EFFECTS OF RECURRENT SELECTION IN TWO SORGHUM POPULATIONS

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CERTIFICATE

This is to certify that the thesis entitled 'Effects of recurrent selection in two sorghum populations' submitted in partial fulfilment of the requirements for the degree of Master of Science in Agriculture of the Andhra Pradesh Agricultural University, Hyderabad, is a record of the bonafide research work carried out by Mr. Prasit Jaisil under my guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee.

No part of the thesis has been submitted for any other degree of diploma or has been published. Published part has been fully acknowledged. All the assistance and help received during the course of the investigations have been fully acknowledged by him.

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INTRODUCTION

The development of quantitative genetic theories and their successful application in the cross-pollinated crops, particularly in maize, have drawn the attention of breeders in the self-pollinated crops to use population improvement procedures with several modifications, in recent years.

Gilmore (1964), Eberhart (1970 and 1972), Doggett and Eberhart (1968), Doggett (1968 and 1972) and Gardner (1972) have clearly demonstrated the need and application of population improvement methods for sorghum in utilizing the vast variability available in its germplasm for the development of improved cultivars and parents for hybrids.

In sorghum, random mating populations were first developed by using cytoplasmic male-sterility. The availability of the genetic male-steriles, particularly the ms_3 and ms_7 traits, which are stable over environments, further helped in the development of new random mating populations.

A systematically designed recurrent selection program should be a useful way to maintain the genetic diversity in populations while improving their overall performance. The importance of a population program in providing useful basic breeding stocks simultaneously to a number of national programs is being increasingly realized. This is particularly true where national program have conventional breeding systems that have been successful in the development of improve varieties and hybrids.

In addition to this back-up support, the improved populations, particularly after a few cycles of recurrent selection, are likely to contribute improved varieties (from intra-population improvement selection) and hybrid parents from complementary population pairs (inter-population improvement). Population improvement promises to be an important breeding system in handling several traits together in an interdisciplinary crop improvement program.

The population improvement program at ICRISAT was initiated with an introduction of a large number of populations from different parts of the world and then, following evaluation, synthesized into new populations based on geographic origin and restoration behaviour to cytoplasmic-male sterility. Initially, S_1 progeny recurrent selection was practiced to improve the population but later on the method was changed to S_2 progeny testing. Three cycles of recurrent selection have been completed in five ICRISAT populations.

Periodic assessment of the progress from recurrent selection is an important step in a population improvement program to understand the nature of changes that have occurred in the populations and to decide the future course of program.

The US/R and US/B populations, which were in the most advanced stages of selection, were chosen for this study. The objectives of the present investigation are as follows:

(1) To study the shift in the mean performance of yield and contributing factors and other associated traits from the original population to that in the third cycle of selection.

(2) To assess the effect of selection on the variability of characters.

(3) Based on the above two measurements to recommend changes in selection methods for these populations and

(4) To contribute to information developing on the usefulness of recurrent selection in sorghum.

REVIEW OF LITERATURE

Recurrent Selection

Recurrent selection in its broadest sense, is any cyclical scheme of plant selection and recombination by which frequencies of favourable genes are increased in plant populations (Hallauer, 1980). Some form of recurrent selection has always been used in plant improvement, but the methods of selection were not always conducted in a systematic manner. Recurrent selection methods were developed primarily for the improvement of traits that are inherited in a quantitative manner. It was realized that different methodologies were needed for the improvement of quantitative traits than those developed for qualitative traits. Traits inherited in a quantitative manner involve a large number of genes, each with a small effect, and genotypes that cannot be classified into discrete classes. Quantitative traits involve some measurement, and statistical parameters (means, variances, and covariances) are used to determine the effects of selection. Direct knowledge of gene or genotypic frequencies is not known, but if selection is effective it is a corollary that the gene or genotypic frequencies are changing in the desired direction. The basic premise of recurrent selection methods is to increase the frequency of desirable genes in a systematic manner to enhance the opportunities of extracting superior genotypes. Success of recurrent selection methods is dependent on the original assemblage of genes in the breeding populations. If the gene frequency of the trait under selection is different among populations, response to selection may be realized but at different rates and levels.

Types of Recurrent Selection

Recurrent selection may take many forms, and may be classified in various ways. Allard (1960) recognized four different types distinguished by the way in which plants with desirable attributes are identified. These types are (1) simple recurrent selection, (2) recurrent selection for general combining ability, (3) recurrent selection for specific combining ability, and (4) reciprocal recurrent selection.

Simple recurrent selection was described by Sprague and Brimhall (1950), who studied oil content in the corn kernel. In simple recurrent selection, plants are divided into a group to be discarded and a group to be propagated further on the basis of phenotypic scores taken on individual plants or their selfed progeny. Since test crosses are not made, the effective use of simple recurrent selection is restricted to characters with sufficiently high heritability for a satisfactory phenotypic evaluation of the character to be made visually or by simple tests. They said it cannot be used with much effectiveness in breeding for improved combining ability for yield or any other quantitative trait.

Recurrent selection for general combining ability developed as an outgrowth from studies of early testing. Early testing, first proposed by Jenkins in 1935, was based on the dual assumptions that there are marked differences in combining ability among plants in open-pollinated populations, the tester used has a broad genetic base, variations in performance in a group of test crosses will be due primarily to differences in general combining ability, and that a selected sample based on tests of combining ability of S_o (or S_1) plants offers promise of yielding a larger proportion of superior lines than a sample drawn from the same population on the basis of visual selection alone.

Recurrent selection for specific combining ability was proposed by Hull in 1945 on the assumption that an important part of heterosis results from the nonlinear interactions of genes at different loci, from interaction between alleles at the same locus, or from both causes in combination. Hull's proposal called for tests to determine whether higher levels of specific combining ability can be achieved by recurrent-selection procedures based on progeny tests with a homozygous tester line.

Reciprocal recurrent selection was proposed in 1949 by Comstock, Robinson and Harvey, as a procedure that would be useful in selecting simultaneously for both general combining ability and for specific combining ability. This type of recurrent selection employs two heterozygous source populations, each of which is the tester for the other.

Penny et al., (1963) divided recurrent selection into two types, phenotypic recurrent selection and genotypic recurrent selection. Phenotypic recurrent selection includes those cases in which the phenotype of the S_o plant is the basis of selection, while genotypic recurrent selection is the genetic worth of the S_o plant as evaluated in some type of progeny test. Progeny evaluation may be done on the basis of selfed-progeny performance or test-cross progeny performance. The test-cross progeny evaluation may be further subdivided on the basis of the degree of heterozygosity or heterogeneity of the tester.

Breeding Systems for Population Improvement

A system was developed by Allard (1960) for use in maize and has the following operational features: (1) Plants from a heterozygous source are self-pollinated and at the same time can be evaluated for some desirable character or characters; (2) Plants with inferior performance for the character or characters under improvement are discarded; (3) The superior plants are propagated from the selfed seed; (4) All possible intercrosses among these superior progenies are made by hand, or, if this is impractical, the intercrosses are made by open-pollination in isolation among the selected progenies; (5) The resulting intercross population serves as source material for the next cycle of selection and intercrossing.

Breeding schemes similar to the above were first suggested in 1919 by Hayes and Garber and independently by East and Jones in 1920. Critical data were not published in either case however, and these suggestions did not lead to use of the method. The first detailed description of this type of breeding scheme was published by Jenkins in 1940 as a result of his experiments with early testing for general combining ability in maize. Later on, Hull (1945) suggested that selection after each of several cycles of intercrossing might be useful in improving specific combining ability.

Several cyclic breeding systems for population and hybrid improvement have been used successfully in maize. They all involve evaluation, selection and recombination but the methods vary greatly in technique used and in length of cycle. Some methods in use are as follows (Gardner, 1972):

1) Intra-population improvement methods such as mass selection half-sib family selection, full-sib family selection and S_1 family selection.

2) Inter-population improvement methods are half-sib reciprocal recurrent selection and full-sib reciprocal recurrent selection.

Mass selection is the easiest of all the methods (Gardner,1972).One or more cycles of selection can be completed each year if the seasons do not differ from each other or there is very little seasonal interaction for the selected trait. The method is very effective for highly heritable characters. In a naturally cross-pollinated crop, open-pollinated plants are selected on the basis of their phenotype and an equal quantity of seed from each selected plant is bulked to form the next cycle of recurrent selection. A system parallel to this was developed in sorghum by Doggett (1968) wherein selection based on male-sterile plants is termed as 'female-choice'. The plants are selected at maturity. On the other hand if selection is based on fertile plants two generations are required per cycle because of an additional season for recombination. Therefore, alternating selfed choice and female choice has been proposed (Doggett, 1968). "In this system selection is done on the basis of open pollinated male-sterile plants in one season and on fertile plants in the following season. In this system generation one is essentially a selection generation and the other recombination as well as selection generation". Mass selection in sorghum was used by Doggett (1972) at Serere. He observed 20% increase in grain yield over three cycles in PRS1 population. Gardner (1961) observed 3.9% linear positive response to selection in the Golden Hays variety of maize.

Full-sib family selection may offer more promise than mass selection for sorghum improvement (Gardner,1972). The plant population density of families being evaluated should be the same as that recommended for sorghum production. Such families are easily formed by crossing selected male-fertile plants on to selected male-sterile ones. Selected families can be recombined using bulked remnant seed and harvesting only male-sterile plants. Moll and Robinson (1966) have had some success with this method in improving maize yields of open pollinated varieties.

Half-sib family selection would not be expected to be as efficient as full-sib family selection, but it is a very easy system to use in sorghum (Gardner,1972).Open-pollinated male-sterile plants tagged at anthesis provided the seed needed for half-sib family testing and selection. Bulked remnant seed of selected families could be used for recombination. Only male-sterile plants produced would be harvested to form the next generation. A half-sib family system obtained with individual plant selection within families has given excellent results in maize. Webel and Lonnquist (1967) showed results obtained from yield tests in each of the first six generations of selection. A gain of 8% per cycle was realized and the system progresses at the rate of a cycle per year.

S_1 family selection appears to be one of the most promising selection schemes in sorghum (Gardner, 1972). Heads of male-fertile plants can easily be bagged to eliminate outcrossing and ensure selfing if this seems necessary, otherwise, male-fertile heads should be tagged at the time of flowering for selection at harvest (unless all male-sterile plants are being tagged). The remnant seed of selected S_1

families can be used for recombination. Only male-sterile plants produced would be harvested to form the next generation. Burton et al. (1971) have increased yield in maize using the S_1 progeny testing procedure.

The S_2 family selection system is a further extension of S_1 family testing. In this, S_2 families (fertile plants from S_1 families) are evaluated in replicated trials. The S_2 family selection requires four generations to complete a cycle. The system is very effective in eliminating undesired genes from the populations (Nath, 1977).

The additive genetic variance among S_2 progenies is one and a half times greater than S_1 progenies. Hence S_2 family selection should be the most effective method of selection, particularly when it is difficult to complete one cycle of S_1 family selection per year (Eberhart, 1972).

Horner et al. (1973) have had good success using S_2 family testing and selection in Florida, however, to compare S_2 selection with S_1 selection, gains must be expressed on an annual gain basis because S_2 testing requires an additional year per cycle. They said for many agronomic traits, S_1 and S_2 family tests do provide more precise evaluations of genotype than do other types of selection, thus greater progress should be possible.

S_2 testing also helps to work with very heterogeneous material, e.g.

height differences, where characters such as these are segregating, it is much easier to select in the S_2 than in the S_1 progenies.

Eberhart (1970) studied factors affecting efficiencies of breeding methods. From statistical genetic studies, he indicated that efficient breeding programs benefit from the improvement of random mating varieties or populations by recurrent selection.

There are several techniques for increasing gain from selection. These are to increase the additive genetic variance, increase the selection intensity, improve plot techniques (Eberhart,1970). The plot techniques can be improved by such things as rotation of fields for trial sites so that the yield trials always follow a uniform crop, use higher rates of fertility to reduce the variability within a replication and use improved machinery to give a more uniform seed bed and more uniform planting depth. Reducing the number of years per cycle with irrigation nurseries is one of the most efficient means of increasing progress.

Many methods of recurrent selection have been proposed (Eberhart, 1970) with varying techniques associated with each method. Statistical genetic parameters estimated from the recurrent selection trials can be used to help the breeder select the most efficient breeding method for a particular set of circumstances. S_1 selection is a very effective method for sorghum and maize when irrigation nurseries permit the breeder to grow three seasons a year. In contrast, full-sib selection is more efficient for maize when the irrigation nursery and the regular growing season permits two seasons per year. Half-sib family selection is more efficient than full-sib selection when irrigation nursery permits the breeder to grow three seasons in two years (Eberhart, 1970). Although mass selection is a very simple method to use, it is relatively inefficient compared to some methods of progeny testing, especially S_1 testing in tropical areas because irrigation nurseries can be used to reduce the number of years per cycle for S_1 testing (Eberhart, 1970). The main reason for this is the great decrease in phenotypic variance of a progeny mean compared to the variance of an individual plant. In most areas, the environmental conditions in the off-season irrigated nurseries are not the same as the regular season, so mass selection can only be done one season per year, For sorghum, the crossing required to produce full-sib family is very laborious and not practical. Hence, S_1 testing offers maximum promise among all methods applicable to sorghum, but only for early maturing populations where three generation can be grown in one year.

