Arunachalam, V. and Katiyar, R. K.
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Composite Populations.
Indian Journal of Genetics and Plant Breeding,
42 (1982): 32-37.

A VIABLE SHORT-TERM STRATEGY FOR BREEDING COMPOSITE POPULATIONS

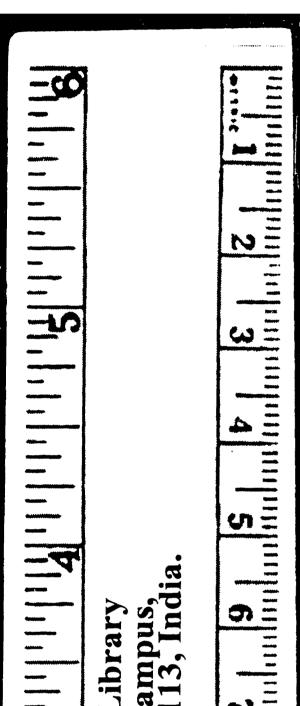V. ARUNACHALAM* and R.K. KATIYAR

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ABSTRACT

A viable short-term strategy has been outlined to breed productive composite populations. The major steps in the strategy are generating a base gene pool, reordering it into a productive gene pool by appropriate systems of mating and syphoning composite populations through effective selection. The strategy was field tested in *Pennisetum typhoides* and *Brassica campestris* and found efficient. The utility and implications of this strategy are discussed.

Most of the methods used for breeding pure lines start with single crosses as their base. In the process of breeding, the potential of the initial base gets diluted both in terms of yield and, in many cases, of resistance though the degree of dilution depends, among other causes, on the specific crop, the nature of the breeding system, the size of the material handled, the mating process generating it and the methods of selection. Moreover, the major strategy to surpass the "yield limit" set by the existing high-yielding varieties still remains hybird breeding. The heterozygous hybrid genotype, being homogeneous can, however, still be exposed to serious disease-pest risks in addition to helping the long-term evolution of virulent races of pathogen.

On the other hand, populations, composite or synthetic, consisting of an array of genotypes "sharing in a common gene pool" (Dobzhansky, 1951) offer a viable alternative with built-in capacity for maximum avoidance of the risks enumerated earlier. Being dynamic gene pools, they can retain the effects of a number of genes contributing to yield and resistance to pests and diseases without the risk of diluting them down the generations. There is scope for maintaining a balance of favourable and cumulative effects of genes by new genic combinations produced every generation. When situation demands, it is easier to replace a population by another in the pipeline, than a pure line derivative by another, as seed production does not impose any serious restriction, as would be seen later. This paper therefore, aims to present a viable approach to generate productive populations based on results achieved in two cross-pollinated crops.

MATERIALS AND METHODS

Brassica campestris var. brown *sarson* is an important oilseed crop in India possessing varying levels of self-incompatibility. Being highly cross-pollinated, it provides ample opportunities to test the basic concepts behind breeding for productive composite populations. The low and stagnant yield levels of this crop can be stepped up if short-term and repeatable strategies of producing composites can be evolved.

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A comparable situation (demanding recourse to population breeding) exists in the case of pearl millet (*Penn setum typhoides* S. & H.) too (Arunachalam, 1981). Despite the availability of several hybrids, yield advantage or stability could not be achieved due mainly to the major disease, downy mildew (*Sclerospora graminicola*) among other causes.

Earlier studies on *Brassica* showed that effective gene pools could be sythesised by inter-varietal single crosses (Devarathinam, Arunachalam and Murty, 1976), well-designed three way crosses (Arunachalam and Katiyar, 1978) and multiple cross-multiple pollen hybrids (Bandyo-padhyay and Arunachalam, 1980). Methods were devised to associate a high (H) or Low (L) general combining ability status to a parent from an evaluation of a set of F_1 crosses (made to a genetic design) for a number of characters spanning the whole duration of the crop (Arunachalam and Bandyopadhyay, 1979). They were also used to classify the specific combining ability of a cross as H or L. Investigations on some crops revealed that a high probability of obtaining desirable heterosis was associated with H × L crosses (where H and L are the gca status of parents), be they single or multiple crosses (Arunachalam and Srivastava, 1980 in triticale; Reddy and Arunachalam 1981, in pearl millet: Katiyar and Arunachalam, 1981 and Bandyopadhyay and Arunachalam, 1980 in *Brassica campestris*).

