Integrative exploration of metabolic syndrome in older men

Blandine Comte, Marion Brandolini-Bunlon, Pierrette Gaudreau, Estelle Pujos-Guillot

Integrative exploration of metabolic syndrome in older men

Blandine COMTE[1], Marion BRANDOLINI-BUNLON[1], Pierrette GAUDREAU[2], **Estelle PUJOS-GUILLOT**[1]

[1] Université Clermont Auvergne, INRAE, UNH, Plateforme d'Exploration du Métabolisme, MetaboHUB Clermont, Clermont-Ferrand, France;

[2] Centre de Recherche du Centre hospitalier de l'Université de Montréal, Montreal, Canada; Département de médecine, Université de Montréal, Montreal, Canada.

Background: Metabolic syndrome (MetS), a cluster of factors associated with risks of developing cardiovascular diseases, is a public health concern because of its growing prevalence. Considering the combination of concomitant components, their development and severity, MetS phenotypes are largely heterogeneous, inducing disparity in diagnosis.

Objective: The objective of the present work was to better characterize metabolic perturbations in MetS and define a comprehensive MetS signature stable over time in older men.

Design: A case/control study was designed within the Quebec NuAge longitudinal cohort on aging. From a 3-year follow-up of 123 stable individuals, we present a deep phenotyping approach based on a multiplatform metabolomics and lipidomics untargeted approach. A full feature selection strategy was developed to build a comprehensive molecular MetS signature, stable over time.

Results: We characterize significant changes associated with MetS, involving modulations of 476 metabolites and lipids, and representing 16% of the detected serum metabolome/lipidome. These results revealed a systemic alteration of metabolism, involving various metabolic pathways (urea cycle, amino-acid, sphingo- and glycerophospholipid, and sugar metabolisms…) not only intrinsically interrelated, but also reflecting environmental factors (nutrition, microbiota, physical activity…). These findings allowed identifying a comprehensive MetS signature, reduced to 26 metabolites for future translation into clinical applications for better diagnosing MetS.

Conclusions The refinement of the comprehensive signature, performed both in terms of measurement reliability, but also by showing the consistent association between the modulated metabolites/lipids and the underlying biological mechanisms, is increasing the value of the proposed biomarker combination within the reduced signature for further investigation and possible clinical application.

Acknowledgements: The NuAge Study was supported by a research grant from the Canadian Institutes of Health Research (CIHR; MOP-62842). All metabolomics and lipidomics analyses were funded and performed within the MetaboHUB French infrastructure (ANR-INBS11-0010).