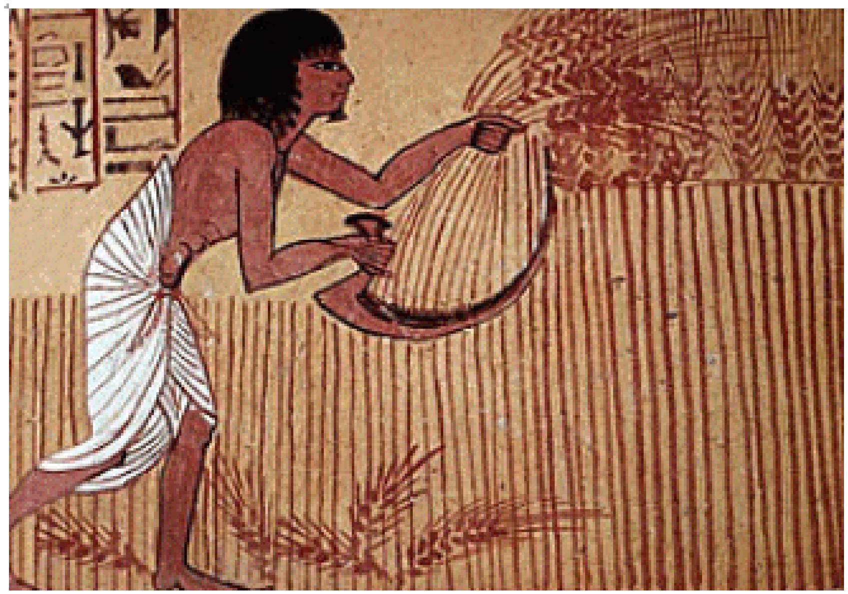
ARS Research in Support of Bioenergy Goals
NP 301 and NP302 Contributions

- ***Cell Walls***
- ***Plant Oils***
- ***Plant Biopolymers***

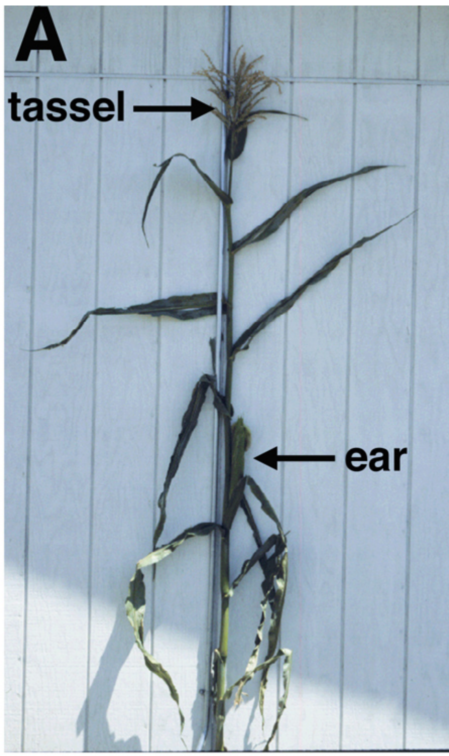
Kay Simmons
NPL, Plant Genetics & Grain Crops

Nov. 30, 2006



Wheat was domesticated around 10,000 years ago

Evolution of maize from wild ancestor, teosinte



maize


teosinte

We have been breeding crops for food for thousands of years,

but improving crops for bioenergy for just a few years.

