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Ralph van Berloo · Piet Stam

Marker-assisted selection in autogamous RIL populations: a simulation study

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Abstract Molecular markers may enable plant breeders to select indirectly for genes affecting quantitative traits by selecting for molecular markers closely linked to these genes (marker-assisted selection, MAS). We have assessed the effectiveness of MAS compared to phenotypic selection. Key variables in this assessment were: trait heritability, selection intensity, genetic architecture and uncertainty in QTL mapping. Simulation studies showed that the application of MAS in autogamous crops, with the objective of obtaining transgressive genotypes, can improve selection results when compared to conventional selection procedures. Marker-assisted selection appears particularly promising when dominant alleles at quantitative trait loci are present and linked in coupling phase. Uncertainty in estimated QTL map positions reduces the benefits of marker-assisted selection, but this reduction remains limited in most cases.

Key words Marker-assisted selection · Simulation · Quantitative trait loci · Complementation

Introduction

The advent of molecular-marker techniques has had a large impact on quantitative genetics. Marker-based methods applied to segregating populations have provided us with a means to locate quantitative trait loci (QTLs) to chromosomal regions and to estimate the effects of QTL allele substitution (Lander and Botstein 1989). The ability to estimate gene effects and locations for quantitative traits can be very useful for the design and application of new, efficient, breeding strategies. A new selection strategy, marker-assisted selection (MAS), has been proposed by many authors as a way to increase gains from selection for quantitative traits (Tanksley 1993; Lee 1995; Kearsey and Pooni 1996). In backcross breeding programs, it has been shown that MAS can be effective in reducing linkage drag and optimising population sizes, by selecting against the donor genome except for the allele(s) to be introduced from the donor (e.g. Hospital et al. 1992). MAS can also improve selection for quantitative traits by selecting for the presence of specific marker alleles that are linked to favourable QTL alleles. This can be done for single marker loci or for an index representing several marker loci. Breeding strategies for autogamous crops are often aimed at obtaining pure homozygous lines that show a superior phenotype. This can be done by generating genetic diversity, for instance a segregating F_2 population, selecting desirable individuals within the population, and then repeatedly selfing and selecting individuals until sufficiently homozygous lines are obtained. Another strategy uses the genetic variation that is present in F_2-derived inbred lines, obtained without selection, commonly referred to as recombinant inbred lines or RILs.

We consider a strategy based on intercrosses of pairs of RILs. We assume that the aim of the selection is to obtain single genotypes containing as many accumulated advantageous alleles as possible. This goal is different from the aim of population improvement studied by most other authors. Lande and Thompson (1990) and Gimelfarb and Lande (1994a, b), for example, did not consider extreme genotypes within a MAS-derived segregating population, but focussed instead on improvement of the mean genotypic value of a population over several generations of selection.

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R. van Berloo (✉) · P. Stam
C.T. de Wit Graduate school of Production Ecology, Department of Plant Breeding, Wageningen Agricultural University, PO box 386, Wageningen, The Netherlands
Fax: +31 317 483457
E-mail: ralph.vanberloo@users.pv.wau.nl

In the present paper, we analyse the possible benefits of MAS in autogamous crops, compared to conventional phenotypic selection. We investigate how the relative performance of MAS and conventional selection depend on the heritability of a trait, the intensity of selection, the genetic architecture (e.g. the number and spacing of markers, and the number and effects of QTLs).

QTL mapping methods have continued to be improved since the earliest papers presenting and applying this approach (Soller and Brody 1976; Lander and Botstein 1989). In particular the use of co-factors in the analysis to account for multiple segregating QTLs can considerably reduce the size of QTL support intervals on the genome (Jansen and Stam 1994). Nevertheless, uncertainty in estimates of QTL map locations and effects are unavoidable. We were interested to see how the performance of MAS is influenced by errors in the estimation of QTL locations and effects.

Our selection material consists of a set of RILs, obtained through single-seed descent from a cross between two homozygous parents, markers having been mapped and QTLs supposedly mapped in the F_2 generation, allowing estimation of dominance effects. RILs are assumed to be completely homozygous. The problem we address is: which pair of RILs from this set is most promising in producing extreme genotypes among their offspring? We define extreme genotypes as those that contain the favourable allele at (nearly) all QTLs detected for the trait of interest. The performance of a pair of RILs is evaluated by considering the simulated F_2 offspring obtained by crossing these RILs (see below for details).

