

Characterizing the Wheat Genome by Random Sample Sequencing National Science Foundation (NSF) Funded Wheat Pilot Project 2005

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The nuclear DNA of bread wheat, *Triticum aestivum*, variety Chinese Spring, will be investigated to determine the content and distribution of genes and other sequences in the large genome of this polyploid species. A total of 220 large fragments of wheat DNA, cloned into a bacterial artificial chromosome (BAC) vector, will be randomly selected and subjected to DNA sequence analysis. The sequence analysis will be done at a low redundancy to maximize the data generated per unit cost. These 220 BACs will also be located to wheat chromosome maps by a novel polymerase chain reaction (PCR) strategy so that the relationship between chromosomal location and DNA sequence content can be assessed. Two gene enrichment techniques, High Cot analysis and Hypomethylated Partial Restriction analysis, that have been proven in maize will be tested for their efficacy in wheat. All generated sequences will be analyzed for gene and repetitive DNA content. Abundant repeats will also be characterized for their degree and nature of sequence divergence and their possible differential distribution across the wheat chromosomes. These experiments and analyses will determine the basic molecular characteristics of the wheat genome, provide insights into the nature of sequence evolution in this polyploid cereal, and lay the foundation for future genomic characterizations of wheat. Access to project outcomes All data and analyses will be made available through a project website (accessible via <http://www.genetics.uga.edu/jlblab/index.html>) and public databases, and also through publication in peer-reviewed scientific journals.