

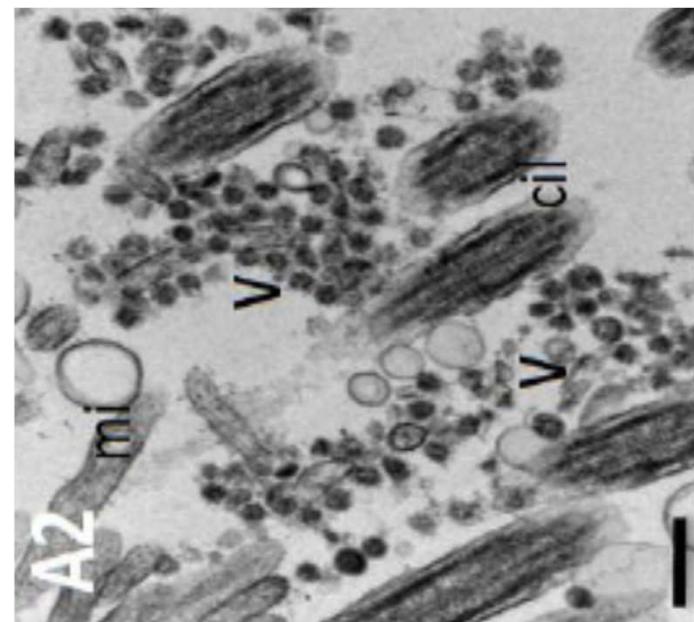
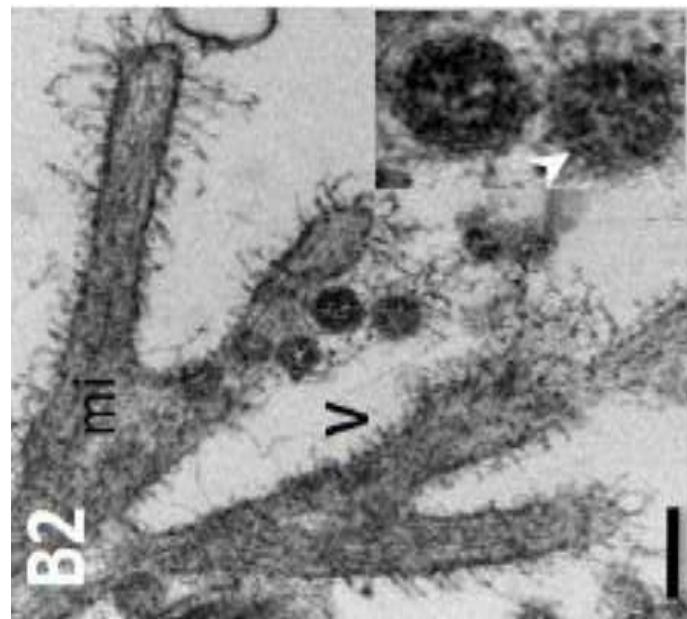


Émergence et diffusion du SARS-CoV-2 en France, bilan de la première vague

Bruno LINA

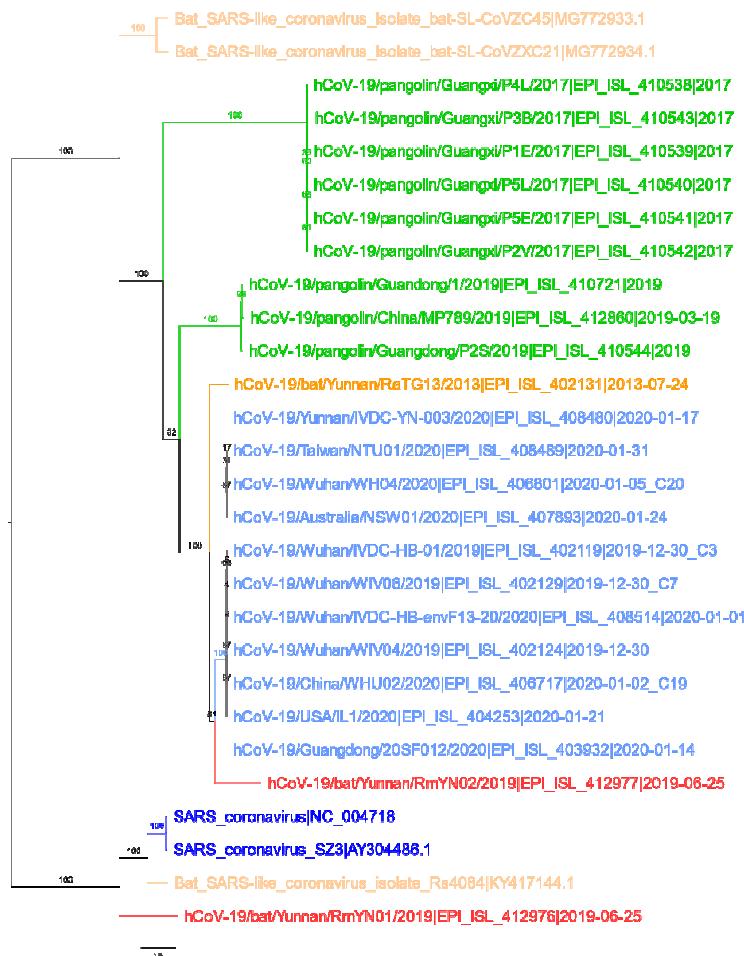
CNR des virus respiratoires, HCL,
Virpath, CIRI, U1111, UMR 5308, ENS, UCBL,
Lyon, France

A - Le Virus, le diagnostic et la clinique



Pizzorno MA et al, in press

Phylogénie genome entier des précurseurs de SARS-CoV-2



- 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(high identity in Orf1ab, greatest difference in Spike protein, recombination or mixed viruses in metagenomic sample, not yet peer-reviewed)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

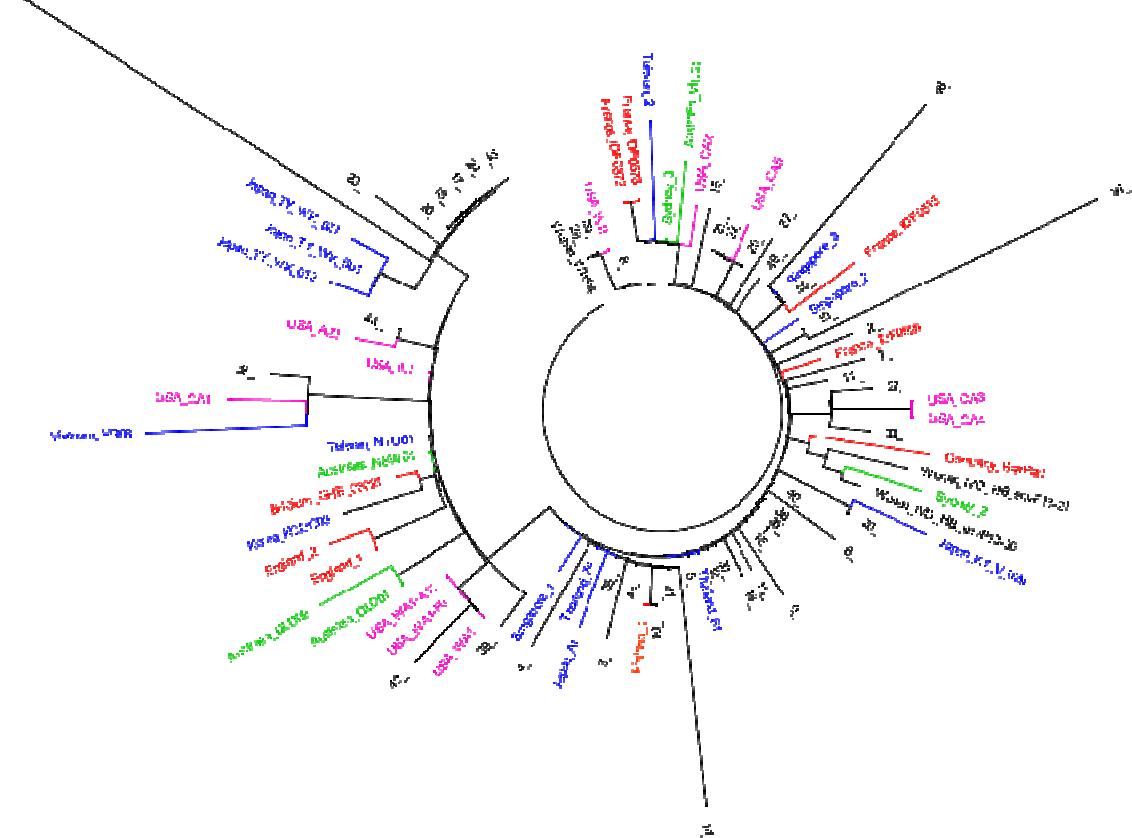
Light Orange ... previous bat CoVs
Orange ... previous closest bat precursor (Yunnan 2013)
Red ... new bat CoVs (Yunnan 2019)
Light blue ... hCoV-19 2019-2020
Green ... pangolin CoV (Southern China 2019)
Blue ... SARS CoV

We gratefully acknowledge the Authors from Originating and Submitting laboratories of sequence data on which the analysis is based.



