Inbred Line Development and Hybrid Evaluation in GEM Breeding Crosses

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Objectives:

Identify GEM breeding crosses and lines with desirable agronomic characteristics, resistance to abiotic and biotic stresses, and high consistent yield performance.

Materials and Methods:

Seventy GEM breeding crosses were evaluated for adaptability, maturity, flowering synchrony, standability, plant and ear height, pest resistance, stay green, grain quality, and drydown. The major diseases were gray leaf spot and anthracnose stalk rot. S_1 lines from five breeding crosses and S_2 lines from one breeding cross were advanced through a modified single seed descent bulk (MSSD) method. Five hundred twenty-six hybrids were evaluated at an irrigated location in collaboration with the Southern GEM Program.

Results:

A joint project to evaluate GEM breeding crosses was conducted by the University of Delaware, USDA-GEM at Ames, Memphis, TN, and Mycogen Seeds at Mount Vernon, IN. Results and recommendations will be presented jointly by the cooperators at the December TSG GEM meeting. We gave higher ratings and suggest the following GEM crosses to breed with: BR105:N99z, BR105:S162699ag, BR105:S162699aj, BR105:S1641, CML341:S99y, CML341:S99y99ah, DKXL212:S11b46, (GEMS-0147/GEMS-0180)-B, NC354:S99y, CUBA173:S0422, SANM126:N1241, and DKB844:S1601 based on per se rating performance. We also suggest CUBA164:S99y, Ki14:S99ad, NS1:S99aa, Tzi8:N99ac, and Tzi9:S21z to use for making new breeding crosses. Based on per se evaluations for plant height, ear placement, stalk and root strength, ear traits, maturity, disease and ECB resistance, 557 S_2 selections were made from two Stiff Stalk (DKXL212:S0928 and DKXL212:S09) and three non-Stiff Stalk (BR105:N16a16b, CL00331:N1834, and CML329:N1834) breeding crosses that had been advanced from the S_1 stage by a modified single seed descent bulk procedure. Fifty seven S_3 ears were selected from one breeding cross DKXL212:S09(MSSDS1BS2B), that had been advanced from the S_2 stage by a modified single seed descent bulk procedure. We are using a modified single seed descent method to more efficiently advance S_1 families to the S_2 stage and S_3 stages

Evaluation of Breeding Methods using GEM Breeding Crosses:

Four breeding methods, Conventional GEM (**CG**) (pedigree emphasizing family selection), Conventional Mass (**CM**) (pedigree with both family and within family selection and more mass selection within the initial breeding cross), Modified Single Seed Descent (**MSSD**) (bulk of 3 S_1 seeds from each selected S_0 plant from the **CM** selections), and Doubled Haploid (**DH**) were compared using three **GEM** (**G**ermplasm **E**nhancement of **M**aize) breeding crosses: Antig01:N16DE4, AR16035:S0209, and DKXL212:S0943b (Figure 1). Fifty hybrids per method were evaluated in 2007 for yield and agronomic performance using **DH** and S_2 lines crossed to one tester. The selected **DH** and

S_3 lines (~25% selection) were further evaluated on two testers in 2008. Note that the original 50 lines from each method had been selected per se from a larger number of S_1 and **DH** lines based on plant appearance, grain dry down, disease resistance, plant and ear height etc. The **MSSD** S_2 lines were evaluated per se using open pollinated ears with improved seed set compared to hand pollinated ears. Low numbers of **DH** lines were recovered for the two stiff stalk breeding crosses thereby reducing the opportunity for per se selection prior to making testcrosses. There were 229, 133, and 117 **DH** lines recovered for the Antig01:N16DE4, AR16035:S0209, and DKXL212:S0943b breeding crosses, respectively. The low numbers of Stiff Stalk **DH** lines was related to low numbers of DH lines recovered and not problems with the induction phase of the **DH** process.

The **DH** hybrids had a wider range of values in the first year results for yield (Y), yield/moisture (Y/M), and grain moisture (M) as expected based on the greater additive variance among inbred vs. S_2 lines (Table 1, for example). In the **MSSD** method, hybrids had higher grain moisture than the other methods perhaps due to per se observation family selection of the 50 S_2 lines from the original 250 S_2 lines which may have emphasized stay green and consequently later maturity. Although the method means for the second year results were generally not significant for Y, Y/M, and M, the **CM** and **MSSD** methods each accounted for about one third of the top five lines selected based on Y and Y/M across the three breeding crosses; whereas, the **CG** and **DH** methods contributed fewer lines to the top five than were expected. A **MSSD** method utilizing S_3 lines for testcrossing (self S_0 in summer and advance S_1 to S_3 in two winter nurseries in the same growing year or in subsequent nurseries in different growing years) may be an effective and efficient alternative to the **DH** and conventional methods for both increasing the additive variance among lines and developing lines with improved yield and agronomic performance from **GEM** breeding crosses. More complete details are provided in the thesis cited below.

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References:

Jumbo, M.B. 2009. Comparison of Conventional, Modified Single Seed Descent, and Doubled Haploid Breeding Methods for Maize Inbred Line Development using GEM Breeding Crosses. Ph.D Dissertation. University of Delaware. Newark. DE, USA.

Breeding Crosses

ANTIG01:N16DE4, AR16035:S0209, DKXL212:S0943b X **Inducer**

Br. Method/ Stage	CG	CM	MSSD	DH	Spring 2005
S_0	Grow 300 & self 300	Grow 1500 plants & self 500			Summer 2005
S_1	250	160	480 kernels (bulk)	229 Antig01 133 Argentine 117 DKXL212	Winter 2005/06
S_1	250 self & select	160 self & select	250 S_2 lines per se evaluation	DH inbreds evaluate & increase	Summer 2006
S_2 testcross (one tester)	60	60	60	70	Winter 2006/07
Yield test & line advance	50	50	50	50	Summer 2007
S_3 testcrosses (2 testers)	10 + 5	10 + 5	10 + 5	10 + 5	Winter 2007/08
Yield test & line advance	14	14	14	14	Summer 2008

Figure 1. Conventional GEM (CG), Conventional Mass (CM), Modified Single Seed Descent (MSSD), and Doubled Haploid (DH) Breeding Method Schemes.

Table 1. Pooled Range of Method Means for Yield (Y), Yield/Moisture (Y/M), and Grain Moisture (M) for 50 S_2 Entries of DKXL212:S0943b x LH287Bt

	Yield ††Mg ha^{-1}	Y/M	Moisture (%)
†Method	50 Entries Range	50 Entries Range	50 Entries Range
CG	9.9 –12.7	0.47 - 0.67	16.9 – 22.0
CM	10.0 - 13.1	0.49 - 0.72	17.3 – 22.1
MSSD	10.0 –12.7	0.50 - 0.66	17.9 – 21.6
DH	9.2 – 13.0	0.41 - 0.76	15.6 – 23.7
Number of reps	6	6	6
Number of Locations	3	3	3

†**CG** = Conventional GEM, **CM** = Conventional Mass, **MSSD** = Modified Single Seed Descent, **DH** = Doubled Haploid. ††Megagrams per hectare.