Speciation of labile metal biomolecule complexes – not always a job for hyphenated mass spectrometric techniques

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The determination of biomolecules containing metals using chromatography coupled to elemental mass spectrometry is very attractive. The reason for that is the species-unspecific response of ICP-MS. The problem is however, if the metals are not covalently bound to the biomolecules.

In this lecture a couple of new quantification and identification strategies for metalloproteins in real samples will be presented.

The first study is generating a copper and zinc isotopically-enriched superoxide dismutase (SOD) which has been used to quantify SOD in liver homogenates using 2 D chromatography ICPMS[1] and GE-LA-ICPMS. It will be made clear that this approach is only feasible when worked under non de-naturing conditions.

The second study is highlighting that hyphenated techniques are not always successful for the detection of metal protein complexes. This will be demonstrated for metal complexes of calprotectin, the most abundant protein in neutrophils. Here the imaging of metals and proteins in addition to the structural features give first identification of the impossible involvement of such metal complexes in biota. Techniques such as 2 D imaging using laser ablation ICPMS and MALDI-TOF-MS as well as histopathology will be shown for an infection caused by the antibiotic-resistant *Staphyllococcus aureus*.[2]

References

[1] C.L. Deitrich, A. Raab, B. Pioselli, J. Thomas-Oates, J. Feldmann, Chemical preparation of an isotopically enriched superoxide dismutase and its characterisation as a standard for species-specific isotope dilution analysis, Anal. Chem. (2007) 79, 8381-8390.

[2] BD Corbin, EH Seeley, A Raab, J Feldmann, MR Miller, VJ Torres, KL Anderson, BM Datillo, PM Dunman, R Gerads, RM Caprioli, W Nacken, WJ Chazin, ER Skaar, Metal chelation as a defence strategy to prevent bacterial growth in tissue abscesses, Science, (2008) 319, 962-965