

Scientific Commercialization



China's First Forage-based Multi-omics Database Platform Established

Milletdb contains the genomes of 7 genera of Millets and 1800 different genomics data, including graphical pangenomics, genome, transcriptomics, epigenomics, variegation, and phenomics, etc. Milletdb also integrates 20 utilities, which can help users quickly identify individual genes, construct regulatory networks from multiple levels, and characterize gene sets, enabling rapid search for candidate genes and their related information. On August 3, the paper was formally published in the academic journal called Plant Biotechnology Journal (Plant Biotechnology Journal).

Milletdb is by far the most comprehensive multi-omics database for millet and wolfsbane, and is also the first multi-omics database focusing on forage grasses in China. It contains and visualizes a large amount of multi-omics data, allowing users to extend the study of individual genes to the level of genetic networks. Milletdb has a user-friendly, bilingual interface and provides operation manuals for all tools, which can effectively promote the gene function study and molecular breeding process of lycopods.



Millets, a group of American wolfsbane, are abiotic stress-resistant, nutritious grasses and coarse grains of high quality. It ensures food security for people living in extreme climatic conditions and provides genetic resources related to abiotic stress tolerance for other crops.

Due to the growing importance of the millet category, the United Nations has declared this year as the International Year of Millet 2023. With the rapid development of genomics technology, the amount of relevant data is increasingly proliferating, but utilizing the data to rapidly mine genes remains a challenge for most researchers. There is not yet a comprehensive and systematic platform for analyzing the multi-omics data of a class of millet, which seriously hampers the mining of important candidate genes and the molecular breeding process.