

Genomewide Selection for Rapid Introgression of Exotic Germplasm in Maize

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ABSTRACT

The length of time needed for prebreeding in adapted \times exotic maize (*Zea mays* L.) crosses has deterred breeders from exploiting exotic germplasm. My objective in this study was to determine, by simulation, the usefulness of genomewide selection for the rapid improvement of an adapted \times exotic cross. I simulated F_2 , BC_1 , and BC_2 populations from an adapted \times exotic maize cross. The adapted inbred had the favorable allele at $L_{\text{Adapted}} = 50$ quantitative trait loci (QTL), whereas the exotic inbred had the favorable allele at $L_{\text{Exotic}} = 50, 25, 10, \text{ or } 5$ QTL. The joint effects of 512 markers were fitted by best linear unbiased prediction. For $L_{\text{Exotic}} \leq 25$, the maximum responses (in units of the testcross genetic standard deviation) to multiple cycles of genomewide selection ranged from 0.38 to 3.81. Responses increased as heritability increased and as the number of testcrosses that were phenotyped in Cycle 0 increased from 144 to 288. Overall, the results indicated that a useful strategy for the rapid improvement of an adapted \times exotic cross involves 7 to 8 cycles of genomewide selection starting in the F_2 rather than in a backcross population, even when the number of favorable alleles is substantially larger in the adapted parent than in the exotic parent. Assuming three generations can be grown per year in a greenhouse or year-round nursery, this procedure would require only 3 yr beyond the time required to develop and phenotype the Cycle 0 testcrosses.

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Abbreviations: QTL, quantitative trait locus/loci; BLUP, best linear unbiased prediction.

THE GERmplasm BASE of U.S. maize (*Zea mays* L.) has become increasingly narrow because new inbreds are developed from crosses among the best available inbreds instead of from broadbase germplasm. Specifically, maize breeding has largely focused on developing new and improved versions of key historical inbreds such as A632, B37, B73, H99, Mo17, Oh43, and PH207 (MBS, 2003; Mikel and Dudley, 2006; Nelson et al., 2008). While exotic germplasm is potentially useful for improving U.S. maize (Wellhausen, 1965; Hallauer, 1978; Goodman, 1985; Goodman et al., 2000), current maize inbreds have very little exotic germplasm (Goodman, 1999; MBS, 2003).

A main reason for this limited use of exotic germplasm in maize breeding is the performance gap between the best adapted germplasm and the best exotic germplasm, particularly for grain yield and moisture, flowering date, and stalk and root lodging (Hallauer and Sears, 1972; Albrecht and Dudley, 1987; Holland et al., 1996). As such, prebreeding via recurrent selection is usually needed in exotic germplasm (Hallauer and Sears, 1972; Johnson et al., 1986; Hallauer, 1994). The length of time needed for prebreeding in adapted \times exotic crosses has subsequently discouraged maize breeders from exploiting exotic germplasm. For example, one cycle of testcross phenotypic selection in maize typically requires 2 yr. If 5 to 10 cycles of testcross phenotypic selection are needed to sufficiently improve the mean performance of an adapted \times exotic cross

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before inbred development (Dudley, 1982), then 10 to 20 yr would be required for prebreeding.

Genomewide selection (Meuwissen et al., 2001) is a marker-based selection procedure that could potentially allow the introgression of exotic germplasm into U.S. maize in a short amount of time. Genomewide selection as proposed in maize involves two steps (Bernardo and Yu, 2007). First, a segregating maize population is genotyped and evaluated for testcross performance. Based on the genotypic and phenotypic data, breeding values associated with a large set of markers (e.g., 256 to 512 markers) are calculated for the traits of interest. Significance tests for markers are not used, and the effects of all markers are fitted as random effects in a linear model by best linear unbiased prediction (BLUP). Second, two or three generations of selection based on all markers are conducted in a year-round nursery (e.g., Hawaii or Puerto Rico) or greenhouse. Trait values are predicted as the sum of an individual plant's marker values across all markers, and selection is subsequently based on these genomewide predictions.

Genomewide selection in a year-round nursery or greenhouse, where three generations can be grown in a year but where phenotypic measurements do not reflect performance in the target environment (i.e., the U.S. Corn Belt), permits the rapid improvement of quantitative traits (Bernardo and Yu, 2007). Whereas 10 cycles of testcross phenotypic selection in an adapted \times exotic cross would require 20 yr, 10 cycles of genomewide selection could be completed in less than 4 yr. But while genomewide selection was shown to result in sustained progress through three cycles of marker-based selection (Bernardo and Yu, 2007), is it unknown whether these gains could be sustained through the 5 to 10 cycles of selection often needed to sufficiently improve an adapted \times exotic cross (Dudley, 1982).

My objective in this study was to determine, by simulation, the usefulness of genomewide selection for the rapid improvement of an adapted \times exotic cross. Previous studies have suggested that if the adapted parent has a higher mean performance than the exotic parent, then selection in a backcross to the adapted parent enhances the probability of obtaining superior inbreds (Dudley, 1982; Albrecht and Dudley, 1987; Crossa and Gardner, 1987; Holland et al., 1996). I therefore examined genomewide selection in F_2 , BC_1 , and BC_2 populations from an adapted \times exotic cross, assuming different proportions of favorable quantitative trait alleles in the adapted and exotic parents.

MATERIALS AND METHODS

Quantitative Trait Loci and Adapted \times Exotic Crosses

A trait controlled by $L = 100$ quantitative trait loci (QTL) was considered. This number of QTL was identical to that considered by Dudley (1982) for phenotypic recurrent selection in adapted \times exotic crosses, and having a large number of QTL was consistent with the large number of QTL that are likely involved

in marker-based selection for multiple traits (e.g., grain yield and moisture; Eathington et al., 2007) in maize. The adapted and exotic parents were fully inbred. The adapted parent had the favorable allele at $L_{\text{Adapted}} = 50$ of the 100 QTL, whereas the exotic parent had the favorable allele at $L_{\text{Exotic}} = 50, 25, 10$, or 5 QTL at which the adapted parent had the less favorable allele. Genetic gain was absent at the loci where both the adapted and exotic parents had the less favorable allele, for example, 40 of the 100 QTL for $L_{\text{Exotic}} = 10$.

At the k th QTL, the testcross effect of the favorable allele was a^k , with $a = (L - 1)/(L + 1)$ as suggested by Lande and Thompson (1990). The testcross effect of the less favorable allele was $-a^k$. The QTL1 therefore had the largest effect, QTL2 had the second-largest effect, and QTL100 had the smallest effect. The adapted parent had the favorable allele at the odd-numbered QTL and the less favorable allele at the even-numbered QTL. With $L_{\text{Exotic}} = 50$, the exotic parent had the favorable allele at the even-numbered QTL and the less favorable allele at the odd-numbered QTL. With $L_{\text{Exotic}} = 25$, the exotic parent had the favorable allele at every fourth QTL starting with the second QTL, i.e., QTL2, QTL6, QTL10, ... QTL98. With $L_{\text{Exotic}} = 10$, the exotic parent had the favorable allele every 10th QTL starting with the second QTL, i.e., QTL2, QTL12, QTL22, ... QTL92. With $L_{\text{Exotic}} = 5$, the exotic parent had the favorable allele at QTL2, QTL22, QTL42, QTL62, and QTL82.

The F_2 , BC_1 , and BC_2 populations from adapted \times exotic crosses were considered as the Cycle 0 (C_0) populations. For a given combination of L_{Adapted} (which was always equal to 50) and L_{Exotic} , the adapted and exotic parents were crossed to form the F_1 . The F_1 was then selfed to form an F_2 population of $N_{C_0} = 144$ or 288 plants. The F_1 was also backcrossed to the adapted parent to form a BC_1 population of $N_{C_0} = 144$ or 288 plants. Lastly, the N_{C_0} BC_1 plants were backcrossed to the adapted parent to form a BC_2 population of $N_{C_0} = 144$ or 288 plants. The Cycle 0 populations were crossed with an unrelated inbred tester, and all phenotypic values were for testcross performance. The F_2 with $L_{\text{Adapted}} = L_{\text{Exotic}} = 50$ was considered the reference population to which all the other populations were compared.

