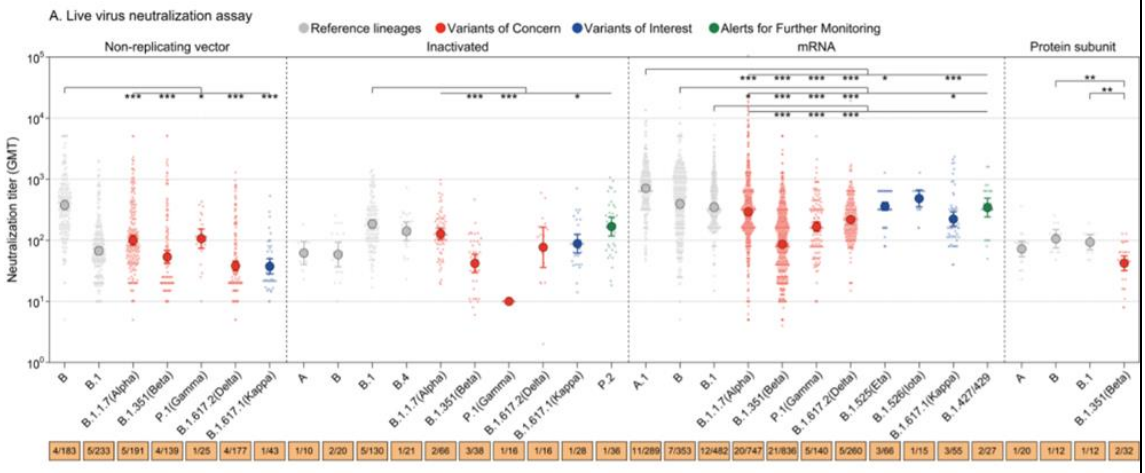
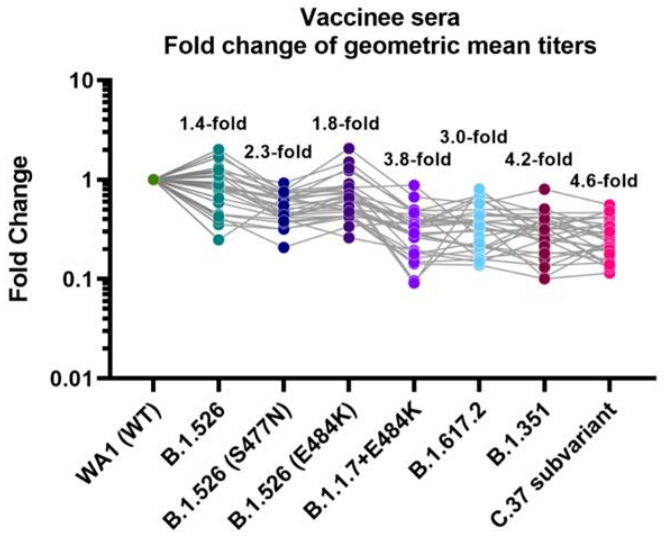
Quoi de neuf en génomique (SRAS-CoV-2)

26 juillet 2021

Publications sélectionnées

Titre	Extrait pertinent
24 juillet Neutralizing antibodies against SARS-CoV-2 variants induced by natural infection or vaccination: a systematic review and pooled meta-analysis	We systematically searched for studies that evaluated neutralizing antibodies titers induced by previous infection or vaccination against SARS-CoV-2 variants and collected individual data. Lineage B.1.351 (Beta), P.1 (Gamma) and B.1.617.2 (Delta) significantly escaped natural-infection-mediated neutralization, with an average of 4.1-fold (95% CI: 3.6-4.7), 1.8-fold (1.4-2.4), and 3.2-fold (2.4-4.1) reduction in live virus neutralization assay, while neutralizing titers against B.1.1.7 decreased slightly (1.4-fold, 95%CI: 1.2-1.6). Serum from vaccines also led to significant reductions in neutralization of B.1.351 across different platforms, with an average of 7.1-fold (5.5-9.0) for non-replicating vector platform, 4.1-fold (3.7-4.4) for mRNA platform, and 2.5-fold (1.7-2.9) for protein subunit platform. Neutralizing antibodies levels induced by mRNA vaccines against SARSCoV-2 variants were similar, or higher, than that derived from naturally-infected individuals. 

23 juillet Reduced neutralizing activity of post-SARS-CoV-2 vaccination serum against variants B.1.617.2, B.1.351, B.1.1.7+E484K and a sub-variant of C.37	Here, we tested a number of currently circulating viral variants of concern/interest in neutralization assays using a panel of post-mRNA vaccination sera. The assays were performed with authentic SARS-CoV-2 clinical isolates in an assay that mimics physiological conditions. The microneutralization assays showed only modest reductions in neutralizing activity against the three B.1.526 variants compared to the wild type WA1 isolate. The geometric mean titer (GMT) of neutralization of the three B.1.526 sublineages was reduced by 1.4-fold (ancestral B.1.526), 1.8-fold (E484K) and 2.3-fold (S477N), respectively. Reduction in neutralizing activity against the B.1.617.2 isolate was moderate with 3-fold change compared to WA1. A more pronounced drop in neutralizing activity was seen with the B.1.1.7+E484K isolate (3.8-fold). As expected and reported before, an even stronger decrease in neutralization (4.2-fold) was found against the B.1.351 isolate. However, the greatest reduction in GMT (4.6-fold) was observed against a C.37 variant isolate. 

23 juillet

[23 July 2021 Risk assessment for SARS-CoV-2 variant: Beta. Public Health England.]

Indicator	RAG*	Confidence	Assessment and rationale
Transmissibility between humans		MODERATE	**Beta is no more transmissible than Alpha** Experimental data (growth in airway epithelium, and animal to animal transmission) suggest that Beta is not highly fit and is likely to be less transmissible than Alpha. Case numbers in England are too low for reliable estimates of secondary attack rate. Based on GISAID data, Beta has persisted at a low to moderate prevalence in the presence of Alpha in many countries, but it does not appear to become predominant in this context. In countries where Beta has previously been highly prevalent, Delta is now consistently establishing predominance.
Infection severity			**Insufficient information** Case numbers in the UK have been too low to assess severity. There are limited published data available.
Naturally acquired immunity		HIGH	**Experimental evidence of evasion of naturally acquired immunity** There is laboratory evidence of reduction in neutralisation by convalescent sera, from multiple laboratories. Although this is true regardless of the nature of the first infection, preliminary data suggest the effect may be more pronounced in convalescent sera from Delta infections in unvaccinated individuals (LOW confidence). Systematic comparative data on clinical reinfections would be required to raise the risk to red.
Vaccine-derived immunity		MODERATE	**Evidence of decreased vaccine effectiveness** There is robust evidence of reduced neutralisation by sera from vaccinated individuals, across multiple studies and vaccines. The change in neutralisation is greater than for other variants of concern, including Delta. Clinical trial and real-world data support a reduction in vaccine effectiveness against symptomatic infection after two doses, which varies by vaccine (MODERATE confidence). The reduction in vaccine effectiveness is greater for some vaccines than the reduction seen for Delta, but for other vaccines there is equivalent effectiveness for Beta and Delta. There is some evidence that vaccine effectiveness against severe disease is similar to that against Delta, however the data include one study which combines Beta and Gamma, and two studies where the studied population is young and does not reflect the composition of the UK population (LOW confidence for VE against severe disease).
Overall assessment of level and nature of risk, and level of confidence			There is strong laboratory and real-world evidence that Beta is antigenically different to other common variants. The immune experience of the UK population will be shaped by which variants have circulated and which vaccines have been used. This will determine the population vulnerability to Beta and should be further explored. Whilst Beta does not appear highly fit or transmissible compared to the currently prevalent variants, it has still achieved widespread global transmission and it is currently difficult to predict whether it may display a selective advantage in the changing virological, immunological and human behavioural landscape in the UK.

The therapeutics risk assessment is under review for all variants and is not included.
*refer to scale and confidence grading slide

[23 July 2021 Risk assessment for SARS-CoV-2 variant: Delta. Public Health England.]

Indicator	RAG*	Confidence	Assessment and rationale
Transmissibility between humans		**HIGH**	**Transmissibility appears greater than wild type (first wave) virus.** All analyses support increased transmissibility for Delta compared to both wild type virus and Alpha. There is in vitro evidence suggestive of increased replication in biological systems that model human airway, and evidence of optimised furin cleavage. There is epidemiological evidence from secondary attack rates, household transmission studies, and growth rate modelling. The finding of lower CT values in routine testing data, compared to Alpha, may be relevant to the mechanism of increased transmissibility, however there may be multiple contributors.
Infection severity		**LOW**	**Increased severity (hospitalisation risk) when compared to Alpha.** There is an apparent increased risk of hospitalisation compared to contemporaneous Alpha cases. Analysis of deaths in England is limited by low numbers but suggests that Delta has at least an equivalent case fatality rate to Alpha (LOW confidence). Further analysis is required of both national surveillance and CO-CIN data to understand the severity and characteristics of disease in hospital.
Immunity after natural infection		**LOW**	**Evidence of increased reinfections** Pseudovirus and live virus neutralisation using convalescent sera from first wave and Alpha infections shows a reduction in neutralisation. National surveillance analysis, adjusted for different variables including age and vaccination, shows a preliminary signal of increased risk of reinfection with Delta compared to Alpha. Further investigations are being undertaken
Vaccines		**HIGH**	**Epidemiological and laboratory evidence of reduced vaccine effectiveness** There are analyses from England and Scotland supporting a reduction in vaccine effectiveness for Delta compared to Alpha against symptomatic infection. This is more pronounced after 1 dose. Iterated analysis continues to show vaccine effectiveness against Delta is high after 2 doses. Current evidence suggests that VE against hospitalisation is maintained. Although this is observational data subject to some biases, it holds true across several analytic approaches and the same effect is seen in both English and Scottish data. It is strongly supported by pseudovirus and live virus neutralisation data from multiple laboratories. There are no data on whether vaccine effectiveness against transmission is affected.
Overall assessment			Delta remains predominant in the UK and the rapid global spread continues. Distinct clades within Delta are beginning to be identified, predominantly distinguished by changes outside spike of uncertain biological significance. Laboratory investigations have been triggered. The changes in this update concern severity and reinfection risk. Both hospitalisation and deaths analyses now point towards severity that is at least as great as that of Alpha, although there is a high level of uncertainty in these findings. Whilst laboratory data and anecdotal reports have long raised the possibility of an increased risk of reinfection, there is now a signal in the national surveillance data. The priority investigations are to improve understanding of asymptomatic transmission in the vaccinated, to further investigate the developing diversity within Delta, and continued investigation of the clinical course of disease.

The therapeutics risk assessment is under review for all variants and is not included.
*refer to scale and confidence grading slide

23 juillet [Pfizer Shot Just 39% Effective Against Delta Infection, But Largely Prevents]	Recent data from Israel's health ministry suggests Pfizer's Covid-19 vaccine is far less effective at preventing infection and symptomatic illness with the Delta variant than with previous strains of coronavirus.

Severe Illness, Israel Study Suggests	A full course of the Pfizer-BioNTech vaccine was just 39% effective at preventing infections and 41% effective at preventing symptomatic infections caused by the Delta Covid-19 variant, according to Israel's health ministry, down from early estimates of 64% two weeks ago. **NOTE: Follow-up period shifted to weeks when delta variant dominated sequenced strains in Israel** The Israel findings also conflict with several other studies (Nasreen *et al.*, Bernal *et al.*, Sheikh *et al.*,) assessing the vaccine's performance against the Delta variant, which indicated only slightly diminished degrees of protection against infection and mild illness (between 80% and 90%), including peer reviewed research from Public Health England published Wednesday. The vaccine still provides very high levels of protection against hospitalization (92%) and severe illness (91%) caused by the Delta variant, the ministry said.

Outcome	20/06-17/07		
	VE	Lower CI	Upper CI
SARS-CoV-2 cases	39.0%	9.0	59.0
Symptomatic COVID-19*	40.5%	8.7	61.2
COVID-19 hospitalization	88.0%	78.9	93.2
Severe COVID-19**	91.4%	82.5	95.7

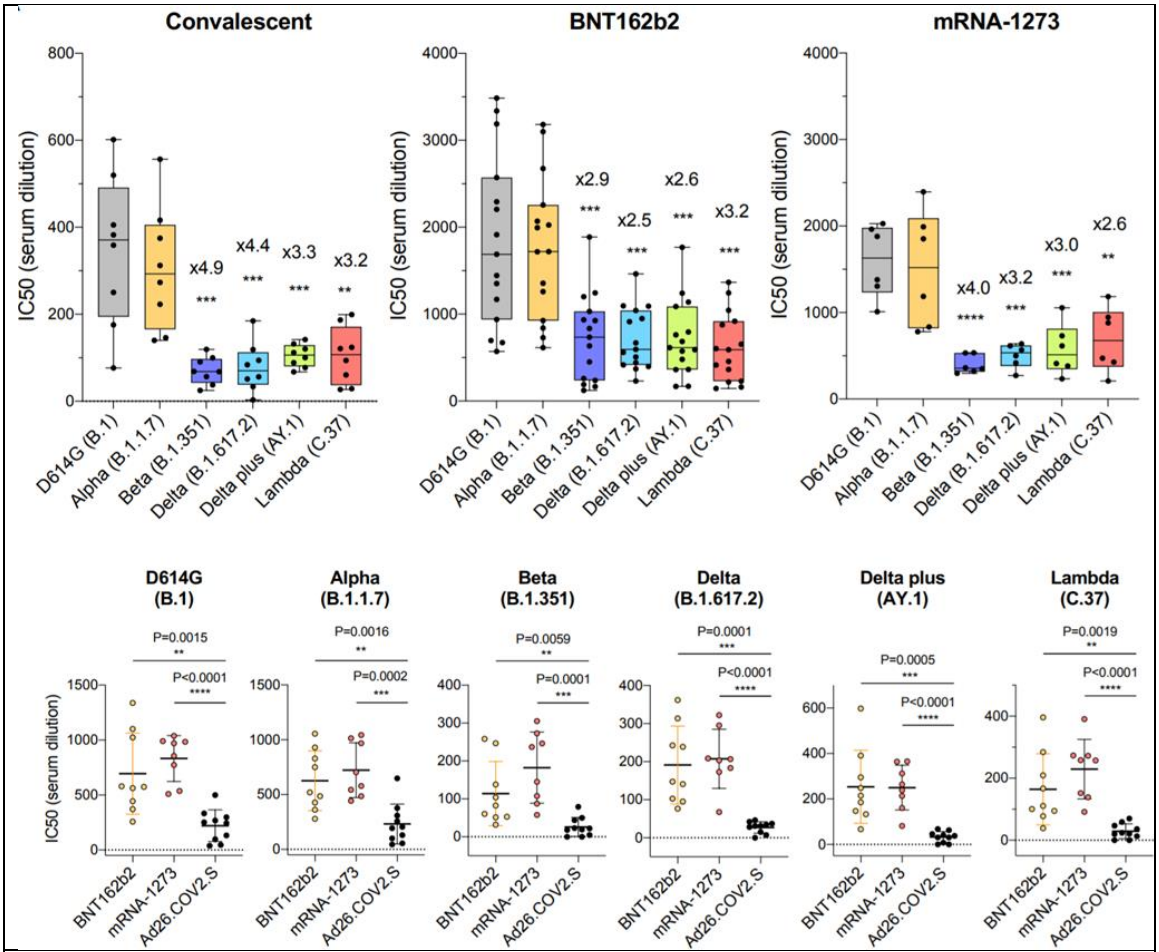
* Fever and/or respiratory symptoms on epidemiologic investigation
** Including severe, critical and deceased COVID-19 (Severe – respiratory rate > 30/minute, oxygen saturation < 94%, and/or PaO2/FiO2 < 300; Critical – invasive mechanical ventilation, shock or major organ failure)

21 juillet

Comparison of Neutralizing Antibody Titers Elicited by mRNA and Adenoviral Vector Vaccine against SARS-CoV-2 Variants

This study compared the neutralization titers of serum antibodies from individuals immunized with three U.S. FDA Emergency use authorization vaccines (BNT162b2, mRNA-1273 and Ad26.COV2.S) against viruses with the VOC and Lambda spike proteins. The study groups were controlled for age, clinical co-morbidity, history of pre-vaccination infection and sera were collected on similar days post-vaccination.