Reciprocal recurrent selection (RRS) is designed to improve the performance of the cross of two populations or of the hybrids of lines derived from the two populations. Half-sib RRS as originally proposed by Comstock et al. (1949) is the most promising in sorghum because it gives a better evaluation of males to be selected. A male-fertile plant in one population can be crossed to several male-sterile plants in the opposite population and seed can be bulked to form the half-sib family. The use of full-sib RRS as discussed by Jone *et al.* (1971) and Hallauer and Eberhart(1970) would give a poorer evaluation of males to be selected and it is impossible to maintain the male-sterile genotype and reproduce the hybrid. In maize, full-sib RRS has the advantage of producing new lines and hybrids, which can be selected and utilized directly in a hybrid program, as well as used to form the next generation involved for the inheritance of the traits under selection, and the type of cultivar required for commercial production. Except for mass selection, all recurrent selection methods include three operations (Hallauer, 1980); development of progenies, evaluation of the progenies in replicated trials, and recombination of the superior progenies to synthesize the population in the next cycle of recurrent selection. Several variations are involved in each of the three operations because of the type of progeny structure, extent of progeny evaluation, selection intensity and methods of recombination.

Recurrent Selection in Maize

Different recurrent selection methods were developed in maize as the experimental evidence became available. The first convincing experimental evidence on the effectiveness of simple recurrent selection in changing gene frequencies was presented by Sprague and Brimhall (1950), who studied oil content in the corn kernel. The mean oil percentage was shifted rapidly upwards, being 4.2 in the original population, 4.97 for the 10 foundation ears selected from the original population, 5.2 for the first cycle, and 7.0 for the second cycle.

Penny et al. (1962) evaluated the progress from three cycles of recurrent selections in an open-pollinated maize variety and an F_2 of a maize single-cross, using an inbred line with a narrow gene-base as the tester. They found an increase in grain yield of 7.1% in the open-pollinated variety and 1.6% in the F_2 population after three cycles.

Russel et al. (1973) suggested the use of recurrent selection in maize for both general and specific combining ability. In their study, they realized a gain of 4.4% grain yield per cycle over five cycles of selection and recombination by using an inbred line as the tester parent.

Burton et al. (1971) reported a significant improvement in grain yield and general combining ability after four cycles using half-sib selection and S_1 testing methods in a maize population. They obtained yield increases of 16.3% in the S_1 series and 6.3% in the half-sib series. Using an inbred line as the tester in a recurrent selection program, Sprague et al. (1959) showed 6.7% and 20.0% yield gains after two cycles in two maize populations. Horner et al. (1973) compared three methods of recurrent selection, namely parental population tester, inbred tester, and S_2 progeny method, for grain yield in a maize population. After five cycles, they obtained a significant linear increase in general combining ability with all methods, with a gain of 4.4% for the inbred tester method, 2.4% for the parental tester method, and 2.0% for the S_2 progeny method.

In a comparision of responses to six cycles of full-sib family selections and reciprocal recurrent selections for grainyield in two maize populations, Moll and Stuber (1971) obtained yield gains of 21% and 17% by the full-sib method and 7% by the reciprocal recurrent selection method. Increases in yield of hybrid between varieties from the two populations were 15% and 21% for the full-sib and reciprocal recurrent selection methods, respectively.

Eberhart _et al_. (1973) evaluated the progress from five cycles of reciprocal recurrent selection in two maize populations and reported a yield gain of 4.6% per cycle in the population cross. They also obtained an increase in grain yield of 2.6% per cycle for seven cycles in another maize population which was improved by half-sib selection with a double-cross tester.

Moll and Stuber (1979) found that the accumulated increases in yield in Indian Chief and Jarvis maize populations following eight cycles of reciprocal recurrent selections were 12% for Indian Chief, 20% for Javis, and 26% for the population hybrid.

"Martin and Hallauer (1980) evaluated 7 cycles of reciprocal recurrent selection in BSSS and BSCB1 maize populations. They observed mid-parent heterosis increased from 14.9% for the C_o population cross to 41.7% for the C_7 population cross. The mean yield of the population crosses increased from 58.5 q/ha for the C_o population cross to 70.7 q/ha for the C_7 population cross".

In addition to yield, recurrent selection procedures have been useful in the improvement of other traits of maize. Penny et al. (1967) reported on three cycles of recurrent selection for first-brood European corn borer (Ostrinia nubilalis, Hubner) resistance. Two cycles of selection were sufficient to shift the frequencies of resistance genes to a high level in all varieties. Three cycles produced essentially borer-resistant varieties in their study. Widstrom et al. (1970) obtained significant progress in increasing the level of earworm resistance in maize from five cycles of recurrent selection.

Jenkins et al. (1954) reported on the use of recurrent selection in conjunction with a backcrossing program in an effort to accumulate genes for resistance to Helminthosporium turcicum, leaf blight in maize. Their data indicated that two cycles of selection and recombination of resistant plants were sufficient to obtain a high level of resistance in most of the material studied. Jinahyon and Russell(1969) reported a change in stalk rot (Diplodia zea) rating from 3.7% to 1.7% following three cycles of recurrent selection in the open-pollinated variety, 'Lancaster Surecrop' of maize.

The success of recurrent selection in improving nutritional quality have also been reported. Zuber et al. (1975) presented evidence to indicate that they were able to increase lysine content in some normal dent maize populations to the level of opaque-2 by recurrent selection.

Changes in morphological and physiological traits associated with recurrent selection for grain yield in maize have been reported by Fakorede and Mock (1978). They concluded that the source (i.e., photosynthetic capacity) was not limiting grain yield in BSSS (R) x BSCB1(R) and BS 12. Increased grain yields that resulted from recurrent selection were consequences of longer grain-filling duration for BSSS(R) x BSCB1(R) and increased translocation of photosynthate from source to sink for both BSSS(R) x BSCB1(R) and BS 12.

Recurrent Selection in some Self-Pollinated Species

Recurrent selection techniques have had limited use in self-pollinated crop species because of the technical difficulties of making the necessary intercrosses among selected progenies in each cycle (Hallauer, 1980). Gilmore (1964) outlined breeding procedures for conducting reciprocal recurrent selection in self-pollinated species in which male-sterile plants (either genetic or cytoplasmic) are wind pollinated, such as sorghum, barley, and perhaps wheat; the procedures were developed particularly for those species that have potential for producing hybrids. Compton (1968) discussed how the obstacle of inter-pollinations can be reduced in a recurrent selection program by use of the single seed descent concept. Brim and Stuber (1973) outlined methods for conducting recurrent selection in soybeans that use genetic male sterile genes to facilitate intercrossing.

Studies illustrating the effects of mass selection without recombination were reported by Frey (1967) and Romero and Frey (1966) in oats and by Fehr and Weber (1968) in Soybeans. Frey (1967) conducted mass selection on seed width and measured the indirect effects of mass selection on 100-seed weight in a composite F_2 population by mixing 5 g samples of 250 oat-crosses. Mass selection on seed width increased the mean 100-seed weight 9% over the comparable unselected population. Because of the heritability (35%) of seed width and the relatively high genotypic correlation (r = 0.69) between seed width and seed weight, indirect selection was effective for increasing 100-seed weight. Other correlated effects of mass selection for seed width was later heading dates and taller plants. In the same F_2 composite, Romero and Frey (1966) reduced plant height nearly 2 cm in F_6 by using mass selection and the mass selected populations had earlier heading dates and greater yield than the unselected population. Fehr and Weber (1968) evaluated the response of mass selection on seed size and specific gravity for their effects on protein and oil composition in soybean populations. Response to selection was realized in all instances, but maximum progress for high protein and low oil was obtained by mass selecting for large seed and low specific gravity.

Matzinger _et_ _al_. (1977) conducted mass selection studies in a broad genetic-base tobacco population, that included intercrossing of selected plants between each cycle of selection. Selections were made before flowering and the intermatings were made among selected individuals to provide seed for the next cycle. They reported that plant height decreased by 6.5 cm per cycle and number of leaves increased by one leaf per cycle for the first five cycles of selection.

Brim (1978) and Burton and Brim (1978) have initiated S_1 and half-sib recurrent selection studies in soybean populations. Two populations of soybean were included, (a) population I was derived from a cross of two adapted lines, one high in percent protein and the second high in percent oil, and (b) population II was developed from a backcross of an adapted line to nine plant introductions. Response to selection was determined after six cycles of selection in population I and five cycles in population II. Percent seed protein increased 0.33% and 0.67% per cycle in population I and II, respectively. In population I, six cycles of recurrent selection increased yield by 9%. In population II, there was a 16% gain in yield from C_o to C_3 cycle and the C_3 cycle composite yielded 20% more than the check. Burton and Brim (1978) also reported on the effectiveness of three cycles of recurrent mass and half-sib family selection for increased seed oil content in soybean population. Tests of the composite populations showed that percent seed oil increased linearly from 18.4 to 19.5%

Recurrent Selection in Forages

Recurrent selection methods have been used effectively for the improvement of traits in forages. The first evaluation of recurrent selection in forages was reported by Johnson (1952) and Johnson and Goforth (1953) comparing the response of S_1 progeny and mass selection for the improvement of forage yield in the sweet clover (Melilotus officinalis) variety, 'Madrid'. A rapid advance in forage yield per plant was realized for both methods of selection, two cycles of S_1 progeny selection increased yield 52%, and four cycles of mass selection increased yield 11%.

Devine and Hanson (1973) have shown the effectiveness of selection for plant vigor in conjunction with selection for anthracnose

(*Colletotrichum trifolli* Bain) resistance in alfalfa. Three cycles of recurrent selection for anthracnose resistance in three populations increased the level of resistance from 4.2 for the original parents to 1.7 after selection (Ratings were 1 for highly resistant to 5 for dead plants). More importantly, the stand for the selected populations were 85 to 95% pure stands whereas the parental varieties had 50% alfalfa plants and 50% weeds.

Cyclical selection programs have been applied extensively to forage grasses and legumes and positive responses have been realized in nearly all instances (Hallauer, 1980). Phenotypic recurrent method for most traits, particularly when the parent can be vegetatively propagated for intercrossing. Mass selection for pest resistance (Hanson *et al.*, 1972, for alfalfa), forage dry-matter yield (Burton, 1974 for Pensacola bahiagrass), seed weight (Trupp and Carlson, 1971, for smooth bromegrass, *Bromus inermiss* Leyss.), and specific leaf weight (Topark-Ngram *et al.*, 1977, for reed canarygrass) has been successful in all instances.

Recurrent Selection in Horticultural Crops

Phenotypic recurrent selection has been used effectively in horticultural crops. Andrus and Bohn (1967) practiced mass selection for nine cycles in a heterozygous base population of cantaloups by use of an index representing 16 fruit characters. Mass selection by index resulted in improvement in most of the index-component traits without any apparent loss of genetic variability. Inbreds extracted from the later cycles of mass selection performed better than those immediately following a cross, indicating selection was effective for increasing the favourable-gene frequencies.

Jones et al. (1976) reported on the results following six cycles of mass selection in sweet potato to combine pest resistance with other desirable production and market qualitites. The method of selection seemed successful because the sixth cycle of mass selection had high frequencies of flowering and seed set, acceptable yield, orange flesh, and resistance to pests.

Recurrent Selection in Sorghum

The concept of population improvement can be easily visualized as appropriate to the breeding behaviour of a cross pollinating species, at first it may seem less applicable to sorghum, a primarily self-pollinating species. However, it may be noted that cross-pollination has been an effective means of introgression in cultivated sorghum landraces as evidenced by the variability they contain and that cross pollination does occur in related species of sorghum (Doggett and Majisu, 1968). For sorghum, it is common to employ genetic male-sterility to ensure recombination. There are several available genes for male-sterility (Ross et al. 1971) which operate as single gene recessives independent of the genetic background. He indicated that the best of these are ms_3 and ms_7. Male-sterile plants must be marked at anthesis because they cannot be distinguished from normal male-fertile plants at maturity. Male-steriles are easily recognizable at flowering due to their small lighter coloured anthers and gaping glumes (Andrews, *et al*. 1977).

Progress in the improvement of hybrids is proportional to the improvement in the breeding populations used as the source material for parental lines. Quantitative genetic theory and applied studies have clarified the role that breeding populations have in a modern breeding program. Breeding populations should be synthesized from elite sorghum germplasm, and genetic male-sterility factors, such as al, ms_3 or ms_7 can be used to maintain random mating populations (Eberhart, 1972).

The first random mating sorghum population was produced by O.J. Webster in Nebraska about 1960 initially using cytoplasmic male-sterility but then changing to the use of ms_3 (Andrews *et al*.,1977).They reported subsequently, several populations were developed in East Africa by H. Doggett and D. Jowett, in West Africa by D.J. Andrews, in the U.S.A. by C.O. Gardner, P.T. Nordquist, W.M. Ross, J.D. Axtell and D.L. Oswalt, in Australia by R.W. Downes and at ICRISAT by Bhola Nath and H. Doggett.

Doggett and Jowett (1963 and 1964) used cytoplasmic male-sterility to apply to recurrent selection to sorghum and Gilmore (1964) suggested methods of utilizing both cytoplasmic and genetic male-sterility for this purpose. Webster (1965) did three cycles of recurrent selection in a bulk population using cytoplasmic male-sterility, and he also set up a further bulk population using the Coes genetic male-sterile, ms_3. "Because there is no evidence that over-dominance or over-dominant types of epistasis are important in sorghum, the extra work required to obtain the test cross seed for reciprocal recurrent selection is not justified" (Doggett and Eberhart, 1968).

The quantitative genetics of a random mating grain sorghum population has been studied in NP3R population by Jan-orn et al., (1976). They studied half-sib, full-sib, and S_1 families derived from the NP3R random mating grain sorghum population. They concluded that dominance variance exceeded additive genetic variance for grain yield per plant and per unit area and for kernels per plant, but the reverse was true for other traits. The trend in grain yield following the use of different breeding procedures was full-sib family means $>$ half-sib family means $>$ S_1 family means indicating that heterosis and inbreeding depression are important for this trait. Heterosis was also indicated for plant height and number of kernels per plant. S_1 families tended to exceed full-sib families which in turn tended to exceed half-sib families for additive and non-additive genetic variance.

