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STRATEGIES FOR PLANT IMPROVEMENT ARISING FROM BASIC GENETIC STUDIES ON SOME CROP PLANTS

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ABSTRACT

Basic studies on pearl millet (*Pennisetum typhoides L.*), rapeseed (*Brassica campestris L.* var. brown sarson) and triticale were utilised to classify parents and hybrids conforming to known designs of mating as of High or Low potential. Methods were devised to pool information, particularly on combining ability and heterosis, on a large number of component characters spanning the entire growth phase of the plant. High \times Low crosses showed, in all crops, a higher frequency of heterotic crosses than High \times High or Low \times Low. These were also efficient as parents of productive three - and four-way crosses. A feasible hypothesis to explain the superiority of High \times Low crosses was provided.

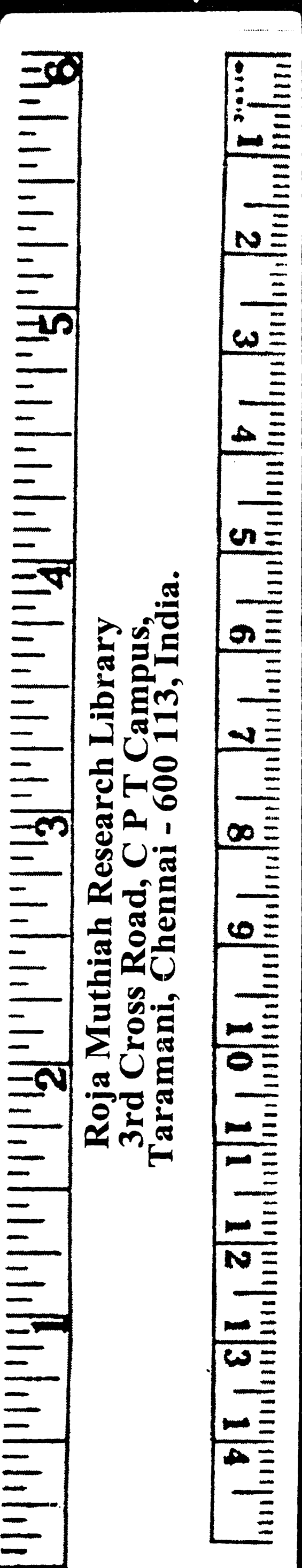
The need for short term strategies for accelerating yield improvement in crop plants per unit time and space is increasingly felt in India in the context of growing population and static area available for agriculture. Such strategies should satisfy certain norms for large scale application. For instance, they should be need-based and repeatable. As far as possible, they should be relatively simple to adopt at field level. They should be flexible enough to accommodate new research information and quick orientation to become increasingly efficient. They should be constructed on easily available basic information and avoid, as a general rule, over-dependence on special human skill. This point gains ground when instances are recollected where phenotypic selection of super-plants, dependent solely on individual skill of spotting them, constitutes a major strategy of breeding some crop plants.

Yield, which is the main interest of

every agricultural scientist, in general, and a plant breeder, in particular, is now acknowledged as a highly complex character and has been a subject of intensive research for a long time. It has a large number of direct and indirect components and disciplines like plant physiology, biochemistry, pathology and entomology which have come to play a greater role in its understanding. Consequently, the goal of the plant breeder is like the proverbial carrot hanging before the donkey pulling the carriage. The goal is nearer since other disciplines help a breeder to understand the structure and function of yield components in better perspective ; at the same time, the goal is far since the number of components a breeder has to consider now has vastly increased, making the task of providing a repeatable genetic basis of breeding arduous.

It is now possible to identify and measure a number of direct and indirect yield components. But they are correlated,

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varying largely in the intensity of association. Most often correlations among important components of yield are negative. Crucial decisions on the mating system and selection to be followed in the next generation depend on the ratio of additive to epistatic components of variance in these yield components which are usually under polygenic control. So much so, these variances need to be estimated with a relatively high precision.

However, the theoretical base of Mendelian genetics rests essentially on single gene diallelic models. Their results are extended to polygenic situations, as a matter of analytical simplicity and theoretical elegance, under untenable assumptions. They find their way wrongly into complex practical applications even now, thereby weakening the reliability of decisions based on them.

The immediate need, therefore, is to identify repeatable methods of evaluating the relative genetic potential of genotypes, not essentially on one gene model or its questionable extensions, but on the phenotypic values of a number of related component characters. Since basic information of breeding value is usually collected on a set of F_1 crosses to start with, it is essential that repeatable methods are devised for such situation.

An attempt is, therefore, made in this paper to evaluate the results of a number of investigations undertaken with these objectives at the Biometrical Genetics Unit of the Indian Agricultural Research Institute, New Delhi during the past decade.