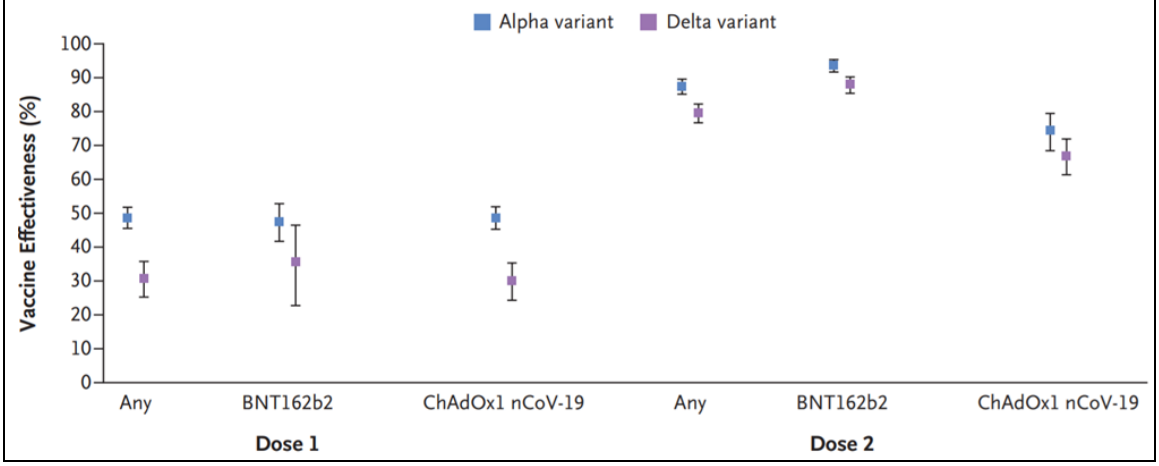
BNT162b2 and mRNA-1273-elicited antibodies showed modest neutralization resistance against Beta, Delta, Delta plus and Lambda variants whereas Ad26.COV2.S-elicited antibodies from a significant fraction of vaccinated individuals were of low neutralizing titer (IC50 <50). The data underscore the importance of surveillance for breakthrough infections that result in severe COVID-19 and suggest the benefit of a second immunization following Ad26.COV2.S to increase protection against the variants.

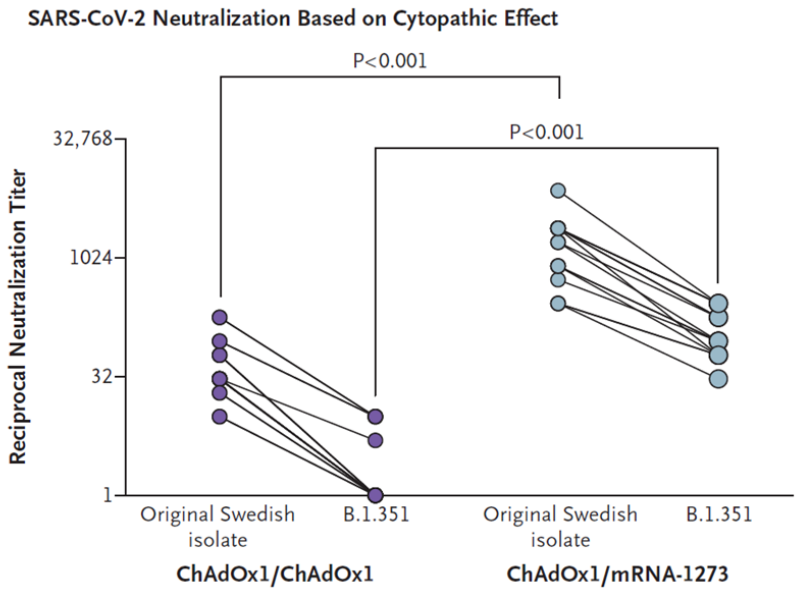


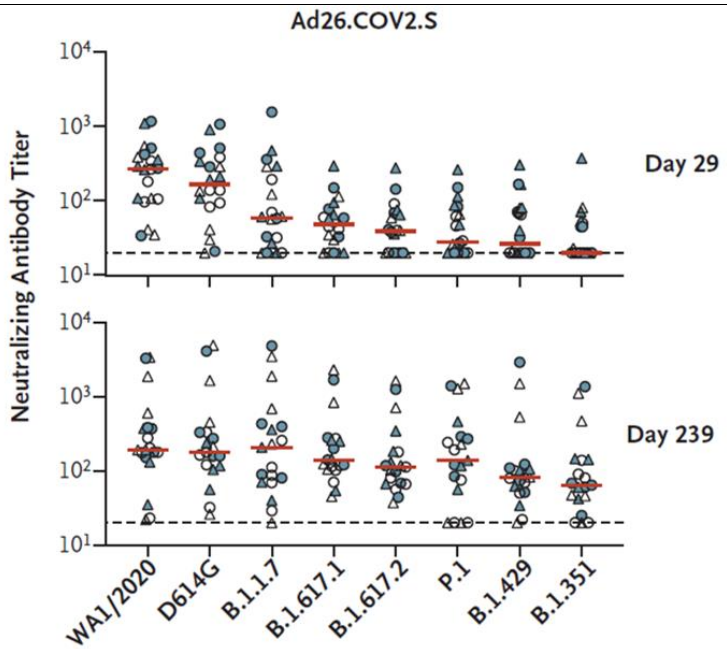
21 juillet

[Effectiveness of Covid-19 Vaccines against the B.1.617.2 (Delta) Variant]

We used a test-negative case–control design to estimate the effectiveness of vaccination against symptomatic disease caused by the delta variant or the predominant strain (alpha variant) over the period that the delta variant began circulating. Data on all symptomatic sequenced cases of Covid-19 in England were used to estimate the proportion of cases with either variant according to the patients' vaccination status.



Results for the first dose were similar for both vaccines, with an absolute difference in vaccine effectiveness against the delta variant as compared with the alpha variant of 11.9 percentage points with the BNT162b2 vaccine and 18.7 percentage points with the ChAdOx1 nCoV-19 vaccine. The difference in vaccine effectiveness was much smaller among persons who had received the second dose of vaccine. With the BNT162b2 vaccine, a small difference in effectiveness between variants was seen after the second dose: 93.7% (95% CI, 91.6 to 95.3) with the alpha variant and 88.0% (95% CI, 85.3 to 90.1) with the delta variant. The effectiveness with two doses of the ChAdOx1 nCoV-19 vaccine was lower than with the BNT162b2 vaccine; however, with the ChAdOx1 nCoV-19 vaccine, the difference in effectiveness between the alpha and delta variants was small (74.5% [95% CI, 68.4 to 79.4] and 67.0% [95% CI, 61.3 to 71.8], respectively).	
14 juillet Heterologous ChAdOx1 nCoV-19 and mRNA-1273 vaccination.	A dose of mRNA-1273 following, by 9 to 12 weeks, a primary dose of ChAdOx1 efficiently stimulated SARS-CoV-2 specific B-cell memory. Those receiving heterologous doses mounted significantly higher reciprocal neutralizing titers and had higher titers against B.1.351 than those receiving homologous doses (p <0.001). 
14 juillet Durable humoral and cellular immune responses 8 months after Ad26.COV2.S vaccinationexternal icon	Durability of humoral and cellular immune responses in experimental group receiving Ad26.COV2.S (Johnson & Johnson/Janssen) vaccination (n = 20) and placebo (n = 5) studied over 8 months. Median neutralizing antibody titers were evaluated by ELISA for the WA1/2020, D614G, B.1.1.7 (Alpha), B.1.617.1 (Kappa), B.1.617.2 (Delta), P.1, B.1.429 (Epsilon), and B.1.351 (Beta) variants. Limitations : Small sample size. -Vaccination with a single dose of Ad26.COV2.S continued to produce humoral and cellular immunity for at least 239 days. Median CD8+ T-cell responses was 0.0545%, 0.0554%, and 0.0734% on days 57, 85, and 239, respectively. -Increased neutralization over time of SARS-CoV-2 variants, including B.1.617.2 (Delta), B.1.351 (Beta) and P.1 (Gamma) suggests maturation of B-cell responses.

	
13 juillet Impact of original, B.1.1.7, and B.1.351/P.1 SARS-CoV-2 lineages on vaccine effectiveness of two doses of COVID-19 mRNA vaccines: Results from a nationwide case-control study in France	We analysed data from an ongoing nationwide case-control study to assess the effectiveness of two doses of mRNA vaccines against COVID-19 with the original SARS-CoV-2 virus and other lineages circulating in France, adjusting for a large series of potential confounders, including socio-demographic characteristics, co-morbidities, occupation, and history of past infection. Information about the infecting virus was based on a screening RT-PCR for either B.1.1.7 or B.1.351/P.1 variants. Included in our analysis were 7 288 adults infected with the original SARS-CoV-2 virus, 31 313 with the B.1.1.7 lineage, 2 550 with B.1.351/P1 lineages, and 3 644 controls. In multivariable analysis, the vaccine effectiveness (95% confidence interval) seven days after the second dose of mRNA vaccine was estimated at 88% (81-92), 86% (81-90) and 77% (63-86) against COVID-19 with the original virus, the B.1.1.7 lineage, and the B.1.351/P.1 lineages, respectively.

Quoi de neuf en génomique (SRAS-CoV-2)

19 juillet 2021

Publications sélectionnées

<table>
<tr><th>Titre</th><th>Extrait pertinent</th></tr>
<tr><td>18 juillet
Tracking variants of the novel coronavirus in Canada</td><td>CTVNews.ca's variant tracker is keeping a daily count of these VOCs, with a provincial breakdown by variant that you can see in the below table. Additionally, CTVNews.ca is now tracking 'screened' COVID-19 cases, which have been identified as mutations but are yet to be confirmed which variant they belong to.
By adding this screened data, we hope to provide a more accurate estimate of how many VOCs are circulating in Canada.

<table>
<tr><th>Province</th><th>Alpha</th><th>Beta</th><th>Gamma</th><th>Delta</th><th>Screened*</th></tr>
<tr><td>Canada</td><td>226 393</td><td>2 341</td><td>19 680</td><td>6 809</td><td>190 966</td></tr>
<tr><td>Ontario</td><td>144 798</td><td>1 466</td><td>4 955</td><td>3 318</td><td>24 226</td></tr>
<tr><td>Alberta</td><td>45 735</td><td>171</td><td>2 801</td><td>969</td><td>77 582</td></tr>
<tr><td>British Columbia</td><td>14 063</td><td>154</td><td>10 695</td><td>1 380</td><td>42 701</td></tr>
<tr><td>Quebec</td><td>7 173</td><td>445</td><td>554</td><td>219</td><td>17 372</td></tr>
<tr><td>Manitoba</td><td>7 065</td><td>73</td><td>230</td><td>474</td><td>8 382</td></tr>
<tr><td>Saskatchewan</td><td>6 963</td><td>10</td><td>410</td><td>424</td><td>4 505</td></tr>
<tr><td>Newfoundland and Labrador</td><td>187</td><td>6</td><td>1</td><td>1</td><td>0</td></tr>
<tr><td>New Brunswick</td><td>180</td><td>4</td><td>1</td><td>0</td><td>0</td></tr>
<tr><td>Nova Scotia</td><td>103</td><td>12</td><td>1</td><td>22</td><td>0</td></tr>
<tr><td>Northwest Territories</td><td>76</td><td>0</td><td>1</td><td>0</td><td>0</td></tr>
<tr><td>Prince Edward Island</td><td>26</td><td>0</td><td>0</td><td>2</td><td>0</td></tr>
<tr><td>Nunavut</td><td>21</td><td>0</td><td>0</td><td>0</td><td>0</td></tr>
<tr><td>Yukon</td><td>3</td><td>0</td><td>31</td><td>0</td><td>0</td></tr>
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<tr><td>16 juillet
Homologous and Variant-Specific Memory B-Cell and Antibody Responses after SARS-CoV-2 mRNA Vaccination</td><td>In this longitudinal cohort study of subjects receiving COVID-19 mRNA vaccine we assessed memory B cell response and functional antibody titers.

