

Acronyms/Abbreviations found in grant proposal

B73: An inbred maize line developed at Iowa State University. Iowa lines are given the designation “B” since there are several corn belt states (Iowa, Illinois, Indiana) that begin with the letter “I”. B73 and its derivatives are widely used in the production of commercial hybrids. This inbred also became the “lab rat” of many maize genomics labs. It is the genotype being sequenced and mapped by the NSF-funded maize genome project.

BACs : **B**acterial **A**rtificial **C**hromosomes - Vectors for cloning large (>100 kb) fragments of DNA into *E. coli*. These are the vectors of choice for making libraries of eukaryotic genomes, including maize.

BLAS : **B**asic **L**ocal **A**lignment **S**earch **T**ools - BLAST programs developed by the National Center for Biotechnology Information are powerful tools for comparing new sequences with previously characterized ones. This allows researchers to identify whether the query sequence is similar or identical to previously cataloged sequences.

<http://www.ncbi.nlm.nih.gov/BLAST/>

BLASTN: **B**asic **L**ocal **A**lignment **S**earch **T**ools **N**ucleotides - Compares a nucleotide query sequence against a nucleotide sequence database.

<http://www.ncbi.nlm.nih.gov/BLAST/>

BLASTX: **B**asic **L**ocal **A**lignment **S**earch **T**ools - Compares a nucleotide query sequence translated in all reading frames against a protein sequence database.

<http://www.ncbi.nlm.nih.gov/BLAST/>

CAP3: **C**ontig **A**ssembly **P**rogram - DNA sequence assembly program developed by Dr. Xiaoqi Huang in the Department of Computer Science at Iowa State University.

<http://genome.cs.mtu.edu/cap/cap3.html>

CEL1: **C**elery endonuclease **1** - Enzyme isolated from celery that cleaves heteroduplexes. This enzyme is used for TILLING.

*Henikoff, S. and Comai, L. (2003) Single Nucleotide Mutations for Plant Functional Genomics, **Annual Reviews of Plant Biology 54:375-401.**

<http://www.annualreviews.org>

CIMMYT: **C**entro **I**nternational de **M**ejoramiento de **M**aize y **T**rigo - International Maize and Wheat Improvement Center outside of Mexico City that researches sustainable development of maize and wheat.

<http://www.cimmyt.org>

Consed: A graphical user interface for editing DNA sequence assemblies.

<http://www.phrap.org/consed/consed.html>

dHPLC: **D**enaturing **H**igh-**P**erformance **L**iquid **C**hromatography - PCR products are partially denatured by heat within a linear acetonitrile gradient. SNPs will cause the formation of heteroduplexes which can be distinguished from homoduplexes.

EMS: **E**thyl **M**ethane **S**ulfonate - Chemical mutagen used to make single base mutations in DNA. Recessive EMS-induced mutations are uncovered in the M₂ generation. **EST** Expressed Sequence Tag - A single-pass sequence of a cDNA clone.

F₁: First filial generation - The generation obtained by crossing two (inbred) parents that typically have allelic differences in multiple genes.

F₁BC: F₁ Backcross - The generation obtained by backcrossing an F₁ to one of its inbred parents.

GenBank: Publicly accessible repository of annotated DNA sequences maintained by the National Institutes of Health. Sequences from over 130,000 organisms are included. <http://www.ncbi.nlm.nih.gov/Genbank/genbankstats.html>

Heterosis: The F₁ hybrid of two inbred lines is typically more robust than either parent. Also known as hybrid vigor. The genetic and molecular basis for heterosis is not yet well understood.

IBM: Intermated B73/Mo17 - Mike Lee and his co-workers, Department of Agronomy, Iowa State University, developed the intermated B73 X Mo17 (IBM) population (n = 350) by intermating an F₂ population derived from the single cross of the inbreds B73 and Mo17 for several generations prior to extraction of recombinant inbred (RI) lines. The genetic resolution in the resulting population was therefore enhanced because additional opportunities for recombination were provided during the intermating generations.

*Lee et al. (2002) Expanding the genetic map of maize with the intermated B73 X Mo17 (IBM) population. **Plant Mol Biol.** 48:453-61.

IDP: Insertion-Deletion Polymorphism - Variation in DNA sequence that involves loss or gain of base pairs; also known as InDel or INDEL.

Lucy: Program to trim vector and low quality portion from a sequence developed by Dr. Hui-Hsien Chou in the Department of Computer Science, Iowa State University. http://www.complex.iastate.edu/hhchou/software_lucy.html

MAGI: Maize Assembled Gene Island. Maize genome assembly project conducted at Iowa State University. Publicly available maize genome survey sequences (GSSs) from gene-rich (High Cot or Methyl Filtered) and BAC end sequences were assembled into contigs (contiguous fragments) using parallel processing. <http://www.plantgenomics.iastate.edu/maize/>

M₂: Second generation after application of a mutagen, e.g. EMS. In this generation, homozygous recessive mutations may be identified via phenotypic screens.

MAS: Marker Assisted Selection - A DNA polymorphism, e.g. a SNP or IDP, is used to follow the segregation of the chromosomal region responsible for a trait of interest. The DNA polymorphism can be detected at an earlier stage (e.g. seedling) than the trait of interest (e.g., height).

