

Press release September, 2016

A new approach for deciphering complex immune responses

The response to infection is highly variable from one individual to another. The Milieu Intérieur consortium, coordinated by Prof. Matthew Albert (Immunobiology of dendritic cells Unit, Institut Pasteur / Inserm) and Dr Lluís Quintana-Murci (Human Evolutionary Genetics Unit, Institut Pasteur / CNRS) seek to establish the parameters that characterize the immune system of healthy individuals and its natural variability. In a study just published (August 25th) in Cell Reports, **and co-authored by Magnus Fontes, founder of Qlucore**, the researchers describe a new approach for analyzing the inflammatory response at the gene expression level in blood samples from healthy individuals, which reproduces the conditions of in-vivo stimulation.

The striking result from this study is that the immune response to complex stimuli such as bacteria, viruses, and fungi could be defined and distinguished based on a small number of genes that were induced by 4 key immune proteins or cytokines. In particular as few as forty-four genes, that were identified by machine learning techniques, could explain the variance present within such diverse immune responses. At a time of high-throughput sequencing approaches which create huge challenges for data analysis and medical applications, this study suggests that simplified approaches if properly targeted may provide more effective solutions with easier clinical translation. In addition, the study highlights that the utilization of highly standardized techniques for all steps including sample collection, sample preparation, and data analysis results in the generation of higher quality and more informative data. “We are excited by the results of this study which demonstrated that a relatively small subset of identified genes could explain the variability in responses to different complex immune stimuli” said Dr Darragh Duffy, immunologist and manager of the Milieu Intérieur consortium at Institut Pasteur, Paris.

In support of the published article, reference values are provided for each immune stimuli which reflects the natural variation of immune responses in humans. An online application was also released which provides an opportunity for the scientific community to exploit these data and to explore which genes are induced by a variety of immune stimuli. This newly established approach is now being applied to the 1000 healthy donors within the Milieu Intérieur cohort, which will enable the dissection of how age, gender, environment, lifestyle, and genetics contribute to variable immune responses. This is a first necessary step on the path towards precision medicine approaches.

Several of the data analyses in this study were carried out using [Qlucore Omics Explorer](#). Most of the up-stream analyses in the study can quickly be reproduced using Qlucore Omics Explorer, directly

downloading the data from Gene Expression Omnibus (GEO). This work is one example of how Qlucore Omics Explorer is used by scientists, who can browse an extensive list of links to many hundreds [more than 300] scientific articles from peer-reviewed journals written by Qlucore clients.

www.qlucore.com/references.aspx.

END

About: <http://www.milieuinterieur.fr/en>

<https://www.synapse.org/milieuinterieur>

Source

Standardized whole-blood transcriptional profiling enables the deconvolution of complex induced immune responses, *Cell Report*, 25 août 2016

Alejandra Urrutia,^{1,2,10,11} Darragh Duffy,^{1,2,3,11} Vincent Rouilly,³ Céline Posseme,³ Raouf Djebali,³ Gabriel Illanes,^{3,4,5} Valentina Libri,³ Benoit Albaud,⁶ David Gentien,⁶ Barbara Piasecka,³ Milena Hasan,³ Magnus Fontes,^{4,7,11} Lluís Quintana-Murci,^{8,9,*} Matthew L. Albert,^{1,2,3,10,12,*} and Milieu Intérieur Consortium

1. Laboratory of Dendritic Cell Immunobiology, Department of Immunology, Institut Pasteur, Paris 75015, France
2. INSERM U1223, Paris 75015, France
3. Center for Translational Research, Institut Pasteur, Paris 75015, France
4. IGDA, Institut Pasteur, Paris 75015, France
5. Centro de Matematica, Facultad de Ciencias, Universidad de la Republica, 11200 Montevideo, Uruguay
6. Institut Curie, Centre de Recherche, Département de recherche translationnelle, Plateforme de Génomique, Paris 75005, France
7. Centre for Mathematical Sciences, Lund University, 221 00 Lund, Sweden
8. Laboratory of Human Evolutionary Genetics, Department of Genomes and Genetics, Institut Pasteur, Paris 75015, France
9. CNRS URA3012, Paris 75015, France
10. Department of Cancer Immunology, Genentech Inc., San Francisco, CA 94080, USA
11. Co-first author
12. Lead Contact