In an average-sized population of RILs it is impracticable to cross and test all possible pairs of lines. Thus we wish to predict, before any RILs are crossed, which pairs are most likely to produce the most extreme genotypes in the F_2, accumulating as many as possible advantageous alleles in a single genotype.

Materials and methods

In MAS, predictions for the performance of the offspring of line-pairs are used. These predictions are based on an index constructed from the genotypes of markers flanking putative QTLs in the pair of lines. In conventional selection, a line's phenotype determines if that line becomes part of a subset of selected lines. From this subset all possible pairs of lines are selected.

Marker index construction

The marker index value is calculated as an index for possible line combinations, based on the marker genotype of the potential F_1 resulting from crossing two parental lines. Since the indices are connected to line pairs, a population of N lines results in $1/2N*(N-1)$ possible line combinations (not counting selfings and reciprocals). For each line-combination an index is calculated. This differs from the usual way combined indices are calculated (see for instance Lande and Thompson 1990; Knapp 1994; Whittaker et al. 1995), in the sense that this method of indexing takes genetic complementation into account. In our model, the smallest indexing unit is the *marker interval*, which consists of two markers located next to each other on the genetic map. If a QTL has been located within a marker interval, the interval is assigned an index number. A table is built connecting the index number with index values. This table contains the index values for three possible situations (see Fig. 1): (1) the favourable QTL allele is homozygous (QQ), (2) the QTL is heterozygous (Qq) or (3) the favourable QTL allele is absent (qq). The magnitude of the index values corresponds to the relative genetic effect of each allele combination; i.e. when the favourable allele is absent the index value is set to zero. It also depends on the dominant or additive character of the QTL:

$$CI = \sum_{chrom} \sum_{intervals} (QTL-effect * Weight), \quad (1)$$

where CI is the combination index; chrom indicates: all chromosomes; intervals indicates: all intervals on a chromosome; (QTL − effect * weight) is the interval index; Weight is as described in Fig. 1.

The overall index is calculated as the sum of all interval indices, according to (1). Because both parents are taken into account in the combination index, it can be seen as a predictor of the usefulness of a pair of lines.

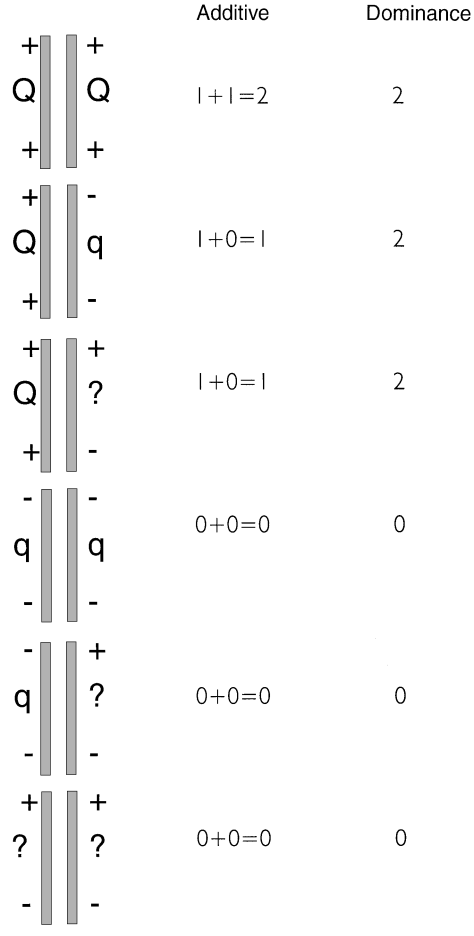

Fig. 1 Marker interval combinations for a hypothetical F_1 between two RILs and contributions to the combination index. The + and − indicate the alternative alleles at marker loci. The QTL alleles (Q/q) are inferred from the flanking markers. In case of uncertainty (?) the unfavourable QTL allele is assumed, and there is no contribution to the line-pair index

Phenotype

The phenotypic value for a recombinant inbred line was calculated by adding an environmental error term, drawn from a normal distribution with mean $\mu = 0$ and variance $\sigma^2 = V_E$ to the line genotypic value. The line genotypic value was determined by the genotype at all QTLs, assuming additivity between QTLs. The magnitude of V_E depends on the trait heritability. Genetic variance V_G was calculated from the RIL genotypes; environmental variance V_E was calculated according to (2), derived directly from the definition of heritability:

$$V_E = [(1–h^2)/h^2]\ V_G, \quad (2)$$

where V_G is the genotypic variance, V_E is the environmental (error) variance and h^2 is the broad-sense heritability.

