GLYCATED PLATELETS PROTEOME

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Despite significant recent advances in hyperglycemia treatments, a precise glycemia evaluation and control through the monitoring of glucose and glycated hemoglobin remain in most diabetic patients a critical challenge. An alternative perspective could be the discovery and analysis of new glycated proteins formed by non-enzymatic reaction with circulatory glucose with a suited proteomics workflow. As a result of glucose exposition, any component of blood is a promising source of glycated proteins to monitor glycaemia and interpret changes at the level of this post-translational modification. The approach based on the differential labeling of proteins with isotopically labeled-glucose ([^{13}C] glucose) or GIL has demonstrated its power for the analysis of protein glycation in human plasma and hemolysate samples. With this approach, the current work presents the investigation of the platelet glycated proteome. The qualitative analysis provided the identification of 13 glycated proteins that are modified at physiological conditions with elucidation of 26 preferential glycation sites. These proteins were Ig kappa chain C, fructose-biphosphate aldolase A, peroxiredoxin 2 and protein disulfide-isomerase, among others. From a biological point of view, these results represent meaningful information since the mechanisms by which glycation influences the progression of diabetes is not completely understood. Further studies in samples with a poor glycaemic control are needed to evaluate quantitative glycation changes. Ultimately, this should help to elucidate the effect of glycation on the biological function of platelet proteins.