MATERIALS AND METHODS

The crops that were used for the investigations were brown sarson (*Brassica campestris* L.) (Bandyopadhyay, 1976 ;

Katiyar, 1978), pearl millet (*Pennisetum typhoides* L.) (Reddy, 1975 ; Goswami, 1976) and triticale (Srivastava, 1975). The designs of mating adopted were line \times tester, diallel, triallel, three- and four-way crosses made in a combined (line \times tester-diallel) system and complex crosses made by pollinating single and triple crosses with mixed pollen from one, two or three varieties. Usually the F_1 generation was raised in randomised block design with two replications with single row plots for the crosses. Optimal agronomic and cultural practices were followed. Observations on characters were made on samples of varying sizes from 3 to 12 plants per plot depending upon the growth conditions. The data were subjected to single plant weighted analysis and genetic information was gathered from the combining ability analysis as detailed in Griffing (1956) and Arunachalam (1974, 1976a, b). Characters which were observed were : days to first flowering (FT), plant height (HT), effective tillers (TL) or primary (PB) and secondary (SB) branches, length of ear (EL) or of main axis (LM), seedling vigour (SV) as dry weight of a sample of seedlings, seed weight (SW), number of ears or heads or number of siliquae on main axis and single plant yield (YD). A number of 'ratio' and 'plot' characters (Bandyopadhyay, 1976) were computed from these data to characterise single plant potential in an efficient manner. Whenever the parent material was suspected to have undergone arbitrary inbreeding, the variation in single plant flowering time was accounted by two parameters—mean and variance of flowering time on the basis of a frequency distribution of plants flowering at various points of time (for details, refer

to Bandyopadhyay, 1976 and Katiyar, 1978).

RESULTS AND DISCUSSION

We attempt only to provide a gist of salient and relevant results emerging in common from the studies. Other results important to the crop concerned are found in the references under 'Materials and Methods' and published papers (Srivastava and Arunachalam, 1976; Reddy and Arunachalam, 1979, 1980; Arunachalam and Reddy, 1980; Bandyopadhyay and Arunachalam, 1980; Arunachalam and Srivastava, 1980).

The main objective is to tag the genetic potential of a parent or a cross or the amount of heterosis over better parent into two distinct extreme classes at least, to be designated as High (H) and Low (L) hereafter. Usually data on a set of crosses in their F_1 generation conforming to a specific design of mating are available to a breeder. Proper analysis of data on a number of component characters spanning the entire growth phase of the plant till maturity provides general (gca) and specific combining ability (sca) effects, in addition to the amount of heterosis over better parent. On the basis of a defined norm of gca effects, a parent, and on sca effects, a cross can be grouped into 'High' or 'Low' category. When this is done, it is unlikely that the genotype records a consistent H or L status for each component character. To overcome this situation, a score of +1 for H, -1 for L and 0 for non-significant effects is given to each component character. The total score over the characters will then represent the pooled information on an entry, parent or cross. On the basis of a defined norm of the total scores, a genotype is finally classi-

fied as overall High or Low. Similarly, the heterosis over the component characters is classified based on the possible distribution of the hybrid in relation to its parents. It has been shown that a cross can be considered heterotic if it shows heterosis over better parent for 'h' component characters out of 'n', where $h = n/4$. These methods have been discussed in detail by Arunachalam and Bandyopadhyay (1979).

The method of classifying a parent or a cross was found to be repeatable. It is to be noted that a specific parent, like *Bele* in brown sarson, for example, may receive different diallel combinations when tested in different environments (in space or time). Since scientific plant breeding is a stochastic process, a breeder needs to take a decision for forwarding his material to the next generation and no more. The classification, if need be, would have to be done afresh in the next generation. Thus the method was found potent and repeatable.

The next logical step was to relate the observed heterosis with the relevant gca and sca status. If the data were examined for individual component characters (Table 1), it was found that, in most of the cases, HL registered the highest probability of recording heterotic crosses followed by HH for the two crops, pearl millet and triticale. In some cases, a relative superiority of LL over HL in this respect was observed, possibly due to the differential expression of component characters in specific residual genetic backgrounds and biotic environments. Further, it was interesting to observe in pearl millet, a higher frequency of heterosis in Dwarf \times Tall as compared to Dwarf \times Dwarf and Tall \times Tall crosses.

status in
different

If, however, overall heterotic performance was analysed (Table 2), HL crosses were invariably superior in all the three crops, whether single or multiple crosses were considered. A high repeatability could be associated with this observation when various sets of crosses or when particular sets over time were examined (Table 2). Moreover, the frequency of heterotic crosses with non-significant sca for every component character was more in HL than in HH group in all the crops. Again HL group of single crosses were found successful as parents of a large number of productive three- and four-way crosses.