While RBDspecific MBCs were readily detectable to all variant RBDs at both timepoints following mRNA vaccination, we noted statistically significant reductions in the MBC frequencies to the each of the variant RBDs after the first vaccine dose ($p<0.025$ for all comparisons, Fig. 3A). Following the second vaccine dose, a significant decrease in the number of reactive MBCs recognizing the Beta, Gamma and Delta RBD variants remained ($p<0.002$ for all comparisons), while the difference in MBC response to the Alpha variant was non-significant (Fig. 3B)</td></tr>
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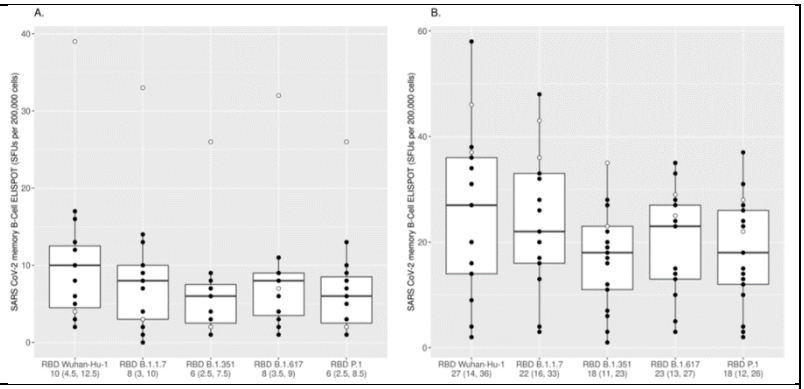
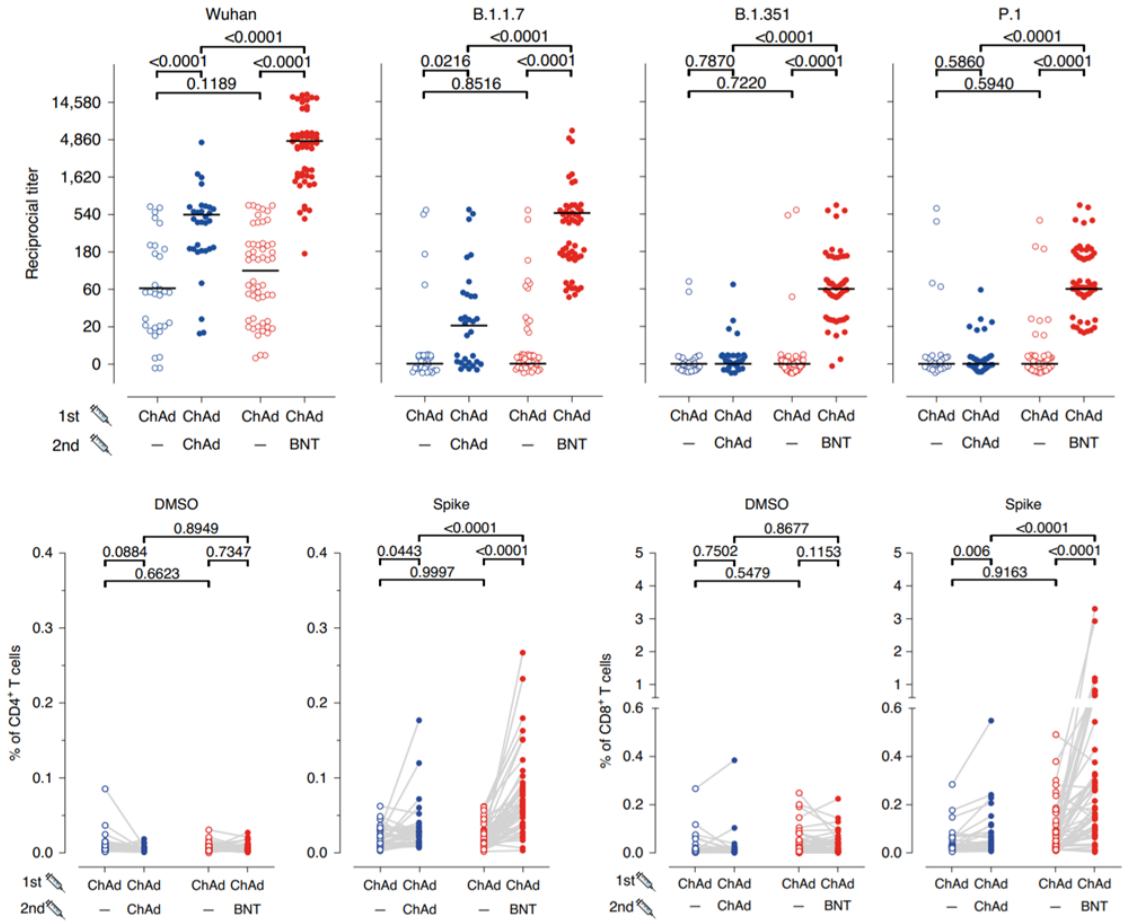
	
16 juillet Cinq fois plus de nouveaux cas de COVID-19 d'ici au 1er août	La semaine dernière (5-11 juillet), le nombre de nouveaux cas dans l'Union européenne a bondi de 60%, augmentant pour la deuxième semaine consécutive selon l'ECDC du fait « du relâchement des mesures et de la progression du variant Delta » originellement détecté en Inde. L'ECDC table sur une incidence de plus de 420 nouveaux cas pour 100 000 habitants pour la semaine s'achevant le 1er août contre moins de 90 la semaine dernière. Si ces projections restent des hypothèses épidémiologiques, ce niveau correspond à celui observé lors des pics de l'automne 2020 et d'avril 2021, selon les données de l'agence de l'UE. Le nombre d'hospitalisations et de décès devrait lui augmenter moins vite, selon l'ECDC, grâce notamment à la campagne vaccinale: le nombre de morts liés à la COVID-19 devrait redépasser la barre des 10, contre 6,8 la semaine passée.
14 juillet Immune responses against SARS-CoV-2 variants after heterologous and homologous ChAdOx1 nCoV-19/BNT162b2 vaccination We used Hannover Medical School's COVID-19 Contact Study cohort of healthcare professionals to monitor ChAd-primed immune responses before and 3 weeks after booster with ChAd (n=32) or BioNTech/ Pfizer's BNT162b2 (n=55). Although both vaccines boosted prime-induced immunity, BNT162b2 induced significantly higher frequencies of spike-specific CD4+ and CD8+ T cells and, in particular, high titers of neutralizing antibodies against the B.1.1.7, B.1.351 and P.1 variants of concern of severe acute respiratory syndrome coronavirus 2.	

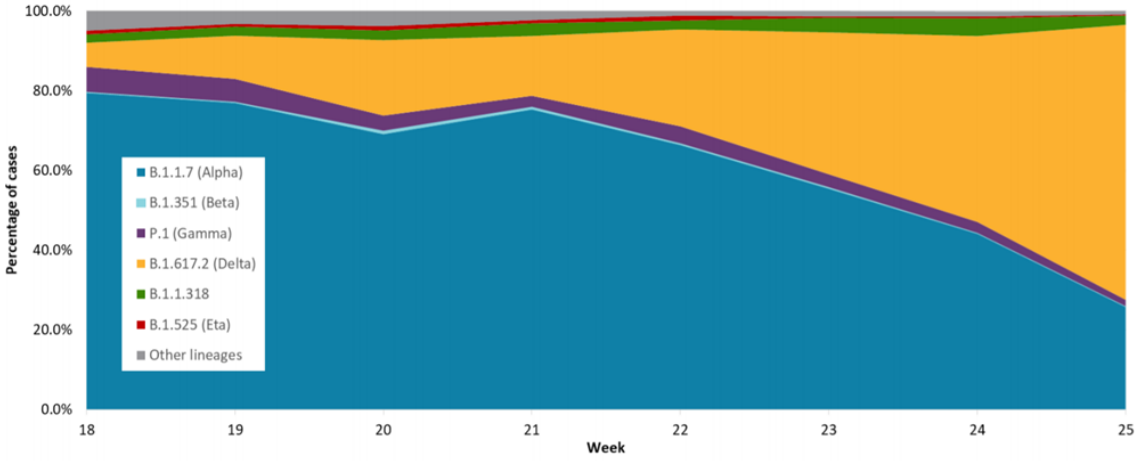


En complément:
[Heterologous ChAdOx1 nCoV-19 and BNT162b2 prime-boost vaccination elicits potent neutralizing antibody responses and T cell reactivity]

14 juillet
[Séquençage du génome entier du SARS-CoV-2 en Ontario, 14 juillet 2021]

-Du 30 mai au 26 juin 2021, 4 771 cas ont été séquencés par le Réseau génomique COVID-19 de l'Ontario aux fins de surveillance représentative. La majorité était de la lignée Pango B.1.1.7 (Alpha; 50,6 %) et les autres étaient des lignées B.1.617.2 (Delta; 41,0 %) et B.1.1.318 (3,2 %).

-La proportion d'échantillons de la lignée B.1.617.2 (Delta) a augmenté de 46,6 % (du 13 au 19 juin) à 69 % (du 20 au 26 juin), devenant ainsi la lignée la plus répandue en Ontario.

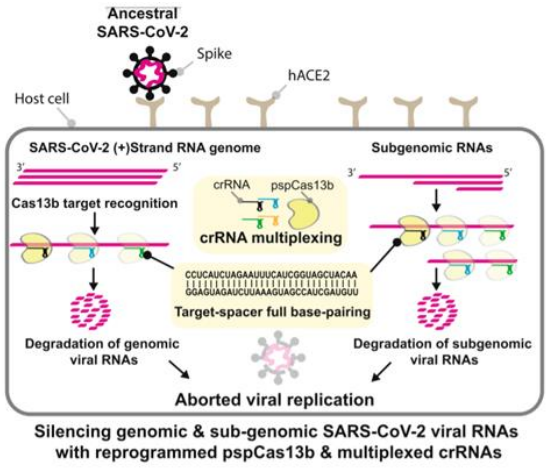


13 juillet

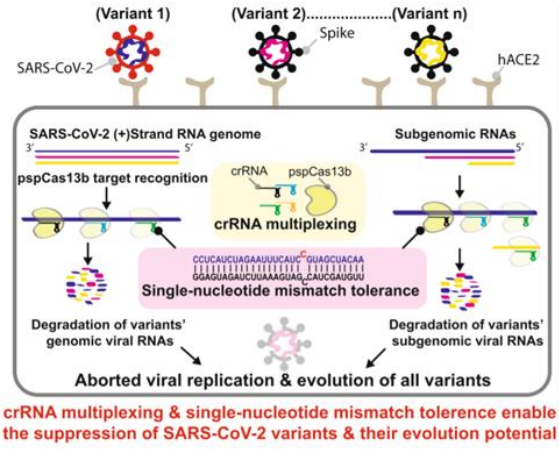
[Reprogrammed CRISPR-Cas13b suppresses SARS-CoV-2 replication and circumvents its mutational escape through mismatch tolerance]

Reprogrammed Cas13b effectors targeting accessible regions of Spike and Nucleocapsid transcripts achieved >98% silencing efficiency in virus-free models. Further, optimized and multiplexed Cas13b CRISPR RNAs (crRNAs) suppress viral replication in mammalian cells infected with replication-competent SARS-CoV-2, including the recently emerging dominant variant of concern B.1.1.7.

The comprehensive mutagenesis of guide-target interaction demonstrated that single-nucleotide mismatches does not impair the capacity of a potent single crRNA to simultaneously suppress ancestral and mutated SARS-CoV-2 strains in infected mammalian cells, including the Spike D614G mutant. The specificity, efficiency and rapid deployment properties of reprogrammed Cas13b described here provide a molecular blueprint for antiviral drug development to suppress and prevent a wide range of SARS-CoV-2 mutants, and is readily adaptable to other emerging pathogenic viruses.

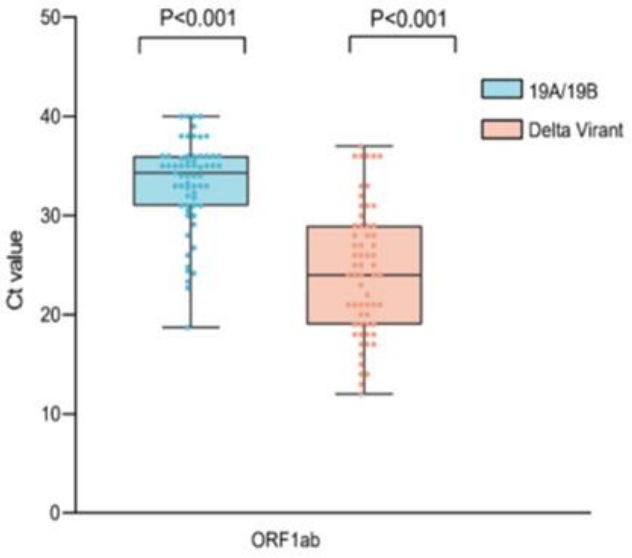


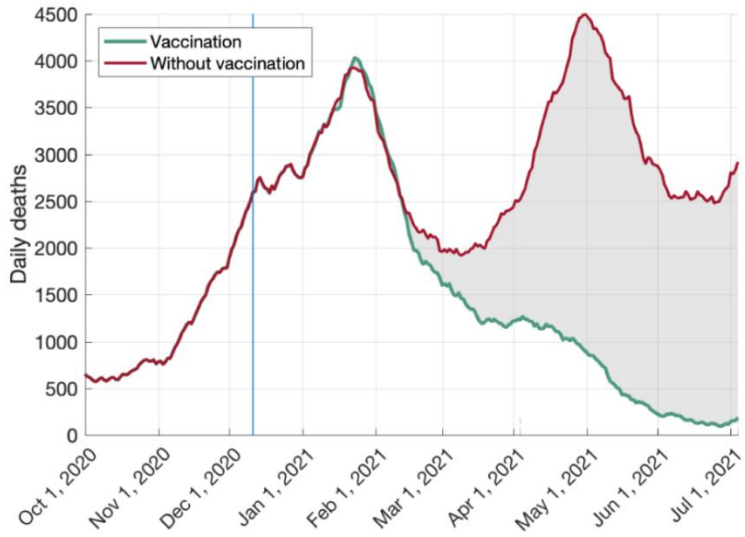
Silencing genomic & sub-genomic SARS-CoV-2 viral RNAs with reprogrammed pspCas13b & multiplexed crRNAs



crRNA multiplexing & single-nucleotide mismatch tolerance enable the suppression of SARS-CoV-2 variants & their evolution potential

A key step in enabling clinical translation of this proof-of-concept approach will be to develop a safe and effective delivery strategy such as lipid nanoparticle formulations for systemic, and possibly, mucosal delivery for testing in animal models.

