

UTILIZING EXOTIC GERMPLASM TO INCREASE SOYBEAN YIELD

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Since 1924, the average U.S. soybean yield has increased from 740 kg/ha on 0.65 million hectares to the highest of 2956 kg/ha on over 30.9 million hectares in 2009. Through all of the changes in breeding and production technology, the average rate of gain per year has been remarkably steady at about 23 kg per hectare per year. U.S. soybean production is based on a relatively small set of ancestral lines. Based on pedigree analysis, only 5 lines contribute more than half of the genes to current cultivars. There is no evidence that indicates that yield increases are not still possible within this limited gene pool but our research has demonstrated that introgressing new soybean genetic diversity can increase the yield of U.S. commercial cultivars. We have improved yield by using modern Asian cultivars as parents but also primitive accessions that predate scientific plant breeding. We have developed experimental lines derived from wild soybean that exceed the yield of the recurrent soybean parent and research with multiple wild soybean accessions indicates that these yield enhancing alleles may not be uncommon in wild soybean accessions. We have developed fertile progeny by backcrossing an accession of the perennial *Glycine tomentella* to soybean and identified lines that significantly exceed the yield of the recurrent parent. Traditionally exotic germplasm has been used primarily as a source of disease or insect resistance that is primarily controlled by a single or few genes. Our research demonstrates that a variety of types of exotic germplasm can also improve complex, quantitatively inherited traits such as yield even though the donor parents are much lower yielding than the elite cultivars being improved.

Utilizing Exotic Germplasm to Increase Soybean Yield

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Why expand the genetic base of soybean production?

- The annual *Glycine* lack diversity

Reported Estimates of Nucleotide Diversity

Species	Θ_w ($\times 10^{-3}$)
<i>Glycine max</i>	0.8 to 1.2
<i>Glycine soja</i>	2.4
<i>Zea mays</i> ssp. <i>Parviglumis</i>	13.4
Modern U.S. <i>Z. mays</i> inbred lines	6.2
<i>Hordeum vulgare</i> ssp. <i>Spontaneum</i>	9.8
<i>Sorghum bicolor</i>	2.3

Why expand the genetic base of soybean production?

- The annual *Glycine* lack diversity
- Most available diversity is unused
- Exotic germplasm increases yield

Germplasm used in breeding

- **China** **1%**
- **U.S.** **0.5%**
- **Japan** **1%**

Why expand the genetic base of soybean production?

- The annual *Glycine* lack diversity
- Most available diversity is unused
- Exotic germplasm increases yield

Types of exotic germplasm

- Plant breeding cultivars

Z. Li et al. 2001. Molecular Genetic Analysis of the U.S. and Chinese Soybean Ancestral Lines. Crop Sci. 41: 1330-1336.

- Wild soybean

Wild soybean Θ_w *Glycine* 2.35

Primitive varieties 1.15

Hyten et al. 2006. PNAS. 103:16666

Examples from $G. \max$

USDA Uniform IV Test – 2010

15 locations

Entry	Pedigree	% exotic	Kg/ha	Mat
<u>LD00-3309</u>			3601	9/22
LG06-5798	LG00-3372 x <u>LD00-3309</u>	50	3843	+5.2

LSD (0.05)

181

PI 561319A (1991) Hui nan zi hua he jia
Fen dou 31 was released in 1990

USDA Preliminary Uniform IV Test – 2012

7 locations

Entry	Pedigree	% exotic	Kg/ha	Mat
IA4004	Check		3467	9/25
LG09-2695	F6 IA3023 x LG03-3020	31	3722	+1

LSD (0.11)

249

PI 91730-1		Jilin, China	1931
PI 227333	Ohozyu	Hokkaido, Japan	1955
PI 427099	Jilin No. 3	Jilin, China	1963
PI 438151		NE China	1980

2012 Group III USB Coop Test

17 Locations

Entry	Pedigree	Kg/ha	Mat
LG11-6210	F6 LG03-3020 x LG03-3780	3514	3
IA3048	Check	3262	0
LSD (0.065)		242	

PI 91730-1	Jilin	1931
PI 227333	Hokkaido	1955
PI 427099	Jilin	1978
PI 438151	NE China	1980
FC 04007B	Unknown	1924
PI 68508	NE China	1926

Mapping Yield QTL

Lawrence x LG96-6607

(F3 Lawrence (4) x PI 68658)

PI 68658 from ChiSRs (602 tested)

194 PI 68658 QTL in 7 environments
USB Soybean Asian Germplasm Evaluation 1998-99

Four from PI 68658 8 Kg/ha

PI 68658 Sept 15 2372 Kg/ha

One from Lawrence

Confirming Yield QTL

LD00-3309 (2) x LG01-16487

Chr 5/Chr 14	Hgt	Mat	Ldg	Kg/ha	Δ
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BD

