(05-1-99)

# Obtaining of functional genes using FOX-hunting system in *Brassica rapa* L.

**Da-Yeong Seo[1], Hyo-Jin Jung[1], Kwon-Kyu kang[2], and Ill-Sup Nou[1*]**

[1]Faculty of plant Science, Sunchon National University, 315 Maegok-Dong, Sunchon 540-742, Korea,
[2]Department of Horticulture Hankyong National University, 67 Seokjeong-dong Anseong city Kyunggi-Do 456-749, Korea

## Objectives

To develop gain-of-function type gene function specifying method. FOX hunting system was used in this study, as a new type genome scale gene function analysis tool. The study feature is that causing gene can be identified within few days due to the gene tagging aspect if phenotype appears.

## Materials and Methods

1. Material
Plant - *Arabidopsis thaliana, Brassica rapa*
2. Methods
Floral-dipping, Hygromycin antibiotics tolerant test, PCR analysis, selfing, Sequence

## Results and Discussion

The FOX-Agrobacteria library was constructed by uniform cDNA library of phage DNA. Plant collection that contains kinds of independent full length cDNA of Arabidopsis can be obtained. It had Independent cDNA of inserted vector in the each Agrobaterium. Selfed seed (T1) were yielded of the Arabidopsis transformation by floral-dipping with Agrobacteria. The T-DNA only 1~2 copy was not inserted in plants generally. According to like transgenic plants were plant clone group, to respectively 1~2 copy full-length cDNA could be over-expression.

It was selected 302 individual transgenic plants by hygromycin antibiotics tolerant test, and obtained 27 individual transgenic mutants. After self-pollination transgenic plants of selected, genomic DNA was extracted from the transgenic mutants. Introduced cDNA was isolated by PCR analysis. Resulting of 5' frame sequencing for 16 cDNA, all of them have a initiation codon. We are now analysis the isolated cDNA sequencing.

Afterward that cDNA reinsert at the T-DNA, and re-introduce it into 'Osome', and we will recheck the phenotype. The next cDNA sequence determined. And we will identification of gene becomes the cause of mutation character.

* *Corresponding author* :Ill-Sup Nou, TEL: 061-750-3249, E-mail: nis@sunchon.ac.kr