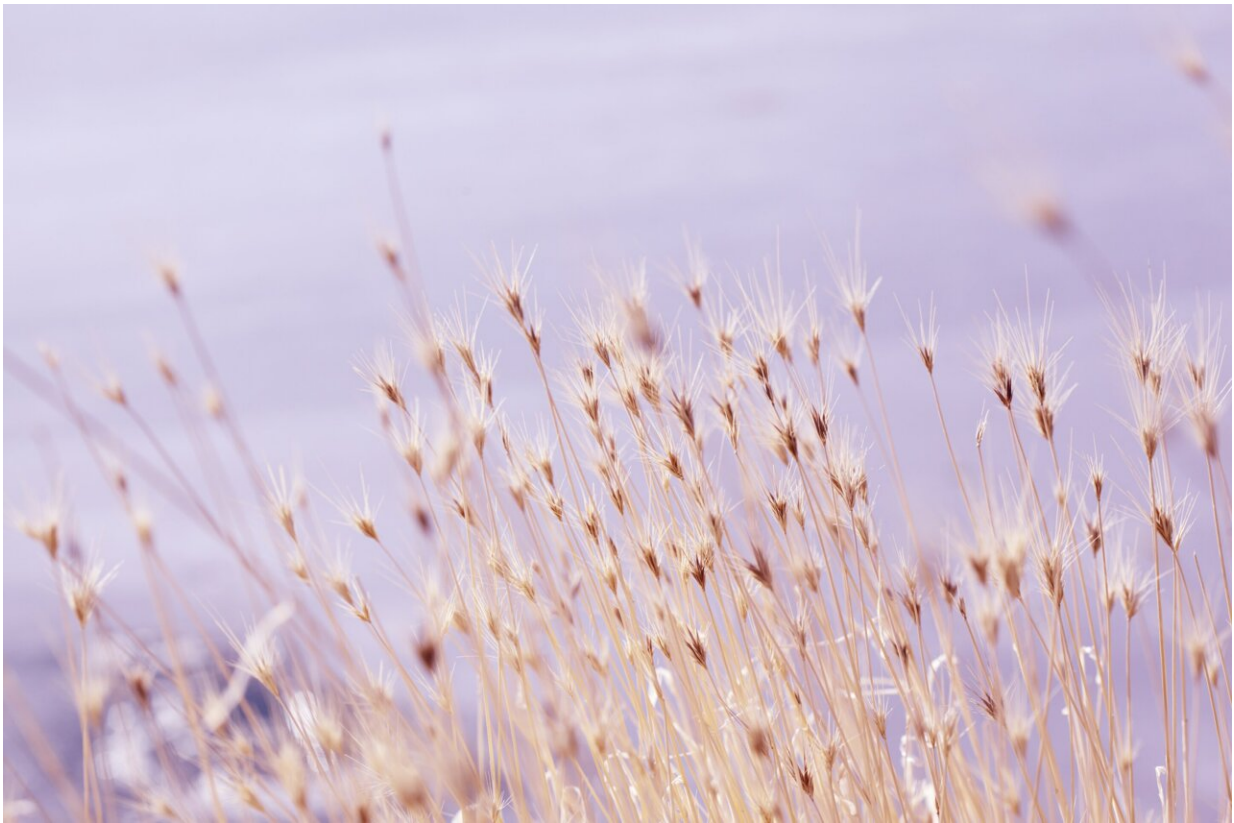


# **New knowledge of ancient grain: Researchers map complete millet genome to help with food security**

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An international team of researchers has unlocked a large-scale genomic analysis of *Setaria* or foxtail millet, an important cereal crop. The study,

led by researchers at the Chinese Academy of Agricultural Sciences and including scientists at NYU, advances our understanding of the domestication and evolution of foxtail millet, as well as the genetic basis for important agricultural traits.

"Foxtail millet is considered to be the foundation for early Chinese civilization," said Michael Purugganan, the Silver Professor of Biology at NYU and NYU Abu Dhabi, and the study's co-senior author.

"Moreover, because it is a crop that can grow across a wide range of environments—including arid lands—it has the potential to be important for food security under [climate change](#)."

Foxtail millet is one of the oldest domesticated grain crops in the world and has been grown by humans for roughly 11,000 years. It held a [dominant position](#) in Chinese agriculture before the introduction of high-input [agricultural practices](#) like irrigation and chemical fertilizers. The protein-rich grain—which employs C4 photosynthesis, a highly efficient form of photosynthesis that helps it adapt to [different environments](#)—is resilient to drought and able to thrive in low-nutrient soils.

"C4 plants constitute only about 3% of flowering [plant species](#), but they surprisingly contribute to approximately 25-30% of global biomass production. The complexity of the genomes of most C4 species has posed challenges for fundamental studies and breeding, but *Setaria* serves as an ideal model system for studying C4 photosynthetic plants in genomics and genetics research," said Xianmin Diao, a professor in the Institute of Crop Sciences at the Chinese Academy of Agricultural Sciences, the study's co-senior author, and the scientist who organized the study.

In their study published in the journal *Nature Genetics*, the researchers established the *Setaria* pan-genome—the entire set of the species' genes—by assembling 110 representative genomes from a worldwide

collection of 1,844 *Setaria* species. They performed large-scale [genetic studies](#) for 68 traits across 22 environments in 13 geographical locations, each with distinct climactic conditions, identifying potential genes and marker-panels for how [foxtail millet](#) has evolved and improved at different geographic sites. For instance, the researchers found that the gene SiGW3 regulates grain yield of foxtail millet.

They also constructed the first graph-based genome sequence of *Setaria*, offering insights into genomic variation across wild and cultivated *Setaria*. This deeper understanding of the comprehensive genomic variation equips researchers with valuable genetic tools to pursue biological research and breeding efforts.

"This paper is a [significant milestone](#), as it paves the way for the next generation of comparative genomics studies that can help to decipher the molecular mechanism of C4 photosynthesis. The large-scale comparative genomics, genome-wide association study, and genomic selection studies of *Setaria* not only provide opportunities for gene discovery and breeding advancements in foxtail millet itself, but also offer insights for other crops to enhance global food security," added Diao.

"Understanding the [genetic basis](#) underlying the domestication and improvement of foxtail millet, along with these important agricultural characteristics, holds significant potential for its enhancement. With our graph-based genome, we can estimate grain quality-related traits and potential yield, providing avenues for foxtail millet breeding for climate change adaptation," said Qiang He, a postdoctoral researcher in the Institute of Crop Sciences at the Chinese Academy of Agricultural Sciences and the study's first author.

**More information:** A graph-based genome and pan-genome variation of the model plant *Setaria*, *Nature Genetics* (2023). [DOI: 10.1038/s41588-023-01423-w](#)

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