Le virus (émergence)

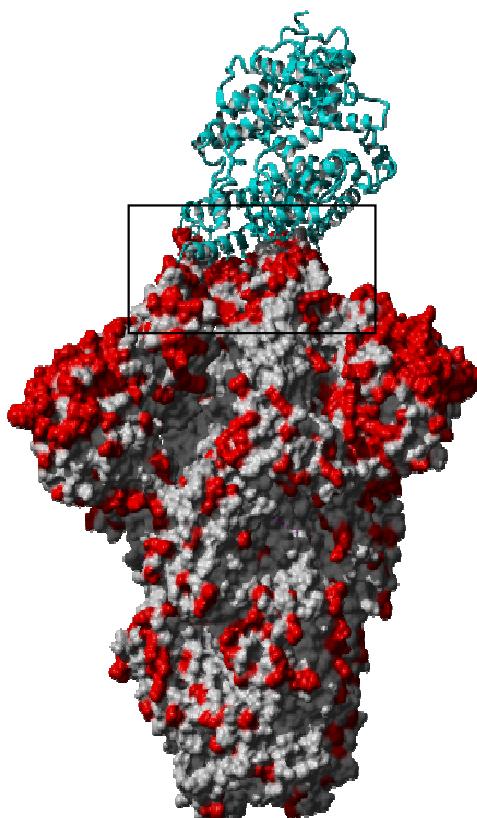
- 11-2-2020



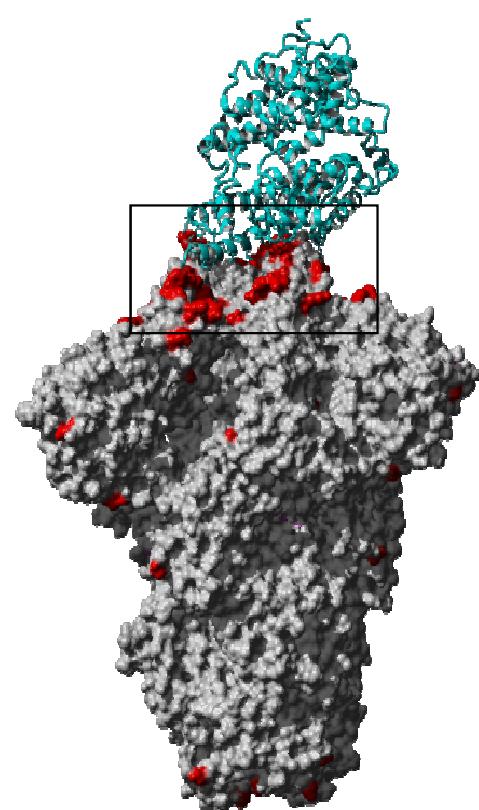
We gratefully acknowledge the Authors from Originating and Submitting laboratories of sequence data on which the analysis is based.



Site d'attachement au receiteur cellulaire : differences entre le SARS, le précurseur chez la chauve-souris (RaTG13) et le SARS-CoV-2



SARS vs SARS-CoV-2



RaTG13 vs SARS-CoV-2

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

- 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

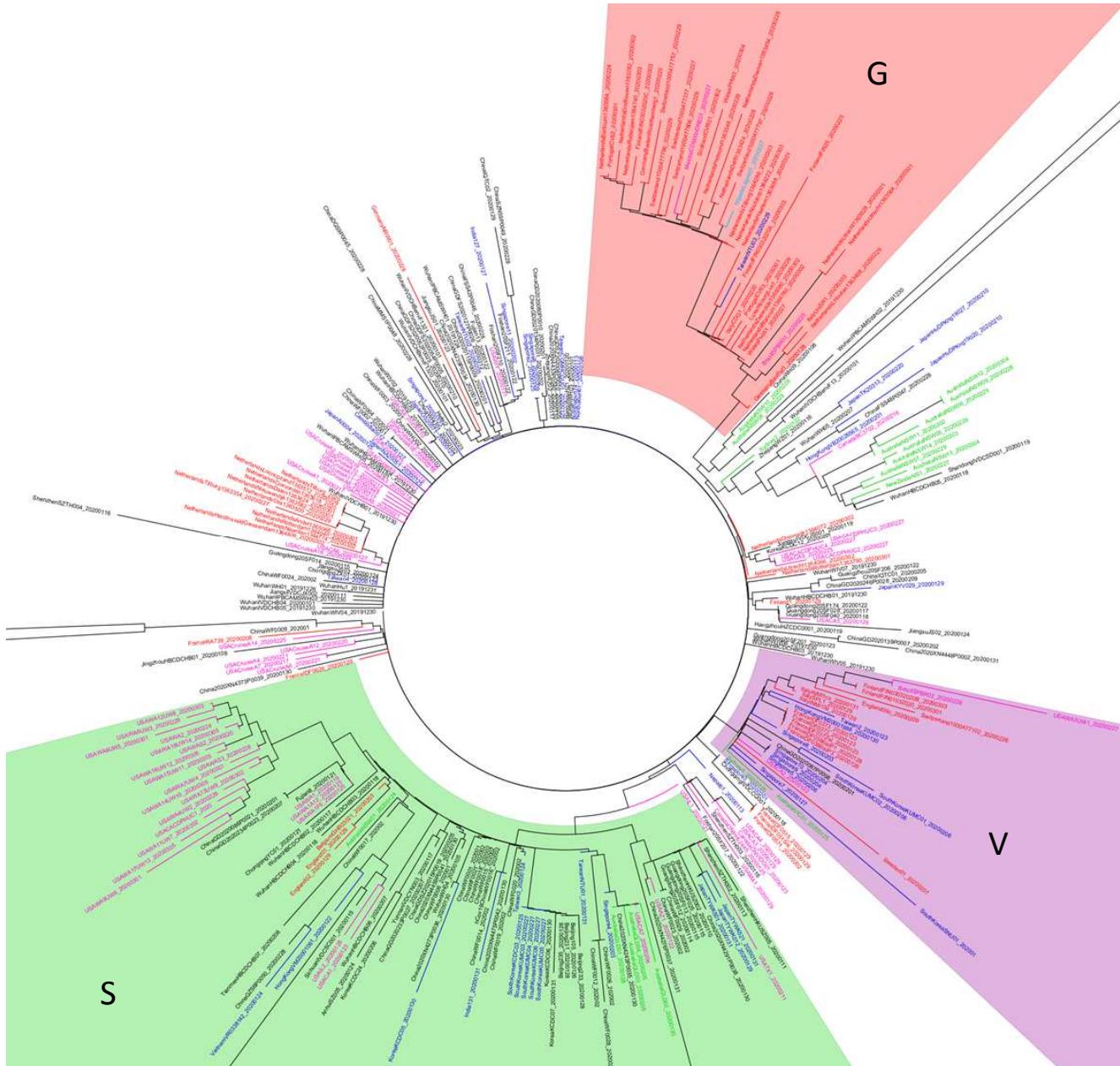
by BII, A*STAR Singapore



Le virus (diffusion)

- 10-3-20

We gratefully acknowledge the Authors from Originating and Submitting laboratories of sequence data on which the analysis is based.