83

9-26

1.5

3494

BC

86

9-26

1.4

3615

121

AD

86

9-26

1.5

3655

161

AC

86

9-26

1.5

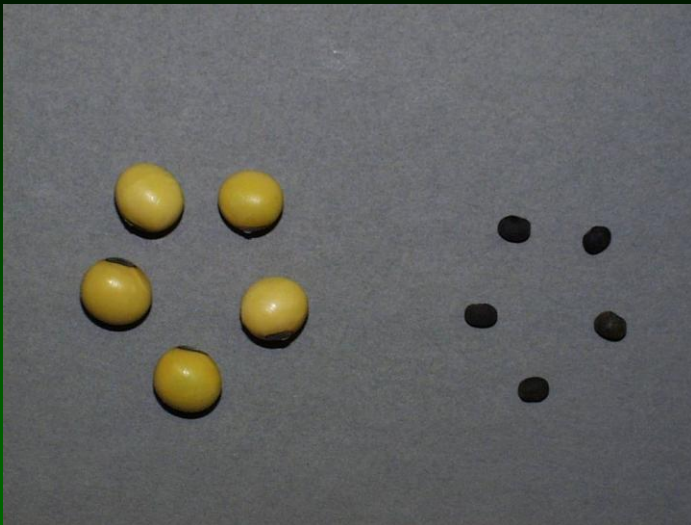
3735

241

A,B alleles: PI 68658; C,D alleles: LD00-3309

Glycine soja

Highly diverse
Difficult parent

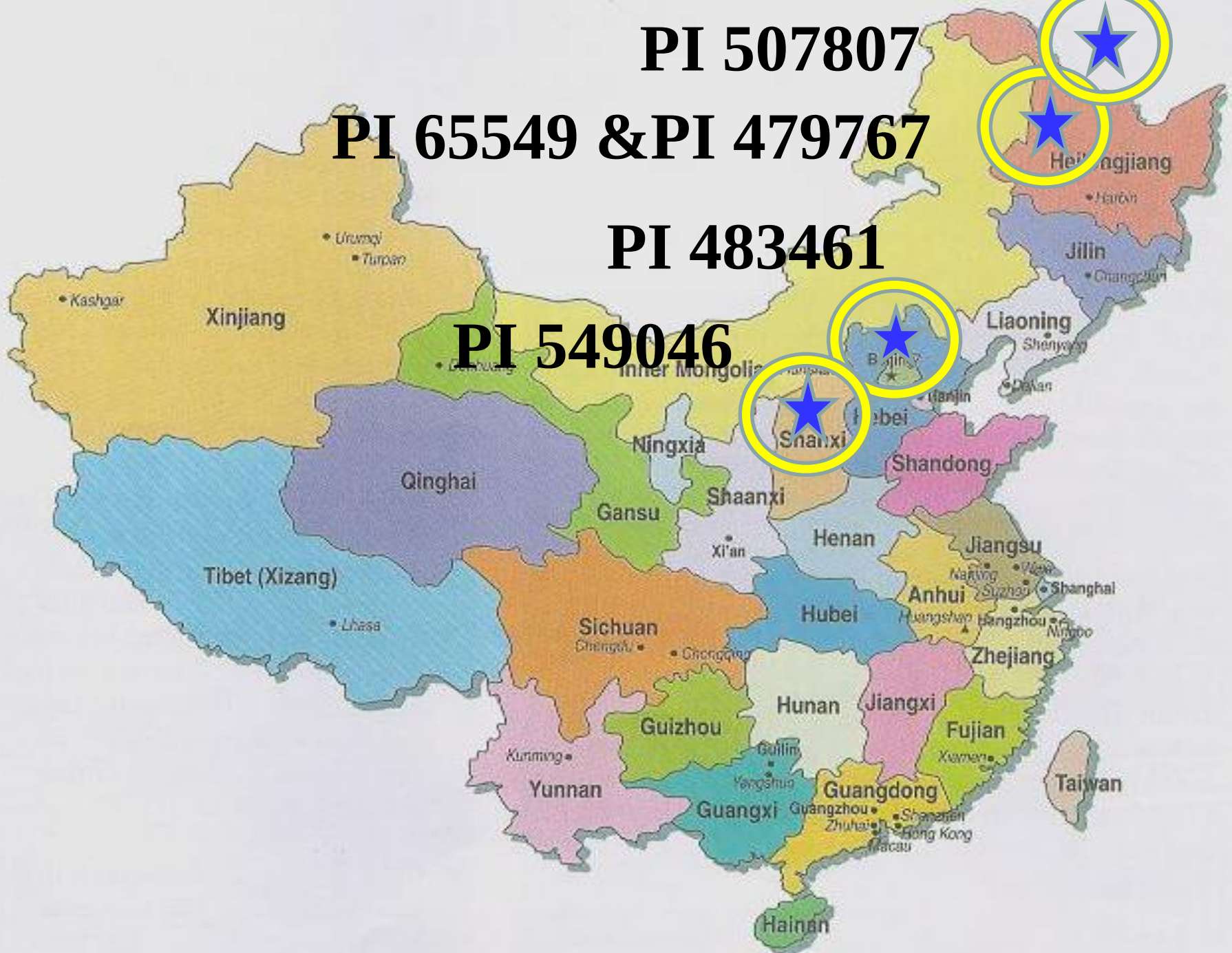


PI 507807

PI 65549 & PI 479767

PI 483461

PI 549046



G. soja-derived lines

9 locations in 2011 and 2012

Entry		Mat	Kg/ha	Donor
Williams 82		0	3413	
LG08-4152	BC2	4	3561	PI 479767
LG08-4195	BC2	-3	3426	PI 483461
LG07-4278	BC1	-7	3393	PI 549046
				PI 479767
LG07-4231	BC2	-3	3494	PI 549046
LG07-4722	BC1	-4	3306	PI 507807
LG07-2165	BC2	-5	3232	PI 65549

G. soja-derived lines

9 locations in 2011 and 2012

Entry		Mat	Kg/ha	Donor	% soja
Williams 82		0	3413		
LG08-4152	BC2	4	3561	PI 479767	
LG08-4195	BC2	-3	3426	PI 483461	
LG07-4278	BC1	-7	3393	PI 549046	
				PI 479767	
LG07-4231	BC2	-3	3494	PI 549046	
LG07-4722	BC1	-4	3306	PI 507807	24
LG07-2165	BC2	-5	3232	PI 65549	30

G. soja-derived lines

9 locations in 2011 and 2012

Entry		Mat	Kg/ha	Donor	% soja
Williams 82		0	3413		
LG08-4152	BC2	4	3561	PI 479767	
LG08-4195	BC2	-3	3426	PI 483461	7
LG07-4278	BC1	-7	3393	PI 549046	7
				PI 479767	4
LG07-4231	BC2	-3	3494	PI 549046	
LG07-4722	BC1	-4	3306	PI 507807	24
LG07-2165	BC2	-5	3232	PI 65549	30

