Standardization of metabolomics analysis protocols in biological samples

In order to ensure the quality of metabolomic data, our group is carrying out several experiments and developing bioinformatics’ tools to standardize different steps of the metabolomic workflow. Some examples, as follows:

CONTROL OF THE BIOLOGICAL SAMPLE STABILITY:

ANALYSIS OF THE FREEZING EFFECT DURING THE SAMPLE STORAGE. Our aim is to assess the stability of biological samples such as urine and plasma, after short-, medium- and long-term (> 2 years) freezing periods.

ANALYSIS OF THE EFFECT OF FREEZING-THAWING CYCLES (FTC). Our interest is to evaluate whether and in which extent FTCs may affect the stability of biological samples. In this sense, we evaluate:

- Short-term FTC: the samples are subjected to short-term freezing periods (hours) between consecutive FTC.
- Long-term FTC: the samples are subjected to long-term freezing periods (days, weeks, etc.) between consecutive FTC.

EFFECT OF THE ANALYSIS TIMES. Depending on the characteristics of the studies, the time between the samples preparation and their analysis may vary (process known as “injection queue time”). Therefore, we are interested in evaluating the sample stability when changing the “injection queue time” variable.

QUALITY CONTROL OF THE DATA ACQUISITION STEP: To evaluate the overall quality of the data acquisition step, our experimental protocols incorporate the analysis of three different quality controls (QC) along the samples injections:

- QC1: Milli-Q water samples.
- QC2: Acqueous standard pools consisting of both endogenous and exogenous metabolites.
- QC3: Reinjection of 10% of randomly selected biological samples.

IMPLEMENTATION OF THE DATA COLLECTION AND ANALYSIS STEPS. Our group is involved in a project to develop and implement a new algorithm designed and adapted to the metabolomic analysis using LC-QToF in collaboration with the group of Dr. Perera from the Universitat Politècnica de Catalunya (UPC), in order to reduce the analysis time and, in turn, improve the annotation and identification of mass features generated during the data acquisition stage. At the same time, the algorithm will also allow powerful multivariate statistical analysis.

IMPLEMENTATION OF THE BIOMARKERS IDENTIFICATION STEP (Computational-Assisted Identification). Our group is also working at the development of tools for the identification of both biomarkers of food intake and effect, and biomarkers of disease risk. The group recently participated to the development of the metabolic workpackage of the database PHENOL EXPLORER. At the same time, we are developing a database focused to increase the knowledge and dimension of the Food Metabolome. On the second point, we are designing a protocol for marking a profile of biomarkers.
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related to several diseases like metabolic syndrome, obesity and cardiovascular disease, among others.

DEVELOPMENT OF PROTOCOLS FOR INTEGRATIVE BIOLOGY. The group works on the development of a protocol which allows the overall analysis of the generated data during a nutritional intervention study. In this sense, this protocol will allow us to integrate the information provided by the analysis of the diet and its components, with socio-demographic aspects, clinical and biochemical tests, and data from metabolomic analysis, in order to obtain a complete image of the nutritional intervention effect.

GROUP PUBLICATIONS:


Source URL: http://www.nutrimetabolomics.com/lineas/protocolos

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