

SARS-CoV-2 / COVID 19 – virologie

Evelyne Schvoerer, mars 2020

- *Le contexte viral*
 - *Variabilité virale et émergence/transmission*
 - *Pouvoir pathogène, détection chez l'Homme*

COVID 19 - Le VIRUS

Yu Chen 2020 & others

- Sous-famille Coronavirinae, genres Beta

Génome **ARN ss(+)** , ~ **30kb**

- Mammifères, oiseaux ...

Origine : Huanan South Seafood Market, Wuhan + transmission interhumaine

- Durée de survie du virus sur surfaces inertes à l'étude,

MERS-CoV →

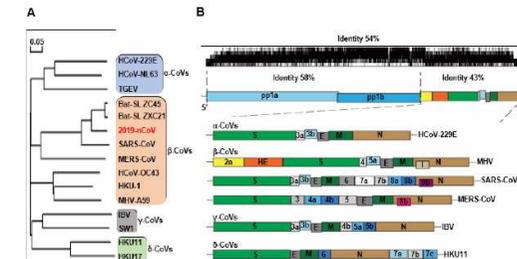
Survie 5 jours (taux d'humidité ≥ 50%) et faible température.

coronavirus sensibles aux désinfectants usuels virucides

(hypochlorite de sodium 0,5%, l'acide peracétique/peroxyde d'hydrogène, l'éthanol ou isopropanol à 70%, glutaraldéhyde)

Figure

Figure 1. The genomic structure and phylogenetic tree of coronaviruses. (A) The phylogenetic tree of representative CoVs, with the new coronavirus 2019-nCoV highlighted in red. (B) The genomic structure of four genera of coronaviruses. Pp1a and pp1b represent the two long polyproteins that are processed into 16 non-structural proteins. S, E, M and N indicate the four structural proteins: spike, envelope, membrane and nucleocapsid. HE, hemagglutinin-esterase. Viral names: HCoV, human coronavirus; TGEV, transmissible gastroenteritis virus; MHV, murine hepatitis virus; HKU1, coronaviruses identified by Hong Kong University; IBV, infectious bronchitis virus.



COVID 19 - Le VIRUS, 'filiation dangereuse'

6 CORONAVIRUS HUMAINS

Tropisme respiratoire préférentiel
Infections aiguës



Séroprévalence \approx 100 % à 5 ans
Réinfections fréquentes au cours de la vie
Infections peu sévères sauf chez populations à risques



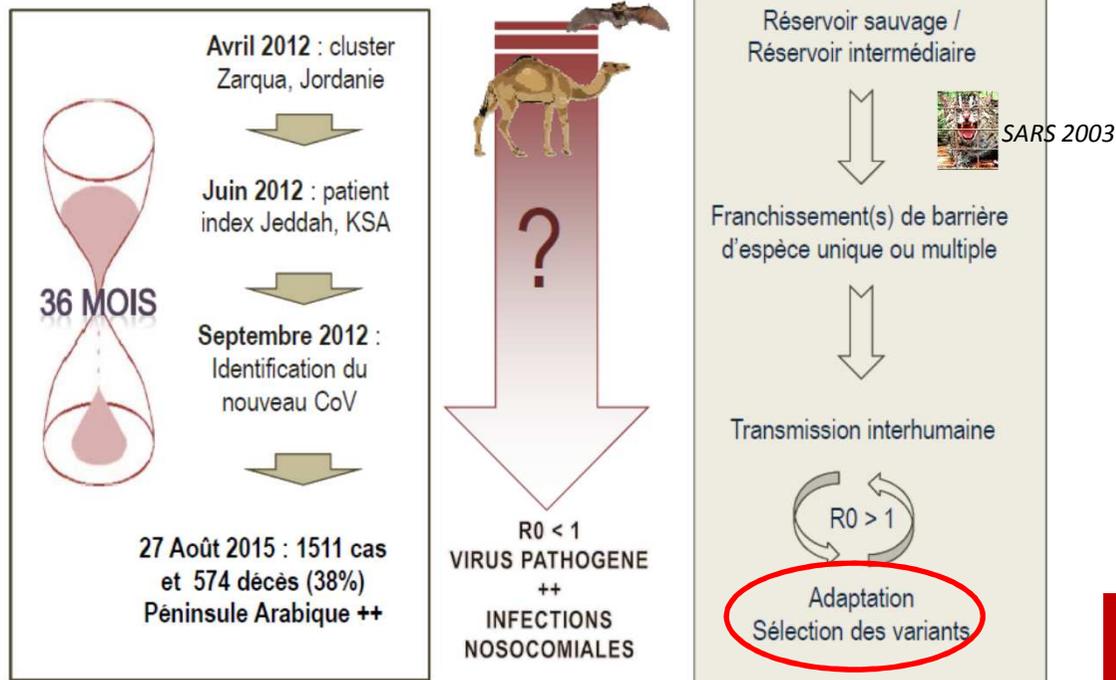
SARS-CoV-2 (nCoV 2019)

**Adaptation d'un virus ancien ?
Sélection de variants viraux ?**

COVID 19 - Le VIRUS, 'filiation dangereuse'

SARS-CoV-2 (nCoV 2019)
p/r à des modèles
(MERS-CoV 2012, SARS-CoV 2003)

EMERGENCE DU MERS - COV : EMERGENCE RÉUSSIE ?