Le virus

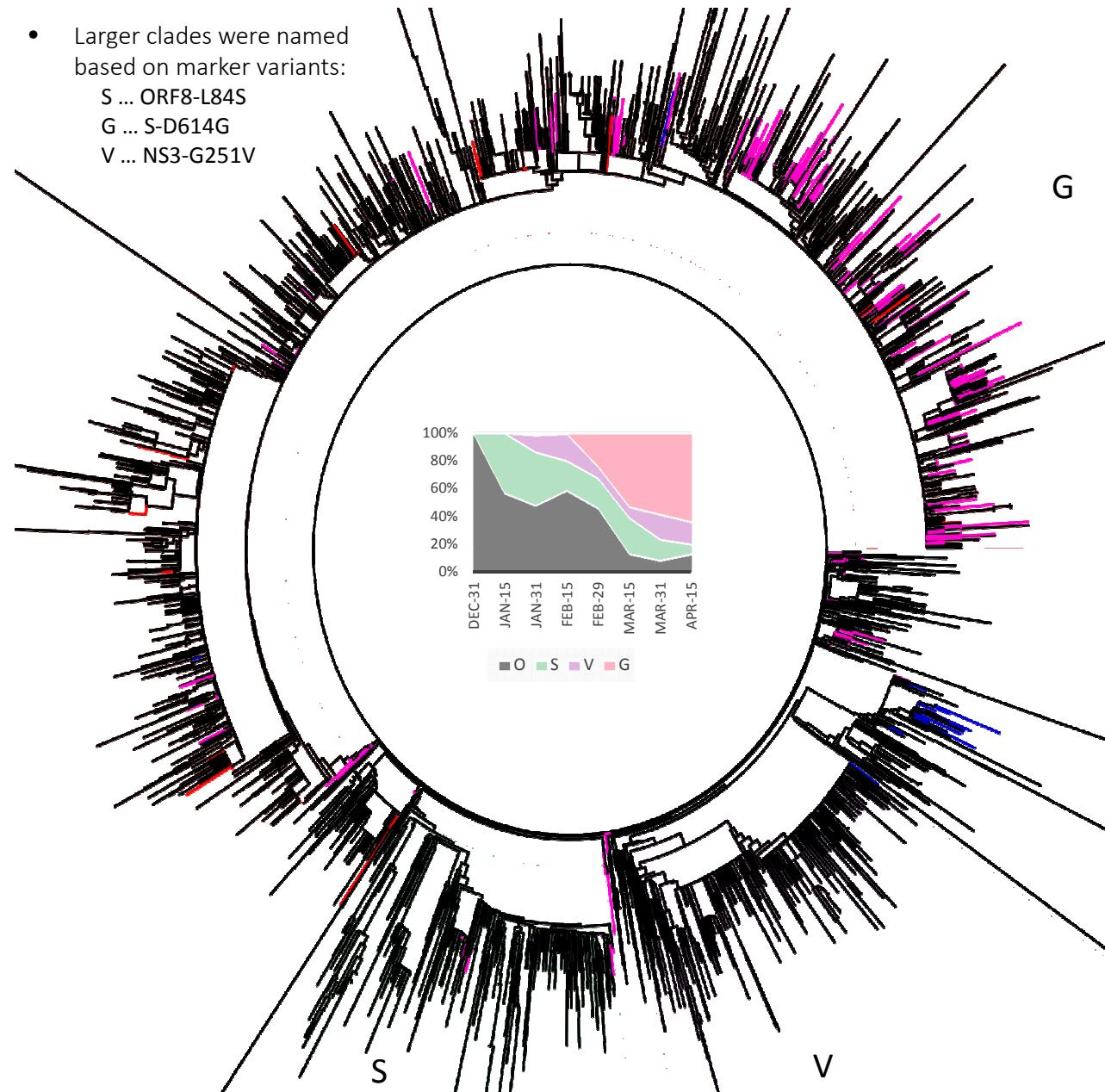
- 30-4-20

- Larger clades were named based on marker variants:

S ... ORF8-L84S

G ... S-D614G

V ... NS3-G251V

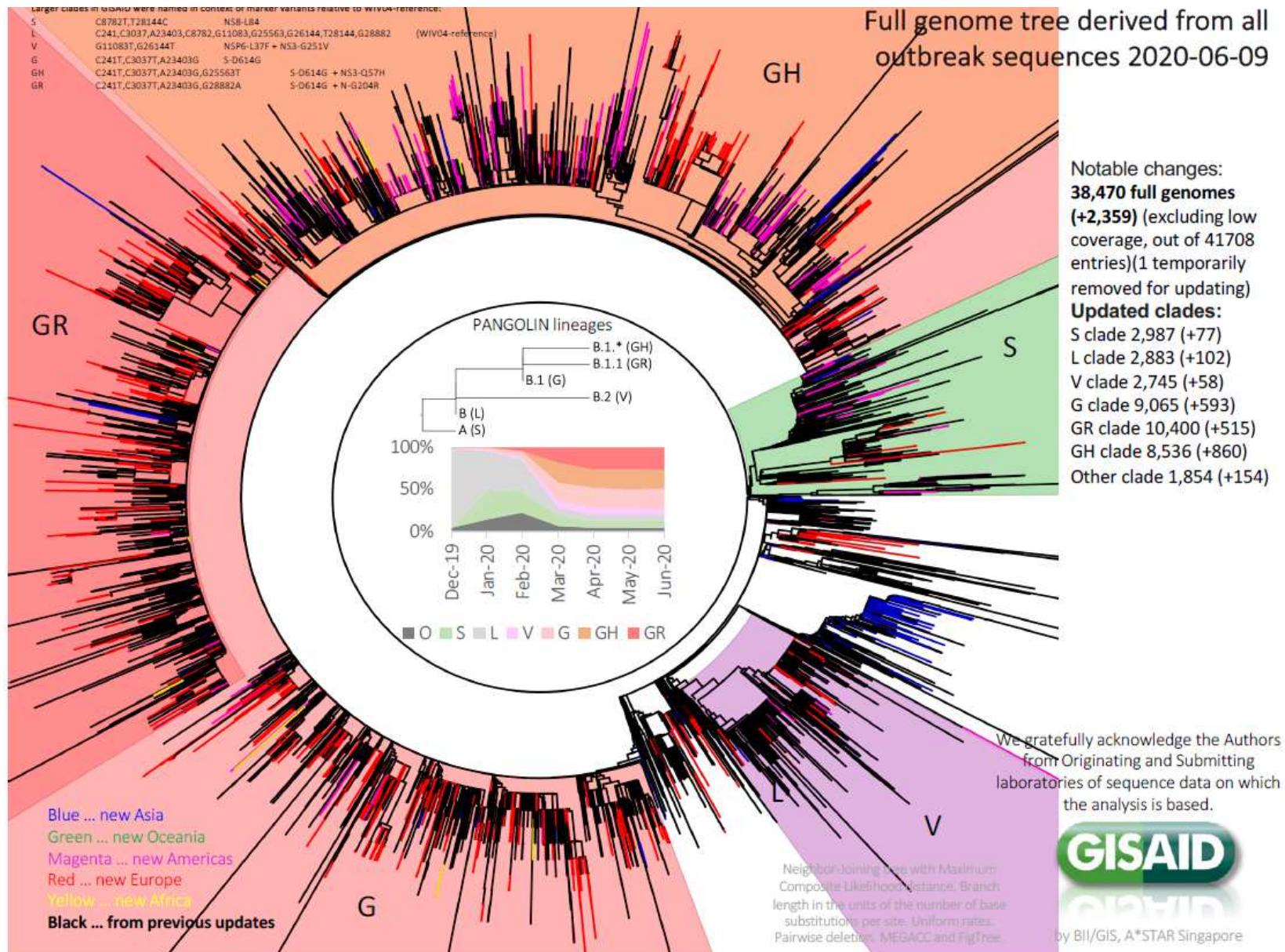


We gratefully acknowledge the Authors from
Originating and Submitting laboratories of
sequence data on which the analysis is based.



Le virus

• 9-6-20

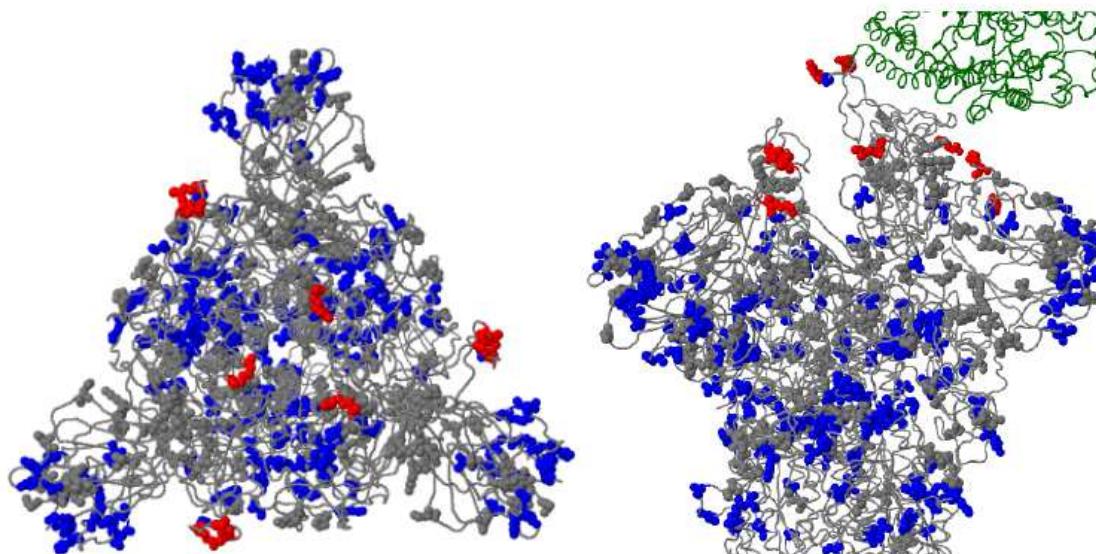


Données sur les évolutions liées au RBS

Receptor binding surveillance for complete genomes 2020-06-09

New occurrence of receptor binding mutations 33x N439K in Scotland, T478I in England, V483F in Belgium, E484K in England.

