BREEDING CORN FOR SILAGE: RESOURCES AND TECHNOLOGIES DEVELOPED IN THE UW PROGRAM

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About 6.4% of the ~87 million acres of corn harvested in the U.S were dedicated to silage production in 2010. Of those, approximately 750,000 acres were located in Wisconsin, the largest silage producing state in the U.S. (USDA, 2010). Maize silage is produced by ensiling the whole plant harvested a few weeks prior to physiological maturity. The starch from the grains and the complex carbohydrates in the cell walls are the primary sources of energy for the complex community of anaerobic microbes that reside in the gastrointestinal tract of ruminant animals (Van Soest, 1994; Coors and Lauer, 2001). Substantial improvements in forage digestibility have been achieved through traditional breeding in maize (Frey et al, 2004; Gustafson et al, 2010) as well as through the incorporation of large mutations such as the brown *midrib3* (Sattler et al., 2010).

For many years, the focus of many corn silage breeding programs has been improving the digestibility of the whole maize plant without a detailed understanding of what plant components on the cell wall of these materials or the relative contribution from the easily digestible grain provided that improvement. This approach has tended to increase the relative proportion of grain in the final forage mix and this has had a detrimental effect on dry matter yield and quality (Coors and Lauer, 2001). While increasing whole plant digestibility is still the primary goal of breeders, a better understanding of the relative contribution of grain relative to stover as well as specific changes in fiber and lignin content and composition has been crucial for the development of more efficient decision making process in breeding programs.

The UW corn silage breeding program has unique germplasm specifically designed to produce high-quality inbreds for use as parents for silage hybrids. An important component in the success of this program relates to fruitful interactions with animal nutritionists and corn extension specialist as well as the development of specific protocols to guide the identification of improved germplasm resources. We will present results that illustrate the technologies used and the resources generated by this program.

References

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