Multi-omics in COVID-19: Seeing the unseen but overlooked in the clinic
COVID-19的多组学研究，照亮被忽视的角落

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Background

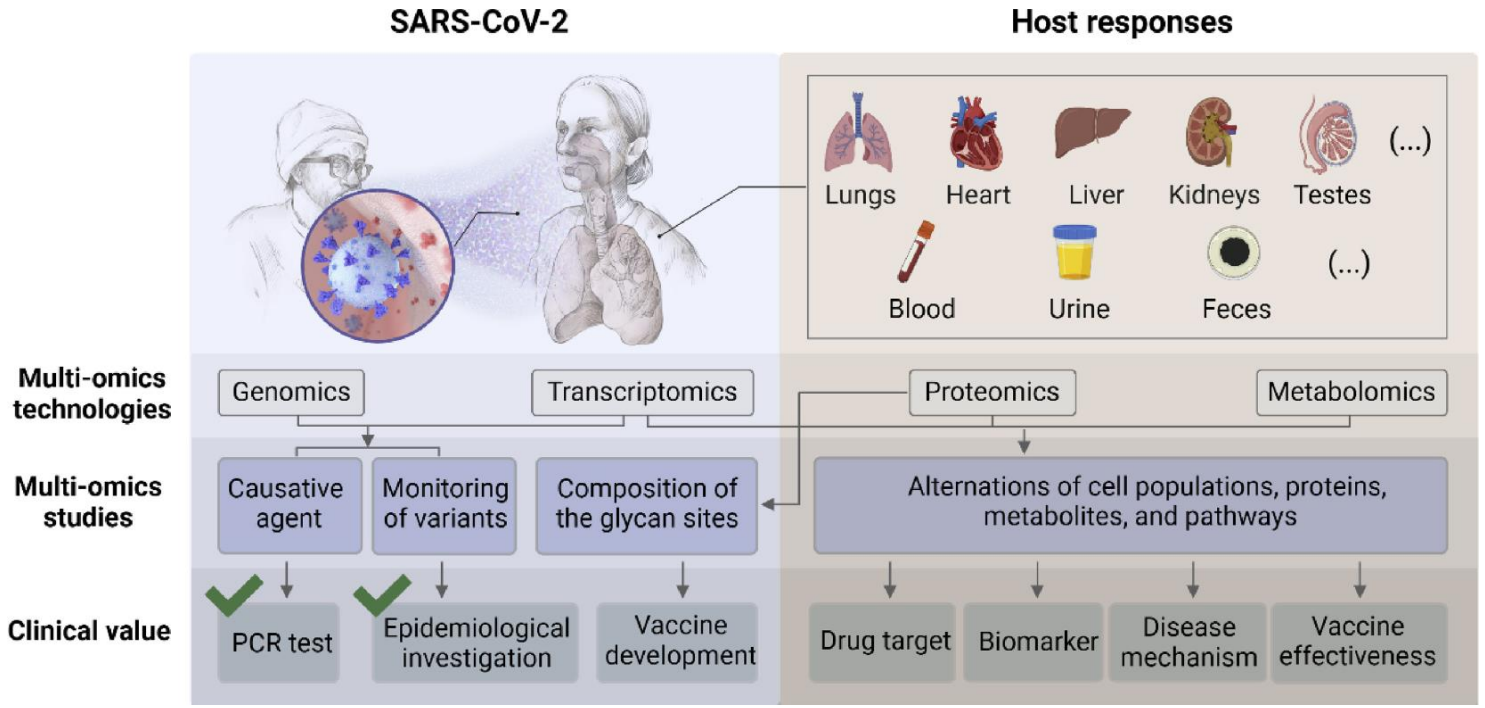
As of February 12, 2022, more than 200 countries and territories have reported over 405 million confirmed cases of COVID-19, and 5.8 million recorded deaths.

While vaccinations have not stopped the spread of SARS-CoV-2, they have reduced the risk of serious disease and death in adults and children.

Investigations deploying multi-omics technologies reveal the underlying molecular structure of the pathogen and molecular host responses to the virus and vaccines.