Linkage Map, Molecular Markers, and Genetic Models

Procedures pertaining to the linkage map, molecular markers, and genetic models were identical to those described by Bernardo and Yu (2007) but are repeated here for convenience. Briefly, the maize linkage map comprised 1749 cM (Senior et al., 1996). A total of $N_M = 512$ evenly spaced, codominant markers were used in genomewide selection. The L QTL were randomly located among the 10 chromosomes according to a uniform distribution across the total genome. Coupling and repulsion linkages between QTL were therefore generated at random. A model with $L_{\text{Adapted}} = 10$ and $L_{\text{Exotic}} = 2$ was also investigated. On average, the 12 segregating loci in this model were unlinked. Differences between the results for this model and for the models with $L = 100$ QTL therefore reflected the effects of linkage among QTL on the response to genomewide selection.

Given that testcross means behave in a purely additive manner (Hallauer and Miranda, 1989, p. 28; Bernardo, 2002, p. 78), dominance was absent. Epistasis was likewise absent. Phenotypic values were calculated by adding random nongenetic

effects to the genotypic values summed across all the QTL. The random nongenetic effects were normally distributed with a mean of zero and a variance of V_E . So that the results would be comparable across different adapted \times exotic crosses, V_E was constant for all values of L_{Exotic} and for all types of populations (F_2 , BC_1 , and BC_2). Specifically, the constant V_E corresponded to a heritability, on a testcross-mean basis, of $H = 0.20, 0.50$, or 0.80 in the F_2 population with $L_{\text{Exotic}} = 50$.

Genomewide Selection

A total of 15 cycles of selection were conducted. Genomewide selection comprised testcross phenotypic selection in Cycle 0 followed by marker-based selection in Cycles 1 to 14. The procedures for genomewide selection were the same as those described by Bernardo and Yu (2007).

Briefly, the $N_{C_0} = 144$ or 288 testcrosses in Cycle 0 were evaluated in six environments. Testcross genetic variance (V_G) and V_E were estimated by equating the observed mean squares to their expectations and solving for the desired variance component. The $N_{\text{Sel}} = 15$ plants with the best testcross performance in Cycle 0 were random-mated to form $N = 576$ or 1152 Cycle 1 plants. The value of N_{Sel} was chosen according to the principle that N_{Sel} should be roughly equal to the number of cycles that selection will be performed (Bernardo et al., 2006). Phenotyping a testcross in five environments currently costs about \$75, whereas genotyping an inbred with 1536 single nucleotide polymorphism markers currently costs about \$40 (Bernardo, 2008). The increased population sizes of $N = 576$ or 1152 plants in Cycles 1 to 15 therefore reflected the still-decreasing costs of large-scale genotyping compared to phenotyping in commercial breeding programs (Bernardo, 2008).

Based on the genotypic and phenotypic data in Cycle 0, breeding values associated with each of the $N_M = 512$ markers were obtained by BLUP (Meuwissen et al., 2001; Bernardo and Yu, 2007). The genetic variance associated with each marker was equal to the estimated V_G for the particular adapted \times exotic cross, divided by $N_M = 512$. Based on genomewide predictions of performance (Meuwissen et al., 2001; Bernardo and Yu, 2007), the best $N_{\text{Sel}} = 15$ plants in Cycle 1 were random-mated to form Cycle 2. Selection before flowering was assumed so that the same generation was used for selection and recombination. The procedures for genomewide selection were repeated until Cycle 15 was obtained.

For comparison, 15 cycles of testcross phenotypic selection were also simulated by repeating the procedures used in Cycle 0 until Cycle 15 was obtained. The population size used in each cycle of phenotypic selection was $N_{C_0} = N = 144$ or 288.

Data Analysis

Each simulation experiment comprised a combination of the type of population (F_2 , BC_1 , or BC_2), L_{Exotic} , N_{C_0} , N , and H . Each simulation experiment was repeated 1000 times and the results were averaged across repeats. Each repeat differed in the location of QTL, the genotypes of the individuals sampled, and their phenotypic values.

So that comparisons can be made across different adapted \times exotic crosses, standardized responses were calculated as $R = (R' - \mu_{\text{Reference}}) / \sigma_{G(\text{Reference})}$, where R' is the response in a given cycle of a particular simulation experiment; $\mu_{\text{Reference}}$ is

the Cycle 0 mean of the F_2 population with $L_{\text{Exotic}} = 50$; and $\sigma_{G(\text{Reference})}$ is the testcross genetic standard deviation in Cycle 0 for the F_2 population with $L_{\text{Exotic}} = 50$. The statistical significance ($P = 0.05$) of differences in selection response was determined with z -tests, using the variances of the selection response across the 1000 repeats of an experiment.

