

## D-D2-41

### 전사조절유전자 특이적 분자마커를 이용한 한국 검정콩 품종의 유전체 특이성 구명

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**ABSTRACT** : The objective of this study is understanding characteristic features of Korean soybean cultivars developed for black bean from genomics view point. I used gene specific molecular markers particularly related Myb transcription factor (TF) genes. Putative promoter region sequences of soybean Myb genes have been traced using comparative sequence analysis of *Medicago truncatula* sequencing database. Eight putative soybean Myb gene specific primers are designed and used as molecular markers to identifying genetic differences. A total of 13 blackbean of Korean soybean cultivars were evaluated by these soybean Myb gene-specific molecular markers. The 12 cultivars could be individually discriminated by eight gene-specific markers in associated Myb transcription factor. Genetic diversity in black bean of Korean soybean cultivars were ranged from 0.42 to 1.00 with an average of 0.72. Based on Nei's genetic distances, the 13 cultivars were classified into 2 groups by the cluster analysis in genetic diversity of 0.75.

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### A genome-wide approach for functional analysis of rice mutants

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Rapid growing of genomic database leads to the remarkable advance of functional genomics. We have proposed a novel methodology of functional analysis using mutants together with their 2-DE analysis and public microarray database. A total of 155 microarray samples from Gene Expression Omnibus (GEO) in NCBI was downloaded followed by constructing gene-coexpression networks over a broad range of biological issues through Self-Organising Tree Algorithm. Some proteins with differential expression pattern were exhibited from high tryptophan mutant rice, probably reflecting new coexpression networks in the mutant.

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