But a single cross has to be characterised before flowering if it is to be used as a parent of a multiple cross. Otherwise, this cross has to be reproduced again for that purpose which results in the loss of a season. Many times, it may not be possible to obtain an exact genetical replicate of the cross again. Hence characterisation was done in all the crops on the basis of early growth characters like seedling vigour and the genetic status was compared with that based on all the character components. The tally was as high as 70 per cent based on seedling vigour alone in some instances and this can be kept up if more seedling characters are used for classification. Work is in progress in this regard.

Langham (1961) has provided a feasible hypothesis for realising transgressive segregation in HL crosses at F_2 level. It can be modified to explain the superiority of HL crosses at F_1 level, as observed in all our studies.

High genotypes possess genes capable of expressing high phenotypic effects but are prevented from doing so by the 'retarding' effect of residual genetic

background (RGB) (Fig.1). Low genotypes possess similarly genes capable of expressing extremely low phenotypic effects but are again prevented from doing so by the 'enhancing' effect of RGB.

Further, High genes express extremely high phenotypes when they, as well as the RGB, are homozygous and nearly equal phenotypes result when they and the RGB are heterozygous. But Low genes can express their potential only in a 'retarding' homozygous RGB. HH and LL crosses result in situations resembling essentially their parents and hence in a low frequency of heterotic crosses, if at all. But HL crosses produce heterozygous progeny genotypes in heterozygous RGB. Their phenotypes express high effects and thus are far superior to their superior parent, resulting in a high frequency of heterotic crosses. More potential transgressive segregants homozygous for High genes expressed in homozygous and enhancing RGB can be selected for in the segregating F_2 and higher generations.

Still one fair criticism can be levelled against the logic behind attaching equal weight to every component character used in characterising an entry as High or Low. But in the absence of a logical and repeatable method of assessing the weights to be attached to the component characters, the characterisation cannot undoubtedly be improved by the use of weights. Since the methods of characterisation are flexible enough to admit of more component characters, the problem of weighting can partially be overcome if we use a large number of component characters spanning the entire growth phase, from seedling to maturity, of the

Table 1. Efficiency of various groups of crosses in producing heterosis for some yield components

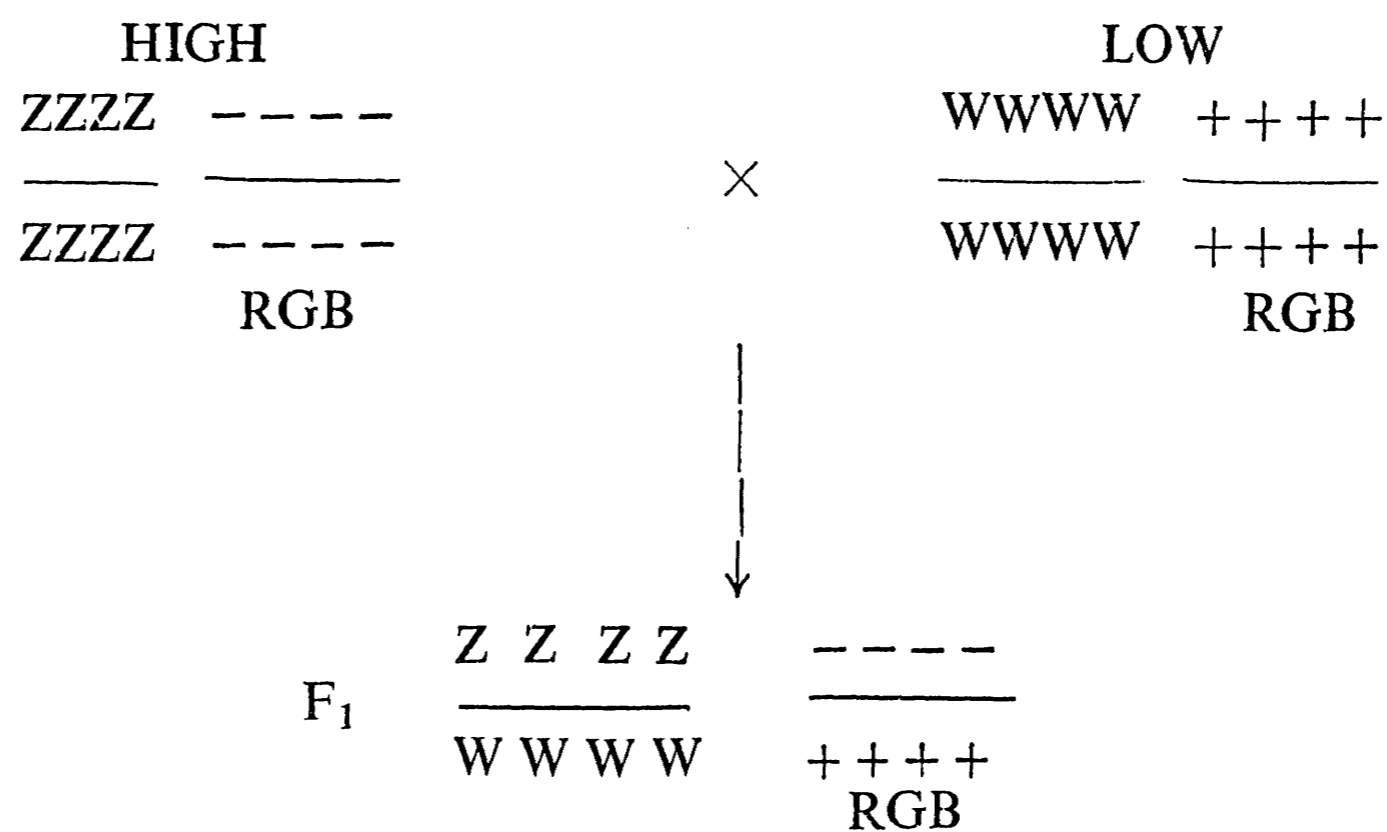
System	Character	HH	HL	LL
<i>Pennisetum typhoides L.</i>				
Single crosses				
Set 1	FT	0	100	0
	HT	54	23	23
	YD	25	75	0
	SW	0	100	0
	EL	40	40	20
Set 2	FT	43	14	43
	HT	14	43	43
	YD	25	50	25
	SW	29	58	13
	EL	20	60	20
*Set 3	FT	23	51	26
	YD	34	43	23
	SW	20	50	30
	EL	35	43	22
Triticale				
Set 1	FT	50	33	7
	TL	65	35	0
	YD	50	45	5
	SW	30	56	14
Set 2	FT	40	40	20
	TL	31	69	0
	YD	57	43	0
	SW	44	47	9

