

XV Reunión Científica de la SECyTA y VII Reunión Nacional de la SEEM

Lipidomics Based On High Resolution Mass Spectrometry: A Novel Strategy Employed In Food and Nutrition Research.

Jana Hajslova. Institute of Chemical Technology, Prague, Czech Republic

This work can be a new approach for the analysis of lipids. HRMS used to be a common strategy for the structural and quantitative characterization of these compounds. Using this tool, they have been developed new strategies for the analysis of lipids exposed to degradative conditions. In fact, the generated compounds have been related with healthy problems. Methods commonly used are hard-working and the accuracy is questionable. For this reason, they propose a faster analysis that permits us a comprehensive and specific information interpretation.

Different strategies were developed in this work to achieve this objective and one of the most interesting was the use of an ambient high resolution mass spectrometry employing Direct Analysis in Real Time (DART) ion source for an assessment of lipid quality with regards to content of primary and secondary oxidation products. In this way, they try to find differences between Spanish and Italian oils. A simple sample treatment was carried out in order to avoid compound discriminations. They compare LC-HESI (+) and DART (+) to evaluate the best option for this analysis. In order to classify samples, it is necessary to find biomarkers that allow us to distinguish oil types and do a fast screening analysis. DART shows a high matrix effect although it was not a problem for oil samples. Both PCA models (LC-HESI (+) and DART (+)) could separate Spanish and Italian samples. So, there are not big differences between both analytical methods.

Finally, they selected DART (+) as the best option because they save a lot of time using this ambient technique needing only 2.5 h for the analysis of all the samples while LC-HESI (+) needs 54 h. So, this work shows the advantages of ambient ionization techniques (DESI, DART, etc.) in order to save time.

Breath Analysis: Transitioning from Bench to Bedside

Pablo Martínez-Lozano Sinues. ETH Zurich, Switzerland

It was a really interesting presentation. Normal human analysis includes blood and urine analysis but the information supply by breath analysis is always ignore. However, it is well-known that exhaled air contain metabolites which may be related with biochemical activity. Furthermore, a high amount of diseases have been detected by the smell through the years. These types of analysis can be labored if a GC-MS determination is used to identify metabolites. Additionally, using sensors the analysis time is shorter but the identification could be a problem.

For these reasons, they have modified the entrance of a QTOF mass spectrometer to allow for real-time analysis of the breath using SESI-MS. Employing this method they could identify an increment in the signal of some metabolites during the disease. In this way, they develop a fast and easy real-time method to add extra-information for the clinical analysis.

This method can be also used for migration analysis of volatile compounds from food packaging to air as, for example, fluorotelomers. It can be a good screening analysis to discriminate between positive and negative samples if the sensitivity of the method is enough for the required levels.

Juan Francisco Ayala Cabrera