

The effect of simulated copper stress on genes associated with the metabolism of polyphosphates and polyhydroxyalkanoates in *Bacillus thuringiensis* Y1

ABSTRACT

Aims: *Bacillus thuringiensis* Y1 is a copper-tolerant bacterium that can serve as a model for the elucidation of the mechanism of energy metabolism under simulated copper stress. This study aimed to elucidate the effects of simulated copper stress on the genes associated with the biosynthesis of polyhydroxyalkanoates (PAH) and the metabolism of polyphosphates (PP). **Methodology and results:** The gene expression study involved the growth of the bacterium in nutrient broth supplemented with two concentrations of copper sulphate (0.4 mM and 0.8 mM), followed by RNA extraction and quantification of four and 11 genes associated with the metabolism of polyphosphate (PP) and polyhydroxyalkanoates (PAHs) respectively, using reverse transcription quantitative polymerase chain reaction (RT-qPCR). Three genes associated with polyphosphate metabolism, which are polyphosphate kinase (ppk), exopolyphosphatase (ppx) and NAD kinase (ppnk), were all shown to be upregulated by both 0.4 mM and 0.8 mM copper, except for the 5'-nucleotidase (surE) gene that was downregulated under the second treatment. Among the 11 genes associated with the metabolism of polyhydroxyalkanoates, only the 3-ketoacyl-CoA-thiolase (phaA) gene was upregulated in both treatments and highly expressed in the second treatment; the majority were downregulated and repressed. **Conclusion, significance and impact of study:** The study demonstrated that copper induces the metabolism of polyphosphates in *B. thuringiensis* Y1 that serve as an alternative source of energy under copper stress. This model can be extended to the study of other species of *Bacillus* under environmental stress.