Main points

1) The pathogen
2) Host responses to the pathogen
3) Host responses to vaccines
4) Why are proteomics and metabolomics largely overlooked in the clinic?
5) Other challenges



The pathogen

1. The virus causing COVID-19 was first identified by metagenomic RNA sequencing → PCR-based assays (diagnose)

2. The discovery of mutations provids crucial information to track the spread of these variants.

3. Mass-spectrometry (MS)-based characterization of the spike (S) glycoprotein of the virus→vaccines

Host responses to the pathogen

1. Expanded our views on circulating molecular changes → biomarkers
    A) Sera
    B) Urine
2. Local responses in multiple solid organs → mechanism

3. Identification of target cells of the virus

Host responses to vaccines

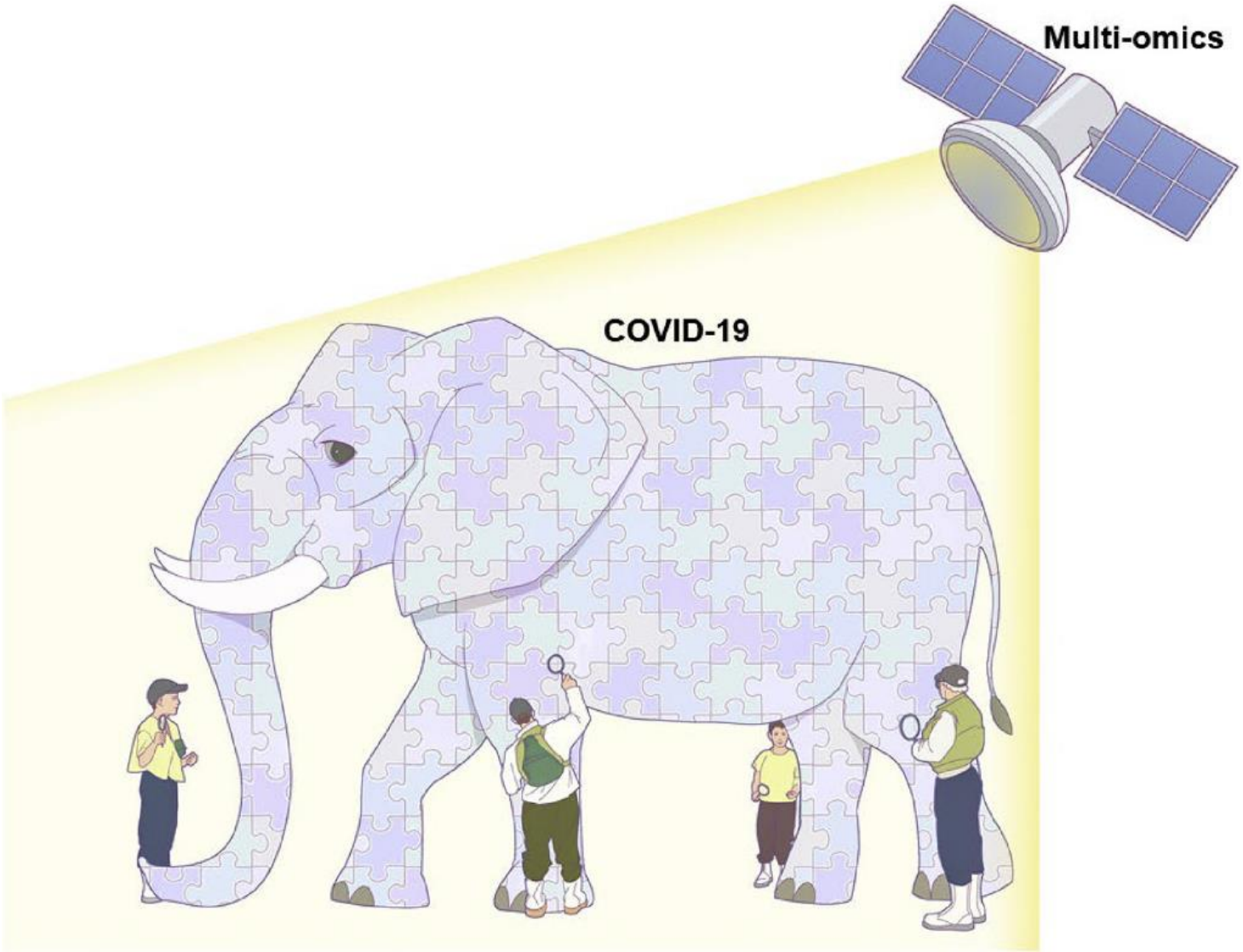
1. mRNA vaccines showed 80% efficacy against symptomatic infection even after only one dose in the absence of detectable neutralizing antibodies.

2. Up to 6% of recipients are seronegative after the second injection.

3. More than 0.004% of recipients experienced severe side effects

4. Breakthrough infections occur in vaccinated individuals

5. Timely monitoring of serological host responses is theoretically informative for epidemiological tracking in a population and could potentially offer useful information to guide vaccine dosage and dose spacing


Multi-omics
COVID-19

Why are proteomics and metabolomics largely overlooked in the clinic?

1. Reproducible?
2. Robust?
3. Cost?
4. The lack of standardization

Other challenges

1. It is inherently not straightforward to integrate multi-omics data by algorithms
2. Collection of potentially infectious samples during the pandemic poses additional challenges.

THANK YOU

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