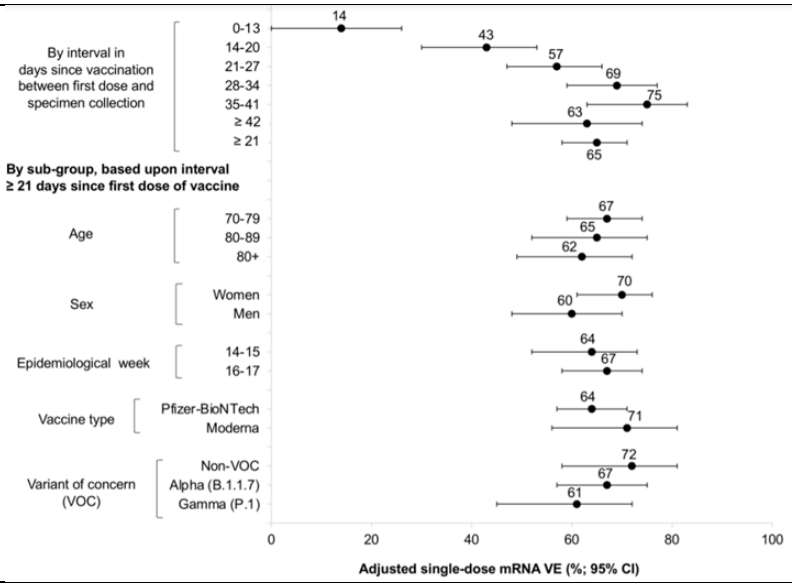
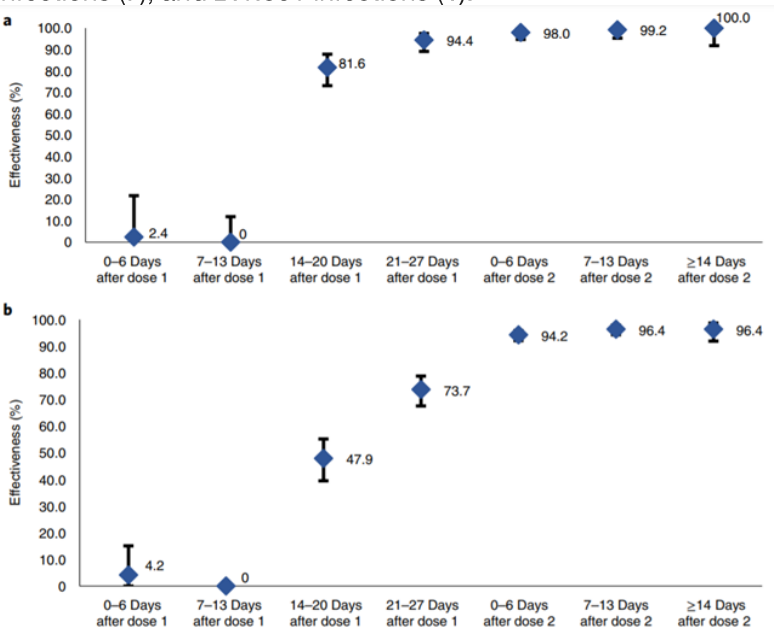
12 juillet Viral infection and transmission in a large well-traced outbreak caused by the Delta SARS-CoV-2 variant	In this study, we characterize a large transmission chain originated from the first local infection of the SARS-CoV-2 Delta variant in mainland China. Compared to the 19A/19 B strains, the relative viral loads in the Delta variant infections (62 cases, Ct value 24.00 (IQR 19.00~29.00) for ORF1ab gene) were 1260 times higher than the 19A/19B strains infections (63 cases, Ct value 34.31 (IQR 31.00~36.00) for ORF1ab gene) on the day when viruses were first detected. 
8 juillet COVID-19 Outbreak Associated with a SARS-CoV-2 P.1 Lineage in a Long-Term Care Home after Implementation of a Vaccination Program – Ontario, April-May 2021	Outbreak investigation among staff and residents at long-term care facility in late April 2021. As of March 2021, 54% (120/224) of staff and 81% (100/121) residents were fully vaccinated with BNT162b2 (Pfizer/BioNTech). Positive SARS-CoV-2 cases were confirmed by RT-PCR, and genomic sequencing was performed. *Limitations*: Small sample sizes resulting in estimates with wide confidence intervals; because not all facility residents were included, vaccine effectiveness rates may be underestimated. Among fully vaccinated residents and staff, 39% (19/48) of residents and 9.3% (4/43) of staff tested positive for SARS-CoV-2 P.1 (Gamma). ○ Severe illness (hypoxemia, hospitalization, or death) was reported among residents only (12.5%). Estimated vaccine effectiveness (VE) was 52.5% (95% CI 26.9%-69.1%) among residents, and 66.2% (95% CI 2.3%-88.3%) among staff. ○ VE against severe illness among residents was 78.6% (95% CI 47.9%-91.2%).

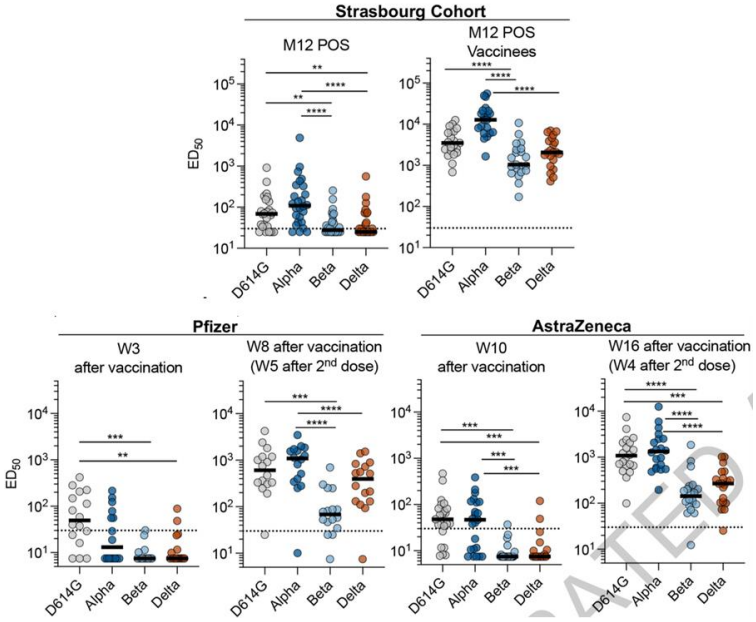
	<table><tr><th rowspan="2">Roles (residents/staff) and outcome</th><th colspan="2">Number (attack rate as %) by vaccine status</th><th rowspan="2">Total‡ (vaccinated & unvaccinated)</th><th rowspan="2">Vaccine effectiveness§ (95% CI)</th></tr><tr><th>Fully vaccinated*</th><th>Unvaccinated†</th></tr><tr><td>Residents</td><td>(n = 48)</td><td>(n = 12)</td><td>60</td><td>-</td></tr><tr><td>SARS-CoV-2 infection</td><td>19 (39.6)</td><td>10 (83.3)</td><td>29</td><td>52.5 (26.9-69.1)</td></tr><tr><td>Symptomatic</td><td>11 (22.9)</td><td>8 (66.7)</td><td>19</td><td>65.6 (33.8-82.1)</td></tr><tr><td>Severe illness¶</td><td>6 (12.5)</td><td>7 (58.3)</td><td>13</td><td>78.6 (47.9-91.2)</td></tr><tr><td>Staff</td><td>(n = 43)</td><td>(n = 40)</td><td>83</td><td>-</td></tr><tr><td>SARS-CoV-2 infection</td><td>4 (9.3)</td><td>11 (27.5)</td><td>15</td><td>66.2 (2.3-88.3)</td></tr><tr><td>Symptomatic</td><td>4 (9.3)</td><td>5 (12.5)</td><td>9</td><td>25.6 (-157.8-78.5)</td></tr><tr><td>Severe illness¶</td><td>0</td><td>0</td><td>0</td><td>-</td></tr></table>
7 juillet Deaths and Hospitalizations Averted by Rapid U.S. Vaccination Rollout	A model, accounting for Alpha, Gamma, and Delta variants, compared the observed epidemiologic trajectory in the U.S. to 2 counterfactual scenarios (For details, see How We Conducted This Study). At a daily vaccination rate 50% of actual, by June 2021 there would have been 121,000 additional deaths and >450,000 hospitalizations. Had there not been a vaccine program, an additional 279,000 deaths and 1.25 million hospitalizations were predicted. 

12 juillet 2021

Publications sélectionnées

Titre	Extrait pertinent
10 juillet Troisième dose ? Des experts ont des réserves En complément (8 juillet): Pfizer/BioNTech va demander l'autorisation pour une 3e dose de vaccin	« Je suis convaincue que cette troisième dose augmente les niveaux d'anticorps présents. Toutefois, il reste à savoir si ce "boost'' est nécessaire et, si oui, quand. Cette troisième dose pourrait être d'intérêt, en particulier pour les gens avec un système immunitaire plus faible, très vieux ou immunocompromis, et ces études sont en cours. » ***-Dre Caroline Quach-Thanh*** « La décision n'est pas mûre dans le sens où on n'a pas d'études cliniques qu'on peut scruter à la loupe pour voir si c'est vraiment nécessaire. On peut avoir une très bonne protection contre le virus même si les anticorps descendent tranquillement. Si on ne contrôle pas la pandémie un peu partout sur la planète, on risque de voir émerger un variant qui va échapper à l'immunité vaccinale et aux anticorps qu'on a faits en faisant la COVID. » ***-Dre Marie-France Raynault*** « le CIQ aura des discussions sur une troisième dose lorsqu'il y aura des données qui montrent une perte d'efficacité vaccinale avec le temps ou dans certains groupes de population ou contre certains variants et que l'ajout d'une troisième dose apporterait un bénéfice ». ***-Dr Gaston De Serres***
9 juillet Single-dose mRNA vaccine effectiveness against SARS-CoV-2, including Alpha and Gamma variants: a test-negative design in adults 70 years and older in British Columbia, Canada	Analyses included community-dwelling adults ≥70-years-old with specimen collection between April 4 (epidemiological week 14) and May 1 (week 17) 2021. Adjusted VE was estimated by test-negative design. Cases were RT-PCR test-positive for SARS-CoV-2 and controls were test-negative. Vaccine status was defined by receipt of a single dose ≥21 days before specimen collection, but a range of intervals was assessed. Variant-specific VE was estimated against viruses genetically characterized as Alpha, Gamma or non-VOC lineages. VE was negligible at 14% (95% CI 0-26) during the period 0-13 days post-vaccination but increased by one week interval thereafter from 43% (95% CI 30-53) at 14-20 days to 75% (95% CI 63-83) at 35-41 days post-vaccination. Summary VE at ≥21 days was 65% (95% CI 58-71) and was similar (within 10% absolute) in participant sub-group analyses, differing by 10% in women (70%; 95% CI 61-76) vs. men (60%; 95% CI 48-70). At ≥21 days since vaccination, a single dose of mRNA vaccine was also significantly protective in variant-pecific analyses, with VE of 72% (95% CI 58-81), 67% (95% CI 57-75) and 61% (95% CI 45-72) for non-VOC, Alpha and Gamma variants, respectively.

	
9 juillet [mRNA-1273 COVID-19 vaccine effectiveness against the B.1.1.7 and B.1.351 variants and severe COVID-19 disease in Qatar]	Figure : Effectiveness of the mRNA-1273 vaccine against B.1.1.7 infections (**a**), and B.1.351 infections (**b**).  -Our analysis demonstrates that the effectiveness of the mRNA1273 vaccine is high, regardless of variant, against both symptomatic and asymptomatic infection, and against COVID-19 hospitalization and death. -Development of vaccine protection against B.1.1.7 infections and COVID-19 hospitalization and death rapidly accelerated in the third and fourth weeks after the first dose, immediately before the second dose, nearly reaching the values attained after the second dose. -Protection against B.1.351 infection exhibited a similar pattern, but mounted at a slower rate and did not achieve its highest value of ~95% until after the second dose.

	-While long-term protection of only one dose could not be assessed beyond 4weeks after the first dose, these findings might suggest that most of the protection from this vaccine is attained using only one dose, apart possibly from its protection against B.1.351.
8 juillet Reduced sensitivity of SARS-CoV-2 variant Delta to antibody neutralization	Sera from convalescents up to 12 months post symptoms (n = 26) were 4-fold less potent against B.1.617.2 compared to B.1.1.7 (Alpha). Sera from recipients of 1 dose of Pfizer or AstraZeneca vaccines barely inhibited B.1.617.2; 2 doses led to a neutralization response in 95% of samples but titers were 3- to 5-fold lower than against B.1.1.7. 

8 juillet

[Public Health England - 8 July 2021 Risk assessment for SARS-CoV-2 variant: LAMBDA (VUI-21JUN-01, C.37)]

8 July 2021 Risk assessment for SARS-CoV-2 variant: LAMBDA (VUI-21JUN-01, C.37) Public Health England

Indicator	RAG*	Confidence	Assessment and rationale
Transmissibility between humans			**Insufficient information** Lambda (C.37) appears to have transmitted successfully in South America with some wider spread. There is a single study with some evidence of enhanced ACE2 binding. There is insufficient genomic structured genomic surveillance to understand the contribution of Lambda (C.37) to the high levels of transmission that have been seen in some South American countries.
Infection severity			**Insufficient information**
Immunity after natural infection		LOW	**Experimental evidence of evasion of naturally acquired immunity** There is only one small study available, which finds find a reduction in neutralisation with convalescent sera when compared to virus from earlier in the pandemic. The magnitude of the reduction in this single study is moderate (less than B.1.351) but further assessments are required. There are no clinical or epidemiological data on reinfections.
Vaccines		LOW	**Very limited experimental evidence of evasion of vaccine derived immunity** There are only 2 pseudovirus studies available (US, Chile). Both find neutralisation by vaccinee sera to be reduced for Lambda compared to viruses from earlier in the pandemic. These are small studies and it is difficult to make any clinical extrapolation from this early data.
Overall assessment			Lambda has spread successfully in South America with evidence of some wider global transmission. There is no evidence as yet of a country where it is outcompeting Delta, though careful monitoring of the epidemiology in Chile and Peru is required. There are a small number of cases in the UK which are largely travel associated. Lambda contains a novel combination of mutations and very limited laboratory data are available. The priority studies are pseudovirus and live virus neutralisation with UK vaccinee sera, assessment of growth using *in vitro* systems and genomic surveillance of those countries where both Lambda (C.37) and Delta are present.

The therapeutics risk assessment is under review for all variants and is not included.
*refer to scale and confidence grading slide

[Public Health England - 8 July 2021 Risk assessment for SARS-CoV-2 variant: Delta (VOC-21APR-02, B.1.617.2)]

8 July 2021 Risk assessment for SARS-CoV-2 variant: Delta (VOC-21APR-02, B.1.617.2) Public Health England

Indicator	RAG*	Confidence	Assessment and rationale
Transmissibility between humans		HIGH	**Transmissibility appears greater than wild type (first wave) virus.** All analyses support increased transmissibility for Delta compared to both wild type virus and Alpha. There is in vitro evidence suggestive of increased replication in biological systems that model human airway, and evidence of optimised furin cleavage. There is epidemiological evidence from secondary attack rates, household transmission studies, and growth rate modelling. The finding of lower CT values in routine testing data, compared to Alpha, may be relevant to the mechanism of increased transmissibility, however there may be multiple contributors.
Infection severity		LOW	**Increased severity (hospitalisation risk) when compared to Alpha.** Iterated analysis continues to suggest an increased risk of hospitalisation compared to contemporaneous Alpha cases. Analyses using 2 different sources of hospital data (SARIwatch sentinel surveillance and routine hospital episode data) do not yet find any evidence of increased severity once in hospital, in hospital inpatients since Delta became predominant. There is a high level of uncertainty in the estimates for the past 2 months due to data lag and these will be iterated. Data from COCIN (hospitalised patients) are broadly consistent with this, but additional analyses are being undertaken to adjust for age and vaccination status.
Immunity after natural infection		LOW	**Experimental evidence of functional evasion of natural immunity but insufficient epidemiological data** Pseudovirus and live virus neutralisation using convalescent sera from first wave and Alpha infections shows a reduction in neutralisation. National surveillance analyses are underway but there is currently insufficient evidence to assess whether the risk of reinfection differs between Delta and Alpha.
Vaccines		HIGH	**Epidemiological and laboratory evidence of reduced vaccine effectiveness** There are now analyses from England and Scotland supporting a reduction in vaccine effectiveness for Delta compared to Alpha against symptomatic infection. This is more pronounced after one dose. Iterated analysis continues to show vaccine effectiveness against Delta is high after 2 doses. Current evidence suggests that VE against hospitalisation is maintained. Although this is observational data subject to some biases, it holds true across several analytic approaches and the same effect is seen in both English and Scottish data. It is strongly supported by pseudovirus and live virus neutralisation data from multiple laboratories. There are no data on whether vaccine effectiveness to prevent transmission is affected.
Overall assessment			Delta is predominant in the UK and there is very rapid global spread. All analyses continue to support increased transmissibility and reduced vaccine effectiveness against symptomatic infection. Whilst risk of hospitalisation appears increased, early data on hospitalised patients does not show indicators of increased severity once in hospital and further analyses are required to resolve this. The priority investigations are to improve understanding of asymptomatic transmission in the vaccinated, to monitor for new mutations occurring on Delta, and continued investigation of the viral kinetics and clinical course of disease.