Simulations

Simulation consisted of the following steps.

(1) Two complementary parents, defining the genetic architecture, were used to generate a set of 100 RILs. The genotype and phenotype of these RILs was calculated. Most simulation runs involved three replications, for each replication a different set of RILs was raised.
(2) For each RIL population marker indices were calculated for all RIL pairs. Based on the combination indices a subset of all RIL pairs was selected for evaluation (MAS, Fig. 2 A). The size of this subset is called the 'selected fraction'.
(3) Another subset of RIL pairs was selected based on the phenotype of the RILs (phenotypic selection, Fig. 2 B). Among the lines, RILs with the highest phenotype were selected and a set of line pairs between the selected RILs was created. The number of lines that was selected was chosen in such a way that the total number of line pairs in this second set was equal to the number in the set selected with MAS.
(4) For each selected RIL pair the F_1 generation was raised and subsequently selfed to obtain a segregating F_2 population of size 1000. For each generated F_2 population the average and standard deviation of the genotype was calculated. For the estimation of population extremes the F_2 progeny was divided into ten random groups of 100 progeny each. The most extreme genotype from each group was recorded and the average over the ten group-extremes was taken as the value for the extreme genotype of the population. In this way we actually obtained an estimate of the extreme genotypic value in an F_2 population of size 100, which is attainable in most practical situations.
(5) The selection response was used to assess the success of each selected pair of RILs. The selection response was defined as the difference between the average extreme genotypic value (G_{ex}) and the average genotype of all RILs (G_{RIL}), divided by G_{RIL} to obtain a relative number. This can be written as: $G_{RIL} = (\sum g_i)/N$ and: selection response $= 100 * (G_{ex} - G_{RIL})/G_{RIL}$; where the RIL population consists of N RILs and the genotype of the i^{th} RIL is denoted as g_i. When the procedure was repeated over several RIL-sets the average selection response was used to assess the success of the selection method.
(6) The selection response obtained using MAS was compared to the selection response after phenotypic selection.

We now describe the specific simulation conditions used to investigate the influences of trait heritability, selection intensity, several aspects of genetic architecture, and uncertainty in QTL locations on the performance of MAS, compared to phenotypic selection. The relevant simulation parameters are: The number of markers, the QTL positions and effects as well as the type of inheritance and linkage between QTLs, the trait heritability, and the fraction of RIL pairs that was selected. Except when stated otherwise, we assume that the mapped positions of markers and QTLs are accurate, no interaction occurs between QTLs, and no interference is present during meiosis. The heritability is only used to estimate the magnitude of the environmental error. We assume that the heritability is determined accurately in a trial of sufficient size.

