Method for Calibration and Correction of Mass Spectrometry with Reduced Interference from Internal Standards

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Technology description

Isotopically labeled internal standards are widely used in mass spectrometry (MS) analysis, with the assumption that there is no interference or cross-talk between the internal standard and analyte. This can result in nonlinear data, limited dynamic range, and inaccurate assessment of analyte concentration.

Two simple equations, derived after experimental determination of one or two constants and an adjustable parameter, are applied to generate a more accurate fit to isotope-caused, nonlinear MS data, to correct the inherent bias (inaccuracy) for many analyte/internal standard pairs. This approach removes much of the difficulty associated with use of stable labeled internal standards, such as deuterium labeling, including chromatographic separation, isotope effects, and cost. The invention could be implemented as a product as analysis software for the MS instrument, or provided as an add-on software module.

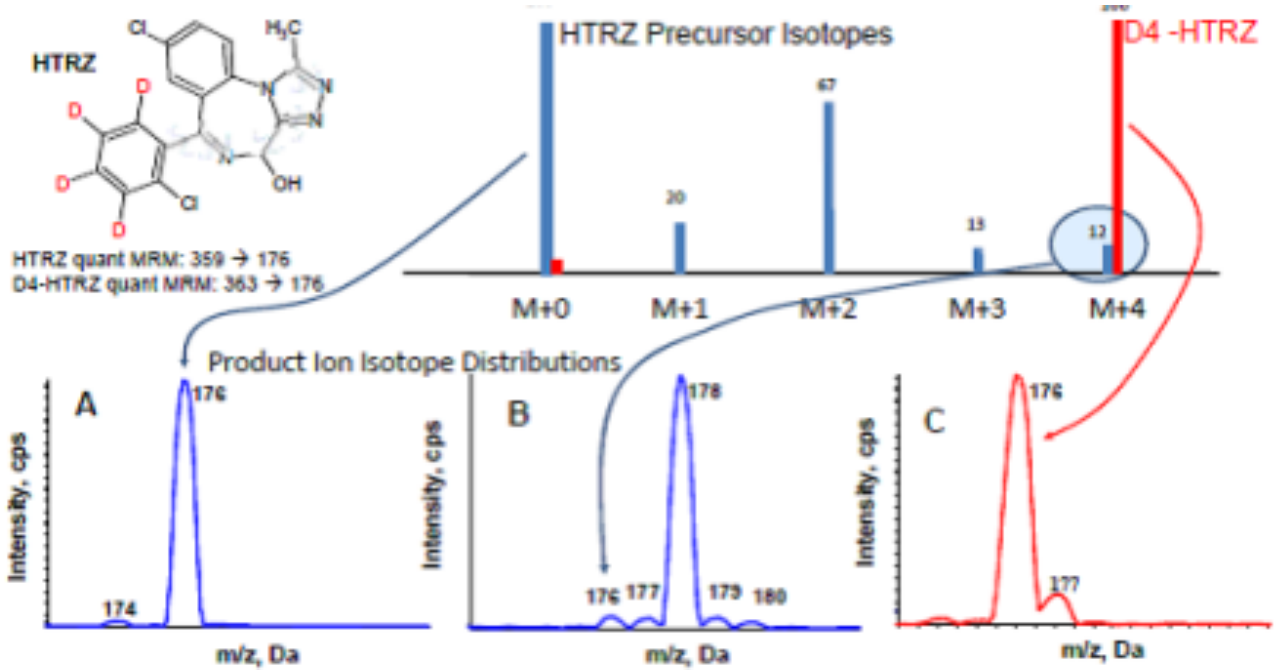
Value Proposition

•Allows for mass spectrometric analyses to span a broader quantitative range with more accuracy across a broader range of concentrations.

•Expands use of analyte/internal standard combinations that would otherwise beimpractical owing to their nonlinear behavior.

•Correction for contributions of analyte isotopes to internal standard signal improves quantitation and provides extended dynamic range.

•Clinical and bioanalytical assays can benefit by providing better fitting regressions andeliminating a source of systematicbias.



Market Opportunity

The spectrometry instrumentation market was estimated to be $10 billion in 2011. Mass spectrometry is an analytic technique with high specificity and a growing presence in clinical laboratory medicine, with applications in toxicology, endocrinology, and metabolomics.

Institution

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