Plant Genetic Resources, Genomics, and Genetic Improvement (NP301)

Components:
1. Plant and Microbial Genetic Resource Management
2. Crop Informatics, Genomics, and Genetic Analyses
3. Genetic Improvement of Crops

USDA ARS

Plant Biological and Molecular Processes (NP302)

Components:

1. Functional utilization of the genome
2. Biological processes that improve crop productivity and quality
3. Plant biotechnology risk assessment

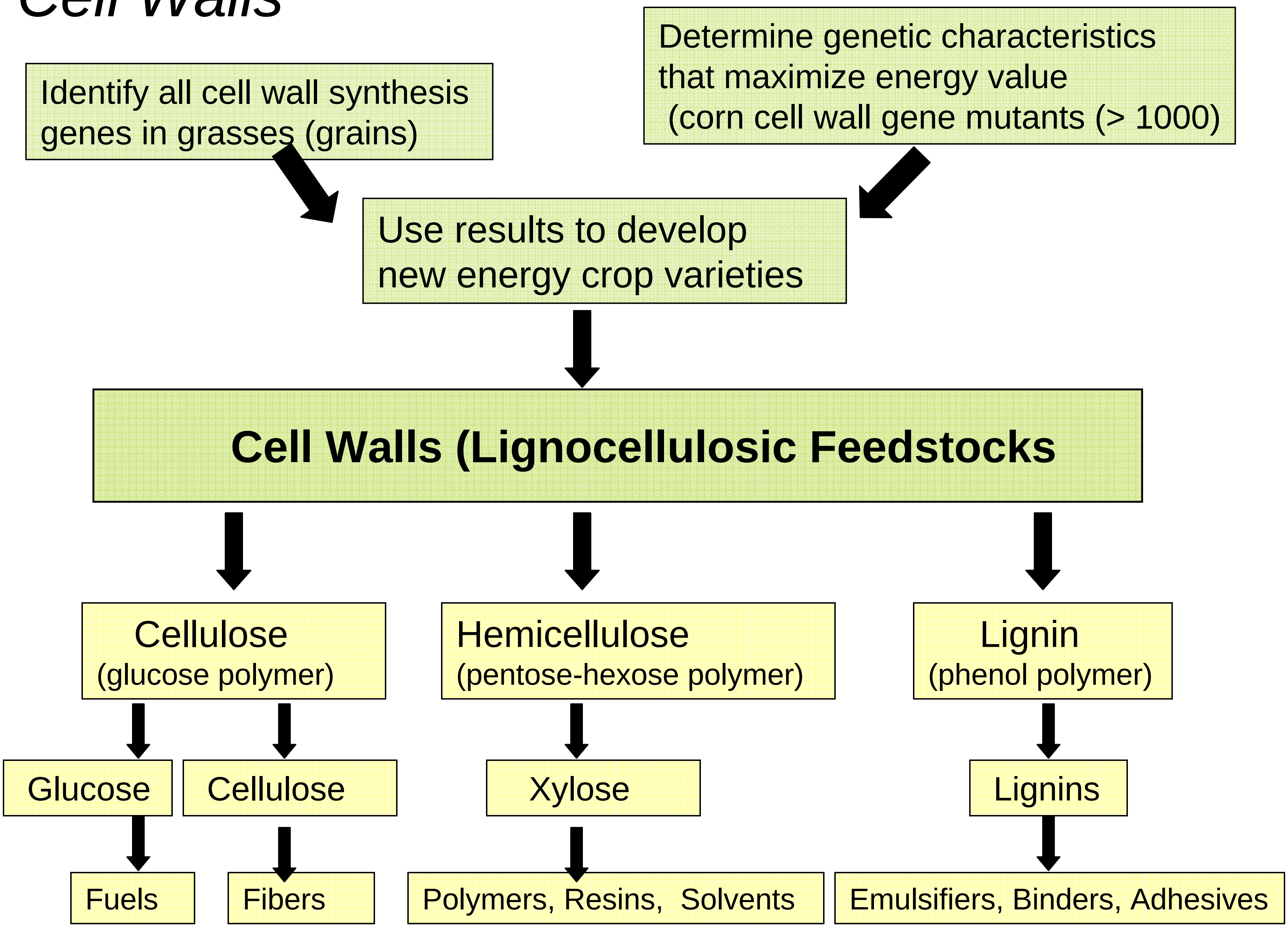
USDA ARS

Cell Walls

- Select for plants with increased mass and walls with more accessible polysaccharides