In pearl millet, several base gene pools were set up by mixing equal amounts of seed of 3- and 4-way crosses tested for general and specific combining ability for yield, number of tillers, plant height and length of earheads. The base gene pools evaluated for their yield in 1975 constituted the I phase. They were advanced to II phase by large scale hand crossing using multiple pollen. Only crossed seeds were used to form the II phase populations. Due to management limitations, they were advanced to III phase by open pollination without isolation. The populations were yield-tested in initial national trials in 1976-77. Their yield potential was tested in large plots of around 650 sq.m. in isolation during 1978. The yield fluctuations between rainy season (July) and winter planting (November) were also checked in 1977-78.

In contrast to the case in pearl millet, the three populations in *Bra ssica campestris* were set up from biparental matings in single crosses in F_3 generation and the rest from similar matings in 3-way crosses in F_2 generation.

RESULTS

PEARL MILLET :

The results clearly showed (Table 1) that the base gene pool (of 1975) was trans-formed into potential gene pool (of 1976) with almost double the yield capacity by one generation of inter-mating. Incidentally this result helps to emphasize the role of inter-

TABLE 1

Progressive yield (q/ha) status of composite populations in pearl millet

*Population	+1975 kh	+1976 kh	+1977 kh	1977 AICMIP	@1978 kh	1978 RB
8	9.6	18.4	17.9	12.6	15.7	8.7
16	8.0	14.4	15.0	—	16.0	10.3
34	7.3	18.6	10.9	12.6	13.9	11.7
Check[1]				17.3	21.3	13.7

*Base gene pool : 8—three 3-way crosses; 16—F_1 Bulk of 11 parent diallel crosses; 34—three 4-way crosses

+ Small plots; @ = Large isolation plots app. 650 sq.m.

kh = Rainy season; RB = Winter season; AICMIP = All-India Coordinated Millet Improvement Project.

[1] : Hybrid BJ 104

mating in upgrading even the low yield level of a base gene pool. However, the next generation (of 1977) raised under open pollination without isolation could just sustain the potential. Contamination in such a process by pollen whose potential was unknown could largely explain the result. The relative performance was maintained under large plots during 1978. The final yield level was, however, lower than the hybird check, indicating the need for further improvement.

The quick attainment of phenotypic uniformity in four years can mainly be attributed to the choice of the base gene pool only. However, it remains to be seen whether the yield level can be toned up in further cycles.

Brassica campestris : Here again the general trend of a slight depression in the yield level of II phase is due to open pollination without isolation allowed in I phase. However, the populations were toned up in further cycles by inter-mating in isolaticn and in particular, population I is doing well in all-India evaluation trials. It is again demcnstrated that an efficient choice of base gene pool can lead to a productive population in 4 or 5 years (Table 2).

TABLE 2

Progressive yield (q/ha) status of composite populations in Brassica campestris

+Population	1975	1976	1977	1978	1979
1	10.4	7.8	14.7	16.7	18.7
					*19.0
2	13.4	10.3	17.9	14.3	15.6
6	13.4	8.0	19.7	11.1	—
Check (Composite Pusa Kalyani)			15.5		17.2

*Large plot of app. 600 sq. m. ⊢ Base gene pool : 1, 2 = Progeny of biparental matings in F_3 of single crosses; 6 = Progeny of biparental matings in F_2 of a three-way cross.

DISCUSSION

A possible short-term approach for population improvement can now be outlined with the following major steps : (A) Creating a base gene pool; (B) Upgrading the base to a potential gene pool by appropriate mating systems; (C) Reordering the potential gene pool into productive populations by selection. Though these steps are known, the method suggested to handle them are capable of ensuring a higher rate of success and repeatability as compared to the existing ones.

