discussion

**Additive genetic variances:** The results of additive variances for different characters (Table 1) under study were non-significant in both the crosses in NCD I. This was due to higher amount of standard errors in all characters. For plant height and intermodal length additive variances were significant in both the crosses in NCD II and III, while they were significant in case of number of nodes per plant, fruit length, number of fruits per plant and average fruit weight in NCD II in both the crosses. In NCD III they were significant for

fruit length, number of fruits per plant and average fruit weight in cross 1 only. For yield character in none of the design additive gene action was observed.

**Dominance genetic variances:** All the dominance variances for different characters (Table 2) were found non-significant in both the crosses in NCD I. Positive significant variances were observed in yield (cross 1), fruit girth (cross 1 and 2) and fruit length (cross 2) in NCD II. Certain variances in NCD III were found significant but they were negative which are due to higher error component and hence are not to be interpreted. Thus component characters like fruit length and fruit girth were found to be governed by dominance gene action.

Negative non-significant variances were also reported by Pushpendra and Ram (1987), Kaur and Thakur (2007) while, positive and significant variance was reported by Chandra *et al.* (2004). Variances with higher SE [Bain *et al.*, (1982), Yunus and Paroda (1983), Reddy and Agrawal (1992a, 1992b) and Patel (2010)] were also observed by several workers in different crops as observed in present study.

**Reliability of mating designs:** The reliability of a mating design depends upon its efficiency to provide unbiased estimates with lower standard error. However, there is no standard procedure for such comparison. Therefore, an attempt was made to find out reliable design considering significance, signs and standard error of both genetic variance components. Both the variances were grouped according to their significance, signs and their standard error and results are given in tables 3 to 6. The distribution of variances according to their significance indicated that none of the additive variance was found significant in NCD I (Table 3). The highest percentage of significant additive variances was observed in NCD II and III (66.67 %). The Chi-square test applied to test the independence of the significance with the mating designs was found significant indicating dependence of the mating design in turning out the additive variance to be significant. The distribution for the dominance variances (Table 3) indicated that the highest per cent (100 %) of significant dominance variances were observed in NCD II followed by NCD III (55.56 %). The test of independence between the designs and the significance of variances indicated that the significance of dominance variance component is not independent of the mating design. The frequencies of both the variances together indicated that the highest percentage of significant variances was observed in NCD II (83.33 %) followed by NCD III (61.11 %). The test of independence indicated that the significance of both types of variances were dependent on mating

designs. Thus, taking both kind of variances into consideration, the NCD II seems to be better for the study of genetic variances. The variances which were classified according to their signs (positive and negative) and presented in table 4 indicated that 83.33 % additive variances were positive in case of NCD I followed by NCD II (66.67 %) and NCD III (55.56 %). The Chi-square test indicated that the signs are independent on mating designs for additive variances. The highest percentage of positive dominance variances were observed in NCD I (61.11 %) followed by NCD III (27.78 %). The test of independence suggested that the signs of dominance variances were dependent on mating designs. The combined results for both types of variances suggested that NCD I (72.22) is better to have higher positive variances followed by NCD II (41.44) and NCD III (41.67). The value of chi-square indicated that the mating designs and signs of combined variances together are dependent. In the distribution of variances according to the magnitude of their standard error ( $SE < \hat{\sigma}^2$  and  $SE > \hat{\sigma}^2$ ) it was observed that in NCD II, 66.67 % additive variances and 22.22 % dominance variances had standard error lower than their estimated variance components (Table 5) followed by NCD III. In NCD I, none of the additive and dominance variances were having SE less than their estimated variance components. The test of independence indicated that the magnitude of standard error of additive variances was dependent while dominance variances were independent on mating designs. The combined results based on standard error for both the type of variances indicated that in NCD II (44.44 %) ranked first to have lesser SE of estimates followed by NCD III (22.22 %). The estimates of standard errors of both the variances were dependent on mating design.