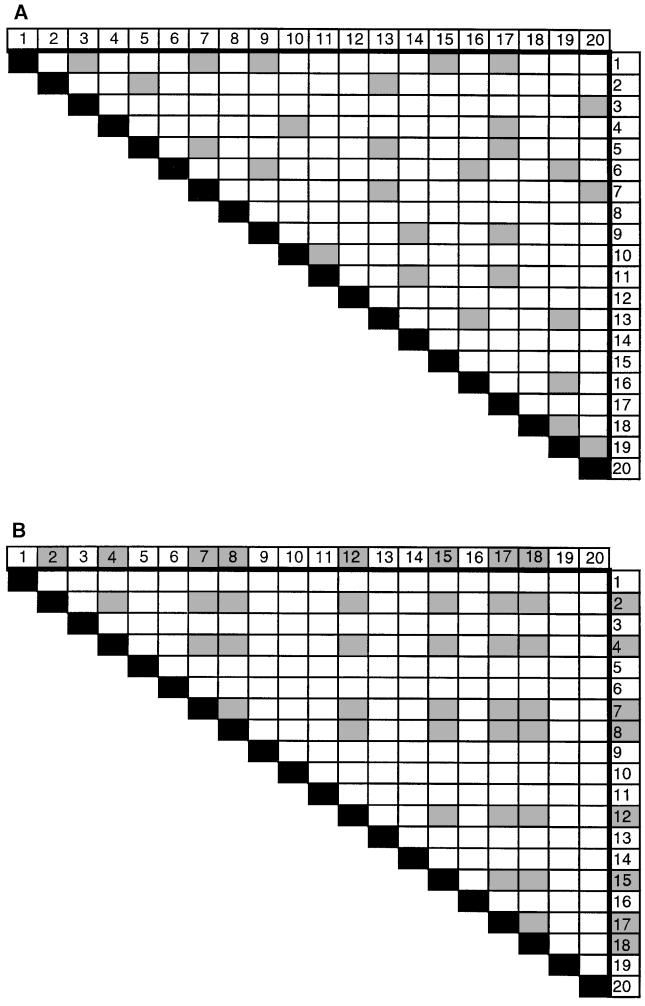

Fig. 2 Comparison of marker-assisted selection procedure (**A**), with conventional phenotypic selection procedure (**B**). With MAS specific line combinations are selected, while with conventional selection lines are selected first and then combined with each other

Trait heritability

Four RIL populations were generated and used for simulation. Simulations were run for genomes containing five identical chromosomes. Nine markers were positioned at 10-centiMorgan (cM) intervals on each chromosome. Two QTLs per chromosome were located at positions 20 and 80, replacing the markers at these positions. The QTLs were linked in coupling phase. All QTLs had the same size effect, and there was no additive interaction between QTLs. We only considered additive effects of allele substitution at each QTL. The fraction of pairs that was selected was 10%. We studied trait heritabilities ranging from $h^2 = 0.1$ to $h^2 = 0.9$.

Selected fraction

As stated earlier, it is ordinarily not feasible, to test all possible line combinations in a set of RILs. For this reason we assessed the

amount of useful material that is lost by decreasing the number of selected RIL pairs. Using the same configuration as for investigating heritability, we varied the fraction of RIL pairs selected, ranging from 5% to 50%, and recorded the selection response. Heritability was held constant at 0.1 and QTLs were linked in coupling phase. Only additive QTL allele effects were considered.

Number of chromosomes, dominance, linkage phase

We investigated the effects of different QTL configurations. For a genome consisting of 5, 10 or 20 chromosomes, we compared the selection response obtained with MAS to the selection response obtained when conventional selection was applied. Nine markers were positioned at 10-cM intervals on each chromosome. Two QTLs per chromosome were located at positions 30 and 70 for the genomes consisting of five and ten chromosomes, replacing the markers at these positions. One QTL per chromosome was located at position 35 for the genome consisting of 20 chromosomes. QTL alleles were linked in either coupling phase or repulsion phase. QTL allele effects were either additive or showed complete dominance. The effects of all QTLs were of the same magnitude. Heritability of the trait was held constant at 0.1 and the selected fraction of RIL pairs was 10%.

Random QTL dispersion and geometric allele effects

We also tested the genetic configuration used by Gimelfarb and Lande (1994 a; Fig. 1). In this setting 25 QTLs are dispersed randomly over ten chromosomes of length 100. The effects of the QTL alleles constitute the 'geometric series of variance contributions' as described by Lande and Thompson (1990). (Among the 25 QTLs there were only a few with a large effect and there were many QTLs with a small effect). It is believed that such a constitution gives a better representation of a naturally occurring situation. We tested this setting with QTLs linked in repulsion and coupling phases. The Gimelfarb and Lande genome has marker loci at every 10 cM: 110 marker loci in total. We also tested the effect of marker loci present every 20 cM, resulting in a map with 60 markers in total. The selected fraction of RIL pairs was 10%. Trait heritability was held at 0.1 or 0.3.

Errors in QTL mapping

To study the effect of uncertainty in QTL number and position we have run simulations for the following situations:

QTLs mapped to incorrect marker intervals

It is assumed that the mapped positions of some QTLs does not correspond to their true positions on the genome. Instead these QTLs are mapped to intervals adjacent to the intervals containing the true positions, leading to the selection of some incorrect marker intervals in the MAS procedure. We tested a configuration with ten chromosomes, carrying 20 QTLs with equal effects linked in coupling phase. Nine markers per chromosome were present at 10-cM intervals. Two QTLs per chromosome were present at locations 30 and 70, replacing the markers at these positions. All QTL effects were additive. Trait heritability was held at 0.1 and the selected fraction of RIL pairs was 10%. The proportion of QTLs that were not assigned to their true marker interval, but rather to a neighbour interval, ranged from 5% to 100%.

