



Coordination of Ni²⁺ and Cu²⁺ to metal ion binding domains of *E.coli* SlyD protein.

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Streszczenie

The C-terminal region of Escherichia coli SlyD is unstructured and extremely rich in potential metal-binding amino acids, especially in histidine residues. SlyD is able to bind two to seven nickel ions per molecule, in a variety of coordination geometries and coordination numbers. This protein contributes to the insertion of nickel into the hydrogenase precursor protein and it has a peptidyl-prolyl cis/trans-isomerase activity which can be regulated through nickel ions. This inspired us to undertake systematic studies on the coordination ability of two histidine-rich peptides from the C-terminus of the SlyD protein with nickel. Also, it is known that histidine-rich regions are part of a Cu(2+) binding domain involved in copper uptake under conditions of metal starvation in vivo in other bacteria. For this reason we decided to examine the complex formation of Ac-AHGHVHGAHDHHHD-NH(2) and Ac-GHGHDHGHEHG-NH(2) fragments with copper ions, which are also reference metal ions in this study. Experiments were performed in a DMSO/water 30:70 solvent. The Ac-AHGHVHGAHDHHHD-NH(2) and Ac-GHGHDHGHEHG-NH(2) fragments were synthesized and their interactions with Ni(2+) and Cu(2+) ions were studied by potentiometric, mass spectrometric, UV-vis, CD, EPR, and NMR spectroscopic techniques in solution. The results show that the Ac-GHGHDHGHEHG-NH(2) fragment forms equimolar complexes with both nickel and copper ions. At physiological pH, the metal ion is bound only through nitrogens from imidazole sidechain of histidine residues. On the contrary, Ac-AHGHVHGAHDHHHD-NH(2) binds 2 metal ions per molecule, at pH range 5 to 7, even if the 1:2 metal:peptide ratios were used. NMR studies indicate the involvement of all His residues in this pH-range in metal binding of the latter peptide. At higher pH, the stoichiometry changes to 1:1 and the His residues are displaced by amide nitrogens.

Adres publiczny

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