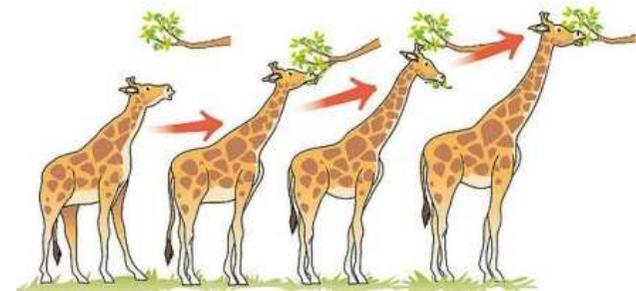


Zaki AM, et al., NEJM 2012

**Adaptation d'un virus ancien ?
Sélection de variants viraux ?**

COVID 19 - Variabilité virale et émergence

- Coronavirus : **variabilité génomique, pouvoir adaptatif**
& corrections partielles /maintien du génome ?
 - Haut potentiel évolutif par **mutations** et **recombinaisons**.
- ⇒ **EMERGENCE** 'réussie'



sélection naturelle/Dibujo_explicativo.jpg

COVID 19 - Variabilité virale et émergence

- Coronavirus, adaptation

⇒ **EMERGENCE à partir de réservoir animaux**

- Phylogénie*
- Machinerie de traduction en acides aminés

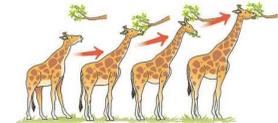
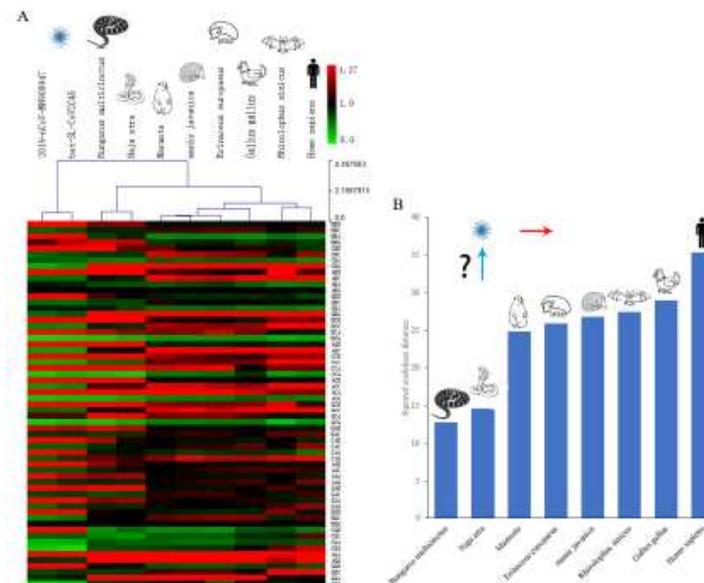


Figure 3 Comparison of relative synonymous codon usage (RSCU) between 2019-nCoV and its putative wildlife animal reservoir(s). A. Heat map resulting from cluster analysis of the RSCU among the 2019-nCoV, bat-SL-CoVZC45, Bungarus multicinctus, Naja atra, Marmota, Erinaceus europaeus, manis javanica, Rhinolophus sinicus, Gallus gallus, Homo sapiens. B. Comparison of squared euclidean distance between 2019-nCoV and different animal species. Squared euclidean distance was calculated based on the RSCU.



