E

BMT-TWA/Maize/2/7-d
ORIGINAL: English
DATE: November 12, 2007

INTERNATIONAL UNION FOR THE PROTECTION OF NEW VARIETIES OF PLANTS
GENEVA

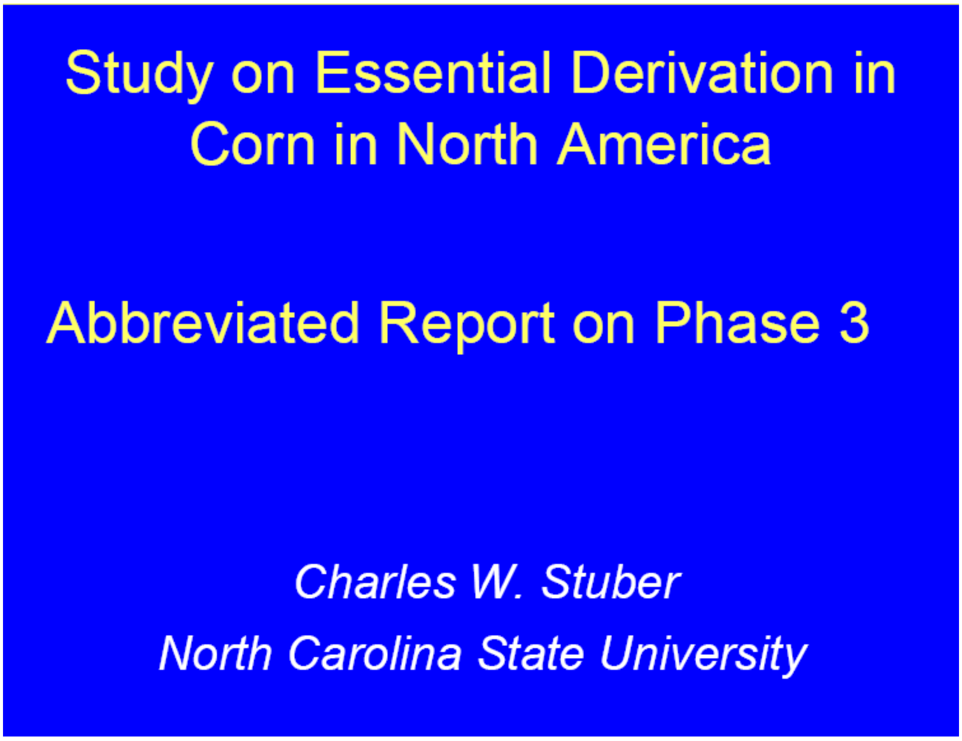
AD HOC CROP SUBGROUP ON MOLECULAR TECHNIQUES FOR MAIZE

Second Session
Chicago, United States of America, December 3, 2007

EDV IN CORN:

STUDY ON ESSENTIAL DERIVATION IN CORN IN NORTH AMERICA - ABBREVIATED REPORT ON PHASE 3

Document prepared by experts from the United States of America

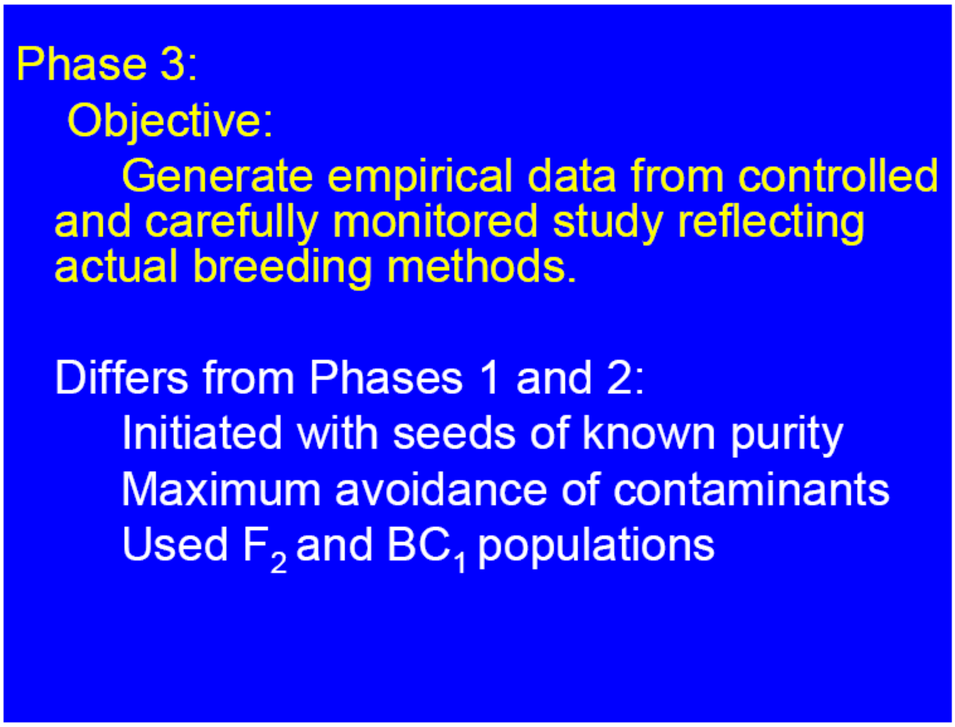


Study on Essential Derivation in Corn in North America

Abbreviated Report on Phase 3

Charles W. Stuber

North Carolina State University



Phase 3:

Objective:

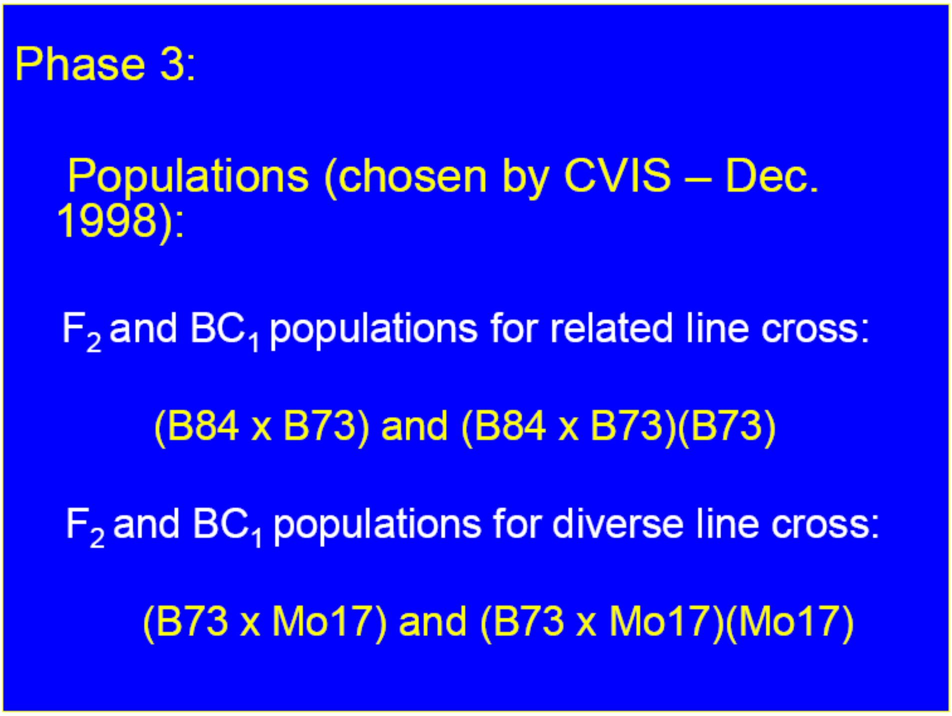
Generate empirical data from controlled and carefully monitored study reflecting actual breeding methods.

Differs from Phases 1 and 2:

Initiated with seeds of known purity

Maximum avoidance of contaminants

Used F_2 and BC_1 populations



Phase 3:

Populations (chosen by CVIS – Dec. 1998):

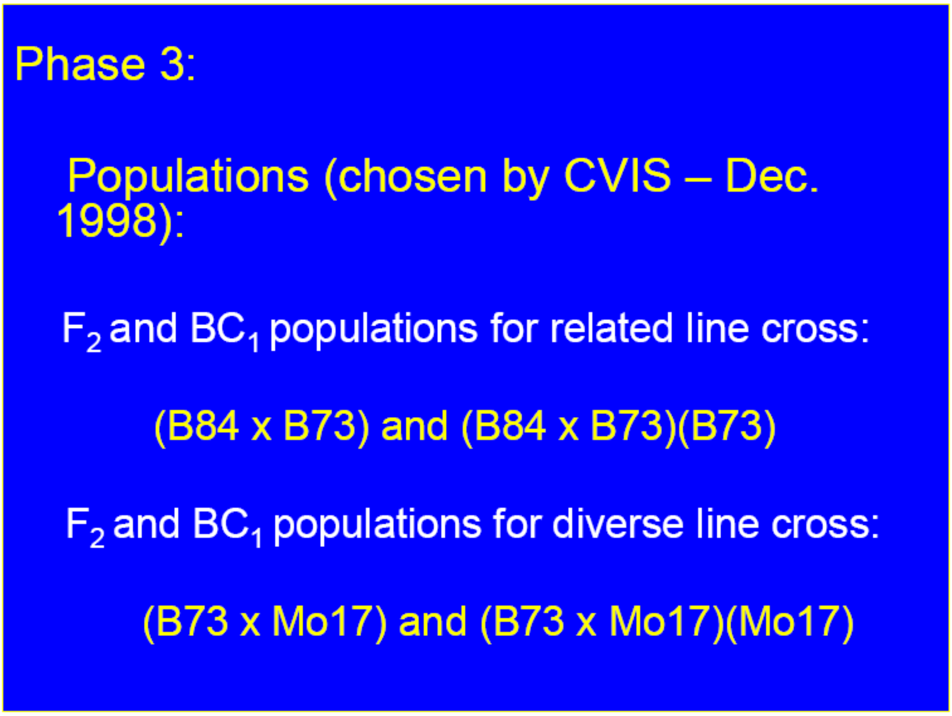
F_2 and BC_1 populations for related line cross:

(B84 x B73) and (B84 x B73)(B73)

F_2 and BC_1 populations for diverse line cross:

(B73 x Mo17) and (B73 x Mo17)(Mo17)

CVIS: ASTA Cultivar Identification Subcommittee



Phase 3:

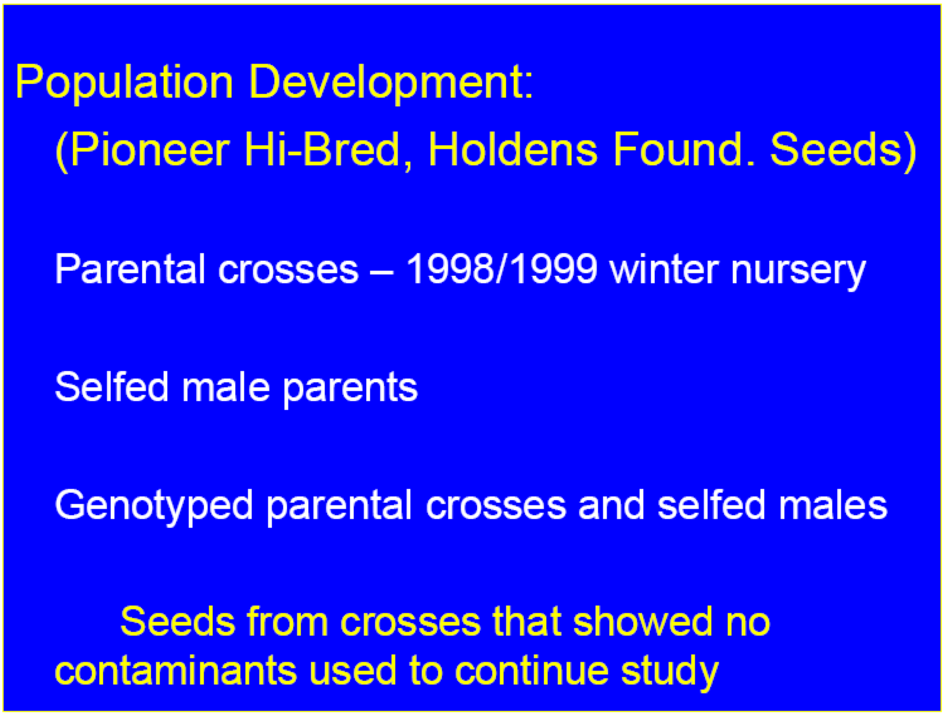
Populations (chosen by CVIS – Dec. 1998):

F_2 and BC_1 populations for related line cross:

(B84 x B73) and (B84 x B73)(B73)

F_2 and BC_1 populations for diverse line cross:

(B73 x Mo17) and (B73 x Mo17)(Mo17)



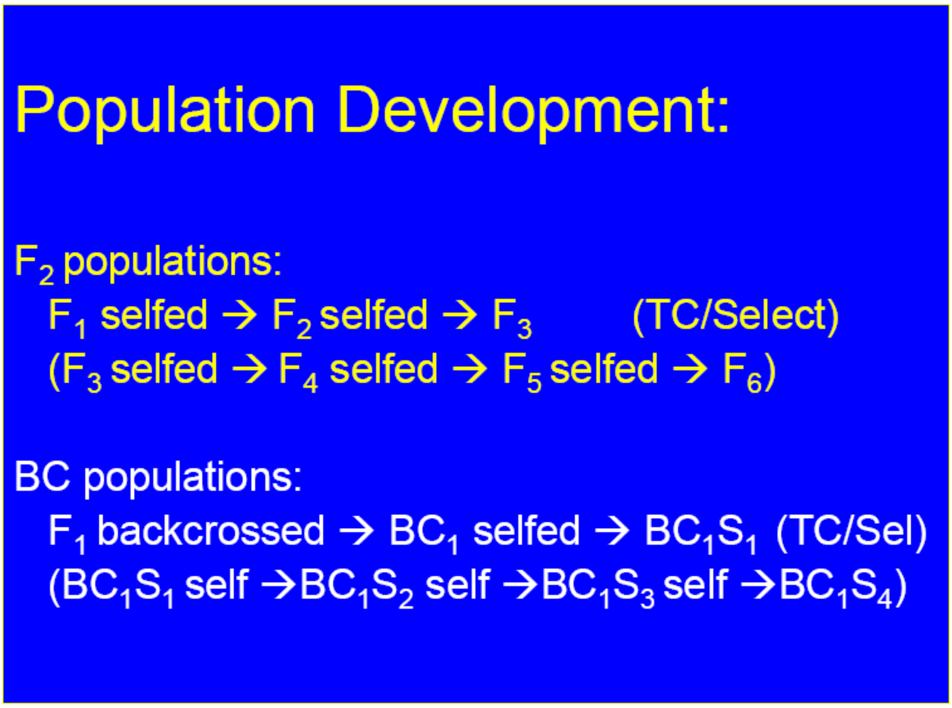
Population Development:
(Pioneer Hi-Bred, Holdens Found. Seeds)

Parental crosses – 1998/1999 winter nursery

Selfed male parents

Genotyped parental crosses and selfed males

Seeds from crosses that showed no contaminants used to continue study

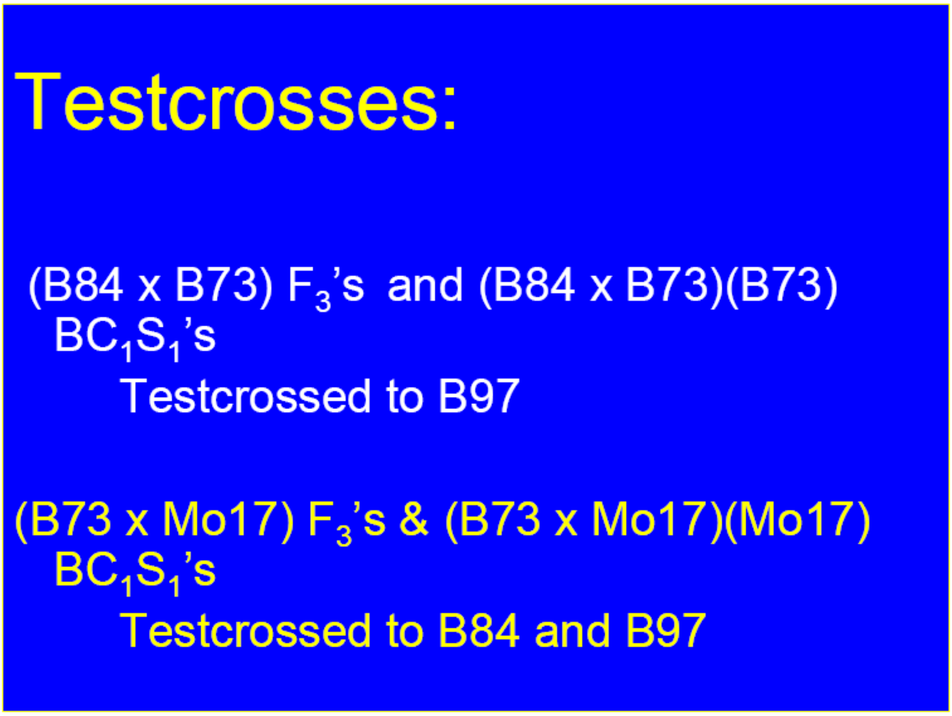


Population Development:

F_2 populations:
F_1 selfed → F_2 selfed → F_3 (TC/Select)
(F_3 selfed → F_4 selfed → F_5 selfed → F_6)

BC populations:
F_1 backcrossed → BC_1 selfed → BC_1S_1 (TC/Sel)
(BC_1S_1 self → BC_1S_2 self → BC_1S_3 self → BC_1S_4)

TC/Select: progeny are selected from yield data for top-crossed progeny



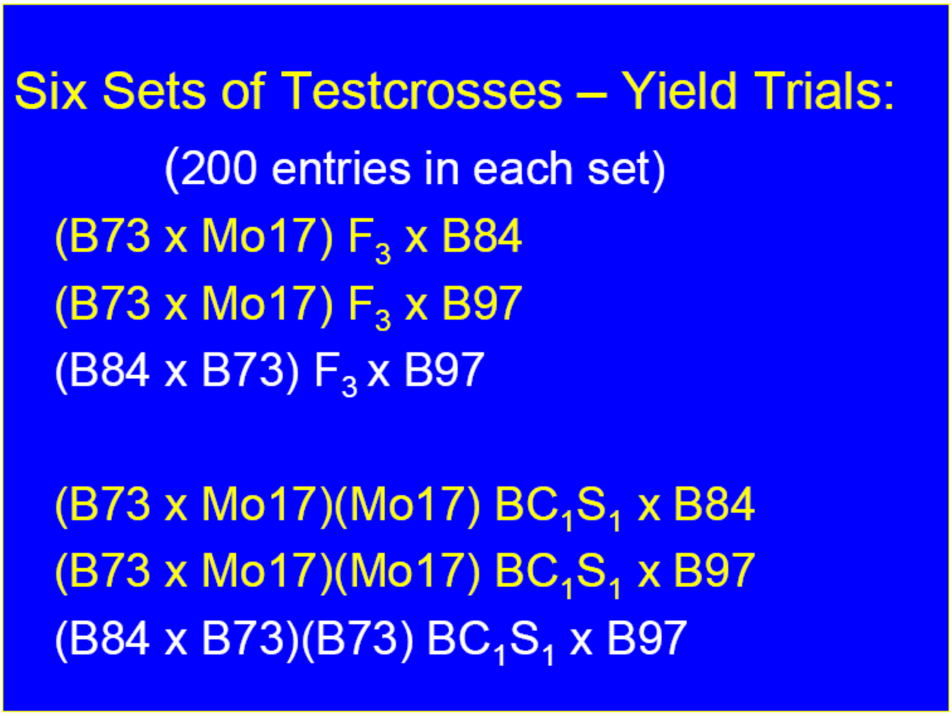
Testcrosses:

(B84 x B73) F_3’s and (B84 x B73)(B73) BC_1S_1’s

Testcrossed to B97

(B73 x Mo17) F_3’s & (B73 x Mo17)(Mo17) BC_1S_1’s

Testcrossed to B84 and B97



Six Sets of Testcrosses – Yield Trials:

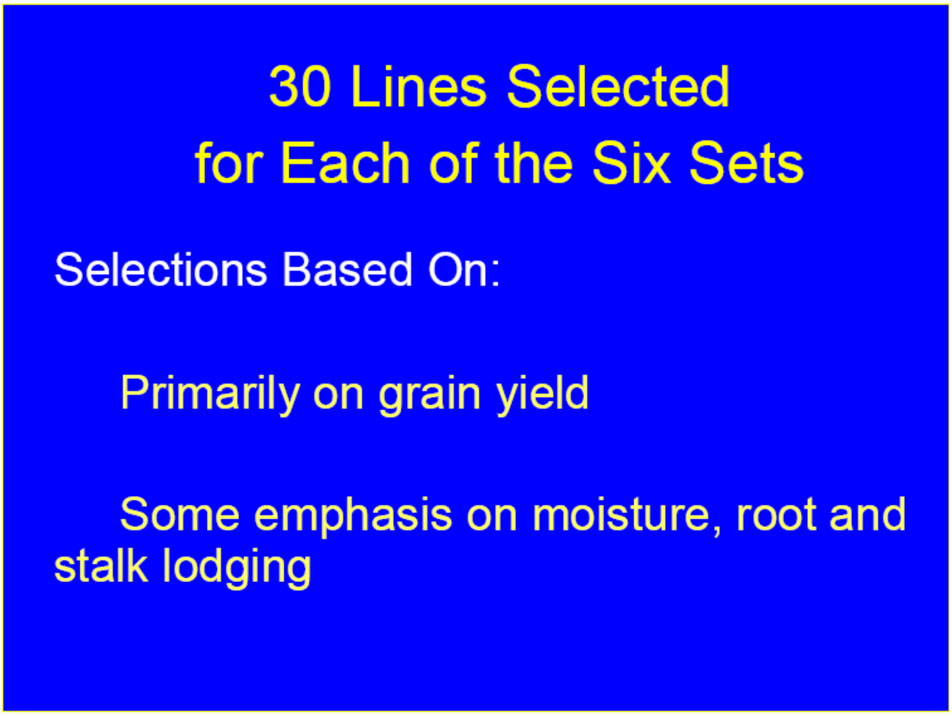
(200 entries in each set)

(B73 x Mo17) F_3 x B84
(B73 x Mo17) F_3 x B97
(B84 x B73) F_3 x B97

(B73 x Mo17)(Mo17) BC_1S_1 x B84
(B73 x Mo17)(Mo17) BC_1S_1 x B97
(B84 x B73)(B73) BC_1S_1 x B97

Yield Trials Conducted in 2001:

AgReliant Genetics
    Ivesdale, IL and Lebanon, IN
Golden Harvest
    Clinton, IL and Fairfield, NE
Hoegemeyer Hybrids
    Elm Creek, NE and Fremont, NE
Holdens Foundation Seeds
    Waco, NE and Williamsburg, IA
Pioneer Hi-Bred International
    Alleman, IA and Johnston, IA
Syngenta
    Glidden, IA and Washington, IA

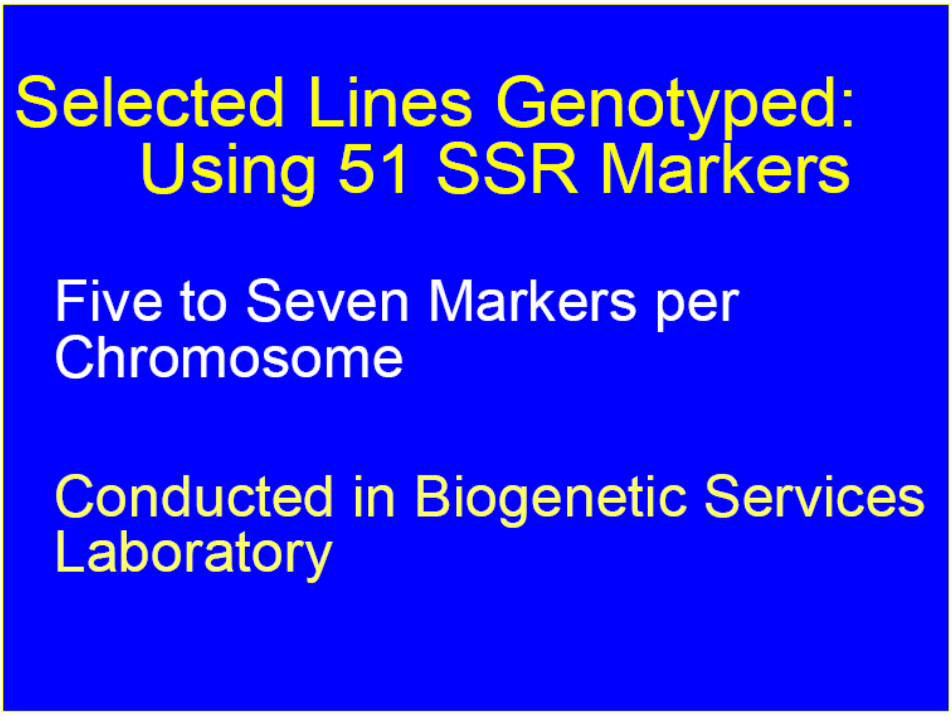


30 Lines Selected
for Each of the Six Sets

Selections Based On:

Primarily on grain yield

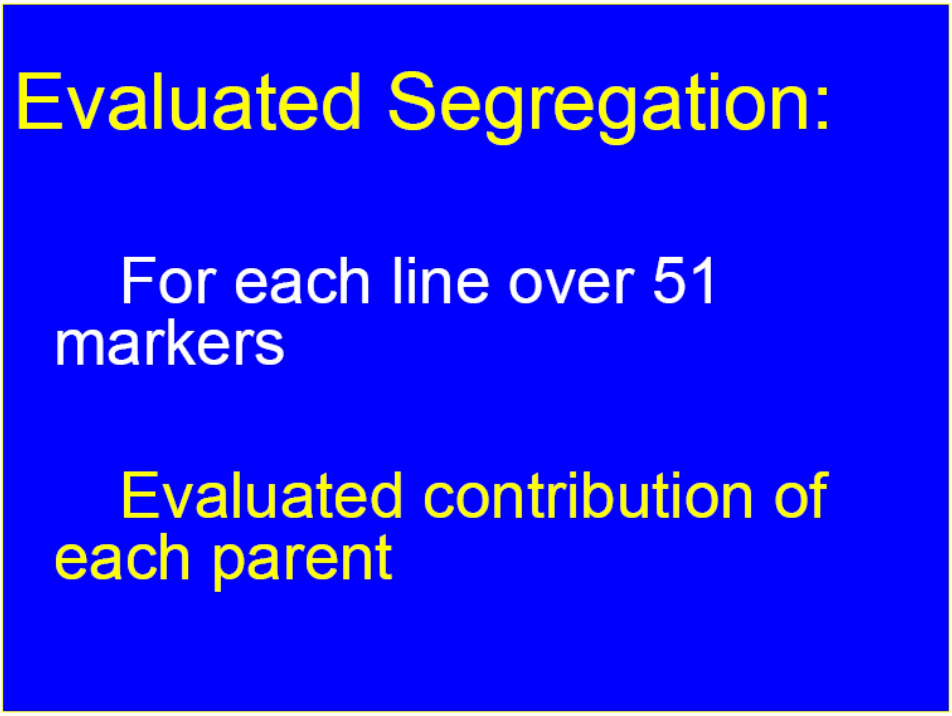
Some emphasis on moisture, root and stalk lodging



Selected Lines Genotyped: Using 51 SSR Markers

Five to Seven Markers per Chromosome

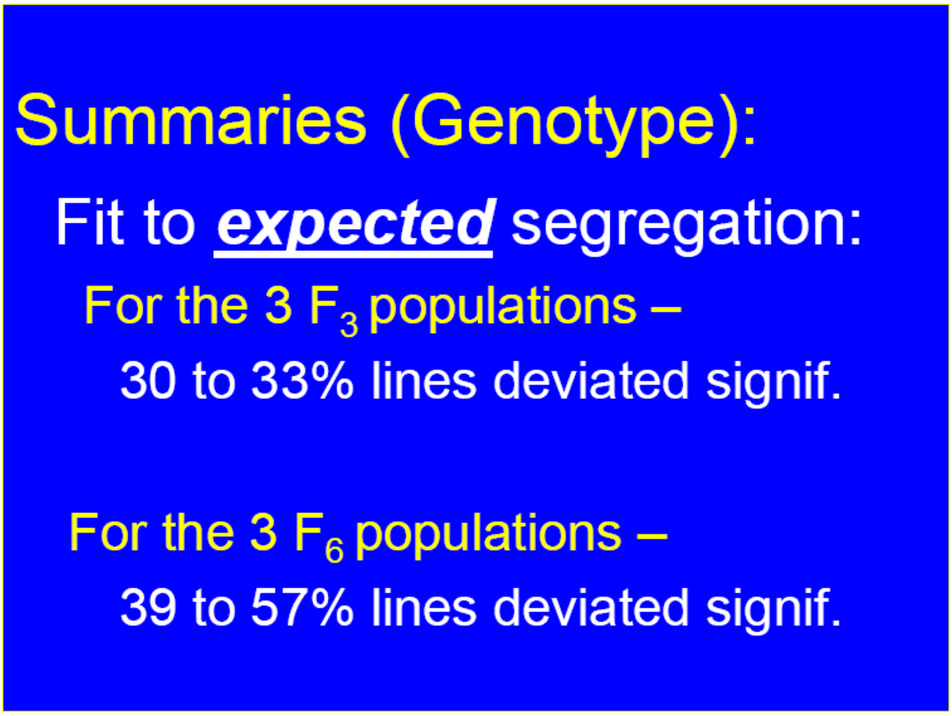
Conducted in Biogenetic Services Laboratory



Evaluated Segregation:

For each line over 51 markers

Evaluated contribution of each parent



Summaries (Genotype):

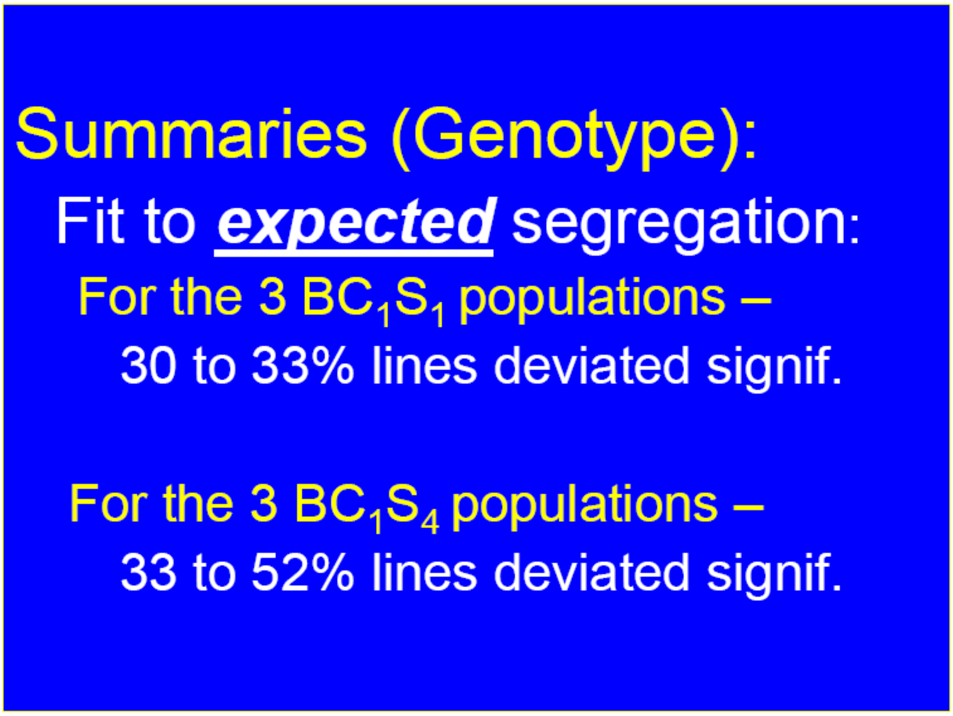
Fit to ***expected*** segregation:

For the 3 F_3 populations –

30 to 33% lines deviated signif.

For the 3 F_6 populations –

39 to 57% lines deviated signif.



Summaries (Genotype):

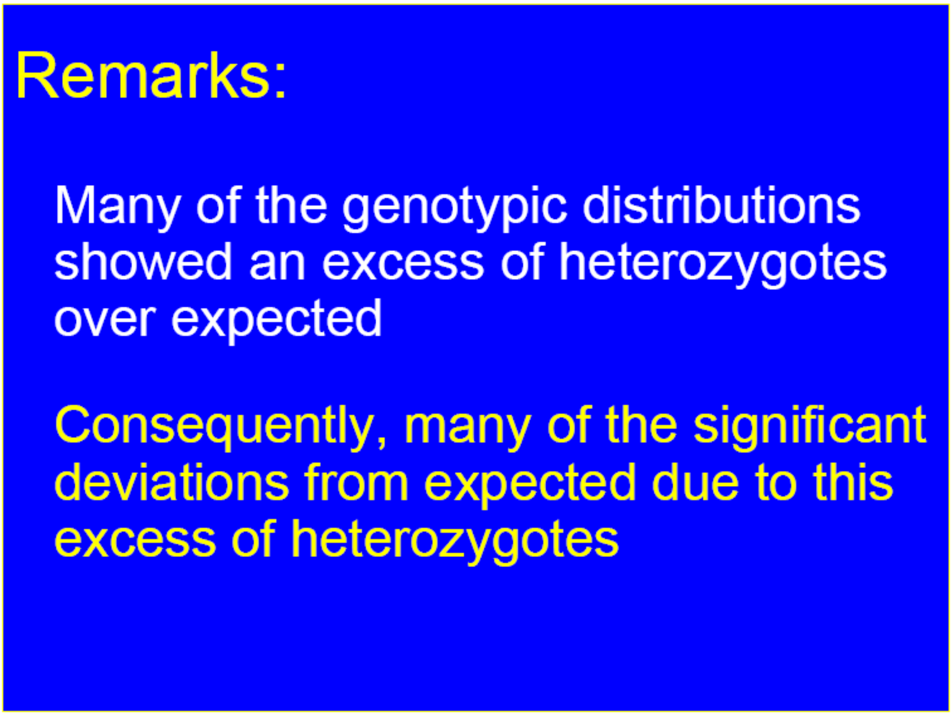
Fit to ***expected*** segregation:

For the 3 BC_1S_1 populations –

30 to 33% lines deviated signif.

