

Title: E-BABE- Status and evolutionary dynamics of cyclic-nucleotide gated ion channels in *Brassicaceae*: systematic characterization and expression profiling of *Brassica rapa* CNGCs

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Cyclic nucleotide-gated channels (*CNGCs*) are ligand-gated calcium signaling channels, involved in important biological functions. However, the origin and function of *CNGC* gene family is not well-investigated in *Brassicaceae* family. In this study, we performed a genome-wide identification and phylogeny of *CNGC* families in sixteen sequenced genomes of crucifer species, followed by systematic characterization and functional analyses of Chinese cabbage (*Brassica rapa*) family genes. We identified 414 *CNGC* genes in sixteen crucifer species, which represent 10 genera of 8 tribes, ranging between 10 (*Arabis alpine*) and 51 (*C. sativa*) *CNGC* genes. The *Brassicaceae* CNGCs can be classified into four major (I-IV) and two sub-groups (IV-A and IV-B), among which, Group-I CNGCs are most recently evolved and Group-II CNGCs are most ancient that eventually disappeared from the genome of *Arabis alpine*. Vegetable crops (*Brassica*) have more *CNGC* genes than other crucifers, except *C. sativa*, implying that *CNGC* genes expanded after divergence from common ancestor. The Chinese cabbage (*Brassica rapa*) contain 29 *CNGC* genes (*BrCNGCs*), which are non-randomly localized on 9 chromosomes, and dispersed into three sub-genomes, namely LF-I, LF-II and LF-III. Analyses of synteny revealed that both whole-genome triplication, and tandem and segmental duplication events contributed to the expansion of *BrCNGC* gene family. Bioinformatics analyses suggest that most *BrCNGCs* can be regulated by phosphorylation and miroRNAs of diverse functionality. RNA-seq data revealed that *BrCNGC* genes are differentially expressed in different tissues, and many of these genes are sensitive to different biotic, abiotic and hormonal stress types. Notably, *BrCNGC-9*, *27*, *18* and *11* exhibited highest response of fold-change against club-root pathogen *Plasmodiophora brassicae*, *Pseudomonas syringae* pv. *maculicola*, methyl-jasmonate, and trace elements. This study provides the foundation for futuristic characterization of this family, and select novel genes for future breeding to improve production, quality and stress resistance in Chinese cabbage.

Biography

Dr. Kaleem Kakar has completed his PhD at the age of 27 years from Zhejiang University and postdoctoral studies from Zhejiang University. He has also served as Foreign Expert at Guizhou Academy of Tobacco Science and Molecular Genetics. He is serving the department of Biotechnology, BUITEMS as the Assistant Professor. He has published more than 18 papers in reputed journals and is the author of a book (Cosmetic Herbs).

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