ABSTRACT

MYCOBACTERIUM SMEGMATIS MC² 155 *fbiC* AND MSMEG_2392 ARE INVOLVED IN TRIPHENYLMETHANE DYE DEGRADATION AND COENZYME F_{420} BIOSYNTHESIS

Triphenylmethane dyes are carcinogenic and widely used in the aquaculture and textile industries. Bioremediation, the use of microorganisms to degrade xenobiotic compounds, may be a more efficient alternative to conventional treatment methods for dye contaminated waste. To identify genes involved in triphenylmethane dye decolorization by mycobacteria, a transposon mutant library of *Mycobacterium smegmatis* mc² 155 was created and screened for mutants unable to decolorize the triphenylmethane dye Malachite Green. One gene identified was *fbiC*, which is essential for the biosynthesis of the electron carrier, coenzyme F_{420}. Also identified was MSMEG_2392, belonging to a superfamily without annotated function. High Pressure Liquid Chromatography revealed that F_{420} was absent in both mutant strains, indicating that, like *fbiC*, MSMEG_2392 is required for the biosynthesis of coenzyme F_{420} and this cofactor is likely the electron donor for the reduction of Malachite Green. This is the first report of this coenzyme in dye decolorization.

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