Prospecting specific protein patterns for high Body Mass Index (BMI), Metabolic Syndrome and Type 2 Diabetes in saliva and blood plasma from a Brazillian population

Carlos Vinicius Ferreira da Silva[1,2,3], Carlos José Ferreira da Silva[2], Youssef Bacila Sade[3], Sandra Mara Nara Scapin[3], Fabiano Lopes Thompson[1], Cristiane Thompson[1], Carina Maciel da Silva-Boghossian[1], Eidy de Oliveira Santos[2]

[1.] UFRJ, Universidade Federal do Rio de Janeiro, Av. Carlos Chagas Filho, 373 - Cidade Universitária, Rio de Janeiro - RJ, 21941-599;
[2.] UERJ-ZO, Universidade do Estado do Rio de Janeiro-Zona Oeste, Av. Manuel Caldeira de Alvarenga, 1203 - Inhoaíba, Rio de Janeiro - RJ, 23070-200;
[3.] Inmetro, Instituto Nacional de Metrologia, Normalização e Qualidade Industrial, Av. Nossa Sra. das Graças, 50 - Xerém, Duque de Caxias - RJ, 25250-020;

Obesity, metabolic syndrome (MeS), and Type 2 Diabetes Mellitus (T2DM) are known to involve shifts in pro-inflammatory and anti-inflammatory proteins, however, changes in the proteome of mixed-race individuals remain uncleared. Our goal was the identification of protein patterns that are uniquely characteristic of higher Body Mass Index, MeS and T2DM in a Brazillian population. Saliva and plasma proteomes, clinical parameters were analyzed in population from the State of Rio de Janeiro, Brazil, a mixed-race population. Volunteers were sorted by their BMI in normal (n=29), overweight (n=25) and obese (n=15) and were compared with individuals with MeS (n=23) and T2DM (n=11). Random Forest predictive model revealed that 3 clinical variables, BMI, HOMA-IR, and fasting blood glucose, are most important for predicting MeS and T2DM. A total of 6 plasmatic proteins (ABCD4, LDB1, PDZ, Podoplanin, Lipirin-alpha-3 and WRS) and 6 salivary proteins (Hemoglobin subunit beta, POTEE, T cell receptor alpha variable 9-2, Lactotransferrin, Cystatin-S, Carbonic anhydrase 6), are enhanced in T2DM and in MeS. Our data revealed similar alterations in protein composition across individuals with abnormal weight gain, T2DM, and MeS. We found that obesity, MeS, and T2DM are related to progressively decrease in tryptophan tRNA synthetase (WRS), a protein involved in tissue and cell damage protection. Conversely, Profilin 1, a protein related to cardiovascular disease, was identified more abundantly in obese individuals, MeS, and T2DM, metabolics diseases related to cardiovascular diseases. Investigating these proteins could help fill the knowledge gap in metabolic diseases, potentially enhancing our understanding of these disease and and paving the way for the development of novel diagnostic tools.

Agradecimentos: We are grateful for all volunteers that participated of this study and the National Institute of Metrology, Quality and Technology (Inmetro) for the support in MS analysis. This work was supported by the funding agencies (CAPES, CNPQ and FAPERJ) for financial resources and grants.