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Molecular Cloning and Characterization of a Glycosyl Hydrolase Family 9 Cellulase Expressed throughout the Digestive Tract of the Emma Field Cricket, *Teleogryllus emma*

Namjung Kim[1,2], Young Moo Choo[1], Kwang Sik Lee[1], Zhigang Hu[1], Seong Jin Hong[2],
Kwang Youl Seol[2], Hung Dae Sohn[1] and Byung Rae Jin[1]*

[1]Department of Applied Biotechnology, College of Natural Resources and Life Science,
Dong-A University, Busan 604-714, Korea
[2]Department of Agricultural Biology, National Institute of Agricultural Science and Technology,
Suwon 441-100, Korea

A novel endogenous -1,4-endoglucanase (EG) gene belonging to the glycoside hydrolase family (GHF) 9 expressed throughout the digestive tract of the emma field cricket, *Teleogryllus emma*, was cloned and characterized. This gene consists of a single exon coding for 453 amino acid residues and exists as a single copy in the *T. emma* genome, named *TeEG-I*. *TeEG-I* shares all the features, including signature motifs and catalytic domains, of the GHF 9 members. The recombinant TeEG-I, which is expressed as a 47-kDa polypeptide in baculovirus-infected insect Sf9 cells, showed the highest activity at 40 °C and pH 5.0. Northern and Western blot analyses and enzyme activity assay revealed that TeEG-I was expressed throughout the digestive tract; TeEG-I shows the highest expression in the salivary gland, followed midgut, foregut and hindgut. These results indicate that TeEG-I was expressed throughout the entire digestive tract of *T. emma*, suggesting involvement of endogenous TeEG-I for a sequential cellulose digestion throughout the *T. emma* digestion tract.

Key words: *Teleogryllus emma,* Baculovirus, cDNA cloning, cellulase, endoglucanase, enzyme, insect cells, emma field cricket

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Production of an Useful Saccharide from an Unused Mushroom Resources by Bacteria

Yong-Seok Lee*, In-Hye Park, Keun-Ki Kim[1], Sun-Gu Kim[1] and Yong-Lark Choi

Major of Biotechnology, Faculty of Natural Resources and Life Science, Dong-a University, Busan, Korea.
[1]Major of Animal Science, Faculty of Natural Resources and Life Science, Pusan National University, Miryang, Korea.

Over 200 microorganisms for producing of an useful saccharide were isolated from Korea soil. One colony has many polysaccharide degrading enzyme, (soluble chitosan, Xylan, soluble starch, and carboxymethyl cellulose). It was identified as *Klebsiella pneumoniae* by 16S rDNA and *rpoB* sequencing analysis. The 16S rDNA sequence were very similar to *K. pneumoniae* with 99% homology. And *rpoB* sequence was very similar to *K. pneumoniae*, with 98% homology. The *K. pneumoniae* gene encoding cellulase was cloned from the genomic library. The cellulase gene was composed of an 1002 bp open reading frame and 334 amino acid with 37kDa enzyme determined by sequencing analysis.

Key words: Oligosaccharide, mushroom, *Klebsiella* sp.