

Research makes plant breeding easier

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The loss of function of RF1A1/ALDH2B2, a fertility restorer (RF) protein causes maize susceptibility to *Helminthosporium maydis*, the causal agent that was responsible for the maize southern corn leaf blight epidemic in 1972. The disease symptoms on a maize leaf are pictured. Credit: Photo by Simeon O. Kotchoni

University of Illinois research has resulted in the development of a novel and widely applicable molecular tool that can serve as a road map for

making plant breeding easier to understand. Researchers developed a unified nomenclature for male fertility restorer (RF) proteins in higher plants that can make rapid advancements in plant breeding.

"Understanding the mechanism by which RF genes suppress the male sterile phenotype and restore fertility to plants is critical for continued improvements in [hybrid technology](#)," said Manfredo J. Seufferheld, U of I assistant professor of crop sciences.

To reach this goal, Seufferheld teamed up with post-doctoral researchers Simeon O. Kotchoni and Emma W. Gachomo of Purdue University, and Jose C. Jimenez-Lopez of the Estacion Experimental del Zaidin, Consejo Superior de Investigaciones Cientificas (CSIC) in Granada, Spain, to develop a simplified genetic-based nomenclature that automatically catalogues the entire RF gene products into families and subfamilies.

"Up to now, there has been no unified nomenclature for naming the RF proteins," Seufferheld said. "As the systematic sequencing of new [plant species](#) has increased in recent years, naming has been simply arbitrary. We have had 'chaos' in the databases. The RF information in the databases could not be adequately handled in the context of comparative functional genomics."

This new tool will help plant breeders and scientists make decisions more quickly. Breeders can now easily match [sterility](#) in plants to male restorer mechanisms. Ultimately, growers may benefit sooner from new developments in [plant breeding](#) since breeders will be able to generate new hybrids at a faster pace, Jimenez-Lopez said.

"Genomic sequencing, coupled with protein modeling, allowed us to begin dismantling this complexity that has held us back in the field of science," Kotchoni said. "Now we can easily compare unknown [gene](#)

[functions](#) to known and well characterized genes in order to determine their functions and family hood."

With many teams of researchers competing to finish this task first, Kotchoni said it has been an honor to have this model accepted as the new standard for RF protein nomenclature. This system has been developed as a building block for plant genomics.

"The nomenclature, which is designed to include new RF genes as they become available in the future, is not based on one species or another, but rather on the function of the gene itself," Seufferheld said. "This allows scientists to work with a wide range of plants and take a gene with known function(s) from one plant and transfer it into another plant to restore male fertility."

Corn growers only need to look back to the southern corn leaf blight epidemic in 1972 to see the importance of this scientific development.

In 1972, Texas-Cytoplasm Male Sterility (T-CMS) corn was heavily used in hybrid seed production because it eliminated the costly practice of hand detasseling. Nearly 85 percent of the U.S. corn crop was produced using T-CMS, which was highly susceptible to *Helminthosporium maydis*, the fungus that causes southern corn leaf blight.

Since then, understanding the function of RF genes in higher plants has been a priority of many researchers. "The first male sterility restorer ever characterized in plants was maize ALDH," Kotchoni said. "When this gene is altered, it causes male sterility."

Seufferheld said this will also be a great tool for studying plant evolution.

"We can follow how plants became domesticated," Seufferheld said. "It

is easier now because we have all the structures of the RF proteins organized and can look at the evolution of these proteins in a systematic manner. If we just look at the sequence of the gene, part of the phylogenetic scene has been lost through evolution. However, the structure of protein provides more information that can go well into the past."

This public gene database will allow scientists to search using the old or new names of RF proteins, Seufferheld said.

More information: "A new and unified nomenclature for male fertility restorer (RF) proteins in higher plants," was published in the December 2010 edition of PLoS ONE. (Ref: PLoS ONE 5 (12): e15906)

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