THE EQUALIZER: A FITNESS-FOR-PURPOSE TOOL

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Introduction

Quantitative interferences[1,2] in ultratrace analyses can be a source of leading errors during the quantification of target analytes, the computation of their isotopically-labeled analogs' recoveries as well as the distortion of congener profiles and chromatographic properties. A quantitative interference is an organic chemical—either extracted from the sample or picked up during the sample handling—that survived the extensive sample fractionation procedure, elutes from the GC column within the retention time window of the target analytes, and is present in relatively high quantities (e.g., 50 ng/sec). It typically manifests itself by causing deflections—usually negative—in the QC check[3] (e.g., PFK) ion's selected ion current profile (SICP). Depending on the retention time of the quantitative interference, it may affect the computation of the various labeled standards recoveries and the uncertainty associated with the determination of isomeric- and congeneric isotope-dilution compounds. By the very nature of true-isotope-dilution, the quantitative interference—except in extreme cases—does not affect the precision and accuracy of the specific congeners for which a ^{13}C isotopically-labeled analogue is present.

Materials and Methods

All analyses were performed on a number of Waters/Micromass AutoSpec-Ultima and AutoSpec-Premier high-resolution mass-spectrometers using GC EI+ SIR acquisition at a resolving power of 10,000 (or >). The custom software described below was created using Microsoft's Visual Studio as a VB.NET Windows application.

Results and Discussion

Two types of quantitative interferences are possible. First, a quantitative interference can originate from specific chemical interferences presenting ions at m/z close to those of the lock-mass (even when operating at high resolution). Alternatively, they might result from a non-specific chemical interference from compounds that do not share ions in common with either the reference compound or the target analytes. The two mechanisms produce the same outcome. The non-specific type detunes or suppresses the ion source by space-charge effects[4] while for the specific-type, the presence of an isobaric interference within the lock-mass window leads to an error in the centroiding of the actual lock mass, and hence to an incorrect determination of the mass drift (the primary purpose of lock-mass correction). This effectively shifts the monitored mass for any target ion to the side of the peak away from its apex. In effect, the "sensitivity" of the detector is reduced by a factor roughly equivalent to the proportion of the negative deflection observed in the QC check ion SICP. Depending on the circumstances, the concentrations of target analytes quantified relative to a labeled internal standard isomer or congener (i.e., different retention time) can be under as well as overestimated. Similarly, under or overestimation of the recovery of the extraction standard—added to the sample before the extraction and measured against the injection standard—can result. Errors can be significant.

A number of approaches are used by laboratories to mitigate the effects of quantitative interferences: i.e., additional fractionation of the extract and re-analysis, or dilution of the extract and re-analysis with a consequent reduction in sensitivity. The options for the former are often limited with compounds such as PCBs, and the loss of sensitivity is also often unacceptable for many studies or regulatory work. A third alternative, discussed here, relies on a custom-made computer program whose function is to normalize the response of the detector to the conditions of the instrument corresponding to the situation where no quantitative interferences are present. The program is referred to as the Equalizer and makes use of the data from the various QC check ions to assess the degree of interference and compute the correction required. A number of special cases also have to be considered such as the consequence of excessive quantitative interferences, and on-going correction from function to function (i.e., mass descriptors). Two sets of data are produced. The first is untreated data (i.e., unequalized) for which the various QC Check Ion SICP are provided showing the quantitative interferences. The second set of data is obtained following the application of the Equalizer program where the various analytes and labeled standards SICPs are displayed along with each corresponding QC Check Ion SICP. The data files are assigned the same name with the

"EQ" appended to it. The program has been refined over the past eight years using actual situations during the analyses of PCDD/F, PCB and PAH in a variety of environmental and biological samples. Validation of the Equalizer was conducted with the analyses of SRMs and replicate analyses as well as other conventional means while comparing the equalized and unequalized results. The validation shows that the Equalizer applied to the analytical raw data lowers the uncertainty (better precision and accuracy) of the measurements and therefore enhance the quality of the decision made by the data end user; i.e., fitness-for-purpose.

References

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