

# Chromosome substitution lines: An effective way to introgress useful genes from other allotetraploid species into Upland cotton *Gossypium hirsutum* L.

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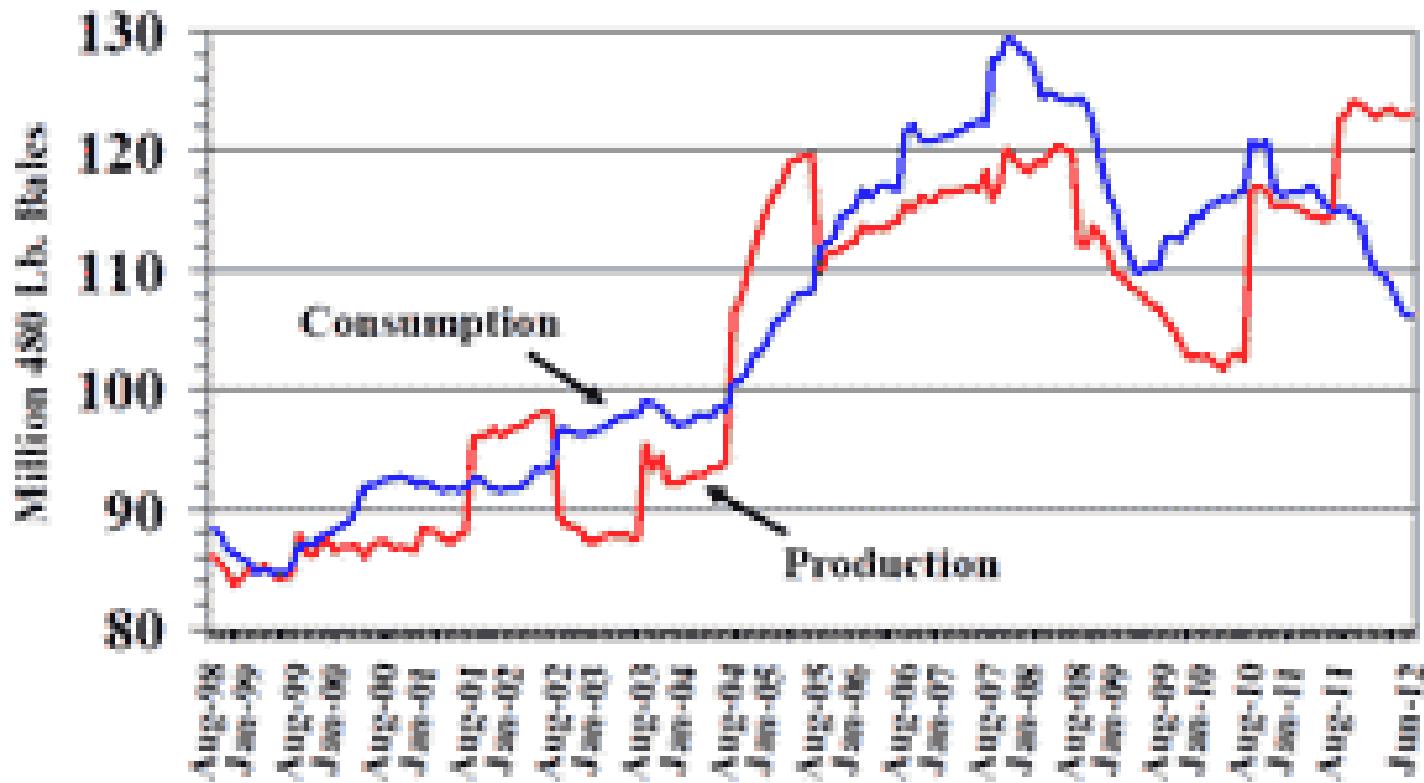
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## Cotton: World Production and Consumption, August 1998/99 – June 2011/2012



Sources: USDA/OCE, Monthly WASDE Report

**“Too Much Cotton, Too Little Demand”**  
**(Source: Cotton Incorporated )**

**Predicted world's mills will consume  
107.6 million bales in 2012/13.**

**This represents the lowest volume  
since the 2003/04 crop year.**

**Clothes containing 51% cotton or  
greater declined 11.8 percent in  
2011 compared to 2010 indicating  
a switch from cotton to synthetic fibers  
among apparel importers.**



# **Some Important Challenges:**

- **Narrow genetic base**
- **Susceptibility to pests and diseases**
- **Lower yields and fiber qualities**
- **Development of new germplasm is an important priority for the public sector**
- **Technological changes in textile industries demand high fiber quality**

# **Gossypium Spp.**

- *The genus Gossypium includes approximately 46 diploid and 5 tetraploid species.*
- *Two widely cultivated tetraploid species- G.hirsutum (95% of the cotton growing areas) and G. barbadense (2% of the cotton growing areas).*
- ***G. hirsutum: Good Agronomic Qualities.***
- ***G. barbadense: Good Fiber Qualities.***

## ***G. tomentosum***

Meredith et al. (1973) reported that nectariless cottons reduce tarnished plant bug numbers (50%), fleahoppers (50%), boll rot (20%) and bollworm damage (20%). They also observed that nectariless lines produced lint yield and fiber quality equal to their isogenic commercial parents. *G. tomentosum* also has strong fiber (Meyer and Meredith, 1978) and is the most heat-resistant species in *Gossypium* (Percival et al., 1999; Aktar et al., 1996).

## *G. mustelinum*

Its foliage has the highest concentrations of the heliocides H<sub>1</sub> and H<sub>4</sub> and moderately high levels of gossypol (Khan et al., 1999). Except for gossypol, foliar concentration of terpenoid aldehydes in the lysigenous glands was highest in *G. mustelinum* relative to 30 species representing A, B, C, D, F, G, K, and AD genomic groups of *Gossypium* (Khan et al., 1999). Many of these allochemicals are potentially useful for improving host-plant resistance in Upland cotton.

# **Problems in interspecific introgression**

- Cytological abnormalities
- Infertility
- Distorted segregation and transmission
- Linkage drag effect
- Loss of germplasm
- Cryptic structural differences in chromosome



- ❖ Fiber Quality
- ❖ Yield
- ❖ Biotic and abiotic stress resistance



# An Alternative Approach:

# Backcrossed Chromosome Substitution Lines



# Cytogenetic stocks

**TWO MAIN TYPES:**

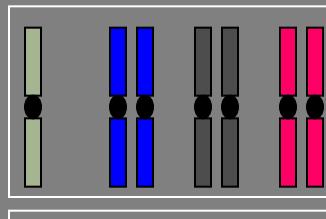
- Reciprocal translocations
  - Hypoaneuploids
-

# UTILIZATION of the most important *intraspecific* *G. hirsutum* cytogenetic stocks

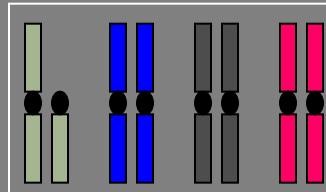
## Hypoaneuploids (chromatin-deficiencies) MAP &

## INTROGRESS:

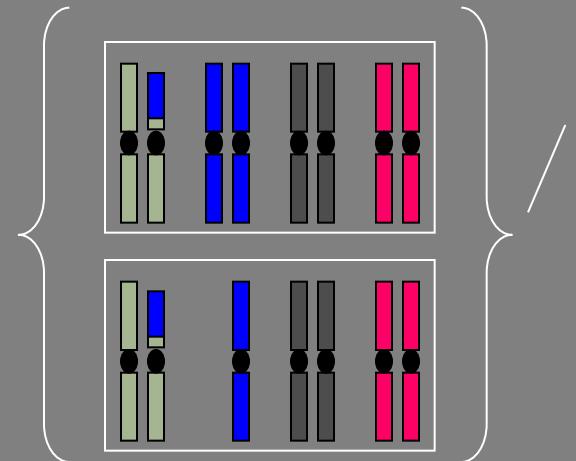
Monosomics



Monotelodisomics



Segmental  
aneuploids



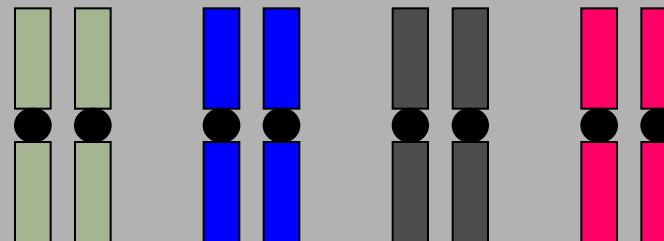
- Whole chromosomes

- Arms, centromeres

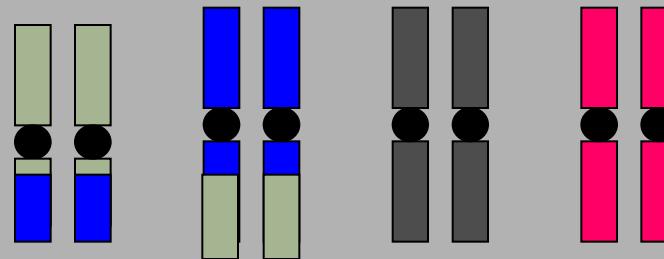
- Chromosome  
segments

# TRANSLOCATIONS

Normal:



Reciprocal  
Translocation



MAJOR USES --

- ID chromosomes
- ID chromosome arms
- CREATE aneuploids

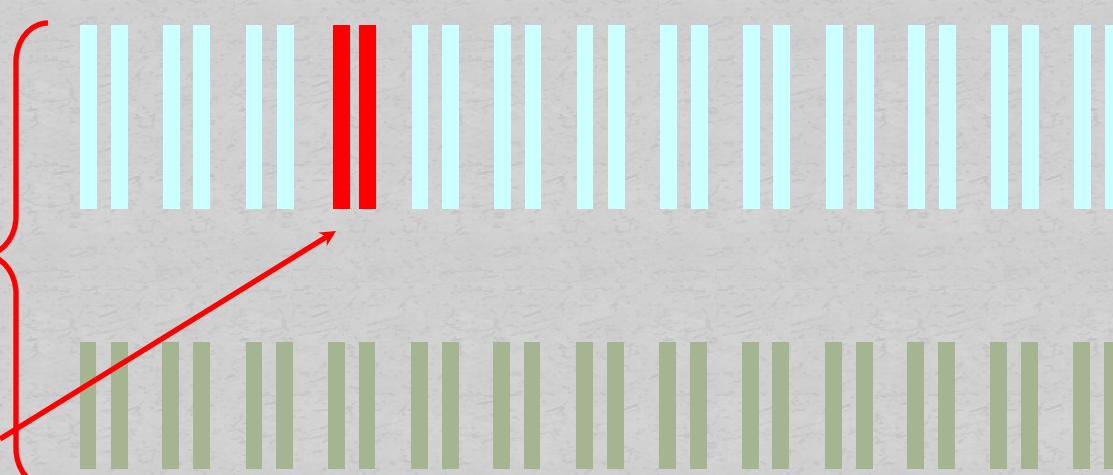
# What is a Chromosome Substitution (CS) Line?

The 52 Chromosomes of cotton  
(2 sets of 13 pairs)

