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Immunopathogenesis of long-COVID: future directions

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MICROBES AND MORE!
CIRCULAR DISCUSSIONS IN HIV
AND OTHER INFECTIONS



Vigevano, June 9-10, 2023
Hotel del Parco

Presentation outline

1. MIDAS project
2. Transcriptomic project

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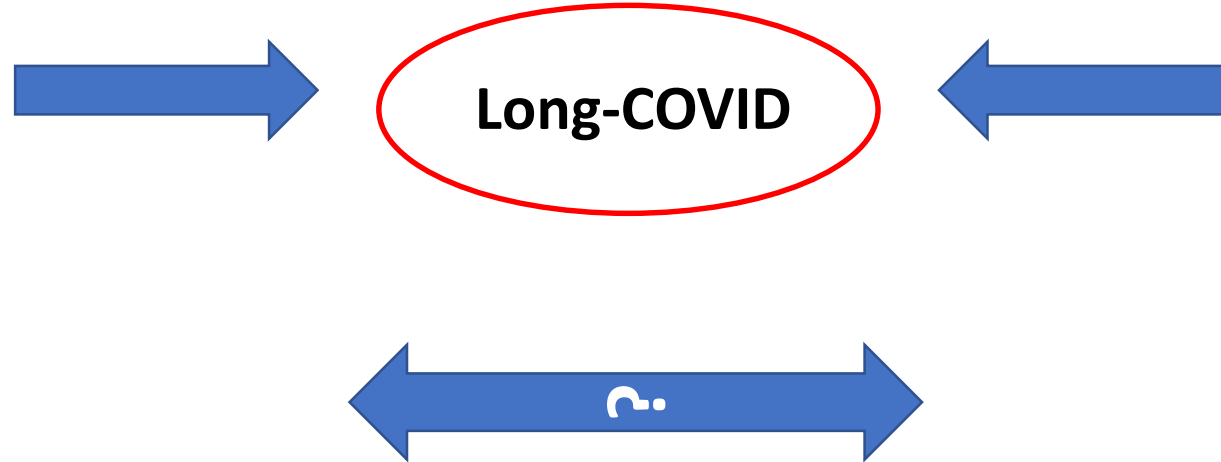
Clinic of Infectious Diseases, Department of Health Sciences, University of Milan

MIDAS project: background

Dysregulated host immune responses

- reduced SARS-CoV-2-specific T cells, increased inflammation, exhausted CD8 T-cells, atypical and naïve B-cells at 1-7 months from symptoms onset;
- increased SARS-CoV-2-specific T cells but reduced functionality (pulmonary symptoms);
- Poorer SARS-CoV-2-specific humoral response.

References: Peluso M et al, Cell Rep, 2021-J Infect Dis 2021; Torres-Ruiz et al, Clin Transl Med 2021; Littlefield K et al, PLoS Pathog, 2022; Garcia-Abellan J et al, Front Immunol, 2022.



Gut dysbiosis

- Gut microbiota dysbiosis at 1 year after infection;
- Gut and airway microbiota dysbiosis is associated with long-COVID neurological symptoms.

References: D. Zhang et al 2023 JKMS; G. Ancona et al, Front Immunol 2023; Q. Su et al MBJ 2023.

MIDAS project: aim of the project

Immunity

$\gamma\delta$ T cell responses

Immunophenotype: CD3, V δ 1, V δ 2, α 4 β 7, CD103, CCR9, HLA-DR

ICS (PMA+IONO stimulation): CD3, V δ 1, V δ 2, PD-1, IFN- γ , TNF- α , IL-17



Gut dysbiosis

Microbiome

Sequencing: whole blood

Gut barrier damage

ELISA: iFABP, Zonulin, cadherin

MT

ELISA: flagellin, LBP, EndoCAB, β -glucan



Long-COVID

Sample size:

1. 20 LC-
2. 20 LC+

Time points:

T0: acute phase of disease
T1: 2-4 months from acute disease

Transcriptomic project

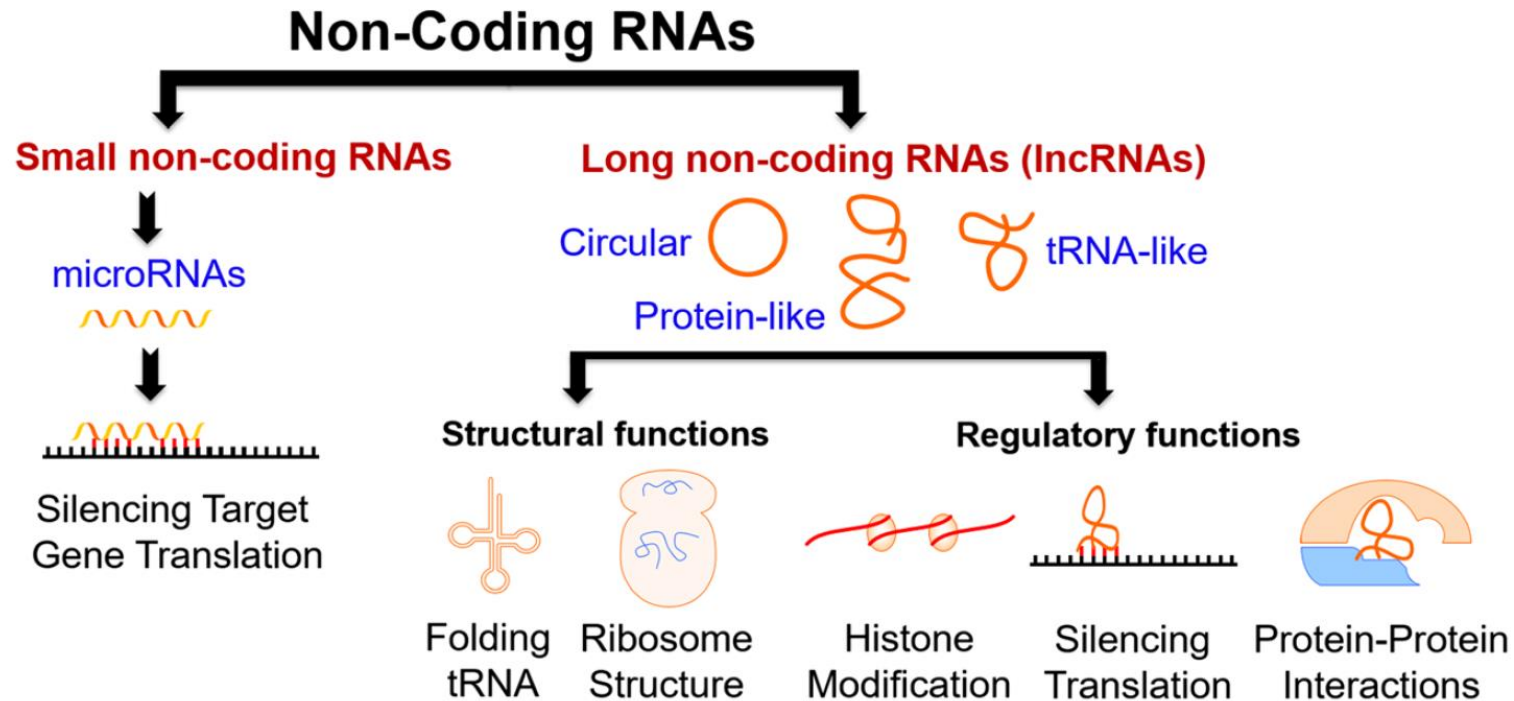
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Transcriptomic project: background

1. Non-coding RNA (miRNAs and lncRNAs) modulates gene expression at transcriptional and post-transcriptional level
2. Released in extracellular fluids, including plasma and saliva
3. Alteration associated with disease, including acute COVID-19



R. Paulmurugan et al, 2019, J Mol med

Transcriptomic project: aim of the project

Identification of a ncRNA immunesignature associated with long-COVID

Transcriptomic project: methods

