

With the increasing application of multi-omics technologies in radish research, researchers are gradually establishing a systems biology framework that links morphological traits, physiological indicators, and specific regulatory genes. This framework not only helps clarify the molecular mechanisms underlying cold tolerance in radish but also accelerates breeding programs based on Marker-Assisted Selection (MAS) and Genomic Selection (GS) for the development of cold-tolerant winter radish cultivars.

## **4 Cold Tolerance Germplasm Resources and Breeding of Radish**

### **4.1 Diversity of Chinese radish germplasm resources**

Radish germplasm resources provide the essential genetic foundation for developing new varieties with strong stress tolerance, high yield, and superior quality. China is one of the major centers of radish diversity and production worldwide, with a cultivation area of about 1.2 million hectares and an annual production exceeding 40 million tons (Xing et al., 2024). At present, more than 2 000 radish germplasm accessions have been collected and conserved in Chinese germplasm repositories, of which approximately 95% are domestic landraces. This reflects the rich in situ genetic diversity and long domestication history of radish in China (Wang et al., 2018). Population genetic studies based on single nucleotide polymorphism (SNP) and structural variation (SV) markers have shown that radish resources from China and other East Asian regions form the major genetic groups. Clear genetic differentiation exists between these groups and European or other regional types. However, relatively frequent gene flow has also been observed among some subpopulations, accompanied by a certain risk of genetic erosion (Li et al., 2023a).

### **4.2 Identification of cold-tolerant landrace resources**

Landraces are generally defined as heterogeneous populations that have evolved through long-term farmer selection under specific ecological, geographical, and cultivation conditions. They are valuable genetic resources for obtaining adaptive traits such as tolerance to abiotic stresses. In radish research, systematic evaluations conducted across different seasons and locations have identified excellent germplasm resources with desirable agronomic traits and strong stress resistance. For example, long-term trials carried out in Jinan, Yangling, Harbin, and other regions screened multiple germplasm accessions with outstanding overall performance based on yield, stress tolerance, and disease resistance (Qu et al., 2002). The conservation of radish germplasm resources in China places particular emphasis on collecting and preserving landraces from their regions of origin as well as resources representing different ecological types. These materials exhibit abundant phenotypic and biochemical variation.

### **4.3 Conventional breeding methods (selection breeding and hybrid breeding)**

Traditional radish breeding mainly focuses on target traits such as high yield, early maturity, late bolting, cold tolerance, drought tolerance, heat tolerance, disease resistance, and high-quality fleshy roots. Through methods including mass selection and pedigree selection within landraces and local populations, as well as intraspecific and interspecific hybridization, favorable alleles can be continuously accumulated, resulting in varieties that combine multiple desirable traits that are difficult to achieve in a single genotype.

With the development of  $F_1$  hybrid seed production systems based on self-incompatibility, identification of S haplotypes in parental lines has become an important step for efficient hybrid seed production. This approach eliminates the need for manual emasculation, greatly improves hybrid seed production efficiency, and accelerates the incorporation of complementary favorable traits, including stress tolerance, into commercial cultivars (Kumar and Kaushik, 2021). In addition, core germplasm collections established from large-scale germplasm resources have been widely used in the development of cytoplasmic male sterility (CMS) lines and new hybrid cultivars, further improving the efficiency of conventional breeding programs.

### **4.4 Molecular breeding strategies (marker-assisted selection and genomic tools)**

In recent years, significant progress has been made in radish genomics research. High-quality reference genomes, genetic linkage maps, SNP and SV marker systems, and molecular markers associated with important agronomic traits have been continuously developed and improved (Kim et al., 2019). Molecular fingerprint maps based on SNPs and SVs can not only be used for accurate germplasm identification, genetic structure analysis, and core germplasm collection construction, but also provide important technical support for marker-assisted selection (MAS) and genomic studies.