Accepted Manuscript

Title: Metabolomics applied to diabetes – lessons from human population studies

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PII: S1357-2725(17)30269-8
DOI: https://doi.org/10.1016/j.biocel.2017.10.011
Reference: BC 5240

To appear in: *The International Journal of Biochemistry & Cell Biology*

Received date: 2-5-2017
Revised date: 30-9-2017
Accepted date: 20-10-2017

Please cite this article as: Liggi, Sonia., & Griffin, Julian L., Metabolomics applied to diabetes – lessons from human population studies.*International Journal of Biochemistry and Cell Biology* https://doi.org/10.1016/j.biocel.2017.10.011

Metabolomics applied to diabetes – lessons from human population studies

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Abstract

The 'classical' distribution of type 2 diabetes (T2D) across the globe is rapidly changing and it is no longer predominantly a disease of middle-aged/elderly adults of western countries, but it is becoming more common through Asia and the Middle East, as well as increasingly found in younger individuals. This global altered incidence of T2D is most likely associated with the spread of western diets and sedentary lifestyles, although there is still much debate as to whether the increased incidence rates are due to an overconsumption of fats, sugars or more generally high-calorie foods. In this context, understanding the interactions between genes of risk and diet and how they influence the incidence of T2D will help define the causative pathways of the disease. This review focuses on the use of metabolomics in large cohort studies to follow the incidence of type 2 diabetes in different populations. Such approaches have been used to identify new biomarkers of pre-diabetes, such as branch chain amino acids, and associate metabolomic profiles with genes of known risk in T2D from large scale GWAS studies. As the field develops, there are also examples of meta-analysis across metabolomics cohort studies and cross-comparisons with different populations to allow us to understand how genes and diet contribute to disease risk. Such approaches demonstrate that insulin resistance and T2D have far reaching metabolic effects beyond raised blood glucose and how the disease impacts systemic metabolism.

List of abbreviations:

α -hydroxybutyrate (α -HB)

Aromatic amino acids (AAAs)

Branched-chain amino acids (BCAA)

Branched-chains keto acids (BCKA)

Cardiovascular Health Study (CHS)

Cardiovascular Risk in Young Finns Study (YFS)

Docosapentaenoate (DPA)

Dongfeng-Tongji (DFTJ)