J Chromatogr Sep Tech 2016, 7:7 (Suppl)
http://dx.doi.org/10.4172/2157-7064.C1.023

Gas chromatographic analysis of degradation products from amine in CO_2 capture: An overview

Shaukat Mazari
Dawood University of Engineering and Technology, Pakistan

This paper elucidates the current gas chromatographic (GC) analytical method and advances in quantitative determination of amine degradation products, emphasizing on influence of sample preparation, column and detector selection. We commented on the literature and found that head space solid phase micro extraction (HS-SPME) is one of the simplest and viable methods for analyzing amines. Plausibly, GC-MS is a well-established method with pre-derivatization, and it is affordable while its library is readily available for searching the detected compounds. Amine degradation is one of the major issues associated with amines based CO_2 absorption in post-combustion CO_2 capture. Therefore, analysis of amines and their degradation products is of utmost importance in determining the viability of the amine. This review presents the applications of GC in amine-based CO_2 capture technology with their corresponding degradation products.

shaukatmazari@gmail.com

Identification of processes related impurities and hepato-enzymatic metabolites for liver cancer radiomedicine, Re-188-MN16ET using HPLC-tandem mass spectrometry

Wei-Hsi Chen
Institute of Nuclear Energy Research, Taiwan (ROC)

The radio-isotope Re-188-labeled ligand with amino-amido-dithiol (N_2S_2) tetradentate and hexadecyl carboxylate ethyl ester (Re-188-MN16ET) dissolved in lipiodol has been served as radio-transcatheter arterial embolization (TAE) therapeutic medicine under preclinical study for hepatocellular carcinoma (HCC). The impurities of its precursor, trimethylphenyl protected- H_3MN16ET arose from the preparative processes and metabolites of Re-MN16ET in hepatic medium were identified by HPLC coupled with electrospray ionization tandem mass spectrometry (HPLC-tandem MS) based on m/z of protonated molecular ions and multi-fragmentation ions obtained from triple quadrupole-linear ion trap (QqQ-LIT) and quadrupole-time of flight (Q-ToF) mass spectrometry. The molecular structure of unknowns (including impurities in protected-H^3MN16ET and metabolites from bio-transformation of Re-MN16ET) were directed by sketching fragmentation profiles. There were 2 impurities identified in protected-H3MN16ET and 2 metabolites (Re-MN16-CO_2H and de-ReO-MN16-CO_2H with disulfide bond) involved in hepatic biotransformation of Re-MN16ET. The potential deteriorate pathways of protected-H3MN16ET were also found. The methodology was advanced applied to solve the identity of derivatives which come from Re-188 labeling process for protected-H_3MN16ET into end-product, Re-188-MN16ET.

whchen@iner.gov.tw