Endocrinología, Diabetes y Nutrición

CO-024 - NMR METABOLOMICS, A SUCCESSFUL STRATEGY TO IDENTIFY A TYPE 2 DIABETES MELLITUS MOLECULAR SIGNATURE BEYOND GLUCOSE IN THE DI@BETES STUDY

N. Amigó[a], E. Ozcariz[a], G. Rojo[b], M. Guardiola[c] y J. Ribalta[c]

[a]Biosfer Teslab. [b]Hospital Universitario Carlos Haya. [c]Universitat Rovira i Virgili.

Resumen

The Di@bet.es Study, the first national study in Spain to examine the prevalence of diabetes and impaired glucose regulation, showed an overall DM2 prevalence of 13.8%. The primary objective of our study was to characterize the NMR metabolomic profile of a sub-group of 720 individuals, with and without DM2 (25%), matched by age, sex, body mass index (BMI) and glucose concentration, to identify a molecular signature associated with DM beyond glucose levels. Lipoprotein and glycoprotein profiles, as well as a set of 13 low molecular weight metabolites (LMWM), including amino acids and catabolic metabolites, were obtained. Univariate analysis showed significant differences ($p < 0.05$) in: triglycerides (TG), tyrosine, isoleucine, TG/cholesterol (TG/C) ratio of VLDL and HDL and in the percentage of small LDL particles (%sLDL). Stronger differences ($p < 0.01$) were observed in: glucose, glutamine, glycine and in the percentage of small VLDL particles. We explored DM associated metabolomic profile by using four multivariate modelling approaches: logistic regression, random forest, extreme gradient boosting and naïve Bayes models discriminating DM individuals to capture DM associated molecular variability. Random forest modelling was preferred showing the higher accuracy (72% and an area under the curve (AUC) value of 0.80) discriminating DM2 -beyond glucose concentration. Although glucose remained having a great relevance in the model, additional predictors showed significant contribution: The TG/C-ratio of VLDL, glutamine, the % of small LDL particles, glycine and creatine were the most contributing variables to DM. ^{1}H-NMR is a powerful tool to characterize DM-associated metabolomic profile, helping to a better understanding of DM molecular signature.