Coordination properties of Cu(II) ions towards the peptides based on the His-Xaa-His motif from *Fusobacterium nucleatum* P1 protein.

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The coordination capacity of the copper(II) ions with peptides (fragments of the P1 protein - one of the outer membrane protein from *Fusobacterium nucleatum*) based on the His-Xaa-His motif was carried out using potentiometric measurements, mass spectrometry and spectroscopic techniques: UV–Vis, CD and EPR. The selected tetrapeptides (**Ac-HGHE-NH$_2$**, **Ac-GHEH-NH$_2$**, **Ac-HEHQ-NH$_2$** and **Ac-EHEH-NH$_2$**) form both mononuclear and bis-complexes with copper(II) ions. In the case of mononuclear complexes the CuL and $CuLH_{-2}$ species dominate in the solution, where the coordination sphere is create by $\{2\times N_{Im}\}$ and $\{2\times N_{Im}, 2\times N^{-}_{amide}\}$, respectively. The **Ac-HGHE-NH$_2$** peptide form more stable the $CuLH_{-2}$ complex with the $4N\{2\times N_{Im}, 2\times N^{-}_{amide}\}$ binding site compared to the other ligands. The presence of glutamic acid residue in sequence **Ac-HEHQ-NH$_2$** produced the destabilization of the $CuLH_{-2}$ complex in comparison to that of the **Ac-HGHE-NH$_2$** sequence. For the $CuLH_{-3}$ complex the coordination process for complexes containing a histidyl residue in the first positions (H^1) proceed towards *C*-terminal sequence of the peptide. The bis-complexes are formed in the solution, where the metal ion is bounded by four imidazole nitrogen atoms $\{4\times N_{Im}\}$.

Słowa kluczowe

P1 protein, Copper(II) complexes, Peptide, histidine, Fusobacterium nucleatum

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