G. hirsutum DNA

1 2 3 4 5 6 7 8 9 10 11 12 13

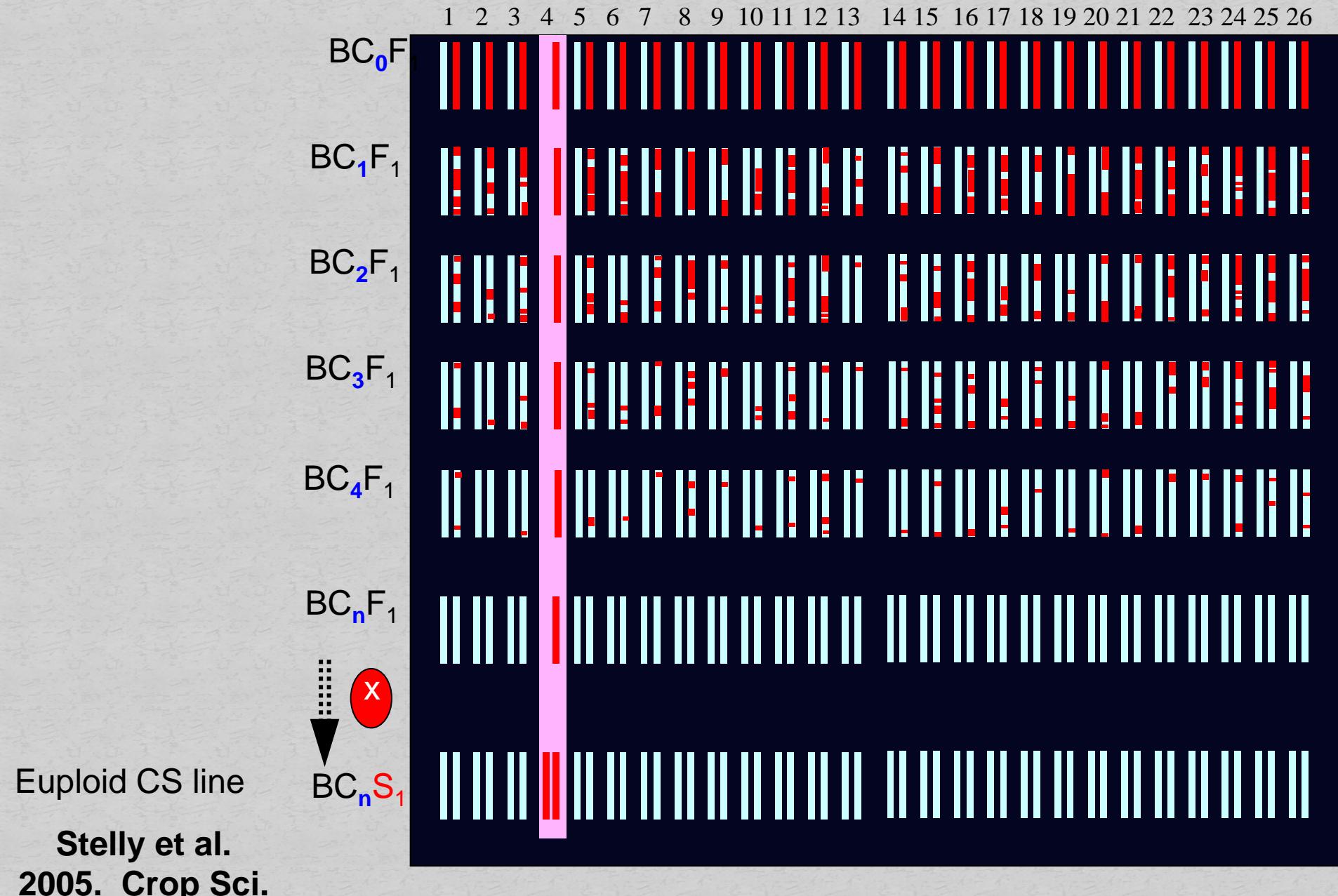
CS Line  
for chr. 4  
*(idealized)*



Alien DNA

14 15 16 17 18 19 20 21 22 23 24 25 26

## Development of a DCS Line (e.g., Chr. 4)

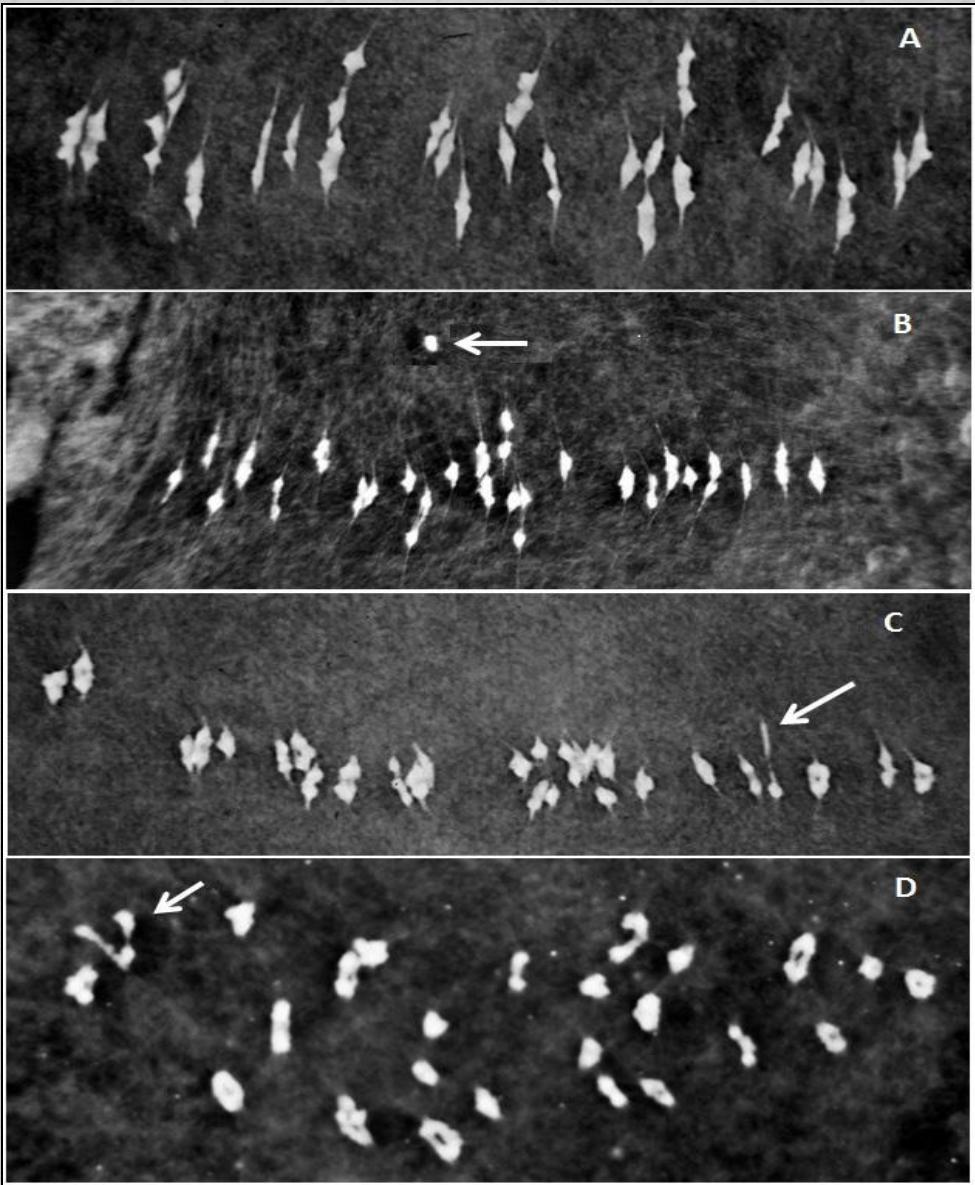


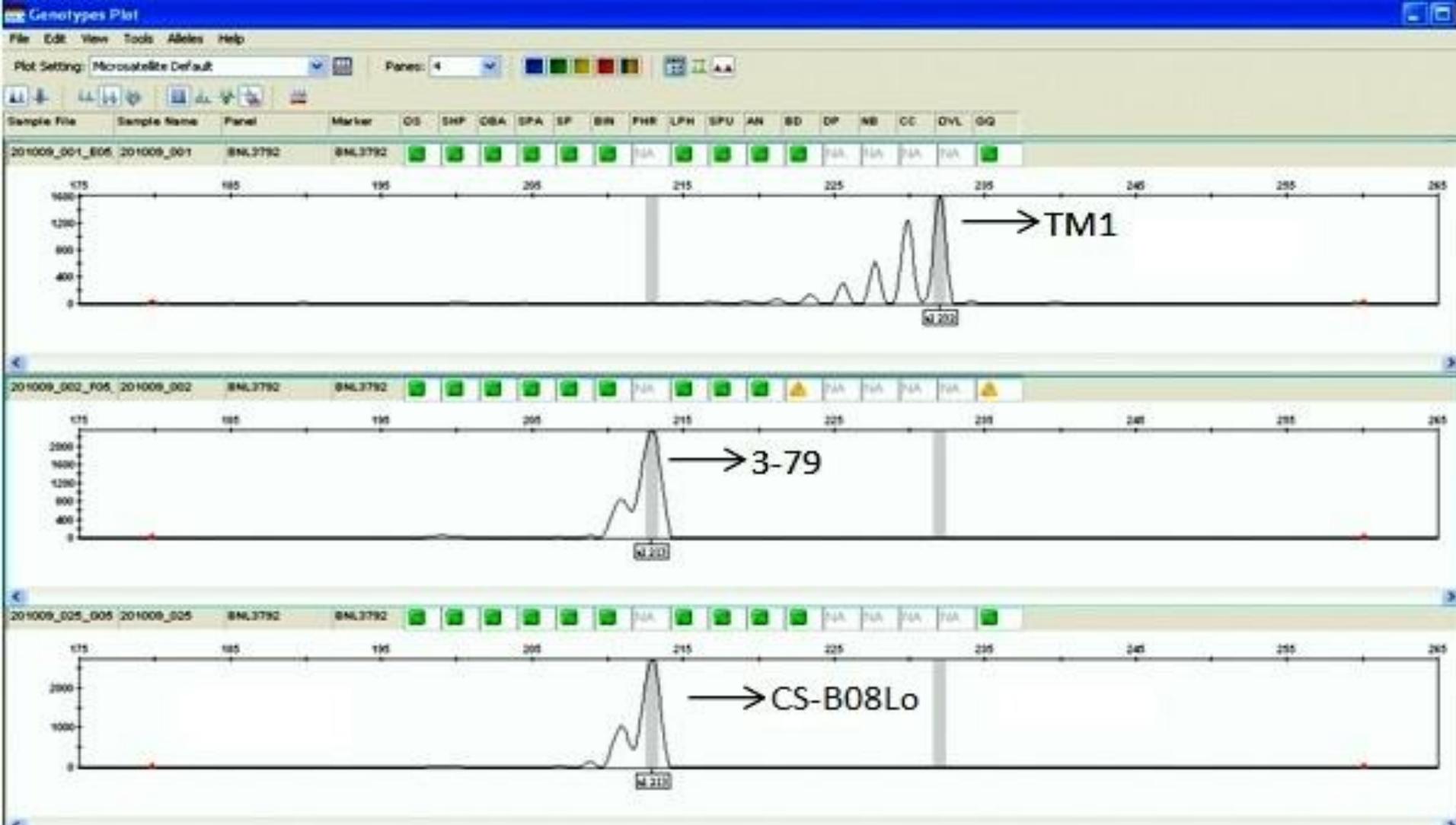
**(A) Metaphase-I showing 26 II (pairs of chromosomes), indicating a normal (euploid) constitution.**