Undetected QTLs (Type-II errors)

Here we allow that the QTL mapping procedure may fail to locate one or more QTLs, causing reduced selection opportunities for MAS. The same configuration was used as described in the section dealing with QTLs mapped to incorrect intervals, but a randomly chosen subset of the QTLs present in the simulated cross were not used for marker-interval indexing. We ran simulations for the cases where 0%, 25%, 50% or 75% of the QTLs were not included in the computation of indices.

False positive QTL detection (Type-I errors)

The QTL mapping procedure may falsely indicate the presence of one or more QTLs at positions where none in fact exist. These 'false QTLs' were used for interval indexing, introducing errors in the overall combination index. Again the same configuration as in the situation of QTLs mapped to adjacent intervals was used. Twenty true QTLs were present, but the number of QTLs used for computing indices ranged from 20 to 40. The 'false QTLs' were added to the genome randomly, but as a constraint no more then four QTLs could be present per chromosome and only one QTL was allowed per marker interval.

Software[1]

A simulation computer program, mimicking Mendelian genetical behaviour, has been created to enable crossing and selection. The smallest model unit, the locus, can be either a marker or a quantitative trait locus. Loci are linked together in linkage groups or chromosomes and Mendelian rules apply to the simulation of recombination during meiosis. QTLs and allele effects remain visible, but are not used for selection. Selection is based only on marker loci and intervals of marker loci. Within the model, indices are calculated for pairs of lines. Based on these index values, pairs of lines are either selected or disregarded from the selected fraction. In conventional selection, phenotypic values are used as the criterion to select RIL pairs. The software was written in Borland Delphi and run on a Pentium PC.

Results

Trait heritability

The results of this experiment are summarised in Fig. 3. With additive QTL effects, MAS resulted in a higher selection response at heritabilities 0.1 and 0.3, while for a heritability of 0.5 the advantage of MAS over phenotypic selection becomes negligible. At trait heritability approaching 1.0 we can see that the phenotypic selection response becomes larger than the selection response after MAS. This observation is probably due to the conservative way index selection is practised. If only one of two markers flanking a QTL is present, no index value is awarded, because it is uncertain which QTL allele is present. In approximately half of the cases this will be the advantageous allele, but in the other half it will be the other, undesirable, allele. In this way some of the advantageous alleles are missed by MAS, so reducing it's power.

[1] The software described in this paper can be obtained from the author.

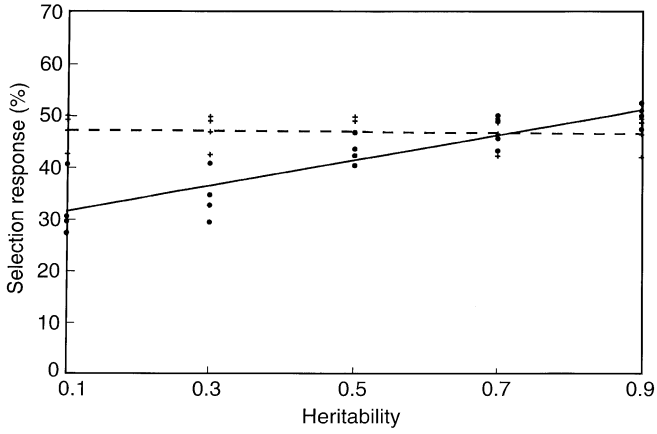

Fig. 3 Comparison of relative selection response for different trait heritabilities. (—●): MAS; (- - - +): phenotypic selection. Lines show a linear regression through replication means.The selected fraction was kept at 10%; the simulated genome consisted of five chromosomes each with nine markers and two QTLs; markers at 10-cM intervals and QTLs at positions 20 and 80. QTLs had additive effects and were linked in coupling phase

