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POTENTIAL OF EXOTIC X ADAPTED MAIZE GERMPLASM FOR SILAGE

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ABSTRACT - Maize (*Zea mays* L.) is used extensively as a forage crop. In the U.S., maize is harvested as silage on about 8% of the total maize acreage of approximately 31 million ha. Our objective was to evaluate the impact of introgressing Latin American germplasm provided by the Germplasm Enhancement of Maize (GEM) project into a silage breeding program with respect to both nutritional quality and yield. Beginning in 1995, 29 GEM breeding crosses (50% exotic) were evaluated as populations per se for stover quality. Traits included neutral detergent fiber (NDF), acid detergent fiber (ADF), lignin, in vitro true digestibility (IVTD), crude protein (CP), and in vitro NDF digestibility (NDFD). Thirty-two breeding crosses that were derived from the 11 breeding crosses selected in 1995 (both 50% and 25% exotic) were further evaluated for stover quality in 1996. Two hundred S_1 families were developed from the four most promising 25% exotic breeding crosses, and these were evaluated for stover quality in 1997. The best 20 families were selfed to produce S_2 families that were then topcrossed to the inbred LH198. These 20 topcrosses and five check hybrids were evaluated for whole-plant silage quality and yield in 2000. Milk production potential was also estimated using the MILK2000 prediction system. Topcrosses involving URZM13085:N0204-6 had the highest forage yield and milk ha^{-1} in the 2000 trial (20 Mg ha^{-1} and 26,486 t ha^{-1}, respectively). Other topcrosses involving ARZM17026:N01013-5 and URZM13085:N0204-1 had above-average yield and quality, and the quality gains were mostly due to high NDFD. These findings suggest that there are several GEM breeding crosses with potential to elevate both yield and quality of silage maize germplasm in the U.S.

KEY WORDS: *Zea mays*; Evaluation; Exotic; Germplasm; Silage.

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INTRODUCTION

Maize is one of the most important crops in the world economy. In 2000, 593 million metric tons of maize were harvested from 139 million hectares (FAOSTAT, 2001). Both human consumption and livestock feed are the main uses for this cereal. Plant breeders have contributed substantially to reach this production level, particularly since the inbred-hybrid concept was established and used in maize breeding programs. In general, genetics gains have been estimated to be responsible for at least 50% of total yield gain at the farm level (Duvick and Cassman, 1999).

The use of maize as an ensilaged forage is common in northern temperate regions of the world, particularly in Europe, Canada, and in the northern Corn Belt of the United States (Coors and Lauer, 2001). The U.S. has the largest maize forage area in the world, and Wisconsin is the principal producer state with about 11.9 million tons in 2000 (USDA, 2001). The total maize forage area varies every year, mainly because U.S. farmers and livestock producers grow maize for both grain and silage, and they usually factor in market conditions before deciding to harvest their fields for a specific purpose. Coors and Lauer (2001) emphasized that maize germplasm with adequate grain yield potential will provide the genetic base for future efforts to improve forage potential in the U.S.

The ideal forage crop includes high dry matter yield, high protein content, high energy content (high digestibility), high intake (low fiber), and optimum dry matter content at harvest for acceptable silage fermentation and storage (Carter *et al.*, 1991). Maize silage exhibits all these characteristics, except the high protein level, which is the main nutritional deficiency of maize silage (Sniffen *et al.*, 1992). Genetic variation in stover and whole-plant composition for populations, inbred lines, and hybrids has been reported (ROTH *et al.*, 1970; CARTER *et al.*, 1991; HUNT *et al.*, 1992; WOLF *et al.*, 1993a,b; LUNDVALL *et al.*, 1994; JUNG *et al.*, 1998; COORS and LAUER, 2001). Whole-plant characteristics influencing silage maize quality and yield have received much attention, but there has not been as much effort dedicated to the evaluation of genetic variability in stover composition (CARTER *et al.*, 1991). Since 1930, the increase in maize forage yield and quality in the U.S. can be attributed mostly to the increase in grain yield, and the quality of the stover has not changed appreciably (LAUER *et al.*, 2001). There are greater ranges in stover cell wall content and digestibility among inbred lines than among hybrids (COORS and LAUER, 2001). Consequently, inbred *per se* evaluations could be useful to identify new potential sources with adequate nutritive value for silage breeding. At the University of Wisconsin, current public and historically important inbred lines have been evaluated for stover composition and digestibility (COORS *et al.*, 1992). Several researchers (Gurrath et al.; 1991; Seitz et al., 1992) have reported significant correlations of inbred stover nutritional composition with derived-hybrid stover composition and have, therefore, recommended that inbreds be prescreened for stover composition before testcrosses are evaluated for forage yield in order to preserve testing capacity for the more promising hybrids.