Heterogeneous half-sib families tended to be most stable over environments, and the S_1 families were least. Heritability estiamtes on an individual plant basis were high for days to flower (0.88) and plant height (0.71), very low for grain yield (0.09), and quite low for heads per plant (0.16) and kernels per plant (0.15). Predicted response from single trait selection was highest for S_1 family selection for most traits, particularly grain yield. Highly heritable traits such as days to flower and plant height, could easily be improved by mass selection. If selection is for yield alone, correlations indicate that the population would become later maturing and taller, therefore, selection procedures must take expected correlated response into account.

Doggett (1972) reported an average increase of 25% in grain yield for four populations after one cycle of S_1 testing. The maximum increase of 33% was observed in PRS1. Eckebil et al. (1977) using 20% selection intensity predicted yield gains of 16.3, 10.2 and 8.7 q/ha per cycle for NP5R, NP3R and NP7R populations, respectively.

At ICRISAT (Andrews et al. 1977), two methods of recurrent selection were considered for improvement of sorghum populations:

- Half-sib family selection, which takes two generations per cycle where gradual improvement under relatively low selection pressure is required, e.g. source populations.

- S_2 testing, which takes four generations per cycle where faster progress is required using higher selection pressures in more advanced populations.

For interpopulation improvement, as yet little progress has been made at ICRISAT because of the complexity of making reciprocal full-sibs, or using the reciprocal inbred tester method, with the superimposed difficulties of maintaining the ms gene frequencies for random mating (Andrews et al.,1977).

Nath (1977) evaluated eight populations of sorghum; RS/R, RS/B. US/R, US/B, Tropical conv., Serere Elite, Fast Lane 'R', and Fast Lane 'B' after two cycles of selection. Six of the eight populations showed positive increases in the mean yield ranging from 21-36%. Only US/R and Fast Lane 'R' populations gave reduced grain yields of 8 and 11%, respectively. The plant height of all the populations was reduced and grain colour improved from brown to white. There was almost no change in maturity.

Obilana and El-Rouby (1980) used recurrent mass selection for improving yield of two random-mating populations of sorghum; B and Y composites. They obtained yield gains of 12.8% and 13.5% cycle, respectively.

MATERIALS AND METHODS

Experimental Materials

Random mating sorghum populations have been developed at ICRISAT. Recurrent selection procedures were used to improve the populations since 1974. Each cycle of selection has been aimed at simultaneous improvement of various traits, namely, grain yield, grain quality and resistance to pests and diseases. No deliberate selection was made for yield components except that bold grains were preferred. Three cycles of selection have been completed.

The populations viz., US/R and US/B were chosen for the present study. The US/R population was constituted by random mating selected early generation lines from Nebraska and Purdue restorer populations $(NP_1 BR+NP_3R+NP_4BR+NP_5R+NP_8R+PP_1R+PP_3R+PP_5R)$. Similarly, the US/B population was synthesized from Nebraska and Purdue non-restorer populations $(NP_2B+NP_6B+PP_2B+PP_6B)$. The first cycle of selection was completed on the basis of S_1 family evaluations and the subsequent two cycles of selection were completed following S_2 family evaluations. Table 1 gives details on number of various progenies evaluated, number of test environments used and number of lines recombined during each recurrent selection cycle. Some additional elite lines from other sources were recombined with the S_2 lines in the third cycle of selection.

An equal quantity of seed of all crosses made on selected lines for recombination at each cycle was bulked and stored for this study.

Table 1: Number of lines evaluated and recombined and number of test environments for progeny evaluation in different cycles of the US/R and the US/B populations

Population	Cycle	No. of progenies evaluated		No. of test environments	No. of lines recombined
US/R	1	S1	-1852	4	104
	2	Half-sib	- 825	-	
		S1	- 433	-	
		S2	- 194	4	38
	3	Half-sib	-1230	-	
		S1	- 473	-	
		S2	- 195	5	$28S_2$+9 elite lines[1]
US/B	1	S1	- 749	4	68
	2	Half-sib	- 700	-	
		S1	- 359	-	
		S2	- 194	4	39
	3	Half-sib	-1165	-	
		S1	- 405	-	
		S2	- 195	5	$33S_2$+5 elite lines[2]

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[1] 1167 intercrosses were made among the lines selected from C_3 for US/R

[2] 1516 intercrosses were made among the lines selected from C_3 for US/B

The material for the present study was the constitution of each of the four populations: C_0 (original population); C_1 (S_1) after one cycle of S_1 testing in C_0; C_2 after one cycle of S_2 testing in C_1 (S_1); and C_3 after 2 cycles of S_2 testing in $C_1(S_1)$. The random mated bulks were grown at Bhavanisagar during 1980 summer. Each bulk consisted of 100 rows each of 4 m length, 50 cm apart with plants spaced 10 cm. Each plot was divided in two equal halves. In one half of each plot male-fertile plants were bagged for selfing and in the other half the male-sterile plants were bagged for making reciprocal crosses between US/R (C_0) x US/B(C_0); US/R(C_1) x US/B(C_1); US/R(C_2) x US/B (C_2); and US/R(C_3) x US/B (C_3). The bulk pollen from male-fertile plants was used for making crosses. The equal seed of reciprocal crosses was mixed. The seed harvested from male-fertile plants produced S_1 progenies. Nearly 100 randomly chosen fertile plants were harvested from each cycle of the two populations. The mixture of equal seeds from 100 male-fertile plants provided the selfed bulk for each cycle of the population.

The following two types of trials were conducted for each population at ICRISAT, Patancheru, Hyderabad, during 1980 rainy season:

1. Population Bulk Trials
2. S_1 Progeny Trials

Each trial was grown in two soil types; Alfisols and Vertisols available at ICRISAT center.

Experimental Design and Planting Plan:

Four separate trials were conducted for this study in each location:

Trial 1 : US/R Population Bulk Trial.

Trial 2 : US/B Population Bulk Trial.

Trial 3 : US/R Population - S_1 Progeny Trial

Trial 4 : US/B Population - S_1 Progeny Trial

List of materials for Trial 1

1. $US/R-C_0$ random mated bulk
2. $US/R-C_1$ random mated bulk
3. $US/R-C_2$ random mated bulk
4. $US/R-C_3$ random mated bulk
5. $US/R-C_0$ x $US/B-C_0$
6. $US/R-C_1$ x $US/B-C_1$
7. $US/R-C_2$ x $US/B-C_2$
8. $US/R-C_3$ x $US/B-C_3$
9. US/R self bulk-C_0
10. US/R self bulk-C_1
11. US/R self bulk-C_2
12. US/R self bulk-C_3
13. CSH-6
14. CSV-4

List of materials for Trial 2

1. $US/B-C_0$ random mated bulk
2. $US/B-C_1$ random mated bulk
3. $US/B-C_2$ random mated bulk
4. $US/B-C_3$ random mated bulk
5. $US/B-C_0$ x $US/R-C_0$
6. $US/B-C_1$ x $US/R-C_1$
7. $US/B-C_2$ x $US/R-C_2$

8. US/B-C_3 x US/R-C_3
9. US/B self bulk-C_0
10. US/B self bulk-C_1
11. US/B self bulk-C_2
12. US/B self bulk-C_3
13. CSH-6
14. CSV-4

<u>List of pedigrees for Trial 3</u>

81 S_1 Progenies of US/R-C_0
81 S_1 Progenies of US/R-C_1
81 S_1 Progenies of US/R-C_2
81 S_1 Progenies of US/R-C_3

<u>List of pedigrees for Trial 4</u>

81 S_1 Progenies of US/B-C_0
81 S_1 Progenies of US/B-C_1
81 S_1 Progenies of US/B-C_2
81 S_1 Progenies of US/B-C_3

Trial 1 and Trial 2 were laid out in randomized complete block design (RBD) with 4 replications. Each plot consisted of 8 rows each of 4 m length and 75 cm width. Trial 3 and Trial 4 were laid out in an 18x18 triple lattice design. Each plot consisted of a single row of 4 m length and 75 cm width.

All trials were conducted at two locations: Alfisols and Vertisols. The planting was done by mechanical planters on ridges 75 cm apart. The seeding was continuous and thinning was done after 12-15 days of planting.

A plant to plant spacing of 10 cm was maintained. 84 kg/ha of N and 84 kg/ha of P_2O_5 (300 kg of 28:28:0) was applied as a basal dose prior to planting, and an additional 46 kg/ha of N (100 kg of Urea) was given as top-dressing after thinning. Weeding and the other usual cultural practices were done as and when necessary. All trials were planted on June 22, 1980 and harvested from September 18 - November 15, 1980 as and when the entries matured. The heads were sun dried for about two weeks before threshing and grain yield were recorded as weights of threshed grain (nearest gram per plot) without any adjustment for slight differences in grain moisture percentage. It was assumed that all the samples attained a constant moisture percent after drying.

Data Recorded

1. Population Bulk Trials (Trial 1 and Trial 2)

   Data on the following characters were recorded on the central six rows of each plot:

   1.1 Plot grain yield:

   Total grain weight was recorded to the nearest gram from each harvested plot (18 m^2) and multiplied by 0.555 to convert to kg/ha.

   1.2 1000-kernel weight:

   The weight of 500 kernels was recorded to the nearest gram from the grain of the plot and multiplied by 2 to get 1000-kernel weight.

2. S_1 Progeny Trials (Trial 3 and Trial 4)

   Five randomly selected competitive plants were tagged in each plot and the following measurements were taken:

2.1 Days to 50% flowering (bloom):

The number of days from planting to the date when a plant had half of its florets in the panicle in anthesis were recorded.

2.2 Plant height:

The plant height from the ground level to the tip of the main panicle was measured in centimeters after seeded set.

2.3 Head length:

The length of individual heads(panicle) from ear base to the tip of the head was measured in centimeters.

2.4 Grain weight:

The grain weight was recorded in grams from five randomly selected competitive plants. This is used in computing grain yield per plant.

The following measurements were taken on whole plot basis (3 m^2).

2.5 Total head weight in grams from each plot was recorded and the head weight from the five randomly selected competitive plant was added to get the plot head weight and multiplied by 3.333 to convert to kg/ha.

2.6 Total grain weight in grams from each plot was recorded and the grain weight of the five randomly selected competitive plants was added to get the plot grain weight and multiplied by 3.333 to convert to kg/ha.

2.7 100-kernel weight:

The weight of 100 kernels sampled from the plot grain weight was recorded in grams.

2.8 Threshing percentage:

The threshing percentage was derived as follows:

$$\text{Threshing \%} = \frac{\text{Plot grain yield}}{\text{Plot head weight}} \times 100$$

Statistical Analysis

1. The Analysis of Variance of the Population Bulk Trials:

Data from Trial 1 and Trial 2 were analysed for each location (Steel and Torrie, 1960) and then combined into a single analysis (Panse and Sukhatme, 1967) by using a general factorial analysis of variance on the PDP-11/45 computer, program written by ICRISAT Computer Service (Anonymous, 1976).

Before pooling, the data from the two experiments for the combined analysis was done only for the characters having homogeneous error variances. The general form of the analysis of variance for the combined analysis is given in Table 2.

Table 2: General form of the analysis of variance for combined analysis (Panse and Sukhatme, 1967)

Source of variation	d.f.
Replications in locations	$\ell(r-1)$
Locations	$\ell-1$
Error (a)	$(r-1)\ (\ell-1)$
Entries	$t-1$
Entries x Locations	$(t-1)\ (\ell-1)$
Pooled error	$\ell(r-1)(t-1)$

Where, ℓ = number of locations
r = number of replications per location
t = number of entries

The analysis of Variance and Standard Errors (S.E.) of the S_1 Progeny Trials:

Data from the triple lattice field design (Trial 3 and Trial 4) at each of the two locations were analysed by using the PDP-11/45 computer and a computer program written by ICRISAT Computer Service (Anonymous,1976). The general form of the lattice analysis of variance is shown in Table 3 The null hypothesis, $H_o = \sigma_p^2 = o$, can be tested by $F(n_p, n_e) = M_p/M_e$, where n_p and n_e are the degrees of freedom associated with the M_p and M_e mean squares for the unadjusted progeny mean. Similarly, for the adjusted progeny means, the null hypothesis $H_o = \sigma^2_{p'} = o$, can be approximately tested by $F(n_{p'}, n_{e''}) = M_{p'}/M_{e''}$ where $n_{p'}$ and $n_{e''}$ are the degrees of freedom associated with the $M_{p'}$ and $M_{e''}$ mean squares (Federer, 1955).

Table 3: General form of the analysis of variance used to analyze data from a triple lattice field design (Mumm, 1972)

Source of variation	d.f.	Mean squares
Total	rk^2-1	
Replications	$r-1$	
Progenies	$p-1$	M_p
Error (RBD)	$(r-1)\ (p-1)$	M_e
Blocks adjusted	$r(k-1)$	M_b
Intra-block error	$(k-1)(rk-k-1)$	$M_{e'}$
Progenies adjusted	$p-1$	$M_{p'}$
Effective error	$(k-1)(rk-k-1)$*	$M_{e''}$

k = number of progenies in each incomplete block

r = number of replications

p = number of progenies = k^2

M_p = progeny mean square

M_e = error mean square (RBD)

M_b = block adjusted mean square

$M_{e'}$ = intra-block error mean square

$M_{p'}$ = progeny adjusted mean square

$M_{e''}$ = effective error mean square

* This formula represents the approximate degrees of freedom (Federer,1955).

The standard errors for lattice analysis were estimated as follows; (Cochran and Cox, 1968)

S.E. of mean between two progenies in the same block $= \frac{2M_{e'}}{r}\{1+(r-1)\mu\}$

and S.E. of mean between two progenies not in the same block $= \frac{2\,M_{e'}}{r}\{1+r\mu\}$

where,

$M_{e'}$ = intra-block error mean square

r = number of replications

$\mu = \frac{(M_b - M_{e'})}{k(r-1)M_{e'}}$

M_b = block adjusted mean square

k = number of progenies in each incomplete block

The coefficient of variation expressed in percent (C.V.%) is estimated as (Mumm, 1972):

$$\text{C.V.\%} = \frac{M_{e''}}{\text{Mean}} \times 100$$

Where, $M_{e''}$=effective error mean square.

The relative efficiency of the lattice design over the RBD is estimated as the ratio of the RBD error variance to the average effective error variance expressed in percent (Mumm, 1972):

$$\text{Relative efficiency} = \frac{M_e}{M_{e''}} \times 100$$

Where,

M_e = error mean square (RBD)

$M_{e''}$ = effective error mean square.

It was observed from the analysis of variance of lattice design that the efficiency of lattice over RBD was negligible, therefore, the design is treated as RBD and analysed accordingly (Cochran and Cox, 1957). The general form of the analysis of variance for an orthogonal break up of lines within cyclesis given in Table 4 (Ostle, 1974).

The standard errors were calculated as follows:

S.E. of mean for any progeny = $\sqrt{\frac{M_e}{r}}$

and S.E. of mean for cycle = $\sqrt{\frac{M_e}{rt}}$

L.S.D. at 5% of mean of any progeny = $t_{.05,\ \text{error d.f.}} \sqrt{\frac{2\,M_e}{r}}$

L.S.D. at 5% of mean for cycle = $t_{.05,\ \text{error d.f.}} \sqrt{\frac{2\,M_e}{rt}}$

Where,

M_e = error mean square

r = number of replications

t = number of progenies in each cycle.

Table 4: General form of an orthogonal break-up of analysis of variance for lines within each of different cycles (Ostle, 1974)

Source of variation	d.f.	Mean square
Replications	r-1	
Progenies	p-1	M_p
Cycles	c-1	M_c
Among progenies within cycles	c(t-1)	M_{pwc}
Among progenies within C_0	t-1	
Among progenies within C_1	t-1	
Among progenies within C_2	t-1	
Among progenies within C_3	t-1	
Replications x Progenies (error)	(r-1)(p-1)	M_e
Total	rp-1	

Where,

r = number of replications
p = number of progenies
c = number of cycles
t = number of progenies within each cycle
M_p = progeny mean square
M_c = cycle mean square
M_{pwc} = progeny mean square within cycle
M_e = error mean square.

The sets of 81 progenies from each cycle were further analysed separately in RBD as given by Steel and Torrie (1960). The analysis of variance for RBD and expected mean squares are given in Table 5.

The genotypic coefficient of variation expressed in percent (G.C.V. %) is estimated as:

$$\text{G.C.V. \%} = \frac{\sqrt{\sigma_g^2}}{\text{Mean}} \times 100$$

Where,

$$\sigma_g^2 = \text{genotypic variance} = \frac{M_t - M_e}{r}$$

The phenotypic coefficient of variation expressed in percent (P.C.V. %) is estimated as:

$$\text{P.C.V. \%} = \frac{\sqrt{\sigma_P^2}}{\text{Mean}} \times 100$$

Where,

$$\sigma_p^2 = \text{Phenotypic variance} = \sigma_g^2 + \sigma_e^2$$

Table 5 : General form of the analysis of variance and expected mean squares for RBD (Steel and Torrie, 1960)

Source of variation	d.f.	Mean Square	
		Observed	Expected
Replications	r-1		
Progenies	t-1	M_e	$\sigma_e^2 + r\sigma_t^2$
Error	(r-1) (t-1)	M_e	σ_e^2
Total	rt-1		

Where,

r = number of replications

t = number of progenies

M_t = progeny mean square

M_e = error mean square

σ_e^2 = error variance

σ_t^2 = variance among progenies

The selection advance for each cycle was calculated from Population Bulk Trials (Trial 1 and Trial 2) as percent change from one cycle to the next cycle. For example, selection advance from C_0 to C_1 was calculated as:

$$\text{Selection advance} = \%\ \text{change} = \frac{\text{Mean of } C_1 - \text{Mean of } C_0}{\text{Mean of } C_0} \times 100$$

Similarly, selection advance for S_1 Progeny Trials (Trial 3 and Trial 4) were calculated as follows:

Selection advance = % change

$$\%\ \text{change} = \frac{\text{Mean of } S_1 \text{ progeny of } C_1 - \text{Mean of } S_1 \text{ progeny of } C_0}{\text{Mean of } S_1 \text{ progeny of } C_0} \times 100$$

The % inbreeding depression for each cycle from random-mated bulk to one generation of selfing was calculated from Population Bulk Trials as follows:

$$\%\ \text{inbreeding depression} = \frac{\text{Mean of self bulk-Mean of random mated bulk}}{\text{Mean of random mated bulk}} \times 100$$

RESULTS

The results of the present investigations are presented under the following sections:

1. Population Bulk Trials:
   - 1.1 The analysis of variance
   - 1.2 Selection advance and inbreeding depression.
2. S_1 Progeny Trials:
   - 2.1 The analysis of variance of the lattice design and comparative performance of S_1 progenies over cycles.
   - 2.2 Means, ranges, genotypic and phenotypic coefficients of variation in different cycles and selection advance for different traits.

1. Population Bulk Trials:

1.1 The analysis of variance ;

The analyses of variance are presented in Table 6 (US/R Population) and Table 7 (US/B Population). The results indicated that there were highly significant differences among entries of Trial 1 (US/R Population) and Trial 2 (US/B Population) for both characters studies (grain yield and 1000-kernel weight) at both locations (Alfisols and Vertisols) and as well as in the combined analysis. From the combined analysis, it was observed that locations and entries x locations interactions were also highly significant for both characters studies. The significance of entries x locations interaction showed that environment plays an important role for grain yield expression.

Table 6 : The analysis of variance and coefficients of variation (C.V.) for grain yield and 1000-kernel weight in the US/R population.

Source of variation	d.f.	Mean squares					
		Grain yield (kg/ha)			1000-kernel weight (g)		
		Alfisols	Vertisols	Combined	Alfisols	Vertisols	Combined
Replications	3	76003	39803	93778	1.956*	2.092**	3.268
Locations	1	-	-	25895000**	-	-	102.300**
Error (a)	3	-	-	22029	-	-	0.776
Entries	13	2554195**	2744994**	5195420**	5.652**	7.032**	11.008**
Entries x Replications	39	28116	21638	-	0.476	0.304	-
Entries x Locations	13	-	-	103765**	-	-	1.676**
Error (b)	78	-	-	24877	-	-	0.388
C.V %		4.4	3.1	x	2.6	1.92	y

* and ** indicate significances at the 0.05 and 0.01 levels of probability, respectively.

x = C.V. % in whole plots = 3.4, and C.V. % in sub-plots = 3.7

y = C.V. % in whole plots = 3.2, and C.V. % in sub-plots = 2.5

Table 7 : The analysis of variance and coefficients of variation (C.V) for grain yield and 1000 - kernel weight in the US/B population

Source of variation	d.f	Mean squares					
		Grain yield (kg/ha)			1000-kernel weight (g)		
		Alfisols	Vertisols	Combined	Alfisols	Vertisols	Combined
Replications	3	162861**	15677	65074	0.472	2.044**	0.716
Locations	1	-	-	49909200**	-	-	284.868**
Error (a)	3	-	-	113464	-	-	1.800
Entries	13	1558345**	1522142**	2950000**	11.080**	5.772**	14.316**
Entries x Replications	39	31401	19459	-	0.612	0.384	-
Entries x Locations	13	-	-	130485**	-	-	2.536**
Error (b)	78	-	-	25430	-	-	0.500
C.V %		4.9	2.8	x	3.1	2.2	y

* and ** indicate significances at the 0.05 and 0.01 levels of probability, respectively.

x = C.V % in whole plots = 7.8, and C.V. % in subplots = 3.8

y = C.V % in whole plots = 4.9, and C.V. % in subplots = 2.6

1.2 Selection advance and inbreeding depression:

Mean grain yield in different cycles, % change over cycles and % inbreeding depression from half-sibs to one generation of selfing are presented in Table 8 for the US/R population and Table 9 for the US/B population. The above information on 1000-kernel weight is presented in Table 10 for the US/R population and Table 11 for the US/B population.

An examination of table 8 indicates that grain yield of random mated bulks, self bulks and crosses between US/R and US/B populations were significantly different from each other in all cases except in C_3 of random mated bulk and US/R-C_3 x US/B-C_3 in Alfisols and in the combined analysis indicating that inbreeding depression as well as heterosis were significant in the US/R population. It was observed that grain yield of crosses was generally higher than random mated bulks followed by self bulks. Based on the combined analysis, the average of inbreeding depression ranged from 5.6% to 23.1%. The rate of inbreeding and heterosis increased from C_0 to C_3.

Observation across cycles in the US/R population revealed that the grain yield increased significantly over each cycle in case of random mated bulks, self bulks as well as in crosses, except in crosses of C_1 over C_0. The rate of selection advance per cycle was 13.5 to 20.2% over each cycle. Poor plant stands in C_0 random mated bulks resulted in an extraordinarily high selection advance of 50.8% based on the combined analysis - the value for this advance was ignored.

Table 8 : Grain yield (kg/ha) and gains from selection for random mated bulks, self bulks and crosses in different cycles of recurrent selection in the US/R population.

	Random[4/] mated bulks	% change		Self[5/] bulks	% change		% in-[6/] breeding depression	cross
		Over 1 cycle	Cumulative		Over 1 cycle	Cumulative		
Alfisols[1/]								
C_0	1975	-	-	2945	-	-	-49.1	3910
C_1	3690	86.8	86.8	3415	16.0	16.0	7.5	4060
C_2	4170	13.0	111.1	3485	2.0	18.3	16.5	4610
C_3	4750	13.9	140.5	3790	8.8	28.7	20.2	4910
Vertisols[2/]								
C_0	3330	-	-	3870	-	-	-16.2	4920
C_1	4300	29.1	29.1	4125	6.6	6.6	4.1	4950
C_2	4945	15.0	48.5	4515	9.5	16.7	8.7	5620
C_3	6200	25.4	86.2	4630	2.5	19.6	25.3	5995
Combined[3/]								
C_0	2650	-	-	3410	-	-	-28.7	4415
C_1	3995	50.8	50.8	3770	10.6	10.6	5.6	4505
C_2	4560	14.1	72.1	4000	6.1	17.3	12.3	5115
C_3	5475	20.1	106.4	4210	5.2	23.6	23.1	5450

1/ Alfisols experiment: L.S.D. for treatment mean at 5%=240 kg/ha, C.V.=4.4%

2/ Vertisols experiment: L.S.D.for treatment mean at 5%=210 kg/ha, C.V.=3.1%

3/ Combined analysis: L.S.D. for treatment mean at 5% = 157 kg/ha, C.V.=3.4% for whole plots and 3.7% for sub-plots.

4/ Bulks of an equal quantity seed from all the intercrosses of selected lines in each cycle.

5/ Bulks of an equal quantity seed from 81 selfed plants in random mated bulks

6/ % reduction due to one generation of selfing in random mated bulks.

7/ US/R x US/B

N.B.: Grain yield of CSH-6 = 4035, 5665 and 4850 kg/ha in Alfisols, Vertisols, and combined analysis, respectively.

: Grain yield of CSV-4 = 2910, 4065 and 3490 kg/ha in Alfisols, Vertisols, and combined analysis, respectively.

The selection advance of 7.9% per cycle based on selfed bulks was, however, meaningful.

The result from US/B population (Table 9) was similar to that of the US/R population. Based on the combined analysis, the rate of inbreeding increased as selection proceeded (13.1% in C_0 to 18.6% in C_3). The performance of crosses US/R-C_0 x US/B-C_0 (4365 kg/ha) increased to 5160 kg/ha in US/R-C_3 x US/B-C_3. However, the difference between US/R-C_0 x US/B-C_0 and US/R-C_1 x US/B-C_1 was not significant statistically in both locations. A selection advance per cycle for grain yield was observed to be 10.9% and 8% on the basis of random mated bulks and self bulks, respectively. The rate of selection gain was maximum in the first cycle (18.1%) in the combined analysis.

An examination of tables 10 and 11 indicates that the 1000-kernel weight of crosses was generally higher than random mated bulks followed by self bulks in the US/B population whereas the difference among them in the US/R population were very marginal. The observations across cycles indicated that the 1000-kernel weight in the US/R population increased due to selection (1% and 0.7% per cycle based on random mated bulks and self bulks, respectively). However, selection in the US/B population resulted in reduced 1000-kernel weight of 0.9% and 0.5% per cycle on the basis of random mated bulks and self bulks, respectively. The rate of inbreeding for 1000-kernel weight ranged from 2.1

Table 9 : Grain yield (kg/ha) and gains from selection for random mated bulks, self bulks and crosses in different cycles of recurrent selection in the US/B population.

