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

May 11th-13th, 2022, Portugal

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.

I.2

Investigating the impact of COVID-19 vaccines on the red blood cell immune function by omics-based approaches.

Joana Saraiva1, Cristina Valentim-Coelho1,2, Fátima Vaz1,2, Marilia Antunes3, Sofia Neves1, Peliano Ricardo1, Odília Andrade4, Armandina Miranda5, Aryse Melo6, Carla Roque6, Raquel Guiomar6, Mohammed H. Semreen7,8, Nelson C. Soares7,8, Deborah Penque1,2 (deborah.penque@insa.min-saude.pt)

[1]Departamento de Genética Humana, Instituto Nacional de Saúde Doutor Ricardo Jorge, Lisboa, Portugal; [2]Toxomics-Centre for Toxicogenomics and Human Health, Nova-School, Lisboa, Portugal ; [3]Centro de Estatística e Aplicações, Faculdade de Ciências, Universidade de Lisboa, Portugal; [4]Sector de Apoio Laboratorial, Instituto Nacional de Saúde Doutor Ricardo Jorge, Lisboa, Portugal; [5]Departamento de Promoção da Saúde e Prevenção de Doenças, Instituto Nacional de Saúde Doutor Ricardo Jorge, Lisboa, Portugal; [6]Departamento Doenças Infeciosas, Instituto Nacional de Saúde Doutor Ricardo Jorge, Lisboa, Portugal; [7]Pharmacy-Department of Medicine Chemistry, University of Sharjah, United Arab Emirates. [8] Sharjah Institute for Medical Research, University of Sharjah, United Arab Emirates.

The role of red blood cells (RBC) in the immune system is increasingly recognized. However, RBC-derived molecules with an immunomodulatory role in health and disease, as well as in vaccine immunogenicity are still poorly investigated [1,2]. Taking as a model the emergent COVID-19 vaccines, we aimed to investigate whether vaccines induce proteome and/or metabolome changes in RBCs able to affect T-cell immune activity, as a mechanistic test for vaccine immunization regulated by RBCs. Our ultimate goal is to identify RBC immunomodulators as potential co-adjuvants in the formulation of next-generation vaccines with bolstered efficacy and duration.

A biobank of blood samples collected longitudinally under ‘omics’ quality control from subjects (n=39) that underwent vaccination for COVID-19 between April and September 2021 was created. This biobank is associated with extensive clinical data, including demographic data, COVID-19 PCR diagnosis, hematological and vaccine effectivity data.

Linear Mixed Models, were used to evaluate the association between biometrical characteristics, health related habits, vaccine technology and vaccine effectivity and hematological parameters, along the different time-points (t0-t4) under study, i.e, before and after (24-72h or 30 days) of the first and second dose of vaccine. Statistical analyses were performed using R software version 4.1.2. Results showed significant differences ($p<0.05$) before/after vaccination in a set of hematological variables (e.g., hemoglobin, lymphocytes and monocytes values), as well in terms of vaccine effectivity and vaccine technology (mRNA or adenovirus – based vaccines).

Preliminary data from proteomics and metabolomics analysis of RBCs along the different timepoints (t0-4) of immunization response will be also presented and discussed.

The knowledge gained with this project can generate important evidence-based recommendations intended to optimize vaccine immunization, by recognizing the impact of blood cells such RBCs in the immune system regulation.

References

1Morera & MacKenzie. Vet. Res. 2011, 42-89

2Antunes et al. Cell Biol. 2011, 89, 111–121

Acknowledgment: to all volunteers that participate in this study, supported by INSARJ and Toxomics-FCT grants.

Project approved by the Ethical Committee of INSA.I.P.-Lisboa and Centro Nacional e Proteção de Dados, Portugal.