For each simulation experiment, the average frequency of the favorable allele in each cycle of selection was calculated across the $L_{\text{Adapted}} = 50$ QTL where the adapted parent was fixed for the favorable allele. Likewise, the average frequency of the favorable allele was calculated across the $L_{\text{Exotic}} = 50, 25, 10$, or 5 QTL where the exotic parent was fixed for the favorable allele.

RESULTS AND DISCUSSION

Reference Population: F_2 of Equal-Performing Parents

Responses to both testcross phenotypic selection and genomewide selection were largest when the adapted and exotic parents were fixed for the favorable allele at equal numbers of QTL ($L_{\text{Adapted}} = L_{\text{Exotic}} = 50$). In Cycle 15, the responses (in units of the testcross genetic standard deviation in the F_2 Cycle 0 population) to genomewide selection in the F_2 ranged from 4.46 to 8.26 across different levels of heritability ($H = 0.20, 0.50$, or 0.80 in the F_2 Cycle 0 population), numbers of progenies evaluated for their testcross performance in Cycle 0 ($N_{C_0} = 144$ or 288), and numbers of plants subjected to marker-based selection in Cycles 1 to 14 ($N = 576$, Fig. 1; results for $N = 1152$ are not shown). The corresponding responses to phenotypic selection (with $N = 144$ or 288 testcrosses evaluated in each cycle) ranged from 6.57 to 10.02 (Fig. 1).

As expected, the responses to genomewide selection increased as heritability and N_{C_0} increased (Fig. 1). In Cycle 15, the responses to genomewide selection in the F_2 ranged from 4.46 to 7.34 with $N_{C_0} = 144$, and from 5.38 to 8.26 with $N_{C_0} = 288$. In contrast, keeping N_{C_0} constant but increasing N from 576 to 1152 during marker-based selection in Cycles 1 to 14 increased the Cycle 15 response by only about 1% (results not shown). Because of these results, the results for genetic models with fewer QTL fixed for the favorable allele in the exotic parent ($L_{\text{Exotic}} = 25, 10$, and 5) are later presented only for $N_{C_0} = 288$ and $N = 576$.

Responses to selection under the reference model of $L_{\text{Adapted}} = L_{\text{Exotic}} = 50$ were obtained only for the F_2 and not for backcross populations because theoretical results have indicated no advantage in selection in a backcross population when the parents have equal or near-equal performance (Bailey, 1977; Ho and Comstock, 1980; Dudley, 1982). Moreover, when the parents have equal numbers of favorable alleles, there is no basis for choosing which inbred should be the recurrent parent in creating a backcross population. As previously mentioned, a main reason for the limited use of exotic germplasm in maize

