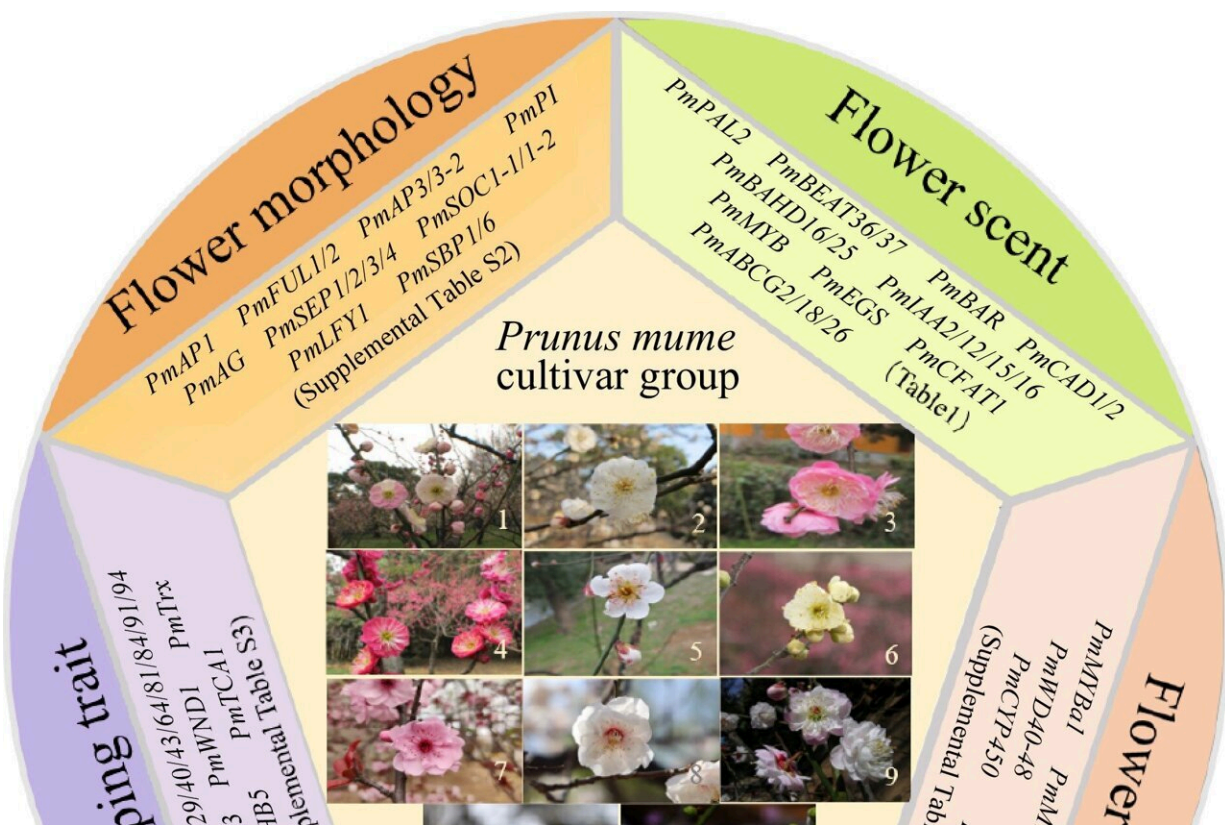# Advancing mei (Prunus mume) breeding: Genomic insights into ornamental and cold resistance traits

April 25 2024

Eleven cultivar groups of Mei and representative functional genes in five aspects. 1, Versicolor Group; 2, Dragon Group; 3, Pendent Group; 4, Cinnabar Purple Group; 5, Single Flowered Group; 6, Flavescens Group; 7, Blireiana Group; 8, Apricot Mei Group; 9, Pink Double Group; 10, Alboplena Group; 11, Green Calyx Group. Credit: *Ornamental Plant Research* (2024). DOI: 10.48130/opr-0024-0004

A research team has provided an overview for understanding the genetic basis of ornamental and cold resistance traits in Mei (Prunus mume), a tree valued both for its ornamental and cultural significance in China.

By employing cutting-edge biotechnological approaches, including whole-genome sequencing and resequencing, scientists have laid a solid foundation for targeted breeding programs. These advancements promise to greatly enhance the efficiency of breeding Mei trees with distinctive characteristics and high resistance, aligning with both aesthetic and practical needs in contemporary horticulture.

Genomics, which delves into the complete genetic blueprint of organisms, has revolutionized plant science by overcoming challenges like large, complex genomes. The pioneering Arabidopsis genome sequence in 2,000 spurred advancements in sequencing technologies, leading to the sequencing of approximately 400 plant genomes, including Mei (Prunus mume).

This progress has enriched our understanding of genetic variation and aided breeding technologies. However, further research is needed to decode the specific genetic mechanisms influencing the ornamental and functional traits of Mei for enhanced breeding applications.

The study published in *Ornamental Plant Research* on 4 March 2024, provides a comprehensive overview of the development and expansion of genome projects over the past decade, highlighting advances in whole-genome sequencing, resequencing, and genetic mapping.

This review highlights the completion of the Mei genome project, which has catalyzed research into the genetic underpinnings of ornamental and cold resistance traits in this culturally significant tree.

Through advanced genomic techniques, researchers have delineated the complex genetic network influencing traits such as flower fragrance, color variation, and cold hardiness. This includes the identification of key gene families like benzyl alcohol acetyltransferase (BEAT), which influences Mei's unique floral scent, and cold-resistance genes.

The review underscores the implications of these discoveries for breeding programs, emphasizing the potential to develop Mei cultivars with enhanced ornamental qualities and environmental adaptability.

According to the study's lead researcher, Prof. Lidan Sun, "The efforts to improve genetic makeup will continue to be greatly impacted by this new information and the resources that are now available."

This foundational genetic insight is set to revolutionize Mei breeding, making it possible to meet aesthetic and practical goals more efficiently.