Despite the great genetic diversity in maize around the world, breeders have concentrated their efforts on relatively few races. Even in the U.S., which is responsible for more than 40% of the world's production, breeders work with a very narrow genetic base. GOODMAN (1990) reported that six inbred lines (C103, Mo17, and Oh43 – Lancaster Sure Crop types; A632, B37, and B73 – Reid types) and their close relatives are represented in approximately 70% of all U.S. hybrids. The risk of genetic vulnerability is well known by maize breeders, thus warranting all activities that broaden genetic base of maize. In this regard, considerable efforts have recently been devoted to adapting exotic germplasm to U.S. conditions (HALLAUER, 1978; GOODMAN, 1985).

Beginning in 1987 the Latin American Maize Project (LAMP) involved 12 countries (Argentina, Bolivia, Brazil, Colombia, Chile, Guatemala, Mexico, Paraguay, Peru, Uruguay, U.S., and Venezuela) in the evaluation of 12,133 accessions (SEVILLA and SALHUANA, 1997). LAMP's results led to the development the Germplasm Enhancement of Maize (GEM) project. The GEM project involved public and private sectors in the U.S., and its goal was to broaden the U.S. maize germplasm base by adapting the best temperate and tropical exotic accessions identified in the LAMP project to conditions in the U.S. Corn Belt (POLLAK, 1997; POLLAK and SALHUANA, 1998). The enhancement protocol used by GEM was to initially cross each of the chosen LAMP accessions to an elite proprietary inbred line to make a 50% exotic breeding cross. Crosses with the elite proprietary inbred lines are made by the individual companies who contribute the lines. Crosses are made such that combining abilities identified in the LAMP project are maintained. In other words, if an accession showed a Stiff Stalk combining ability pattern, the elite inbred used to make the breeding cross would be a Stiff Stalk type. The proprietary lines themselves, as well as their exact pedigree, are not available to the other members of the GEM project.

Once the 50% breeding crosses were developed, the more promising were crossed once more to elite proprietary lines in the same manner to produce 25% exotic breeding crosses. For any specific breeding cross, the company contributing the proprietary inbred was different from that one used to produce the 50% breeding cross. As with the 50% breeding crosses, the Stiff Stalk (S) and non-Stiff Stalk (N) combining ability patterns were maintained as determined from the original LAMP evaluations. In some instances, when the combining ability patterns were not clear, both S and N breeding crosses were made from the original accession (POLLAK and SALHUANA, 2001).

The strategy that we chose to evaluate GEM material for silage potential included the following steps. First, we sampled the most productive 50% breeding crosses that had the best chance of being adapted to Wisconsin conditions. Second, based on that preliminary trial we chose the 50% breeding crosses (as well as related materials – 25% breeding crosses) with the most promising stover composition, based on both quality and maturity, for additional evaluation. Third, we developed S_1 families for stover evaluation. The best 20 S_1 families were selfed to the S_2 level and then testcrossed to an elite inbred line. Fourth, the hybrid performance of testcrosses was evaluated based on whole-plant characteristics.

The objectives of this study were to characterize the performance of several of the most promising GEM breeding crosses for fiber composition and digestibility when harvested as forage, and to evaluate the potential of these breeding crosses for silage breeding purposes in the northern U.S. Corn Belt.

TABLE 1 - *Maize accessions used and their racial classification.*

Country	Race	Accession
Argentina	Dentado Blanco Rugoso	ARZM01150
	Dentado Blanco	ARZM03056
	Cristalino Colorado	ARZM13035, ARZM16021, ARZM16026, ARZM16035, ARZM17026, ARZM17056
Chile	Camelia	CHZM04030, CHZM05015
USA	Southern Dent	FS8-AS (Mixed), FS8-AT (Mixed), FS8-BT (Mixed)
	Corn Belt Dent	CASH, Golden Queen
Uruguay	Semidente Riograndense	URZM05017
	Dente Branco	URZM10001, URZM11002, URZM13010
	Cateto Sulino	URZM13085, URZM13088