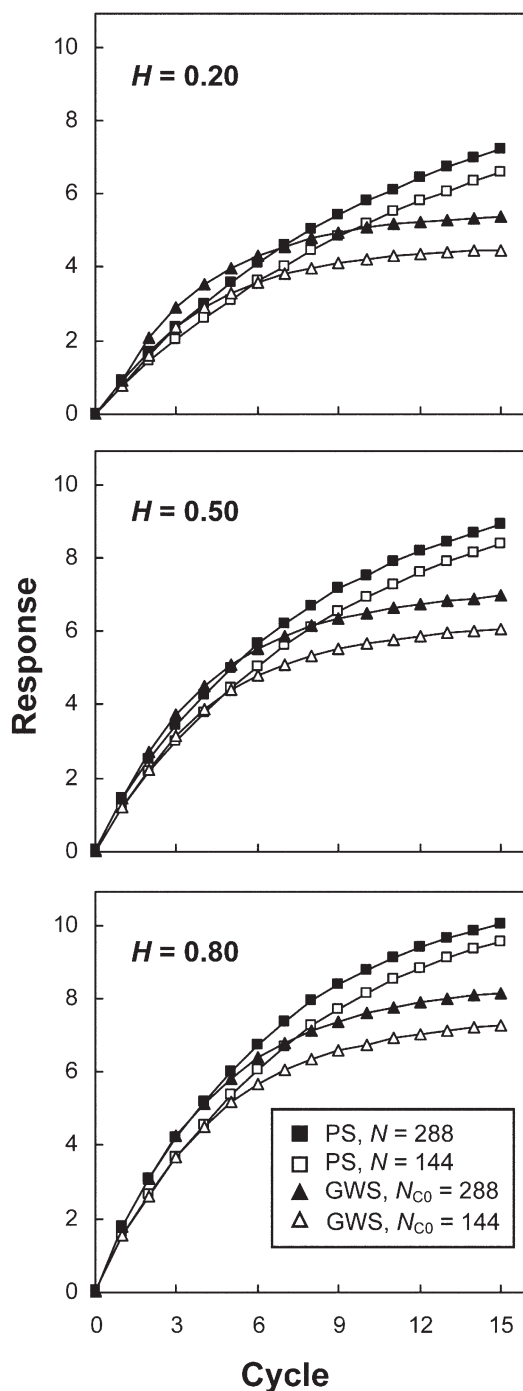


Figure 1. Response to testcross phenotypic selection and genomewide selection in the F_2 between parents with equal numbers of quantitative trait loci fixed for the favorable allele ($L_{\text{Adapted}} = L_{\text{Exotic}} = 50$). Responses are expressed as a deviation from the Cycle 0 mean and divided by the testcross genetic standard deviation in Cycle 0. Testcross-mean heritability (H) refers to that in Cycle 0. Solid squares: response to testcross phenotypic selection (PS) with a population size of $N = 288$ in each cycle; open squares: response to PS with $N = 144$; solid triangles: response to genomewide selection (GWS) with $N_{C0} = 288$ testcrosses phenotyped in Cycle 0 and $N = 576$ plants subjected to marker-based selection in Cycles 1 to 14; open triangles: response to GWS with $N_{C0} = 144$ and $N = 576$. In all cases, $N_{\text{Sel}} = 15$ individuals were selected in each cycle. The LSD ($P = 0.05$) was approximately 0.03 to 0.09.

breeding has been the performance gap between the best adapted germplasm and the best exotic germplasm (Hallauer and Sears, 1972; Albrecht and Dudley, 1987; Holland et al., 1996). The F_2 reference population with $L_{\text{Adapted}} = L_{\text{Exotic}} = 50$ was therefore unrealistic for adapted \times exotic crosses. However, the results for this reference population provided a benchmark for comparing the gains obtained with fewer numbers of loci at which the exotic parent was fixed for the favorable allele.

Genomewide Selection with Exotic Donor Parents

Compared with the responses for the F_2 reference population with $L_{\text{Adapted}} = L_{\text{Exotic}} = 50$, the responses decreased when the adapted parent had the favorable allele at $L_{\text{Adapted}} = 50$ QTL but the exotic parent had the favorable allele at $L_{\text{Exotic}} = 25, 10$, or 5 QTL (Fig. 2; all results shown are for $N_{C0} = 288$ and $N = 576$). The mean of the adapted parent, expressed as a standardized deviation from the mean of F_2 reference population, was 0.13. The least significant difference ($P = 0.05$) for the responses in Fig. 2 ranged from 0.03 to 0.09, and a one-sided z -test indicated that a mean greater than 0.15 was significantly greater than the mean of the adapted parent. The latter indicated improvement due to favorable alleles from the exotic donor parent. For $L_{\text{Exotic}} = 25$, responses to genomewide selection were largest in the F_2 of the adapted \times exotic cross (Fig. 2). Significant improvement over the adapted parent was achieved by Cycle 2 regardless of the level of heritability studied. By Cycle 15, these responses increased to 1.93 with $H = 0.20$, 3.07 with $H = 0.50$, and 3.81 with $H = 0.80$. The increases in mean performance leveled off toward the later cycles particularly with $H = 0.20$. The responses in the BC_1 and BC_2 were substantially smaller than those in the F_2 , with only a slight difference in response between the BC_1 and BC_2 populations.