G. soja-derived lines

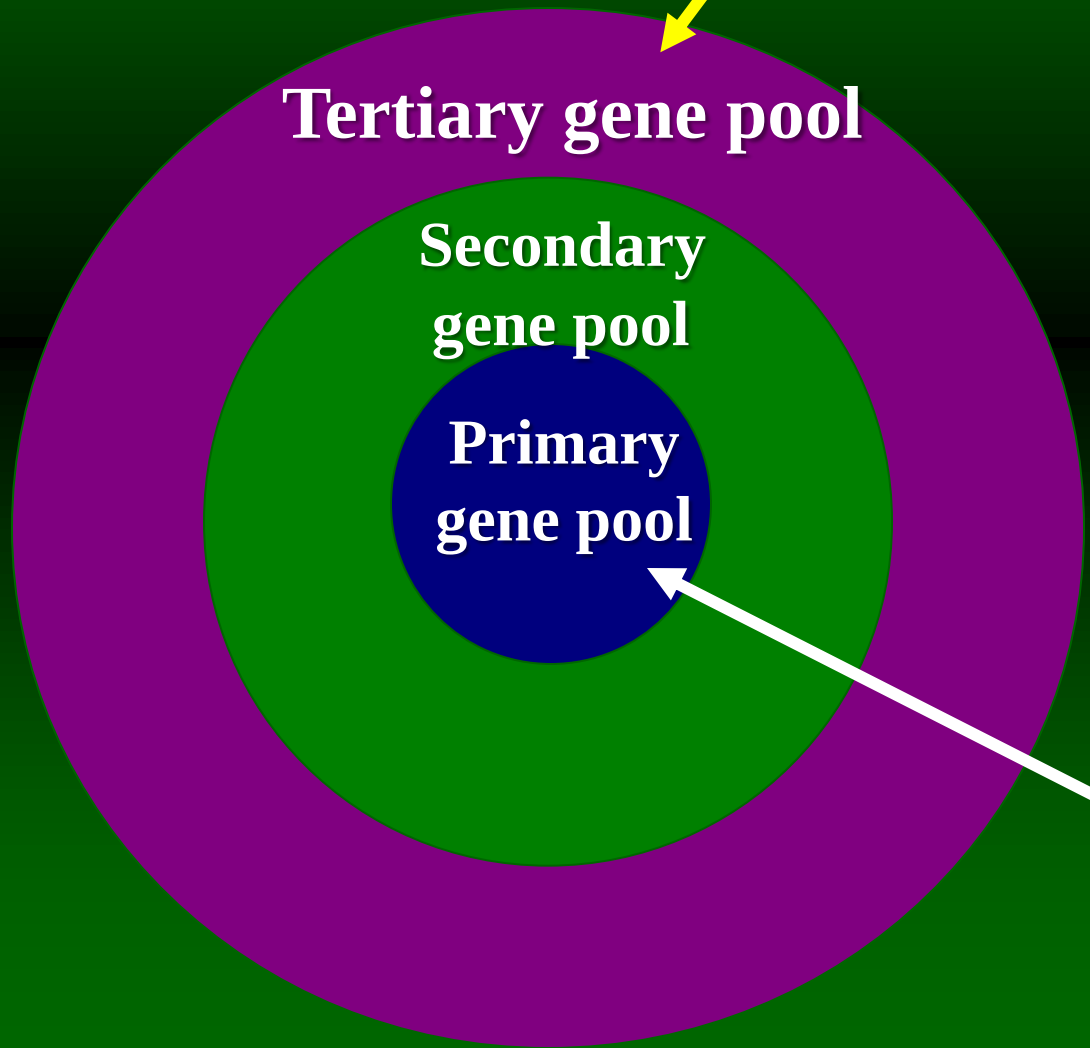
9 locations in 2011 and 2012

Entry		Mat	Kg/ha	Donor	% soja
Williams 82		0	3413		
LG08-4152	BC2	4	3561	PI 479767	9
LG08-4195	BC2	-3	3426	PI 483461	7
LG07-4278	BC1	-7	3393	PI 549046	7
				PI 479767	4
LG07-4231	BC2	-3	3494	PI 549046	6
LG07-4722	BC1	-4	3306	PI 507807	24
LG07-2165	BC2	-5	3232	PI 65549	30

Average % introgression by *G. soja* donor

Donor	# lines	BC	% soja SNPs	
PI 65549	12	2	7 to 32	19
PI 479767	39	2	4 to 29	13
PI 483461	17	2	3 to 19	11
PI 549046	16	2	1 to 27	14
PI 507807	5	1	8 to 24	13

subgenus *Glycine*:
includes the 26 perennial
species



Tertiary gene pool

Secondary
gene pool

Primary
gene pool

subgenus *Soja*:
soybean (*G. max*)
and wild soybean
(*G. soja*) both with
 $2n=40$



