What do we know about SARS-CoV-2

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CNR des virus respiratoires, HCL,
Virpath, CIRI, U1111, UMR 5308, ENS, UCBL,
Lyon, France
A - The Virus

Pizzorno MA et al, in press
Full genome tree of hCoV-19-related precursors

- New nearest bat precursor from Yunnan 2019 (high identity in Orf1ab, greatest difference in Spike protein, recombination or mixed viruses in metagenomic sample, not yet peer-reviewed)
- Nearest pangolin precursors from Guangdong (Southern China)
- Previous closest bat precursor also from Yunnan (Southern China) but sample from 2013

We gratefully acknowledge the Authors from Originating and Submitting laboratories of sequence data on which the analysis is based.
The virus (emergence)

• 11-2-2020

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Host receptor binding site differences between SARS, bat precursor (RaTG13) and human outbreak BetaCoV

- Surface proteins are 76% and 98% identical, respectively.
- Antigenic surface highly divergent compared to SARS.
- Bat precursor differences in receptor binding interface indicative of changes that allowed host switch.

Cyan — ACE2 human host receptor
Gray — CoV spike glycoprotein
Red — mutations between either SARS (left side) or bat precursor RaTG13 (right side) vs human outbreak WIV04 CoV

SARS vs BetaCoV
RaTG13 vs BetaCoV

by BII, A*STAR Singapore
The virus (diffusion)

- 10-3-20
The virus

• 30-4-20

Larger clades were named based on marker variants:
S ... ORF8-L84S
G ... S-D614G
V ... NS3-G251V

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B – Clinical Impact
A. Probability of hospitalization given infection by age and gender.

B. Probability of ICU admission given hospitalization by age and gender.

C. Probability of death given hospitalization by age and gender.

D. Infection fatality ratio (IFR) by age and gender.
C - Diagnosis

CT Scan
- Ground-glass opacities
- Inter-/intra-lobular septal thickening
- Air space consolidation
- Bronchovascular thickening
- Traction bronchiectasis
- Available earlier
- Check severity of condition
- Check possible infection
- Track lung based recovery

Nasopharyngeal swab
- Nucleic acid amplification for viral DNA
- Measures current infection
- Increased accuracy
- Targets different components of viral genome
- Individual can be monitored to prevent disease progression
- Identify patients with COVID-19

Stool
- Measures antibody
- Detection of past exposure to SARS-CoV-2
- Detection of immune individuals
- Identify individuals with antibodies for potential use as therapy
- Identify susceptible individuals
- Aid in tracing individuals in contact with infected person

Plasma & Blood
- Rapid processing
- Easily accessible
- Relatively inexpensive
- Laboratory not required to process samples
Mean Ct values and standard deviations obtained using five PCR-based methods for SARS-CoV-2 detection. Serial dilutions of SARS-CoV-2 cell culture supernatants were used and are represented by a single colour (10^{-5} blue, 10^{-6} red, 10^{-7} pink, 10^{-8} green).

A point in the ND (non-detected) column (Ct value axis) indicates a negative result for one replicate.
Viral excretion (Preliminary data)

Lescure X et al, Lancet ID 2020
Virus detection in respiratory samples (load)

Viral load at admission: 5.9 log10 copies/mL (4.1-7.9)

Viral load at admission is larger in patients arriving early after symptom onset.
Virus load evolution to negativation

Confidential data from French COVID Group
Immune response to infection
Serology first set of data
Immune response to infection

Troullet-Assant S et al, JACI 2020

Zhou F et al, Lancet 2020
Evolution of the cases
Diagnostic strategy
Incubation (2-12d) Respiratory symptoms (0-30d)

Mild cases (RT-PCR+ > 20 days)

Severe cases requiring O2

ICU most severe cases

RT-PCR detection

RT-PCR detection with high CT (possible intermittent detection)

Switch timing
Virus diffusion – some examples
Contamine cluster: super-spreading

Figure 1

Danis K et al, CID 2020
Virus diffusion in nursing homes

Arons MM et al NEJM 2020
Virus diffusion in nursing homes

Figure 3. Cycle Threshold Values Relative to First Evidence of Fever, Cough, or Shortness of Breath.

Arons MM et al NEJM 2020
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