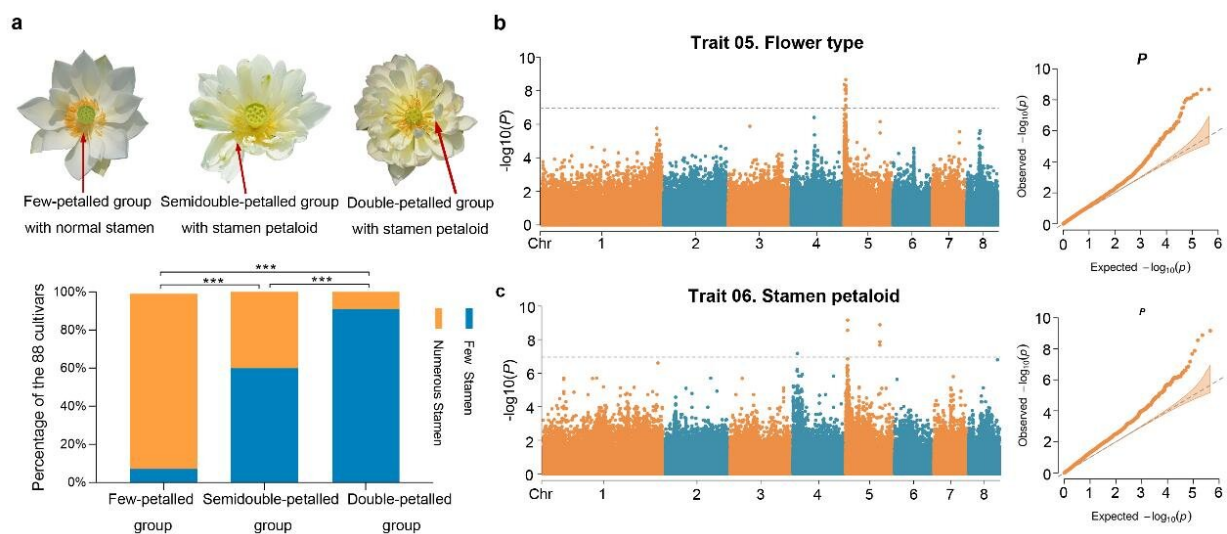


Genetic architecture of multiple correlated traits in the sacred lotus mapped for the first time

December 13 2022, by Zhang Nannan



GWAS of flower type and stamen petaloid. Credit: Gao Zhiyan

The sacred lotus enjoys an astonishing diversity of floral traits, particularly petal number, color, and flower type. Previous studies have discussed the molecular mechanisms underlying a single trait for flower development based on transcriptomes and methylations; however, no systematic study has determined the genetic architecture of multiple correlated traits in a population using a genome-wide association study (GWAS) in lotus.

Researchers from the Wuhan Botanical Garden of the of the Chinese Academy of Sciences (CAS) investigated the genome resequencing and high-density [single nucleotide polymorphism](#) (SNP) markers of 88 flower lotus cultivars with 12 well-recorded horticultural traits obtained in a common-garden condition to address the question of the genetic variants underpinning multiple crucial horticultural traits of this complex flower through GWAS.

Results reveal a total of 149 [candidate genes](#), including several pleiotropic genes (like NnKUP2) linked to SNPs that were significantly associated with the developmental and colorful variations of floral organs and plant size in a continuous distribution of lotus individuals.

Moreover, a 2.75-kb presence-and-absence genomic variant fragment carrying seven transposons (including three miniature inverted-repeat [transposable elements](#)) and two small-RNA-binding regions was found to significantly affect the formation of double- petalled flowers and stamen petaloid in lotus by interfering with nearby gene expressions (Petaloid-Related Formation, PRF gene).

Additionally, this genomic variant fragment was also verified to be significantly associated with flower types and stamen petaloid by re-examining the 136 accessions with sufficient sequencing abundance from another published study.

This work provides insight into the genetic variations underlying remarkable diversity in complex traits of the lotus flower.

Results were published in *Frontiers in Plant Science*, in an article titled "Genome-wide association study of traits in sacred lotus uncovers MITE- associated variants underlying stamen petaloid and petal number variations."

More information: Zhiyan Gao et al, Genome-wide association study of traits in sacred lotus uncovers MITE-associated variants underlying stamen petaloid and petal number variations, *Frontiers in Plant Science* (2022). [DOI: 10.3389/fpls.2022.973347](https://doi.org/10.3389/fpls.2022.973347)

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