For the 3 BC_1S_4 populations –

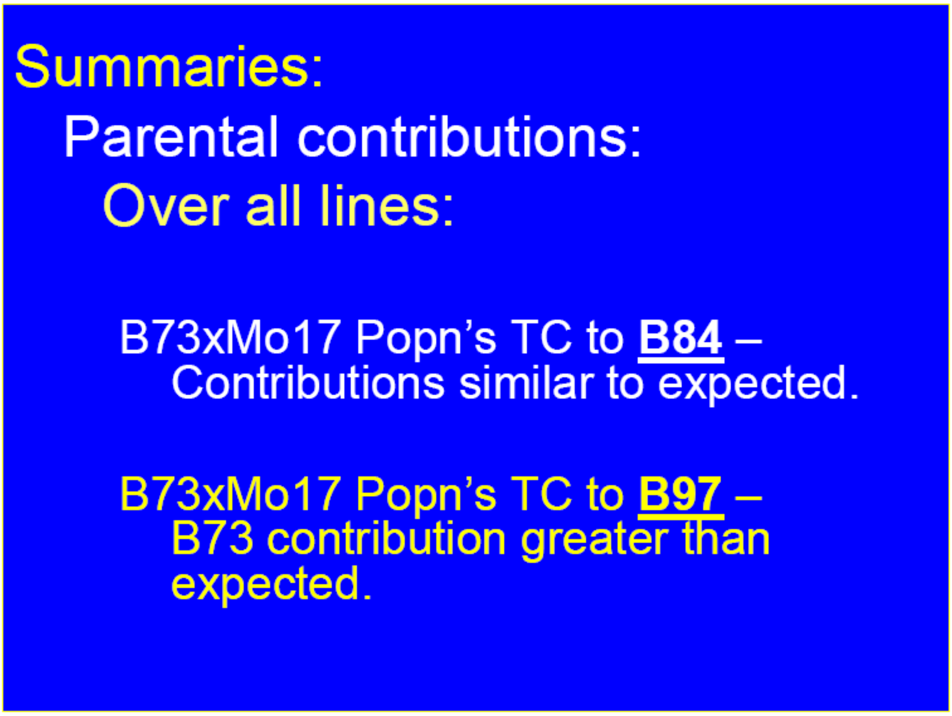
33 to 52% lines deviated signif.



Remarks:

Many of the genotypic distributions showed an excess of heterozygotes over expected

Consequently, many of the significant deviations from expected due to this excess of heterozygotes



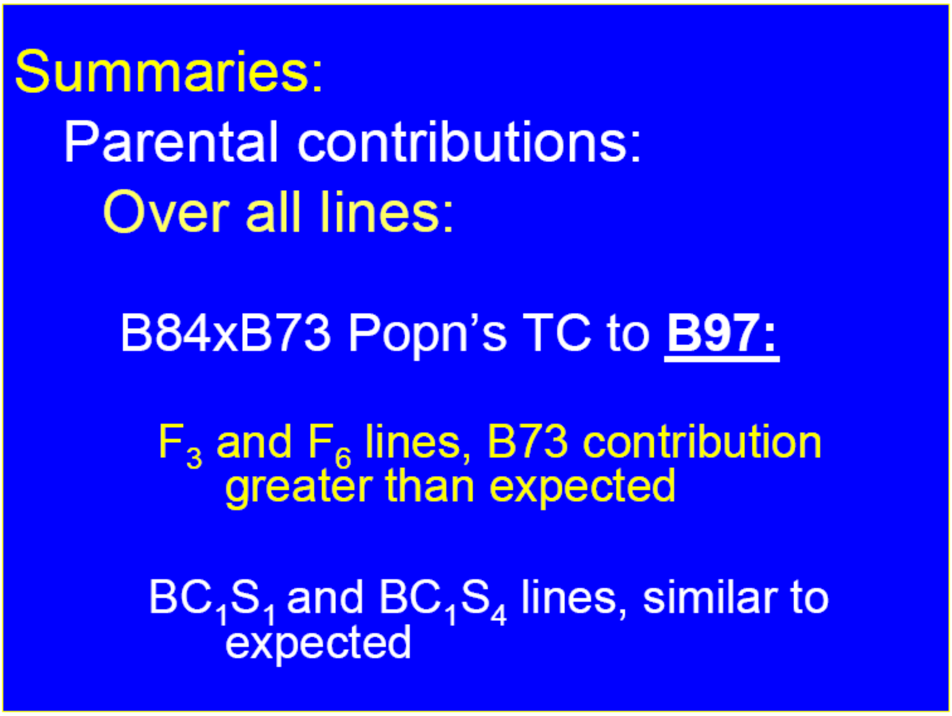
Summaries:

Parental contributions:

Over all lines:

B73xMo17 Popn’s TC to **B84** – Contributions similar to expected.

B73xMo17 Popn’s TC to **B97** – B73 contribution greater than expected.



Summaries:

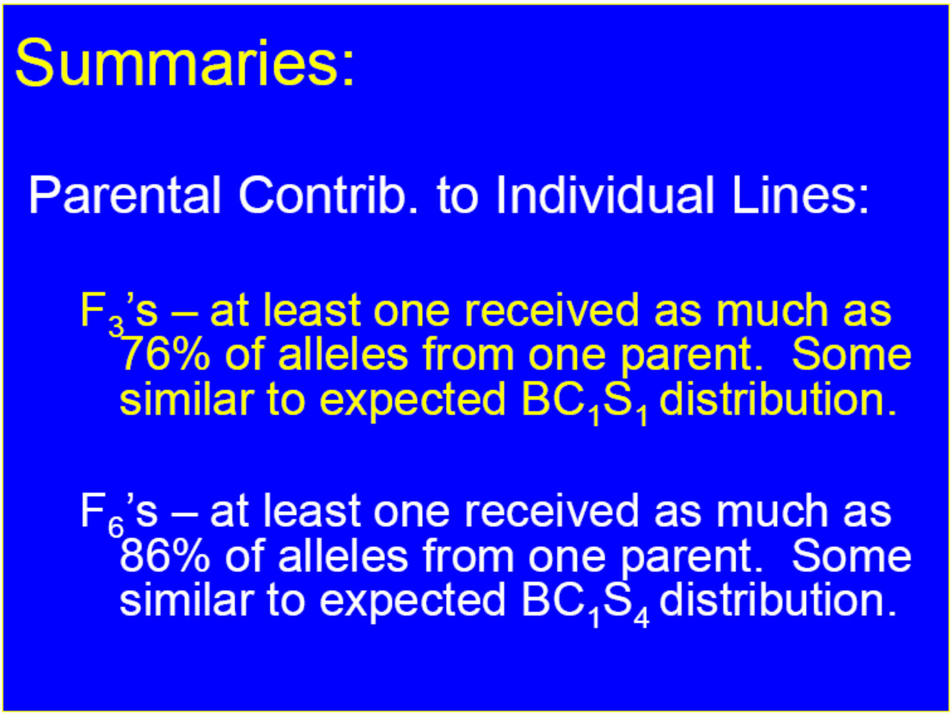
Parental contributions:

Over all lines:

B84xB73 Popn's TC to **B97:**

F_3 and F_6 lines, B73 contribution greater than expected

BC_1S_1 and BC_1S_4 lines, similar to expected

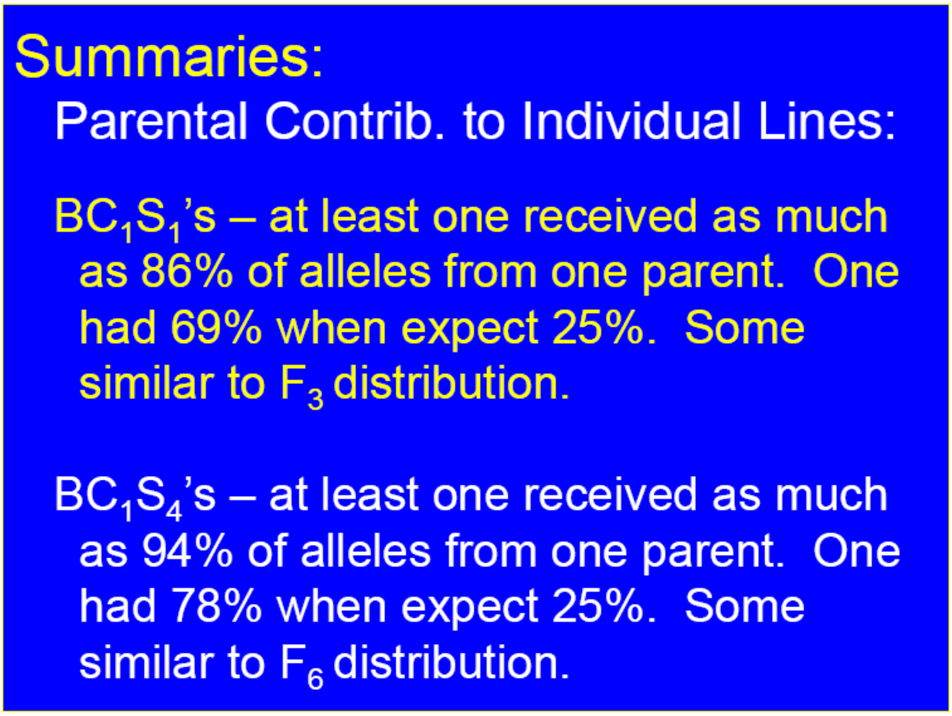


Summaries:

Parental Contrib. to Individual Lines:

F_3's – at least one received as much as 76% of alleles from one parent. Some similar to expected BC_1S_1 distribution.

F_6's – at least one received as much as 86% of alleles from one parent. Some similar to expected BC_1S_4 distribution.

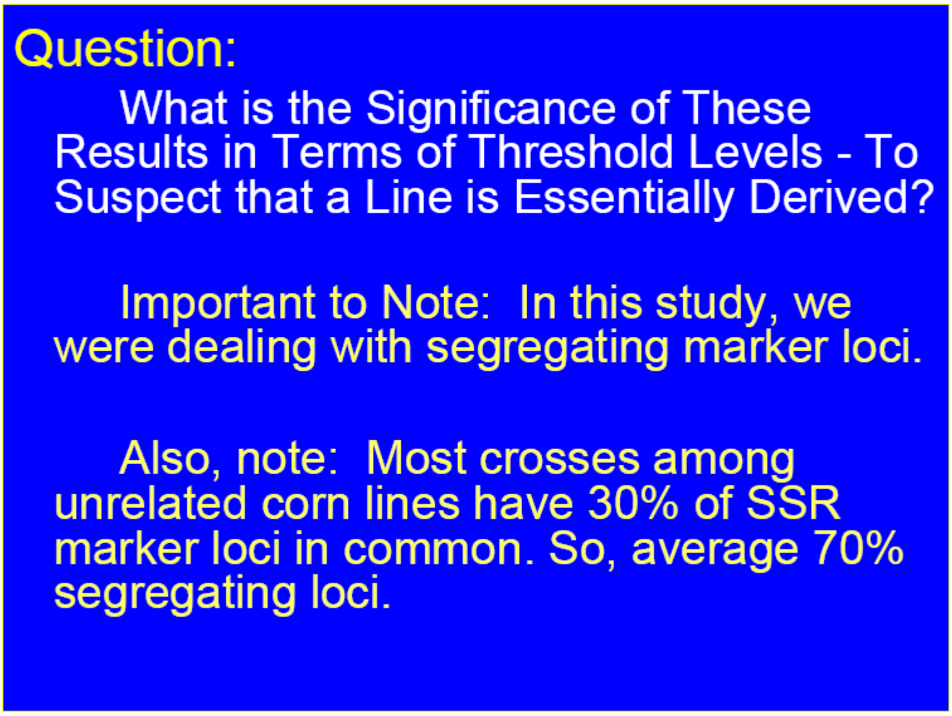


Summaries:

Parental Contrib. to Individual Lines:

BC_1S_1's – at least one received as much as 86% of alleles from one parent. One had 69% when expect 25%. Some similar to F_3 distribution.

BC_1S_4's – at least one received as much as 94% of alleles from one parent. One had 78% when expect 25%. Some similar to F_6 distribution.



Question:

What is the Significance of These Results in Terms of Threshold Levels - To Suspect that a Line is Essentially Derived?

Important to Note: In this study, we were dealing with segregating marker loci.

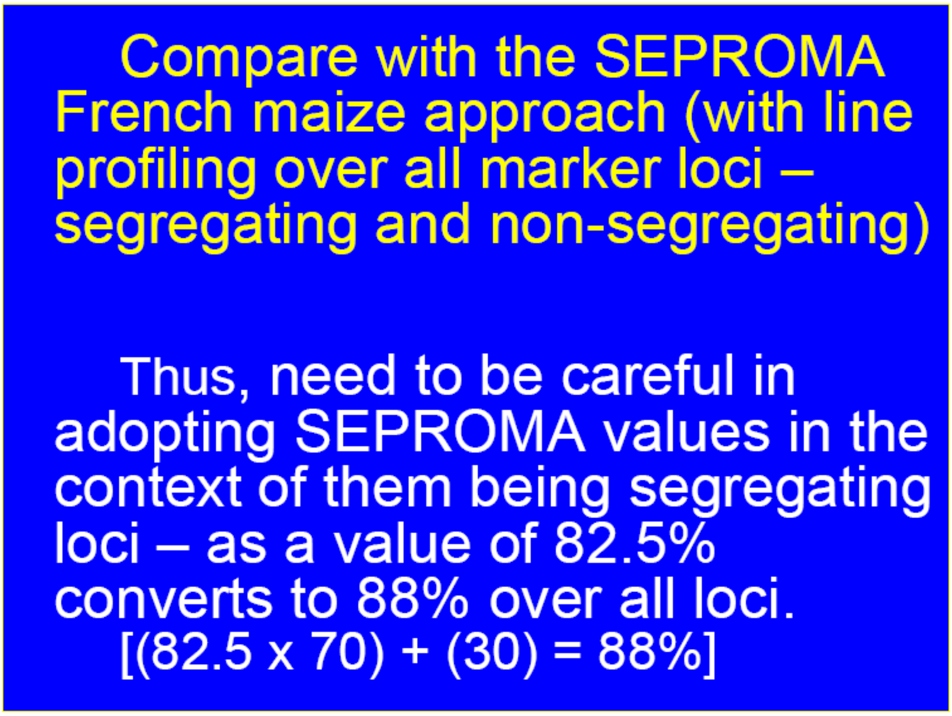
Also, note: Most crosses among unrelated corn lines have 30% of SSR marker loci in common. So, average 70% segregating loci.

Assume 100 SSR marker loci:

Suppose you are comfortable with threshold (boundary) of 75% for segregating loci –

Then, 75% of 70 segregating loci = 52.5 + 30 not segregating = 82.5% over all marker loci.

If 80% of 70 segregating loci = 56 + 30 not segregating = 86% over all marker loci.



Compare with the SEPROMA French maize approach (with line profiling over all marker loci – segregating and non-segregating)

Thus, need to be careful in adopting SEPROMA values in the context of them being segregating loci – as a value of 82.5% converts to 88% over all loci.

[(82.5 x 70) + (30) = 88%]

Need to Consider:

Defining acceptable threshold level for EDV, segregating and non segregating loci important.

