

Comprehensive Analysis of the CDPK-SnRK Superfamily Genes in Chinese Cabbage and Its Evolutionary Implications in Plants

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Figure S1 Schematic diagram of amino acid motifs and gene structures of *BrCDPK-SnRK* genes in *Arabidopsis* and *B. rapa*.

Figure S2. Alignments of *A. thaliana* and *B.rapa* CPK, CRK, PEPRK, PPCK and SnRK proteins. Conservations and consensus were demonstrated under the alignments.

Figure S3. The phylogenetic trees of the *BrCDPK-SnRK* genes from 13 Angiospermae.

Figure S4 (a) The phylogenetic tree of the *BrCDPK-SnRK* genes from 13 Angiospermae, one Pteridophyta, one Bryophyta and two Chlorophyta species. **(b)** The genetic distance among clades *CPK*, *CRK*, *PEPRK*, *PPCK* and *SnRK*.

Figure S5 Information of *CPK*, *CRK*, *PEPRK*, *PPCK* gene family clades in *Brassica rapa*, *Arabidopsis thaliana*, *Carica papaya*, *Populus trichocarpa*, *Vitis vinifera* and *Amborella trichopoda*. The α , β , γ , and salicoid duplications and the Brassica-specific triplication are indicated on the branches of the trees according to the Plant Genome Duplication Database. To classify these *CPK*, *CRK*, *PEPRK*, *PPCK* genes, phylogenetic trees with *CPK*, *CRK*, *PEPRK*,

PPCK genes for each of the five species by maximum likelihood using MEGA5, respectively.

Figure S6 Information of *SnRK* gene family clades in *Brassica rapa*, *Arabidopsis thaliana*, *Carica papaya*, *Populus trichocarpa*, *Vitis vinifera* and *Amborella trichopoda*. The α , β , γ , and salicoid duplications and the Brassica-specific triplication are indicated on the branches of the trees according to the Plant Genome Duplication Database. To classify these *SnRK* genes, phylogenetic trees with *SnRK* genes for each of the five species by maximum likelihood using MEGA5, respectively.

Figure S7. Phylogenetic analysis of the *CPK* gene family in angiosperms. Protein sequences were aligned by ClustalW2. A phylogenetic tree was constructed by maximum likelihood (ML) and bootstrap values were calculated with 1000 replications using MEGA5.2. Gene losses are possibly indicated by X. α , β , and γ duplications as well as the Brassica triplication are indicated. green pentagons indicate the Brassica triplication.

Fig. S8. Expression patterns analysis of the *CDPK-SnRK* genes in *Arabidopsis thaliana* and *Brassica rapa*. Expression patterns of the *CPK*, *CRK*, *PEPRK*, *PPCK* and *SnRK* in five tissues, including the root, stem, leaf, flower and silique. Gene expression was determined using the AtGenExpress Visualization Tool and *B. rapa* RNA-Seq data. The bar at the bottom of each heat map represents the relative expression values.

Fig. S9. Interaction network of *CDPK-SnRK* genes in between *Arabidopsis thaliana* and *B.rapa*. (a,b,c,d) Specific protein interactions of *CPK*, *SnRK* in *A. thaliana* and *B.rapa* were constructed using STRING (Search Tool for the Retrieval of Interacting Genes/Proteins; <http://string-db.org/>).