





**Genomes to Fields
2014 Workshop**

***Coalition Building
Rodney Williamson***

***Chicago, IL
December 10***

We asked: Should we sequence the Corn Genome?

- ✧ How many genes are in a corn plant?
- ✧ How much will it cost to sequence all the genes in corn?
- ✧ Will seed companies collaborate or want proprietary sequence information?
- ✧ HOW ARE WE GOING TO DO THIS????



NATIONAL
CORN GROWERS
ASSOCIATION



Gene Sequencing - New Frontier

One Hundred Fifth Congress
of the
United States of America
AT THE FIRST SESSION
Begun and held at the City of Washington on Tuesday,
the seventh day of January, one thousand nine hundred and ninety-seven

An Act

Making appropriations for the Departments of Veterans Affairs and Housing and Urban Development, and for sundry independent agencies, commissions, corporations, and offices for the fiscal year ending September 30, 1998, and for other purposes.

Be it enacted by the Senate and House of Representatives of the United States of America in Congress assembled, That the following sums are appropriated, out of any money in the Treasury not otherwise appropriated, for the Departments of Veterans Affairs and Housing and Urban Development, and for sundry independent agencies, commissions, corporations, and offices for the fiscal year ending September 30, 1998, and for other purposes, namely:

APPROVED

OCT 27 1997

William Jefferson Clinton

"Medical care" for necessary expenses in implementing those provisions authorized in the Omnibus Budget Reconciliation Act of 1992 (31, 51, 53, and 55), the funding source for which is set as the "Compensation and pensions" appropriated there, That such sums as may be earned on an individual basis, shall be reimbursed to "Medical fund" to augment the funding of individual medical

The Dynamic Maize Genome

Maize has a strikingly dynamic genome: two maize varieties show as much DNA sequence variation as that observed between two different species. Also, genes present in one maize variety may be absent in another. Such variation is evidence of rapid genome change that occurred during the evolution of maize. The grass lineage that includes maize and teosinte diverged from rice and wheat approximately 50 million years ago. Subsequently, the full complement of chromosomes doubled in number in the ancestor of teosinte. Analysis of the sequenced genome of the Midwestern variety, B73, demonstrates that this ancestral duplicated genome underwent significant rearrangement, with pieces of chromosomes inverted, exchanged, transposed, further duplicated, or lost. Transposons contributed substantially to genome variation. Some classes of transposons cluster near centromeres, while others are found near genes that lack the chemical modification of methylation. Most, however, are located in heavily methylated, intergenic regions, contributing to the distinctive genome of each inbred variety. Comparative genomics studies are useful to identify genes in maize that are similar to those found in other plant species. Using these methods, study of the genome of the Mexican maize landrace, *Palomero toluqueño*, identified genes under selection homologous to those that are suspected to be involved in metal processing. Genome analysis demonstrates that landraces and worldwide varieties are highly diverse, making preservation of their unique molecular heritage important for cultural, scientific, and agricultural reasons.

Two maize genomes sequenced recently were B73, an elite inbred line grown in the Midwestern United States (right: Image: Ruth Swanson-Wagner and Patrick S. Schnable, Iowa State University; reprinted by permission from Springer-Plant Sciences), and Palomero toluqueño, a popcorn landrace grown in the highlands of Mexico (left: Image: Jaime Padilla, Irapuato, Guanajuato, Mexico).

Sequence analysis of the maize variety, B73, shows the dynamic nature of the maize genome. The outer rings are maize chromosomes (labeled 1 to 10) with duplicate regions connected by ribbons, showing the large related segments derived from each of the ancestral genomes (Image: From Schnable et al., *Science* 326 (5956) (2009); DOI: 10.1126/Science.1178437).

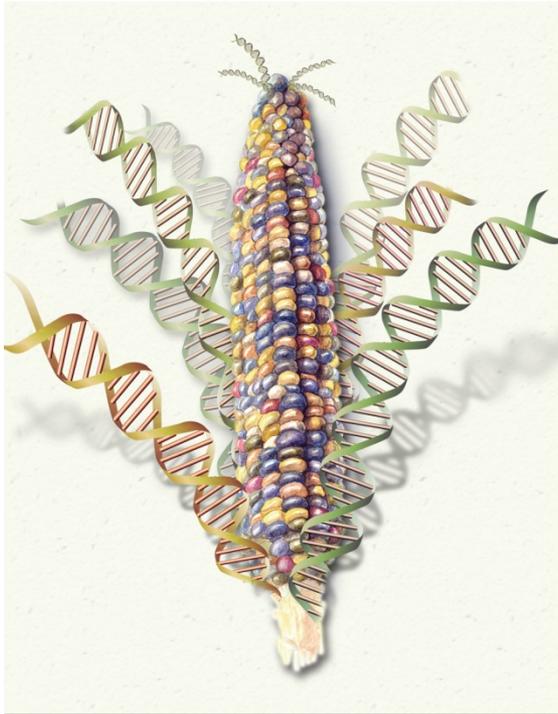
- Recombination rate (cM/Mb) 0 to 7
- Alu insertions (sites/Mb) 0 to 109
- MF Enrichment (% reads) 0.1 to 0.3
- Repeat coverage (%) 0 to 100
- Gene density (genes/Mb) 0 to 74
- Rice chromosomes 1 to 12
- Sorghum chromosomes 1 to 10



Source: Poster from AAAS

Synergy

$$1 + 1 = 3$$



**DROUGHT, SUNLIGHT,
TEMPERATURE, SOILS, RAINFALL,
FERTILITY**



Synergy

$$1 + 1 = 3$$

- 1 Phenotyping Company
- 14 Universities
- 8 Seed Companies
- ARS USDA
- 1 Weather Company

Funding from:

- 4 State Commodity Groups
- National Corn Growers Assn



Genomes to Fields

Revolutionize Plant Science

- \$25 million/yr for 10 years
- Industry support (\$ and in-kind)
- Commodity & organization support (\$ and political)

- Utilize the investment in gene sequencing
- Sequester more carbon
- Feed a growing population
- Develop rural economy
- Improve efficiency of land and fertilizer



Chemicals, Plastics, Detergents, Food Additives, Antibiotics, Cosmetics, Pharmaceuticals, Adhesives, Soap, Fireworks, Pro Dyes & Chalk
Fires