Total: 26 different rare variants near the binding interface not known to be linked to severity. 246x N439K (244 Scotland, England, Romania), 66x **T478I** in England, 30x V483A (26 USA/WA, 2 USA/UN, USA/CT, England), 10x G476S (8 USA/WA, USA/OR, Belgium), 7x S494P (3 USA/MI, England, Spain, India, Sweden), 6x V483F (4x Spain, England, Belgium), 4x **A475V** (2 USA/AZ, USA/NY, Australia/NSW), 3x G446V (2 Australia/Vic, England), 3x F490S in England, 2x V483I in England, 2x F490L (Australia/Vic, USA/LA), 2x **Q493L** in USA/WI, , 2x **G446S** in England, F456L in USA/TX, V445I in England, V503F in USA/NY, Y495N in Luxembourg, L455F in England, K444R in Spain, E484A in Spain, G476A in England, E484Q in India, E484D in Thailand, R403K in Australia/Vic, N501Y in USA/NY, E484K in England.



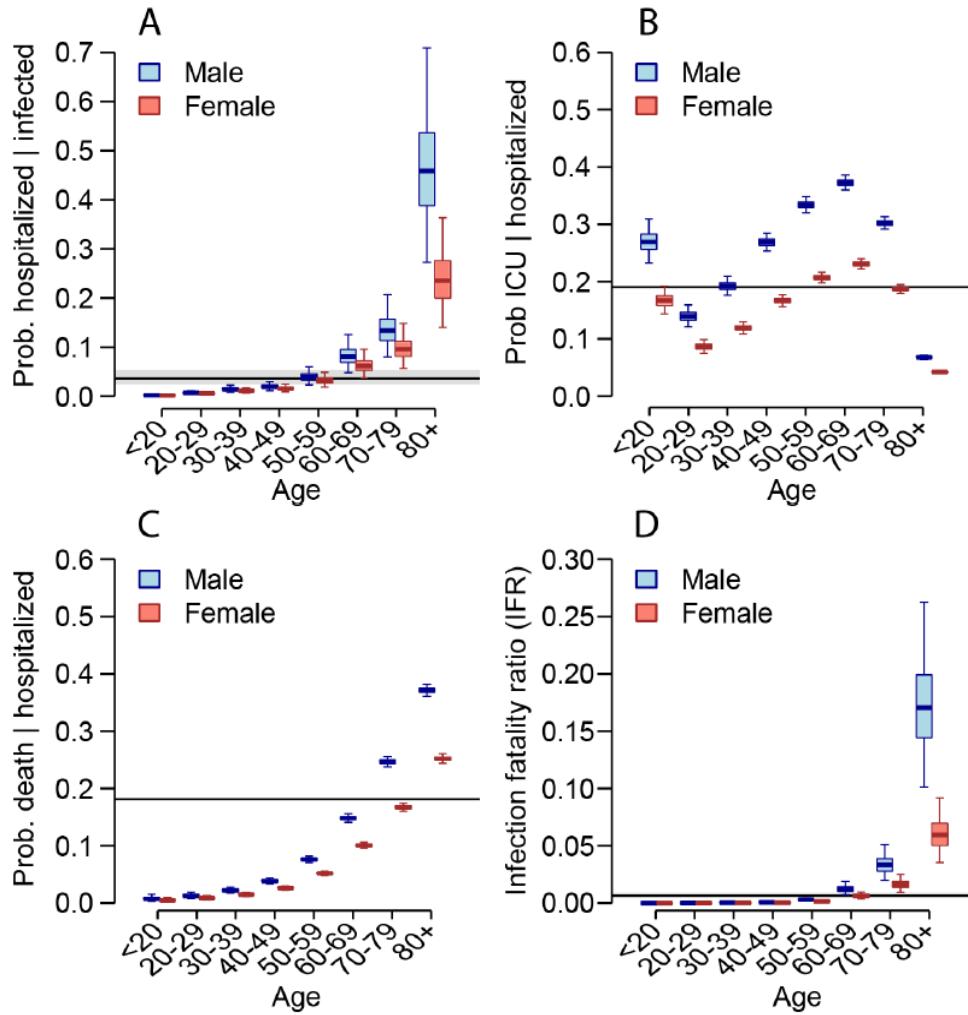
Mutations in the spike glycoprotein for the 2359 new complete genomes are shown here.

We gratefully acknowledge the Authors from Originating and Submitting laboratories of sequence data on which the analysis is based.

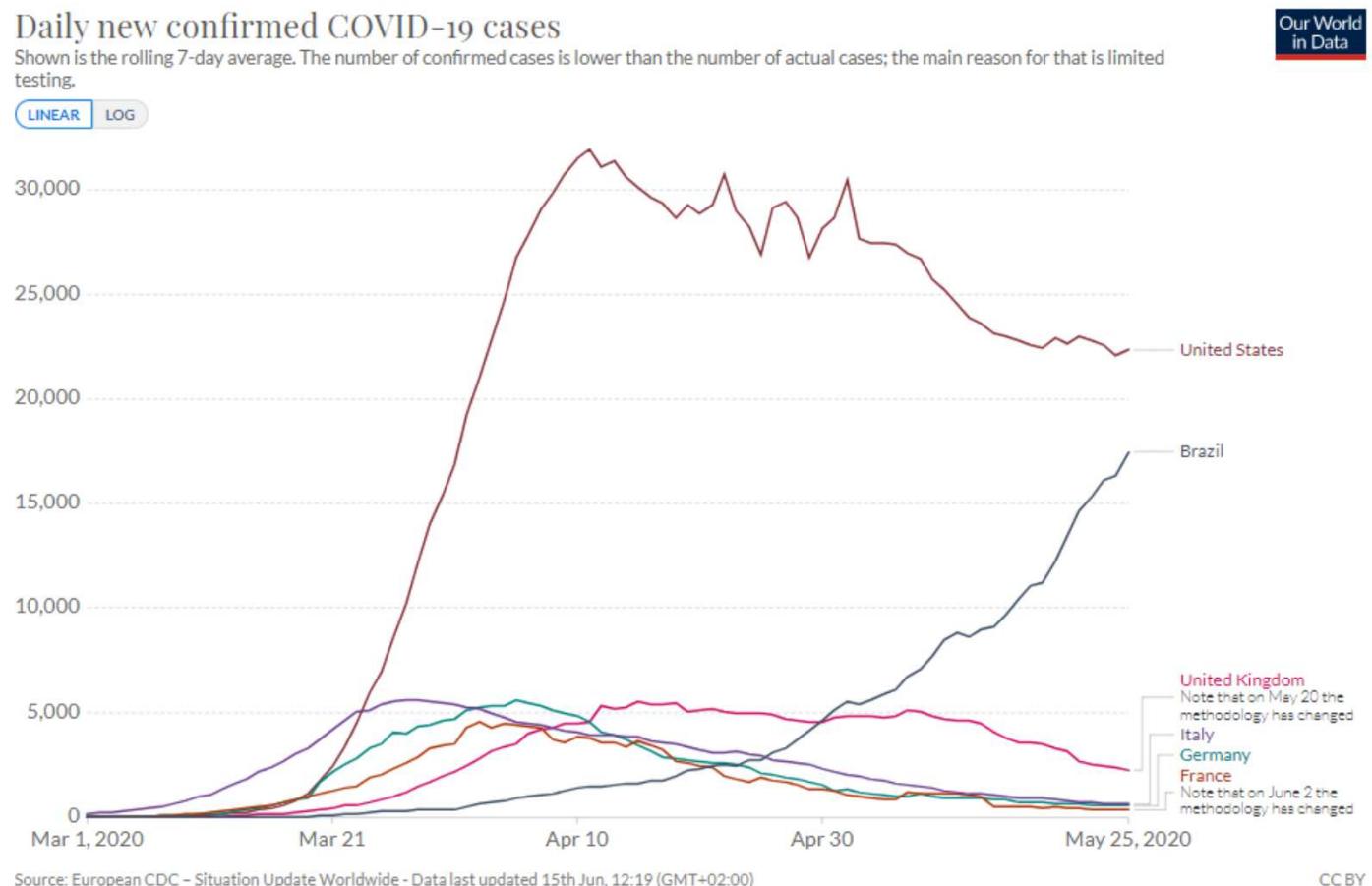
Green ... ACE2 human host receptor
Gray ... CoV spike glycoprotein trimer
Gray balls ... Spike glycoprotein variation occurring once (in EpiCoV)
Blue balls ... Spike glycoprotein variation occurring more than once (in EpiCoV)
Red balls ... Spike glycoprotein variation near host receptor
Yellow ... Insertion/deletion