COVID 19 - Pouvoir pathogène

Wu et al, 2020

Table 1 continued

Variables	Patients (n=80)
Signs and symptoms at admission	
Fever	63(78.75%)
Cough	51(63.75%)
Shortness of breath	30(37.50%)
Muscle ache	18 (22.50%)
Headache and mental disorder symptoms	13 (16.25%)
Sore throat	11(13.75%)
Rhinorrhoea	5(6.10%)
Chest pain	3(3.75%)
Diarrhoea	1(1.25%)
Nausea and vomiting	1(1.25%)
More than one sign or symptom	66(82.50%)
Chest x-ray and CT findings	
Bilateral pneumonia	36 (45.00%)
Unilateral pneumonia	19 (23.75%)
No abnormal density shadow	25 (31.25%)

COVID 19 - Pouvoir pathogène à explorer

Li et al, jmv 2020

The neuroinvasive potential of SARS-CoV2 may be at least partially responsible for the respiratory failure of COVID-19 patients

Yan-Chao Li^{1*}, Wan-Zhu Bai², Tsutomu Hashikawa³

¹Norman Bethune College of Medicine, Jilin University, Changchun, Jilin Province, China 130021

²Institute of Acupuncture and Moxibustion, China Academy of Chinese Medical Science, Beijing, China 100700

³Advanced Technology Development Group, RIKEN Brain Science Institute, Saitama, Japan 351-0198

Running title: The neuroinvasive potential of the SARS-CoV-2

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*CORRESPONDENCE TO:

Yan-Chao Li, Norman Bethune College of Medicine, Jilin University, Changchun, Jilin Province, China, 130021. E-mail: liyanchao@jlu.edu.cn

Abstract

Following the severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV), another highly pathogenic coronavirus named SARS-CoV-2 (previously known as 2019-nCoV) emerged in December 2019 in Wuhan, China, and rapidly spreads around the world. This virus shares highly homological sequence with SARS-CoV, and causes acute, highly lethal pneumonia (COVID-19) with clinical symptoms similar to those reported for SARS-CoV and MERS-CoV. The most characteristic symptom of COVID-19 patients is respiratory distress, and most of the patients admitted to the intensive care could not breathe spontaneously. Additionally, some COVID-19 patients also showed neurologic signs such as headache, nausea and vomiting. Increasing evidence shows that coronaviruses are not always confined to the respiratory tract and that they may also invade the central nervous system inducing neurological diseases. The infection of SARS-CoV has been reported in the brains from both patients and experimental animals, where the brainstem was heavily infected. Furthermore, some coronaviruses have been demonstrated able to spread via a synapse-connected route to the medullary cardiorespiratory center from the mechano- and chemoreceptors in the lung and lower respiratory airways. In light of the high similarity between SARS-CoV and SARS-CoV2, it is quite likely that the potential invasion of SARS-CoV2 is partially responsible for the acute respiratory failure of COVID-19 patients. Awareness of this will have important guiding significance for the prevention and treatment of the SARS-CoV2-induced respiratory failure. (229 words)

→ message :

Participation au Sd de détresse respiratoire par potentielle **neuro-invasion** par le SARS-CoV-2



COVID 19 – Diagnostic = PCR/Imagerie*

Corman 2020

Corman* et al, Berlin / Rotterdam / Londres

- 1^{ère} technique RT-PCR en ligne

- Institut Pasteur (Paris), combinaison RT-PCR duplex RdRp et gène E

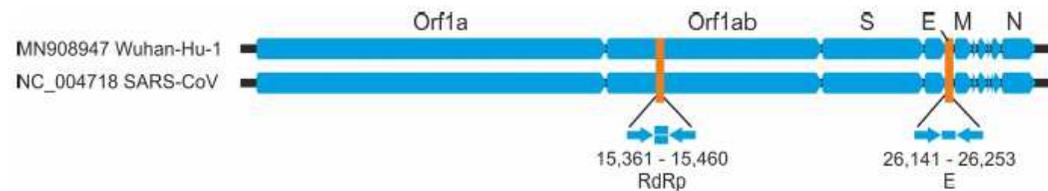


Figure 1 relative positions of amplicon targets on SARS-CoV an 2019-nCoV genome. ORF: open reading frame; RdRp: RNA-dependent RNA polymerase. Numbers below amplicon are genome positions according to SARS-CoV, NC_004718.

COVID 19 - Diagnostic biologique = PCR

- Prélèvement respiratoire : haut et bas

Préleveurs : EPI et triple emballage

- Diagnostic d'infection (et d'excrétion virale)

Prélèvements respiratoires	Matériel de collection
1. Écouvillon nasopharyngé/oropharyngé	Écouvillons
+/- 2. Expectoration, LBA, aspiration trachéale ...	Réceptacle stérile



“Dépistage”

- PCR sur 2 gènes viraux (pol, E) du nCoV 2019 (=virus COVID = SRAS-CoV-2)

- Astreinte technique **PFGM** (7/7 journées) + biologistes

COVID 19 – Questions virologiques à résoudre

- Potentiel de **mutation génomique** et **pouvoir adaptatif** du SARS-CoV-2 :
espèces animales, tropisme tissulaire
- Combinaison optimale d'examens paracliniques :
RT-PCR (sites de prélèvement, chronologie) & **Imagerie**
- **Prévention** antivirale ...

