Proteo Vilamoura

Abstract Book



SEProt Sociedad Española de Proteómica

fps French Proteomics Society

PROCURA OMICS PT

Proteo Vilamoura

2nd Joint Meeting of Spanish, French and Portuguese Proteomics Societies

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More than 30 years after the introduction of the word proteomics, which quickly spread through the scientific literature and beyond, the instrumental development, the development of bioinformatics, the integration with other omics, the sharing of data between researchers, the integration with data coming from other scientific activities, allowed an enormous development of knowledge on living organisms (dead or alive) from viruses to humans but also showed new difficulties and most of all created new challenging opportunities. In all human activities where proteins happen or may come to be proteomics either already exist or will certainly be there in the future. Our proteomics meeting is divided into 4 main sessions referring to: technical and methodological aspects; to different applications; its complementarity with other areas and methodologies (named mixomics); and examples of state-of-the-art works. Reference invited speakers were carefully chosen to share and discuss from the most basic aspects to new subjects that most are unaware of. We also want science to be shared by all who want to do so. Small talks, flash talks and of course posters are programmed so that everyone can share and discuss their work and we all learn together.

SHOTGUN PROTEOMICS OF RED BLOOD CELLS FROM OBSTRUCTIVE SLEEP APNEA PATIENTS UNDER POSITIVE AIRWAY PRESSURE (PAP) TREATMENT

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Obstructive Sleep Apnea (OSA) syndrome is characterized by recurrent episodes of apneas and hypopneas during sleep, leading to recurrent intermittent hypoxia and sleep fragmentation. No treated OSA can result in metabolic and cardiovascular diseases. By 2D gel-based proteomics approach we have demonstrated that OSA can cause alterations in the red blood cells (RBC) proteome that may be associated with OSA outcomes [1,2]. OSA induces alterations in the redox/oligomeric states of RBC proteins such as gyceraldehyde-3-phosphate dehydrogenase (GAPDH) and peroxiredoxin-2 (PRDX2) that can be reverted or modulated by PAP treatment [3].
In this study, we applied a shotgun proteomics strategy to further investigate the RBC proteome from patients with OSA before and after PAP treatment to better understand the regulation of RBC homeostasis in the context of OSA and/or under effect of PAP treatment.
As a first approach, RBCs samples, corresponding to Snorers patients as control (n=23) and patients with OSA before and after six months of PAP treatment (n=33/condition) were selected from our biobank[1]. Samples were randomly pooled (n=3 per group/condition) and lysed 1:6 with 5mM sodium phosphate buffer containing 100 mM of N-ethylmaleimide, a reagent that alkylates free sulfhydryl groups, before haemoglobin depletion by using Hemovoid^{TM} system. Depleted samples were alkylated, reduced and digested with trypsin and chymotrypsin. The resulting peptides were cleaned with C18 columns and analysed in triplicate by a Nano High Performance Liquid Chromatography (nanoHPLC) on-line coupled to a high-resolution accurate-mass Orbitrap mass spectrometer (Q Exactive, Thermo Scientific) with a nano electrospray ionization source (nanoESI). The acquired mass spectrometry data were analysed by MaxQuant v1.5.8.3 and Perseus v2.0.3.1 software.
The preliminary results corroborated our previous findings by showing that proteins associated with stress response and antioxidant regulatory system were the most changed in OSA RBC compared with Snorers ones. The active catalytic cysteine (Cys 51) in the PRDX2 was identified trioxidized $–SO_3H$ almost exclusively in OSA RBC before PAP treatment. Further analyses and validation of these data are in progress, which will certainly provide a better understanding of RBC molecular mechanisms and their proteins/PTMs associated with OSA pathology and/or response to PAP therapy.

1. A. Feliciano et al, BBA Molecular Basis of Disease (2017); 863(2): 621–629.
2. A. Feliciano et al, Data in Brief (2017); 103–110.
3. C. Valentim-Coelho et al, Antioxidants (2020); 9(12):1184.

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