	Random mated bulks 4/	% change		Self bulks 5/	% change		% inbreeding depression 6/	Crosses 7/
		Over 1 cycle	Cumulative		Over 1 cycle	Cumulative		
Alfisols 1/								
C_0	2895	-	-	2755	-	-	4.8	3730
C_1	3755	29.7	29.7	2895	5.0	5.1	22.9	3870
C_2	4270	13.7	47.5	3040	5.0	10.3	28.8	3980
C_3	4470	4.7	54.4	3710	22.0	34.7	17.0	4555
Vertisols 2/								
C_0	4805	-	-	3930	-	-	18.2	4995
C_1	5335	11.0	11.0	4305	9.5	9.5	19.3	5005
C_2	5475	2.6	13.9	4530	5.2	15.3	17.3	5345
C_3	5745	4.9	19.5	4600	1.6	17.0	19.9	5765
Combined 3/								
C_0	3850	-	-	3345	-	-	13.1	4365
C_1	4545	18.1	18.1	3600	7.6	7.6	20.8	4435
C_2	4875	7.3	26.6	3785	5.1	13.2	22.4	4665
C_3	5105	4.7	32.6	4155	9.8	24.2	18.6	5160

1/ Alfisols experiment: L.S.D. for treatment mean at 5% = 253 kg/ha, C.V. = 4.9%

2/ Vertisols experiment: L.S.D. for treatment mean at 5% = 199 kg/ha, C.V. = 2.8%

3/ Combined analysis : L.S.D. for treatment mean at 5% = 159 kg/ha, C.V. = 7.8% for whole plots and 3.8% for sub-plots

4/ Bulks of an equal quantity seed from all the intercrosses of selected lines in each cycle.

5/ Bulks of an equal quantity seed of 81 selfed plants in random mated bulks.

6/ % reduction due to one generation of selfing in random mated bulks.

7/ US/^{B} x US/^{R}

N.B.: Grain yield of CSH-6 = 4660, 5555 and 5105 kg/ha in Alfisols, Vertisols, and combined analysis, respectively.

: Grain yield of CSV-4 = 3290, 4170 and 3730 kg/ha in Alfisols, Vertisols, and combined analysis, respectively.

Table 10: 1000-kernel weight (g) and gains from selection for random mated bulks, self bulks and crosses in different cycles of recurrent selection in the US/R population.

	Ramdom-mated bulks 4/	% change		Self-bulks 5/	% change		% inbreeding depression 6/	Crosses 7/
		Over 1 cycle	Cumulative		Over 1	Cumulative		
Alfisols 1/								
C_0	27.58	-	-	26.22	-	-	4.9	27.42
C_1	27.28	-1.1	-1.1	26.14	-0.3	-0.3	4.2	26.90
C_2	27.68	1.5	0.4	26.76	2.4	2.1	3.3	28.38
C_3	27.82	0.5	0.9	25.84	-3.4	-1.5	7.1	28.06
Vertisols 2/								
C_0	29.06	-	-	27.84	-	-	4.2	27.62
C_1	29.86	2.8	2.8	28.42	2.1	2.1	4.8	28.80
C_2	30.00	0.5	3.2	29.36	3.3	5.5	2.1	29.58
C_3	30.64	2.1	5.4	29.40	0.1	5.6	4.0	28.84
Combined 3/								
C_0	28.32	-	-	27.02	-	-	4.6	27.52
C_1	28.56	0.9	0.9	27.28	1.0	1.0	4.5	27.84
C_2	28.84	1.0	1.8	28.06	2.9	3.9	2.7	28.98
C_3	29.22	1.3	3.2	27.62	-1.6	2.2	5.5	28.44

1/ Alfisols experiment: L.S.D. for treatment mean at 5% = 0.98 g. C.V. = 2.6%

2/ Vertisols experiment: L.S.D. for treatment mean at 5% = 0.78 g. C.V. = 1.9%

3/ Combined analysis: L.S.D. for treatment mean at 5% = 0.62 g. C.V. = 3.2% for whole plots and 2.3% for sub-plots.

4/ Bulks of an equal quantity seed from all the intercrosses of selected lines in each cycle.

5/ Bulks of an equal quantity seed of 81 selfed plants in random mated bulks.

6/ % reduction due to one generation of selfing in random mated bulks.

7/ US/R x US/B

N.B.: 1000-kernel weight of CSH-6 = 21.40, 26.62 and 24.00 g in Alfisols, Vertisols and combined analysis, respectively.

: 1000-kernel weight of CSV-4 = 24.92, 26.82 and 25.86 g in Alfisols, Vertisols and combined analysis, respectively.

Table 11: 1000-kernel weight (g) and gains from selection for random mated bulks, self bulks and crosses in different cycles of recurrent selection in the US/B population.

	Random mated bulks[4]	% change		Self bulks[5]	% change		% inbreeding depression[6]	Crosses[7]
		Over 1 cycle	Cumulative		Over 1 cycle	Cumulative		
Alfisols[1]								
C_0	26.98	-	-	24.60	-	-	8.8	26.56
C_1	25.80	-4.4	-4.4	24.06	-2.2	-2.2	6.7	26.88
C_2	26.76	3.7	-0.8	26.06	8.3	5.9	2.6	27.36
C_3	26.48	-1.1	-1.9	24.44	-6.2	-0.7	7.7	27.46
Vertisols[2]								
C_0	29.28	-	-	28.40	-	-	3.0	30.80
C_1	28.94	-1.2	-1.2	29.48	3.8	3.8	-1.9	29.36
C_2	29.12	0.6	-0.6	29.32	-0.5	3.2	-0.7	30.02
C_3	28.36	-2.6	-3.1	27.74	-5.4	-2.3	2.2	30.12
Combined[4]								
C_0	28.14	-	-	26.50	-	-	5.8	28.68
C_1	27.36	-2.8	-2.8	26.76	1.0	1.0	2.2	28.12
C_2	27.94	2.1	-0.7	27.68	3.4	4.5	0.9	28.68
C_3	27.42	-1.9	-2.6	26.10	-5.7	-1.5	4.8	28.80

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[1] Alfisols experiment: L.S.D. for treatment mean at 5% = 1.12 g. C.V. = 3.1%

[2] Vertisols experiment: L.S.D. for treatment mean at 5% = 0.88 g C.V. = 2.2%

[3] Combined analysis : L.S.D. for treatment mean at 5% = 0.70 g. C.V. = 4.9% for the whole plots and 2.6% for sub-plots.

[4] Bulks of an equal quantity seed from all the intercrosses of selected lines in each cycle.

[5] Bulks of an equal quantity seed of 81 selfed plants in random mated bulks.

[6] % reduction due to one generation of selfing in random mated bulks.

[7] US/B x US/R

N.B.: 1000-kernel weight of CSH-6 = 24.62, 25.62 and 25.02 g. in Alfisols, Vertisols and combined analysis, respectively.

: 1000-kernel weight of CSV-4 = 24.60, 27.04 and 25.82 g. in Alfisols, Vertisols and combined analysis, respectively.

to 7.1% in the US/R population and -1.9 to 8.8% in the US/B population.

2. S_1 Progeny Trials:

2.1 The analysis of variance of the lattice design and comparative performance of S_1 progenies over cycles:

Eighty one S_1 progenies from each of 4 cycles (C_0 to C_3) of the US/R and US/B populations were grown in 18 x 18 triple lattice as separate trials. The analysis of variance, trial means, standard errors, coefficient of variation (C.V.%) and relative efficiencies of the lattice design over the RBD for seven agronomic traits at two locations are presented in Table 12 and Table 13 for the US/R and US/B populations, respectively. The Bartlett's tests of homogeneity of variance indicated that the error variances for the two locations are heterogeneous for all characters. Therefore, the combined analysis of the data was not attempted.

The mean squares for lines and lines adjusted in Table 12 and Table 13 were highly significant at both locations for all the characters studied indicating significant differences among lines of both populations. It was interesting to note that the efficiency of lattice over the RBD was negligible in both experiments for all characters, including grain yield. The coefficient of variation (C.V.%) were quite low (2.9 to 13.9%) in the US/R population - S_1 progenies trial and 2.4 to 10.6% in the US/B population - S_1 progenies trial.

Table 12 : The analysis of variance, means, standard errors (S.E.), coefficients of variation (C.V.) and relative efficiencies of the lattice design for seven agronomic traits observed at two locations in US/R population - S_1 progenies.

Source of variation	d.f.	Mean squares					
		Bloom(days)		Height (cm)		Yield/plant (g)	
		Alfisols	Vertisols	Alfisols	Vertisols	Alfisols	Vertisols
Replications	2	3.0	61.3*	1602.6**	52.9	87.1**	121.5*
Lines	323	59.1**	57.5**	1607.3**	2179.5**	104.3**	281.1**
Error (RBD)	646	3.1	3.8	138.4	174.2	12.2	19.2
Blocks adjusted	51	4.1	4.7	166.4	189.7	12.7	21.7
Intra-block error	595	3.0	3.8	136.0	172.8	12.2	19.0
Lines adjusted	323	60.1**	58.2**	1635.4**	2195.5**	104.6**	283.1**
Effective error	595	3.1	3.8	137.9	174.1	12.2	19.2
Mean		60	62	160	168	25	35
S.E.		1.0	1.1	6.8	7.6	2.0	2.5
C.V. %		2.9	3.2	7.4	7.9	13.9	12.7
Relative efficiencies of lattice		100.8	100.4	100.3	100.1	100.0	100.1

* and ** indicate significances at the 0.05 and 0.01 levels of probability, respectively.

Table 12 : (Contd.)

Source of variation	d.f.	Mean squares							
		Yield/ha (kg)		Head length(cm)		100-kernel weight(g)		Threshing (%)	
		Alfisols	Vertisols	Alfisols	Vertisols	Alfisols	Vertisols	Alfisols	Vertisols
Replications	2	1771161**	1622777**	38.8**	22.8**	0.032	0.105	29.3*	13.9*
Lines	323	1173720**	3088548**	21.3**	24.2**	0.226**	0.284**	11.8**	13.0**
Error (RBD)	646	129364	206318	2.8	3.3	0.023	0.030	5.0	3.2
Blocks adjusted	51	138741	251148	2.8	4.3	0.026	0.036	7.4*	3.7
Intra-block error	595	128560	202475	2.8	3.2	0.022	0.030	4.8	3.1
Line adjusted	323	1180960**	3114680**	21.4**	24.5**	0.230**	0.290**	12.1**	13.1**
Effective error	595	129305	205573	2.8	3.2	0.020	0.030	5.0	3.2
Mean		2781	3529	23	26	2.59	2.83	59	58
S.E.		207.7	262.2	1.0	1.0	0.09	0.10	1.3	1.0
C.V. %		12.9	12.9	7.2	6.8	5.8	6.1	3.8	3.1
Relative efficiencies of lattice		100.0	100.4	100.0	100.8	100.2	100.3	101.4	100.2

* and ** indicate significances at the 0.05 and 0.01 levels of probability, respectively.

Table 13 : The analysis of variance, means, standard errors (S.E.), coefficients of variation (C.V.), and relative efficiencies of the lattice design for seven agronomic traits observed at two locations in US/B population - S_1 progenies.

Source of variation	d.f.	Mean squares					
		Bloom(days)		Height(cm)		Yield/plant (g)	
		Alfisols	Vertisols	Alfisols	Vertisols	Alfisols	Vertisols
Replications	2	55.5**	147.7**	383.3	2243.3**	8.7	16.0
Lines	323	40.0**	44.5**	1725.0**	2198.2**	83.6**	296.3**
Error (RBD)	646	2.4	2.2	116.1	112.4	11.3	13.4
Blocks adjusted	51	2.5	3.2*	99.3	110.0	11.2	17.1
Intra-block error	595	2.4	2.1	117.6	112.6	11.3	13.1
Lines adjusted	323	40.2**	45.6**	1749.5**	2202.8**	83.6**	301.0**
Effective error	595	2.4	2.2	115.9	112.4	11.3	13.4
Mean		59	62	166	170	29	40
S.E.		0.9	0.9	6.2	6.1	1.9	2.1
C.V %		2.6	2.4	6.5	6.2	11.6	9.3
Relative efficiencies of lattice		100.0	101.3	100.2	100.0	100.0	100.6

* and ** indicate significances at the 0.05 and 0.01 levels of probability, respectively.

Table 13 : (Contd.)

Source of variation	d.f.	Mean squares							
		Yield/ha (kg)		Head length(cm)		100-kernel weight(g)		Threshing (%)	
		Alfisols	Vertisols	Alfisols	Vertisols	Alfisols	Vertisols	Alfisols	Vertisols
Replications	2	361073	3520058**	21.3**	40.6**	0.038	0.032	8.0	3.9
Lines	323	1242660**	2542321**	17.2**	21.5**	0.173**	0.284	10.2**	10.0**
Error (RBD)	646	138139	130814	2.2	2.2	0.025	0.021	4.1	1.5
Blocks adjusted	51	132715	185942*	3.0*	3.2*	0.030	0.018	4.2	1.6
Intra-block error	595	138604	126089	2.1	2.1	0.024	0.021	4.0	1.4
Lines adjusted	323	1246340**	2590000**	17.6**	21.9**	0.180**	0.290**	10.3**	10.0**
Effective error	595	138119	129293	2.1	2.2	0.020	0.020	4.1	1.5
Mean		3511	4006	24	26	2.58	2.85	61	61
S.E.		214.6	208.8	0.8	0.9	0.09	0.08	1.2	0.7
C.V. %		10.6	9.0	6.1	5.6	6.1	5.0	3.3	2.0
Relative efficiencies of lattice		100.0	101.2	100.9	101.2	100.4	100.2	100.0	100.1

* and ** indicate significances at the 0.05 and 0.01 levels of probability, respectively.

