D-D2-41

전사조절유전자 특이적 분자마커를 이용한
한국 검정콩 품종의 유전체 특이성 구명

박나영[1], 김민진[1], 정도원[1], 정일민[1], 김성기[2], 정종일[3], 정우석[1*]

[1]건국대학교 응용생물과학과 , [2]경기도 농업기술원, [3]경상대학교 식물자원환경학부,

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.

D-D2-42

A genome-wide approach for functional analysis of rice mutants

Won Cheol Yim[1], Dong Sub Kim[2], Jun-Cheol Moon[1], Cheol Sung Jang[3], Sung Don Lim[1], Kyung-Hee Kim[1], Ji-Suk Park[1], Sang-Kyu Lee[1], and Byung-Moo Lee[1*]

[1]Department of Plant Biotechnology, Dongguk University, Seoul 100-715, Korea

[2]Department of Radiation Plant Breeding and Genetics, ARTI, KAERI, Jungeup, 580-185, Korea

[3]Institute of Life Science & Natural Resources, Korea University, Seoul 136-713, Korea

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.

*Corresponding author : Tel. 02-2260-3307, e-mail : bmlee@dongguk.edu