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2nd International Conference on
Current Trends in Mass Spectrometry
July 20-22, 2016   Chicago, USA

Mass spectrometry with inductively coupled plasma as a technique for analysis of complex matrix

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Mass spectrometry with inductively coupled plasma (ICP MS) takes the leading position among the instrumental techniques for elemental analysis. Main advantages of ICP-MS are: extremely high sensitivity (limits of detection down to ppt), multielement capability (detection of the elements from Li to U in one cycle from sample volume about 1 mL), high throughput, user friendly operation (not high qualification of an operator), gradually decreasing price. However as all instrumental techniques, ICP-MS suffers from spectral interferences and matrix effects – the dependence of analytical signal on the composition of a sample. These effects can strongly affect the accuracy of the analysis. Different types of interferences exhibit serious role in the analysis of the samples with complex composition e.g. biological samples (human liquids, bones, hairs), pharmaceuticals, strongly acidified resulting liquids after a solid sample digestion and so on.

The strategy of accounting for or, et best, eliminating these effects depends on the types of the ICP-MS instrument. Basically two types of instruments are now widely used – quadrupole ICP MS (QMS) and Sector Field MS (SFMS). The first has low mass resolution (not better than 600), but is much cheaper. The second has resolution up to 7000, but is about 3-4 times more expensive. Evidently, the QMS instruments occupy larger part of the market. The problems of interferences are much stronger pronounced for the QMS instruments.

The results obtained in my group with a simple QMS will be presented in the talk. Different strategies of the accounting and elimination of the interferences will be exemplified on the developed strategy of the analysis of bio-samples and strongly acidic liquids after rock sample digestion. In case of bio-sample analysis two techniques of a sample pretreatment were compared - 1) acid mineralization (in open or closed vessels or MW digestion), and 2) dilution by the mixture of reagents. It was found that combination of instrumental parameters optimization and use of internal standard (IS) provides adequate accuracy of the determination in blood and hair samples for crucial elements - Al, Cr, Mn, Co, Cu, Zn, As, Se, Cd, Pb. Not trivial was the finding of the analytical strategy, which allows using one and any IS independent on its mass or ionization potential. Another approach was developed for analysis of acidic liquids. The pretreatment procedure and measurement strategy will be discussed in the talk.

In the end a brief overview of recent improvements of QMS instruments will be presented. These results are based on my lectures in MSU.

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Functional Proteomic Approach in Dry Eye Disease

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Identifying important biomarker(s) for a disease is a major challenge in clinical proteomics. In this paper we have introduced a metadata approach to classify proteomes from aqueous deficient dry eye (ADDE) disease. After initial selection of tear samples from control and ADDE subjects a disease specific proteome set was constructed using a simple set theory based reduction method. The properties for each of such protein members were then evaluated, and the properties having highest discriminatory power (between control and ADDE) were chosen. The electrostatic charge distribution and amino acid composition and to some extent overall hydrophobicity seemed to be the important discriminatory features. The ADDE patients thus showed a positive bias in their proteome as compared to control subjects. Similarly, the disease specific proteome contained lesser percentage of glycine and higher percentage of threonine. The meta-proteomic analysis thus implied that ADDE specific proteins have lesser flexibility in their conformation. The results seemed to have some correspondence with our recent finding that ADDE is a protein conformational disease having higher propensity for occurrence of aggregated proteins.

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J Chromatogr Sep Tech 2016
ISSN: 2157-7064 JCGST, an open access journal

Mass Spectrometry 2016
July 20-22, 2016

Volume 7, Issue 4(Suppl)

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