

# Maps of *Miscanthus* genome offer insight into grass evolution

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University of Illinois crop sciences professor and Energy Biosciences Institute program leader Stephen Moose and his colleagues mapped the *Miscanthus sinensis* genome, a first step towards a full genome sequence. Credit: L. Brian Stauffer

*Miscanthus* grasses are used in gardens, burned for heat and energy, and converted into liquid fuels. They also belong to a prominent grass family that includes corn, sorghum and sugarcane. Two new, independently produced chromosome maps of *Miscanthus sinensis* (an ornamental that likely is a parent of *Miscanthus giganteus*, a biofuels crop) are a first step toward sequencing the *M. sinensis* genome. The studies reveal how a new plant species with distinctive traits can arise as a result of chromosome duplications and fusions.

The two studies were published this year: The first, led by the [energy crop](#) company Ceres, appeared in the journal [PLoS ONE](#); the second, from a team led by researchers at the University of Illinois, is in the

journal [BMC Genomics](#). The data, materials, methods and [genetic markers](#) used in the latter study are available to the public for further research.

Before this work, scientists knew that *M. sinensis* had a base set of 19 [chromosomes](#) and was closely related to sorghum, which has a base set of 10. (Humans have a base set of 23). But without a map and sequence of the *Miscanthus* genome, researchers who hope to maximize yields or discover which genes give *Miscanthus* its desirable traits are working in the dark, said Stephen Moose, a University of Illinois [crop sciences](#) professor and Energy Biosciences Institute program leader who led the [BMC Genomics](#) study.

Moose and his colleagues used information gleaned from the sugarcane genome to develop hundreds of genetic markers to target specific regions of the *M. sinensis* genome. Then they crossed two *M. sinensis* plants and grew 221 offspring in the lab. By comparing how the genetic markers from each parent were sorted in the offspring, the team reconstructed 19 "linkage groups" corresponding to the 19 chromosomes of *Miscanthus*. This rough map of the chromosomes is a first step toward a *Miscanthus* genome, Moose said.

The researchers also used the sorghum genome as a comparative reference. Their analysis indicated that *M. sinensis* arose as a result of a duplication of the sorghum genome, with a later fusion of some chromosome parts.

"Some plants will duplicate their genomes and then there's some sorting that goes on," Moose said. "Sometimes whole chromosomes are lost and sometimes there are fusions." Once there are two copies of each chromosome in a base set, each will proceed along its own evolutionary trajectory. "Often what will happen is even though there are two (versions of the same chromosome), one of them will start to deteriorate

over time," Moose said. "Some positions and some genes will win out over the others."

Genome duplications may undermine the viability of a plant or give it an advantage. One immediate advantage of doubling, tripling or otherwise duplicating the genome is that it increases the size of the plant, or of certain plant parts, Moose said.

"Humans have selected for these traits," he said. "Strawberries, for example, are octoploids; they have eight chromosome sets. Sugarcane has eight sets, and it's bigger (than its wild cousins)."

Moose and his colleagues were surprised to find a high degree of similarity between the *Miscanthus* and sorghum genomes.

"I would say that for about 90 percent of the *Miscanthus* markers, their chromosomal order corresponds to what is known for [sorghum](#)," he said.

The new findings and the eventual publication of the *Miscanthus* genome will help scientists understand the evolution of grasses and the genetic mechanisms that give them some of their useful traits, such as cold tolerance, Moose said.

The *BMC Genomics* team also included researchers from the University of California, Berkeley; the Polish Academy of Sciences; the department of plant biology at the University of Illinois; the Department of Energy Joint [Genome](#) Institute; and the National Institute of Horticultural and Herbal Science, in South Korea. Moose is an affiliate of the Institute for Genomic Biology at Illinois.

Provided by University of Illinois at Urbana-Champaign

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