

Investigation on the metal binding sites of a putative Zn(II) transporter in opportunistic yeast species *Candida albicans*.

Autorzy

Denise Bellotti

Dorota Łoboda

Magdalena Rowińska-Żyrek

Maurizio Remelli

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Streszczenie

In the present work, we focus on C4YJH2, a protein sequence of 199 amino acid residues, found in the genome of *Candida albicans*, and suggested to be involved in metal transport. *Candida albicans* is a member of the normal human microbiome; under certain circumstances that allow it to grow out of control, it can transform into a very dangerous fungal pathogen. The most probable Zn(II) binding domain of this sequence was identified at its C-terminus, a histidine-rich region, well conserved in numerous fungal Zn(II) transporters. The Zn(II) binding behaviour towards the three peptides Ac-FHEHGHSHSHGSGGGGGG-NH₂ (residues 131–148), Ac-SHSHSHSHS-NH₂ (residues 157–165), and Ac-FHEHGHSHSHGSGGGGGGSDHSGDSKSHSHSHS-NH₂ (residues 131–165) was explored by means of different thermodynamic and spectroscopic techniques. Cu(II) was also investigated since this endogenous metal can compete with Zn(II) for the same binding sites. The results indicate that the peptides under investigation have the ability to tightly coordinate Zn(II), at physiological pH, thus suggesting that the whole protein sequence can play a role in Zn(II) acquisition and regulation. Cu(II) is able to form even stronger complexes than Zn(II) but it is normally present in very low concentrations in the biological environment. The competition between Zn(II) and Cu(II) could be exploited to impair the Zn(II) acquisition routes of *Candida albicans*. Among the two binding sites, the affinity of both Zn(II) and Cu(II) is higher for that located at the residues 131–148, although the coordination geometry is rather different for the two metal ions.

Adres publiczny

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