



Selection Mapping in Two Maize Populations Improved for Northern Leaf Blight Resistance



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Genetic Diversity

	Pool 29	Pool 30	Total*
No. of Loci	120	151	115
% Polymorphic	100%	100%	100%
No. of Alleles	771	852	879
Mean Allele No./Locus	6.4	5.7	7.6
No. Private Alleles	218	188	406
Mean No. Private alleles/Locus	1.9	1.6	3.5

*This total does not include loci that could not be compared due to run variation in genotyping.

Discussion

- Both pools had a similar amount of within population genetic diversity. There was also allelic variation found between the pools, indicating that there is considerable genetic diversity both within and between the pools.
- Some significant marker loci co-localized with reported QTL, while others did not. This suggests that the regions without reported QTL, where significant markers were located could represent previously unidentified QTL for NLB or genomic regions that were selected for other agronomic traits as significant gains were also made for yield and common rust resistance by Ceballos *et al.* (1991).
- One putative QTL was validated using a segregating F₂ family. This locus maps to maize bin 8.06 which is known to carry several QTL, and several candidate genes for resistance to NLB. This region also carries the major genes *Ht2* and *HtLV1*, which could have been selected as well.
- Changes in allele frequency did not correlate between populations. This suggests that different SSR alleles are in linkage disequilibrium with putative resistance alleles in each population and/or that different resistance alleles were under selection.

Future Research Objectives

- Tissue has been collected for 45 individuals from C₀ and C₁ for Pools 28, 31, 33, and 34. These pools will also be evaluated for changes in allele frequency at selected loci. Evaluation of these pools will allow us to determine which, if any, loci are putatively under selection in all of the populations.
- An F₂ family which carries the favorable allele from Pool 29 at umc11-49 (8.06) is being grown for evaluation to determine if the same trait-marker association can be found in a separate pool.
- Additional loci in Pool 30 are also being tested. This will further validate any putative QTL that were identified by selection mapping.
- We are currently conducting experiments to determine if the resistance gene identified in 8.06 is HNL1. We are also designing SNP-based markers for the candidate genes in 8.06 to determine changes in SNP frequency.

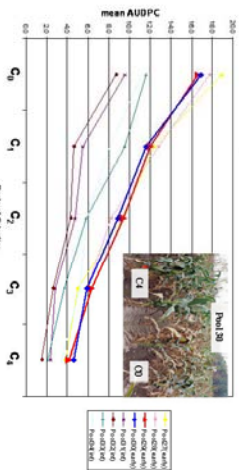
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Introduction

Recurrent selection (RS) is commonly used for trait improvement in crop species. Selection Mapping (SM) is an approach for locating putative quantitative trait loci (QTL) by identifying significant changes in allele frequency in RS populations. We conducted SM on two RS populations that were improved for resistance to northern leaf blight (NLB, causal agent *Exserohilum turricum*) at the International Maize and Wheat Improvement Center. We examined the extent to which common loci or chromosomal segments were associated with RS in two distinct, but similarly selected, populations. In the two populations, 120 simple sequence repeat (SSR) loci were evaluated, and 25 and 31 loci exhibited significant deviations from drift. Of these, 11 loci exhibited significant deviations in both populations. However, the alleles that increased in frequency in the two populations were different. The results presented here suggest that there were several common loci associated with NLB selection between these populations but there is little correlation between the SSR allele(s) that increased in frequency.

Materials and Methods

Ceballos *et al.* (1991) achieved significant gains for NLB through 4 cycles of full-sib S₁ recurrent selection (base cycle = C₀; cycle 1 = C₁;...; cycle 4 = C₄). There were also significant gains for common rust resistance, which was selected as a secondary characteristic.

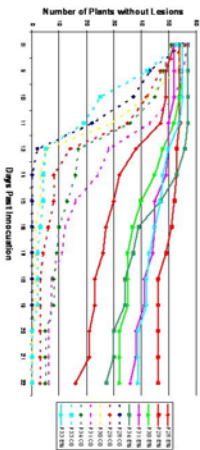


CIMMYT; Ceballos *et al.*, 1991 Crop Sci.

Ninety individuals were sampled from Pool 30 and Pool 29 (45 C₀ + 45 C₄). Simple sequence repeat (SSR) loci (n=120) were analyzed in both populations and allele frequencies calculated. A simulation-based test statistic was developed (derived from a test described by Waples [1989]) and used to identify loci exhibiting significant deviations from genetic drift (R. Wisser and S. Murray, unpublished).

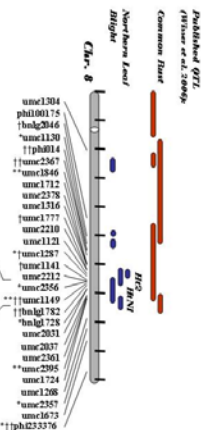
Phenotypic Evaluation

To determine if the increase in resistance from selection could be observed under our field conditions, 50 – 60 individuals from C₀ and C₄ were evaluated for Incubation Period (IP; number of days to appearance of necrotic lesions) in Aurora, NY during July–Aug 2006. There was a large and highly significant difference in all of the pools between the C₀ and C₄. There was also a significant difference between different pools from the same round of selection.



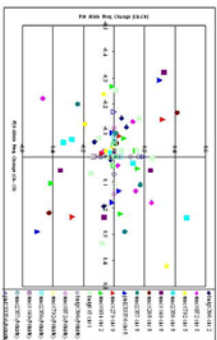
Selection Mapping

The null hypothesis of genetic drift was rejected for 25 loci in Pool 30 and 31 loci in Pool 29 (α = 0.05; corrected for multiple tests). Of these loci, 11 were significant in both populations. Loci that were significant in both populations lend additional support for the putative QTLs identified. On the other hand, significant loci that were found in only one population could be unique alleles for that set of germplasm.



Several regions of the genome were found to be putatively under selection in one or both populations. In maize bins 8.05/8.06, several SSR loci were putatively associated with selection. Other studies have associated this chromosomal segment with QTL and major genes for NLB and QTL for common rust.

Using a segregating F₂ population derived from an individual in Pool 30(C₄) x B73, the favorable allele at markers umc11-49 and umc2356 was shown to associate with increased incubation period. These two markers were found to co-localize to a single BAC which is partially sequenced (R. Wisser *et al.*, unpublished).



While there were many loci which significantly deviated from drift in both populations, there was not a clear correlation between the alleles that changed in frequency in one population and the same alleles in the other population.

Maize BAC AC15355 contained several candidate genes for resistance to *Exserohilum turricum* including a peptidase, an esterase, and a glutathione S-transferase (all putative). These are intriguing candidate genes because they are members of gene families associated with detoxification and were identified as significantly associated with disease QTL in rice (Wisser *et al.*, 2005).