The therapeutics risk assessment is under review for all variants and is not included.
*refer to scale and confidence grading slide

<table>
<tr>
<td>7 juillet
Progressive Increase in Virulence of Novel SARS-CoV-2 Variants in Ontario, Canada, from December to July, 2021</td>
<td>We sought to use Ontario's COVID-19 case data to evaluate the virulence of N501Y-positive variants relative to earlier SARS-CoV-2 strains, and also to evaluate the virulence of the delta variant of SARS-CoV-2 relative to N501Y-positive variants of concern.

After adjustment for age, sex, comorbidities, and temporal trend, large and significant increases in the risk of hospitalization, ICU admission, and death were seen with both N501Y-positive VOC, and probable delta variant infections, relative to non-VOC.

Increases were larger with delta variant infection than with N501Y-positive VOC, with a relative increase in risk of hospitalization, ICU admission and death of 54%, 91% and 65%, respectively (Table 3).

<table>
<tr><th rowspan="2">Outcome</th><th colspan="3">Effect of Delta vs. N501Y+ VOC</th></tr>
<tr><th>OR</th><th>LCL</th><th>UCL</th></tr>
<tr><td>Hospitalization</td><td>1.54</td><td>1.46</td><td>1.63</td></tr>
<tr><td>ICU Admission</td><td>1.91</td><td>1.70</td><td>2.15</td></tr>
<tr><td>Death</td><td>1.65</td><td>1.44</td><td>1.89</td></tr>
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<tr>
<td>2 juillet
Temporal maturation of neutralizing antibodies in COVID-19 convalescent individuals improves potency and breadth to circulating SARS-CoV-2 variants</td>
<td>We monitored the neutralizing activity and NPI of convalescent individuals longitudinally up to 10 months after symptom onset. Furthermore, an additional qualitative parameter, neutralization breadth index (NBI), which represents the relative neutralizing activities to parental strain versus those to VOC strain, was also quantitated. This parameter allowed us to visualize changes in neutralization breath independent of the magnitudes of neutralizing antibody titers to the parental virus strain.

Despite the quantitative decay of antibody titers Alpha and Gamma and total neutralizing activities, we demonstrated a time dependent increase in NPI and NBI during the late convalescent phase beyond 3 months after symptom onset. The progressive increase in these qualitative parameters against circulating SARS-CoV-2 variants was highly correlated with the affinity maturation of IgG antibodies against RBD conserved sites that were durably maintained.

Thus, maturation of the antibody response to SARS-CoV-2 potentiates cross-neutralizing ability to circulating variants, suggesting that declining antibody titers may not be indicative of declining protection.</td>
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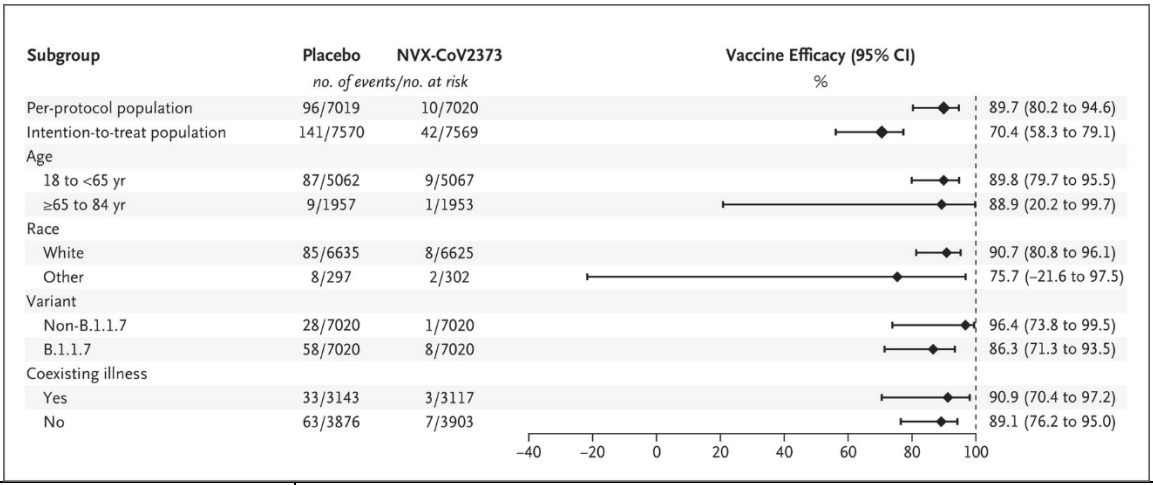
30 juin
Safety and Efficacy of NVX-CoV2373 Covid-19 Vaccine

-Two-dose regimen of NVX-CoV2373 (Novavax) provided 89.7% protection overall, with high efficacy demonstrated against the B.1.1.7 variant in a UK-based 33 site trial with 14,039 participants conducted between September 28 and November 28, 2020.



Subgroup	Placebo	NVX-CoV2373	Vaccine Efficacy (95% CI)
	no. of events/no. at risk		%
Per-protocol population	96/7019	10/7020	89.7 (80.2 to 94.6)
Intention-to-treat population	141/7570	42/7569	70.4 (58.3 to 79.1)
Age			
18 to <65 yr	87/5062	9/5067	89.8 (79.7 to 95.5)
≥65 to 84 yr	9/1957	1/1953	88.9 (20.2 to 99.7)
Race			
White	85/6635	8/6625	90.7 (80.8 to 96.1)
Other	8/297	2/302	75.7 (−21.6 to 97.5)
Variant			
Non-B.1.1.7	28/7020	1/7020	96.4 (73.8 to 99.5)
B.1.1.7	58/7020	8/7020	86.3 (71.3 to 93.5)
Coexisting illness			
Yes	33/3143	3/3117	90.9 (70.4 to 97.2)
No	63/3876	7/3903	89.1 (76.2 to 95.0)

28 juin
SARS-CoV-2 mRNA vaccines induce persistent human germinal centre responses

Antigen-specific B cell responses in blood (n = 41) and draining lymph nodes (n = 14) were examined after 2 doses of BNT162b2. PBs binding to SARS-CoV-2 protein was measured by enzyme-linked immune absorbent spot (ELISpot). Limitations: Small sample size, especially for subset analysis.

- BNT162b2 (Pfizer/BioNTech) vaccination induced strong IgG-dominated plasmablast (PB) responses, peaking 1 week post 2nd dose.
- Robust S-binding germinal center (GC) B-cell responses were detected for up to 12 weeks in lymph node aspirates in a subset of 14 participants.
- PB responses preceded high levels of anti-S binding and neutralizing antibodies (NAbs) to several emerging variants, especially in 8 participants infected prior to vaccination.

BNT162b2 vaccination elicits prolonged GC responses for antibody-mediated immunity in humans. Durable memory B cell immunity may indicate longer lasting humoral immunity than NAb levels alone may suggest.

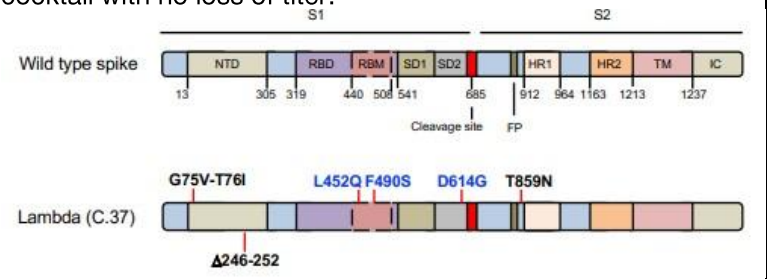
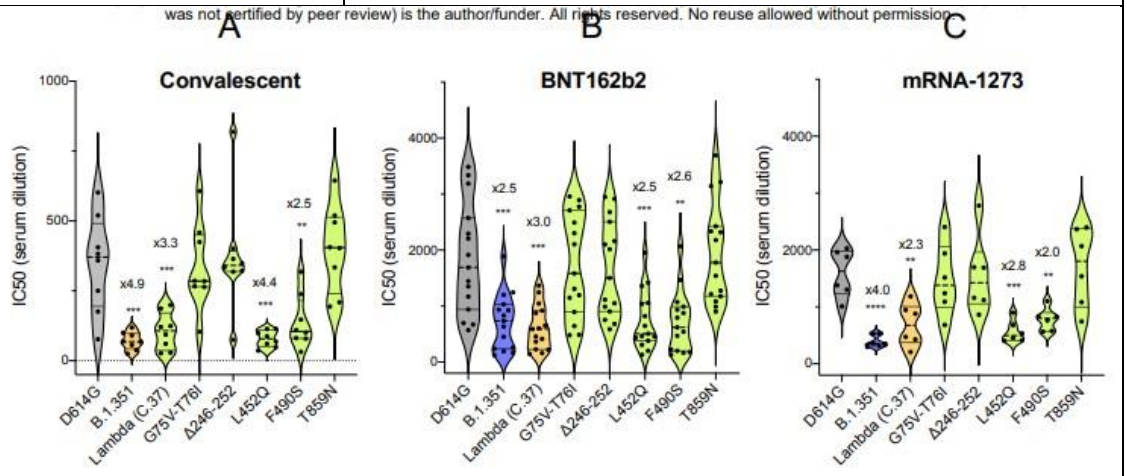
5 juillet 2021

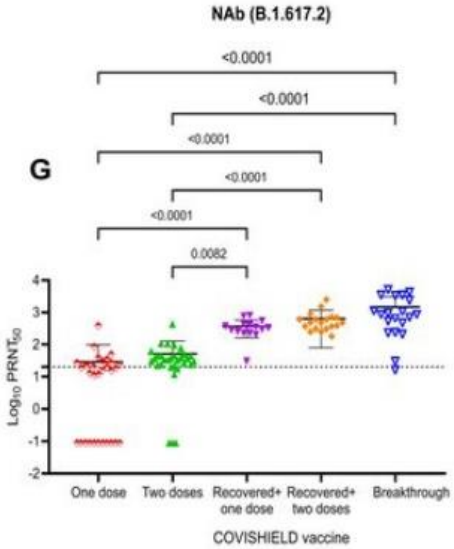
Publications sélectionnées

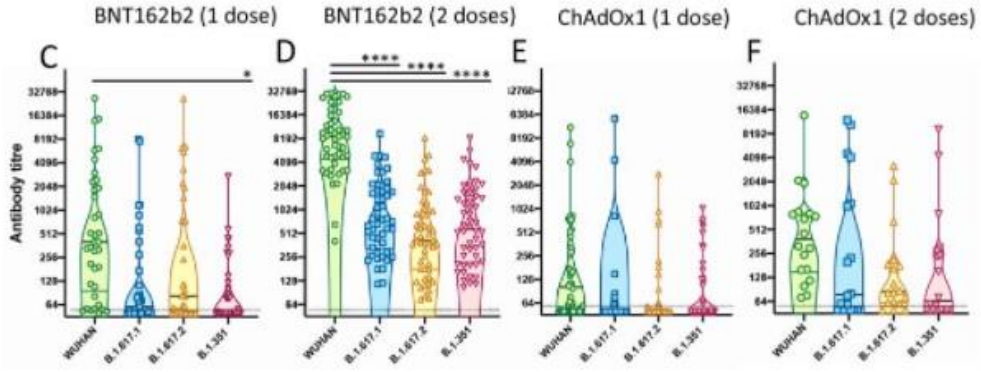
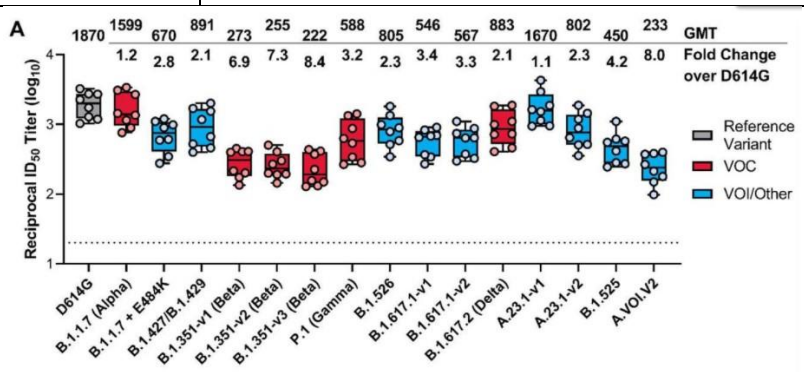
Titre	Extrait pertinent
5 juillet Le journal de Montréal - Vaccins: en Israël, crainte d'une efficacité moindre face au variant Delta	Le rebond des contaminations à la COVID-19 en Israël (>100 cas/jour), où plus de la moitié (55%) de la population est entièrement vaccinée avec le vaccin de Pfizer-BioNTech, constitue un «signe préliminaire» d'une efficacité vaccinale potentiellement moindre sur les «cas modérés» du variant Delta, a estimé lundi un expert. (…) Selon des chiffres officiels, environ la moitié des nouveaux cas sont recensés parmi des enfants et l'autre moitié chez des adultes pour la plupart (85%) vaccinés. Ce rebond est clairement imputé au très contagieux variant Delta, devenu «la souche principale» du virus en Israël (90% des nouveaux cas)
3 juillet Medrxiv - Effectiveness of COVID-19 vaccines against variants of concern, Canada	We conducted a test-negative design study using linked population-wide vaccination, laboratory testing, and health administrative databases in Ontario, Canada. Over the study period (14 December 2020 and 30 May 2021), we identified 421,073 symptomatic community-dwelling individuals who were tested for SARS-CoV-2, with 28,705 (6.8%) positive for non-VOC SARS-CoV-2 and 40,828 (9.7%) positive for a VOC (Table 1). We identified 14,168 individuals with a COVID-19 hospitalization or death (Table 2). A single dose of BNT162b2, mRNA-1273 or ChAdOx1 provide good to excellent protection against symptomatic infection and severe outcomes caused by the 4 currently circulating variants of concern.

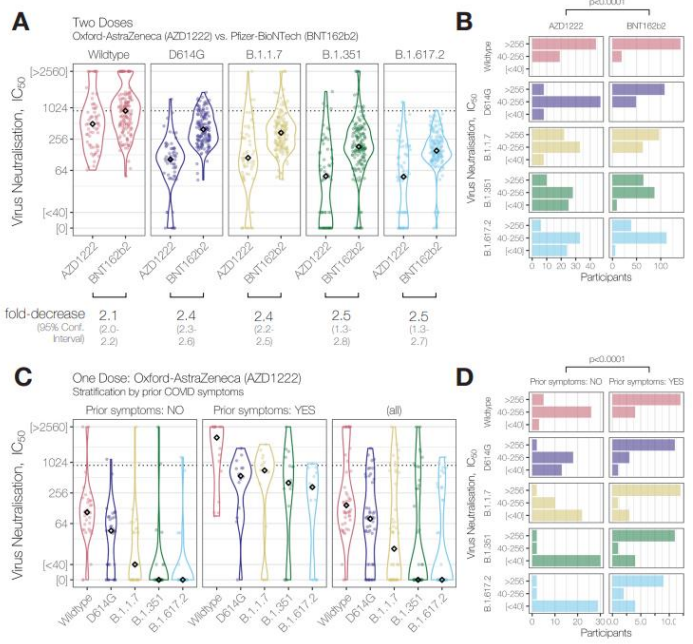
Table 3. Vaccine effectiveness against Alpha (B.1.1.7), Beta (B.1.351)/Gamma (P.1), and Delta (B.1.617.2) variants of concern by outcome, vaccine product, and number of doses received for those tested for SARS-CoV-2 between 14 December 2020 and 30 May 2021 in Ontario, Canada.

