

Interplay between copper and zinc homeostasis through the transcriptional regulator Zur in *Enterococcus faecalis*

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Resumen

By integrating the microarray expression data and a global *E. faecalis* transcriptional network we identified a sub-network activated by zinc and copper. Our analyses indicated that the transcriptional response of the bacterium to copper and zinc exposure involved the activation of two modules, module I that contains genes implicated in zinc homeostasis, including the Zur transcriptional repressor, and module II containing a set of genes associated with general stress response and basal metabolism. Bacterial exposure to zinc and copper led to the repression of the zinc uptake systems of module I. Upon deletion of Zur, exposure to different zinc and copper conditions induced complementary homeostatic mechanisms (ATPase efflux proteins) to control the intracellular concentrations of zinc. The transcriptional activation of zinc homeostasis genes by zinc and copper reveals a functional interplay between these two metals, in which exposure to copper also impacts on the zinc homeostasis. Finally, we present a new zinc homeostasis model in *E. faecalis*, positioning this bacterium as one of the most complete systems biology model in metals described to date.

Palabras clave

KeyWords Plus: [Bacillus-Subtilis Zur](#); [Corynebacterium-Glutamicum](#); [Uptake System](#); [Functional-Analysis](#); [Escherichia-Coli](#); [Gene-Expression](#); [Binding;Protein](#); [Networks](#); [Pathogen](#)

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