MATERIAL AND METHODS

Field trials

1995 evaluations

In 1995, the UW GEM project evaluated silage nutritional value for 29 breeding crosses (50% exotics) derived from 21 LAMP accessions (Table 1). Photoperiod sensitivity is critical for maize development in temperate areas. Therefore, accessions and breeding crosses suitable for Wisconsin conditions were considered to initiate this study. These populations and three checks were evaluated at two locations, Madison and Arlington, WI. The experimental design for both trials was a randomized complete block with three replications in each location. Plots consisted of two rows 5.5 m long and 0.76 m between rows planted at a density of 68,860 plants ha^{-1}. The trials were harvested at approximately 300 to 400 g kg^{-1} whole plant dry matter. Ears were removed from one row, which was then harvested as stover. Each row was mechanically harvested using a one-row forage chopper. The fresh weight was recorded for each harvested row and a 1-kg sample was dried at 50°C for 7 d for moisture determination and quality analyses.

1996 evaluations

In 1996, the UW GEM project analyzed 32 breeding crosses for silage nutritive value. These breeding populations included 11 selected 50% breeding crosses based on 1995 results, and 21 25% breeding crosses that were developed from those 11 populations. These populations and eight checks were evaluated in Madison and Arlington, WI. The experimental design for both trials was a randomized complete block with three replications in each location. Plots were one row 5.5 m long and 0.76 m between rows planted at a density of 68,860 plants ha^{-1}. The breeding crosses were stagger-planted over three planting dates according to their maturity, so that they would be at a common physiological stage at harvest. At approximately 300 to 400 g kg^{-1} whole plant dry matter content, ears were removed from each row, and each row was then harvested as stover alone. Samples (1-kg) were collected and dried for quality analysis as in 1995. In addition, all of the 25% breeding crosses were placed in the UW nursery for selfing to develop S_1 families for further testing.

1997 evaluations

Based on results from 1996, 217 S_1 families from ARZM17026:N1019 (49 S_1 families), ARZM17026:N1013 (86 S_1 families), URZM13085:N0204 (46 S_1 families), and URZM13085:N0204 (46 S_1 families) were selected for inbred *per se* stover evaluation in 1997. These S_1 families and checks were evaluated at Madison, WI, using a randomized complete block design with three replications. Plots consisted of one row 5.5 m long with 0.76 m between rows planted at a density of 68,860 plants ha^{-1}. These plots were harvested at the mid-silk stage (<200 g kg^{-1} whole plant dry matter content) rather than at 300 to 400 g kg^{-1} whole plant dry matter content, the stage at which hybrids and populations are normally harvested for silage. The mid-silk stage was used in order to avoid confounding effect of stover composition with ear-fill effects, which can be pronounced in inbred evaluations. COORS *et al.* (1997) observed great variation in stover composition due to ear-fill effects and suggested this stage to obtain a more reliable evaluation of the stover composition. Samples were analyzed for composition during the winter of 1997 and spring of 1998. A quality index, weighted by heritability of each quality measure, was used to evaluate S_1 families.

2000 evaluations

Based on S_1 families evaluation in 1997, the best 20 (derived from four 25% breeding crosses) were selfed to the S_2 level. In 1999, these S_2 families were crossed to LH198. In 2000, these 20 topcrosses and five checks were evaluated at two locations, Madison and Arlington, WI. The experimental design used was a randomized complete block with two replications at each location. Plots consisted of two rows 5.5 m long and 0.76 m between rows. Trials were harvested at approximately 300 to 400 g kg^{-1} whole plant dry matter. Each row was mechanically harvested using a one-row forage chopper. The fresh weight was recorded for each harvested row, and a 1-kg sample was dried at 50°C for 7 d for moisture determination and quality analyses.

Laboratory procedures for quality analysis

All chemical and digestibility constituents are reported on a dry matter basis. Near infrared reflectance spectroscopy (NIRS) was used to predict all constituents. In 1995, an internal NIRS calibration set was developed for stover concentrations of neutral detergent fiber (NDF), acid detergent fiber (ADF), and lignin. Crude protein (CP) and in vitro true digestibility (IVTD) were estimated using the UW Department of Agronomy global NIRS calibration set developed in the 1992 and 1993 growing seasons (LAUER *et al.*, 2001). In 1996, an internal NIRS calibration set was developed for stover NDF, ADF, lignin, CP, and IVTD. In 1997, an internal NIRS calibration set was developed for stover NDF, CP, and IVTD. In 2000, whole-plant NDF, CP, IVTD, and starch were estimated using an updated global NIRS calibration set developed over the 1992 to 1998 growing seasons (http://uwsilage-breeding.agronomy.wisc.edu).