Considering that grain yield/ha is the most important among the characters studied, the ranked mean of lines for grain yield/ha were studied in greater detail. A sample of the best 32 lines (10%) was taken from each population and lines were classified into cycles according to their origin. In table 14 the mean grain yield (kg/ha)and the composition(%) of the top 10% of progenies on Alfisols and Vertisols from the US/R and US/B populations-S_1 progeny trials are presented. It was observed that the maximum number of high yielding progenies belonged to cycle 3 of each population at each location (84.4 and 71.9% from C_3 of the US/R and 65.6 and 59.4% from C_3 of the US/B population in Alfisols and Vertisols, respectively). The top yielding S_1 progenies (US/R) from C_3 at both locations are 5090 kg/ha on Alfisols and 6485 kg/ha on Vertisols. The top yielding S_1 progenies (US/B) on Alfisols is 5360 kg/ha from C_3 and on Vertisols is 6955 kg/ha from C_2.

Since the lattice design did not show any efficiency over RBD, the design was treated as RBD. In order to test the differences among cycles an orthogonal break-up of the analysis of variance was done.

The orthogonal break-up of the analysis of variance for progenies in the US/R and US/B population is presented in Tables15 and 16, respectively.

The results from Tables 15 and 16 showed that the mean squares due to lines, cycles, among lines within cycles and among

Table 14 : Grain yield (kg/ha) and composition (%) of the top 10% progenies on Alfisols and Vertisols from the US/R and US/B populations - S_1 progeny trials.

	Mean grain yield (kg/ha)							
l No.	US/R population - S_1 progeny				US/B population - S_1 progeny			
	Cycle	Alfisols	Cycle	Vertisols	Cycle	Alfisols	Cycle	Vertisols
1	C_3	5090	C_3	6485	C_3	5360	C_2	6955
2	C_3	4665	C_3	6165	C_3	5010	C_1	6540
3	C_3	4470	C_3	6045	C_3	4965	C_1	6500
4	C_3	4365	C_3	6030	C_2	4940	C_3	6165
5	C_3	4280	C_3	5615	C_3	4860	C_3	6075
6	C_3	4205	C_3	5500	C_3	4835	C_3	6065
7	C_3	4075	C_2	5465	C_3	4800	C_3	5955
8	C_3	4055	C_3	5405	C_3	4755	C_3	5890
9	C_3	4045	C_2	5365	C_3	4750	C_3	5810
10	C_3	4030	C_3	5345	C_3	4705	C_2	5795
11	C_3	4015	C_0	5325	C_3	4695	C_3	5780
12	C_3	3970	C_3	5280	C_2	4685	C_3	5735
13	C_3	3920	C_1	5275	C_2	4670	C_1	5695
14	C_2	3895	C_3	5240	C_3	4665	C_1	5680
15	C_3	3855	C_2	5215	C_0	4645	C_3	5620
16	C_3	3855	C_3	5205	C_3	4630	C_3	5525
17	C_3	3840	C_3	5195	C_3	4580	C_2	5485
18	C_3	3830	C_3	5135	C_1	4575	C_2	5470

(Contd.)

Table 14 : (Contd)

Sl No.	Mean grain yield (kg/ha)							
	US/R population - S_1 progeny				US/B population - S_1 progeny			
	Cycle	Alfisols	Cycle	Vertisols	Cycle	Alfisols	Cycle	Vertisols
19	C_3	3805	C_3	5130	C_3	4540	C_3	5465
20	C_1	3775	C_3	5115	C_3	4535	C_2	5405
21	C_3	3775	C_2	5085	C_3	4525	C_3	5390
22	C_2	3770	C_3	5060	C_2	4515	C_3	5365
23	C_3	3765	C_3	5055	C_3	4430	C_2	5350
24	C_3	3745	C_3	5050	C_3	4415	C_3	5325
25	C_3	3710	C_3	5040	C_3	4400	C_3	5320
26	C_2	3670	C_2	5040	C_1	4395	C_3	5305
27	C_3	3665	C_3	4955	C_3	4380	C_1	5300
28	C_3	3665	C_3	4955	C_1	4375	C_2	5295
29	C_3	3655	C_2	4950	C_1	4365	C_3	5275
30	C_3	3645	C_2	4935	C_3	4360	C_3	5260
31	C_3	3645	C_3	4930	C_2	4345	C_3	5240
32	C_2	3640	C_3	4905	C_2	4335	C_2	5240
Composition (%)								
	C_0	0.0		3.1		3.1		0.0
	C_1	3.1		3.1		12.5		15.6
	C_2	12.5		21.9		18.8		25.0
	C_3	84.4		71.9		65.6		59.4

lines within each cycle were highly significant for all characters under study in both populations at all locations except for among cycles for threshing percentage on Alfisols in the US/B population and among lines with C_3 on Alfisols of the US/R population.

It was interesting to note that the cycles were significantly different for all characters in both populations.

2.2 S_1 progeny means, ranges, genotypic and phenotypic coefficients of variation in different cycles and selection advance for different traits:

The sets of 81 S_1 progenies of each cycle were analyzed separately in RBD and cycle means, ranges, genotypic coefficients of variation (G.C.V.) and phenotypic coefficients of variation (P.C.V.) were calculated for all characters under study.

The performance of seven characters under study based on S_1 progenies in different cycles of the US/R population on Alfisols and Vertisols is presented in Tables 17 and 18, respectively. The performance of the US/B population - S_1 progenies is given in Table 19 for Alfisols and Table 20 for Vertisols. The selection advances based on S_1 progeny means for different cycles at both locations in the US/R population are given in Table 21 and for the US/B population in Table 22.

The results of the above analysis are described below for each character, separately.

Days to 50% flowering (Bloom):

The mean days to 50% flowering increased steadily over each cycle from C_O to C_3 for both populations at both locations (from 57 days in C_O to 65 days in C_3 on Alfisols and from 58 days to 66 days on Vertisols for the US/R population and from 56 days to 62 days on Alfisols and from 59 days to 65 days on Vertisols for the US/B population). The flowering was delayed at the rate of 4.7 and 4.6% per cycle in the US/R population on Alfisols and Vertisols, respectively. The delay in flowering of US/B population was at a slightly lower rate (3.6% per cycle on Alfisols and 3.4% per cycle on Vertisols). It was further noticed that the delay in maturing occurred mainly in the third cycle of selection, particularly in the US/R population in which additional elite lines were incorporated.

The observation on ranges in bloom days indicated that the range was generally narrowed down in the later cycles. This observation was further substantiated by the G.C.V. and P.C.V.

The % G.C.V. reduced from 6.8 to 4.9 and 6.8 to 4.1 on Alfisols and Vertisols, respectively from C_O and C_3 of the US/R population. In the US/B population, the % G.C.V. of 5.3 was maintained in the C_3 on Alfisols whereas it was reduced from 6.2% in the C_O to 5.0% in C_3 on Vertisols.

Plant height (cm):

Mean plant height reduced from C_1 to C_2 but increased in C_3 for both

Table 15 : The orthogonal break up of the analysis of variance for seven agronomic traits observed at two locations in the US/R population - S_1 progenies.

Source of variation	u.f.	Mean Squares					
		Bloom (days)		Height (cm)		Yield/plant (g)	
		Alfisols	Vertisols	Alfisols	Vertisols	Alfisols	Vertisols
Replications	2	3.0	61.3**	1602.6**	52.9	87.1**	121.5*
Lines	323	59.1**	57.5**	1607.3**	2179.5**	104.3**	281.1**
Cycles	3	2577.8**	2495.0**	20173.3**	28601.3**	3288.6**	8952.0**
Among lines within cycles	320	141.9**	138.4**	5732.8**	7727.3**	297.6**	799.3**
Among lines within C_0	80	48.0**	51.3**	1769.8**	2473.6**	72.2**	185.8**
Among lines within C_1	80	31.0**	37.2**	1705.0**	2429.3**	53.3**	176.2**
Among lines within C_2	80	28.7**	24.5**	1468.6**	1863.0**	90.5**	161.8**
Among lines within C_3	80	34.2**	25.4**	789.4**	961.4**	81.6**	275.5**
Replications x lines (Error)	646	3.1	3.8	138.4	174.2	12.2	19.2

* and ** indicate significances at the 0.05 and 0.01 levels of probability, respectively.

Table 15 : (Contd)

Source of variation	d.f.	Mean squares							
		Yield/ha (kg)		Head length (cm)		100-kernel weight (g)		Threshing %	
		Alfisols	Vertisols	Alfisols	Vertisols	Alfisols	Vertisols	Alfisols	Vertisols
Replications	2	1771161**	1622777**	33.8**	22.8**	0.032	0.105	29.3*	13.9*
Lines	323	1173720**	3088548**	21.3**	24.2**	0.226**	0.284**	11.8**	13.0**
Cycles	3	51073968**	139056000**	23.4**	11.5*	0.786**	4.600**	191.3**	813.0**
Among lines within cycles	320	2823619**	7255405**	85.3**	97.3**	0.883**	0.976**	44.7**	40.4**
Among lines within C_0	80	589302**	2107248**	17.6**	25.5**	0.262**	0.232**	16.1**	15.8**
Among lines within C_1	80	516629**	1589194**	30.5**	30.3**	0.259**	0.260**	13.3**	11.1**
Among lines within C_2	80	819920**	1831782**	20.2**	22.5**	0.196**	0.228**	10.3**	8.7**
Among lines within C_3	80	897768**	1727181**	17.0**	19.0**	0.166**	0.256**	5.0	4.8**
Replication x Lines (Error)	646	129364	206318	2.8	3.3	0.023	0.030	5.0	3.2

* and ** indicate significances at the 0.05 and 0.01 levels of probability, respectively.

Table 16 : The orthogonal break up of the analysis of variance for seven agronomic traits observed at two locations in the US/B population - S_1 progenies.

Source of variation	d.f.	Mean squares					
		Bloom (days)		Height (cm)		Yield/plant (g)	
		Alfisols	Vertisols	Alfisols	Vertisols	Alfisols	Vertisols
Replications	2	55.5**	147.7**	383.3	2243.3**	8.7	16.0
Lines	323	40.0**	44.5**	1725.0**	2198.2**	83.6**	296.3**
Cycles	3	1474.5**	1486.8**	20887.7**	28067.8**	1258.8**	6551.3**
Among lines within cycles	320	106.1**	124.1**	6181.4**	7822.6**	290.2**	950.7**
Among lines within C_0	80	28.8*	41.7**	1877.3**	2460.7**	78.7**	176.2**
Among lines within C_1	80	21.6**	26.7**	1882.9**	2460.1**	50.7**	318.6**
Among lines within C_2	80	20.6**	22.0**	1207.8**	1619.7**	66.3**	225.8**
Among lines within C_3	80	35.1**	33.7**	1213.4**	1282.1**	94.5**	230.1**
Replications x Lines(Error)	646	2.4	2.2	116.1	112.4	11.3	13.4

* and ** indicate significances at the 0.05 and 0.01 levels of probability, respectively.

Table 16: (Contd)

Source of variation	d.f.	Mean squares							
		Yield/ha (kg)		Head length (cm)		100-kernel weight (g)		Threshing %	
		Alfisols	Vertisols	Alfisols	Vertisols	Alfisols	Vertisols	Alfisols	Vertisols
Replications	2	361073	3520058**	21.3**	40.6**	0.038	0.032	8.0	3.9
Lines	323	1242660**	2542321**	17.2**	21.5**	0.173**	0.284**	10.2**	10.0**
Cycles	3	36170315**	89962367**	30.1**	31.0**	0.567**	1.813**	162.2	594.3**
Among lines within cycles	320	3660853**	6891031**	68.3**	85.6**	0.679**	1.078**	38.5**	30.2**
Among lines within C_0	80	988114**	1684396**	18.0**	19.1**	0.191**	0.259**	8.8**	9.9**
Among lines within C_1	80	824150**	1782236**	17.1**	26.2**	0.162**	0.238**	10.0**	7.0**
Among lines within C_2	80	675061**	1894529**	17.0**	23.4**	0.140**	0.251**	7.9**	7.0**
Among lines within C_3	80	1173528**	1529870**	16.2**	16.9**	0.186**	0.330**	11.8**	6.3**
Replications x Lines(Error)	646	138139	130814	2.2	2.2	0.025	0.021	4.1	1.5

* and ** indicate significances at the 0.05 and 0.01 levels of probability, respectively.

populations at both locations. The means of height were 160, 152, 154 and 172 cm on Alfisols and 165, 158, 164 and 183 on Vertisols for C_o, C_1, C_2 and C_3, respectively in the US/R population. In the US/B population, the plant height means were 170, 154, 163 and 175 on Alfisols and 171, 158, 168 and 184 cm Vertisols for C_o,C_1,C_2 and C_3 respectively. The plant height was increased at the rate of 2.5 and 3.8% per cycle on Alfisols and Vertisols of the US/R population, respectively. The increase in the plant height of the US/B population was at slightly lower rate (1.0% per cycle on Alfisols and 3.4% per cycle on Vertisols). It was further noticed that the increase in height occurred only in the third cycle of selection.

The observation on ranges in the plant height over cycles indicated that the range was generally maintained from C_1 to C_2 but was narrowed down in the third cycle. This observation was further substantiated by the G.C.V. and P.C.V.%. The G.C.V. reduced from C_O (14.7%) to C_3 (8.6%) on Alfisols and from 16.9% to 8.9% on Vertisols in the US/R population. Similarly, the G.C.V. of the US/B population reduced from C_O (14.3%) to C_3 (10.9%) on Alfisols and from 16.4 to 10.7% on Vertisols. It was observed that generally the G.C.V. reduced at slightly lower rate from C_1 to C_2 and at higher rate from C_2 to C_3.

