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EFFECTIVENESS OF SIBMATING IN WHEAT BREEDING

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ABSTRACT

The effectiveness of sibmating was compared with conventional selfing in two intervarietal crosses, WH 416 x UNC 1 and HSW 147 x Kalyan Sona of breadwheat. Sibmating proved to be more effective in improving the mean performance for most of the characters studied in both the crosses. The lower limit of the range in sibs also improved in desired direction for most characters. Sibs population maintained sufficiently high genetic variation for most of the characters in HSW 147 x Kalyan Sona but the reverse trend was observed in WH 416 x UNC 1. Sibs also exhibited improvement in the heritability estimates and genetic advance for some of the characters.

Key words: Breadwheat, sibmating.

The conventional pedigree method of selection has been the most commonly used breeding procedure in wheat and has been quite successful in evolving a large number of improved varieties throughout the world. However, it is difficult to get the rare recombinants in the material handled by this method because of rapid fixation of linkage blocks. In order to achieve maximum gene recombination and maximum fitness in self-pollinated crops, Palmer [1] and Andrus [2] suggested sibmatings in early generations and recognized the chances of getting better segregants after sibcrossing. The present study aims to assess the genetic variability generated through sibmating approach in wheat.

MATERIALS AND METHODS

Large F_2 populations (about 3000 plants) of two crosses, namely, WH 416 x UNC 1 and HSW 147 x Kalyan Sona, were raised to exercise visual selection. Total of 300 plants were selected in each F_2 population of the two crosses and data recorded for grain yield per plant. The best 10% plants were selected for grain yield and raised in F_3 progeny rows, where five

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plants randomly selected from each progeny and sibmated as well as selfed. The parents of each cross were mated to have the F_1 seed. The F_1 generation of the two crosses was raised at Wellington (Tamil Nadu) for generation advancement. The 150 sibs and their selfed progenies, original F_2 and the parents of the two crosses were evaluated in randomized block design with three replications. Each plot was 3 m long with row-to-row distance 30 cm and plant-to-plant distance 10 cm. The observations were recorded on five random competitive plants per row in each replication for six quantitative traits. The populations were compared on the basis of mean, range, genotypic and phenotypic coefficients of variation (GCV and PCV), heritability ($\hat{h}^2$) and genetic advance (GA) for each character calculated by the standard statistical procedures.

RESULTS AND DISCUSSION

A comparison of mean values of different characters in the sibs, F_2 and F_4 populations of the two crosses (Table 1) revealed that all the character means in the sib-populations were significantly superior than in F_2 and F_4 base populations. Superior mean performance of sibs than F_2 and F_4 appeared to be due to a consequence of greater genetic variability by breakage of undesirable linkages which otherwise conceal the genetic variation in the small size F_2 population [3, 4]. Nonrandomness in crossing of the segregates, which was

Table 1. Comparative mean performance and range of characters in different populations derived from two crosses of wheat

Population	Cross	Tillers per plant	Grains per ear	1000-grain weight	Grain yield per plant	Biological yield/plant	Harvest index (%)
Sibs	WH 416 x UNC 1	10.9 ± 0.7^{a}	56.1 ± 1.9^{a}	43.6 ± 1.0^{a}	20.2 ± 1.4^{a}	53.3 ± 2.6^{a}	30.8 ± 1.8^{a}
		(5.4–15.6)	(40.8–74.6)	(37.8–50.3)	(11.0–33.8)	(27.6–90.0)	(31.6–45.1)
	HSW 147 x Kalyan Sona	9.2 ± 0.8^{a}	59.9 ± 2.9^{a}	46.0 ± 1.1^{a}	19.9 ± 2.3^{a}	48.6 ± 3.7^{a}	40.7 ± 1.4^{a}
		(4.2–19.6)	(38.2–80.6)	(38.4–49.9)	(8.6–39.9)	(20.0–95.0)	(31.9–49.6)
F_2	WH 416 x UNC 1	7.1 ± 1.3^{c}	54.5 ± 4.9^{c}	41.8 ± 1.4^{c}	11.0 ± 1.3^{c}	30.0 ± 3.4^{c}	36.2 ± 1.4^{c}
		(2.0–23.0)	(23.9–121.0)	(22.2–63.9)	(4.1–32.8)	(11.5–84.5)	(28.1–48.0)
	HSW 147 x Kalyan Sona	7.8 ± 1.2^{c}	49.1 ± 3.7^{c}	43.6 ± 1.2^{c}	11.5 ± 1.6^{c}	32.3 ± 4.0^{c}	35.6 ± 1.3^{b}
		(3.0–22.0)	(23.0–102.0)	(28.1–59.7)	(4.0–40.5)	(11.0–113.0)	(28.9–46.3)
F_4	WH 416 x UNC 1	8.9 ± 1.1^{b}	46.1 ± 2.1^{b}	41.6 ± 1.5^{bc}	11.6 ± 1.7^{bc}	33.2 ± 1.8^{b}	34.9 ± 1.4^{b}
		(4.4–19.8)	(27.4–74.0)	(29.1–49.2)	(4.7–24.5)	(13.6–71.0)	(28.0–49.1)
	HSW 147 x Kalyan Sona	8.2 ± 0.5^{b}	46.8 ± 2.4^{b}	44.5 ± 1.8^{bc}	12.3 ± 0.9^{bc}	30.9 ± 2.3^{b}	39.7 ± 0.7^{a}
		(4.2–16.2)	(27.1–64.4)	(24.2–47.7)	(5.3–20.9)	(13.6–51.0)	(29.7–49.9)

a–c—Character means of different populations followed by the same letter not significantly different at 0.05 probability level by Z test.

unavoidable for characters like tillers per plant due to required synchrony in flowering time, would also contribute towards better mean values of sib populations. The sibs invariably exhibited a narrower range of values for almost all the traits studied. However, the shorter range in the sibs was accompanied by shift in desired direction for almost all the characters studied.