INDIA

HONG KONG

THAILAND

VIETNAM

MALAYSIA

SINGAPORE

INDONESIA

CHINA

KOREA

JAPAN

TAIWAN

PHILIPPINES

AUSTRALIA

NEW ZEALAND

*Glycine
pescadrensis*

PI 440996



Glycine curvata

PI 505166



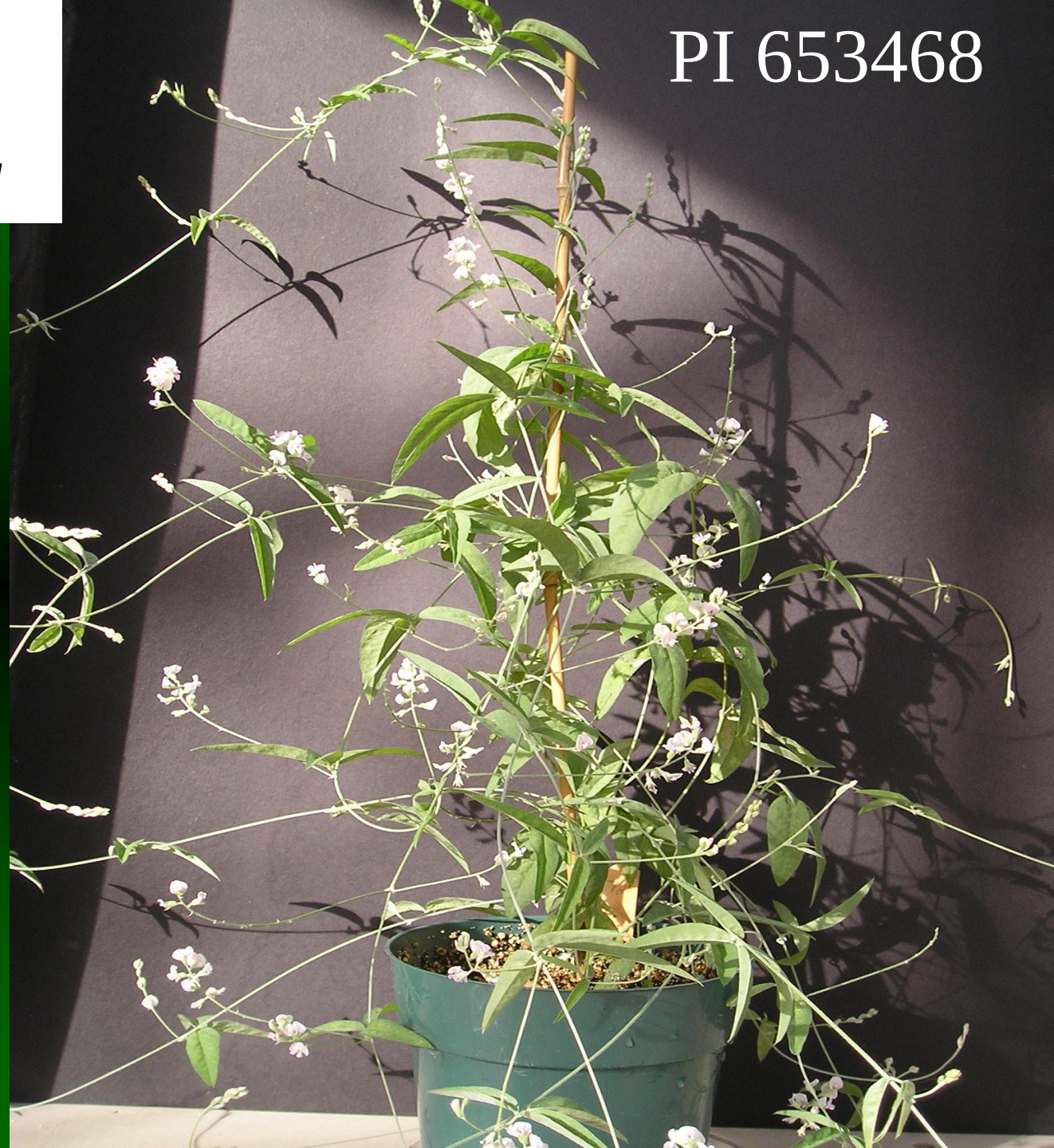
Glycine canescens



PI 509457

Glycine *canescens*

PI 653468



Glycine falcata

PI 653462



G. falcata



$2n=78$

G. tomentella

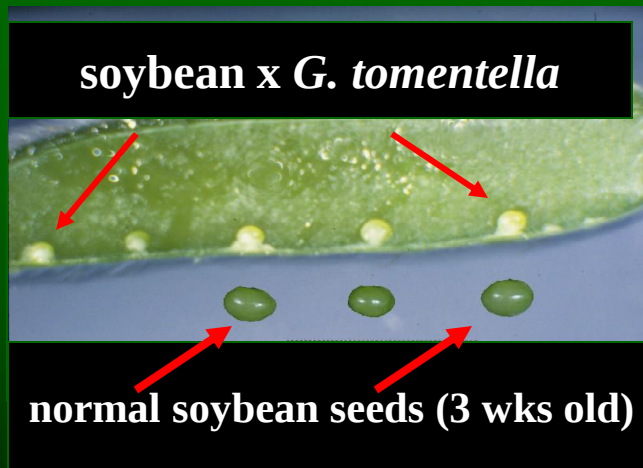
PI 441001





Wide hybridization

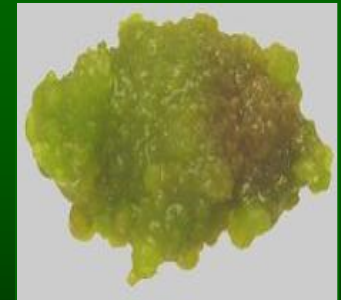
G. max cv. Dwight x **G. tomentella (PI 441001)**
2n=40 **2n=78**