Standard NIRS procedures were used to select calibration sets for wet laboratory analyses (MARTENS and NAES, 1989; SHENK and WESTERHAUS, 1991; 1994). Assays for NDF, ADF, lignin (permanganate method), and IVTD were conducted as described by GOERING and VAN SOEST (1970) with two modifications. The modification of the NDF procedure was the treatment of samples with 0.1 ml of alpha-amylase during refluxing and again during sample filtration (MERTENS, 1991). The modified 48-hour fermentation IVTD procedure was performed in centrifuge tubes as described by MARTEN and BARNES (1980), but buffer and mineral solutions were those described by GOERING and VAN SOEST (1970). Tubes were put in a freezer after they were removed from the incubator, and the NDF procedure previously described was used to eliminate undigested residues. Crude protein was calculated by multiplying total nitrogen (BREMNER and BREINTENBECK, 1983) by 6.25.

NDF and IVTD estimates were used to calculate neutral detergent fiber digestibility (NDFD) by the following equation (VAN SOEST, 1982):

$$NDFD = \{[NDF - (100 - IVTD)]/NDF\} \times 100$$

From the data obtained in the laboratory, prediction equations were developed relating NIR wavelengths to each of the quality variables (SHENK and WESTERHAUS, 1991; 1994). High coefficients of multiple determination and low standard error of calibration and cross validation were considered to select equations.

For the whole-plant analyses in 2000, milk Mg^{-1} of forage and milk ha^{-1} were estimated based on the MILK2000 equations (www.wisc.edu/dysci) developed by UW Agronomy and Dairy Science Departments. MILK2000 uses forage composition (NDF, IVD, NDFD, CP, and starch) to estimate potential milk production. MILK2000 silage performance indices (milk Mg^{-1} of forage and milk ha^{-1}) are calculated using the energy content (NEL) of maize silage, which is estimated using a modification of a published summative energy equation (WEISS *et al.*, 1992).

RESULTS AND DISCUSSION

1995 evaluations

The most desirable genotype is one with low stover NDF, ADF, and lignin, and high stover CP, IVTD, and NDFD. Breeding populations differed for all stover yield and quality measurements, except lignin (Table 2). The range in the dry matter yield among entries was 12.7 Mg ha^{-1}. The highest yielding breeding crosses were URZM11002:S14 (17.3 Mg ha^{-1}) and FS8A(T):N18 (17.0 Mg ha^{-1}). Stover moisture varied from 512 to 705 g kg^{-1}, and checks had lower values than GEM breeding crosses. The breeding cross FS8B(T):N18 had the lowest values of NDF (574 g kg^{-1}) and ADF (322 g kg^{-1}). These means were lower than those reported by LAUER *et al.* (2001) for stover yield and quality performance of maize cultivars developed in different eras in the northern U.S. Corn Belt. Breeding crosses derived from Argentinian accessions exhibited a relatively high CP on average. Low protein content has been considered the most limiting nutritional factor for maize silage (SNIFFEN *et al.*, 1992). However, CARTER *et al.* (1991) emphasized that protein is not the main factor for maize silage evaluation because silage-based rations can be readily supplemented with other protein sources. Forage CP concentration has not changed significantly in the northern U.S. Corn Belt cultivars since 1930 (LAUER *et al.*, 2001).

The check population WFISILO C3 had the highest means for IVTD (725 g kg^{-1}) and NDFD (585 g kg^{-1}). WFISILO C3 was developed using three cycles of S_1 family selection for decreased fiber (NDF and ADF) and lignin concentration of stover tissue at mid-silk stage. This was accomplished in previous research evaluating the relationship of fiber composition and resistance to the European corn borer [*Ostrinia nubilalis* (Hübner)] (OSTRANDER and COORS, 1997). Therefore, WFISILO C3 represents the attainable potential for selection based on improved stover composition. Two breeding crosses, FS8A(T):N18 and URZM13085:N02, did not differ significantly from WFISILO C3 for IVTD. All breeding crosses with 50% exotics had lower means than the checks for NDFD.

Additional agronomic observations, such as days from July 1 to mid-pollen date (data not provided) and ear percentage, showed that many of the 50% breeding crosses were not adapted to conditions in Wisconsin. The large range in maturity across populations may have influenced the laboratory assessments of nutritive value in 1995. Therefore, based on agronomic performance in Wisconsin in 1995, the following breeding crosses were sampled for evaluation in 1996: ARZM01150:N04, ARZM16021:S09, ARZM16035:S19, ARZM17026:N10, ARZM17056:S12, CHZM04030:S09, CHZM05015:N15, GOQUEEN:N16, URZM1001:N17, URZM13085:S19, and URZM13085:N02. Among the 11 selected breeding crosses, URZM10001:N17 had notably higher nutritional value. This population had low NDF, ADF, and lignin concentrations, and high protein. Its low cell wall components concentrations indicate that it may have high intake potential.