A comparison of PCV and GCV in the sibs, F_2 and F_4 populations for six traits in the two wheat crosses (Table 2) indicated that the estimates of PCV were generally higher than GCV for all the characters. This may be due to the involvement of high environmental and genotype x environment interactions effects in character expression. The estimates of GCV were relatively higher in the F_4 population than in the sibs in the WH 416 x UNC 1 for all the characters except 1000-grain weight and harvest index. This indicated the predominance of coupling phase linkages for these characters in the parents. Sibmating might have broken such linkages and consequently, resulted into the lower variability. But in HSW 147 x Kalyan Sona, the reverse trend was observed, i.e. the proportion of desired variation for yield and some of its component traits was most pronounced in the sibmated population than in F_4 population, indicating more chances of isolating better segregate from the population. This enhanced variability in the sib populations could be attributed to the accumulation of

Table 2. Phenotypic and genotypic coefficients of variation (PCV, GCV) in different populations derived from two crosses of wheat

Population	Cross	CV	Tillers per plant	Grains per ear	1000-grain weight	Grain yield per plant	Bio-logical yield per plant	Harvest index
Sibs	WH 416 x UNC 1	GCV	12.2	7.0	5.3	16.4	15.1	7.6
		PCV	13.8	7.8	5.8	17.9	15.9	8.0
	HSW 147 x Kalyan Sona	GCV	17.6	9.9	4.3	21.3	22.3	5.4
		PCV	19.8	10.9	4.9	24.3	23.6	6.4
F_2	WH 416 x UNC 1	GCV	50.5	32.7	13.4	42.5	38.9	10.4
		PCV	59.4	36.1	14.7	47.2	43.5	12.4
	HSW 147 x Kalyan Sona	GCV	46.4	25.3	12.1	47.5	45.4	10.7
		PCV	53.9	28.5	13.1	53.2	50.3	12.5
F_4	WH 416 x UNC 1	GCV	17.6	7.9	5.1	24.1	26.3	6.9
		PCV	22.2	9.1	6.3	28.4	26.8	8.0
	HSW 147 x Kalyan Sona	GCV	12.9	8.8	7.6	15.4	14.1	5.5
		PCV	14.5	10.2	8.6	16.9	15.9	5.8

favourable genes of low frequency otherwise spread over the population [5]. The superior performance of sibs in respect of genetic variation over F4 selfed progenies was also expected from the release of hidden variability by breaking undesirable linkages and even some role of dominance component towards increase in the variance of the sibmated progenies. Sibmating in second segregating generation have broken such repulsion phase linkages in HSW 147 x Kalyan Sona and resulted into concentration of favourable genes in the segregants.

The estimates of heritability in broadsense for all the characters in both the crosses (Table 3) revealed that sibs population had either higher or equal estimates of heritability as compared to F_2 and F_4 base populations for most of the characters in both crosses. Higher heritability estimates in case of BIPs as compared to selfed progenies were also reported earlier [5] for some of the characters in the populations generated through intermating in segregating generations. The estimates of genetic advance for six characters in both the crosses (Table 3) showed that sibs and F_4 population had less genetic advance than the F_2 base population. However, sib populations had either greater or comparable genetic advance for most of the characters studied in both crosses as compared to F_4 population. In sibmated population higher magnitude of heritability was not accompanied

Table 3. Heritability ($\hat{h}^2$) and genetic advance (GA) in different populations derived from two crosses of wheat

Population	Cross	Parameter	Tillers per plant	Grains per ear	1000-grain weight	Grain yield per plant	Biological yield per plant	Harvest index
Sibs	WH 416 x UNC 1	$\hat{h}^2$	77.9	80.7	84.0	83.9	90.2	89.0
		GA	2.4	7.3	4.4	6.3	15.7	5.6
	HSW 147 x Kalyan Sona	$\hat{h}^2$	78.8	80.6	75.4	77.3	89.3	71.9
		GA	2.9	10.9	3.5	7.7	21.1	3.9
F_2	WH 416 x UNC 1	$\hat{h}^2$	72.0	81.8	83.5	81.0	79.7	70.3
		GA	6.3	33.2	10.6	8.7	21.5	6.5
	HSW 147 x Kalyan Sona	$\hat{h}^2$	74.8	78.8	86.2	79.9	81.3	73.5
		GA	6.4	22.7	10.1	10.1	27.3	6.8
F_4	WH 416 x UNC 1	$\hat{h}^2$	63.3	74.3	65.9	72.2	95.7	75.3
		GA	2.6	6.4	3.6	4.9	17.6	4.3
	HSW 147 x Kalyan Sona	$\hat{h}^2$	78.9	74.8	76.5	82.4	78.0	88.3
		GA	1.9	7.3	6.1	3.5	7.9	4.2

by high genetic advance for all the characters. This inconsistency may be attributed to low magnitude of phenotypic standard deviation which was an important component of genetic advance [6].

Hence the present study shows that sibmating approach can substantially supplement the conventional wheat breeding procedure by way of improving the mean performance and creating more desirable genetic variability because of the accumulation of favourable genes in the wheat populations, and thus improving the efficiency of selection.

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