Thus, the overall results of these frequencies distribution suggested that NCD II had maximum variances with SE lower than their estimated variances. So, statistically NCD II can be considered as most comprehensive for such studies. The designs which give maximum significant positive variances with lower standard error can be considered as comparatively better. To have a weighted effect of all these criteria, a score value of 4 for significant and positive, 3 for non-significant, positive and SE less than  $\hat{\sigma}^2$ , 2 for non-significant, positive and SE greater than  $\hat{\sigma}^2$  and 1 for non-significant and negative variances were given and weighted score was calculated (Table 6). More or less similar score values were observed in both the crosses ( $C_1$  and  $C_2$ ) in NC designs with respect to both the variances. The highest total score was observed in NCD II with respect to additive and dominance variances among all the three NCDs. On the basis of the combined scores NCD II (45.00) ranked first

followed by NCD III (34.00) and NCD I (31.00). Similar findings were also reported by Singh *et al.* (1986) and Sentz (1971).

Thus, overall results suggested that statistical point of view NCD II is comparatively better mating design for the estimation of genetic variances among all the NC Designs in okra as well as additive and dominance genetic variation.

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**Table 1.** Estimates of additive variance ( $\hat{\sigma}_A^2$ ) with their SE for different traits in Okra.

S. No.	Source		Yield / plant (g)	Plant height (cm)	No. of nodes / plant	Internodal length (cm)	Fruit length (cm)	Fruit girth (cm)	No. of fruits /plant	Ave. fruit weight (g)	Days to flowering
<b>Cross 1 (HRB-55 x Kamini)</b>											
1	NCD I	$\hat{\sigma}_A^2$	126.35	8.92	1.32	0.40	1.61	0.02	2.13	0.73	-0.73
		SE	1215.75	156.85	9.49	2.75	16.88	0.19	20.47	6.76	12.62
2	NCD II	$\hat{\sigma}_A^2$	0.00	32.54*	1.40*	0.25*	0.71*	0.00	2.30*	1.25*	0.00
		SE	3.19	6.87	0.23	0.06	0.17	0.01	0.65	0.31	0.05
3	NCD III	$\hat{\sigma}_A^2$	-12.78*	135.41*	-0.15	0.54*	0.15*	-0.01	0.57*	1.14*	-1.07*
		SE	2.25	2.10	0.24	0.01	0.02	0.01	0.06	0.07	0.19
<b>Cross 2 (BO-13 x Parbhani Kranti)</b>											
1	NCD I	$\hat{\sigma}_A^2$	-60.94	13.22	0.50	0.18	0.09	0.01	0.96	0.53	-0.05
		SE	327.22	130.00	4.06	1.69	9.91	0.15	20.36	10.07	14.30
2	NCD II	$\hat{\sigma}_A^2$	0.00	26.32*	0.47*	0.15*	0.19*	0.00	3.64*	2.18*	0.00
		SE	2.86	5.58	0.09	0.03	0.04	0.01	0.56	0.34	0.07
3	NCD III	$\hat{\sigma}_A^2$	-1.88	129.59*	-0.18*	0.07*	0.01	0.01	0.06	-0.16*	-1.34*
		SE	7.62	6.70	0.03	0.03	0.03	0.01	0.06	0.07	0.09

