

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

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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 unclear. Our goal was the identification of protein patterns that are uniquely characteristic of higher Body Mass Index, MeS and T2DM in a Brazilian 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, POTE, 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, metabolic 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 paving the way for the development of novel diagnostic tools.

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