

DEPENDENCE OF MATRIX EFFECT ON IONIZATION POLARITY IN LC-ESI-MS

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Matrix effect (ME), the influence of co-eluting components on the ionization efficiency of the analyte, affects the trueness and precision of LC-ESI-MS analysis [1]. Both derivatization [2,3] and the use of negative ionization mode can reduce or eliminate ME. In order to investigate the effect of ionization polarity on the ME during analysis using derivatization, a quantitative LC-ESI-MS/MS method was validated for 22 amino acid DEEMM-derivatives in 15 samples. ME was investigated in alternating ESI ionization mode using the sample dilution approach, where relative standard deviation of back-calculated concentrations was used as indicator of presence of ME [3].

In the positive ion mode, ME was stronger in honeys (average RSD=20%) compared to the herbal extracts (average RSD=10%). The negative ion mode was free of ME (average RSD=8%), with only three exceptions in honeys. The ME was eliminated in the positive ion mode by sample dilution and agreement between concentrations from the two ion modes was achieved in case of all samples for most amino acids. [4]

This research shows, that when combining DEEMM derivatization, which has proven to be less influenced by the ME, and negative ionization mode, it is possible to achieve ME free analysis of low concentrations of amino acids in complex matrices. In addition, LoD and LoQ of analyses in negative ionization mode were similar to those in positive ionization mode. Those findings can be used when developing new derivation reagents. Usually, better ionization in positive ionization mode is targeted through incorporation of permanent positive charge to derivatives. As demonstrated in this work, negative ionization mode provides comparable LoD and LoQ but is virtually free from ME. [4]

References

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