**(B) 25 II + 1 I (univalent, see arrow), indicating a primary monosomic constitution ( $2n-1$ ).**

**(C) 25 II + 1 li (unequal bivalent), indicating a monotelodisomic plant ( $2n=52$ , but missing most of one arm).**

**(D) 24 II + 1 III (trivalent), indicating tertiary monosity and  $2n=51$ .**

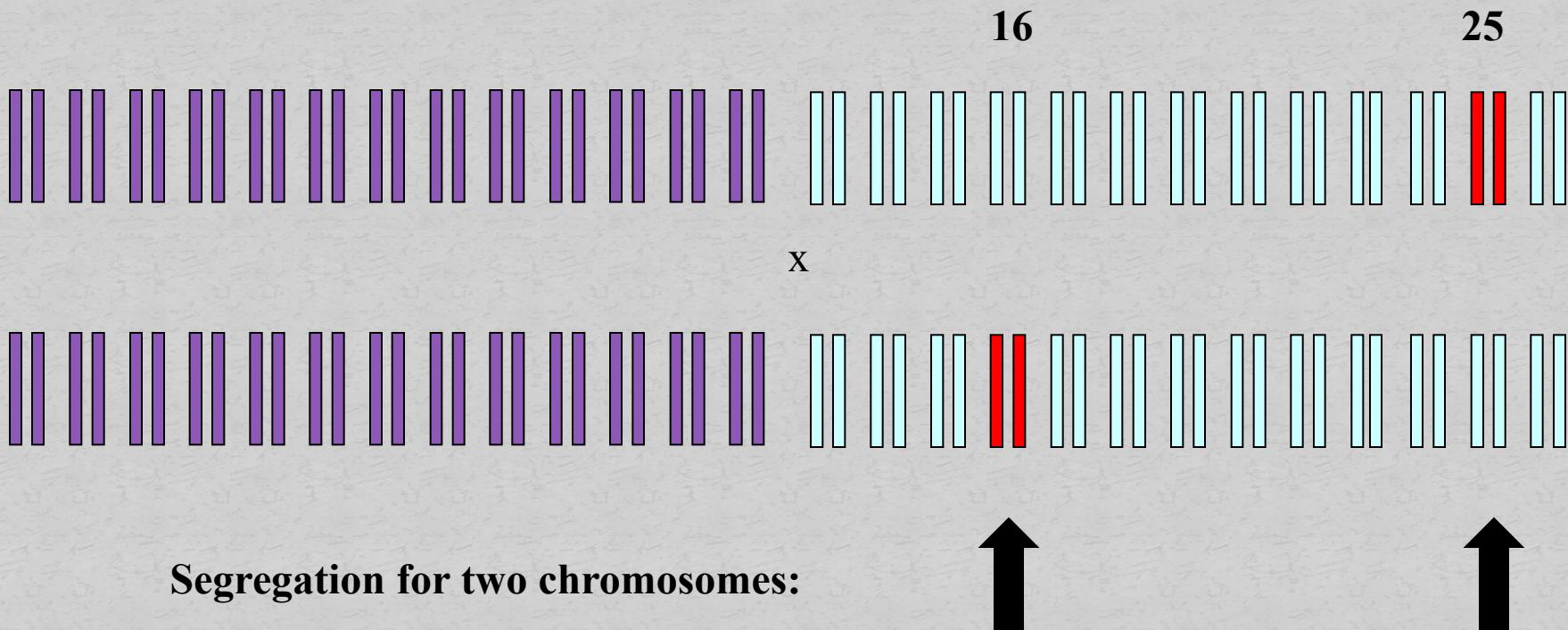




Comparisons of the three electropherograms show that the CS-B08sh line has only the 3-79 allele for BNL3792, previously mapped to linkage group c08. The results are concordant with expectations