*The groups of crosses in this case were Tall × Tall, Dwarf × Tall, and Dwarf × Dwarf. Figures represent the percentage of heterotic crosses found in each group.

Table 2. Efficiency of various groups of crosses in producing heterosis

Crop	System	HH	HL	LL
<i>Brassica campestris L.</i>	Single crosses	29	57	14
	Three-way crosses	33	58	8
	Multiple crosses	26	52	22
<i>Pennisetum typhoides L.</i>	Single crosses Set 1	35	47	18
	Set 2	11	53	36
	Set 3	21	56	23
	Triallel crosses	26	57	17
Triticale	Single crosses Set 1	48	46	6
	Set 2	53	37	10

Figures represent the percentage of heterotic crosses falling in each group.



Z = High gene; W = Low gene; RGB = Residual genetic background;
 + = Enhancing; - = Retarding

Fig. 1. Genetic basis for superiority of High × Low cross.

plant. This, in a way, is also an attempt to take into account the phenotypic expression of a large sample of genes that define the genotype. Yet, searching for sound alternatives for characterisation into High and Low is an open area for research.

Vast literature supports our results on the utility of High × Low crosses in practical plant breeding. High × Low multiple-top crosses were found useful in corn improvement as far back as 1939 (Mangelsdorf, 1939). Dwarf × Tall crosses were frequently successful in rice, wheat, triticale, sorghum and in plantation crops like coconut (Bavappa and Sukumaran, 1976). Exotic × Indian and Temperate × Tropical crosses were the base for the development of pure lines and hybrids of sorghum in India (Rao and Rana, 1978). Winter × Spring combinations are now being tried in a large scale in wheat to transgress the existing yield levels. Even by subjecting winter varieties to summer adaptation and *vice-versa* it was possible to step up the yields of soybean (Tsai, Lu and Oka, 1967). Recently, High × Low combinations were found to rank first in yield potential in barley (Fejer and Jui, 1979).

Our work and those reported in literature thus point to the need for incorporating genetical, geographical and combining ability divergence in the choice of fruitful parents for hybridisation.

With the methods and concepts reported in this paper, it is now possible to set short-term and mission oriented breeding approaches in clearer perspective.

(a) Since wide genetic base is a better starting point than narrow one, it is useful to start with specific multiple crosses with known heterotic and combining ability status.

(b) If breeding for a pure line is the goal, a heterotic HL multiple cross with non-significant sca for every component character will provide a safe starting point. The initial choice of non-epistatic gene effects can help in sustaining more additive gene combinations in subsequent generations when compared to starting with a cross that is heterotic on the strength of high epistatis effects.

(c) If breeding for a hybrid is the goal, a HH or HL single cross which is highly heterotic on the strength of high sca (very high heterosis with low sca is a rare event) can be tested over time for

stability of performance. As usual, the problem of large scale seed production has to be solved prior to release.

(d) Heterotic multiple crosses with low sca can also form a resourceful initial gene pool from which 'composite' populations can be generated, as described in detail by Arunachalam (1976, 1978) and Das (1979).

The methods and concepts set above thus aim at cutting down, with a high

probability, the time that traditional breeding procedures usually take to derive a desirable genotype.

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