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## The bile acid-inducible baiF gene from Eubacterium sp. strain VPI 12708 encodes a bile acid-coenzyme A hydrolase.

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### Abstract

The human intestinal Eubacterium sp. strain VPI 12708 has been shown to have a multistep biochemical pathway for bile acid 7 $\alpha$ -dehydroxylation. A bile acid-inducible operon encoding 9 open reading frames has been cloned and sequenced from this organism. Several of the genes in this operon have been shown to catalyze specific reactions in the 7 $\alpha$ -dehydroxylation pathway. The baiF gene from this operon was cloned, expressed in Escherichia coli, and found to encode a novel bile acid-coenzyme A (CoA) hydrolase. The subunit molecular mass of the purified bile acid-CoA hydrolase was calculated to be 47,466 daltons and the native enzyme had a relative molecular weight of 72,000. The  $K_m$  and  $V_{max}$  for choly-coenzyme A (CoA) hydrolysis was approximately 175 microm and 374 micromol/min per mg protein, respectively. The enzyme used choly-CoA, 3-dehydrocholy-CoA, and chenodeoxycholy-CoA as substrates. No hydrolytic activity was detected using acetyl-CoA, isovaleryl-CoA, palmitoyl-CoA, or phenylacetyl-CoA as substrates. Amino acid sequence database searches showed no significant similarity of bile acid-CoA hydrolase to other thioesterases, but significant amino acid sequence identity was found with Escherichia coli carnitine dehydratase. The characteristic thioesterase active site Gly-X-Ser-X-Gly motif was not found in the amino acid sequence of this enzyme. Bile acid-CoA hydrolase from Eubacterium sp. strain VPI 12708 may represent a new family of thioesterases.

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