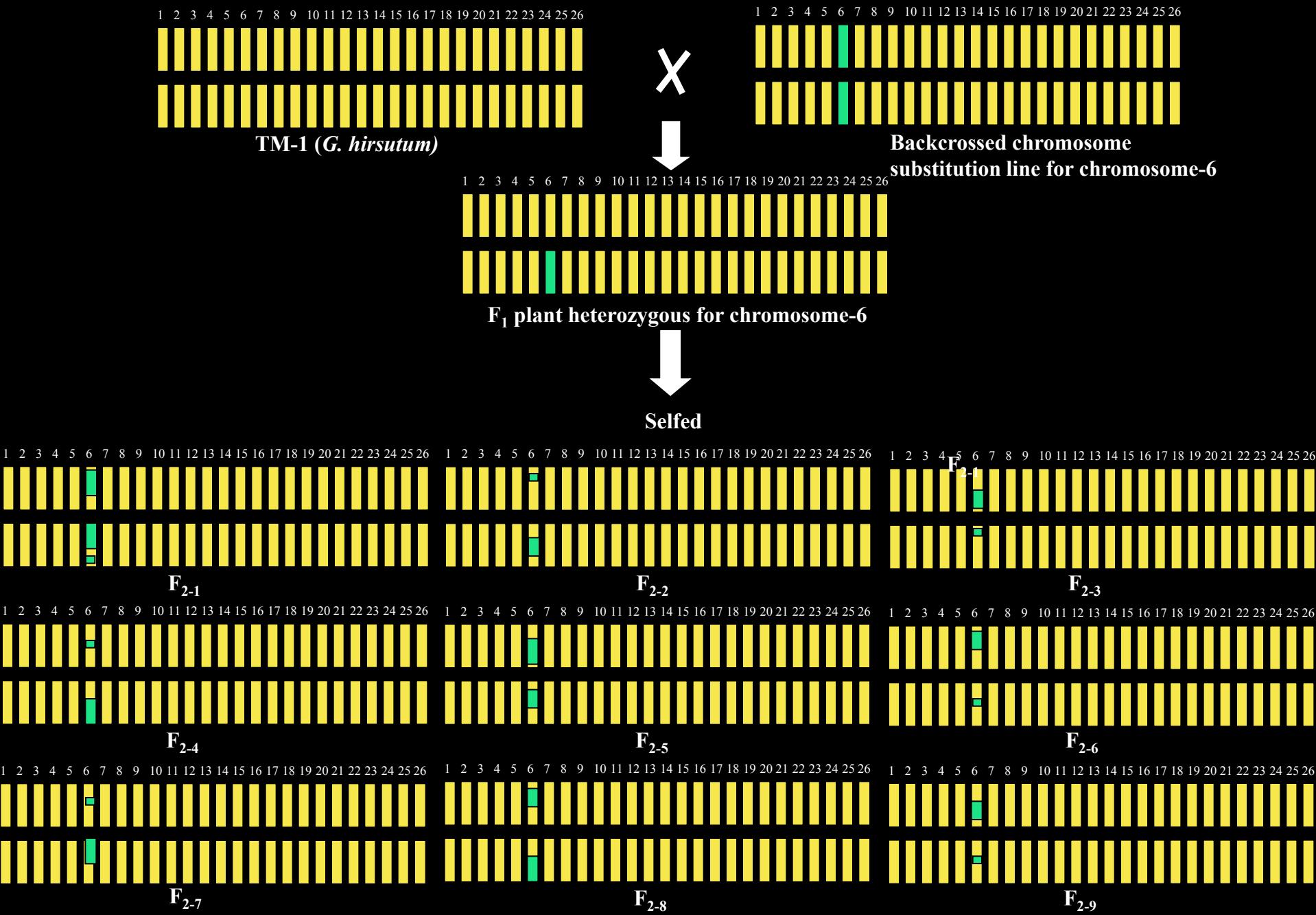
# Intercrosses of CS-B Lines

**Ideally, each CS-B intercrosses is similar to this,  
e.g. CS-B25 x CS-B16:**

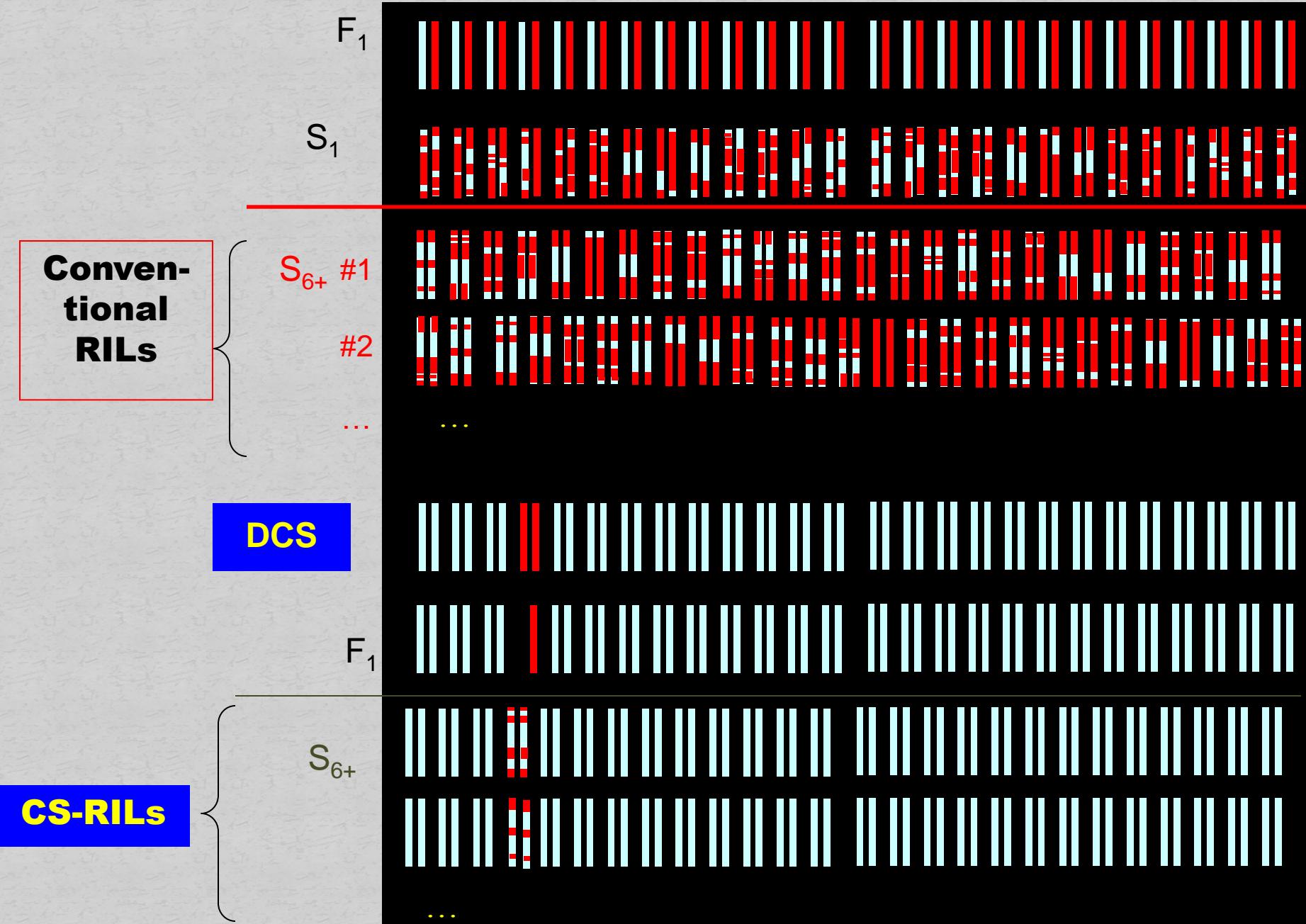


**In reality, CS-B line (BC5) has some cryptic 3-79 beneficial alleles**

# Chromosome-6 Specific F<sub>2</sub> Population



# RILs versus Chromosome-specific RILs





TM-1

Pima 3-79



***G. mustelinum***



**CS-M line**



# **Te22LoSubBC4F2**



# **(TM-1xTe22LoSubBC4F1)F2**

# Comparisons of CS-B Line F2s -> variance

Vp%	Proportions of estimated variance components for agronomic and fiber traits								
	Parameter	Sd-cotton	Lint	Lint%	Wt Boll	Mic	2.5 SPL	Elongation	Strength
8 - 33	Va/Vp	0.15 **	0.11 **	0.15 **	0.24 **	0.29 **	0.33 **	0.08 *	0.23 **
0 - 61	Vd/Vp	0.09 *	0.14 **	0.61 **	0.33 **	0.21 **	0.00	0.34 **	0.20 **
0 - 21	Vae / Vp	0	0	0.05 *	0.21 **	0	0	0	0
0 - 55	Vde / Vp	0.55 **	0.55 **	0.12 **	0	0.30 **	0.44 **	0.34 **	0.23 **
8 - 35	Ve / Vp	0.21 **	0.21 **	0.08 **	0.23 **	0.20 **	0.23 **	0.24 **	0.35 **

Subscripts:  
 a = additive  
 d = dominance  
 e = environment  
 ae, de = interaction effects

- High to v.high G and/or GE
- For G: A vs D differs by trait.
- For GE: DE >> AE effects

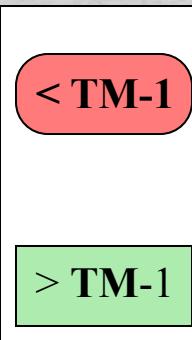
# Direct Comparisons of CS-B Lines

*Deviations (+- SE) from the grand mean.*

Lines	Lint	Lint%	Length	Elong.	Strength
CS-B line	Lint yield (kg/ha)	Lint ( %)	2.5% Span length (mm)	Elongation (%)	Strength (kNm/kg)
CS-B02	121 ± 26 <sup>+</sup>	0.30 ± 0.18**	-0.39 ± 0.10 <sup>+</sup>	-1.05 ± 0.16 <sup>+</sup>	4.79 ± 2.59**
CS-B04	94 ± 23 <sup>+</sup>	-1.18 ± 0.16	0.30 ± 0.10 <sup>+</sup>	1.24 ± 0.18*	-7.58 ± 2.10 <sup>+</sup>
CS-B06	170 ± 21 <sup>+</sup>	-0.18 ± 0.09**	-0.49 ± 0.16 <sup>+</sup>	0.06 ± 0.17 <sup>+</sup>	-6.39 ± 2.00 <sup>+</sup>
CS-B07	99 ± 16 <sup>+</sup>	-0.55 ± 0.07 <sup>+</sup>	-0.06 ± 0.10 <sup>+</sup>	0.29 ± 0.15	-6.59 ± 2.59 <sup>+</sup>
CS-B16	-164 ± 28**	2.73 ± 0.41**	-0.81 ± 0.19**	-0.24 ± 0.19 <sup>+</sup>	-14.07 ± 2.79 <sup>+</sup>
CS-B17	13 ± 27**	-4.20 ± 0.09**	-0.97 ± 0.14**	1.17 ± 0.23*	-6.49 ± 2.20 <sup>+</sup>
CS-B18	-208 ± 25**	1.04 ± 0.14**	-0.39 ± 0.13 <sup>+</sup>	0.30 ± 0.15	0.80 ± 1.70 <sup>+</sup>
CS-B25	23 ± 21**	-3.13 ± 0.18**	1.01 ± 0.18**	-0.70 ± 0.14**	16.57 ± 3.59**
CSB05sh	35 ± 29 <sup>+</sup>	1.31 ± 0.26**	-0.87 ± 0.13**	-0.22 ± 0.11**	-17.27 ± 2.50**
CS-B14sh	-107 ± 26**	-0.84 ± 0.43	1.01 ± 0.21**	-0.49 ± 0.08**	-1.30 ± 2.99 <sup>+</sup>
CS-B15sh	151 ± 34 <sup>+</sup>	-1.24 ± 0.12*	0.65 ± 0.17**	0.38 ± 0.17	0.50 ± 2.50 <sup>+</sup>
CS-B22sh	-59 ± 23**	3.54 ± 0.14**	-1.99 ± 0.11**	-0.94 ± 0.16**	-10.88 ± 2.40 <sup>+</sup>
CS-B22Lo	158 ± 39 <sup>+</sup>	4.85 ± 0.13**	-1.04 ± 0.13**	-0.71 ± 0.19**	-6.89 ± 2.40 <sup>+</sup>
TM1	136 ± 27	-0.76 ± 0.11	-0.04 ± 0.14	0.20 ± 0.07	-6.29 ± 2.50
3-79	-461 ± 24	-1.70 ± 0.36	4.07 ± 0.21	0.70 ± 0.15	60.78 ± 2.50

\* = sig. diff. (p<.05) from 'TM-1'

(Saha et al. 2004 J. Cotton Science)



# Comparisons of Topcrosses - Strength

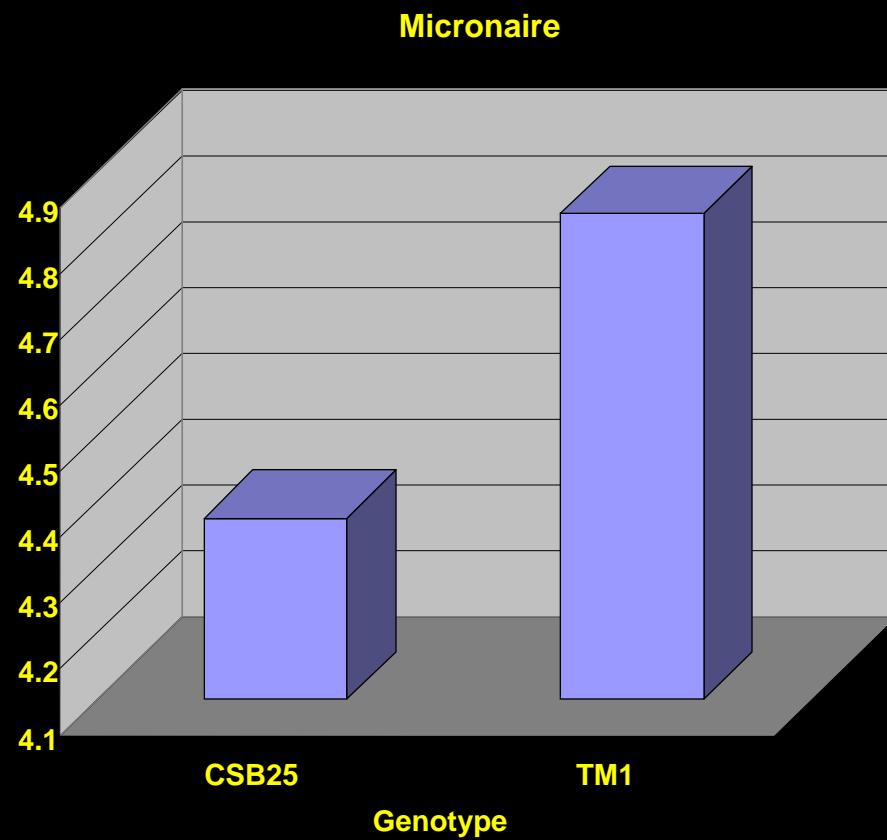
Heterozygous dominance effects (SCA)

