

Complete Circular Genome Sequence and Temperature Independent Adaptation to Anaerobiosis of *Listeria weihenstephanensis* DSM 24698.

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Abstract

The aim of this study was to analyze the adaptation of the environmental *Listeria weihenstephanensis* DSM 24698 to anaerobiosis. The complete circular genome sequence of this species is reported and the adaptation of *L. weihenstephanensis* DSM 24698 to oxygen availability was investigated by global transcriptional analyses via RNAseq at 18 and 34°C. A list of operons was created based on the transcriptional data. Forty-two genes were upregulated anaerobically and 62 genes were downregulated anaerobically. The oxygen dependent gene expression of selected genes was further validated via qPCR. Many of the differentially regulated genes encode metabolic enzymes indicating broad metabolic adaptations with respect to oxygen availability. Genes showing the strongest oxygen-dependent adaptation encoded nitrate (*narGHJ*) and nitrite (*nirBD*) reductases. Together with the observation that nitrate supported anaerobic growth, these data indicate that *L. weihenstephanensis* DSM 24698 performs anaerobic nitrate respiration. The wide overlap between the oxygen-dependent transcriptional regulation at 18 and 34°C suggest that temperature does not play a key role in the oxygen-dependent transcriptional regulation of *L. weihenstephanensis* DSM 24698.

KEYWORDS:

Listeria weihenstephanensis; adaptation to anaerobiosis; complete circular genome sequence; nitrate respiration; temperature; transcriptome

PMID: 28919887 PMCID:[PMC5585140](#) DOI:[10.3389/fmicb.2017.01672](#)