

VII. MOLECULAR AND FUNCTIONAL DIVERSITY OF MAIZE  
(www.panzea.org)

**Panzea's Nested Association Mapping Population: A Powerful Phenomics Resource for the Maize Community**

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"If you build it they will come." Well, the Panzea project has built it:

**The ultimate germplasm resource to date for localizing QTLs in maize!**

The Panzea project (a.k.a. 'Molecular and Functional Diversity of the Maize Genome'; NSF DBI 0321467) is a five-year NSF project headed by John Doebley and involves eight additional investigators at seven institutions (University of Wisconsin, Cornell University, North Carolina State University, University of Missouri, University of California-Irvine, Cold Spring Harbor Laboratory and USDA-ARS). Our overall objectives are to address the two major questions '*How has selection shaped molecular diversity?*' and '*How does this molecular diversity relate to functional trait variation?*' To address these questions, we have performed large-scale SNP discovery in maize and its wild progenitor, teosinte, in more than 3000 randomly chosen genes and in more than 1000 candidate genes for traits of agronomic, developmental, evolutionary and ecological importance. Based on this sequence data, we found that about 2-4% of genes in the maize genome were detectably influenced by artificial selection during the domestication and subsequent improvement of maize (Wright et al., *Science* 308:1310-14, 2005; Yamasaki et al., *Plant Cell* 17:2859-72, 2005). You can read more about the results to date from this project (and from its five-year forerunner) via our project publications web page: <http://www.panzea.org/lit/publication.html>.

Now that we have completed our objectives relating to our first major question, we are devoting our focus to the characterization of functional diversity in both teosinte and maize. To this end, we are engaged in QTL and association mapping experiments both in modern maize and in crosses between teosinte and maize. We are currently working with two teosinte association mapping populations, three teosinte-maize backcross QTL mapping populations, a maize association mapping population and a maize 'Nested Association Mapping' (NAM) population.

The maize NAM population is the centerpiece of our project. Of the numerous resources that we are generating, we expect the NAM population to be the most significant to the maize research community. Nested Association Mapping is a powerful new method for localizing QTL which uses a multifamily RIL mapping population derived from crosses to a common parent (i.e., B73) in order to perform a joint QTL and association analysis. By employing a genomic scan of common parent-specific SNPs in the progeny RILs combined with high density genotyping (or sequencing) of the parental lines, the NAM strategy captures the best of both worlds: the statistical power of QTL analysis is combined with the high chromosomal resolution of association analysis.

We are pioneering the NAM approach in maize. Our NAM population consists of >5000 RILs from 25 families, with 200 RILs per family, all being genotyped at 1500 SNP loci. It forms a permanent QTL mapping resource for the benefit of the maize community. The families were generated by crossing 25 diverse maize inbred lines with B73 as a common parent. Additionally, the well-known IBM mapping population is included as the 26<sup>th</sup> family. Finally, a collection of 280 diverse maize inbreds from around the world that serves as an association mapping platform for maize has also been included in these experiments.

This summer we will be planting out all of these RILs in three locations (Raleigh, NC; Ithaca, NY; Champaign-Urbana, IL). The parental lines are being sequenced over the next year and a half--these data will make it possible to analyze all populations as one unified experiment, potentially with gene-level QTL resolution. A list of the traits that we are scoring in the NAM population will soon be available from [www.panzea.org](http://www.panzea.org). We are scoring a number of the most obvious agronomic and developmental traits in these populations, but are unable to score some of the more complex traits. We have created this NAM resource with the hope that maize researchers working on complex, specialty traits will use it to uncover the genetic basis of these traits in a broad sample of maize inbreds.

**We invite interested maize researchers to score their own phenotypes of interest in one or more of our NAM 'Fields of Dreams'.**

Our only stipulation is that your data set must be deposited in our project database, Aztec, where it will be held privately for two years (members of the Panzea group will not be allowed to analyze it either, without prior permission from you), and then released to the public via [www.panzea.org](http://www.panzea.org).

We also have extensive experience in creating barcoding tools for phenotyping, and can provide help with this. For further details or to arrange your phenotyping visit(s), please contact:

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Jim Holland, USDA-ARS/North Carolina State University (James\_Holland@ncsu.edu), or  
Torbert Rocheford, Univ. of Illinois (trochefo@uiuc.edu).

If you are unable to make it to one of our fields this summer, do not fret! Plans are afoot to have public grow-outs of the NAM population for as many as four subsequent years, as part of the maize phenomics initiative touted by the MGEC. However, at this point funding support is guaranteed only for this summer's grow-out. For educators at institutions focusing primarily on undergraduate teaching, the NAM resource provides an ideal opportunity for research involving undergraduate or Masters students, potentially funded via the NSF's 'Research Opportunity Awards'. Resources from these awards could potentially be pooled with those from other sources to fund one or more future 'public' grow-outs of the NAM population. In addition, for researchers interested in growing out all or part of the NAM population themselves, seed from the entire, fully-genotyped NAM population will be available from the Maize Stock Center in 2008. So if you miss out on this summer, it should not be too late to realize your maize phenomic dream!