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The precise measurement of biological response in metabolomics using the IROA protocol: Yeast toxicity profiles

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Abstract

The IROA protocol generates isotopically signed cells, i.e. cells in which all of the biomolecules (DNA, RNA, and metabolites) carry distinctive isotopic signatures. Since these signatures may be distinguished from one another, artifacts may be removed, and multiple samples prepared and analyzed in a single analytical process, thereby reducing all sample-to-sample variances, including ion suppression, and increasing data quality. The signature for each molecule also carries information defining its molecular structure making its identification less prone to error. The significantly enhanced quantization of having a biochemically complex internal standard present in every experimental sample is an additional benefit of the IROA protocol. We will present the development of toxicological mechanism of action (MOA) profiles using an IROA protocol. In yeast, *S. cervisiae* S288C, the MOA to flucytosine is clearly and easily seen. Additional metabolic pools that are secondarily affected by the primary mechanism of toxicity are also easily determined. Thus the full biological response to the toxin may be easily defined.

Biography

Beecher was a member of the Department of Pathology, University of Michigan School of Medicine until 2011 when he founded NextGen Metabolomics. He was also one of the founders of Metabolon, and Metabolic Analyses. His PhD was granted in 1985 in Pharmaceutical Sciences specializing in Natural Products drug discovery. He has more than 25 years of experience in metabolomics and drug discovery and development, has published over 80 peer-reviewed papers, and is listed as the inventor of 8 patents in metabolomics.