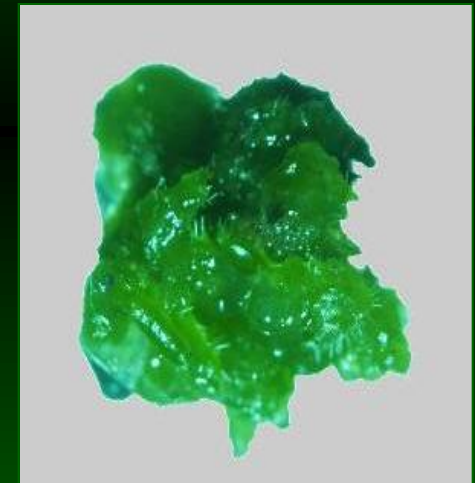
Seed



Embryo



Callus



Small Embryos



Embryonic Shoots



**Growth
Container**

Wide hybridization

G. max cv. Dwight x **G. tomentella (PI 441001)**
 $2n=40$ $2n=78$

↓

F₁
 $2n=59$



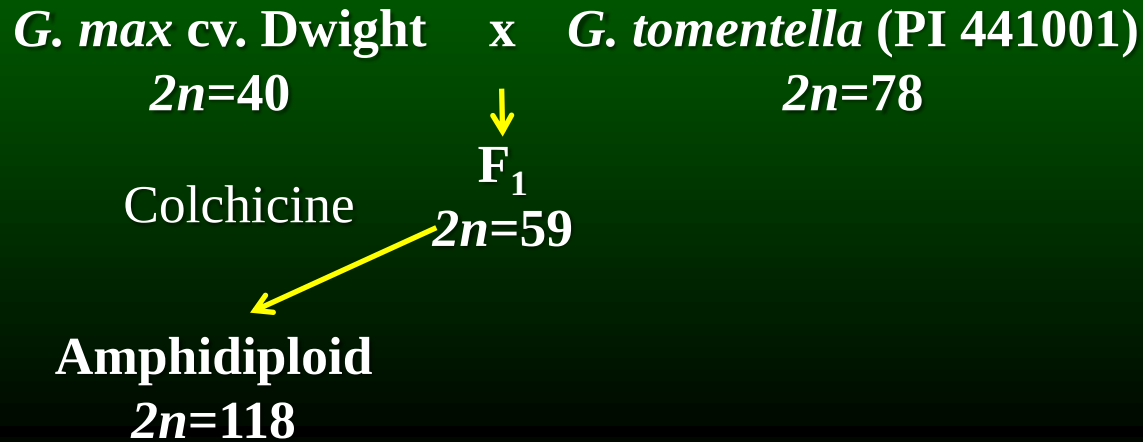
Sterile hybrid plant

59 chromosomes:

20 from soybean

39 from *G. tomentella*

Wide hybridization

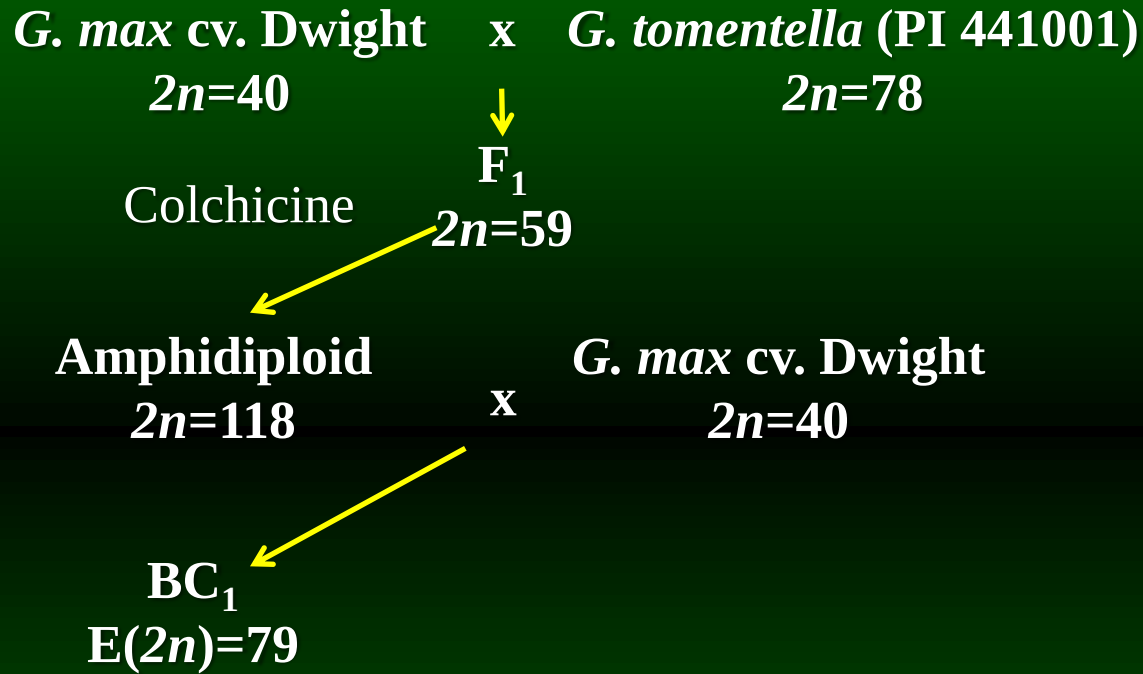




Amphidiploid plant
 $2n=118$

40 from soybean
78 from *G. tomentella*

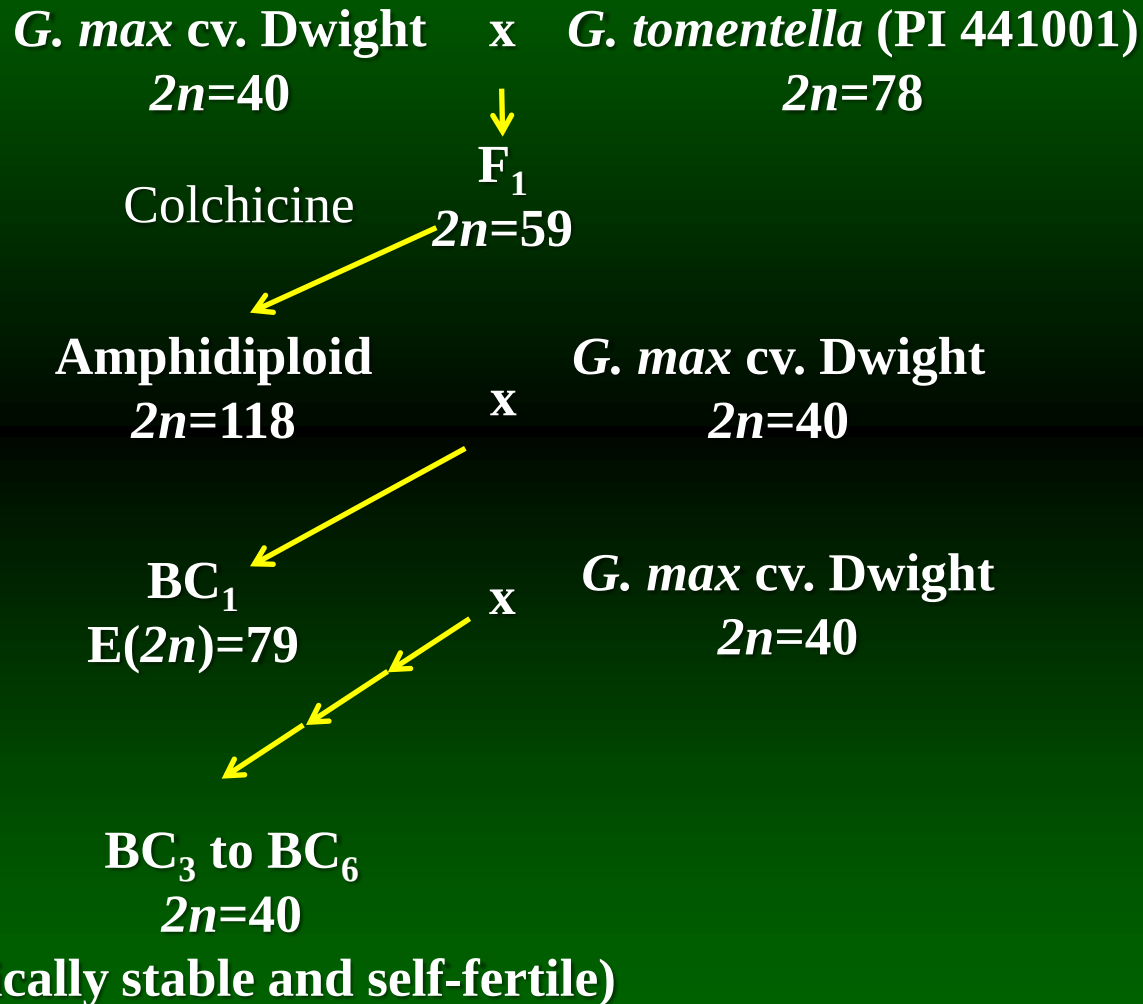
Wide hybridization



**Crossed back to
Dwight (BC1)
79 chromosomes**



Wide hybridization



2012 Illinois Tests

2 locations

Entry	Pedigree	Kg/ha	Mat
LG09-11465	F3 Dwight (6) x PI 441001	3884	4
Dwight	Check	3259	0
LD02-4485	Check	3407	-2
LSD (0.3)		390	