For $L_{\text{Exotic}} = 10$, the initial responses to genomewide selection were largest in the BC_2 (Fig. 2). The maximum responses in the BC_2 all occurred in Cycle 2 and were 0.47 with $H = 0.20$, 0.80 with $H = 0.50$, and 1.02 with $H = 0.80$. The means in both the BC_1 and BC_2 decreased, however, after Cycle 2. Across all cycles of selection, maximum responses for $L_{\text{Exotic}} = 25$ were achieved in the F_2 population. These maximum responses, which were achieved in either Cycle 7 or 8, were 0.53 with $H = 0.20$, 1.24 with $H = 0.50$, and 1.65 with $H = 0.80$.

For $L_{\text{Exotic}} = 5$, the responses to genomewide selection were lower than but followed the same trends as the responses for $L_{\text{Exotic}} = 10$ (Fig. 2). With $H = 0.20$, a maximum response of 0.38 occurred in BC_2 Cycle 2. But when H was higher, maximum responses of 0.81 with $H = 0.50$ and 1.10 with $H = 0.80$ occurred in F_2 Cycle 7.

The large decreases in mean performance after continuous genomewide selection in the BC_1 and BC_2

populations, particularly with $L_{\text{Exotic}} = 10$ and 5 (Fig. 2), were accompanied by unfavorable changes in the average frequencies of favorable alleles from the adapted and exotic parents. Consider the BC_1 population with $H = 0.50$ and $L_{\text{Exotic}} = 10$. In Cycle 0, the expected frequencies of favorable alleles were $p_{\text{Adapted}} = 0.75$ across the $L_{\text{Adapted}} = 50$ QTL fixed for the favorable allele in the adapted parent and $p_{\text{Exotic}} = 0.25$ across the $L_{\text{Exotic}} = 10$ QTL fixed for the favorable allele in the exotic parent. By Cycle 2, p_{Adapted} increased slightly to 0.78 and p_{Exotic} increased to 0.35. The p_{Exotic} continued to increase to 0.66 in Cycle 15. But with continued genomewide selection, p_{Adapted} decreased slightly to 0.72 in Cycle 15. A similar trend in p_{Adapted} and in p_{Exotic} was found in the BC_2 population. Because the effects of QTL were unequal, changes in p_{Adapted} and p_{Exotic} (which are average frequencies across QTL) cannot entirely account for the changes in mean performance. Nevertheless, the above results indicated that the eventual decrease in the mean of the BC_1 and BC_2 populations was associated with a decrease in p_{Adapted} .

In contrast to backcross populations, p_{Adapted} in F_2 populations increased from 0.50 to ≥ 0.80 across the different combinations of L_{Exotic} and H . The p_{Exotic} generally ranged from 0.45 to 0.60. For example, in the F_2 population with $H = 0.50$ and $L_{\text{Exotic}} = 10$, p_{Adapted} increased to 0.87, whereas p_{Exotic} remained equal to 0.50 in Cycle 7. These results indicate that genomewide selection is useful in the F_2 of an adapted \times exotic cross because the procedure increases the frequency of favorable alleles inherited from the adapted parent while maintaining a moderate frequency of favorable alleles inherited from the exotic parent. As indicated below, the slight decreases in the means of the later cycles of genomewide selection in the F_2 (Fig. 2) can be attributed to linkage disequilibrium among QTL.

The decrease in p_{Adapted} after continuous genomewide selection in BC_1 and BC_2 populations can be explained by the effect of p_{Adapted} and p_{Exotic} on the testcross average effect of a favorable allele in Cycle 0 (Bernardo, 2002, p. 64). However, the following simple example suffices to illustrate the expected changes in allele frequencies in a backcross population. Suppose a trait is controlled by only two loci with favorable alleles Q_1 and Q_2 . The adapted parent has the $Q_1Q_1q_2q_2$ genotype, whereas the exotic parent has the $q_1q_1Q_2Q_2$ genotype. The adapted \times exotic cross is backcrossed to the adapted parent so that the allele frequencies are $p_{\text{Adapted}} = 0.75$ (i.e., Q_1) and $p_{\text{Exotic}} = 0.25$ (i.e., Q_2). If only the $Q_1Q_1Q_2Q_2$ individuals are selected in the BC_1 to form the next cycle of selection, the change in p_{Exotic} is $(1.0 - 0.25) = 0.75$, whereas the change in p_{Adapted} is only $(1.0 - 0.75) = 0.25$.

