Breeding Progress for Increasing Soybean Yield: Past, Present, and Future

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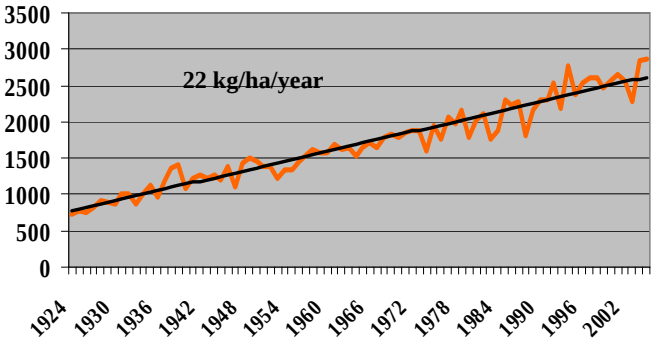
Eras of U.S. Soybean Breeding

- Soybean introduction (to 1943)
  - Varieties introduced from Asia
  - Within and among variety selection
- Scientific plant breeding (1944-1965)
  - 15 soybean breeders in North America
  - Fewer than 2 varieties/year
  - Hand planting and harvesting

Eras of U.S. Soybean Breeding

- Expansion and mechanization (1966 to 1995)
  - Tractor planting and combines
  - Computers for data management
  - More private and public breeders
  - Transition to proprietary varieties
- Transgenics (1996 to present)
  - Equipment advances
  - Off season nurseries
  - Marker assisted selection
  - Increase in genetic research

Changes in US yield (kg/ha)



What determines average yield?

- Environment
  - Rainfall
  - Soil type
- Diseases and pests
- Genetic base of the crop
- Genetic potential of each variety

Where are we?

✓We are still making progress

✓Gains per unit input are decreasing

✓There is potential for increase

How do we increase yield?

- Improve physiological efficiencies
- Provide protection from diseases and pests
- Tolerance to abiotic stresses

What can plant breeders do?

- Change breeding efficiency
- Expand the genetic base
- Incorporate transgenes

Increasing breeding efficiency

Variety development time

Improved selection techniques

- Marker assisted selection
  - Disease and insect resistance
  - Yield
    - Parent selection
    - Within population selection
- Improved field testing

Expanding the Genetic Base

- Current U.S. genetic base
  - 35 ancestors account for 96% of genes
  - 6 ancestors provide 60% of the genes
  - 7 crosses contributed 70% of the genes
  - Pool ~85% complete by 1954
  - Pool ~95% complete by 1970