1996 evaluations

In 1996, the UW GEM project analyzed 32 breeding crosses including 11 50% exotics that were selected in 1995 and 21 25% exotics that were developed from them. In 1995, the trial was not stag-

TABLE 2 - *Mean values for stover yield, stover moisture, and stover composition*[λ] *for 29 GEM breeding crosses of maize and three checks averaged over two WI environments in 1995.*

GEM Breeding Cross*	Dry matter yield	Moisture	NDF	ADF	Lignin	CP	IVTD	NDFD	EAR%[δ]
	Mg ha^{-1}				g kg^{-1}				%
ARZM01150:N04	12.1	667	586	324	42	82	706	497	42.2
ARZM03056:N09	14.6	671	583	335	45	86	698	491	35.9
ARZM13035:S11b	13.9	648	588	325	44	78	706	492	37.1
ARZM16021:S09	10.8	682	625	353	45	68	694	511	49.2
ARZM16026:S17	13.4	705	579	330	44	85	707	501	36.8
ARZM16026:N12	12.4	694	648	369	49	81	696	531	45.8
ARZM16035:S19	13.4	678	603	339	44	74	706	515	37.7
ARZM16035:S02	13.3	679	592	334	43	74	706	508	33.2
ARZM17026:N10	11.1	689	608	343	43	80	705	517	50.2
ARZM17056:S16	10.8	655	631	358	49	75	694	518	41.3
ARZM17056:S12	13.4	671	601	340	42	78	707	518	37.0
CHZM04030:S09	11.9	663	620	351	46	66	692	505	47.0
CHZM05015:N15	9.9	670	623	351	44	80	701	517	45.7
CHZM05015:N12	12.0	676	638	362	46	79	700	530	44.2
FS8A(S):S09	13.0	677	602	338	45	69	691	484	41.1
FS8A(T):N18	17.0	662	585	323	43	80	713	505	23.7
FS8B(T):N18	15.2	671	574	322	43	80	701	482	40.3
FS8B(T):N11a	14.9	633	588	327	43	80	700	497	37.7
URZM05017:S04	14.3	666	598	333	44	80	699	495	35.8
URZM10001:S18	15.5	668	586	330	44	78	698	486	35.5
URZM10001:N17	13.4	666	587	327	42	83	706	507	42.4
URZM11002:S14	17.3	659	582	327	43	81	702	494	32.4
URZM13010:S13	12.7	658	608	341	45	79	694	497	40.8
URZM13010:N06	12.9	661	615	345	44	75	693	495	38.4
URZM13085:S19	13.7	684	599	334	44	75	708	512	42.2
URZM13085:N02	13.4	685	594	330	42	76	709	511	42.9
URZM13088:S06	12.1	658	618	347	43	70	701	521	41.4
CASH:N14	10.3	657	635	349	43	69	692	508	45.4
GOQUEEN:N16	11.2	666	634	356	45	65	695	519	44.8
Checks									
J4120	7.9	520	645	345	41	69	718	566	50.1
P3737	7.2	585	703	392	49	66	694	557	52.0
WFISILO C3	4.6	512	644	353	44	78	725	585	47.4
LSD (0.05)	0.8	34	36	26	NS	6	16	22	9.6
CV(%)	5.4	4.4	5.3	6.8	10.4	7.1	2.0	3.8	20.4

* 50% exotic breeding cross = Accession; S (cross with Stiff Stalk) and N (cross with non-Stiff Stalk); two digits are the cooperator code.
[λ] NDF = Neutral detergent fiber; ADF = Acid detergent fiber; CP = Crude Protein; IVDT = In vitro true digestibility; NDFD = Neutral detergent fiber digestibility.
[δ] EAR% = 100[(whole-plant weight – stover weight) / whole-plant weight].

ger planted to overcome confounding by maturity, and the 1996 results likely provide a more reliable measure of composition. WQS C0 was developed by crossing WFISILO C3 with two U.S. Corn Belt inbreds with good stover nutritional value, H99 and Mo17. Thus, of the eight check entries, WQS C0 represents the optimum overall stover composition (Table 3). In 1995, URZM10001:N17 had high protein concentration, as well as low NDF, ADF, and lignin concentrations. However, in 1996, even though protein concentration remained high for URZM10001:N17 and its related 25% breeding cross (URZM10001:N1702), several other advanced breeding crosses had better overall composition.