Grain yield per plant in grams:

The mean grain yield/plant (g) increased in each cycle from

C_0 to C_3 in both populations at both locations except in the US/B population on Alfisols; Mean grain yield/plant in the US/R populations were 22 g in C_0 and 30 g in C_3 on Alfisols; 29 g in C_0 and 43 g in C_3 on Vertisols, whereas the US/B population cycle means were 27 g in C_0 and 31 g in C_3 on Alfisols and 34 g in C_0 and 45 g in C_3 on Vertisols. The grain yield/plant increased at the rate of 12.1 and 16.1% per cycle in the US/R population on Alfisols and Vertisols respectively. In the US/B population, rate of increase was 4.9 and 10.8% per cycle on Alfisols and Vertisols, respectively.

The observation on ranges in the grain yield/plant revealed that the ranges were increased in the later cycles. In the US/R population, the G.C.V. tended to reduce from 20.3% in C_0 to 15.6% in C_3 on Alfisols and from 26.2% in C_0 to 21.4% in C_3 on Vertisols. Similarly, the G.C.V. in the US/B population were also reduced but slightly at the lower rate than in the US/R population (from 17.9% in C_0 to 17.0% in C_3 on Alfisols and 21.9% to 19.0% on Vertisols).

Grain yield (kg/ha):

The means of grain yield/ha over cycles increased steadily in each cycle from C_0 to C_3 for both populations at both locations (from 2355 kg/ha in C_0 to 3390 kg/ha in C_3 on Alfisols and from 2815 kg/ha in C_0 to 4495 kg/ha in C_3 on Vertisols in the US/R population and from 3035 kg/ha in C_0 to 3920 kg/ha in C_3 on Alfisols and from 3380 kg/ha in C_0 to 4695 kg/ha in C_3 on Vertisols in the US/B population). Grain yield/ha was increased at the rate of 14.6 and 19.9% per cycle in the US/R population on Alfisols and Vertisols, respectively. The rate of increase in the US/B population was at a slightly lower rate (9.7 and 12.9% per cycle on Alfisols and Vertisols, respectively). It was further observed that the rate of increase in grain yield/ha in the US/R population was more consistent than in the US/B population.

The observation of ranges in grain yield/ha indicated that the range was generally more in the later cycles. However, the G.C.V. and P.C.V.% reduced for both populations at both locations. In the US/R population, the G.C.V. reduced from 17.0% in C_O to 14.7% in C_3 and from 28.5% in C_O to 15.5% in C_3 on Alfisols and Vertisols, respectively. Similarly, the G.C.V% of the US/B population reduced from 17.8% in C_O to 15.0% in C_3 and 21.3% in C_O to 14.4% in C_3 on Alfisols and Vertisols, respectively.

Head length (cm):

The means of head length (cm) were almost unchanged over cycles in both populations at both locations except on Vertisols in the US/R population. Mean head length in the US/R population was constant at 23 cm in each cycle on Alfisols but slightly increased (1.3% per cycle) on Vertisols. The mean head length in the US/B population was constant at 24 cm on Alfisols and 26 cm on Vertisols. The G.C.V.% slightly reduced from 9.7 to 9.5% and 10.5 to 8.6% on Alfisols and Vertisols, respectively, from C_O to C_3 in the

US/R population. Similar results were observed on the US/B population.

100-kernel weight (g):

The means of 100-kernel weight increased in each cycle from C_O to C_3 for both populations at both locations (from 2.54 g in C_O to 2.66 g in C_3 on Alfisols and from 2.67 g in C_O to 2.99 g in C_3 on Vertisols in the US/R population and from 2.57 g in C_O to 2.63 g in C_3 on Alfisols and from 2.79 g in C_O to 2.96 g in C_3 on Vertisols in the US/B population). The rate of increase in the mean of 100-kernel weight was slightly higher (1.6 and 4.0% per cycle on Alfisols and Vertisols, respectively) in the US/R population than in the US/B population (0.8 and 2.0% per cycle on Alfisols and Vertisols, respectively).

The observation of ranges on 100-kernel weight indicated that the range was generally narrowed down in the later cycles except on Vertisols in the US/R population. The G.C.V.% of the US/R population reduced from 11.3(C_O) to 8.2% (C_3) and from 9.7(C_O) to 9.2% (C_3) on Alfisols and Vertisols, respectively. The G.C.V.% in the US/B also reduced from 9.1 (C_O) to 8.9% (C_3) on Alfisols but increased from 10.2 (C_O) to 10.8% (C_3) on Vertisols.

Threshing Percentage:

The means of threshing percentage were slightly greater in both populations at both locations (from 73% in C_O to 75% in C_3 on Alfisols and 70% in C_O to 74% in C_3 on Vertisols in the US/R population and from 75% in C_0 to 77 % in C_3 on Alfisols and 74% in C_0 to 78% in C_3 on Vertisols in the US/B population). The rate of increase in the threshing % was slightly higher (0.9 and 1.9% per cycle in the US/R population on Alfisols and Vertisols, respectively) than in the US/B population (0.9 and 1.8% per cycle on Alfisols and Vertisols, respectively).

The observation of ranges in threshing % indicated that the range was generally narrowed down in the later cycles of the US/R population but increased in the US/B population. The G.C.V.% in the US/R population reduced from 3.5 (C_0) to 1.8% (C_3) and 4.4 (C_0) to 1.9% (C_3) on Alfisols and Vertisols, respectively. Similarly, the G.C.V. % of the US/B population also reduced from 3.0 (C_0) to 2.5% (C_3) and 3.4 (C_0) to 3.0% (C_3) on Alfisols and Vertisols, respectively.

Table 17 : S_1 progeny means, ranges, genotypic coefficients of variation (G.C.V.), and phenotypic coefficients of variation (P.C.V.) for seven agronomic traits in different cycles of US/R population - S_1 progenies on Alfisols.

Cycle		Bloom (days)	Height (cm)	Grain Yield/ plant (g)	Grain yield/ha (kg)	Head length (cm)	100-kernel weight (g)	Threshing %
C_0	Mean	57	160	22	2355	23	2.54	73
	Range	50-71	107-226	14-37	1475-3440	18-29	1.98-3.37	65-80
	G.C.V.%	6.8	14.7	20.3	17.0	9.7	11.3	3.5
	P.C.V.%	7 4	16.1	25.9	22.0	12.1	12.4	6.8
C_1	Mean	59	152	23	2510	23	2.55	73
	Range	52-69	100-211	14-32	1735-3775	18-34	1.93-3.27	65-81
	G.C.V. %	5.2	15.0	16.8	14.4	13.1	10.9	3.4
	P.C.V. %	6.0	17.0	21.1	20.1	15.2	12.7	5.6
C_2	Mean	60	154	25	2870	23	2.61	74
	Range	54-76	102-232	11-44	1150-3890	15-31	2.15-3.27	62-81
	G.C.V.%	4.9	13.6	20.6	16.7	10.5	9.2	3.1
	P.C.V.%	5.6	15.7	24.5	21.0	12.7	10.9	5.0
C_3	Mean	65	172	30	3390	23	2.66	75
	Range	60-72	142-216	20-48	2085-5090	18-29	2.21-3.34	71-82
	G.C.V.%	4.9	8.6	15.6	14.7	9.5	8.2	1.8
	P.C.V.%	5.7	11.0	20.5	18.6	11.8	10.0	3.7
L.S.D.of mean for cycle at 5%		0.3	2.2	0.6	64	0.3	0.03	0.3
C.V. %		2.9	7.4	13.9	12.9	7.2	5.8	3.8

Table 18: S_1 progeny means, ranges, genotypic coefficients of variation (G.C.V.), and phenotypic coefficients of variation (P.C.V.) for seven agronomic traits in different cycles of the US/R population - S_1 progenies on Vertisols.

Cycle		Bloom (days)	Height (cm)	Grain Yield/ plant (g)	Grain yield/ha (kg)	Head length (cm)	100-kernel weight (g)	Threshing %
C_0	Mean	58	165	29	2815	26	2.67	70
	Range	50-70	95-250	14-48	1440-5290	19-35	1.87-3.25	62-79
	G.C.V.%	6.8	16.9	26.2	28.5	10.5	9.7	4.4
	P.C.V.%	7.8	18.4	29.0	32.1	12.6	11.8	6.5
C_1	Mean	61	158	32	3055	26	2.78	71
	Range	52-70	96-217	16-52	1555-5300	21-36	2.03-3.48	64-77
	G.C.V.%	5.5	12.8	22.3	22.2	11.4	10.0	3.5
	P.C.V.%	6.2	15.6	26.9	26.8	13.8	11.7	5.6
C_2	Mean	62	164	34	3750	27	2.88	72
	Range	56-73	106-240	18-54	2075-5460	19-35	2.26-3.67	66-78
	G.C.V.%	4.3	14.4	20.3	19.8	9.5	8.9	3.1
	P.C.V.%	5.2	16.6	24.0	22.8	11.4	10.8	4.6
C_3	Mean	66	183	43	4495	27	2.99	74
	Range	60-73	144-220	23-74	2435-6500	21-34	2.48-4.02	70-78
	G.C.V.%	4.1	8.9	21.4	15.5	8.6	9.2	1.9
	P.C.V.%	5.0	11.4	23.9	19.3	10.6	10.9	3.6
L.S.D. of mean for cycle at 5%		0.3	2.2	0.8	81	0.3	0.03	0.3
C.V. %		3.2	7.9	12.7	12.9	6.8	6.1	3.1

Table 19 : S_1 progeny means, ranges, genotypic coefficients of variation (G.C.V.) and phenotypic coefficients of variation (P.C.V.) for seven agronomic traits in different cycles of the US/B population - S_1 progenies on Alfisols.

Cycle		Bloom (days)	Height (cm)	Grain Yield/ plant (g)	Grain yield/ha (kg)	Head length (cm)	100-kernel weight (g)	Threshing %
C_0	Mean	56	170	27	3035	24	2.57	75
	Range	51-68	100-217	15-43	1855-4645	18-31	2.01-3.31	68-80
	G.C.V.%	5.3	14.3	17.9	17.8	9.6	9.1	3.0
	P.C.V.%	6.0	15.6	20.9	21.1	11.3	11.2	4.3
C_1	Mean	58	154	27	3390	24	2.51	75
	Range	52-65	104-213	19-38	2145-4575	18-30	1.95-3.07	68-82
	G.C.V.%	4.4	15.8	13.3	14.0	9.2	8.5	2.8
	P.C.V.%	5.1	17.2	18.5	18.0	11.3	10.6	4.7
C_2	Mean	59	163	31	3700	24	2.59	76
	Range	54-68	98-210	22-41	2255-4935	18-30	2.14-3.25	67-81
	G.C.V.%	4.2	11.7	13.5	11.3	9.3	7.6	2.6
	P.C.V.%	4.9	13.4	18.0	15.4	11.1	9.7	4.1
C_3	Mean	62	175	31	3920	24	2.63	77
	Range	57-73	126-213	15-44	2265-5365	19-29	2.09-3.39	57-82
	G.C.V.%	5.3	10.9	17.0	15.0	9.0	8.9	2.5
	P.C.V.%	5.9	12.6	20.0	17.7	10.9	10.4	5.9
L.S.D. of mean for cycle at 5%		0.3	1.9	0.6	66	0.3	0.03	0.3
C.V. %		2.6	6.5	11.6	10.6	6.1	6.1	3.3

Table 20 : S_1 progeny means, ranges, genotypic coefficients of variation (G.C.V.) and phenotypic coefficients of variation (P.C.V.) for seven agronomic traits in different cycles of US/B population - S_1 progenies on Vertisols.

Cycle		Bloom (days)	Height (cm)	Grain yield/ plant (g)	Grain yield/ha (kg)	Head length (cm)	100-kernel weight(g)	Threshing %
C_0	Mean	59	171	34	3380	26	2.79	74
	Range	53-74	101-229	16-57	2100-5070	21-32	1.94-3.80	67-79
	G.C.V.%	6.2	16.4	21.9	21.3	9.0	10.2	3.4
	P.C.V.%	6.6	17.4	23.7	23.8	10.9	11.2	4.4
C_1	Mean	61	158	37	3625	27	2.78	74
	Range	54-67	104-233	18-69	2140-6520	20-34	2.02-3.45	68-80
	G.C.V.%	4.6	17.7	27.0	20.4	10.5	9.7	2.8
	P.C.V.%	5.4	19.0	29.6	22.9	11.8	11.0	3.8
C_2	Mean	63	168	42	4325	27	2.88	76
	Range	57-70	94-223	22-72	1925-6945	21-32	2.29-3.53	70-81
	G.C.V.%	4.1	13.3	20.1	17.9	9.9	9.6	2.8
	P.C.V.%	4.7	14.9	21.8	19.4	11.2	10.9	3.4
C_3	Mean	65	184	45	4695	26	2.96	78
	Range	58-74	139-227	21-68	2940-6195	22-33	2.31-4.14	72-85
	G.C.V.%	5.0	10.7	19.0	14.4	8.5	10.8	2.4
	P.C.V.%	5.4	12.2	20.3	16.7	10.3	11.9	3.0
L.S.D. of mean for cycle at 5%		0.3	1.9	0.6	64	0.3	0.03	0.3
C.V.%		2.4	6.2	9.3	9.0	5.6	5.0	2.0

Table 21: S_1 progeny means and gains from selection for seven agronomic traits in different cycles of recurrent selection in the US/R population.

