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## Identification of genetic factors related to human health promoting functional compounds in Chinese Cabbage

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The functional genomics and molecular breeding researches have been rapidly expanded to understand metabolic pathways and related gene functions on important functional compounds in Chinese cabbage (*B. rapa*). We analyzed and identified the accessions which are enriched with health promoting functional compounds such as glucosinolates, anthocyanins, vitamins,  $\beta$ -carotene, total sugars, lutein, flavonol, Fe, Ca, etc. Further, we have generated double haploid (DH) lines through microspore culture to investigate various aspects of nutrigenetics and nutriomics of these inbred lines. For glucosinolates, we have performed a conventional QTL analysis using F2/3 mapping population of *B. rapa* combined with genome-wide association approach by using natural population to identify the genomic region and genes regulating glucosinolate biosynthesis in *B. rapa* crops. Similarly anthocyanin, the predominant flavonoids in red/purple crops, were tested for its inhibitory effects in cultured endothelial cells and hyperlipidemic apolipoprotein E-deficient mice using anthocyanin-rich extract from red Chinese cabbage and found to reduce the risk of vascular inflammatory diseases. Furthermore, we generated biparental mapping population from red and green Chinese cabbage and QTL mapping coupled with genotyping by sequencing (GBS) approach was used to identify genomic loci associated for anthocyanin biosynthesis. The transcriptome sequencing of both parents along with QTL mapping revealed 703 differentially expressed genes regulating anthocyanin biosynthesis. Among these, 211 positively associated genes are identified in leaf tissues of red Chinese cabbage samples. Our overall results will be additive resource for future studies on nutritional breeding of enriched varieties of *B. rapa* and their subspecies for human health.

PLENARY TALKS

ORALS

POSTERS

WORKSHOPS