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Data Article

Evening and morning alterations in Obstructive Sleep Apnea red blood cell proteome

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ABSTRACT

This article presents proteomics data referenced in [1] Using proteomics-based evaluation of red blood cells (RBCs), we have identified differentially abundant proteins associated with Obstructive Sleep Apnea Syndrome (OSA). RBCs were collected from peripheral blood of patients with moderate/severe OSA or snoring at pre- (evening) and post-night (morning) polysomnography, so that proteome variations between these time points could be assessed. RBC cytoplasmic fraction depleted of hemoglobin, using Hemovoid™ system, were analyzed by two-dimensional fluorescence difference gel electrophoresis (2D-DIGE), the 2D image software-based analyzed and relevant differentially abundant proteins identified by mass spectrometry (MS). MS identified 31 protein spots differentially abundant corresponding to 21 unique proteins

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possibly due to the existence of post-translational modification regulations. Functional analysis by bioinformatics tools indicated that most proteins are associated with catalytic, oxidoreductase, peroxidase, hydrolase, ATPase and anti-oxidant activity. At morning a larger numbers of differential proteins including response to chemical stimulus, oxidation reduction, regulation of catalytic activity and response to stress were observed in OSA. The data might support further research in OSA biomarker discovery and validation.

Specifications Table

Subject area	Biology
More specific subject area	Molecular Medicine; Clinical Proteomics
Type of data	Figures, graphics and tables
How data was acquired	Two-dimensional fluorescence difference gel electrophoresis (2-D DIGE) - based proteomics followed by image analysis with Progenesis SameSpots, version 4.5 software (Nonlinear Dynamics, UK). Protein identification by mass spectrometry (MALDI/TOF/TOF). Pathway analysis by open source DAVID software [2].
Data format	Filtered, analysed
Experimental factors	RBC samples were hemoglobin (Hb) depleted, using Hemovoid™ system, before analysis.
Experimental features	Samples from OSA and Snorers (controls) patients biobank collected at evening and morning time (i.e, before and after night polysomnographic diagnosis) were enrolled.
Data source location	Lisbon, Portugal,
Data accessibility	Data is with this article

Value of the data

- For the first time (evening/morning) changes in OSA RBC proteome are shown probably induced by nocturnal intermittent hypoxia and sleep disruption experienced by these patients.
- The provided data set may help to get new insights into RBC homeostasis which dysregulation can be a source of oxidative-stress and/or inflammation causally linking OSA to cancer and cardiometabolic disorders.
- These data could be used in further verification/validation assays to selected candidates biomarker of OSA severity and/or treatment response.

1. Data

2-D gel reference image of OSA RBC cytoplasmic fraction depleted from hemoglobin was shown. Graphics representing the identified variations for the different PRDX2 and Catalase proteoforms between groups and conditions were highlighted as examples. The 31 proteins spots identified by MALDI/TOF/TOF MS are displayed in detail in the Table. Fold-change histograms and pathway analysis