Outcome	Adjusted VE* (95% CI)			
	Non-VOC	Alpha	Beta/Gamma†	Delta‡
Symptomatic infection				
BNT162b2 (Pfizer-BioNTech)				
≥14 days after dose 1 only§	61 (54, 68)	66 (64, 68)	60 (52, 67)	56 (45, 64)
≥7 days after dose 2	93 (88, 96)	89 (86, 91)	84 (69, 92)	87 (64, 95)
mRNA-1273 (Moderna)				
≥14 days after dose 1 only§	54 (28, 70)	83 (80, 86)	77 (63, 86)	72 (57, 82)
≥7 days after dose 2	89 (65, 96)	92 (86, 96)	-¶	-¶
ChAdOx1 (AstraZeneca)				
≥14 days after dose 1 only§	67 (38, 82)	64 (60, 68)	48 (28, 63)	67 (44, 80)
≥7 days after dose 2	-**	-**	-¶	-¶
Hospitalization or death				
BNT162b2 (Pfizer-BioNTech)				
≥14 days after dose 1 only§	68 (54, 78)	80 (78, 82)	77 (69, 83)	78 (65, 86)
≥7 days after dose 2	96 (82, 99)	95 (92, 97)	95 (81, 99)	-¶
mRNA-1273 (Moderna)				
≥14 days after dose 1 only§	57 (28, 75)	79 (74, 83)	89 (73, 95)	96 (72, 99)
≥7 days after dose 2	96 (70, 99)	94 (89, 97)	-¶	-¶
ChAdOx1 (AstraZeneca)				
≥14 days after dose 1 only§	-¶	85 (81, 88)	83 (66, 92)	88 (60, 96)
≥7 days after dose 2	-¶	-**	-¶	-¶

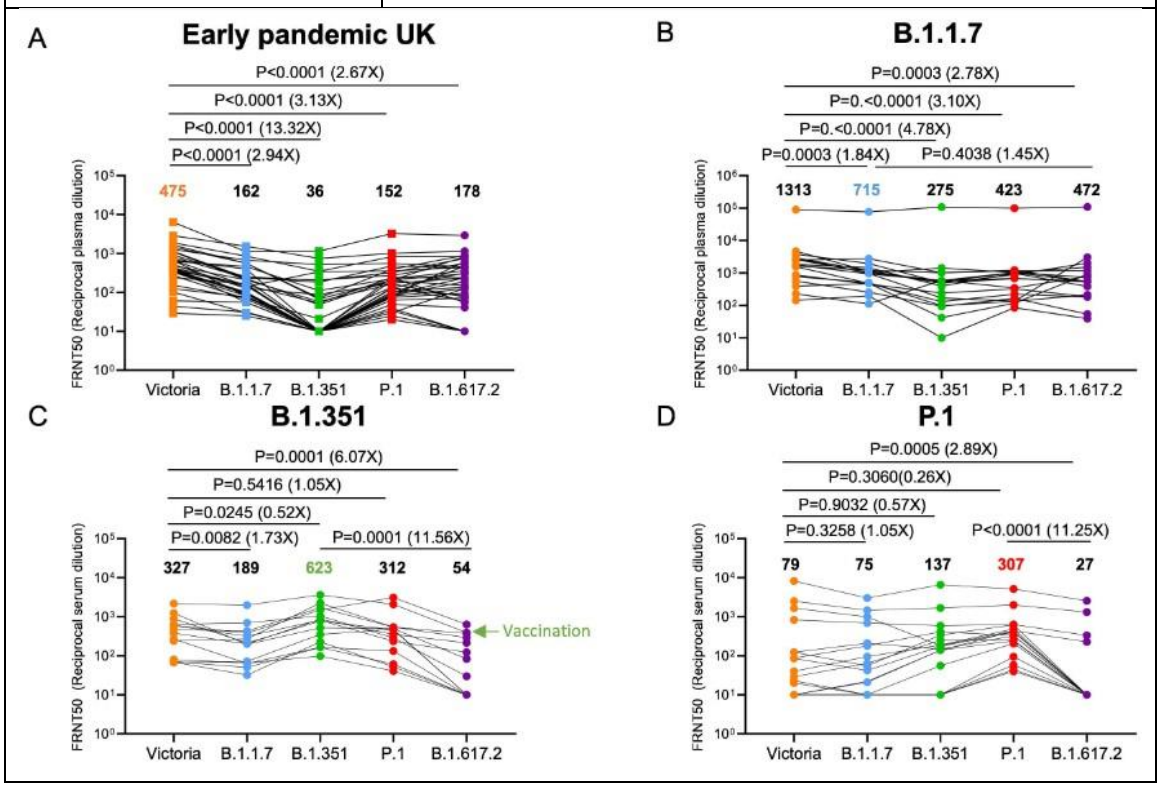
3 juillet Biorxiv - SARS-CoV-2 Lambda Variant Remains Susceptible to Neutralization by mRNA Vaccine-elicited Antibodies and Convalescent Serum **En complement (1 juillet):** Medrxiv - Infectivity and immune escape of the new SARS-CoV-2 variant of interest Lambda	Virus with the lambda spike (lineage C.37; L452**Q** and F490S mutation in the receptor binding domain) had higher infectivity (by 2-fold on ACE2.293T cells; and 3-fold increase sACE2 binding due to the L452Q mutation) and was neutralized by convalescent sera (n=8) and vaccine-elicited antibodies (n=21) with a relatively minor 2.3-3.3-fold decrease in titer on average (compared to the parental D614G spike). The virus was neutralized by the Regeneron therapeutic monoclonal antibody cocktail with no loss of titer. 
  	
3 juillet Medrxiv - Clinicogenomic analysis of breakthrough infections by SARS CoV2 variants after ChAdOx1 nCoV- 19 vaccination in healthcare workers	A total of 1858 HCWs were enrolled in the study (India). The HCWs were divided in two groups vaccinated - **AstraZeneca** - (88.2%, 1639/1858) and non-vaccinated (11.7%, 210/1858). (Table1) The vaccinated group was further subdivided as partially vaccinated (17.8%, 293/1639) and fully vaccinated (82.12%, 1346/1639). Overall SARS CoV2 infections was seen in 219 (11.79%) HCWs during the study period (January to May 2021). The non-vaccinated subjects were at a significantly higher risk of developing infection as compared to partial (RR 1.57, (95% CI 1.07-2.31) p=0.02) and fully vaccinated subjects (RR 2.49 (95%CI 1.83-3.39) p=< 0.001). Partially vaccinated subjects were at a higher risk of developing infection compared to fully vaccinated group (RR 1.58 (95% CI, 1.13- 2.22) p=0.01). None of the vaccinated subjects had severe infection requiring ICU admission and no death was reported.

2 juillet Biorxiv - Neutralization of Delta variant with sera of Covishield vaccinees and COVID-19 recovered vaccinated individu	A comparative assessment of Covishield™ (**AstraZeneca**) vaccinated individuals' (India, n=116) sera in different categories was performed against prototype strain B.1 (D614G) and Delta variant. The findings of the study demonstrated that the breakthrough cases and the COVID-19 recovered individuals with one or two dose of vaccine had relatively higher protection (Nab titers) against Delta variant in comparison to the participants who were administered either one or two doses of Covishield™. 
30 juin The New York Time - As Delta Variant Surges, Outbreaks Return in Many Parts of the World	From **Africa to Asia**, countries are suffering from record Covid-19 caseloads and deaths, even as wealthier nations with high vaccination rates have let their guard down, dispensing with mask mandates and reveling in life edging back toward normalcy. In **Indonesia**, grave diggers are working into the night, as oxygen and vaccines are in short supply. In Europe, countries are slamming their doors shut once again, with quarantines and travel bans. In **Bangladesh**, urban garment workers fleeing an impending lockdown are almost assuredly seeding another coronavirus surge in their impoverished home villages. And in countries like **South Korea and Israel** that seemed to have largely vanquished the virus, new clusters of disease have proliferated. **Chinese** health officials announced on Monday that they would build a giant quarantine center with up to 5,000 rooms to hold international travelers. **Australia** has ordered millions to stay at home.
29 juin CTV News - Where is the Delta variant most prevalent in Canada?	As of Tuesday afternoon, there have been more than 4,100 cumulative cases of the Delta variant in Canada, with Ontario accounting for 42 per cent of the cases in the country and British Columbia accounting for 31 per cent. **En complément** : Au cours des prochaines semaines, l'ASPC présentera un nouveau graphique qui comprendra tous les variants préoccupants et les variants d'intérêt.

28 juin Medrxiv - Reduced neutralisation of the Delta (B.1.617.2) SARS-CoV-2 variant of concern following vaccination	Sera were collected from 156 healthy individuals (United Kingdom) who had received one dose (n = 37) or two doses (n = 50) of BNT162b2 (**Pfizer-BioNTech**), or one dose (n= 50) or two doses (n = 18) of ChAdOx1 (**Oxford/AstraZeneca**) vaccines. Neutralising antibody titres elicited by vaccination with two doses of BNT162b2 were significantly higher than those elicited by vaccination with two doses of ChAdOx1. Fold decreases in the magnitude of neutralisation titre following two doses of BNT162b2, conferred reductions in titre of 7.77, 11.30 and 9.56-fold respectively to B.1.617.1, B.1.617.2 and B.1.351 pseudoviruses, the reduction in neutralisation of the delta variant B.1.617.2 surpassing that of B.1.351. Fold changes in those vaccinated with two doses of ChAdOx1 were 0.69, 4.01 and 1.48 respectively.
	
28 juin Biorxiv - Serum Neutralizing Activity of mRNA-1273 against SARS-CoV-2 Variants	Sera from the phase 1 mRNA-1273 (**Moderna**) clinical trial (8 participants, 1 week following Dose 2) were evaluated against each variant. Results showed minimal effects on neutralization titers against the B.1.1.7 (Alpha) variant (1.2-fold reduction compared with D614G); other VOCs such as B.1.351 (Beta, including B.1.351-v1, B.1.351-v2, and B.1.351-v3), B.1.617.2 (Delta), and P.1 (Gamma) showed decreased neutralization titers ranging from 2.1-fold to 8.4-fold reductions compared with D614G, although all remained susceptible to mRNA-1273–elicited serum neutralization.
	

28 juin The Lancet - AZD1222-induced neutralising antibody activity against SARS-CoV-2 Delta VOC	We carried out a second initial analysis of Legacy study participants vaccinated with AZD1222 (**AstraZeneca**, n=106 participants). Legacy was initiated in early 2021 by University College London Hospitals and the Francis Crick Institute in London, UK, to track serological responses to vaccination during the national COVID-19 vaccination programme in prospectively recruited healthy staff volunteers. Two doses of AZD1222 generated NAb activity against the Wildtype strain bearing a spike identical to that encoded by the vaccine in all participants (median NAbT IC_{50}=419), with a 2·1–fold (95% CI 2·0–2·2) reduction in median NAbT relative to two doses of BNT162b2 (appendix p 2). Moreover, median NAbTs against all SARS-CoV-2 variants were further reduced relative to BNT162b2. Whereas nearly all participants had a quantifiable NAbT against the D614G and B.1.1.7 variants (55 [87%] of 63 [95% CI 76–94%]), significantly fewer participants had quantifiable NAbTs against B.1.351 and B.1.617.2 VOCs after two doses of AZD1222 (38 [60%] of 63 [95% CI 47–72%] against B.1.351; and 39 [62%] of 63 [49–74%] against B.1.617.2), relative to the former two variants (χ^2 test p<0·0011). This contrasts strongly with our previous results, which showed that more than 95% of participants had quantifiable NAbTs against B.1.351 and B.1.617.2 after two doses of BNT162b2 (189 [97%] of 195 against B.1.351; and 186 [95%] of 195 against B.1.617.2). After a single AZD1222 dose, participants with prior COVID-19 symptoms (16 [32%] of 50) had significantly higher NAbTs against all strains than those without prior COVID symptoms ($5{\cdot}1 \times 10^{-5}$ ≤$3{\cdot}1 \times 10^{-4}$).
	

17 juin Cell - Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum	To get an idea of how people previously infected with B.1.1.7, B.1.351 and P.1 were protected from B.1.617.2, we compared the neutralization titres to B.1.617.2 to the neutralization of the homologous infecting lineage. For B.1.1.7 serum neutralization of B.1.617.2 was 1.5-fold reduced (p=0.4038) compared to B.1.1.7, for B.1.351 serum neutralization was 11.6-fold reduced (p=0.0001) compared to B.1.351 and for P.1 was 11.3- fold reduced (p<0.0001) compared to P.1 (Figure 6B-D). Serum from donors infected with B.1.1.7 appears to give good protection against all variants of concern whereas, protection from B.1.617.2 afforded by previous infection with B.1.351 and P.1 is much more compromised. Inspection of the neutralization curves using B.1.351 and P.1 serum (Figure 6E,F) show that in many cases neutralization is almost completely lost to B.1.617.2, most profoundly for P.1, suggesting that individuals infected with B.1.351 and P.1 may be at risk of reinfection with B.1.617.2.



