D-47 Isolation of a chitin-degrading bacterium, Cellulosimicrobium cellulans CH10 and its antifungal activity. Kwang Youll Lee, Han Woo Kim, Ok Ju Chun,
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A bacterial strain with colloidal chitin hydrolysis activity was isolated from tomato cultivated healthy soil at Taejeo, Pusan. The isolate was identified as *Cellulosimicrobium cellulans* CH-10 by analyzing its morphological, physiological properties and 16S rDNA sequences. *C. cellulans* CH-10 was shown to excrete chitinases into the culture supernatant when cultivated in a liquid culture containing colloidal chitin. After concentration of the culture supernatant by precipitation with ammonium sulfate, the induced chitinases was analyzed by in-gel chitinase assay using carboxymethyl-chitin-remazol brilliant violet 5R (CM-chitin-RBV) as a substrate. Three protein bands possessing chitinase activity were obtained with apparent molecular masses of about 33, 47 and 73 kDa, respectively. When *C. cellulans* CH-10 isolate was co-cultured with the fungal pathogen *Fulvia fulva* TF13, causing tomato leaf mold, in PDB media, the CH-10 isolate showed a potent antifungal activity against the pathogen. The microscopic analysis suggested that the chitinase produced from the CH-10 isolate might act on the cell wall of *F. fulva* resulting in malformation of fungal hyphae.

D-48 Cloning and expression of two chitinase genes from Bacillus licheniformis
N-1 and B. licheniformis CH-1. Han Woo Kim, Kwang Youll Lee, Kwang
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We cloned chitinase genes from bacterial isolates from upland soils, *Bacillus licheniformis* N1 strain showing high antifungal activity and CH-1 strain possessing chitinase activity. The CH-1 strain was identified as *Bacillus licheniformis* CH-1 by analysis of 16S rDNA sequences. The chitinase genes of the N1 strain and the CH-1 strain were cloned by PCR using PCR primers based on chitinase gene sequence of *B. licheniformis* TP1. Two chitinase genes exhibited 96% of identity of deduced amino acids sequence by Clustal W analysis. The nucleotide sequence of two genes revealed a single open reading frame encoding 598 amino acids with an expected molecular mass of about 66 kDa. The deduced amino acid sequence of chitinase gene appeared to have three functional domains, such as catalytic domain (amino acid residues 44 to 433), fibronectin typeIII like domain (amino acid residues 460 to 541) and chitin-binding