Breeding populations differed for all quality measurements (Table 3). Among 50% exotic breeding crosses, URZM13085:N02 showed the most promising values for cell wall components (NDF, ADF, and lignin) and digestibilities (IVTD and NDFD). This population had an average CP. SALHUANA *et al.* (1998) reported on breeding potential of maize accessions from Argentina, Chile, USA, and

TABLE 3 - *Mean values for stover composition for 32 GEM breeding crosses of maize and eight checks averaged over two WI environments in 1996.*

GEM Breeding Cross*,λ	Neutral detergent fiber	Acid detergent fiber	Lignin	Crude protein	In vitro true digestibility	Neutral detergent fiber digestibility
	g kg⁻¹					
ARZM01150:N04	591	329	40	73	705	500
ARZM16021:S09	622	347	44	68	677	481
ARZM16035:S19	589	332	42	71	701	492
ARZM17026:N10	613	345	40	75	692	497
ARZM17056:S12	584	329	40	75	705	490
CHZM04030:S09	586	325	41	71	712	510
CHZM05015:N15	615	346	42	69	692	499
GOQUEEN:N16	606	345	42	67	695	496
URZM10001:N17	582	324	40	76	704	493
URZM13085:S19	567	315	38	72	722	510
URZM13085:N02	564	316	36	72	736	533
ARZM01150:N0420	582	321	43	74	711	504
ARZM16035:S1910	579	324	39	74	715	509
ARZM17026:N1019	566	319	38	79	727	518
ARZM17026:N1013	595	331	39	71	710	511
ARZM17056:S1216	608	344	45	68	689	488
ARZM17056:S1217	631	350	43	75	688	505
ARZM17056:S1219	579	325	42	74	710	498
ARZM16021:S0908b	597	333	42	73	693	485
ARZM16021:S0913	605	339	44	70	693	493
ARZM16021:S0915	586	325	42	73	704	495
CHZM04030:S0906	630	351	44	69	683	497
CHZM04030:S0916	642	359	48	66	670	486
CHZM04030:S0917	608	332	40	72	697	502
GOQUEEN:N1612	611	341	41	68	687	488
GOQUEEN:N1603	639	356	45	64	680	500
URZM13085:S1906	613	341	42	69	694	501
URZM13085:N0204	571	317	39	75	723	515
URZM13085:S1912	584	326	39	72	712	507
URZM13085:N0207	609	343	41	72	712	527
URZM10001:N1702	604	332	40	77	704	511
URZM10001:N1708b	619	346	43	69	686	492
Checks						
J4120	671	370	46	61	661	496
P3737	658	372	45	64	681	515
P3573	639	359	42	63	684	505
C4327	612	343	42	74	703	514
H99 x Mo17	601	337	41	68	700	500
B73 x WQS C0	587	336	42	71	712	510
WQS C0	595	332	37	74	720	530
B86 x DE811	619	340	43	72	682	487
LSD (0.05)	32	19	4	5	20	19
CV(%)	5.5	6.0	10.5	6.9	3.0	3.9

* 50% exotic breeding cross = Accession; S (cross with Stiff Stalk) and N (cross with non-Stiff Stalk); two digits are the cooperator code.
λ 25% exotic breeding cross = Accession; S (cross with Stiff Stalk) and N (cross with non-Stiff Stalk); first two digits are the first cooperator code; second two digits are the second cooperator code.

Uruguay. Their results indicated that the accession URZM13085 had outstanding grain yield when topcrossed to Oh43 x Mo17. Our results showed that URZM13085, consisting of 50% non-Stiff Stalk germplasm, could also be useful for silage breeding. Among the 25% breeding crosses, two (ARZM17026:N1019 and URZM13085:N0204) had high overall nutritive value equivalent to WQS C0.

ARZM17026:N1019 also had the highest CP concentration of all entries. SALHUANA *et al.* (1998) had previously emphasiszed the high *per se* grain yield of accession ARZM17026 in evaluations conducted by LAMP in Argentina, Chile, USA, and Uruguay.