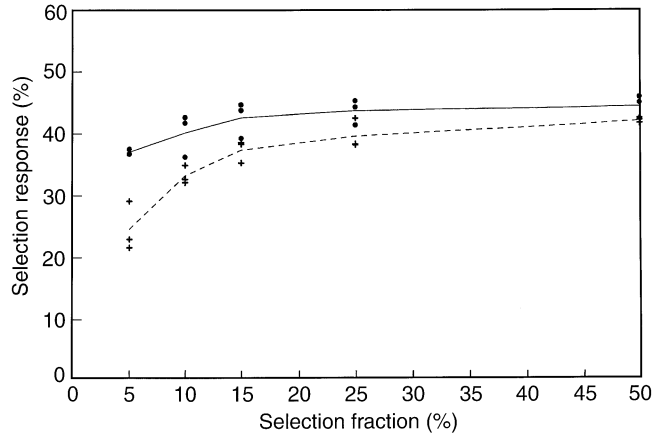

Fig. 4 Comparison of relative selection response as a function of the selected fraction of RIL pairs. (●): marker-assisted selection, the *solid line* connects averages over replications; (+): phenotypic selection, the *dashed line* connects averages over replication. Trait heritability was kept at 0.1; QTL alleles had additive effects. The genetic architecture was the same as described in Fig. 3

To keep the number of tested settings practicable, we decided to set the trait heritability at 0.1 or 0.3 in the other tests, because this is where we expect the contrasts between MAS and phenotypic selection to be the largest.

Selected fraction

We show the selection response for a range of selected fractions of RIL pairs in Fig. 4. The superiority of MAS decreased as the fraction of selected RIL pairs increased. The reduced selection response of MAS and conventional selection at smaller selected fractions of RIL pairs reflects the cost of missing some of the most promising RIL pairs when testing too few of them. The reduction in selection response for phenotypic selection was expected, because we select for extremes and a smaller subset of the population is less likely to contain the best combining lines. When a desirable line remains unselected in phenotypic selection this will affect several RIL pairs that would have included this line, thus lowering the selection results of conventional selection as a whole. This effect is not seen for MAS because in MAS, for each RIL *pair* selection is decided independently. However, marker-assisted selection still showed a drop in selection response if fewer RIL combinations were selected. This effect would not be expected if the combination index were able to predict without error the usefulness of a cross for breeding. However, the conservative way the index value is constructed ensures that the index value of a RIL pair never overestimates, but may underestimate, the utility of a RIL pair, because of the occurrence of crossovers inside marker intervals used for indexation. This underestimation may result in missing some of the most promising RIL pairs when the selected fraction is small. To limit the number of possible parameter settings, unless indicated otherwise, we arbitrarily chose to select 10% of all RIL pairs in the following simulation experiments. For a population consisting of 100 lines this meant selection of 495 line pairs out of a possible 4950.

Number of chromosomes, dominance, linkage phase

The general results of these experiments are summarized in Table 1. Selection response is presented for MAS and phenotypic selection. In all the tested configurations marker-assisted selection gave a higher selection response, compared to phenotypic selection. The effect is larger when QTL alleles are linked in coupling phase. The difference is also larger when QTL alleles exhibit dominance. This can be explained by the way the selection index is constructed. Conventional selection uses the phenotype of the RI lines, while MAS uses the genotype of the F_1, obtained from a cross between two RILs, for selection. In this way, heterozygous F_1 progeny that are advantageous because of accumulated dominant genes can be selected by MAS. After selfing they can give rise to a segregating population containing more extreme genotypes. If the final objective is to obtain inbred lines for hybrid production these numbers give an indication of the progress that can be achieved. For purely autogamous crops the dominance effect will be lost in later generations of inbreeding and only the additive QTL effects remain.

Table 1 Relative selection responses[a] in conventional phenotypic selection (CS) and marker-assisted selection (MAS) for different genetic configurations, types of inheritance and linkage conditions. The data shown are averaged over three different RIL sets. The genome consisted of chromosomes of length 100-cM with evenly spaced markers at 10-cM intervals. The configuration containing 20 chromosomes contained only one QTL per chromosome, at 45-cM. All other configurations contained the QTLs per chromosome located at 35 and 75 cM linked in coupling phase or repulsion phase. QTL effects were of equal size for all QTLs. Trait heritability was fixed at 0.1 and the selected fraction of RIL pairs was 10%

Type		5 chrom, 10 QTLs		10 chrom, 20 QTLs		20 chrom, 20 QTLs
		Coupling	Repulsion	Coupling	Repulsion	
Additive	CS	32%	34%	27%	23%	34%
	MAS	52%	47%	42%	32%	44%
Dominant	CS	59%	56%	51%	48%	33%
	MAS	84%	72%	68%	58%	45%