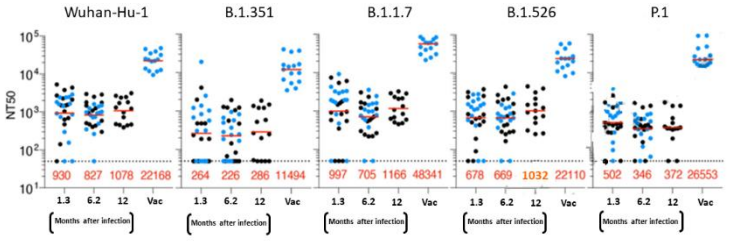
28 juin 2021

Publications sélectionnées

Titre	Extrait pertinent
28 juin Covid-19 : AstraZeneca-Oxford testent un vaccin contre le variant Beta	L'université d'Oxford a annoncé dimanche 27 juin avoir commencé à injecter à des volontaires un vaccin mis au point avec AstraZeneca contre le variant beta ("sud-africain") du coronavirus, dans le cadre d'essais cliniques destinés à mesurer son efficacité. Le candidat vaccin utilise la même technologie dite "à vecteur viral" (adénovirus) que celui actuellement déployé contre le Covid-19 dans le monde. Des données provisoires de ces essais cliniques sont attendues plus tard cette année et elles seront soumises aux régulateurs pour évaluation dans le cadre d'une procédure accélérée, selon le communiqué.
25 juin SARS-CoV-2 variants of concern and variants under investigation in England Technical briefing 17	- C.37 (Lambda), previously a signal in monitoring, was designated a new Variant Under Investigation on 23 June 2021 based on global spread and a novel combination of mutations; further data is provided - Very **preliminary results for live virus neutralisation of AY.1** (a lineage of Delta with K417N), with a small number of sera from vaccine recipients **are reassuring**, however further testing is required (data provided by Genotype to Phenotype consortium). - PCR cycle threshold (Ct) values appear to be persistently lower in Delta than Alpha cases based on routine national testing data.
25 juin Le variant Delta pourrait surcharger les hôpitaux canadiens cet hiver	Selon les prévisions de l'ASPC, la capacité hospitalière au pays pourrait être dépassée en janvier si une nouvelle vague est causée par le variant Delta, indique l'Agence. Celle-ci pourrait être beaucoup plus importante que celle qu'on a vécue cet hiver. Selon l'ASPC, on a observé une multiplication par 4 du nombre de cas de Delta au Canada entre le 25 avril et le 23 mai. D'après les données compilées par CBC et Radio-Canada, il y a présentement un peu plus de 3000 cas au pays liés au variant Delta. Rappelons que le variant Delta est 50 % plus transmissible que le variant Alpha. Les cas de Delta sont 54 % plus susceptibles d'être hospitalisés que les cas reliés au variant Alpha. La majorité des cas de Delta au Canada sont des personnes non vaccinées ou partiellement vaccinées. Selon les dernières données canadiennes :

	• 0,14 % des personnes vaccinées ont été infectées plus de 14 jours après leur première dose; • 0,08 % des personnes entièrement vaccinées ont été infectées plus de 7 jours après la deuxième dose.
23 juin NEJM – Special report - SARS-CoV-2 Variants and Vaccines	Variants of concern have been evolving since the beginning of the Covid-19 pandemic, with **selective advantage generally favoring more transmissible variants**. **Variants of concern with resistance against natural or vaccine-induced immunity would probably supplant previously circulating strains only if this immune evasion capability resulted in increased fitness, including transmissibility.** However, prolonged viral replication in the presence of partial immunity in immunocompromised persons or circumstances in which rapid transmission of high titers of virus occurs could have contributed to the development of variants that can at least partially escape human immune responses. The use of antibody-based treatments in circumstances in which they are of limited or undemonstrated efficacy may further contribute to the evolution of variants of concern that could evade not only these but also other antibody responses. **Partially effective interventions may therefore encourage viral evolution. In addition, the larger the number of infected persons, the greater the chance that new variants of concern will arise.**
23 juin Journal de Montréal - Virus: le variant Delta devrait devenir très dominant dans l'UE d'ici août	Le variant Delta du coronavirus, particulièrement contagieux, **devrait représenter 90% des nouveaux cas de COVID-19 dans l'Union européenne d'ici fin août**, a estimé mercredi le Centre européen de prévention et de contrôle des maladies (**ECDC**), en appelant à la vigilance. Pour faire rempart à l'émergence du **variant**, qui est **40 à 60% plus transmissible que l'Alpha** selon l'agence sanitaire, l'ECDC appelle à accélérer les vaccinations. En laboratoire ou en vie réelle, les études convergent sur un point: **recevoir une seule dose de vaccin n'apporte qu'une protection limitée contre le variant Delta**. « À ce stade, il devient crucial que la deuxième dose de vaccin soit administrée dans l'intervalle minimum autorisé après la première dose, afin d'accélérer le rythme auquel les personnes vulnérables sont protégées »
21 juin Nature medicine - Has SARS-CoV-2 reached peak fitness?	More-fit variants can be expected to emerge over time, but we believe that these will not continue to emerge indefinitely: nothing is infinite in nature, and eventually the virus will reach its form of 'maximum transmission'. After then, new variants will provide no further advantage in infectivity. The virus will thus stabilize and this 'final' variant will prevail and become the dominant strain, experiencing only occasional, minimal variations.

	On the other hand, the most-potent vaccines seem to dramatically hinder viral replication and thus transmission. Because of this, a considerable advantage for the virus could therefore be provided by mutations that cause the emergence of variants that evade vaccine-induced immunity. These would still replicate in the vaccinated host in communities in which the proportion of vaccinated people is very high. We cannot, of course, exclude the possibility of their emergence even in the near future, but molecular data gathered thus far have made it clear that the 'evolutionary space' that SARS-CoV-2 has for evading vaccine-induced immunity is remarkably narrow relative to that available for increases in transmission rates. Some evolutionary virologists believe complete or nearly complete resistance to the current vaccines is an inevitability, which is a prediction that cannot be discounted or ignored.
20 juin L'Indépendant - Variant Delta - 77% des personnes infectées au Royaume-Uni sont non-vaccinées	L'étude ZOE Covid réalisée en lien avec le King's Collège de Londres indique que ces nouveaux cas positifs touchent essentiellement des personnes non-vaccinées. 77% des personnes infectées lors des semaines passées n'étaient pas vaccinées. Quant aux personnes vaccinées qui ont été testées positivement, elles n'avaient reçu, majoritairement, qu'une seule dose du vaccin dans un pays qui a massivement injecté de l'AstraZeneca, le vaccin le moins protecteur (autour de 80% d'efficacité) contre la souche classique comme sur les variants. Les chercheurs du King's College de Londres ont calculé le risque de nouvelle infection quotidienne au Covid: • Chez les non vaccinés : il y a une chance sur 2.093 d'être infecté • Après 1 dose de vaccin : le risque grimpe à une chance sur 5.508 • Après 2 doses de vaccin : le risque est le moins élevé avec une chance sur 16.101
18 juin Biorxiv - A novel bivalent DNA vaccine encoding both spike protein receptor-binding domain and nucleocapsid protein of SARS-CoV-2 to elicit T cell and neutralising antibody responses that cross react with variants	We report that the linkage of the N protein to the modified Fc enhances T cell immunity, and show that the inclusion of this N-modified Fc fusion alongside the RBD antigen in a bivalent DNA vector stimulates strong cellular and humoral immunity to both antigens. High titre antibody responses that exhibited pseudotype neutralisation with a 50% reduction in infective dose (ID50) of >5000 was induced. High frequency CD8 and Th1 CD4 T cell responses to both RBD and N proteins were stimulated. Finally, we demonstrate the induction of variant cross-reactive immune responses and the flexibility of this DNA platform for targeting SARS-CoV-2 variants.

17 juin Biorxiv - SARS-CoV-2 spike P681R mutation enhances and accelerates viral fusion	The **P681R mutation** that is highly conserved in this lineage **enhances the efficacy to viral fusion** and further accelerates its speed of action. The fact that the B.1.617 variants as well as the **P681R mutant efficiently form syncytia** and the S P681R mutant accelerates and promotes cell-cell fusion suggests that **switching the preference of viral replication mode** from cell-free infection to cell-cell infection **may be a unique strategy of the B.1.617 variants to evade antiviral immunity**. Switching viral infection mode by the P681R mutation may relate to the severity and/or unusual outcome of viral infection, therefore, the epidemic of the SARS-CoV-2 variants harboring the P681R mutation should be surveyed in depth.
16 juin Journal of infection - The incubation period of the SARS-CoV-2 B1.1.7 variant is shorter than that of other strains	Poisson regression analysis showed that the **incubation period of the B.1.1.7 variant was 0.66 times shorter than that of other strains** (95% CI: 0.38, 0.71). This **study** had several **limitations**. First, almost all of the patients infected with the B.1.1.7 variant were infected in 3C environments, such as restaurants or bars. It is possible that they were exposed to more virus particles in closed, unventilated, crowded environments. **However, when incubation periods were compared among similar 3C environments, the incubation period of the B.1.1.7 variant was significantly shorter than that of other strains.**
14 Juin Naturally enhanced neutralizing breadth against SARS-CoV-2 one year after infection	**Key findings:** • Among unvaccinated convalescent individuals, SARS-CoV-2 neutralizing activity after infection was not significantly different at 6 and 12 months. • Among convalescent individuals 12 months after infection, neutralizing activity against SARS-CoV-2 variants was greater (21- to 71-fold) among mRNA-vaccinated compared with non-vaccinated individuals (Figure). *Limitations*: Small sample sizes. 
3 juin Ouest-France - Difficile à détecter, le variant breton du coronavirus intrigue	L'émergence de cette « spécialité régionale », aujourd'hui contenue, a fait couler beaucoup d'encre, jusqu'en Chine où *le South China Morning Post* relatait tout récemment « la perplexité des soignants » de l'hôpital de Lannion, confrontés cet hiver à des patients présentant les symptômes du Covid-

encore les scientifiques du monde entier	19, mais avec des retours de tests RT-PCR la plupart du temps négatifs (**« Seuls 15 % des patients ayant contracté la maladie avaient eu un premier test RT-PCR nasopharyngés positif. »).** **« On pense qu'une migration peut-être plus rapide de la zone nasale à la zone pulmonaire rend cette souche mutante du Covid-19 difficilement détectable »,** avait avancé l'Agence régionale de santé (ARS). L'étude aborde notamment la question de la dangerosité du « variant breton », posée par le **taux de mortalité établi à 43 %.** Une létalité élevée qui est probablement à nuancer en raison du profil de ces patients chez lesquels le variant a été détecté (plus âgés ou présentant des comorbidités) : cette détection faisant suite, souvent, à un échantillon respiratoire profond, principalement motivé par la gravité de la maladie.

21 juin 2021

Publications sélectionnées

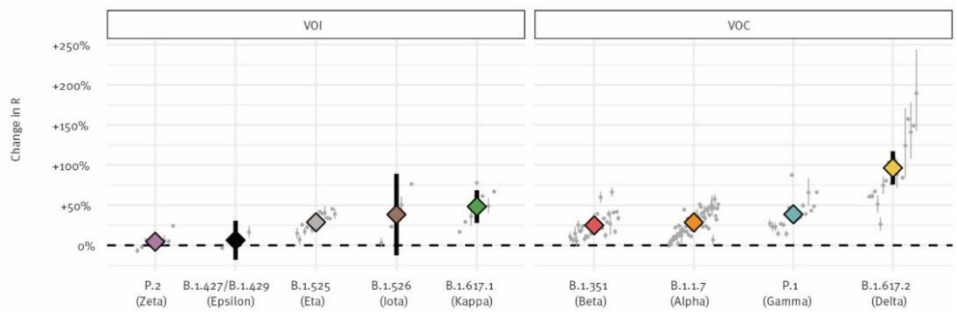
<table>
<tr><th>Titre</th><th>Extrait pertinent</th></tr>
<tr><td colspan="2">18 juin
Public Health England - Risk assessment for SARS-CoV-2 variant Delta: 18 June
18 June 2021 Risk assessment for SARS-CoV-2 variant: Delta (VOC-21APR-02, B.1.617.2) Public Health England
<table>
<tr><th>Indicator</th><th>RAG*</th><th>Confidence</th><th>Assessment and rationale</th></tr>
<tr><td>Transmissibility between humans</td><td></td><td>HIGH</td><td>Transmissibility appears greater than wild type (first wave) virus
Delta continues to demonstrate a substantially increased growth rate compared to Alpha, across multiple analyses. Secondary attack rates and household transmission studies support increased transmissibility. There is in vitro evidence suggestive of increased replication in biological systems that model human airway. It is highly likely that Delta is more transmissible than Alpha.</td></tr>
<tr><td>Infection severity</td><td></td><td>LOW</td><td>Increased severity (hospitalisation risk) when compared to Alpha
Early evidence from England and Scotland suggests there may be an increased risk of hospitalisation compared to contemporaneous Alpha cases. A large number of cases are still within the follow-up period and there is a limited understanding of clinical course of disease.</td></tr>
<tr><td>Immunity after natural infection</td><td></td><td>LOW</td><td>Experimental evidence of functional evasion of natural immunity but insufficient epidemiological data
Pseudovirus and live virus neutralisation using convalescent sera from first wave and Alpha infections shows a reduction in neutralisation. National surveillance analyses are underway but there is currently insufficient evidence to assess whether the risk of reinfection differs between Delta and Alpha.</td></tr>
<tr><td>Vaccines</td><td></td><td>HIGH</td><td>Epidemiological and laboratory evidence of reduced vaccine effectiveness
There are now analyses from England and Scotland supporting a reduction in vaccine effectiveness for Delta compared to Alpha against symptomatic infection. This is more pronounced after one dose (absolute reduction of approximately 15% to 20% after one dose). Iterated analysis continues to show vaccine effectiveness against Delta is higher after 2 doses but that there is a reduction for Delta compared to Alpha. Current evidence suggests that VE against hospitalisation is maintained.
Although this is observational data subject to some biases, it holds true across several analytic approaches and the same effect is seen in both English and Scottish data. It is strongly supported by pseudovirus and live virus neutralisation data from multiple laboratories. There are no data on whether prevention of transmission is affected. The acquisition of the mutation K417N, which may be antigenically significant, in a small number of cases is noted.</td></tr>
<tr><td>Overall assessment</td><td></td><td></td><td>Delta is predominant. All analyses continue to support increased transmissibility and reduced vaccine effectiveness against symptomatic infection. The interplay between the current findings of increased risk of hospitalisation and preserved vaccine effectiveness against hospitalisation requires careful consideration. The clinical course of disease and severity of hospitalised illness also require further detailed assessment. It is too early to assess the case fatality ratio compared to other variants. The priority investigations are more detailed analysis of hospitalised cases, characterisation of the generation time, viral load and period of infectivity, and epidemiological studies of reinfections.</td></tr>
</table>
The therapeutics risk assessment is under review for all variants and is not included.
*refer to scale and confidence grading slide.</td></tr>
<tr><td>18 juin
La presse - Variant Delta - Les cas ont bondi de 66 % au Canada</td><td>L’administratrice en chef de la santé publique du Canada, la D^{re} Theresa Tam, a déclaré vendredi qu’il y avait un peu plus de 2000 cas confirmés du variant.

Il y a à peine trois jours, l’Agence de la santé publique du Canada indiquait à La Presse Canadienne qu’il y avait 1187 cas confirmés.

« Le variant Delta est maintenant dans toutes les provinces et au moins un de nos territoires », a déclaré M^{me} Tam au comité de la santé de la Chambre des communes.

Cependant, les données sur le variant au Canada sont limitées et elles n’ont pas encore été ajoutées au site web de Santé Canada signalant les cas de variants.</td></tr>
<tr><td>18 juin
Global news - Delta COVID-19 variant becoming dominant strain globally, WHO official says</td><td>The Delta variant of COVID-19, first identified in India, is becoming the globally dominant variant of the disease, the World Health Organization’s chief scientist said on Friday.

