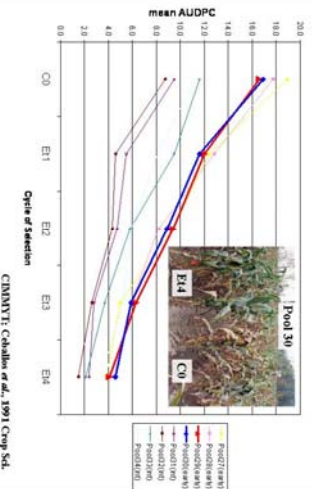


Introduction

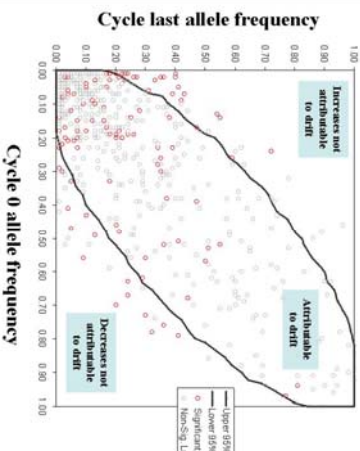
Recurrent selection (RS) is commonly used for trait improvement. Using RS, the International Maize and Wheat Improvement Center (CIMMYT) achieved significant gains for resistance to northern leaf blight (NLB), a disease of global significance, in eight diverse subtropical maize populations (Ceballos *et al.*, 1991). In two of the populations, putative quantitative trait loci (QTL) for NLB resistance were identified by RS mapping from significant changes in allele frequencies between different cycles of selection. The loci identified are likely to be linked to the genes under selection. The purpose of this study was to evaluate to what extent common loci or chromosomal segments were associated with RS in separate, similarly selected, populations.

Materials and Methods

Ceballos *et al.* (1991) achieved significant gains for NLB through 4 cycles of full-sib S₁ recurrent selection.



Ninety individuals were sampled from Pool 30 and Pool 29 (45 C₀ + 45 C₄ [E4]). Simple sequence repeat (SSR) loci (n=120) were analyzed in both populations and allele frequencies calculated. Significant changes in allele frequency between the two cycles were determined by combining a simulation of drift in the respective populations with a χ^2 test (R. Wisser and S. Murray, unpublished; R. Weaples, 1989).



Results

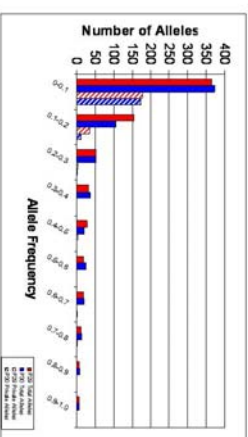
Comparable amount of genetic diversity

These two pools had a comparable amount of genetic diversity. Both of the pools averaged ~ 6 SSR alleles per locus. There was a relatively high number of private alleles (46%) with an average of 3.5 private alleles per locus.

	Pool 29	Pool 30	Total*
Number of Loci	120	151	115
Proportion Polymorphic	100%	100%	100%
Number of Alleles	771	852	879
Mean Allele # / Locus	6.4	5.7	7.6
# Private Alleles	218	188	406
Mean # Private alleles/ Locus	1.9	1.6	3.5

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

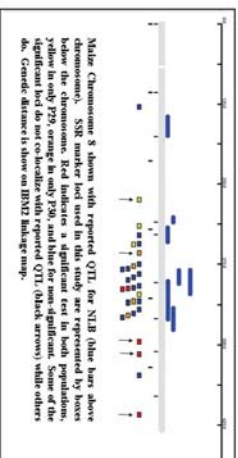
Most alleles were at low frequency



There were many rare alleles found at the loci tested. In addition there were many private alleles which were found almost exclusively at a frequency of less than 20%.

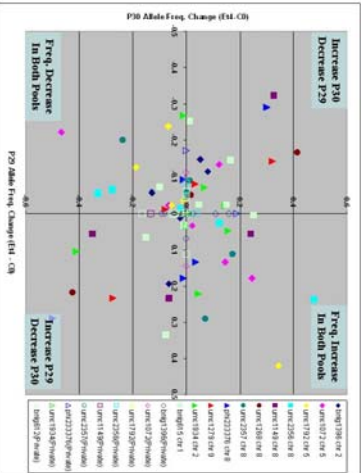
Some loci were significant in both populations

Many significant marker loci co-localize with published QTL for NLB, while other markers are located in regions not previously reported to have disease QTL. Some markers that exceeded expectations of drift were significant in both populations.



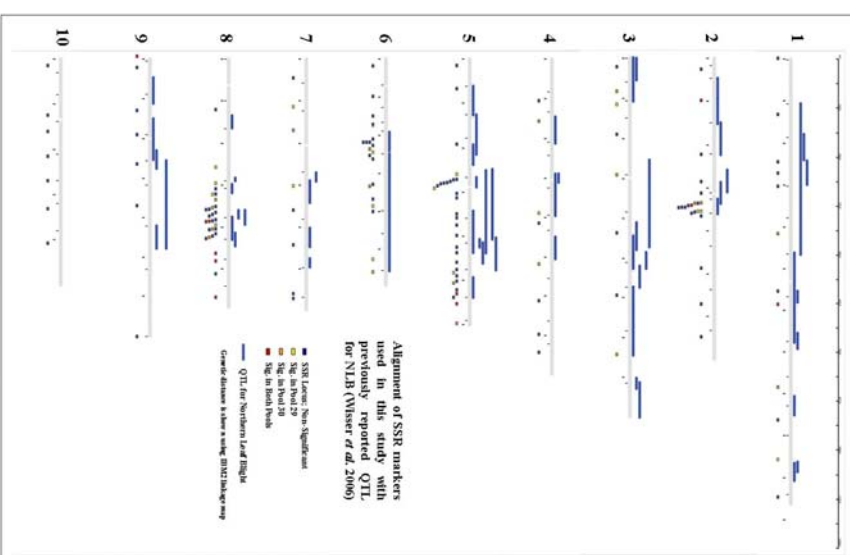
Maize Chromosome 8 shows with reported QTL for NLB (blue bars above the chromosome) and significant loci in both populations (red and black arrows below the chromosome). Red indicates a significant test in both pools of the cycle in only P29, orange in only P30, and blue for non-significant. Some of the significant loci do not co-localize with reported QTL (black arrows) while others do. Genetic distance is shown on IBM2 linkage map.

Changes in allele frequency do not correlate between populations



At loci that 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.

Alignment of SSR Marker Loci with Reported QTL for Northern Leaf Blight



Alignment of SSR markers used in this study (with previously reported QTL for NLB (Wisser *et al.* 2006))

■ SSR Locus: This significant
■ The in Pool 29
■ The in Pool 30
■ The in Both Pools
— QTL for Northern Leaf Blight
--- Candidate's values using IBM2 linkage map

Conclusions

- Both pools had a comparable amount of within population genetic diversity.
- There was a relatively high amount of rare allelic variation found 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, because significant gains were also made for yield and common rust resistance by Ceballos *et al.* (1991).
- 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.

References

- Ceballos, H., J.A. Duvick, and H. Gertner (1991). Recurrent selection for resistance to *Ascochyta blight* in eight adapted maize populations. *Crop Science* 31:964-971.
- Wright, R. S. (1989). Temporal stability of allele frequencies: Testing the right hypothesis. *Evolution*, 43:1256-1251
- Wisser, R.J., P.J. Baker, Bart, and R.J. Nelson (2006) The Genetic Architecture of Disease Resistance in Maize: A Systematic of Published Studies. *PopGen* 7(2): 115-129