Even though changes in p_{Exotic} are expected to be larger than changes in p_{Adapted} in backcross populations, the changes in both p_{Exotic} and p_{Adapted} are expected to be positive if the QTL are unlinked. But when QTL are linked, selection in

a finite F_2 or backcross population may lead to undesired changes in allele frequencies. Comparisons with a model of $L_{\text{Adapted}} = 10$ and $L_{\text{Exotic}} = 2$ indeed showed that unfavorable changes in p_{Adapted} and p_{Exotic} may result from unfavorable linkage disequilibrium. With $L_{\text{Adapted}} = 10$ and $L_{\text{Exotic}} = 2$, the average distance between segregating QTL on the same chromosome was 146 cM (i.e., unlinked). With $L_{\text{Adapted}} = 10$ and $L_{\text{Exotic}} = 2$ and with $H = 0.50$, p_{Adapted} increased from 0.75 to 0.86 and p_{Exotic} increased from 0.25 to 0.87 in the BC_1 Cycle 15 population. In other words, changes in both p_{Adapted} and p_{Exotic} were favorable when linkage was largely absent. Selecting and recombining more than $N_{\text{Sel}} = 15$ individuals during genomewide selection would reduce unfavorable linkage disequilibrium among a large number of QTL. However, increasing N_{Sel} would also reduce the selection differential and result in a lower response to selection.

Application in Breeding Programs

The results from this study indicate that the choice of generation for selection (Dudley, 1982) is a key factor that

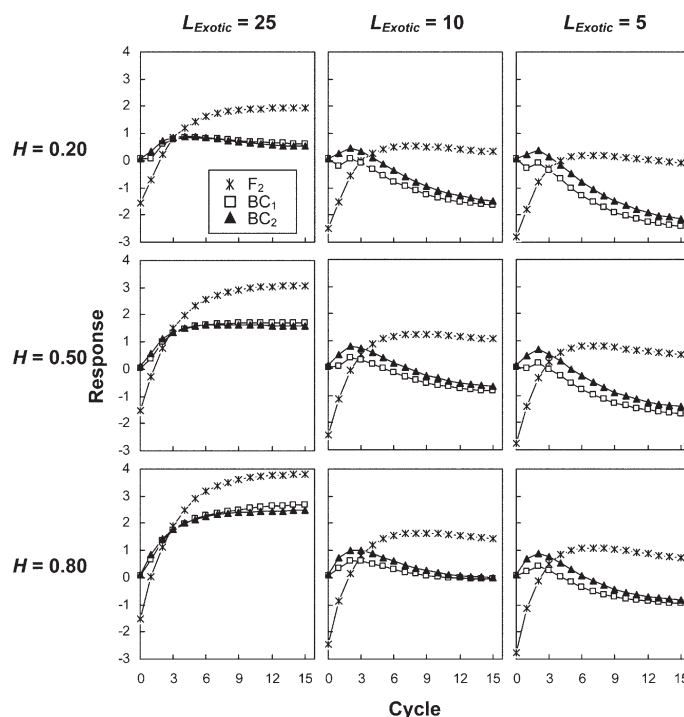


Figure 2. Response to genomewide selection with $L_{\text{Adapted}} = 50$ quantitative trait loci (QTL) with the favorable allele in the adapted parent and $L_{\text{Exotic}} = 25, 10$, or 5 QTL with the favorable allele in the exotic parent. Responses are for the F_2 (asterisks), BC_1 (open squares), and BC_2 (solid circles) of an adapted \times exotic cross. Responses are expressed as a deviation from the mean of the reference population (i.e., F_2 Cycle 0 with $L_{\text{Adapted}} = L_{\text{Exotic}} = 50$) and divided by the testcross genetic standard deviation in the reference population. Testcross-mean heritability (H) likewise refers to that in the reference population. In all cases, $N_{C0} = 288$ testcross progenies were phenotyped in Cycle 0, $N = 576$ plants were subjected to marker-based selection in Cycles 1 to 14, and $N_{\text{Sel}} = 15$ individuals were selected in each cycle. The LSD ($P = 0.05$) was approximately 0.03 to 0.09.