The 50% exotic breeding populations tended to be slightly higher quality than the 25% exotic breeding crosses, on average, but there was not a consistent trend across breeding populations. For example, the breeding crosses ARZM17026:N1019 and ARZM17026:N1013 (25% exotic) had better quality than ARZM17026:N10 (50% exotic), with the exception of CP in ARZM17026:N1013. On the other hand, the breeding cross URZM13085:N02 (50% exotic) had higher quality than URZM13085:N0204 and URZM13085:N0207 (25% exotic), except for CP in URZM13085:N0204.

1997 evaluations

Based on 1996 results, 217 S_1 families from ARZM17026:N1019, ARZM17026:N1013, URZM13085:N0204, and URZM13085:N0207 were selected for inbred *per se* stover evaluation in 1997. Breeding crosses ARZM17026:N1013 and URZM13085:N0207 were included because of their close relation to the other two and because all populations tracing to URZM13085:N02 had excellent NDFD.

The mean of all S_1 families was slightly inferior in nutritive value to the mean of the three public inbred lines used as checks (Table 4). However, the top 20 S_1 families means were superior to the checks for all traits, except CP. The best S_1 family, from URZM13085:N0204, showed particularly low NDF, along with relatively high IVTD and NDFD. Unfortunately, this family had low CP. Among the breeding crosses, URZM13085:N0204 showed the best overall stover composition. The best performance by the nutritional index was observed for the brown midrib commercial hybrid F657. The bm_3 allele is known for reduced lignin and increased digestibility (COORS and LAUER, 2001). However, brown midrib maize hybrids usually yield 20 to 25% less grain and 10 to 15% less stover than their normal counterparts and have increased susceptibility to stalk lodging (LUNDWALL *et al.*, 1994).

2000 evaluations

GEM topcrosses differed for all whole-plant forage yield, quality and estimated milk production measurements (Table 5). The topcross with URZM13085:N0204-6 had a higher dry matter yield (20.0 Mg ha^{-1}), as well as higher NDFD and CP than the highest yielding check NK4687 (17.8 Mg ha^{-1}), a "leafy" hybrid. NK4687 contained a dominant leafy gene that tends to increase the number of leaves above the ear by four or more when compared with normal maize (SHAVER, 1983). Approximately 16% of North American silage production is from leafy hybrids (DWYER *et al.*, 1998). However, COORS and LAUER (2001) emphasized that more studies are needed to confirm that leafy hybrids have nutritional advantages other than possible increase in whole-plant yield.

Among 20 GEM topcrosses, ranges were 81 g kg^{-1} for NDF, 58 g kg^{-1} for IVTD, and 53 g kg^{-1} for NDFD. In general, these NDF, IVTD, and NDFD ranges were less than those reported by WOLF *et al.* (1993a), who observed ranges of 143 g kg^{-1} for NDF, 106 g kg^{-1} for IVTD, and 115 g kg^{-1} for NDFD among S_2 families derived from exotic germplasm. On the other hand, our ranges were greater than those they reported for the 24 LH74 topcrosses involving these S_2 families, which were 60 g kg^{-1} for NDF, 28 g kg^{-1} for IVTD, and 43 g kg^{-1} for NDFD. Among commercial hybrids, ALLEN *et al.* (1990) reported ranges of 90 g kg^{-1} for NDF, 47 g kg^{-1} for IVTD, and 72 g kg^{-1} for NDFD.

GEM topcrosses with LH198 showed high predicted potential for increased milk production using the MILK2000 animal response model for Milk Mg^{-1} forage and Milk ha^{-1} (Table 5). Several GEM topcrosses had excellent silage potential. In particular, URZM13085:N0204-6 had the highest forage yield and milk ha^{-1} in the trial (20.0 Mg ha^{-1} and 26,486 Milk ha^{-1}). Others, such as ARZM17026:N1013-5 and URZM13085:N0204-1, had above-average forage yield as well as nutritional quality, mostly due to high NDFD. From these data alone, however, it is difficult to attribute silage potential solely to the GEM parent since all testcrosses involved LH198 as one of the parents. From previous evaluations of the inbred B73, which is closely related to LH198, and other inbreds derived from the Stiff Stalk Synthetic (COORS and LAUER, 2001), there is little indication that LH198 would impart exceptional nutritional quality to testcrosses.

In general, these preliminary evaluations suggest that several GEM breeding crosses have good potential to contribute to silage breeding in the northern U.S. Corn Belt. The most promising results were observed with 25% exotic breeding crosses, particularly with accessions from Argentina and Uruguay that showed the best performance for Wisconsin conditions (Table 5).