- Transgenes that break down lignin in the right cell types

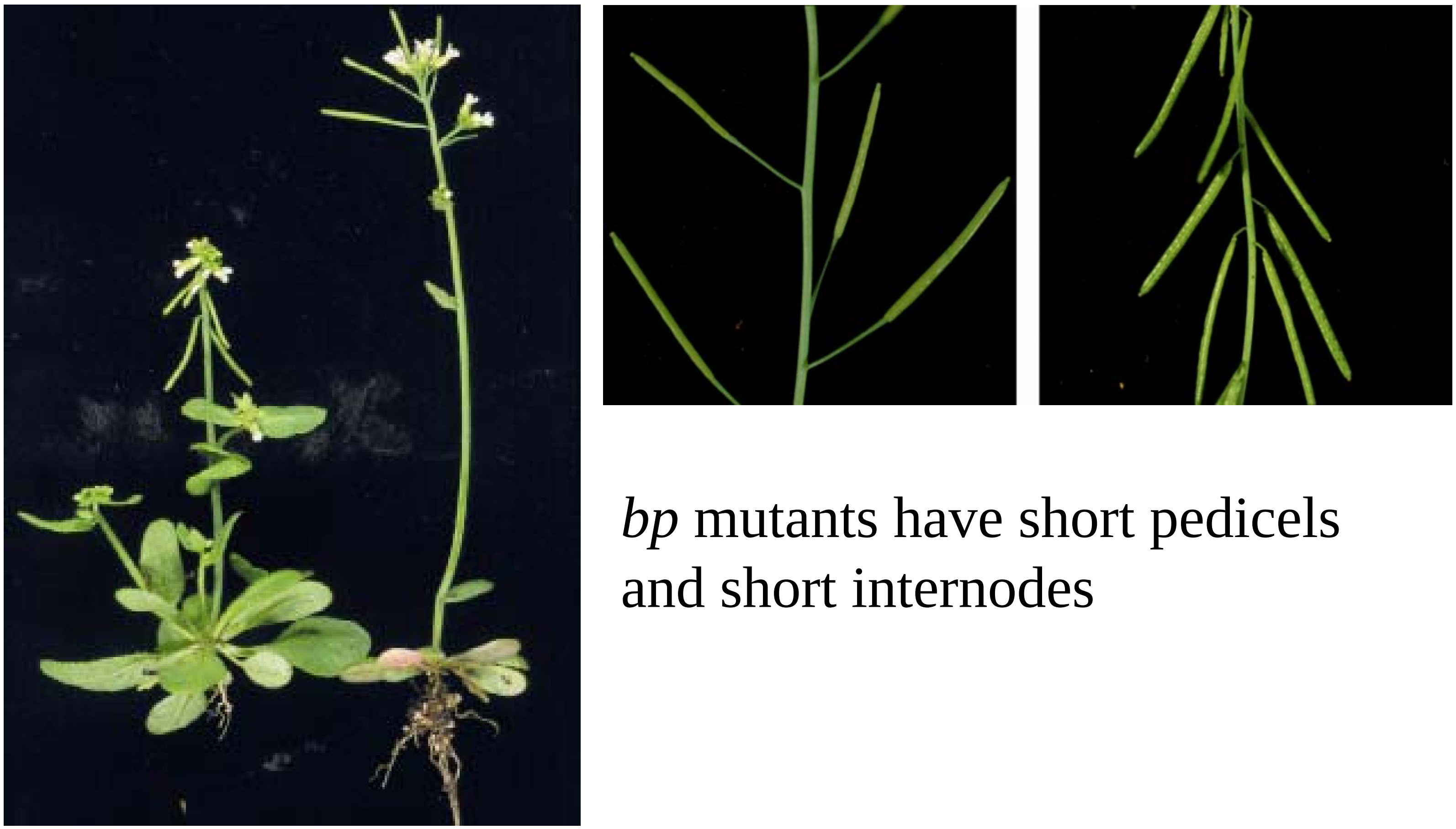
Cell Walls


Identify all cell wall synthesis genes in grasses (grains)
Determine genetic characteristics that maximize energy value (corn cell wall gene mutants (> 1000)
Use results to develop new energy crop varieties
Cell Walls (Lignocellulosic Feedstocks
Cellulose (glucose polymer)
Hemicellulose (pentose-hexose polymer)
Lignin (phenol polymer)
Glucose
Cellulose
Xylose
Lignins
Fuels
Fibers
Polymers, Resins, Solvents
Emulsifiers, Binders, Adhesives

Using plant genetics/genomics to find genes that affect cell wall composition

Sarah Hake
USDA-ARS Plant Gene Expression Center
Albany, CA

KNOX mutant, (bp1) affects cell wall synthesis by negatively regulating the lignin pathway