Impact Clinique

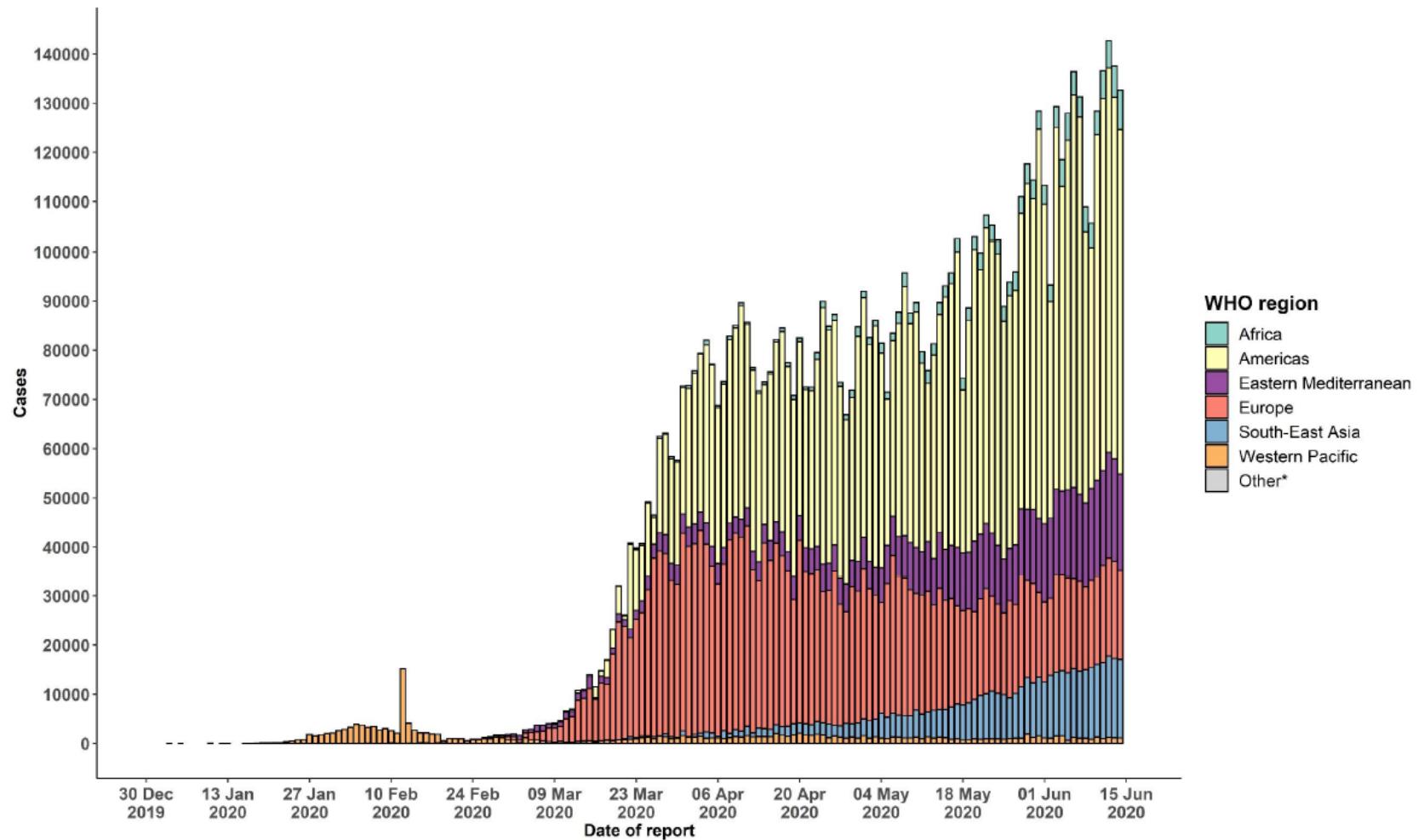
Impact de l'âge et du sexe



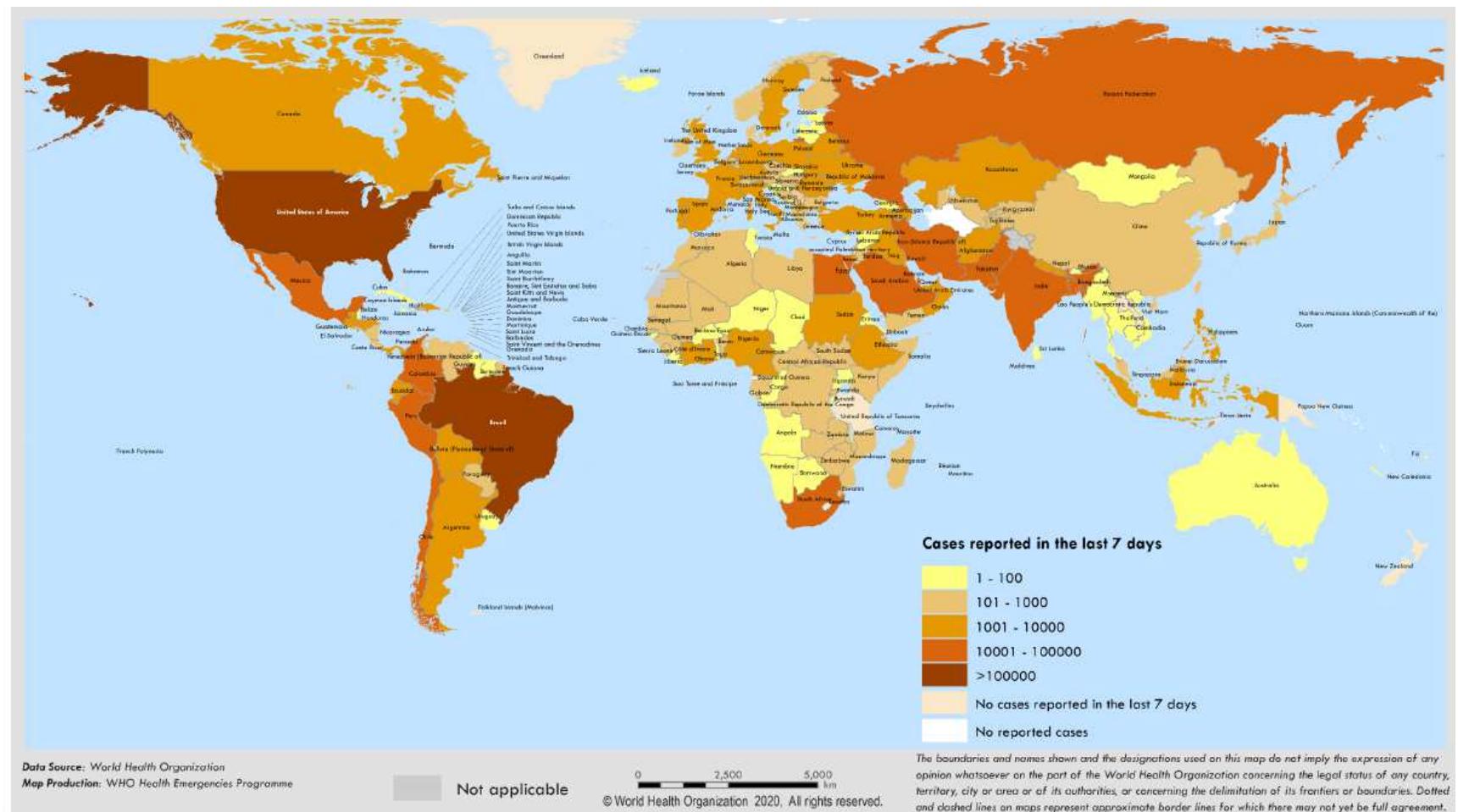
B – Situation Epidemiologique (nb de cas)

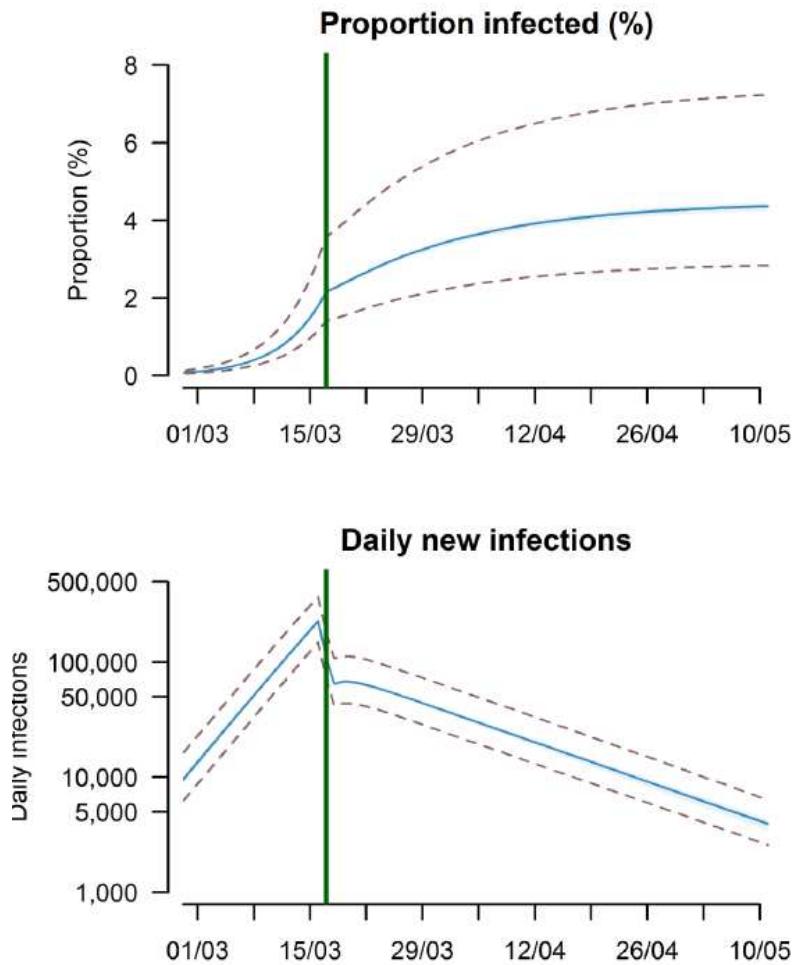


Nombre de cas sur 7 jours glissés (Données OMS)

