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# Molecular Characterization of Epoxide Hydrolase from *Aspergillus niger* LK Using Phylogenetic Analysis

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## Abstract

Epoxide hydrolase gene from *Aspergillus niger* LK, a fungus possessing the enantioselective hydrolysis activity for racemic epoxides, was characterized by phylogenetic analysis. The deduced protein of *A. niger* LK epoxide hydrolase shares significant sequence similarity with several bacterial EHs and mammalian microsomal EHs(mEH) and belongs to the α/β hydrolase fold family. EH from *A. niger* LK had 90.6% identity with 3D crystal structure of lqo7 in Protein Data Bank. Sequence comparison with other source EHs suggested that Asp$^{192}$, Asp$^{348}$ and His$^{374}$ constituted the catalytic triad. Based on the multiple sequence comparison of the functional and structural domain sequence, the phylogenetic tree between relevant epoxide hydrolases from various species were reconstructed by using Neighbor-Joining/UPGMA method. Genetic distances were so far as 1.841～2.682 but characteristic oxyanion hole and catalytic triad were highly conserved, which means they have diverged from a common ancestor.