How Do Advances in Corn Breeding Improve the Corn for Silage?

World Dairy Expo 2017
Dairy Forage Seminar Stage
Natalia de Leon – Department of Agronomy – University of Wisconsin

October 5th, 2017
Outline

✧ Silage Breeding and the UW Program?
✧ Tools to Increase Breeding Outcomes
✧ Future Challenges
Demand for Silage?

✧ While income growth in emerging economies is projected to be weaker, increased global population is expected to increase demand for dairy products.
Seed to Seed: 800X Biomass Return

~30 kg seed/ha

~12 Mg/ha vegetative biomass at flowering

~75 days

~12 Mg/ha grain

~45 days
Relative Contribution of Grain vs Stover

~$130 / ton VS ~$50 / ton
Has Harvest Index Remained Constant in Corn?

Grain and stover yields increased across decades.
Variation for Stover Yield Among Elite Grain Hybrids

*Equivalent for grain yield and flowering time

Where is Biomass Quality Coming From?

- **Comparison:**
  - $bm3$ (=COMT) vs isoline ~10 to 20% increase in NDFD
  - Increase blade sheath by 50% ~5% increase in NDFD
Relationship between Digestibility and Anatomical Traits

Genotypes with low sugar release

Genotypes with high sugar release
Silage Production and the UW Program

火花 Approximately 7% of the corn acreages harvested in the U.S. in 2016 were silage acres and WI is the largest producer with ~790,000 acres
火花 The UW program focuses on the development of corn varieties with enhanced compositional attributes and forage yield
   火花 High yield
   火花 High energy (high digestibility)
   火花 High intake potential (low fiber)
   火花 High protein
   火花 Proper moisture at harvest for storage
Scope of the Program

✴ Between 2,000 and 3,000 evaluation plots are dedicated to the silage breeding program yearly
✴ Evaluation includes two main locations – West Madison and Arlington, WI
✴ Advanced lines are evaluated by the UW Extension Program at an additional 3 to 4 location based on relative maturity
✴ Additional silage plots are dedicated to silage research activities which varies from year to year
✴ Release more than 8 breeding populations, UW NIRS silage quality prediction equations and 25 inbred lines since inception
**Selection Criteria – MILK 2006**

2005 EXPT WQ5198 - Forage yield and nutritional evaluation (Maddock and Arlington)

<table>
<thead>
<tr>
<th>Entry</th>
<th>Dry matter</th>
<th>Yield</th>
<th>NDF</th>
<th>IVD</th>
<th>IVNDFD</th>
<th>Protein</th>
<th>Starch</th>
<th>Milk/ton</th>
<th>Milk/acre</th>
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<td>47.8</td>
<td>80.6</td>
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<td>8.41</td>
<td>45.7</td>
<td>80.4</td>
<td>67.1</td>
<td>7.91</td>
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**University of Wisconsin Corn Silage Evaluation System**

Field Tests Lab Tests

http://www.uwex.edu/ces/dairynutrition/documents/milk2006cornsilagev.xls
Quality Analysis Methods

✧ **Neutral detergent fiber (NDF); Acid detergent fiber (ADF); Acid detergent lignin (ADL) and In vitro true digestibility (IVTD) following Goering and Van Soest, 1970 with modifications (ANKOM system)**

✧ **Protein** = Measure nitrogen using the Leco FP-528 nitrogen analyzer (N × 6.25)

✧ **Starch** = Predicted using whole plant silage global NIRS equation
2016 NIRS Global Equation Calibration

2016 NDF (GBL – LAB)
- 1586 samples
- RSQ = 0.865

2016 ADF (GBL – LAB)
- 1586 samples
- RSQ = 0.898

2016 STARCH (GBL – LAB)
- 1017 samples
- RSQ = 0.844

2016 PROTEIN (GBL – LAB)
- 1586 samples
- RSQ = 0.849
Selection Protocol

GQS - CUBA164:S1517 and CUBA117:S1520 populations are from the Stiff Stalk Synthetic background (75%)

WQS - Broad-based high quality synthetic (low fiber, lignin and silica) then crossed by H99 and Mo17 (100 to 110RM)

Also germplasm from the Germplasm Enhancement of Maize (GEM) program
WQS Germplasm

WQS derived lines

brown midrib3 lines

Joe Lauer - Data from UW Extension - Corn Trial
Outline

- Silage Breeding and the UW Program?
- Tools to Increase Breeding Outcomes
- Future Challenges
Cost per Raw Megabase of DNA Sequence

Moore’s Law

National Human Genome Research Institute

[genome.gov/sequencingcosts]
Exploiting Genetic Variability

Average height = 100

CTGTTAT

Average height = 50

CTGATAT
Phenotypic Selection

Genomic Selection

http://b4fa.org/bioscience-in-brief/plantbreeding/what-is-plant-breeding/
Silage includes many traits
Phenotyping
Growth Rate and Tasseling

Nathan Miller
Spalding Lab
Outline

✧ Silage Breeding and the UW Program?
✧ Tools to Increase Breeding Outcomes
✧ Future Challenges
Phenotypes are Modified by the Environment over Time

<table>
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<tr>
<th>Factor</th>
<th>VE</th>
<th>V6</th>
<th>V12</th>
<th>V18</th>
<th>R1</th>
<th>R6</th>
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<td>Frost (&lt; 28 F)</td>
<td>0</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>0</td>
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<tr>
<td>Hail (max)</td>
<td>0</td>
<td>53</td>
<td>81</td>
<td>100</td>
<td>100</td>
<td>0*</td>
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<tr>
<td>Drought/Heat (%/day)</td>
<td>--</td>
<td>--</td>
<td>3</td>
<td>4</td>
<td>7</td>
<td>0</td>
</tr>
<tr>
<td>Flooding (&lt;48 h)</td>
<td>severe</td>
<td>severe</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

* Assuming no ear dropage

http://corn.agronomy.wisc.edu/Management/L011.aspx
What Our Eyes Cannot See

Edgar Spalding
UW Madison
Take Home Message:

✧ Need for varieties with improved silage characteristics is expected to continue to increase due to international demand
✧ Equipment and management tools have helped research
✧ Genotypic information is cheap, meaningful, high-throughput phenotyping is the bottleneck
✧ Interdisciplinary developments are needed to increase efficiency of phenotyping (current bottleneck)
✧ The UW Corn Silage Breeding Program continues to serve as a source of germplasm, research and a tool for training of students
Acknowledgements:
THANK YOU.

- Shawn Kaeppler and UW Group
- Edgar Spalding group – UW Madison
- Robin Buell group – Michigan State
- Candy Hirsch – Univ of MN