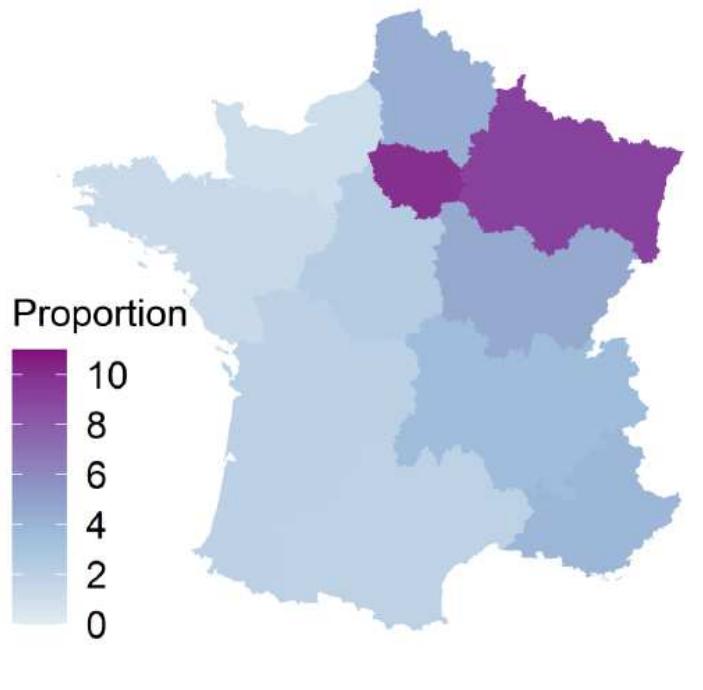


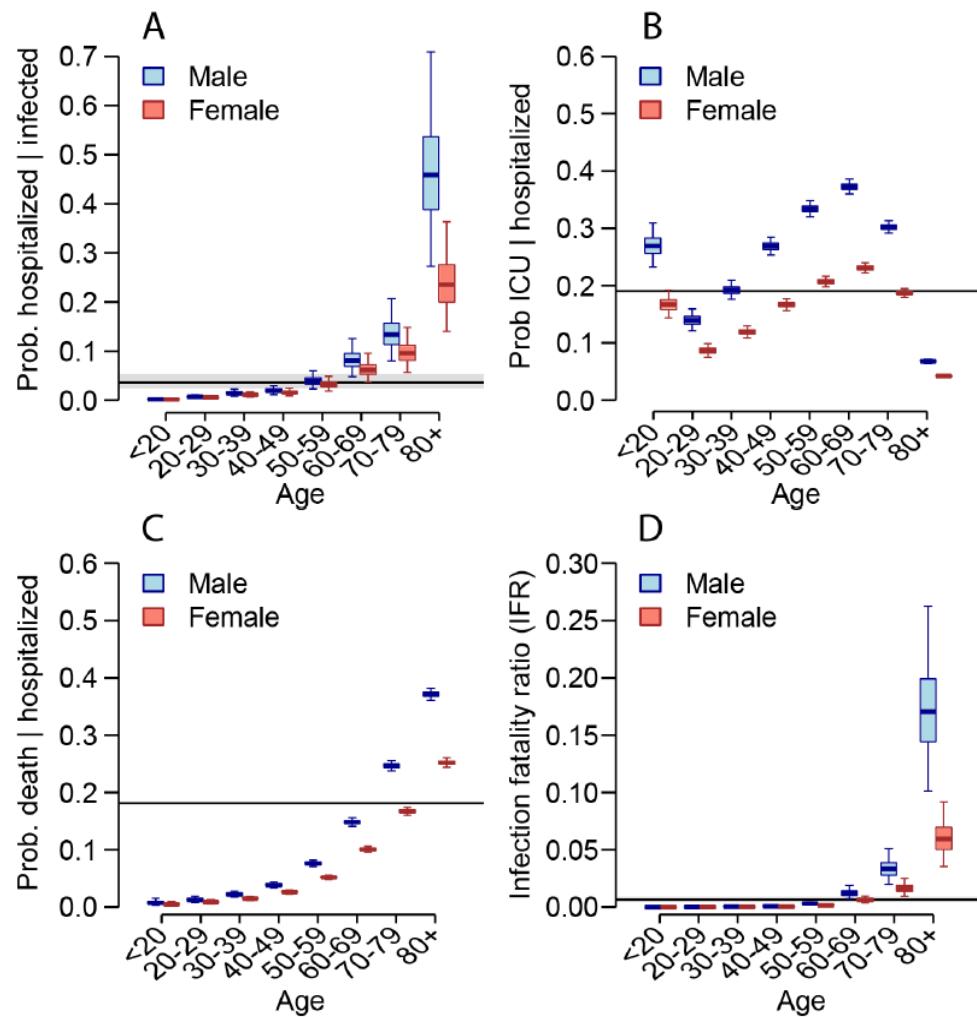
Nombre de cas sur 7 jours glissés (données OMS)



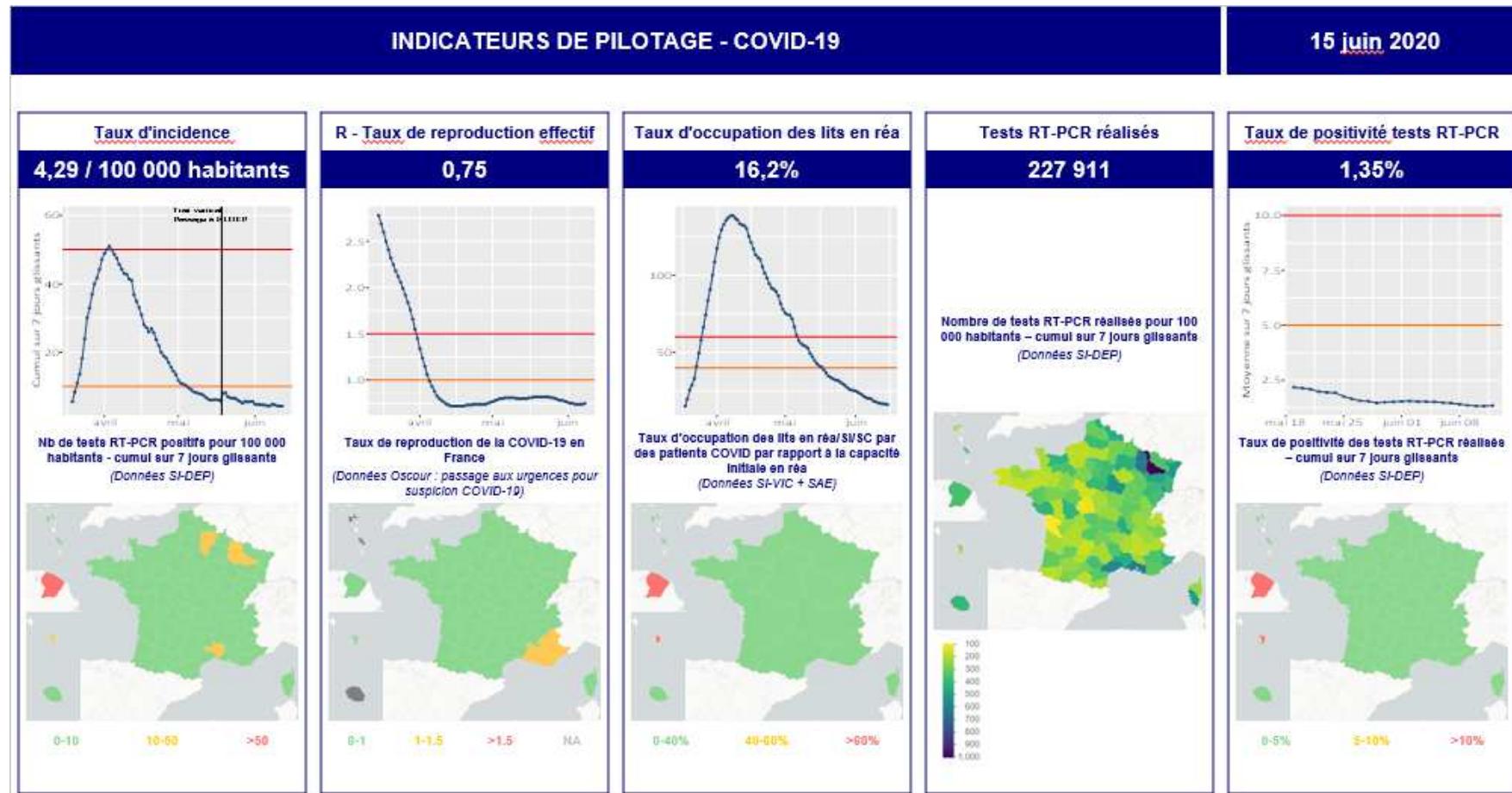


Proportion infected - May 11th (%)