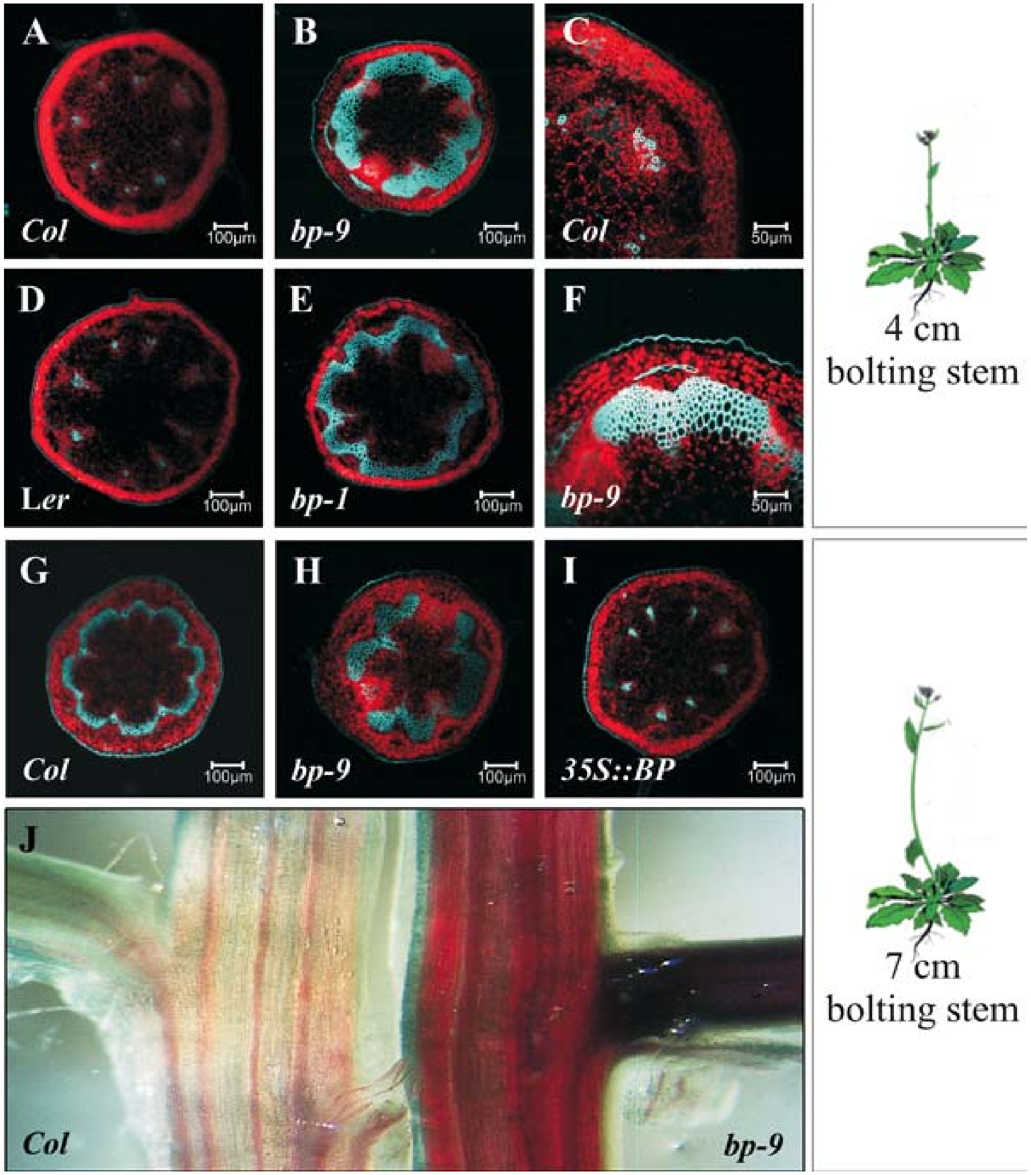


bp mutants have short pedicels and short internodes

Source: Sarah Hake

Can we manipulate transcription factors like KNOX1 in biomass plants to have less lignin and thus more available cellulose?

Source: Sarah Hake



Recessive *knox* mutants have increased lignin.

Plants overexpressing *knox* have decreased lignin

Source: Sarah Hake

Brachypodium distachyon, a model temperate grass

- Small size, small genome, short generation time, self fertile etc.)