MF: Methyl-Filtered DNA is cloned into *mcrBC+* *E.coli* strains that allow proliferation only of hypomethylated DNA. Regions of the maize genome that are rich in genes tend to be hypomethylated. Methyl filtration is an important technology in cloning genic DNA from large genome organisms.

*Palmer LE, Rabinowicz PD, O'Shaughnessy AL, Balija VS, Nascimento LU, Dike S, de la Bastide M, Martienssen RA, McCombie WR. (2003) Maize genome sequencing by methylation filtration. **Science Vol 302 No 5653:2115-7.**

<http://www.oriongenomics.com/tech-genethresher-1.html>

Mites: Miniature Inverted Repeat Transposable Elements - Small nonautonomous DNA transposable elements that appear to be associated with genes.

*Zhang Q, Arbuckle J, Wessler S R (2000). Recent, extensive, and preferential insertion of members of the miniature inverted-repeat transposable element family Heartbreaker into genic regions of maize. **Proc Natl Acad Sci USA**. 1;97:1160-5.

Mo17: Missouri 17 - Inbred maize line developed at the University of Missouri. This inbred and its derivatives are widely used in the production of hybrids. Mo17 is in a different heterotic group (genetic background) than is B73. B73 X Mo17 exhibits a high degree of heterosis and has been an important commercial hybrid.

NR: Non-redundant protein and nucleotide databases maintained by NCBI where completely identical entries of sequences have been merged. <http://www.ncbi.nih.gov/blast/db/nr.tar.gz>

Overgo: OVERlapping oliGOnucleotide - A set of two approximately 40 nt oligos used as primers and templates. The 2 partially overlapping sequences prime each other in a synthesis reaction that incorporates a high level of radioactivity. An overgo probe can be used to identify similar short sequences in genomic DNA. The overlap is similar to the overlap of the two arrows as shown in the image at right.



<http://www.maizegdb.org/overgo.php>

PCAP: Parallel Contig Assembly Program - A whole genome assembly program that was tested on a mouse whole-genome data set developed by Dr. Xiaoqiu Huang in the Department of Computer Science at Iowa State University.

<http://seq.cs.iastate.edu/>

PCR: Polymerase Chain Reaction - Using a heat stable polymerase and oligonucleotide primers of about 20 nt, a DNA sequence is amplified by multiple rounds of denaturation, primer annealing, and primer extension. Taq polymerase can amplify targets of up to 1- 2 kbp; proprietary polymerases with proof reading functions can amplify larger fragments. PCR is used for genotyping, diagnostics, and forensics. PCR products can be cloned, sequenced, or analyzed for heteroduplex formation.

Phred: Program used to call bases and assign confidence values to the base assignments from sequencing chromatograms. Provides a check to the base calls produced by the software that is packaged with the sequencing equipment.

<http://www.phrap.org>

Polymorphism: More than one allele of a gene is present in a population. The difference(s) between alleles may be detectable by a phenotype or only at the DNA level by Southern blot, PCR or sequence analysis.

QCing : Quality Controlling - Researchers manually check on automated analysis of data, e.g. examination of sequencing chromatograms to check on the base calls.

REU: Research Experience for Undergraduates - Internships in research laboratories, usually paid.

RFLP: Restriction Fragment Length Polymorphism - Variation in DNA sequence that is a recognition site for a restriction endonuclease; detectable via Southern blot hybridization.

RI: Recombinant Inbred - A collection of plant lines that has been outcrossed then selfed for several generations e.g. the IBM population. The crossing procedure creates F₁ plants heterozygous at many loci; recombination during the production of gametes during the F₁ and subsequent generations creates new allelic combinations (haplotypes). Several generations of inbreeding results in plants homozygous for different haplotypes. Such lines are valuable for the production of genetic maps.

SNP: Single-Nucleotide Polymorphism - Variation in one nucleotide in a DNA sequence between individuals in a population.

S_{Nu}PE: Single Nucleotide Primer Extension - A method to detect SNPs. A primer is annealed to a DNA sequence flanking an SNP and allowed to extend using the appropriate fluorescently tagged ddNTP.

SSR: Simple Sequence Repeats - Tandem repeats of 1-6 nt sequences. The number of such repeats tends to be variable due to inexact base pairing during recombination.

TGCE: Temperature Gradient Capillary Electrophoresis - Mixed PCR products from a test strain and a control strain are denatured, allowed to renature, and electrophoresed. If there are no sequence differences between the two strains a single electrophoretic peak will result. If there are sequence differences, multiple peaks will result. A single base pair difference can be detected.

TILLING: Targeting Induced Local Lesions in Genomes - A tool for conducting reverse genetics experiments. DNA from EMS-treated plants is pooled and analyzed for formation of heteroduplexes with control DNA. Sequence differences can then be correlated with phenotypic changes to understand the function of that region of DNA.

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This article can be found online at <http://www.annualreviews.org>

More information on TILLING can be found at <http://faculty.washington.edu/comai/tilling.htm>.

UTR: Untranslated Region - 5' or 3' region of mRNA that does not code for protein.