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Commentary

Matrix effects in Protien Analysis by lC-MS Method

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Even in the early stages of chromatography with conventional detectors (UV / VIS, FID, etc.), it is clear that different sample matrices contain unique interfering chemicals to obtain effective quantitative results. It emphasizes the importance of using a spike matrix calibrator. However, while the main problem under these conditions was the presence of co-eluting chemicals with the same detector response, the risk of altering the detector response of the analyte was not yet an issue. Improved sample pretreatment and chromatographic separation, sample dilution, and the use of internal standards are some of the methods used to eliminate, minimize, or compensate for matrix effects.

No matrix is completely consistent, but the matrix effect is significantly reduced by using a variety of techniques such as standard addition, matrix conformance calibration, and the use of isotope analogs of the analyte as an internal standard. And can be corrected. Biofluids, ionization types, and sample preparation methods all affect the matrix effect. Both types of ionization show a matrix effect, but ESI has been shown to be more sensitive and APCI has been shown to be less sensitive. The method of sample preparation and the choice of internal standard have a significant impact on the matrix effect. Matrix effects that cause ion suppression or enhancement of the target analyte due to co-elution of residual components are common in isolated regions of the chromatogram. Matrix effects have been studied using approaches such as post-column injection and post-extraction addition.

LC-MS is one of the most sensitive and selective analytical techniques, but matrix effects are more likely to occur, especially when using ESI to analyze extracts from complex matrices. In the presence of co-eluting chemicals within the same matrix, the matrix effect is often caused by changes in the ionization efficiency of the target analyte. The matrix effect can be thought of as a decrease in response (ion suppression) or an increase in response (ion stimulation) (ion enhancement). Ion suppression and enhancement have a significant impact on the analytical performance of the method. Therefore, the matrix effect must be taken into account when validating the LC-MS method.

Since the discovery of the matrix effect, researchers have been working to understand the mechanism and reduce its impact. The sources of matrix effects and strategies for assessing, mitigating, and / or modifying them are reviewed in this commentary. Introducing the Matrix Effect Coefficient (MEF) based on the Stable Isotope Labeling Internal Standard (SILIS) and its applications. The MEF reflects the loss / increase from both sample preparation and the "traditional" matrix effect caused by co-eluting components during ionization with a mass spectrometer (MS) ion source. Order this to compensate for the matrix effect and recovery.

Matrix effects can have a significant impact on the identification of objects to be analyzed and the performance of quantitative analysis. For example, when using a high resolution MS, the mass accuracy may vary due to the matrix effect. False-negative results can occur due to ion suppression, and false-positive results can occur if the internal standard (IS) signal is more suppressed than the analyte signal. There is a sex. Studies of the matrix effect are specifically recommended by the US FDA Guidelines for Bioanalytic Analysis. Matrix effect can be measured using two different protocols: post-column injection and post-extraction addition.

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