- A model grass to understand where dicot and monocot biology diverge (e.g. cell wall composition)

Source: Olin Anderson, USDA-ARS, Albany, CA

Plant Oils - Oilseeds

Oilseeds & New Crops contribute to production of biodiesel and non-petroleum based lubricants

Research Priorities

Genomic and biotech approaches to achieve:

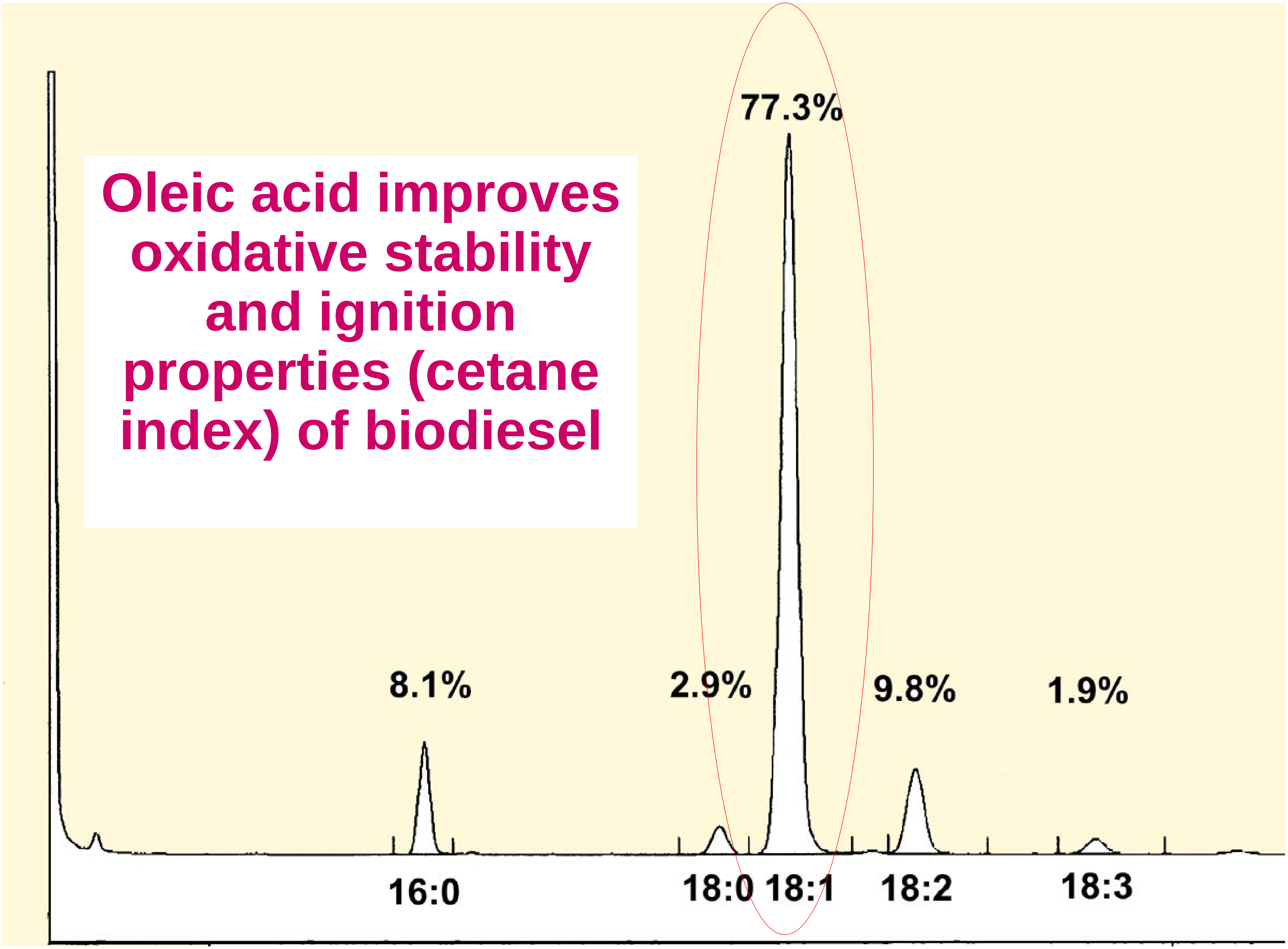
- **Increased oil concentration**
- **Higher oleic acid & lower saturated fatty acid concentration**
- **Hydroxy-fatty acids for oleochemicals and superior lubricants**