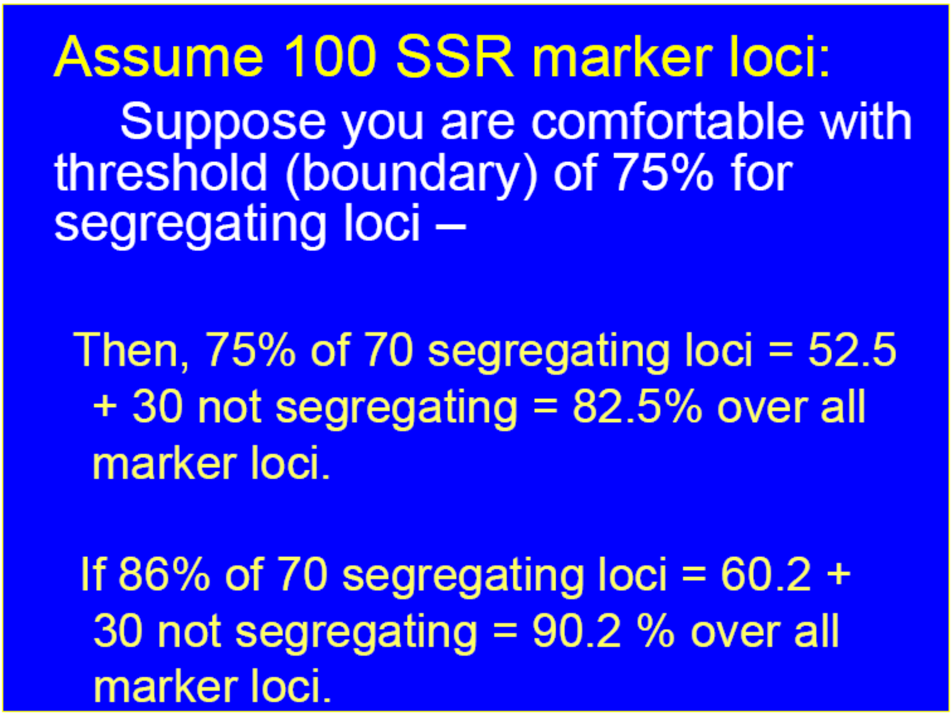
Also, threshold value chosen realistically only triggers need for further information (additional markers, morphological data, pedigree info, etc.)

Parental Contribution Threshold Levels:

(Expect 50%)

	70-75	75-80	80-85	85-90
B73xMo17 - F_6 lines				
Tester B84	1^{*}_{Mo17}			1_{B73}
Tester B97	1_{Mo17}	2_{B73}		1_{B73}
B84xB73 - F_6 lines				
Tester B97	1_{B73}	1_{B73}		

* Number of total of 28 lines

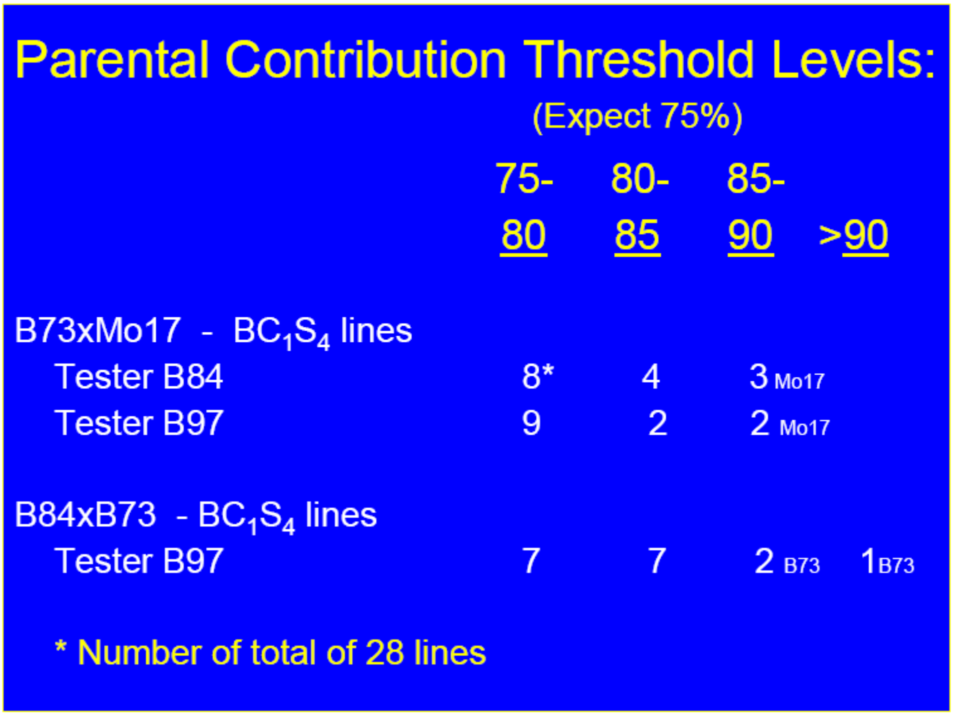


Assume 100 SSR marker loci:

Suppose you are comfortable with threshold (boundary) of 75% for segregating loci –

Then, 75% of 70 segregating loci = 52.5 + 30 not segregating = 82.5% over all marker loci.

If 86% of 70 segregating loci = 60.2 + 30 not segregating = 90.2 % over all marker loci.

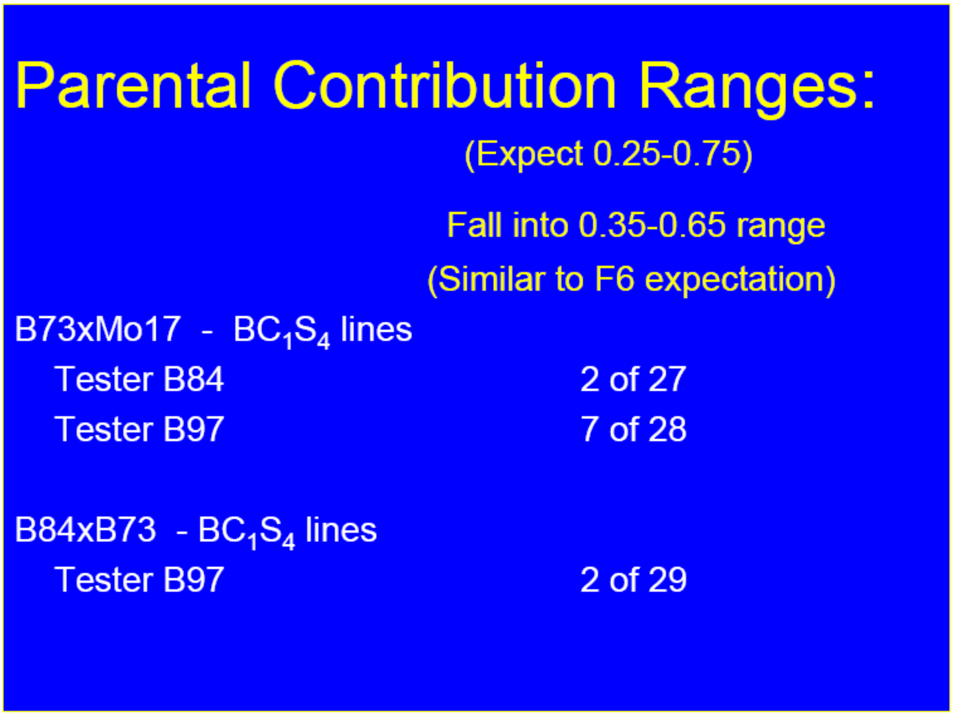


Parental Contribution Threshold Levels:

(Expect 75%)

	75-80	80-85	85-90	>90
B73xMo17 - BC_1S_4 lines				
Tester B84	8*	4	3 Mo17	
Tester B97	9	2	2 Mo17	
B84xB73 - BC_1S_4 lines				
Tester B97	7	7	2 B73	1 B73

* Number of total of 28 lines



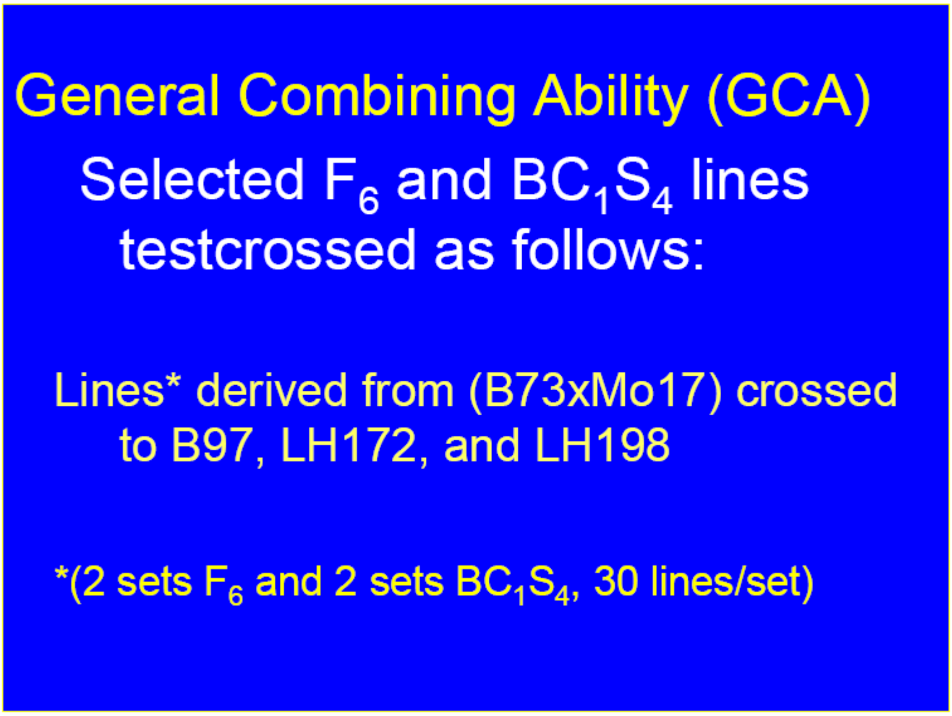
Parental Contribution Ranges:

(Expect 0.25-0.75)

Fall into 0.35-0.65 range

(Similar to F6 expectation)

B73xMo17 - BC_1S_4 lines	
Tester B84	2 of 27
Tester B97	7 of 28
B84xB73 - BC_1S_4 lines	
Tester B97	2 of 29

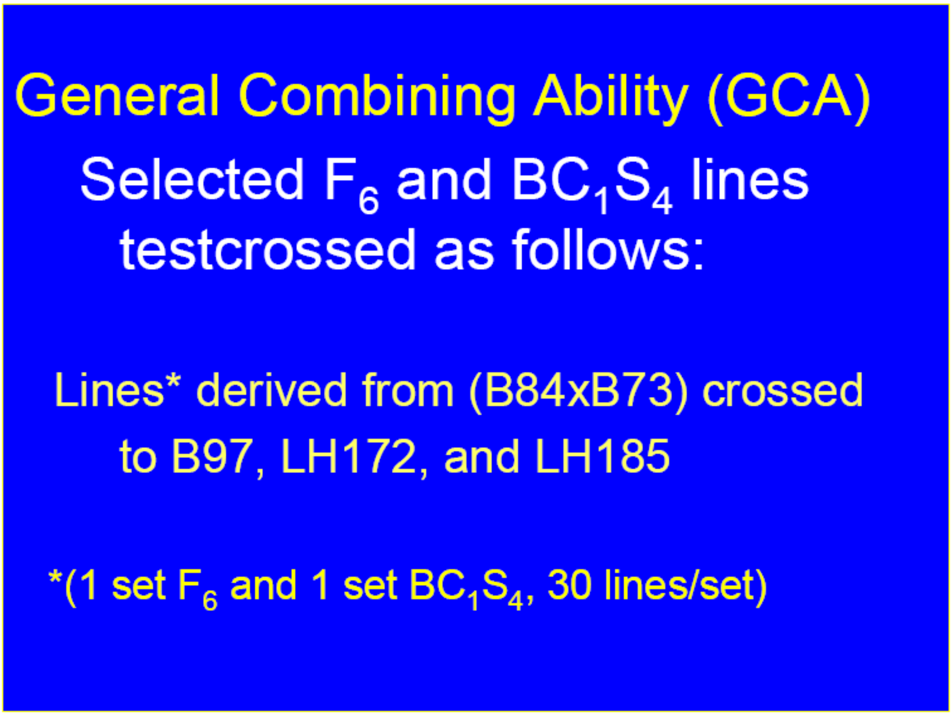


General Combining Ability (GCA)

Selected F_6 and BC_1S_4 lines testcrossed as follows:

Lines* derived from (B73xMo17) crossed to B97, LH172, and LH198

*(2 sets F_6 and 2 sets BC_1S_4, 30 lines/set)

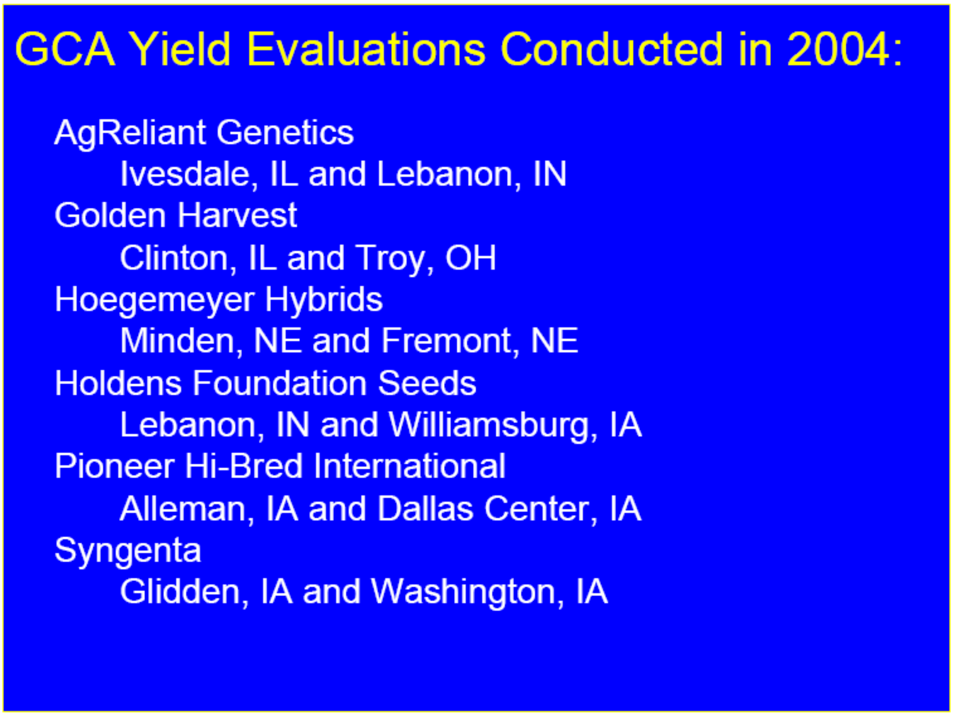


General Combining Ability (GCA)

Selected F_6 and BC_1S_4 lines testcrossed as follows:

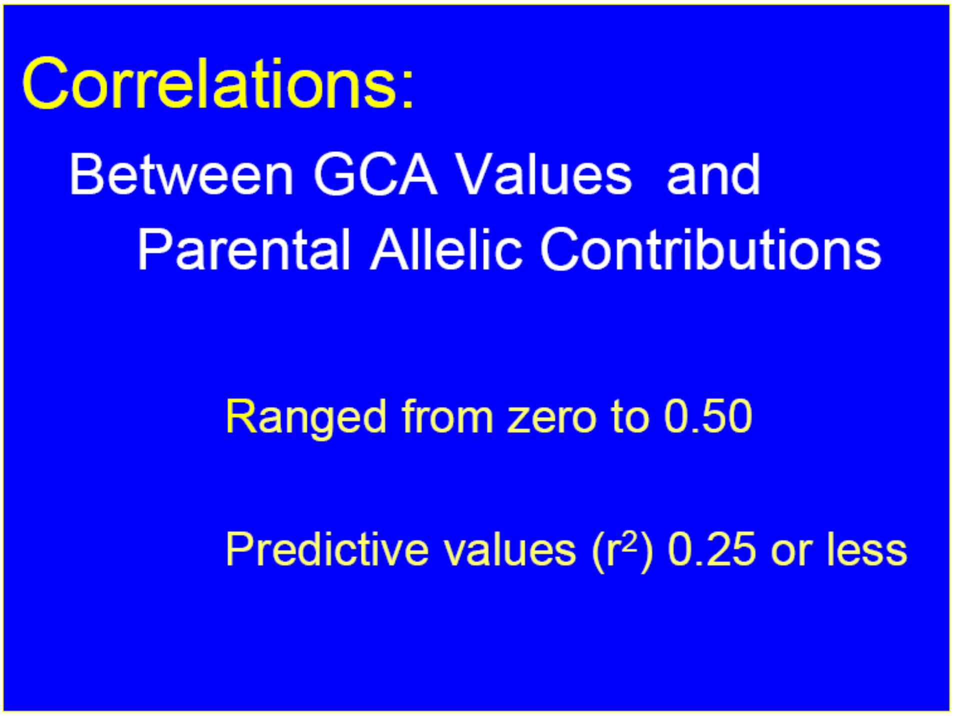
Lines* derived from (B84xB73) crossed to B97, LH172, and LH185

*(1 set F_6 and 1 set BC_1S_4, 30 lines/set)



GCA Yield Evaluations Conducted in 2004:

AgReliant Genetics
    Ivesdale, IL and Lebanon, IN
Golden Harvest
    Clinton, IL and Troy, OH
Hoegemeyer Hybrids
    Minden, NE and Fremont, NE
Holdens Foundation Seeds
    Lebanon, IN and Williamsburg, IA
Pioneer Hi-Bred International
    Alleman, IA and Dallas Center, IA
Syngenta
    Glidden, IA and Washington, IA



Correlations:

Between GCA Values and
Parental Allelic Contributions

Ranged from zero to 0.50

Predictive values (r^2) 0.25 or less

[End of document]