Japanese Soybean Gene Pool

53 ancestors account for 80% of genes

18 ancestors account for 50% of genes

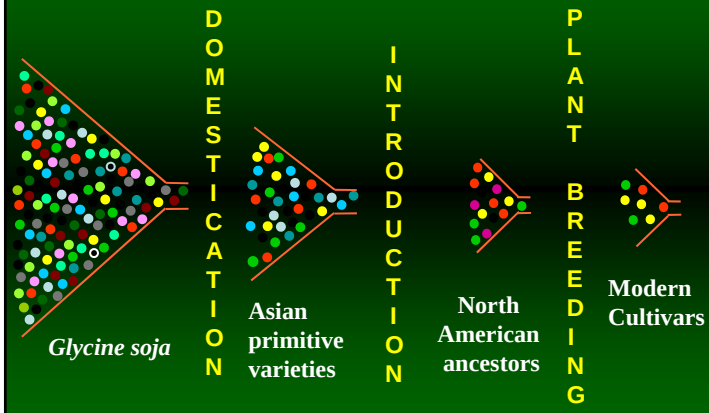
91% of ancestral lines from Japan

Regionally distinct gene pools

Low coefficient of parentage among cultivars

Zhou et al. 2000. Crop Sci. 40:1794–1802

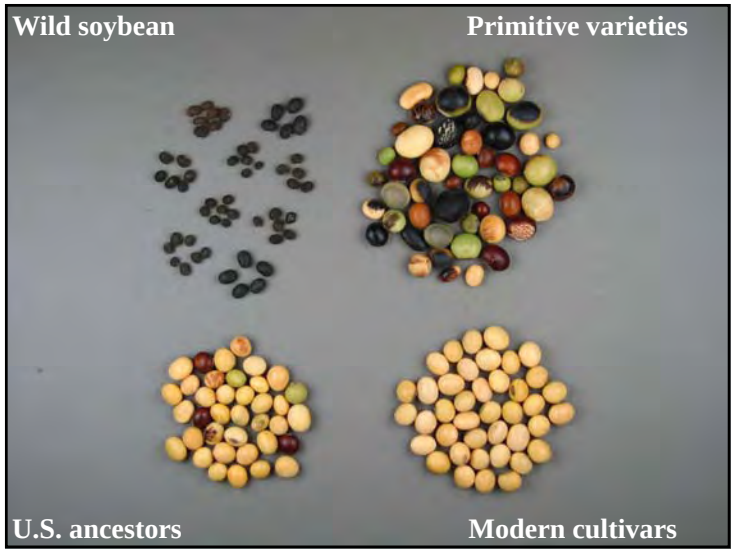
Conventional View of Genetic Diversity



Sequence Analysis of Cultivated and Wild Soybean

- 26 *G. soja* accessions from China, Korea, Japan and Russia.
- 52 Asian *G. max* primitive varieties from China, Korea and Japan
- 17 major ancestors of N. American cultivars
- 25 modern U.S. cultivars

Hyten et al. 2006. PNAS 103: 16666



Sequence Analysis of 120 Cultivated and Wild Soybean Genotypes

111 Sequence Tagged Sites derived from 102 complete GenBank genes and cDNAs

21.9 kbp coding
17.9 kbp intron
11.2 kbp '3 & 5' UTR
2.2 intergenic sequence

Total = 53.1 kbp

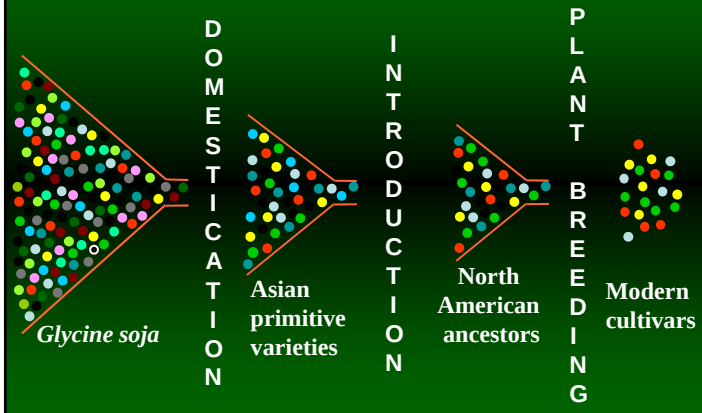
Nucleotide Diversity Terminology

Watterson's θ = Mean SNPs per site adjusted for population size (θ_w = 0.001 = 1 SNP/kbp)

Nucleotide Diversity, θ_w (x 10^3) in Coding and Non-coding Regions in Four Soybean Populations

Population	Total coding	Total non-coding	Total
Wild soybean	1.63 a	3.06 a	2.35 a
Asian primitive varieties	0.81 b	1.36 b	1.15 b
N. American ancestors	0.73 b	1.16 bc	1.00 bc
Modern cultivars	0.59 b	0.92 c	0.83 c

Revised View of Genetic Diversity



Allele frequency changes in 102 genes

Domestication bottleneck

G. soja/Prim. varieties: 61 genes

Introduction bottleneck

Prim. varieties/N. Am. Ancestors: 28 genes

Improvement bottleneck

N. Am. ancestors/Elite cultivars: 7 genes

Expanding the Genetic Base

- Current genetic base
- Understanding genomic control
- Sequencing of the soybean genome
- Many germplasm lines not used

PI 90566-1 x Williams 82 (4)

Entry	Kg/ha	Mat	Ldg	Hgt
Williams 82	3272	9-27	1.7	109
LG05c-1341	3910	9-27	1.9	109
IA3023	4078	9-20	1.4	91

PI 90566-1 came from Jilin, China in 1930

LG05c-1341 has 93% of Williams 82 genes
And 7% of the genes from PI 90566-1

Uniform IV Test 2007-08
22 locations

Entry	Pedigree	Kg/ha	Mat
LG04-6000	HS93-4118 x LG97-9912	3964	3.9
LD00-3309	Check	3669	0.0

Jilin 15 is derived from 3 primitive Chinese varieties and was released in 1978.