Variation in Oil Concentration

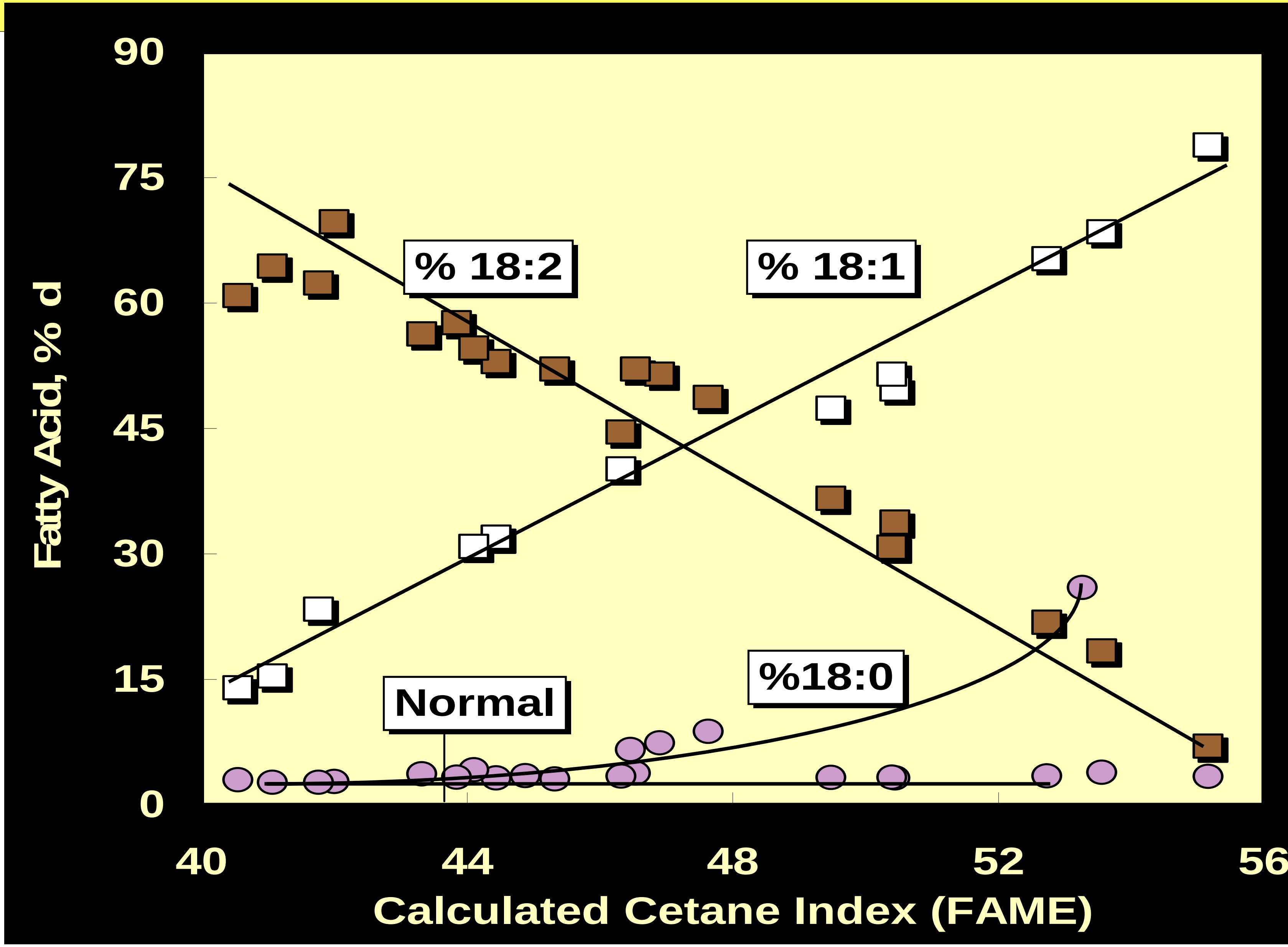
• Soybean	7.0 to 26%
• Sunflower	9.0 to 53%
• Canola	12 to 42%
• Cotton	20 to 30%
• Lesquerella	4 to 29%
• Peanut	30 to 65%

An increase from 20 to 30% oil in soybean seed equals a 50% gain in oil content per bushel

Oleic acid improves oxidative stability and ignition properties (cetane index) of biodiesel



Cetane Index of Genetically Modified Soybean Oils



Genetic Enhancement of Oleic Acid Concentration in Soybean

Mutation	18:1	18:2	18:3
	% crude oil		
Normal	23	53	9
FAD2-1α	36	53	3
FAD2-1β	62	24	2
FAD2-1α & 1β	70	15	3
Anti-sense FAD2-1	79	3	6

New Sources of Oleic Acid

Crop	18:1	18:2	18:3
	% crude oil		
Soybean	60	26	2
	22	55	8
Canola	74	15	3
	62	19	9
Sunflower	65	26	<1
	14	75	<1
Peanut	80	5	<1
	37	41	<1

Lesquerella

Breeding Improvement Potential

- Seed oil has potential to increase above 40%
- 85% Hydroxy fatty acid concentration is possible
- Seed yields could increase to 3000 lbs per acre

