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PROCESO SELECTIVO POR EL SISTEMA DE ACCESO LIBRE PARA INGRESO EN LA ESCALA DE TECNICOS SUPERIORES ESPECIALIZADOS DE LOS ORGANISMOS PÚBLICOS DE INVESTIGACIÓN, CONVOCADO POR RESOLUCION DE 16 DE DICIEMBRE DE 2020 (BOE Nº 341 DE 31 DE DICIEMBRE)

Tercer ejercicio:

Traducción directa al castellano

Programa: EXPERIENCIA EN ÓMICAS, BIOINFORMÁTICA Y MANIPULACIÓN GENÉTICA DE PLANTAS.

- No abra el ejercicio ni lo empiece hasta que se le indique.
- El ejercicio consistirá en una traducción directa al castellano, sin diccionario, durante un periodo máximo de una hora, de un texto determinado por el Tribunal en el idioma elegido por el aspirante, relacionado con los aspectos técnicos del programa al que se presenta.
- Una vez abierto el ejercicio, compruebe que consta de una página y que sea legible. En caso contrario solicite uno nuevo al personal del aula.
- Cumplimente su datos personales en las hojas autocopiativas.
- El tiempo para la realización de este ejercicio será de sesenta (60) minutos.
- NO SEPARE ninguna de las copias de las hojas autocopiativas. Una vez finalizado el ejericio, el personal del aula le indicará los pasos a seguir.
- El ejercicio se podrá utlizar como borrador y se podrá llevar por el opositor al finalizar el tiempo marcado para el ejercicio.

ULTRA-HIGH-PERFORMANCE LIQUID CHROMATOGRAPHY HIGH-RESOLUTION MASS SPECTROMETRY (UHPLC–HRMS) VARIANTS FOR METABOLOMICS RESEARCH

In this Review, the authors cover the technical aspects of UHPLC–HRMS approaches, including (1) current popular technologies and alternatives with respect to sample preparation, stationary phase and ionization, (2) the advent of ion mobility mass spectrometry, (3) the power of orthogonal approaches in metabolite separation, (4) different tandem mass spectral approaches and (5) integration in multiplatform data acquisition. Combinations of these approaches have boosted the number of metabolites that are routinely detectable from hundreds to a few thousand, with attempts to push these limits approaching ranges above 5,000 putative metabolites. However, there are large discrepancies between the number of mass features and the effective number of metabolites in biological matrices. Thus, reports about the ever-increasing number of detected untargeted metabolites should be approached with caution. The authors explain how the combination of different analytical techniques renders such approaches the most powerful tools in enhancing the comprehensiveness of metabolomics. This Review focuses mainly on technical aspects and will not cover computational approaches. Additionally, for all practical purposes, the authors consider lipidomics as a particular case of metabolomics; hence, most topics discussed in this article are just as relevant to such platforms. Finally, the authors provide a perspective on future challenges faced by metabolomics research at the start of its third decade.

Improvements in column technology.

Column technology has evolved rapidly in the last decades with the advent of UHPLC and the introduction of sub-2-μm particles and superficially porous particles (SPPs), providing more efficient separation with shorter analysis times. Smaller particle size provides higher chromatographic efficiency with comparable peak capacity, the maximum number of resolvable peaks, in a given amount of time. Sharper peaks also improve chromatographic sensitivity, providing lower limits of detection. Such fast chromatographic runs require equally fast mass analyzers that can acquire sufficient data points for reliable quantification across a chromatographic peak. Additionally, faster scan times in MS usually come at the cost of mass resolution. Therefore, achieving high accuracy in determination of mass-to-charge (*m*/*z*) values often requires longer scan times, which might be incompatible with typical peak widths using UHPLC.

The solid-phase composition of UHPLC columns is dominated by reverse phases (RPs), particularly ODS18-based phases with multiple modifications to improve the phases' stability under different conditions (for example, extreme pH and a high proportion of aqueous mobile phase). The high resolution and stability achieved for most medium-polarity and hydrophobic metabolites come at the cost of low retention for hydrophilic compounds. A common approach to circumvent such limitations is the use of ion pairing to improve retention. However, most modifiers involved in ion pairing are incompatible with MS systems. Therefore, hydrophilic interaction liquid chromatography (HILIC) is often used as an alternative for analyzing highly polar metabolites. It provides a complex separation system based on multiple mechanisms with a substantial contribution from the partitioning of analytes between the mobile phase and an aqueous layer semi-immobilized by the stationary phase. This mechanism is highly complementary to ODS18 phases. In comparison to ODS18 phases, HILIC has several disadvantages, including reduced reproducibility in retention times, longer inter-run stabilization and high use of organic solvents, affecting sample solubility. These factors have important effects on throughput and have also hindered the widespread adoption of HILIC as an orthogonal method.