

Comparative analysis of metal-binding properties of C-terminal FeoB peptide models from selected Gram-negative bacteria

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Streszczenie

In our previous work, we analyzed the coordination chemistry of the peptidic model of the C-terminal part of *E. coli* FeoB protein, regarded as the most important Fe(II) bacterial transporter in Gram-positive and Gram-negative bacteria. The C-terminal region of FeoB contains conserved cysteine and histidine residues, which create a potent metal-binding site, exhibiting high affinity towards Fe(II), Mn(II), and Zn(II). The C-terminal FeoB sequences in Gram-negative bacteria vary in the number and position of additional potential metal-binding residues, aspartic and glutamic acids, which could affect the affinity of the region towards metal ions and potentially even the specificity of the metal binding. Therefore, in this work, we have decided to investigate the metal-binding properties of the peptidic models of the C-terminal FeoB region of three Gram-negative bacteria: *Yersinia pestis* (**L1**, Ac-RRARSRTVRLQNSEPANCCRSSGSNCH), *Klebsiella pneumoniae* (**L2**, Ac-RRARSRVDSLLATRKTPASCCSSPAGDCH), and *Salmonella typhimurium* (**L3**, Ac-RRARSRVDIELLATRKKNVSSCCSGTAGNCH). With a variety of physicochemical methods (potentiometry, ESI-MS, NMR, CD), we have described complexes of Fe(II), Mn(II), and Zn(II) with the studied ligands and discussed the influence of the specific residues on the metal-binding properties of the peptidic models. These findings enhance our understanding of FeoB-mediated metal transport and provide insights into pathogen-specific metal homeostasis mechanisms.

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