TRANSCRIPTIONAL REGULATION OF PYRIDOXINE BIOSYNTHESIS AND ITS INTEGRATION INTO THE REGULATORY NETWORK MODEL OF CORYNEBACTERIUM GLUTAMICUM

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Background: PdxR belongs to the MocR subfamily of GntR-type transcription regulators with an N-terminal HTH domain and a class I aminotransferase motif in the C-terminal region. It is involved in regulating pyridoxine biosynthesis in Corynebacterium glutamicum.

Objectives: Investigation of the PdxR regulon in C. glutamicum and its integration into the genome-wide transcriptional regulatory network model of this organism.

Methods: The pdxR gene was deleted and its target genes were identified by DNA microarray hybridization and RT-PCR. Potential DNA binding sites were detected with bioinformatic tools. Transcription start sites of the pdxST and pdxR genes were mapped by RACE-PCR.

Results: The pdxR gene is located upstream of pdxST, encoding the PLP synthase complex involved in the DXP-independent pathway of vitamin B₆ biosynthesis. Deletion of the regulatory gene pdxR resulted in pyridoxine auxotrophy. RT-PCR assays of the pdxR deletion mutant compared to the wild-type strain showed decreased relative expression for the pdxST genes. The pdxS-pdxR intergenic region contains DNA binding sites for PdxR and the SOS response regulator LexA. Defined deletion of the lexA gene in the wild-type strain also influenced differential gene expression of pdxST.

Conclusion: PdxR and LexA coregulate the genes for pyridoxine biosynthesis in C. glutamicum.

References:

