Implementation of a QA/QC system for untargeted GC×GC analysis.

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Over the past few decades, the field of analytical metabolomics has witnessed continuous growth, particularly in the realm of investigating human health through untargeted analyses. The primary goal has been to detect and identify a broad spectrum of small molecules [1]. The integration of comprehensive two-dimensional gas chromatography (GC×GC) has been a pivotal advancement in facilitating these untargeted analyses [2]. However, as this technology has become an indispensable part of research in this domain, the pressing need for enhancing and standardizing quality assurance (QA) and quality control (QC) practices in untargeted metabolomics has come to the forefront. The metabolomics quality assurance and quality control consortium (mQACC) have played a significant role in developing various QA/QC systems [3]. Despite these efforts, the field continues to face challenges, with a noticeable lack of documentation and standardization, highlighting the importance of addressing these gaps for the advancement of untargeted metabolomics research [4].

In our research, we delved into the establishment of a robust QA/QC system tailored for untargeted analysis, employing two distinct GC×GC-TOFMS systems. Initially, we conducted a thorough comparison of the analytical capabilities of two GC×GC instruments, each equipped with a different modulator system—a cryogenic and a Peltier system. Our investigation involved scrutinizing the analytical performance through the analysis of alkanes (C8-C20) standard solutions and QC solution mix comprising 37 compounds with diverse chemical properties derived from high-quality analytical grade standards.

Subsequently, we devised a comprehensive method for monitoring the behavior of 37 different compounds utilizing both systems. Indeed, the comparison between the two systems has revealed that, despite having similar analytical parameters and systems (including the same column set, injection and chromatographic methods, as well as mass spectrometry (MS) systems), some variations on compounds detectability can be observed. This underscores the importance of implementing a robust QA/QC system.

The analytical method developed for monitoring the 37 compounds, each exhibiting varying volatility and response due to the diverse chemical functions represented in the panel, has proven effective. Compounds are distributed across the entire 2D chromatogram, demonstrating good distribution and separation in both first and second dimensions over a 35-minute run.

In examining the control charts generated for both instruments over the last few months, no deviations for retention times were observed for all compounds, indicating the system's suitability for extended run periods. Additionally, the areas remained stable over months, with an average deviation of 7.73% ± 4.85 for all 37 compounds. This method not only showcased the versatility of the systems but also highlighted its efficacy in handling a diverse range of compounds.

Finally, to ensure the reliability and stability of our analytical processes, we implemented a sophisticated QA/QC system featuring control charts. This system meticulously tracked the evolution of retention time and response (area values) for all 37 compounds over six months. Our final goal is to extend this systematic follow-up to encompass all four GC×GC systems within our laboratory. By doing so, we aim to establish a

standardized and robust QA/QC framework that will contribute to the precision and reproducibility of our analytical endeavors in the long run for untargeted metabolomics.

References:

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