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A recombinant bacterial ferulate esterase

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L ignocellulosic biomass refers to plant biomass that is composed of cellulose (35-50%), hemicellulose (20-35%), and lignin L(10-20%). Because lignocellulosic biomass is renewable and sustainable, the cost effective conversion of these materials to fuels and chemicals is a global priority to overcome limited petroleum resources. The two major polymer components of lignocellulosic biomass (cellulose and hemicellulose) are covalently bound through ester linkages to the third component (lignin) via a variety of hydroxycinnamic acids including ferulic, ρ -coumaric, sinapic and ρ -cafferic acid. The tight ester-ether bridges among the polysaccharides form the interwoven mesh-like plant cell wall structure. Ferulic acid esterases break down the ester bonds between hydroxycinnamates and sugar. We have identified a bacterial ferulate esterase from plate assay, and the specific ferulate esterase gene was amplified from genomic DNA and cloned into pET28b vector. The recombinant ferulate esterase was expressed in *E. coli* cells. The purified enzyme showed optimal activity at pH 6.5 and 37°C. Kinetic parameters determined by the Hanes-Woolf method showed a Vmax of 0.99 µmol/min/mg and Km of 0.60 mM. The enzyme can be produced at higher levels when the culture was grown at 32°C, and maximum activities were detected after 6 hr of induction. Ferulate esterase is an important component of enzyme mixtures that degrade lignocellulosic biomass materials, particularly the cross link between lignin and hemicellulose. This enzyme can be used for biomass hydrolysis and for production of hydroxycinnamic acids as well as for readily digestible animal feed.

Biography

Liu received Ph.D. degree in Plant Molecular Genetics from the University of Illinois, Urbana-Champaign. Dr. Liu has been a research molecular biologist at USDA-ARS-NCAUR since 2002. Dr. Liu's work involves developing new biocatalysts for converting lignocellulosic biomass materials to biofuels and bioproducts. Specific research includes using whole genome sequencing, proteomics and genetic engineering techniques to design and improve metabolic pathways, and using microbial physiology and biochemical methods to discover new enzymes and value-added co-products. Dr. Liu has authored and coauthored more than 54 peer reviewed publications. Dr. Liu has authored and co-authored four invited book chapters.

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