Male parents	DP90	SG747	PSC355	ST474	FM966
TM-1	-8.45 ± 3.04	2.25 ± 3.18	9.94 ± 2.89	-1.11 ± 3.16	-12.57 ± 4.53
CS-B02	-3.93 ± 2.92	8.62 ± 4.48	3.51 ± 3.79	-10.05 ± 3.08*	4.69 ± 2.26*
CS-B04	0.03 ± 3.24	3.11 ± 3.45	0.52 ± 6.99	-1.14 ± 3.95	1.70 ± 3.09*
CS-B06	-2.25 ± 3.01	3.34 ± 3.23	-12.39 ± 2.62*	1.06 ± 3.61	-6.76 ± 4.00
CS-B07	3.50 ± 3.40*	-9.64 ± 2.49*	-10.45 ± 3.90*	4.51 ± 7.11	8.11 ± 3.23*
CS-B16	4.58 ± 3.06*	-0.64 ± 2.38	4.54 ± 4.29	-1.15 ± 3.19	-12.98 ± 5.16
CS-B17	-5.55 ± 3.19	-4.81 ± 3.60	-1.23 ± 2.28*	5.53 ± 3.05	-1.05 ± 2.89*
CS-B18	-5.58 ± 4.02	-1.00 ± 2.95	2.42 ± 2.97	-7.38 ± 2.87	10.20 ± 4.69*
CS-B25	0.95 ± 3.05*	-6.68 ± 3.50	6.78 ± 3.51	7.45 ± 4.14	3.48 ± 4.14*
CS-B05sh	-0.76 ± 3.08	0.67 ± 3.02	4.26 ± 2.51	-2.96 ± 4.27	-7.55 ± 3.46
CS-B14sh	-4.86 ± 4.15	5.78 ± 4.41	-9.20 ± 4.13*	-2.17 ± 3.57	-0.22 ± 2.90*
CS-B15sh	-6.96 ± 3.00	-5.16 ± 2.59	4.13 ± 3.23	10.59 ± 6.94	-2.24 ± 2.57
CS-B22sh	-16.80 ± 4.24	1.38 ± 3.36	8.15 ± 2.46	-4.10 ± 3.39	-11.68 ± 4.30
CS-B22Lo	-4.32 ± 4.53	4.97 ± 3.37	-7.29 ± 3.18*	-2.28 ± 4.51	8.40 ± 4.66*
Gb 3-79	15.15 ± 7.64*	-13.90 ± 4.51*	6.15 ± 5.45	11.94 ± 6.10	4.78 ± 4.78*

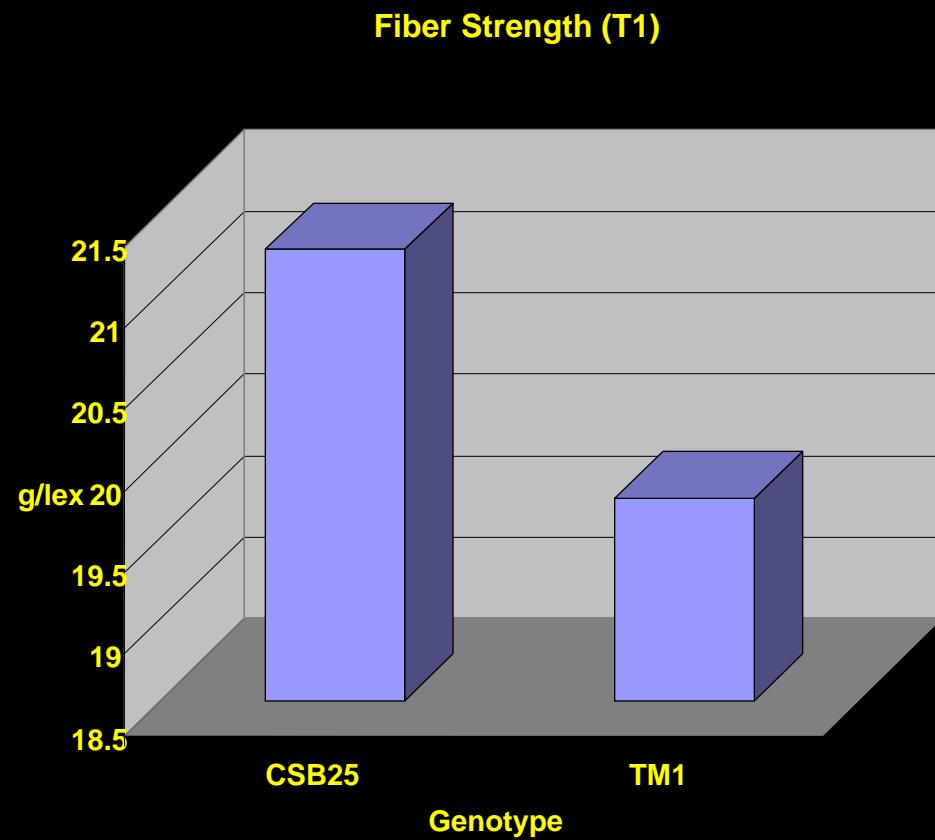
Sig.: Significantly different from TM-1 ( $p < 0.05$ )

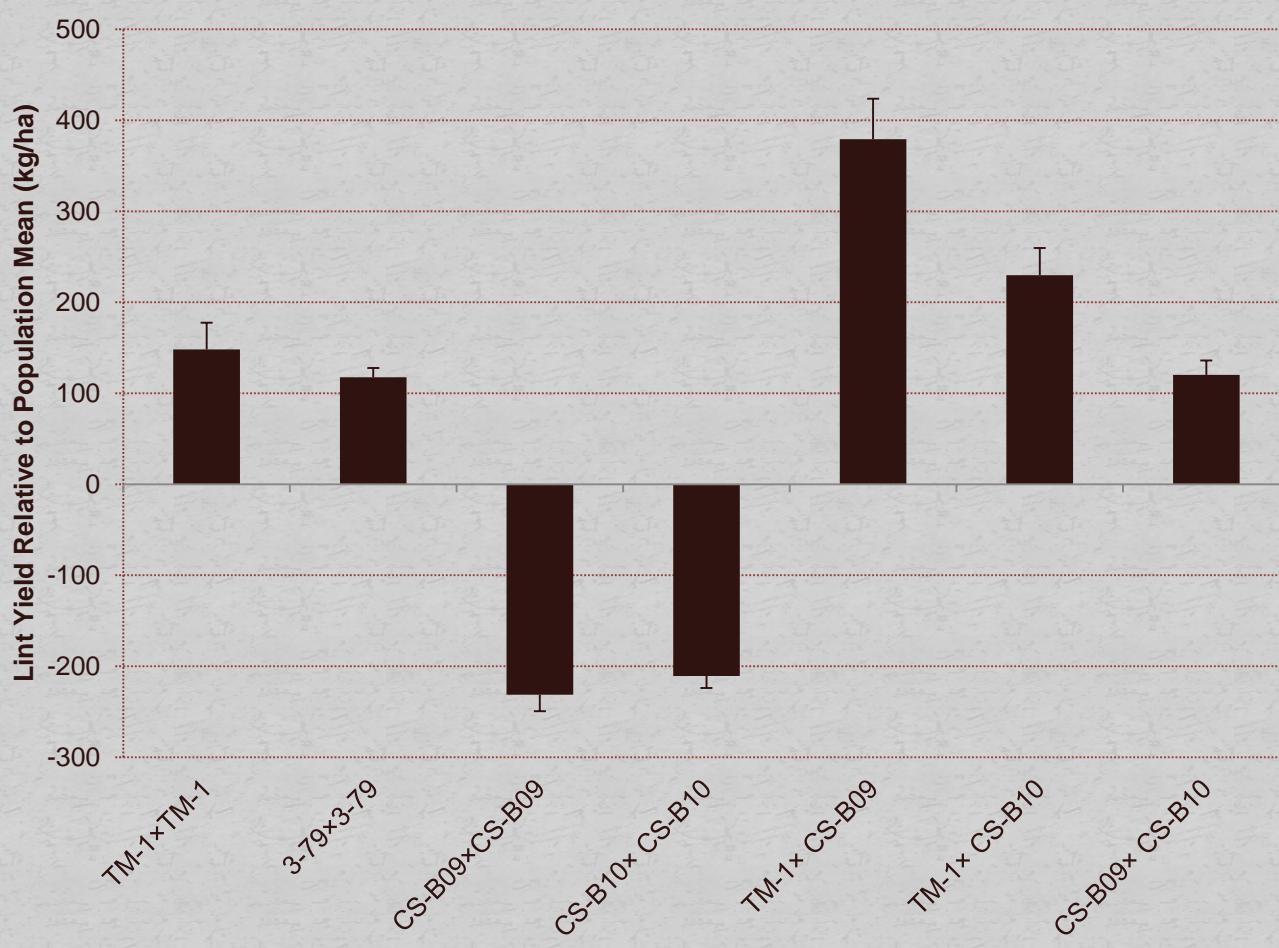
\* Indicates significant difference from TM-1.