Base Gene Pool: This is the most crucial step of the strategy. At the same time, it can admit of a good deal of flexibility. For instance, the number of entries and the

amount of seed in each entry which should be mixed to construct the base gene pool cannot be fixed *a priori*. But it would be desirable to have a large and diverse base gene pool. It would be a good practice to include source genotypes for disease and insect resistance and for a range of yield components like plant height, maturity, tillering capacity etc. The choice and constitution of the base gene pool may fruitfully be made on a quantitative evaluation of the constituent genotypes which could be parents or F_1 crosses. Results of earlier studies emphasise the need to incorporate heterotic H × L crosses with non-significant, overall low or high sca in that order of preference. This is borne out by the observation that heterotic crosses are found in high frequency in H × L category which incorporates divergence in direction and magnitude of the overall gca effects over a number of component characters. The probability of sustaining the heterosis in further generations is high if the source heterotic crosses are associated with non-significant or low sca since undesirable segregation due to epistatic interactions will then be low. Absence of dominance-based interactions is expected to hasten establishment of phenotypic homogeneity in further generations. Base gene pool generated by H × H crosses and by elite material may rank next.

The procedure outlined here lays emphasis on constructing a base gene pool with constituents tested for their genetic status in terms of gca, sca and heterosis. Subsequent steps operate entirely within this genetic frame and the new genic combinations arise by recombination within this base gene pool.

This is a significant departure from some of the methods in vogue which lay stress on selection of full-sib and half-sib families based on yield in Step (B) — potential gene pool in the terminology of this paper. It must be remembered that the half-sibs referred to result from unknown pollinators whose genetic potential is unknown. Considering further that yield alone cannot be fruitful in judging the genetic potential with a desired level of 'repeatability', one cannot completely dispel the causes for hit-and-miss in this process. The very same reasons would weigh against the argument that production and selection of half and full-sib families are relatively simple to practise.

On the other hand, the construction of the base gene pool as outlined in this paper, would require only one testing of the gca and sca (based on F_1). In cross-pollinated crops where composite populations are anyway relevant, it is quite easy to start with a large number F_1's. This therefore need not impose any severe restriction on the number of constituents of the base gene pool, especially when one can include both parents and crosses in it. An evaluation of gca and sca in F_1 on a number of important yield components and yield takes only one season, in addition to the one season taken for making the crosses. The greatest advantage is that, once the base gene pool is filtered to contain constituents that would enhance the chances of sustaining the additive gene action and heterosis, subsequent steps will not only ensure a productive composite but also obtain it in a few generations of inter-mating. The need for a choice of the base gene pool on a quantitative evaluation of its constituents is thus clear.

Potential Gene Pool: This is the important link between base gene pool and productive populations. Recombination and transgressive segragation are the two main phenomena that should be catalysed to transform base into potential gene pool. The easiest method is to grow a large plot in isolation and allow large scale inter-mating. In wind-pollinated crops like pearl millet and maize, this method will work more successfully as compared to crops like sunflower and *Brassica* since the extent of inter-mating is dependent on the activity of bees, the main pollinating agent in the lattter. In such a situation, large scale hand crossing using multiple pollen, wherever feasible, is a sound alternative. The next phase of the population breeding should be intiated from the crossed seeds only.

When the crop is grown in isolation, there may be chances for a high frequency of selfing too. A successful population should hence be able to stand some selfing also (where relevant). However, if selfing percent crosses a threshold value, the productivity of the population will start declining especially when inbreeding depression can occur. One way to check this event is to keep the size of the isolation plot where inter-mating is allowed sufficiently large.

Repeated cycles of inter-mating in isolation *without* selection will strengthen the potential gene pool with productive recombinants. It is a healthy practice to refrain from eliminating low phenotypes in any cycle in order to provide better chances for H $\times$ L mating, which has, in turn, a high chance of generating transgressive segregants. The number of cycles of inter-mating cannot again be fixed *a priori*: usually 3 to 4 cycles should do provided the base gene pool is assembled on the lines suggested earlier. Otherwise more number of inter-mating cycles may be needed which may not always assure of a potential gene pool capable of yielding productive populations.

