E311 Changing Pattern of Isoenzymes by Salt Stress in *Mycosphaerella melonia*의

Young-Ho Kim[1,2*], Ju-Hwan Cho[1], Soo-Ki Kim[1], Young-Keun Lee[3], Young-Keel Choi[2], and Ki-Sung Lee[1]

[1]Research Center for Biomedicinal Resources(Bio-Med RRC) and Division of Life Sciences, Pai-Chai University, [2]Department of Biology, Hanyang University and [3]Radiation Application Team, KAERI.

동위효소는 같은 기질에 작용하고 같은 생성물로 전환할 수 있으며 구조의 차이에 의해 전기영동상에서 분별될 수 있다. 이들 동위효소는 다양한 환경요인에 대하여 서로 다르게 반응하며 같은 아미노산 서열을 갖는다 할지라도 전하, 촉매능력 및 환경변화에 대한 반응이 다를 수 있다. *Mycosphaerella melonia*는 수박덩굴마름병을 일으키는 식물병원성 진균류로 NaCl의 농도에 따른 세포내 환경변화를 관찰하고자 세포내 중심물질대사 및 에너지저장계의 물질대사에 관여하는 중요한 효소의 조절양상을 조사하였다.

Esterase(EST)는 (-)극으로 이동하는 monomorphic enzyme으로 NaCl양의 증가할 때 효소의 양이 증가하였으며, Phosphoglucomutase(PGM)와 Maltate dehydrogenase(MDH), Glucose-6-phosphate dehydrogenase(G-6PD)는 (-)극으로 이동하는 monomorphic enzyme으로 NaCl의 증가에 따라 PGM과 MDH는 효소의 양이 감소하였으나 G-6-PD는 양적변화를 보이지 않았다. Acid phosphatase(ACK)는 (+)극과 (-)극에 각각 1개씩의 효소를 가진 dimorphic enzyme으로 나타났고, NaCl의 양이 증가함에 따라 효소의 양이 감소하였다.

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E312 Cloning of the *Legionella pneumophila panB* gene encoding ketopantoate hydroxymethyltransferase and Overexpression of the enzyme

Se Jin Kim*, Jin Koo Kim, Kwang Dong Kim, Jong-Seok Lim, Hee Gu Lee, Nicholas P. Cianciotto[1] and Yong-Kyung Choe

Korea Reaserch Institute of Bioscience and Biotechnology.
[1] Department of Microbiology-Immunology, Northwestern University.

Legionella pneumophila, the cause of Legionnaires' disease, is able to survive intracellularly in eukaryotic cells such as monocytes, macrophages, and protozoan organisms. The *panB* gene from *Legionella pneumophila* encoding the first enzyme of the panthothenate biosynthesis pathway, ketopantoate hydroxymethyl-transferase (KPHMT), has been isolated by functional complementation of *E. coli* Hfr300 YA139, which carries the *panB* mutation and lacks KPHMT activity. Positive clones were analyzed by BLASTP and ORF search of the National Center for Biotechnology Information (NCBI) protein data bases. The first ORF, which is not complete, is 229 bp in length, and the second is 789 bp. Amino acid sequence comparison of the ORF with the NCBI data base revealed that the first ORF were sequence similarity with the sequence of *panC* and that the second ORF were similar with the *panB* gene. The *panB* gene is encoding a protein of 262 amino acids with a predicted Mr of 28,591. *panB* and *panC* lie adjacent to one another, which is oriented in the same direction. *L. pneumophila panB* was determined by sequence comparison using an unweighted Clustal W method. The resulting phylogenetic tree of these proteins could be divided into the two groups. The most homologous was the *panB* encoded by *Bacillus subtilis.*