determines the effectiveness of genomewide selection in an adapted \times exotic cross. As noted in the introduction, previous studies have suggested that if the adapted parent has a higher mean performance than the exotic parent, then phenotypic selection should start in a backcross population to the adapted parent (Dudley, 1982; Albrecht and Dudley, 1987; Crossa and Gardner, 1987; Holland et al., 1996). The results from this study indicate, however, that genomewide selection in an adapted \times exotic cross should start in the F_2 rather than in a backcross population, even if the number of favorable alleles is substantially larger in the adapted parent than in the exotic parent. Choosing the starting generation for selection in an adapted \times exotic cross is therefore simpler with genomewide selection than with phenotypic selection, for which the most appropriate generation could be an F_2 , BC_1 , BC_2 , or even a BC_3 generation (Dudley, 1982). On the other hand, the results also indicate that a sustained response to genomewide selection will likely not continue beyond 7 to 8 cycles of selection, particularly when the number of favorable QTL alleles is much smaller in the exotic parent than in the adapted parent ($L_{\text{Adapted}} = 50$ and $L_{\text{Exotic}} = 10$ or 5) and when heritability is low ($H = 0.20$).

Overall, a strategy for the rapid improvement of an adapted \times exotic cross for a quantitative trait therefore involves 7 to 8 cycles of genomewide selection starting in the F_2 . Assuming three generations can be grown per year in a greenhouse or year-round nursery, genomewide selection for 7 to 8 generations would require only three years beyond the time required to develop and phenotype the Cycle 0 testcrosses. Even if further gains from genomewide selection are possible beyond Cycles 7 or 8 (e.g., in the F_2 with $L_{\text{Exotic}} = 25$; Fig. 2), after three years, a breeder would likely want to field-evaluate testcrosses of the latest cycles to monitor the progress from genomewide selection. If the field results indicate that gains from genomewide selection have been made and if substantial marker and trait variation remains in Cycle 7 or 8, then an updated genomewide selection index can be constructed based on the Cycle 7 or 8 marker and phenotypic data. Previous studies have shown that such periodic reestimation of a marker-based selection index may lead to a renewed increase in selection response (Hospital et al., 1997).

A relevant question is whether two cycles of testcross phenotypic selection (which would require 4 yr) leads to a larger response than 7 to 8 cycles of genomewide selection (which, as mentioned above, would require 3 yr). The results indicated that the gains from 7 to 8 cycles of genomewide selection were consistently larger than the gains from two cycles of testcross phenotypic selection. Specifically, the difference in the means of F_2 Cycle 8 of genomewide selection and F_2 Cycle 2 of testcross phenotypic selection ranged from 1.25 for $L_{\text{Exotic}} = 5$ and $H = 0.80$, to 2.40 for $L_{\text{Exotic}} = 50$ and $H = 0.80$.

The results indicate that the number of progenies phenotyped in Cycle 0 (N_{C0}) and the heritability in Cycle 0 are critical factors that affect the success of genomewide selection in an adapted \times exotic cross. Simulation studies have previously indicated that for three cycles of genomewide selection in an adapted \times adapted cross, a population size of $N_{C0} = 144$ was generally sufficient (Bernardo and Yu, 2007). But results from the current study showed a clear advantage in using a larger population size ($N_{C0} = 288$) for medium-term improvement of an adapted \times exotic cross. Furthermore, the larger responses with $H = 0.50$ or 0.80 than with $H = 0.20$ indicate that field tests of Cycle 0 progenies need to be replicated sufficiently across several environments to increase the entry-mean heritability. This may include evaluating the Cycle 0 progenies in at least 2 yr so that genotype \times year interaction can be sampled. The impact of genotype \times year interaction increases as the number of cycles of marker-based selection increases. Having a second year of field evaluation of the Cycle 0 testcrosses will add 1 yr to the total number of years needed for 7 to 8 cycles of genomewide selection, but it would help mitigate the influence of genotype \times year interaction on the response to multiple cycles of genomewide selection in the adapted \times exotic cross.

Lastly, epistasis was assumed absent in this study. In contrast, continuous selection in elite germplasm may lead to coadapted gene complexes (Mayr, 1954, p. 165) that comprise favorable combinations of epistatic genes. Introgression of exotic germplasm, either through phenotypic selection or marker-based selection, may lead to an undesired disruption of such gene complexes. Empirical experiments are needed to assess the usefulness of genomewide selection under the actual genetic mechanisms for quantitative traits in elite and exotic germplasm.

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