TABLE 4 - *Summary of mean values for stover composition traits from maize stover, for 217 S_1 families derived from four GEM breeding populations and five checks evaluated in 1997.*

Entry	Neutral detergent fiber (NDF)	In vitro true digestibility (IVTD)	Neutral detergent fiber digestibility (NDFD)	Crude protein (CP)	Index$^{\phi}$
	g kg^{-1}				
All S_1 families (217)	698	705	573	134	444
Top 20 S_1 Families	678	738	613	131	482
Best S_1 (UR13085:N0204)	656	768	646	125	515
Breeding cross:					
AR17026:N1013 (86)	686	704	570	132	444
AR17026:N1019 (49)	694	700	568	137	441
UR13085:N0204 (46)	687	710	579	137	453
UR13085:N0207 (36)	695	706	578	133	447
WQS C0	633	780	654	118	527
F657(bm_3)	691	813	729	122	565
Public inbreds (3)	680	720	589	138	464
LSD (0.05)	30	39	48	12	
CV(%)	2.7	3.5	5.2	5.7	

$^{\phi}$ Index = (0.41) IVTD + (0.51) NDFD + (0.38) CP – (0.27) NDF ; Each term was weighted by its heritability.

TABLE 5 - *Means of whole-plant forage yield and moisture, whole-plant composition, and estimated milk production for twenty S_2 maize families topcrossed to LH198 and five checks average over two WI environments in 2000.*

GEM Breeding Cross	Dry matter yield	Moisture	Neutral detergent fiber	In vitro true digestibility	Neutral detergent fiber digestibility	Crude protein	Milk Mg^{-1}	Milk ha^{-1}
	Mg ha^{-1}	g kg^{-1}	kg Mg^{-1}	kg ha^{-1}				
ARZM17026:N1019-1	17.1	690	508	708	425	76	1078	22 638
ARZM17026:N1019-2	17.5	692	511	709	431	72	1073	22 921
ARZM17026:N1019-3	18.7	729	569	676	431	76	1001	22 935
ARZM17026:N1013-1	12.9	675	535	699	437	73	1041	16 417
ARZM17026:N1013-2	12.4	670	489	734	456	73	1139	17 249
ARZM17026:N1013-3	15.3	680	488	722	430	75	1126	20 898
ARZM17026:N1013-4	11.0	631	518	711	443	70	1029	13 695
ARZM17026:N1013-5	16.8	669	507	729	466	77	1128	23 561
ARZM17026:N1013-6	14.5	652	517	715	450	74	1067	18 810
URZM13085:N0204-1	16.4	688	525	719	464	78	1130	22 852
URZM13085:N0204-2	17.7	692	517	706	435	77	1081	23 629
URZM13085:N0204-3	16.1	677	498	720	437	71	1117	22 000
URZM13085:N0204-4	16.7	677	539	684	413	73	994	19 944
URZM13085:N0204-5	16.9	710	543	686	423	75	1015	20 813
URZM13085:N0204-6	20.0	709	530	703	440	72	1079	26 486
URZM13085:N0204-7	15.0	702	504	709	423	69	1100	19 859
URZM13085:N0204-8	17.8	705	528	707	443	74	1083	23 462
URZM13085:N0204-9	16.3	699	507	706	420	76	1069	21 489
URZM13085:N0204-10	16.2	694	519	702	425	79	1061	20 804
URZM13085:N0207-1	17.9	702	531	691	418	75	1035	22 857
Checks								
F657 (brown midrib)	12.3	699	479	753	484	73	1260	18 609
NK4687 (Lfy)	17.8	648	519	702	427	67	1044	22 857
P33A14	17.2	690	543	686	422	73	1018	21 521
P35R58	17.2	674	536	686	415	70	1021	21 416
Dairyland Stealth 1297	13.8	532	472	727	420	73	1048	17 539
LSD (0.05)	3.4	40	49	33	31	6	100	5 738
CV%	14.8	8.7	6.8	3.3	5.0	5.8	6.6	18.9

LAUER *et al.* (2001) reported that since 1930 forage quality in northern Corn Belt hybrids has improved at the rate of 3.0 kg Mg^{-1} forage y^{-1}, and when combined with yield, has increased by 156 kg milk ha^{-1} y^{-1}. These gains in nutritional quality and productivity were mostly unintentional and were based mostly on increased grain yield because there have been no significant silage breeding programs in the U.S. until recently. The GEM evaluations reported here show that there is tremendous potential for accelerating the improvement in silage quality by using selection procedures that directly utilize nutritional components in germplasm hitherto ignored by maize breeders.

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