D-D2-41

전사조절유전자 특이적 분자마커를 이용한
한국 검정콩 품종의 유전체 특이성 구명

박나영1, 김민진1, 정도원1, 정일민1, 김성기2, 정종일3, 정우석1

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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.

D-D2-42

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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