Jilin 15 is 13% of the parentage of LG04-6000.

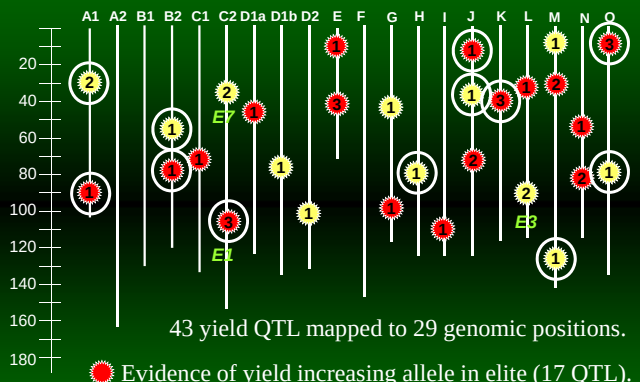
2008 Uniform IV Test at 11 locations

Entry	% exotic	Pedigree	Kg/ha	Mat
LG04-5190	(50)	LG97-9384 x LG97-9301	3944	2.5
LG04-5372	(37)	Rend x LG97-9301	3937	-2.2
LG04-4866	(25)	LG97-9015 x HS93-4118	3863	3.9
LD00-3309		Check	3837	0.0

Origin of "Exotic" parents

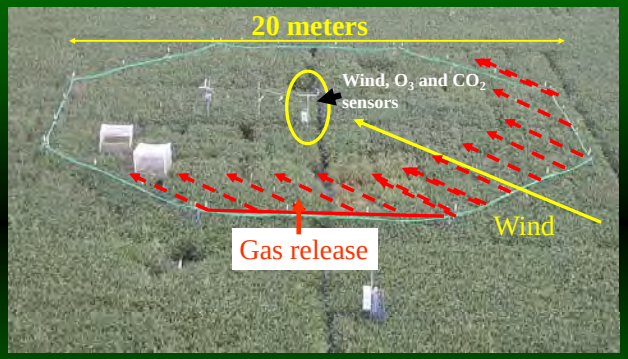
PI number	Cultivar	Origin	Year
PI 90566-1		China	1930
PI 253665D		China	1958
PI 283331		Morocco	1962
PI 391594	Jilin No. 8	China	1974
PI 436682	Jilin No. 15	China	1979
PI 437851A		China	1980

Yield QTL in Exotic by Elite Populations



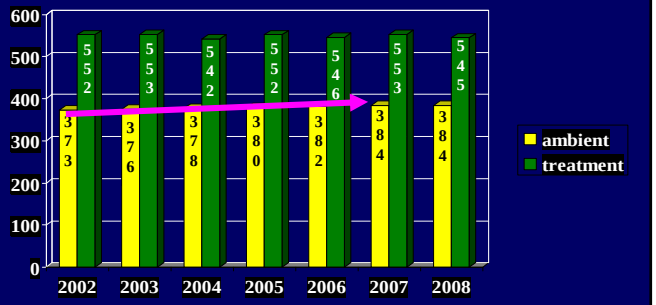
43 yield QTL mapped to 29 genomic positions.

- Evidence of yield increasing allele in elite (17 QTL).
- No evidence of yield increasing allele in elite (12 QTL)
- Currently confirming with near isogenic lines (13 QTL)



Soybean Free Air Concentration Enrichment

CO_2 Concentration (ppm)



Differential CO_2 Responders

5 year average increase from elevated CO_2

Entry	Kg/ha Ambient	Kg/ha Elevated	%Δ
Loda	3621	4488	24%
HS93-4118	3541	3661	4%

Differential O_3 Responders

5 year average decrease from elevated O_3

Entry	Kg/ha Ambient	Kg/ha Elevated	%Δ
Dwight	3742	3225	-14%
LN97-15076	3191	2997	-6%

Transgenics

- Mostly proprietary research
- Broad spectrum disease resistance?
- Yield is genetically complex
- Second generation genes?

How to Increase Soybean Yield

- Shorter variety development time
- Selection for disease/pest resistance
- Understanding the genetics of yield
- Selection for parents and lines
- Use of exotic germplasm for yield
- Use of transgenes

Questions?