

과제 일련번호: 6
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### Hundred thousand genes from *Brassica rapa*

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On the basis of strong support by Brassica Genomics Team of NIAB, our research group of BioGreen21 successfully accomplished possession of 100,041 EST (Expressed Sequence Tag) stock from over 20 cDNA libraries of *Brassica rapa* ssp. *pekinensis* (Chiifu inbred, reference line of Chinese cabbage for The Multinational Brassica Genome Project). This number would be the largest EST stock among *Brassica* species in the world. As a result of Contig assembly, unigenes appear to be 25,634 which may uncover 60% of Chinese cabbage genes. They are composed of 13,336 singlet and 12,298 consensus sequences. Transcription factor, tissue-specific and disease-resistant genes are 1,443, 1,558 and 119, respectively. *In-silico* localization analysis suggests that all genes were evenly distributed on *Arabidopsis* 5 chromoosomes. However, about 11% of Chinese cabbage genes have no similiar *Arabidopsis* counterpart. In the poster, we will discuss many other results obtained from EST analysis. We will prepare oligo-Chip using EST sequences, which provide a springboard for functional genomics study in Chinese cabbage as well as in other Brassica species.

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