Products from Lesquerella

Waxy grains – More efficiently converted to alcohol

Waxy (low amylose) endosperm wheats

Waxy stains pink with iodine

Wild-type stains blue with iodine

Northerly adapted waxy (low amylose) sorghum

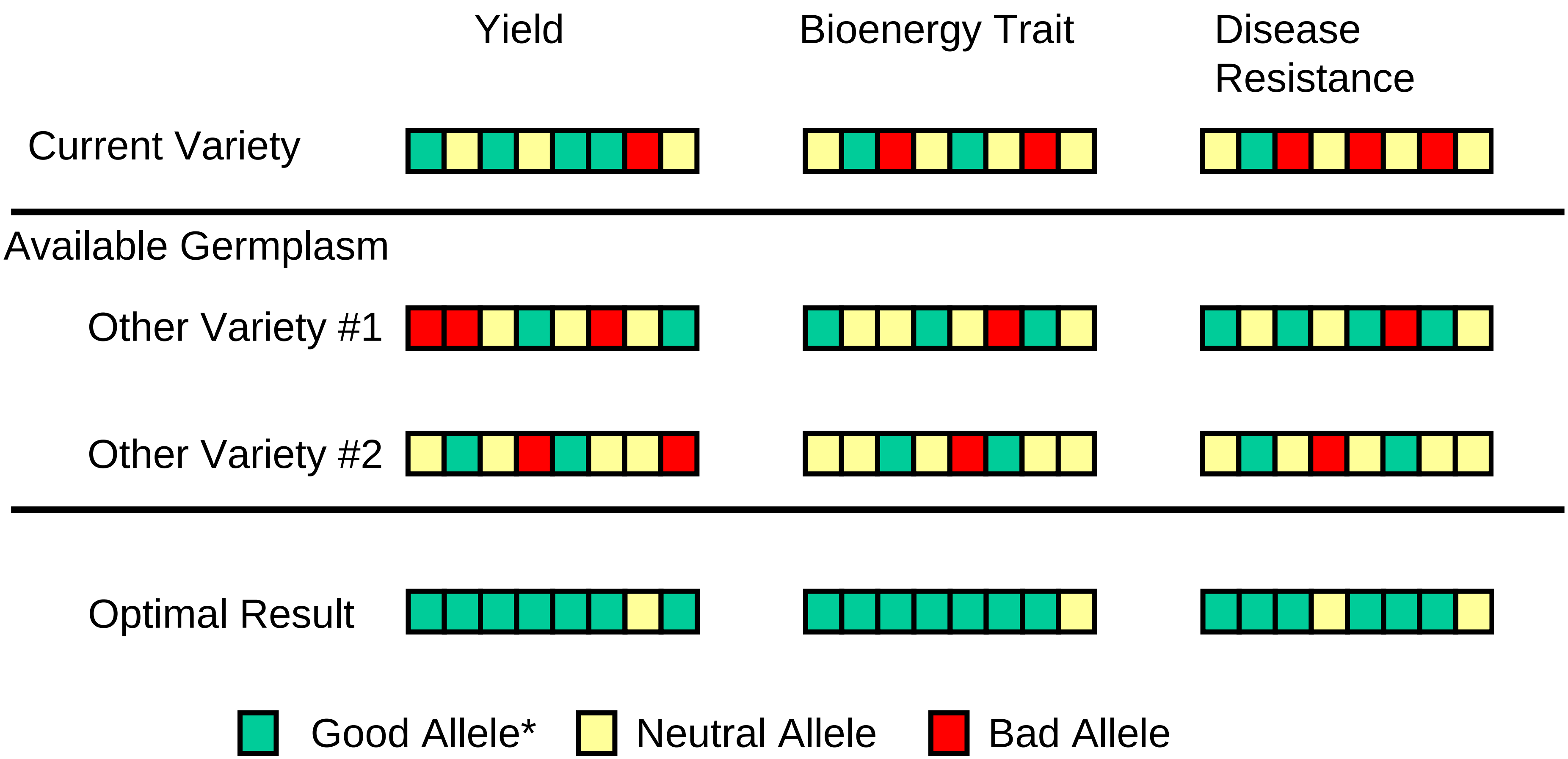
Jeff Pedersen, Bob Graybosch, and Ken Vogel, Lincoln

Applying statistical, genetic, and genomic approaches for dissecting complex traits in maize and perennial grasses

Ed Buckler, Ithaca, NY

Genomics-Enabled Genetic Improvement

- More efficient breeding made possible by comprehensive trait and DNA profiling of the national germplasm collections



*alternate forms of a gene affecting a trait

Genomics-Enabled Genetic Improvement