Composite Populations : These are the ultimate products of the potential gene pool. When a reasonable level of phenotypic uniformity of potential gene pool is attained in the course of inter-mating, mild mass selection practised with the main aim of achieving optimum plant density per unit area capable of optimal yield under optimal agronomic management, will provide the composite population. The number of cycles of mass selection can again be variable: usually it need not exceed 3 or 4. In every cycle attention is drawn to maintaining phenotypic (and not genetic) uniformity only.

The steps outlined above are quite flexible to admit of new sources of germplasm and other productive genotypes. Since the genetically heterogeneous base gene pool cannot be maintained over time, new sources cannot be simply added to it at any point of time. Hence they should preferably be included at the stage of constituting the base gene pool. The process of testing the combining ability components of the constituents will filter out poor combining source material avoiding addition to the total time of breeding composite populations.

Thus, with the strategy evolved to generate such populations with ease, it is possible to work on the concept of replacement of such populations when their performance shows a declining trend with a new productive one in the pipeline, rather than regenerating them which would necessitate maintenance of the components of the base

gene pool. When the base gene pool can be generated by a variety of means like tested individual genotypes, single crosses, multiple crosses or a combination of any or all of these, maintaining the genetically segregating components of the base gene pool over time is impossible, nullifying the chances of regenerating a composite.

New procedures like the diallel selective mating (Jensen, 1970) lay emphasis on techniques of broadening the initial base but they do not prescribe methods to take into account the genetic nature of its constituents at any time. As a consequence, they become ineffective in assuring improvement in a short time. In contrast, the procedures outlined in this paper maintain effectively the genetic heterogeneity of populations and at the same time are tuned to bring in rapid phenotypic homogeneity.

The last important point in favour of composite populations is the minimal requirements for seed production. The only need is to confine seed multiplication to large plots of a few hectares in isolation, to avoid erosion of genetic heterogeneity by sampling. The cost of seeds can then be kept low retaining other advantages associated with populations, which should, therefore, be a successful proposition for farmers.

REFERENCES

Arunachalam, V. (1981). Genetic basis of population improvement with particular reference to pearl millet. In 'Trends in Genetical Research on *Pennisetums*" Ed. V. P. Gupta & J. L. Minocha, P A U Ludhiana, Ap. 35-40

Arunachalam, V. and R.K. Katiyar. (1978). Genetic diversity and breeding potential from disrup. tive selection in *Brassica campestris* cv brown *sarson*. *Exptl. Agric.* Camb., 14:73-79.

Arunachalam, V. and A. Bandyopadhyay. (1979). Are multiple-cross multiple pollen hybrids an answer for productive populations in *Brassica campestris* var, brown *sarson?* I. Methods for studying mucromphs *Theor. appl. Genet.* 54:203-207.

Arunachalam, V. and B.B. Reddy. (1981). Evaluation of heterosis through combining ability in pearl millet. II. Multiple crosses. *Indian. J. Genet.* 41:73-81.

Arunachalam, V. and P.S.L. Srivastava. (1980). Assessment of genetic potential of multiple crosses in triticale. *Genet. Agr.* 35:117-127

Bandyopadhyay, A. and V. Arunachalam. (1980). Are multiple cross-multiple pollen hybrids an answer for productive populations in Brassica campestris var. brown sarson? Part 2: Evaluation of 'mucromphs'. *Theor. appl. Genet.* 58:5-10.

Devarathinam, A.A., V. Arunachalam and B. R. Murty. (1976) A quantitative evaluation of intervarietal hybrids of *Brassica campestris* L. *Theor. appl. Genet.*, 48:1-8

Dobzhansky, T. (1951). Mendelian populations and their evolution. Chap. 25:573-589, in *Genetics in the 20th century* (ed). L.C. Dunn, New York: Macmillan Co.

Jensen, N.F. (1970). A diallel selective mating system for cereal breeding. *Crop Sci.*, 10:629-635.

Katiyar, R.K. and V. Arunachalam. (1981). Single and three-way crosses for generating composite populations in rapeseed *Indian J. Genet.*, 41:95-103.

Reddy, B.B. and V. Arunachalam. (1981). Evaluation of heterosis through combining ability in pearl millet. I. Single crosses. *Indian J. Genet.*, 41:66-72.