 \* Significant at  $P < 0.05$

**Table 2. Estimates of dominance variance ( $\hat{\sigma}_D^2$ ) with their SE for different traits in okra**

S. No	Source		Yield / plant (g)	Plant height (cm)	No. of nodes /plant	Internodal length (cm)	Fruit length (cm)	Fruit girth (cm)	No. of fruits /plant	Ave. fruit weight (g)	Days to flowering
<b>Cross 1 ( RB-55 x Kamini)</b>											
1	NCD I	$\hat{\sigma}_D^2$	125.60	-18.95	-3.05	-0.50	2.45	-0.01	2.12	-0.04	8.98
		SE	1761.52	395.74	13.98	3.31	25.87	0.32	29.56	10.12	41.29
2	NCD II	$\hat{\sigma}_D^2$	45.35*	-28.80*	-1.15*	-0.36*	-0.09*	0.12*	-0.61*	-0.61*	-0.74*
		SE	8.69	3.09	0.17	0.04	0.04	0.02	0.02	0.11	0.20
3	NCD III	$\hat{\sigma}_D^2$	2.50	-11.38*	-8.24*	-0.16*	-0.01	-0.02*	-0.06*	-0.14*	0.34
		SE	5.60	4.12	0.52	0.03	0.05	0.01	0.02	0.06	0.37
<b>Cross 2 (BO-13 x Parbhani Kranti)</b>											
1	NCD I	$\hat{\sigma}_D^2$	415.49	11.98	-1.66	-0.29	3.24	0.01	4.87	0.71	7.28
		SE	1445.40	193.21	7.82	2.89	26.27	0.31	43.98	22.90	38.09
2	NCD II	$\hat{\sigma}_D^2$	-12.44*	-17.76*	-0.47*	-0.52*	0.11*	0.05*	-2.62*	-0.53*	-0.96*
		SE	6.06	3.69	0.09	0.05	0.04	0.01	0.27	0.19	0.13
3	NCD III	$\hat{\sigma}_D^2$	4.24	-14.14	0.04	-0.15*	-0.10*	-0.01	-0.36*	-0.25*	0.56
		SE	7.01	7.27	0.06	0.05	0.04	0.01	0.06	0.05	0.40

\* Significant at P=<0.05

**Table 3. Frequency distribution of variances according to their significance in different NC designs**

Particular	NC design			Chi square value
	I	II	III	
<b>Additive variance</b>				
Significant	00	12	12	21.6*
Non-significant	18	06	06	
% of significant	0.0	66.67	66.67	
<b>Dominance variance</b>				
Significant	00	18	10	36.19*
Non-significant	18	0	08	
% of significant	0.0	100	55.56	
<b>Combined</b>				
Significant	00	30	22	53.70*
Non-significant	36	06	14	
% of significant	0.0	83.33	61.11	

\* Significant at  $P = < 0.05$ **Table 4. Frequency distribution of variances according to their signs of variances in different NC designs**

Particular	NC design			Chi square value
	I	II	III	
<b>Additive variance</b>				
Positive	15	12	10	3.26
Negative	03	06	08	
% of positive signs	83.33	66.67	55.56	
<b>Dominance variance</b>				
Positive	11	04	05	6.82*
Negative	07	14	13	
% of positive signs	61.11	22.22	27.78	
<b>Combined</b>				
Positive	26	16	15	8.25*
Negative	10	20	21	
% of positive signs	72.22	44.44	41.67	

\* Significant at  $P = < 0.05$

**Table 5. Frequency distribution of variances according to their standard error in different NC designs**

Particular	NC design			Chi square value
	I	II	III	
<b>Additive variance</b>				
SE less than $\hat{\sigma}^2_A$	00	12	07	17.70*
SE greater than $\hat{\sigma}^2_A$	18	06	11	
% of $\hat{\sigma}^2_A$ with $SE < \hat{\sigma}^2_A$	0.0	66.67	38.89	
<b>Dominance variance</b>				
SE less than $\hat{\sigma}^2_D$	00	04	01	5.73
SE greater than $\hat{\sigma}^2_D$	18	14	17	
% of $\hat{\sigma}^2_D$ with $SE < \hat{\sigma}^2_D$	0.0	22.22	5.56	
<b>Combined</b>				
SE less than $\hat{\sigma}^2_D$	00	16	08	20.57*
SE greater than $\hat{\sigma}^2_D$	36	20	28	
% of $\hat{\sigma}^2_D$ with $SE < \hat{\sigma}^2_D$	0.0	44.44	22.22	

\* Significant at  $P = < 0.05$

**Table 6. Weighted scores of variance components for different NC designs**

Design	$\hat{\sigma}^2_A$			$\hat{\sigma}^2_D$			Total ( $\hat{\sigma}^2_A + \hat{\sigma}^2_D$ )
	C1	C2	Average	C1	C2	Average	
NCD I	17	16	16.50	13	16	14.50	31.00
NCD II	30	30	30.00	15	15	15.00	45.00
NCD III	24	20	22.00	11	13	12.00	34.00