Active-Site Engineering Expands the Substrate Profile of the Basidiomycete L-Tryptophan Decarboxylase CsTDC.

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Abstract

Aromatic L-amino acid decarboxylases (AADCs) catalyze the release of CO_2 from proteinogenic and non-proteinogenic L-amino acid substrates and are involved in pathways that biosynthesize neurotransmitters or bioactive natural products. In contrast to AADCs from animals and plants, fungal AADCs have received very little attention. Here, we report on the in vitro characterization of heterologously produced Ceriporiopsis subvermispora AADC, now referred to as CsTDC, which is the first characterized basidiomycete AADC. This study identified the enzyme as a decarboxylase that is strictly specific for L-tryptophan and 5-hydroxy-L-tryptophan. The tdc gene was subjected to saturation mutagenesis so as to vary the key active site residue, Gly351. Aliphatic amino acid residues, L-serine, or L-threonine at position 351 added L-tyrosine and 3,4-dihydroxy-L-phenylalanine (L-DOPA) decarboxylase activity while retaining stereospecificity and L-tryptophan decarboxylase activity.

Involved units

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