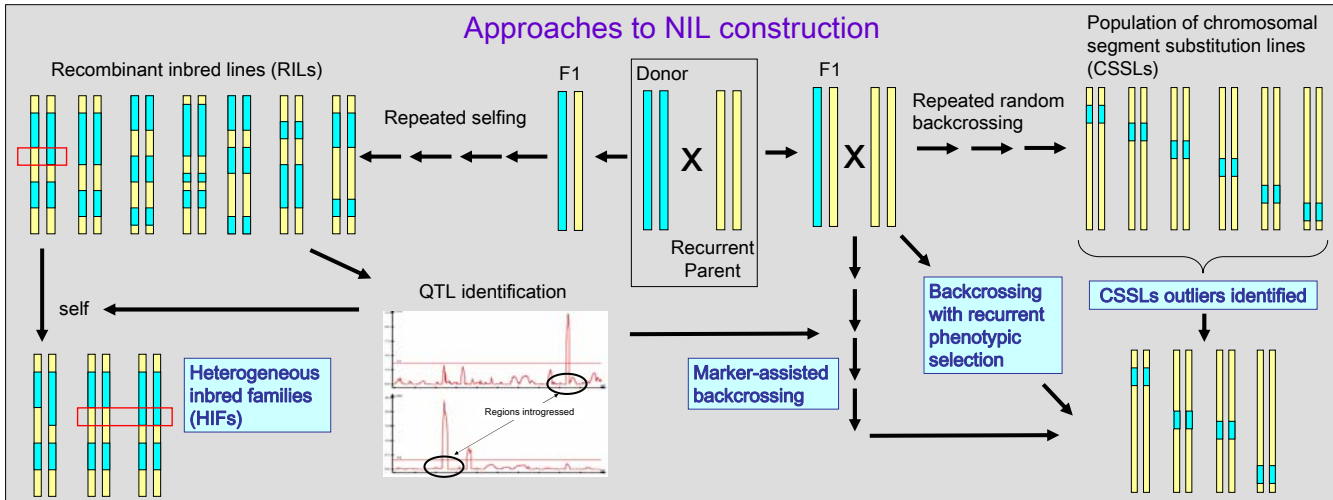


Introduction: To allow detailed study of quantitative trait loci (QTL), it is necessary to create near isogenic lines (NILs) that differ only for the QTL of interest. In this way, the effects of the QTL can be isolated from other genetic effects. Here we detail the production and analysis to date of NILs that differ for disease resistance QTL.

Approaches to NIL construction



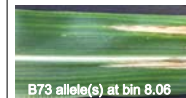
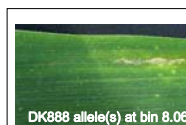
38 bins associated with multiple disease resistance QTL were targeted for NIL construction, based on a consensus map of disease QTL in maize (Wisser *et al.* 2006). HIF-derived NILs were constructed from B73 x CML52 and B73 x DK888. The tropical lines CML52 and DK888 were chosen based on their superior resistance to NLB, GLS, SLB, and other diseases. The NIL pairs are now being characterized for resistance to northern leaf blight (NLB), gray leaf spot (GLS), southern leaf blight (SLB), anthracnose leaf blight (ALB), common rust, and common smut.

NILs derived from heterogeneous inbred families (HIFs)

Cross of origin	Contracting regions in available NIL pairs (bin)	Disease resistance (allele conferring resistance)						Differential in resistance, but causative QTL unknown
		NLB	GLS ^b	SLB ^b	ALB ^b	Rust ^b	Smut ^b	
B73 / CML52	1.06	CML527 ^a	No	No	No	No	No	SLB, ALB
	1.07/08	CML527 ^a	No	No	No	No	No	
	2.04/06	No	No	No	No	No	No	SLB
	2.10, 5.03	CML52 or B73 (epistatic bin QTL in bin 2, 10 and 5, 03)	No	No	No	No	No	
	3.06	No	No	No	No	No	CML52 ^b	NLB, ALB, rust
S11 / DK888	6.05	CML52	No	No	No	No	No	SLB, ALB
	7.04	No	No	No	No	No	No	NLB, rust
	8.02/03	CML527 ^a	No	No	No	No	CML52 ^b	CML52 ^b
	3.04	No	No	No	No	No	No	
S11 / DK888	5.04	No	DK888 ^a	No	No	No	No	S11 ^b
	5.06	No	No	No	No	No	No	
	6.05	No	No	No	No	No	No	
	8.06	DK888	No	No	No	No	No	

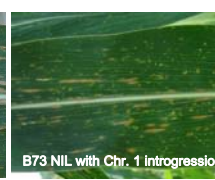
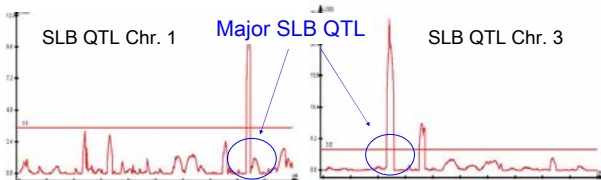
^a The NLB-QTL was identified from corresponding heterogeneous inbred families in 2005 to 2006, but significant phenotypic contrast was not detected in selected NIL pairs at Aurora, 2007.
^b Data based on one-year field trials, and need to be further validated. (Common rust and common smut are from natural infection.)

NIL pairs inoculated with NLB



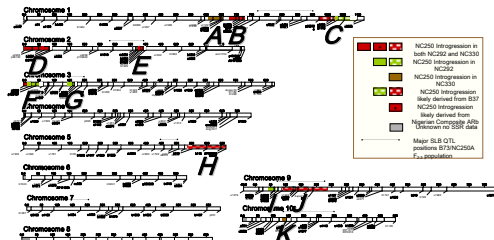
NILs derived from marker-assisted backcrossing

B73 NILs inoculated with SLB in the field

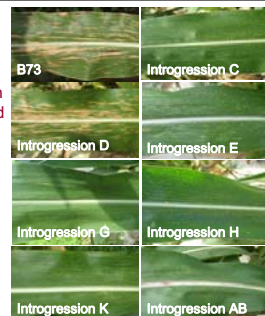


NILs derived from backcrossing with recurrent phenotypic selection

The sister lines NC292 and NC330 were derived in the 1980s by Don Thompson at NCSU by repeatedly backcrossing a B73 / NC250 hybrid to B73 and selecting for SLB resistance at each generation. The resulting lines are more than 90% B73 genome-derived while retaining much of the original SLB resistance from NC250. We scanned the genomes of NC292 and NC330, and identified the 11 introgressed regions (shown right). We then constructed and tested B73 NILs carrying each of the introgressed regions alone (far right).



B73 NILs inoculated with SLB in the field



NILs derived from identified CSSL outliers

The TBBC3 population (Szalma *et al.* 2007) consists of 90 lines with an average 89% B73 constitution. Each line carries a different set of introgressions from the line Tx303. We screened this population for lines that differed significantly in disease resistance from the B73 recurrent parent lines and from the rest of the population.

B73 NILs inoculated with NLB in the field



B73 NILs infected with GLS in the field

