

An effective method for studying gene function of Chinese cabbage

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Heading Chinese cabbage (*Brassica rapa* ssp. *pekinensis*), a cruciferous family species, is a common leafy vegetable crop native to northern China. Pan-genome and population variome analysis of *B. rapa* have been completed in recent years, laying

a foundation for the study of gene functions in Chinese cabbage. In the current era of functional genomics, large-scale, high-throughput genome sequencing technologies are frequently used to study gene functions, and mutants are

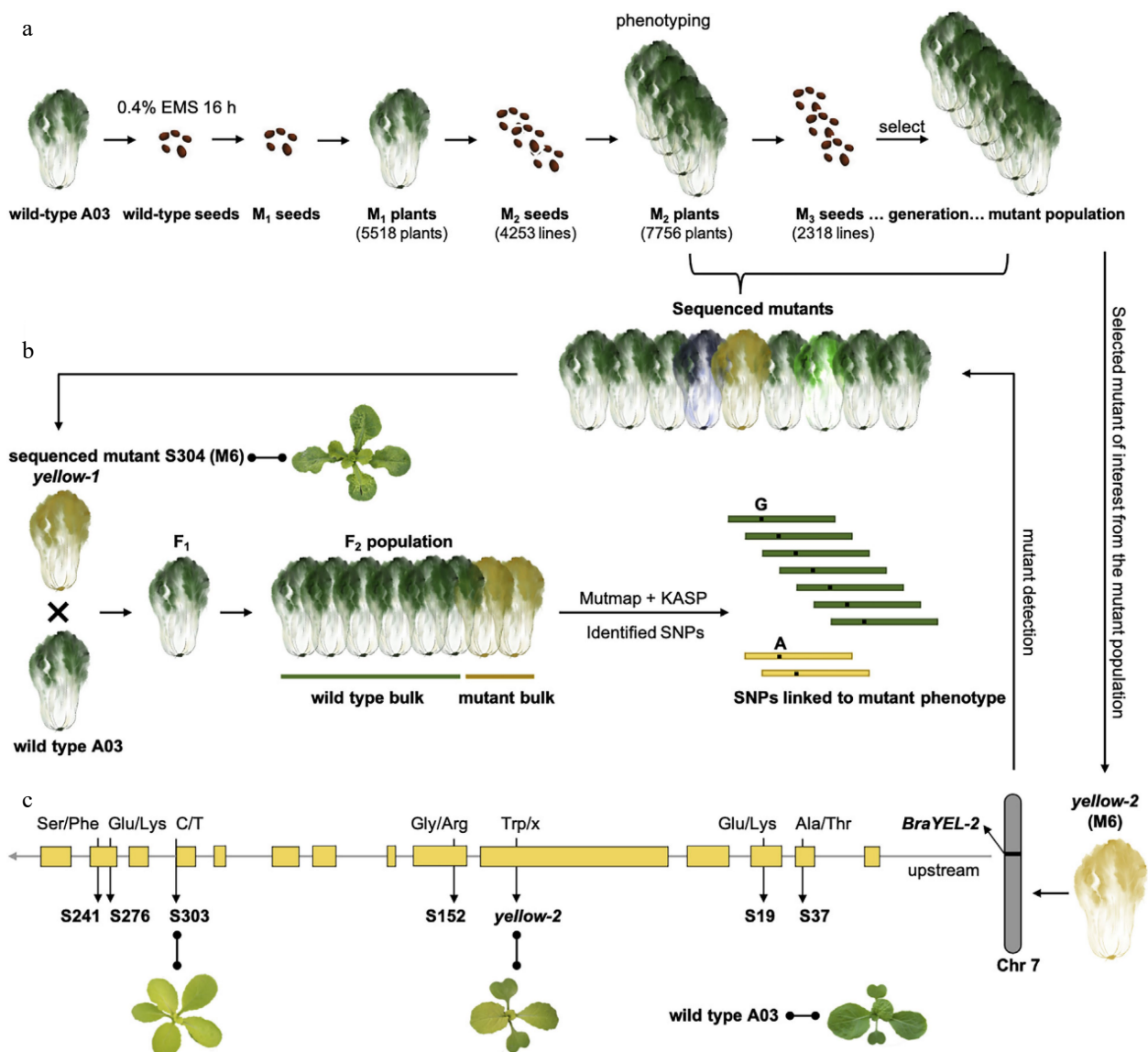


Fig. 1 Workflow for the use of the Chinese cabbage EMS mutant population in a functional genomics study (Cite from Sun et al., 2022, Molecular Plant <https://doi.org/10.1016/j.molp.2022.02.006>).

important materials for conducting related gene studies.

In a recent study (<https://doi.org/10.1016/j.molp.2022.02.006>), more than 8,000 Chinese cabbage mutants were created by EMS mutagenesis from an inbred line A03 which genome has been used as a reference for high-throughput functional characterization of mutations across the genome (Fig. 1). Subsequently, a total of 300 EMS mutants were phenotypically screened and sequenced, yielding 750,629 SNPs and 46,272 InDel mutations, covering 98.27% of A03 genome, with 86.49% located in the gene coding region. Each gene had three functional SNP variants on average, and the genes were highly variable.

The forward genetics method was used successfully to identify two chloroplast-related genes, *BraYL-2* and *BraYL-4*, whose mutations cause the yellow leaf trait in plants. Reverse genetics methods were also used to investigate the relationship between mutations in five genes of the glucosinolate biosynthesis pathway and changes in plant glucosinolate content. These findings indicate that EMS mutant libraries can be used to identify candidate genes and target traits using genetic methods. Meanwhile, the Chinese cabbage mutant

database CCEMD was established, which not only aids in obtaining a large amount of genetic and phenotypic variation information, but also aids in rapidly mining candidate genes for important traits, providing great convenience to those engaged in related research both at home and abroad.

Conflict of interest

The author declares that there is no conflict of interest.

Dates

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