## SL308

# Transcriptional Regulation of *phn* Operon Which is Responsible for Phosphonate Degradation in Enteric Bacteria

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Phosphonates(Pn) are biogenic and xenobiotic compounds containing the stable C-P direct bond found in a variety of organisms. In some organisms, phosphonopeptides and phosphonolipids are synthesized, while in others ingested phosphonates serve as a sole source of carbon or phosphate. The phosphonates are using as antibacterial, antifungal, or antiviral agents in industry and agriculture and their toxicity are concerning in the environment. Microorganisms can cleave or metabolize the phosphonates and remove their toxicity.

Two pathways exist for cleavage of the carbon-phosphorus(C-P) bond of phosphonates, the C-P lyase and the phosphonatase pathways. It was previously demonstrated that *Escherichia coli* carries genes (named *phn*) only for the C-P lyase pathway and that *Enterobacter aerogenes* carries genes for both pathways (K. S. Lee, W. W. Metcalf, and B. L. Wanner, J. Bacteriol. 174:2501-2510, 1992). In contrast, *Salmonella typhimurium* LT2 carries genes only for phosphonatase pathway. The *phn* gene cluster (*phnXWRSTUV*) encodes for phosphonate cleavage and transport by the phosphonatase pathway of *Salmonella typhimurium* LT2. It appears to consist of two operons that are divergently transcribed (W. Jiang, W. W. Metcalf, K.-S. Lee, and B. L. Wanner, J. Bacteriol. 177:6411-6421, 1995).

We have tested the transcriptional regulation of *phn* promoters($P_{phnW}$, $P_{phnR}$, and $P_{phnS}$) of *Salmonella typhimurium* LT2 transferred in *Escherichia coli* which is well characterized in phosphate(*pho*) regulon control. The expression of *phn* operon is induced by Pi starvation and requires the *phoB* function, a transcriptional activator gene of the *pho* regulon. Here, we report the transcriptional regulation in both *in vivo* and *in vitro* of *phn* operons that encode phosphonate degradation in Enteric Bacteria.