[a] The selection response was calculated as: $100 * (G_{ex} - G_{RIL})/G_{RIL}$, where G_{ex} is the average of the realised extreme genotypes of the F_2 progenies resulting from the selected RIL pairs, and G_{RIL} is the average RIL genotypic value

Random QTL dispersion and geometric allele effects

The selection response for MAS and phenotypic selection for the data set derived from the Gimelfarb and Lande (1994 a) map are summarised in Table 2. Again we see that MAS results in a higher selection response compared to phenotypic selection. When the number of marker loci is reduced from 110 to 60 (the interval size is increased from 10 cM to 20 cM), the frequency of having more than one QTL within a marker interval increases. This results in a reduction of the selection response for MAS, especially when QTLs are linked in repulsion phase, because the overall effect of the marker interval will become small when neighbouring QTLs within a marker interval partly counterbalance each others effect.

Table 2 Relative selection responses[a] in conventional phenotypic selection (CS) and marker-assisted selection (MAS) for different heritabilities and marker spacings in the case of random dispersed QTLs and geometric QTL effects. The data presented are averaged over three different RIL sets. The genome consisted of ten chromsomes of length 100 cM with evenly spaced markers at 10-cM or 20-cM intervals. The distribution of QTLs and their effects were as specified by Gimelfarb and Lande (1994 a). QTL effects were assumed additive. Linkage between QTLs on the same chromosome was either in coupling phase or in repulsion phase. Trait heritability was kept at 0.1 or 0.3. The selected fraction of RIL pairs was 10%

		Coupling		Repulsion	
		10 cM	20 cM	10 cM	20 cM
$h^2 = 0.10$	CS	27%	27%	20%	20%
	MAS	51%	49%	27%	23%
$h^2 = 0.30$	CS	33%	33%	**22%**	22%
	MAS	51%	49%	27%	23%

[a] The selection response was calculated as described in Table 1

Errors in QTL mapping

QTLs mapped to incorrect marker intervals

The performance of MAS is affected when QTLs are not mapped at their true position. The magnitude of this effect can be seen in Fig. 5. A reduction in selection response was observed as the number of incorrectly located QTLs increased, but the effect was small. We believe this is because using a neighbouring marker interval for calculation of the index will in most cases still result in the same index. Only when recombination has occurred within either or both of the correct and incorrect intervals will the resulting index be affected, and thus the performance of a RIL pair be inaccurately predicted.

Undetected QTLs (Type-II errors)

QTLs that have an influence on the phenotype are not always detected at the mapping stage. As a result, these QTLs can not be selected by the MAS procedure. The size of the reduction in selection response caused by undetected QTLs is shown in Fig. 6. A reduction in selection response was observed as the proportion of undetected QTLs increased. However, even when only 25% of the QTLs are mapped and indexed the selection response obtained after applying marker-assisted selection is still 4% larger than the response after applying phenotypic selection. This indicates that (for low heritability traits) it is worthwhile to pursue marker-assisted selection, even if the phenotypic data did not allow the detection of all QTLs.

False positive QTL detection (Type-I errors)

The introduction of false QTLs – QTLs that are not actually present genetically, but were identified by the QTL mapping procedure – showed no effect on the

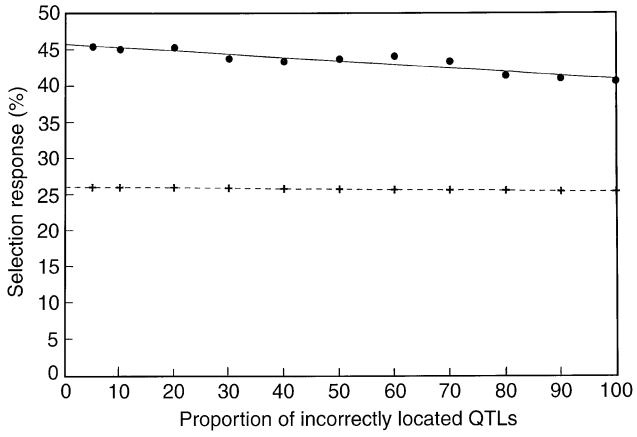

Fig. 5 MAS relative selection response as a function of the proportion of incorrectly located QTLs. (●): marker-assisted selection; (+): phenotypic selection. Trait heritability was kept at 0.1. The selected fraction of RILs was 10%. The genetic architecture was the same as described in Table 1 for loci linked in coupling phase and QTL alleles with additive effects

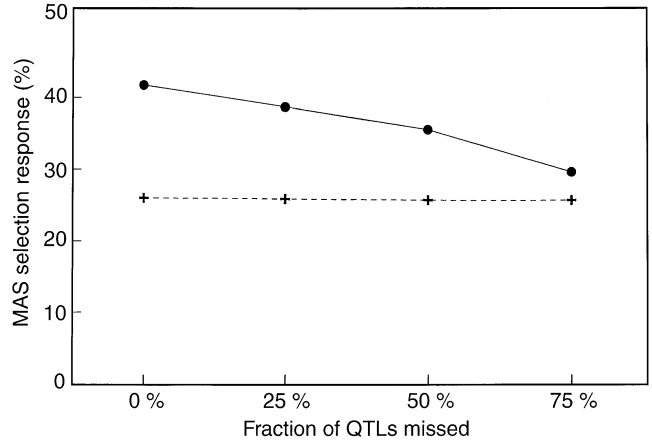

Fig. 6 MAS relative selection response when indices are incomplete because of undetected QTLs. (●): marker-assisted selection; (+): phenotypic selection. Trait heritability was 0.1. The selected fraction was 10%. The genetic architecture was the same as described in Table 1 for loci linked in coupling phase and QTL alleles with additive effects

MAS selection results (data not shown). Even when the number of false QTLs equalled the number of true QTLs no significant decrease in selection response was found.

Apparently the MAS procedure does not suffer much from extra information. This may be due to the configuration we tested. All QTLs were linked in coupling phase, so adding QTLs to the map will inflate the index value, but the order of index values and the line pairs that will be selected will not change dramatically.

Discussion

We have assumed that a set of RILs obtained from a given cross, well characterised in terms of marker genotypes and QTL positions, is available as a starting point for further crossing and selection.

We have not focussed on population improvement by MAS but rather on the 'breeding behaviour' of pairs of RILs. The results indicate that marker data can be a valuable extra source of information on which to base selection, especially when heritability is low. Marker information appears to add little to phenotypic information at high heritability, but at low heritability it does so. This is in agreement with results on recurrent MAS for population improvement (Lande and Thompson 1990; Gimelfarb and Lande 1994 a, b; Gallais & Charcosset 1994).

In all simulations we have assumed that all QTLs affect a single trait. This is, of course, a simplification but not a limitation; one can easily imagine the case where the QTLs of the model are divided into subsets, each set affecting a different trait. The 'final trait' could then be an index value, composed of a linear combination of traits. This will not change our general results, as long as the traits involved are comparable in their importance to the breeder. When many QTLs are to be accumulated the chance of obtaining them all with just one pair of lines is small. In this case, one may think of an extension of the procedure to three-way crosses or four-way crosses.

Trait heritability is the most important factor influencing the effectiveness of MAS. MAS seems to be most promising for traits with low heritability. But trait heritability is also of major importance for accuracy in the mapping of QTLs. Low heritability reduces the power of detecting QTLs, which is based on the correlation between phenotype and marker genotype. This could mean that for well-mapped QTLs MAS may add little to phenotypic selection, while for traits with a very low heritability the underlying QTLs cannot be identified. It is the area in between these two extreme cases that looks most promising for the application of MAS. If QTLs can be mapped for a trait having a low heritability the accuracy of the QTL position may not be very high, which is reflected in a large QTL support interval on the genetic map (Lee 1995). Our simulations have shown that this does affect the effectiveness of MAS, and is only marginal in most cases.

To practical breeders these result may be an incentive to continue to use marker data as a source of information on which to base selection. In most cases MAS will give better selection results than phenotypic selection, for a low-heritability trait. The breeder can decide if the increased selection results are worth the extra cost involved in obtaining the marker data. Index-based selection opens new ways to quantify performance with regard to several traits into one index value, and use markers to select for those plants that give an optimisation of this index in the current or

a future generation. This may facilitate breeding for several traits simultaneously. In future more and more marker and QTL information will be collected; also existing breeding populations will be screened for markers and QTLs. An efficient way to use this information and to predict useful crosses would require prediction and selection procedures similar to those described in this paper.

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