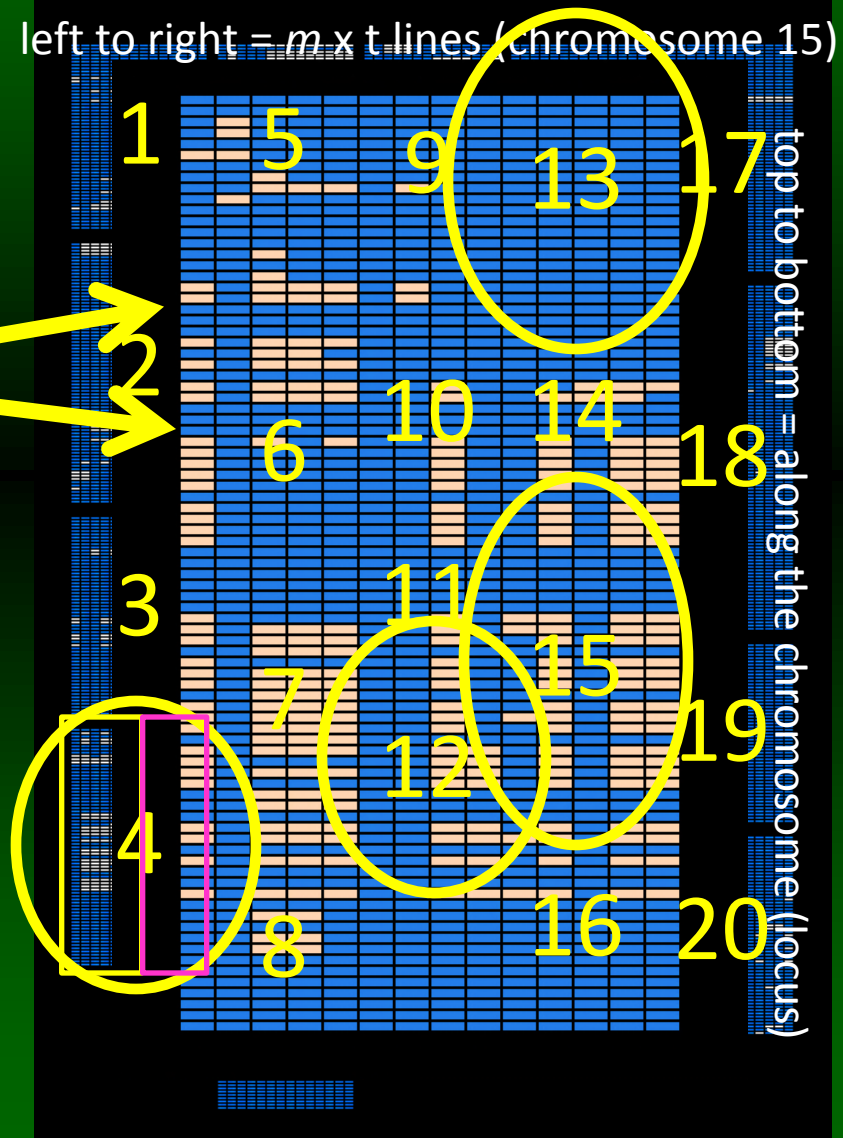
2011- 2012 Illinois Tests

3 locations

Entry	Pedigree	Kg/ha	Mat
LG10-13076	F3 Dwight (6) x PI 441001	3501	1
LD02-4485	Check	3467	-4
Dwight	Check	3151	0

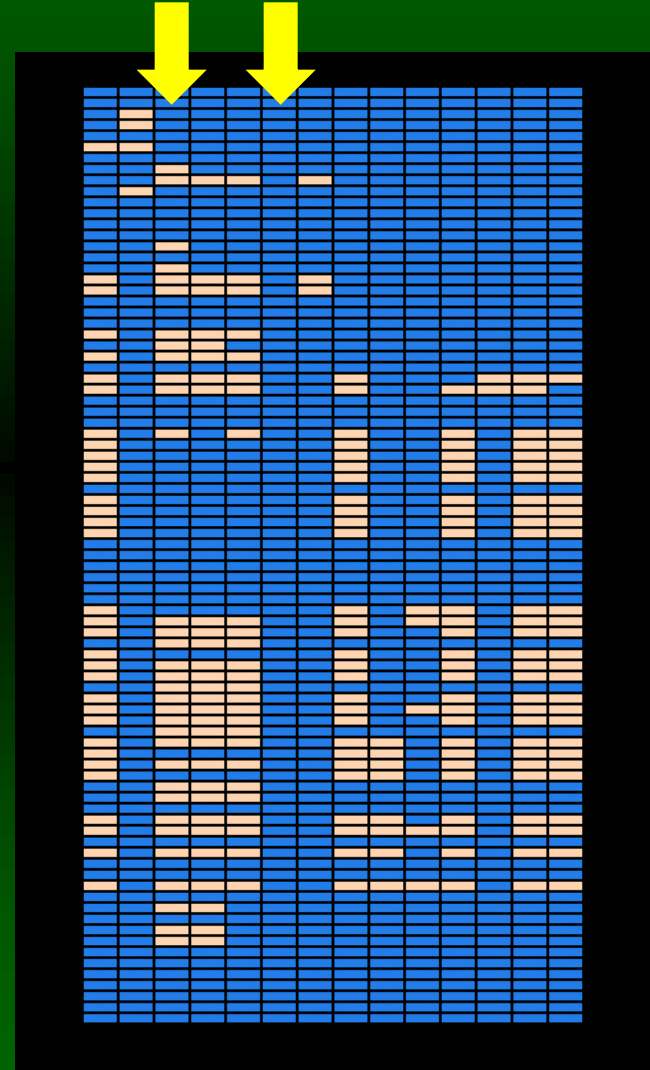
Where is the *G. tomentella* DNA?

- 1536 single nucleotide polymorphisms (SNPs)
- Derived lines (left to right)
- Orange: Different from Dwight
- 20 soybean chromosomes (blocks)
- Genomewide differences
 - Indicates recombination
 - Variation among chromosomes
 - Variation among lines



Where is recombination occurring?

- 1536 single nucleotide polymorphisms (SNPs)
- Derived lines (left to right)
- Orange: Polymorphic with Dwight
- 20 soybean chromosomes (blocks)
- Genomewide polymorphisms
 - Indicates recombination
 - Variation among chromosomes
 - Variation among lines



Summary

- We are still making progress
- Rate of yield gain less than input change
- Exotic germplasm increases yield
- Gene pool expansion is an opportunity

Thanks!

Brian Diers
Ram Singh

Yield QTL mapping
Wide hybridization

Graduate Students

Carol Bonin
Abraham Akperley

QTL confirmation
Wild soybean BC evaluation

ARS support scientist

Ed Johnson

Yield testing

Thanks!



Questions?