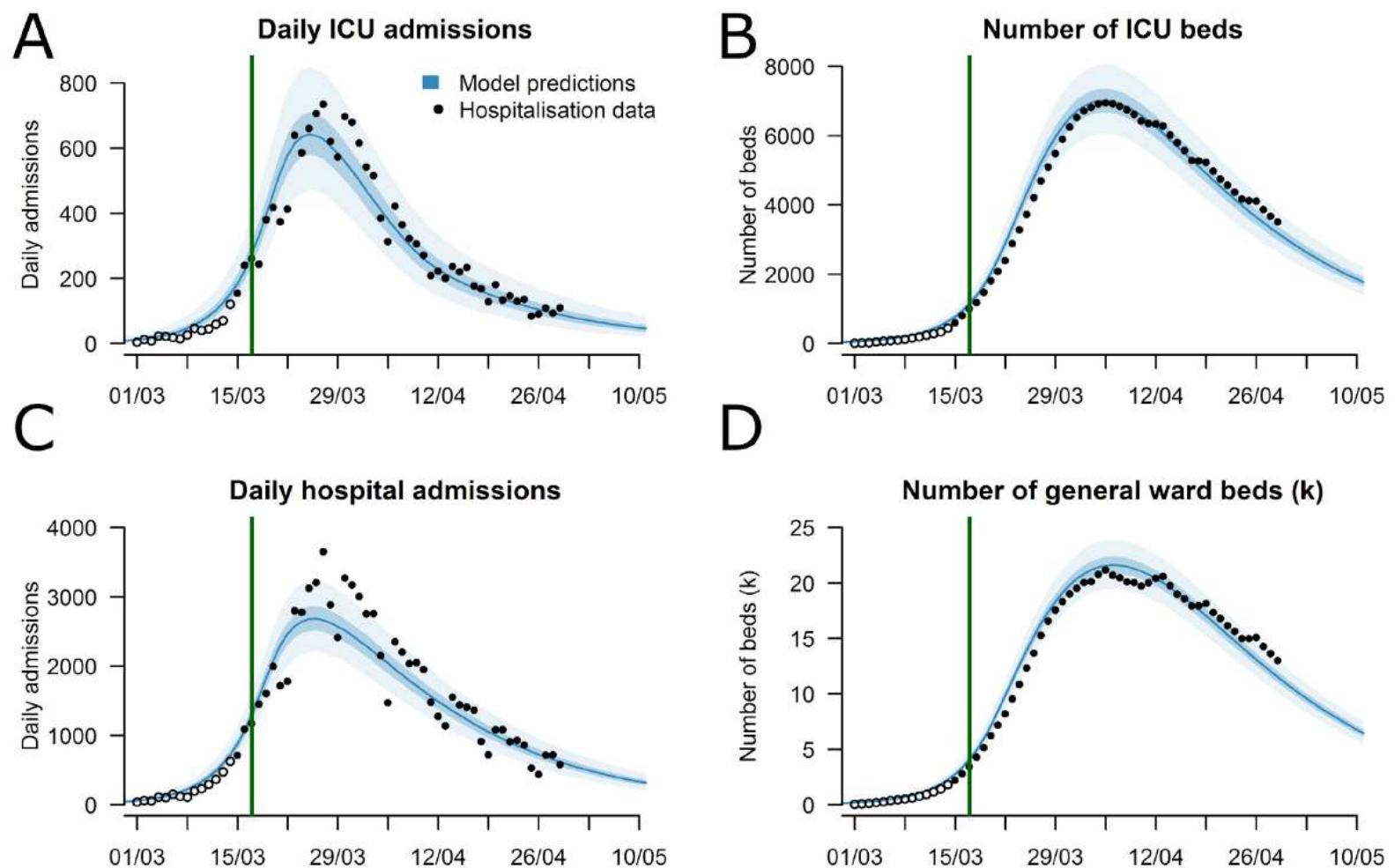




Evolution de la situation

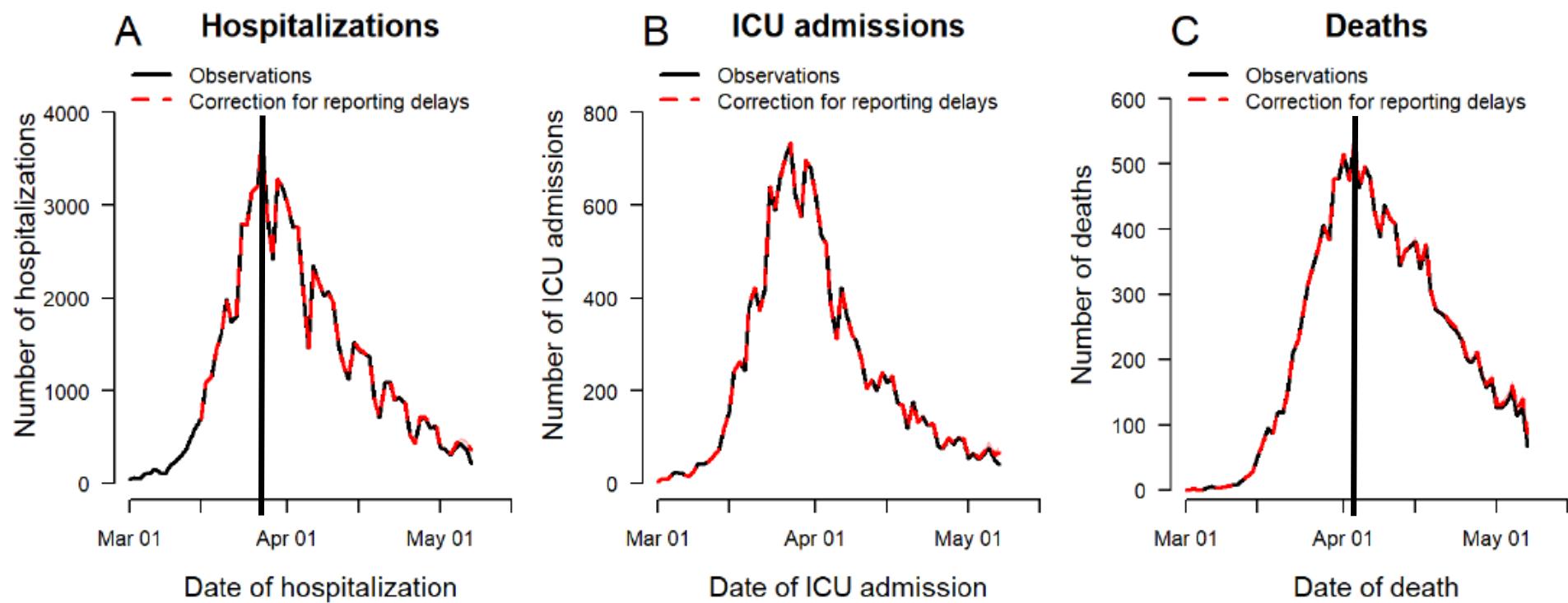


situation COVID-19 au 5 mai 2020



situation COVID-19 au 05 mai 2020

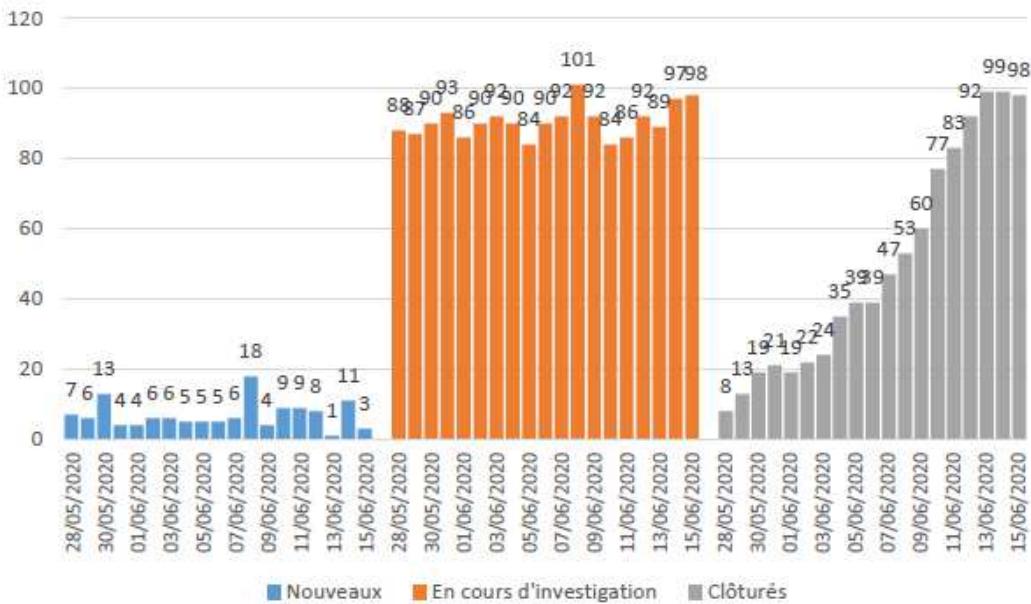
Figure S15 : Time-series of hospitalizations, ICU admissions and deaths corrected for reporting delays



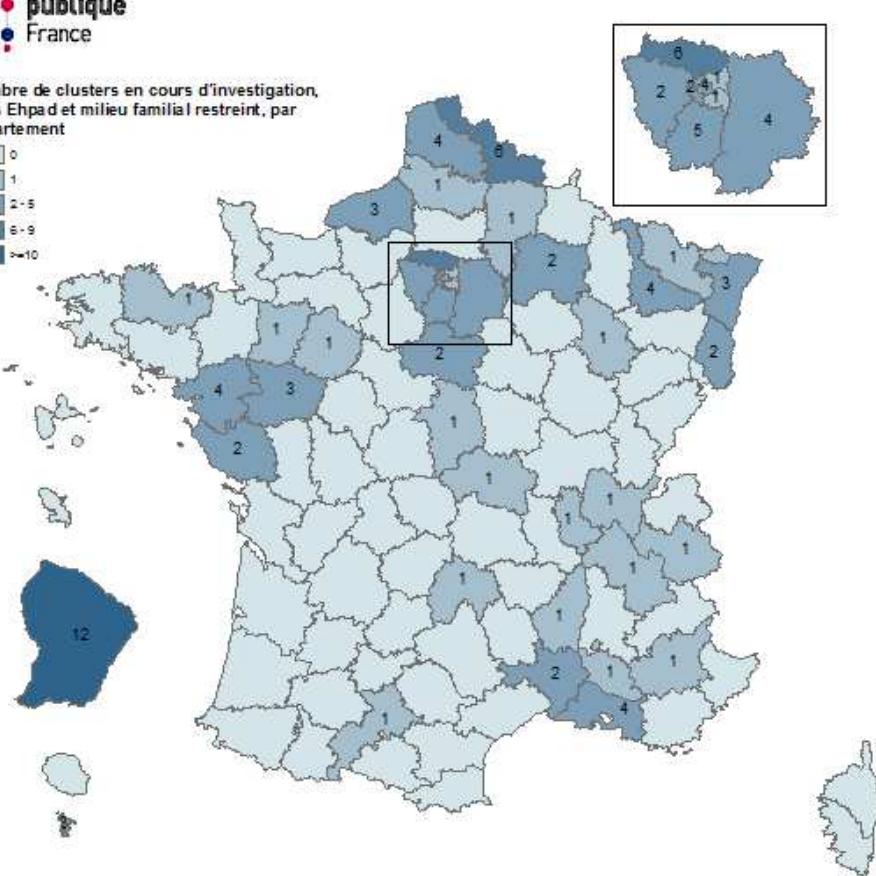
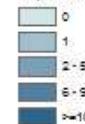
Salje H et al, Science, 2020

situation COVID-19 au 15 juin 2020

Evolution du nombre de clusters (CCS, données SPF)

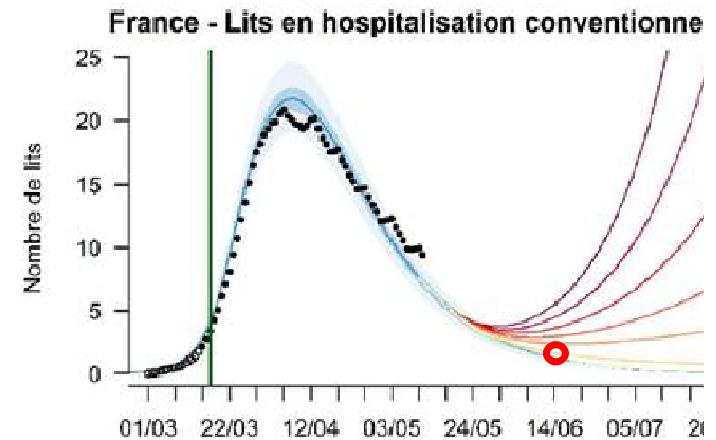
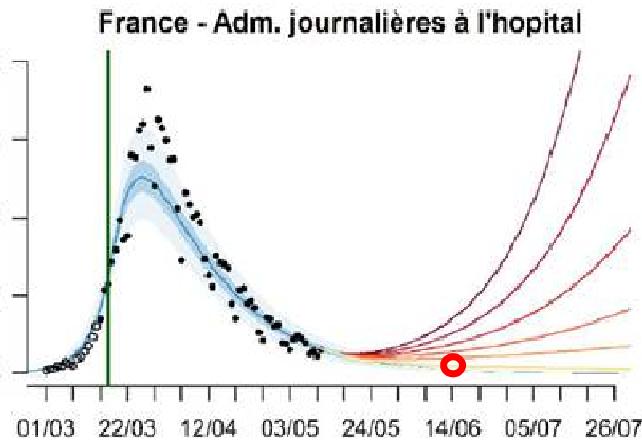
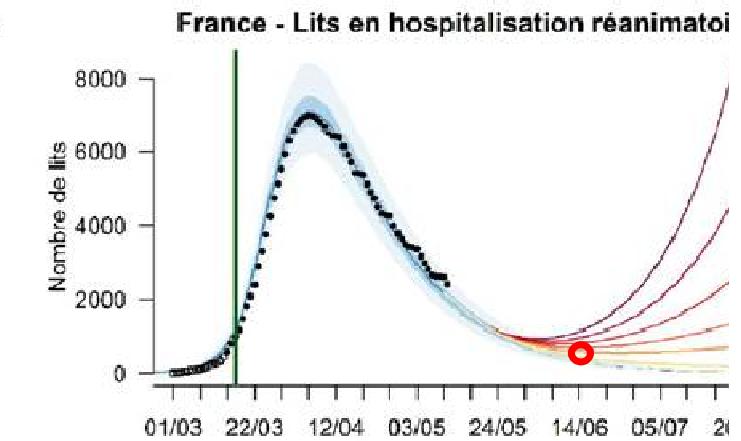
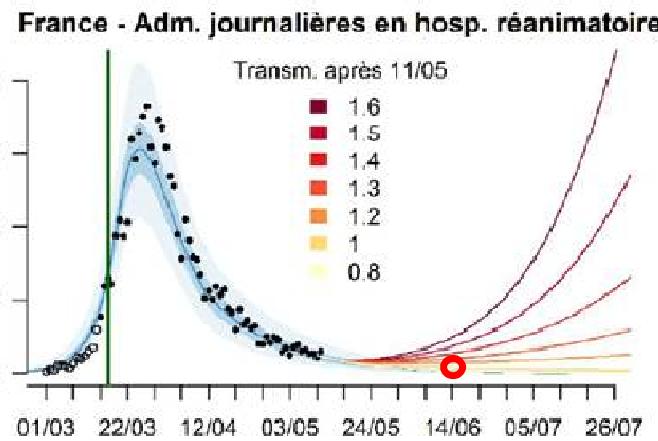


Nombre de clusters en cours d'investigation, hors Ehpad et milieu familial restreint, par département



Source : Santé publique France

Hypothèses d'évolution épidémique



Données Cauchemez S

Questions ?

- Anticorps facilitateurs
 - Réponse anticorps autres coronavirus
- Durée immunité
 - Plus de 2 ans?
- Différents sérotypes
 - Génogroupes S, V et G
- Autres...

L'avenir ???

- Cet été
- Cet automne
- Cet hiver
- Les autres virus

En fait, il faut bien comprendre que tout dépend de nous, rien que de nous



Remerciements

- CNR et labo IAI
 - Gregory Destras
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 - Martine Valette
 - Geneviève Billaud
 - Laurence Josset
 - Frédéric Laurent
 - Florence Morfin