# Micronaire



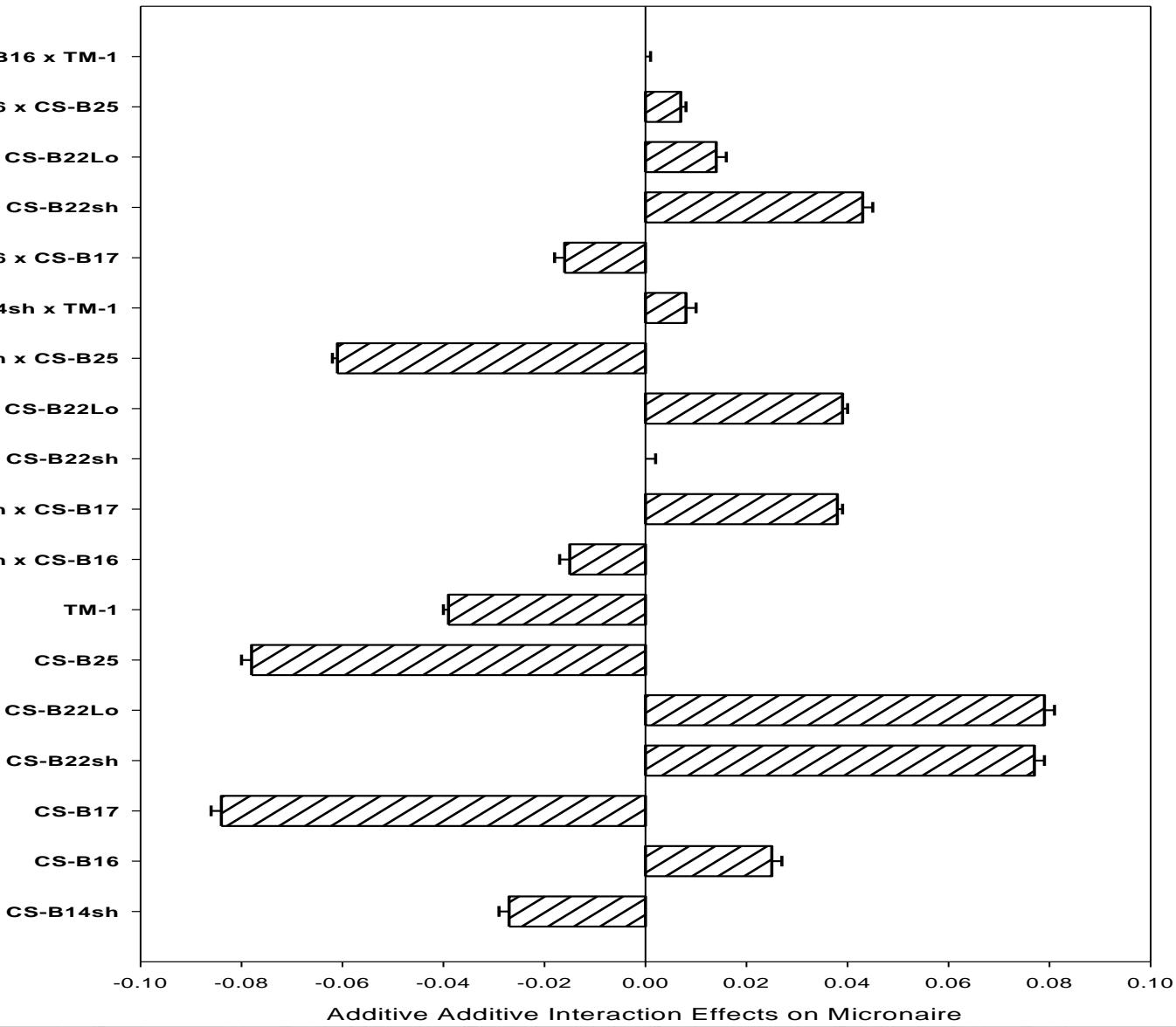
# Fiber Strength

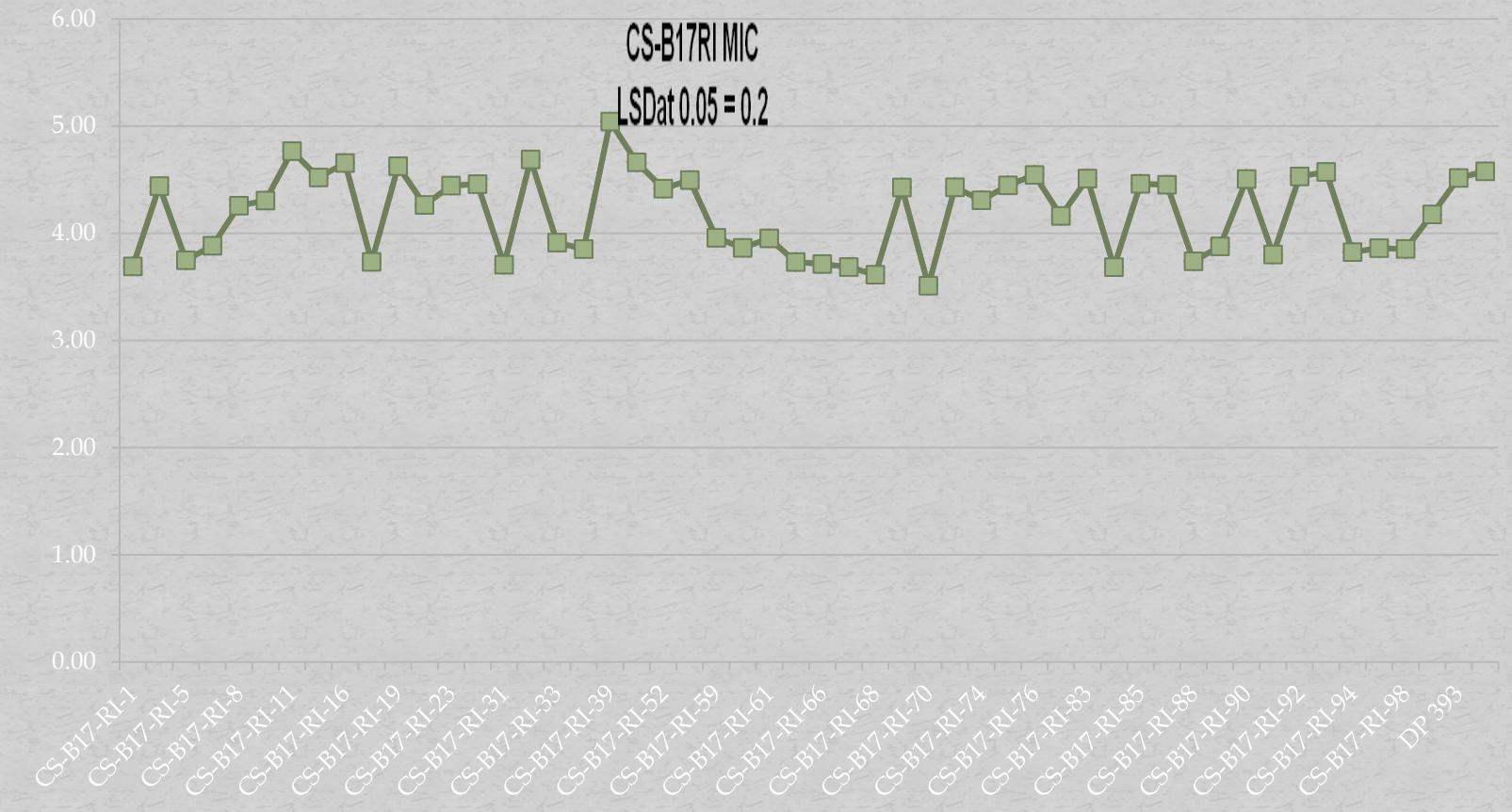




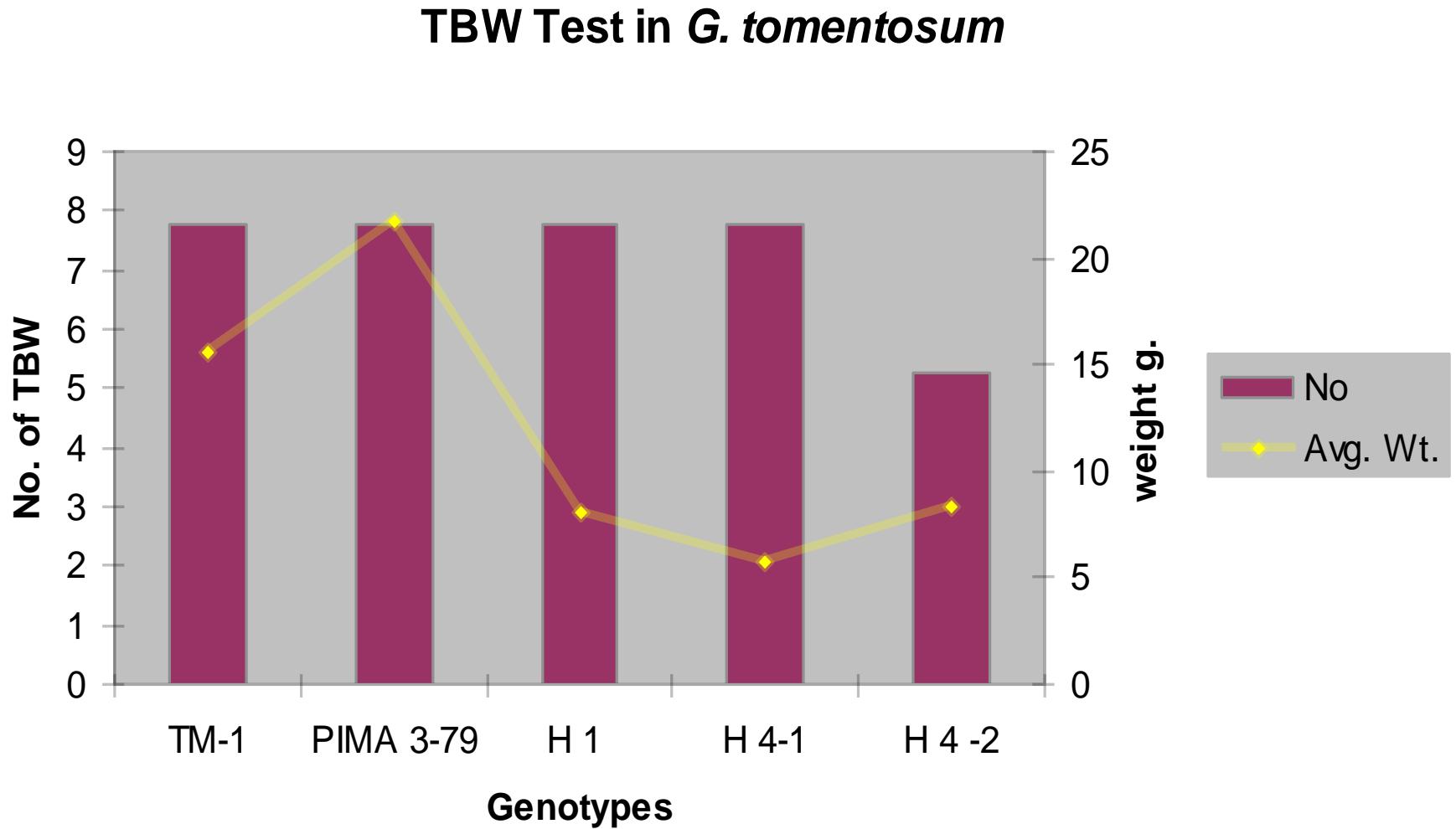
**Predicted dominance effects on lint yield of the selected CS-B lines, TM-1, and 3-79**

Saha et al. 2012 Theor Appl Genet.  
DOI 10.1007/s00122-012-1965-9.

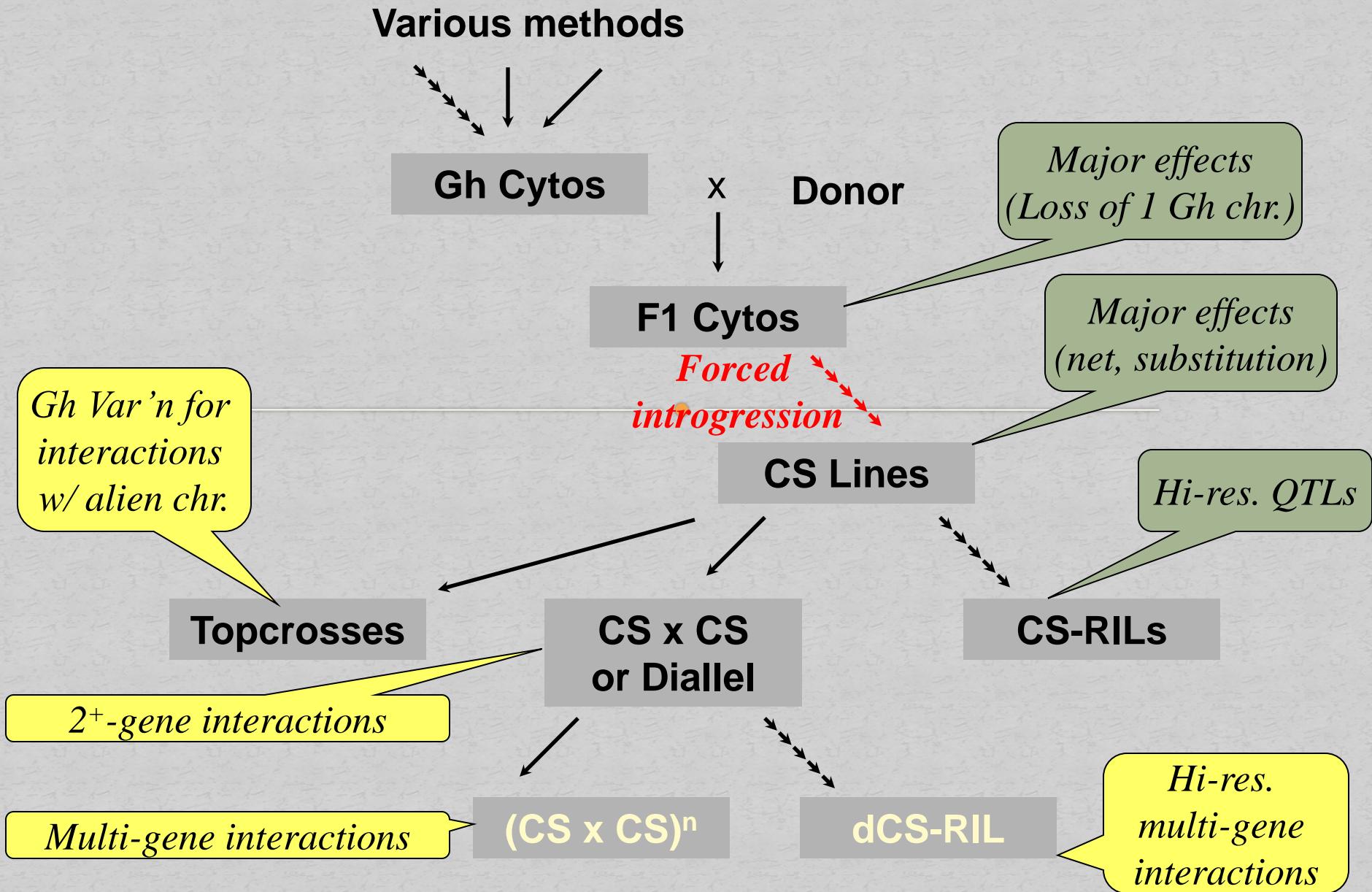




# Results



# CS Line Development & Application



# CS: Potential Impact Areas

## Usable genetic diversity

- Introgression
- Recombination
  - Selection
- 27 CS-B lines, 14 CS-T lines , 9 CS-M lines, several CSRILs, top crosses

## Genetic identification of traits

- QTLs
- Markers
- Genes
- Cryptic alleles
- Epistasis

## Genomics

- Resources
- Technologies
- Information

## An integrated cytogenomics & breeding research

- Affordability
- Accessibility

# Collaborator

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# Thank You

