

Conservation, Management, Enhancement and Utilization of Plant Genetic Resources

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The Need

In the United States, sweet corn is the third most consumed vegetable, following tomato and potato. In 2020, New York state sweet corn was harvested from 25,000 acres, with a production value of \$36.9 million. Sweet corn varieties grown in New York need to have superior productivity and quality, but they also must be adapted to the state's climate and production systems. However, commercial seed companies are primarily focused on breeding for agroecosystems of the Midwest. This neglect for the Northeast's growing conditions has negative consequences for New York state growers in terms of market share. Notably, there is a premium price paid by the consumer for sweet corn that matures before the general sweet corn crop, due to less market competition.

The Approach

Seeking a solution for New York state growers, this project leveraged plant breeding and genetics methods to enhance the productivity of sweet corn. Through interactions with the National Plant Germplasm System, this work was positioned to genetically characterize the complete sweet corn germplasm collection maintained at the North Central Regional Plant Introduction Station (NCRPIS) in Ames, Iowa. The collection was evaluated using a combination of modern genomic and phenomic tools to help better understand the genetic basis of how sweet corn responds to a range of environments in Upstate New York. Until this work, this collection had been only minimally characterized at the genetic level. In total, the project evaluated more than 400 sweet corn inbred lines, and scored roughly 200,000 genetic markers, with a close look at leaf architecture and physiological variables.

The Impacts

The information generated from this research will contribute to the genetic improvement of sweet corn for the Northeastern United States, as well as support the conservation and utilization of the sweet corn collection. By employing high-throughput phenotyping — a method of screening that uses digital instruments to rapidly collect large amounts of data in a non-destructive manner — this project's results enhance our understanding of the genetic basis of leaf architecture in sweet corn and pave the way for the manipulation of leaf physiological attributes in breeding practices. By allowing for rapid adaptation of sweet corn varieties to succeed in different and changing growing environments, this work is intended to benefit seed companies, growers, food processors and consumers.

Related information: [The Gore Lab website](#)