	Bloom(days)			Height (cm)			Yield/plant (g)		
	Mean	% change		Mean	% change		Mean	% change	
		Over 1 cycle	Cumulative		Over 1 cycle	Cumulative		Over 1 cycle	Cumulative
Alfisols									
C_0	57	-	-	160	-	-	22	-	-
C_1	59	3.5	3.5	152	-5.0	-5.0	23	4.5	4.5
C_2	60	1.7	5.3	154	1.3	-3.8	25	8.7	13.6
C_3	65	8.3	14.0	172	11.7	7.5	30	20.0	36.4
LSD at 5%	0.3			2.2			0.6		
C.V. %	2.9			7.4			13.9		
Vertisols									
C_0	58	-	-	165	-	-	29	-	-
C_1	61	5.2	5.2	158	-4.2	-4.2	32	10.3	10.3
C_2	62	1.6	6.9	164	3.8	-0.6	34	6.3	17.2
C_3	66	6.5	13.8	183	11.6	10.9	43	26.5	48.3
LSD at 5%	0.3			2.2			0.8		
C.V. %	3.2			7.9			12.7		

Table 21 : (Contd.)

	Yield/ha(kg)			Head length(cm)			100-kernel weight(g)			Threshing %		
	Mean	% change		Mean	% change		Mean	% change		Mean	% change	
		Over 1 cycle	Cumula-tive		Over 1 cycle	Cumula-tive		Over 1 cycle	Cumula-tive		Over 1 cycle	Cumula-tive
Alfisols												
C_0	2355	-	-	23	-	-	2.54	-	-	73	-	-
C_1	2510	6.5	6.5	23	0	0	2.55	0.4	0.4	73	0	0
C_2	2870	14.3	21.7	23	0	0	2.61	2.4	2.8	74	1.4	1.4
C_3	3390	18.1	43.8	23	0	0	2.66	1.9	4.7	75	1.4	2.7
LSD at 5%	64.0			0.3			0.03			0.3		
C.V. %	12.9			7.2			5.8			3.8		
Vertisols												
C_0	2815	-	-	26	-	-	2.67	-	-	70	-	-
C_1	3055	8.6	8.6	26	0	0	2.78	4.1	4.1	71	1.4	1.4
C_2	3750	22.7	33.3	27	3.8	3.8	2.88	3.6	7.9	72	1.4	2.9
C_3	4495	19.9	59.7	27	0	3.8	2.99	3.8	12.0	74	2.8	5.7
LSD at 5%	80.7			0.3			0.03			0.3		
C.V. %	12.9			6.8			6.1			3.1		

Table 22: S_1 progeny means and gains from selection for seven agronomic traits of different cycles of recurrent selection in the US/B population.

	Bloom(days)			Height (cm)			Yield/plant(g)		
	Mean	% change		Mean	% change		Mean	% change	
		Over 1 cycle	Cumulative		Over 1 cycle	Cumulative		Over 1 cycle	Cumulative
Alfisols									
C_0	56	-	-	170	-	-	27	-	-
C_1	58	3.6	3.6	154	-9.4	-9.4	27	0	0
C_2	59	1.7	5.4	163	5.8	-4.1	31	14.8	14.8
C_3	62	5.1	10.7	175	7.4	2.9	31	0	14.8
LSD at 5%	0.3			1.9			0.6		
C.V. %	2.6			6.5			11.6		
Vertisols									
C_0	59	-	-	171	-	-	34	-	-
C_1	61	3.4	3.4	158	-7.6	-7.6	37	8.8	8.8
C_2	63	3.3	6.8	168	6.3	-1.8	42	13.5	23.5
C_3	65	3.2	10.2	184	9.5	7.6	45	7.1	32.4
LSD at 5%	0.3			1.9			0.6		
C.V. %	2.4			6.2			9.3		

Table 22: (Contd.)

	Yield/ha(kg)			Head length(cm)			100-kernel weight(g)			Threshing %		
	Mean	% change		Mean	% change		Mean	% change		Mean	% change	
		Over 1 cycle	Cumulative		Over 1 cycle	Cumulative		Over 1 cycle	Cumulative		Over 1 cycle	Cumulative
Alfisols												
C_0	3035	-	-	24	-	-	2.57	-	-	75	-	-
C_1	3390	11.7	11.7	24	0	0	2.51	-2.3	-2.3	75	0	0
C_2	3700	9.2	22.0	24	0	0	2.59	3.2	0.8	76	1.3	1.3
C_3	3920	5.9	29.2	24	0	0	2.63	1.5	2.3	77	1.3	2.7
LSD at 5%	66.0			0.3			0.03			0.3		
C.V. %	10.6			6.1			6.1			3.3		
Vertisols												
C_0	3380	-	-	26	-	-	2.79	-	-	74	-	-
C_1	3625	7.3	7.3	27	3.8	3.8	2.78	-0.4	-0.4	74	0	0
C_2	4325	19.3	28.0	27	0	3.8	2.88	3.6	3.2	76	2.7	2.7
C_3	4695	8.5	38.8	26	-3.7	0	2.96	2.8	6.1	78	2.6	5.4
LSD at 5%	64.3			0.3			0.03			0.3		
C.V. %	9.0			5.6			5.0			2.0		

DISCUSSION

Recurrent selection in predominantly cross-pollinated crops has been found as an effective system of selection in accumulating favourable alleles at a large number of loci and in providing increased opportunities for selection of plants with favourable character combinations in the selected population. The information on the success of such a population improvement program in self-pollinated crops in general, where its application has started only recently, is limited.

The common experience of sorghum breeders in national programs is a reduction in genetic variability in breeding material as the programs move ahead. This poses a limitation in the choice of parental material in the development of appropriate segregating populations by conventional breeding methods. Maintenance of variability is necessary to sustain the progress in breeding for improved varieties and hybrids. The most important method to diversify the genetic variability in conventional programs is by introduction and adaptation of germplasm from outside of the program. Population improvement using recurrent selection techniques is another method.

The use of population improvement procedures in sorghum was advocated by Gilmore (1964), Eberhart (1970), Doggett and Eberhart (1968). The availability of the stable genetic male-steriles in sorghum facilitated the development of freely out crossing random mating populations similar to those in cross-pollinated crops.

Following these developments, a substantial program on improvement of sorghum populations was undertaken at ICRISAT. Currently several populations are available which are being subjected to cycles of selection and recombination. Two of these populations, US/R and US/B, in which three cycles of recurrent selection have been completed were taken for this investigation. As indicated earlier, S_1 progeny testing was used in the first cycle of selection and in the following two cycles S_2 family selection was employed. The selection intensities varied from cycle to cycle (Table 1). The objective of selection during each cycle was to improve the populations simultaneously for several economically important characters, including resistance to diseases and pests and grain quality aspects. However, in the present investigation only flowering, plant height, grain yield and its components were studied. The progress due to traits such as grain color, grain quality and overall desirability of plant type that are difficult to measure were not reported. However, there has been a substantial positive shift for these characters over three cycles of selection.

Two types of trials were conducted, population bulk trials consisting of random mated bulks, selfed bulks of C_0, C_1, C_2 and C_3 and their crosses C_0 x C_0 to C_3 x C_3 between the US/R and US/B populations. CSV-4 was used as a varietal check and CSH-6 as a hybrid check. The S_1 progeny trials consisted of 81 S_1 progenies derived from each of the four cycles of a population. The data from population bulk trials on grain yield and 1000-kernel weight was to substantiate the results obtained from S_1 progeny trials as the measurements on these characters on limited plant samples and/ or on a single row basis could be misleading.

The results for grain yield have clearly indicated that there has been a positive shift in the population means for both populations. The average per cycle gain in the US/R and US/B populations were 17.2 and 11.3%, respectively. In the earlier studies, Eckebil et al. (1977) predicted 16.3% selection advanced per cycle of S_1 families in the NP5R population and Doggett (1972) observed 25% selection advance after three cycles of S_1 testing in the African population. The rate of selection advance for grain yield was slightly greater in the US/R population than in the US/B population. The differential rate is accounted because of higher variability in the US/R population as indicated by the coefficients of genetic variation in the populations. The observations for each cycle indicated that gains from selection in the US/B population appear to be of similar magnitude from C_1 to C_3, while the gains in the US/R population were greater in later cycles. The maximum gains were noted in the third cycle during which additional lines were incorporated. The gains appear commensurate with the variability in the populations.

The observations on the gains for yield components indicates that while the mean head length remained unchanged, there were marginal increases in the kernel weight and threshing percentage of both populations. It is realized that there was no deliberate selection for these yield components during selection except that bold grains were generally preferred. The increase in grain yield can be accounted for increased in the threshing percentage and kernel weight and also perhap due to an increase in grain number per head which was not calculated.

The results of Tables 8 and 9 indicated that all cycles of both populations produced higher grain yields than CSV-4, the improved variety. The comparison between CSH-6, the hybrid check, and random mated bulks indicates that C_3 of the US/R population produced significantly higher grain yield than CSH-6 and C_3 of the US/B was on par with CSH-6. It can, therefore, be expected that it should be possible to select lines of comparable or superior yields, as compared to CSH-6, from the advanced cycles of population improvement.

The superiority of advance cycles for grain yield was further substantiate from the comparisons of individual S_1 progeny yields. It was noted that an increasingly higher proportion of S_1 lines were derived from the later cycles of both populations. These results clearly demonstrate that with increase in the mean yield of the populations, the opportunity of deriving high yielding lines is also increased. These results are in accordance with the expection of Eberhart (1972) that the improvement in breeding populations results in parallel improvement in the lines derived from the population at the end of each selection cycle.

It was noted from Tables 17, 18, 19 and 20 that the selection in both populations resulted in a delay in maturity. The base populations were earlier in maturity than desired. Progeny evaluations were conducted primarily at Indian locations where there was advantage to later types. A selection pressure was applied towards lateness so that the populations are better adapted to Indian conditions. It is interesting to note that the range in maturity is sufficiently large to modify the populations in any desired direction. The genotypic coefficient of variation reduced in later cycles indicating that the advanced cycles were more homogeneous and uniform than the base population. It is further noted that the delay in maturity is maximum in the third cycle of selection in which additional lines were incorporated. These additional lines were better adapted to Indian conditions in that they were generally later in maturity than the lines from the population.

The observations on plant height are similar to those of maturity except that the height was significantly reduced in the first cycle of selection. The height was maintained from C_1 to C_2 in the US/B population whereas there was a little increase in the US/R population. The plant height increased in the third cycle of both populations after additional lines were incorporated.

The effect of recurrent selection on the relationship between yield, plant height and maturity in these populations does not appear relevant as there has been almost a linear increase in grain yield over cycles whereas the plant height has been fluctuating from cycle to cycle, for example, there was an increase of 7.5% in the grain yield in the first cycle of selection over the base in the US/R population but the plant height in the same cycle was reduced by 4.7%. On the other hand, in C_3 of the same population there was 19% increase in grain yield followed by 11.5% increase in the plant height. It is extrapolated therefore that the change in plant height appears to be mainly a function of direction of selection rather than the associated effect of increased yield.

The observation on % genotypic and phenotypic coefficients of variation in different cycles for different characters indicated that except for plant height and maturity the genetic variability for all characters was maintained very close to that of the original populations. The addition of new lines in the third cycle helped in increasing the variability which was slightly reduced over the first two cycles. Based on the observations from these results it can be concluded that recurrent selection in these two populations has been very successful in increasing the mean of the population in the desired direction simultaneously for all characters. Without losing variability except for plant height and maturity and it is anticipated that a per cycle gain in yield of about 14% could be continuously maintained for many more cycles of selection. It was apparent that a much higher rate of selection advance can be realized for any one particular trait than was observed in this study if selection pressure is applied for only that trait, i.e., it has been observed that as the number of traits selected for increases, the gain per cycle for each trait decreases compared to a situation where selection is for only one of the traits.

SUMMARY

Field experiments were conducted at the Center of the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, during the rainy season of 1980 to examine the effects of recurrent selection on two random mating populations of sorghum (US/R and US/B).

Two types of trials were conducted for each population: Population Bulk Trials - consisting of C_0, C_1, C_2 and C_3 random mated and selfed bulks and crosses between $C_o \times C_0$, $C_1 \times C_1$, $C_2 \times C_2$ and $C_3 \times C_3$ of US/R and US/B populations along with a varietal check and a hybrid check; and, S_1 Progeny Trials - consisting of 81 S_1 progenies derived from each of four cycles in each population.

Both trials were grown on two types of soils: Alfisols and Vertisols available on the farm. The data were recorded on: Days to 50% flowering, plant height, grain yield/plant, grain yield/ha, head length, 100-kernel weight and threshing percentage from the S_1 Progeny Trials. The data were also collected from the Population Bulk Trials on grain yield/ha and 1000-kernel weight to supplement the results from the S_1 Progeny Trials as well as to calculate inbreeding depression from half-sibs to one generation of selfing in each cycle of selection.

On the basis of the above two trials the following observations were made:

1) Three cycles of recurrent selection in both populations resulted in increased grain yield. The selection advance per cycle for grain yield was higher in the US/R population (17%),

which has greater genetic variability, than in the US/B population (11%).

2. Increased grain yield in both populations may be accounted for from increased threshing percentage, slight increase in kernel weight and also possibly due to increase in grain number per plant.

3. Advanced cycles of populations, particularly the third cycle where additional lines were incorporated into the population resulted in a delay in maturity as indicated by days to 50% flowering.

4. The plant height varied from cycle to cycle and increased mainly in the third cycle in which additional lines were incorporated.

5. Three cycles of selection resulted in reduced variability in plant height and maturity of both populations indicating that advanced cycles became more homogeneous for plant height and maturity. The variability for other characters was nearly the same as in the base populations.

On the basis of the above observation, it was concluded that recurrent selection following progeny selection (S_1 and S_2) is very successful in increasing the mean of the population in the desired direction without losing much variability and selection advance of about 14% per cycle can be expected to be maintained in further cycles.

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