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Genome-wide association study to dissect the genetic regulation of metabolism and resistance to *Sclerotinia sclerotiorum* in *Brassica napus*

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Brassica napus is one of the three major oil crops in the world. *Sclerotinia stem rot (SSR)* is caused by fungal pathogen *Sclerotinia sclerotiorum*, which is one of the most devastating diseases worldwide and has strong negative impacts on seed yield and quality. Many researches have shown that the resistance to *S. sclerotiorum* in *B. napus* was mainly controlled by minor multiple quantitative trait loci (QTLs). But so far, all the QTLs identified for *S. Sclerotinia* resistance only explained a small portion of the phenotypic variation, and it is difficult to identify the candidate genes for these major resistance QTLs. In recent years, metabolome-based genome-wide association study (mGWAS) plays a vital role in understanding plant metabolic pathways and the functional gene identification. Combing these advantages with our previous work, a panel of 420 inbred lines of *B. napus* from all over the world was genotyped by re-sequencing. GWAS will be conducted with the phenotype of disease resistance and the metabolites content of leaves without and with the pathogen (12h) in our association mapping. We will widely identify the key candidate genes which are highlighted and mapped to defense metabolites pathway. Our results will reveal a plant defense metabolite for disease resistance trait, combine with the genetic determinants of *B. napus* metabolism identified, promote efficient utilization of metabolites in improvement of disease resistance breeding.

PLENARY TALKS

ORALS

POSTERS

WORKSHOPS