



Evolution of mustard (*Brassica juncea* Coss) subspecies in China: evidence from the chalcone synthase gene

F.B. Chen, H.F. Liu, Q.L. Yao and P. Fang

Department of Life Sciences, Yangtze Normal University, Fuling, Chongqing, China

Corresponding author: H.F. Liu
E-mail: chenfabo963@126.com

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ABSTRACT. To explore the phylogenetic relationship, genome donor, and evolutionary history of the polyploid mustard (*Brassica juncea*) from China, eighty-one sequences of the chalcone synthase gene (*Chs*) were analyzed in 43 individuals, including 34 *B. juncea*, 2 *B. rapa*, 1 *B. nigra*, 2 *B. oleracea*, 1 *B. napus*, 1 *B. carinata*, and 2 *Raphanus sativus*. A maximum likelihood analysis showed that sequences from *B. juncea* were separated into two well-supported groups in accordance with the A and B genomes, whereas the traditional phenotypic classification of *B. juncea* was not wholly supported by the molecular results. The SplitsTree analysis recognized four distinct groups of *Brassicaceae*, and the median-joining network analysis recognized four distinct haplotypes of *Chs*. The estimates of Tajima's *D*, Fu and Li's *D*, and Fu and Li's *F* statistic for the *Chs* gene in the B genome were negative, while those in the A genome were significant. The results indicated that 1) the *Chs* sequences revealed a high level of sequence variation in Chinese mustard, 2) both tree and reticulate evolutions existed, and artificial selection played an important role in the evolution of Chinese

mustard, 3) the original parental species of Chinese mustard are *B. rapa* var. *sinapis arvensis* and *B. nigra* (derived from China), 4) nucleotide variation in the B genome was higher than that in the A genome, and 5) cultivated mustard evolved from wild mustard, and China is one of the primary origins of *B. juncea*.

Key word: *Brassica juncea*; *Chs* genes; Evolution; Mustard; Polyploid