Britain has reported a steep rise in infections with the Delta variant, while Germany’s top public health official predicted it</td></tr>
</table>

	would rapidly become the dominant variant there despite rising vaccination rates. Coronavirus variants were cited by CureVac (mRNA vaccine) when the German company this week reported its vaccine proved only 47 per cent effective at preventing disease, shy of the WHO's 50 per cent benchmark. **En complement:** CureVac COVID vaccine let-down spotlights mRNA design challenges
17 juin Eurosurveillance - Increased transmissibility and global spread of SARS-CoV-2 variants of concern as at June 2021	We analysed 1,722,652 SARS-CoV-2 sequences uploaded to the Global Initiative On Sharing All Influenza Data (GISAID) hCoV-19 database, considering only VOC or VOI reported at least 25 times in at least three countries. Despite differences between countries, our analysis showed a statistically significant increase in the pooled mean effective reproduction number relative to non-VOC/VOI of B.1.1.7 at 29% (95% confidence interval (CI): 24–33), B.1.351 at 25% (95% CI: 20–30), P.1 at 38% (95% CI: 29–48) and B.1.617.2 at 97% (95% CI: 76–117) (Figure 1). Of the six variants currently designated as VOI, five were considered in our analysis and among these, only B.1.617.1 and B.1.525 demonstrated a statistically significant increase in the effective reproduction number of 48% (95% CI: 28–69) and 29% (95% CI: 23–35), respectively. 
16 juin CTV news -Too soon to tell if Delta variant symptoms are different: experts	A recent U.K.-based study indicates that the symptoms associated with the Delta variant of COVID-19 may differ from the symptoms experienced earlier on in the pandemic, but Canadian experts say they haven't seen that among patients. The main symptoms to look for since the start of the pandemic have been a loss of taste and smell, fever and cough, but the U.K. study suggests that more people are reporting symptoms that are similar to that of a summer cold: fatigue, chills and generally feeling "off." Experts say it could potentially be evolution of the virus, but it may also have something to do with the age of those infected.
16 juin Santé publique Ontario - Ce que nous savons jusqu'à	**Transmissibilité**

présent sur… le variant d'intérêt B.1.617 de la COVID-19	• Au Royaume-Uni, le Scientific Advisory Group for Emergencies (SAGE) a rapporté avec une grande confiance que le B.1.617.2 pouvait être jusqu'à 50 % plus transmissible que le VP B.1.1.731 • Une étude de modélisation menée par le groupe de travail sur la COVID-19 du Centre for Mathematical Modelling of Infectious Diseases a estimé le taux de reproduction (R) de B.1.617.2 à 1,64 (IC à 95 % : 1,61 à 1,67) • Les données recueillies au Royaume-Uni entre le 29 mars et le 4 mai 2021 permettent de dégager des taux d'infection secondaire plus élevés chez les contacts du ménage et de l'extérieur du ménage des 1446 cas infectés par le B.1.617.2 comparativement aux contacts des cas infectés par le B.1.1.7 et à ceux dont les antécédents de voyage sont nuls ou inconnus **Gravité** • Au Royaume-Uni, on avait dénombré 12 décès sur 5599 cas d'infection par le B.1.617.2 en date du 25 mai 2021, avec un taux de létalité de 0,2 % (IC à 95 % : 0,1 % à 0,4 %), comparativement à 2,0 % (IC à 95 % : 1,9 % à 2,0 %) pour le B.1.1.7. **Incidence sur le dépistage** • Il n'existe jusqu'à maintenant aucune preuve que les tests moléculaires sont moins efficaces dans le diagnostic du B.1.617 **Immunité et réinfection** • Quatre prépublications portant sur des expériences de neutralisation in vitro signalent également une neutralisation moins importante de B.1.617 ou des sous-lignées B.1.617.1 et B.1.617.2 par les plasmas de convalescent. • L'étude SIREN, qui surveille les infections à la COVID-19 chez les travailleurs de la santé du National Health Service au Royaume-Uni, a rapporté seulement un cas de réinfection (statut de VP non indiqué) entre le 22 avril et le 21 mai 2021 **Efficacité vaccinale** • Arès seulement une dose, l'efficacité de la vaccination chez des patients symptomatiques avec le variant B.1.617.2 était réduite d'environ 20 % par comparaison aux patients infectés par B.1.1.7. Cependant, la réduction de l'efficacité vaccinale après deux doses était très légère : ex. 87,9 % c. 93,4 % pour le vaccin de Pfizer.
15 juin	**VOI Lambda**

WHO - Weekly epidemiological update on COVID-19 - 15 June 2021	On 14 June 2021, a variant assigned to Pango lineage C.37, GISAID clade GR/452Q.V1, NextStrain clade 20D, was designated as a global VOI, and assigned the WHO label “Lambda”.

Variants of Interest (VOIs):					
Epsilon	B.1.427/ B.1.429	GH/452R.V1	21C	United States of America, Mar-2020	5-Mar-2021
Zeta	P.2	GR/484K.V2	20B/S.484K	Brazil, Apr-2020	17-Mar-2021
Eta	B.1.525	G/484K.V3	21D	Multiple countries, Dec-2020	17-Mar-2021
Theta	P.3	GR/1092K.V1	21E	Philippines, Jan-2021	24-Mar-2021
Iota	B.1.526	GH/253G.V1	21F	United States of America, Nov-2020	24-Mar-2021
Kappa	B.1.617.1	G/452R.V3	21B	India, Oct-2020	4-Apr-2021
Lambda	C.37	GR/452Q.V1	20D	Peru, Aug-2020	14-Jun-2021

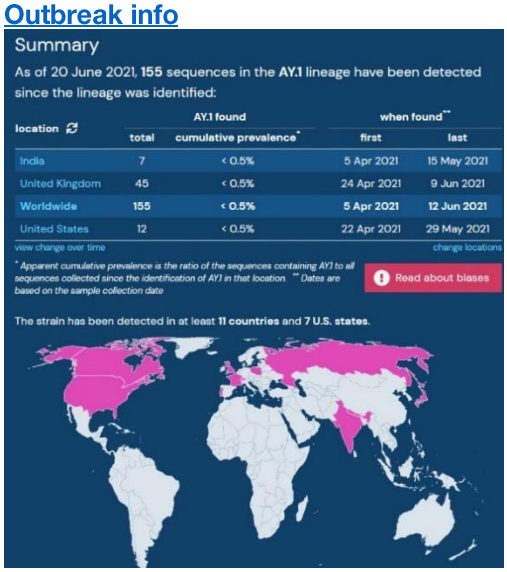
Lambda has been associated with substantive rates of community transmission in multiple countries, with rising prevalence over time concurrent with increased COVID-19 incidence.

Lambda carries a number of mutations with suspected phenotypic implications, such as a potential increased transmissibility or possible increased resistance to neutralizing antibodies. It is characterised by mutations in the spike protein, including G75V, T76I, del247/253, L452Q, F490S, D614G and T859N

There is currently limited evidence on the full extent of the impact associated with these genomic changes (…) Further studies are also to validate the continued effectiveness of vaccines.

En complement - Public Health Agency of Canada (communication au LSPQ) In Canada, 2 detections at the Border (AB & QC); 3 domestic cases (AB & ON) reported to NML; 3 sequences in GISAID (BC & ON). Earliest Canadian detection Feb 2021.

Outbreak info

15 juin News abp live - Delta Variant Of Coronavirus Mutates To 'Delta Plus', Should India Be Worried?	**'Delta plus' or AY.1' variant** While the Delta variant is still impacting not only India but the world, the virus has now mutated further to form the 'Delta plus' or AY.1' variant. The sequences have recently been designated as lineage AY.1 (B.1.617.2.1), a sublineage of Delta, due to concerns about K417N is one of the mutations found in the Beta variant (B.1.351) **En complement - Public Health Agency of Canada (communication au LSPQ)** In Canada, 1 case uploaded to GISAID from ON (25 May 2021) **Outbreak info** 
15 juin BMJ - Delta variant: What is happening with transmission, hospital admissions, and restrictions?	**Are covid-19 hospital admissions increasing?** Yes. **Is this because of the delta variant?** Public Health England figures show that the variant now accounts for 90% of UK cases, with the total number exceeding 42 000. Research indicates that delta is associated with an estimated 60% higher risk of household transmission than the alpha variant (…). There are also suggestions that delta could carry a much higher risk of hospital admission. (…) However, the most recent PHE analysis of 14 019 delta cases (14 June) indicates that two doses of either vaccine are still highly effective against hospital admission: 96% for Pfizer-BioNTech and 92% for Oxford-AstraZeneca. **What is different about the delta variant?** The delta variant has got two important mutations in its spike protein, or sets of mutations. One is at the furin cleavage site, which we think is quite important for the fitness of the virus in the airway.

	Why is delta able to transmit more easily? The current data indicated that the virus was "fitter in human airway cells," meaning an increased amount of the virus in the infected person, and so they may expel more virus out into the air to pass on to the next person. This is supported by the testing data, which show that the CT value (…) seems to be lower in samples from delta infected people, meaning they contain more virus. Another suggestion is that if this variant is better at infecting human airway cells, people may become infected after a lower exposure. **Does delaying the easing of covid-19 restrictions make a difference?** Yes, because it allows more people to receive two doses of the vaccine. **Even if the death rate with delta is lower, could the healthcare system still be overwhelmed?** Absolutely. Rising hospital admission rates would increase pressure on the already exhausted health system and could overwhelm it. **Are more children becoming ill?** There are no official figures on this (…) We're not seeing any evidence of an increase in paediatric admissions with covid. (…) "Our experience over the last 15 months is that many children who test positive have come into hospital for something else, like broken bones. At the moment the situation in the UK is stable. The number of children in hospital with covid remains very low."
15 juin BMJ - Risk of hospital admission for patients with SARS-CoV-2 variant B.1.1.7: cohort analysis	**What is already known on this topic** • The SARS-CoV-2 B.1.1.7 variant was discovered in England in December 2020 and thereafter became the dominant lineage owing to a higher transmissibility than wild-type SARS-CoV-2 • Some evidence suggests that B.1.1.7 is associated with more severe disease, but the studies that have found an association with increased mortality may have been limited by confounding • Hospital admission as a measurement of disease severity is less likely than mortality to be positively confounded by hospital burden **What this study adds** • Patients with covid-19 who tested positive for the B.1.1.7 variant had a 1.52-fold hazard of hospital admission within 1-14 days of the first positive test compared with wild-type variants • The results likely reflect a more severe disease associated with the SARS-CoV-2 B.1.1.7 variant, particularly in patients aged 30 or older

14 juin Lancet - SARS-CoV-2 Delta VOC in Scotland: demographics, risk of hospital admission, and vaccine effectiveness	The Delta VOC in Scotland was found mainly in younger, more affluent groups. Risk of COVID-19 hospital admission was approximately doubled [hazard ratio (HR) 1·85 (95% CI 1·39–2·47)] in those with the Delta VOC when compared to the Alpha VOC, with risk of admission particularly increased in those with five or more relevant comorbidities. Both the Oxford–AstraZeneca and Pfizer–BioNTech COVID-19 vaccines were effective in reducing the risk of SARS-CoV-2 infection and COVID-19 hospitalisation in people with the Delta VOC, but these effects on infection appeared to be diminished when compared to those with the Alpha VOC. AstraZeneca = 73% (95% CI 66–78) for *S* gene-negative cases (Alpha) versus 60% (53–66)] for those *S* gene-positive (Delta); Pfizer = 92% (95% CI 90–93) S gene-negative, 79% (75–82) S gene-positive]. We had insufficient numbers of hospital admissions to compare between vaccines in this respect. Given the observational nature of these data, estimates of vaccine effectiveness need to be interpreted with caution.

Fait saillants de la veille scientifique (pour le rapport génomique hebdomadaire - 15 juin)

15 juin. Le variant B.1.617.2 est maintenant retrouvé dans au moins 66 pays à travers le monde.

14 juin. Selon une étude en prépublication des autorités de santé publique d'Angleterre (PHE), les vaccins de Pfizer-BioNTech et d'Oxford-AstraZeneca sont efficaces à 75 % après 1 dose et à 94 % après 2 doses (données combinées pour les deux vaccins) pour prévenir les hospitalisations causées par le variant B.1.617.2 (Delta). Ces données sont comparables à celles observées pour le variant B.1.1.7 (Alpha), soit 78 % d'efficacité après 1 dose et 92 % après 2 doses (Stowe et coll. 2021).

Les analyses sont en cours pour établir l'efficacité de ces vaccins pour prévenir les décès causés par le variant B.1.617.2 (Delta). Cependant, comme pour les autres variants, le niveau de protection devrait être élevé (PHE, communiqué de presse).

Concernant le vaccin de Moderna, aucune donnée d'efficacité vaccinale n'a été rapportée contre le variant B.1.617.2 (Delta), que ce soit pour prévenir les infections ou les hospitalisations.

11 juin. Selon PHE, le variant de lignée B.1.617.2 (Delta) est maintenant le variant prédominant en Angleterre, soit 74 % des nouveaux cas séquencés (PHE, breffage technique #15). Cette progression rapide du variant B.1.617.2 (Delta) au détriment du variant B.1.1.7 (Alpha) dans ce pays serait attribuable à une combinaison de facteurs, dont le contexte (population et lieu de transmission) et certaines caractéristiques biologiques du virus connues à ce jour, dont une transmissibilité accrue et un potentiel d'échappement immunitaire.

En effet, comparativement à la lignée B.1.1.7 (Alpha), le variant B.1.617.2 (Delta) serait 1,6 fois plus transmissible, selon une étude cas-témoin nationale en milieu résidentiel (PHE, breffage technique #15).

Selon une étude en prépublication de PHE, après 1 seule dose, une efficacité vacinale réduite pour prévenir les infections symptomatiques causées par le variant B.1.617.2 (Delta) est observée, comparativement à la lignée B.1.1.7 (Alpha) (34 % contre 51 % ; données combinées pour les vaccins Pfizer-BioNTech et Oxford-AstraZeneca). Néanmois, après 2 doses, cette réduction d'efficacité vaccinale entre les deux variants est faible (81 % contre 87 % ; données combinées pour les deux vaccins) (Lopez Bernal et coll., 2021).

Selon une étude de cohorte chez les travailleurs de la santé vaccinés (étude SIREN), il n'y a eu d'augmentation des cas de COVID-19 parmi les participants durant la période où le variant B.1.617.2 (Delta) est devenu prévalent, et les cas de réinfection demeurent faibles (PHE, breffage technique #15).

Le variant de lignée B.1.617.2 (Delta) serait toutetois associé à une augmentation du risque d'hospitalisation en Angleterre et en Écosse (environ 2 fois) dans les 14 jours suivant un dépistage, comparativement au variant B.1.1.7 (Alpha) (PHE, breffage technique #15)

31 mai 2021. L'Organisation mondiale de la santé (OMS) a reclassifié certains variants du SRAS-CoV-2 à la lumière des connaissances actuelles sur leurs impacts épidémiologiques ou cliniques. Entre autres, concernant le variant B.1.617 ayant émergé en Inde, la sous lignée B.1.617.2 (Delta) demeure un variant préoccupant, alors que la sous-lignée B.1.617.1 (Kappa) est maitenant un variant d'intérêt et la sous-lignée B.1.617.3 est considéré comme un variant commun (OMS, Tracking SARS-CoV-2 variants).

En raison de la situation sanitaire internationale lié au variant B.1.617 du SRAS-CoV-2, l'Institut national de santé publique du Québec (INSPQ) a publié un état de situation sur ce variant et des recommandations pour en rehausser la surveillance au Québec (INSPQ, document intérimaire).

14 juin 2021

Publications sélectionnées

<table>
<tr><th>Titre</th><th>Extrait pertinent</th></tr>
<tr><td>14 juin
Variant Delta : Deux doses de Pfizer ou d'AstraZeneca efficaces contre l'hospitalisation
https://www.lapresse.ca/covid-19/2021-06-14/variant-delta/deux-doses-de-pfizer-ou-d-astrazeneca-efficaces-contre-l-hospitalisation.php</td><td>L'étude de Public Health England (PHE) montre une protection à 96 % contre les hospitalisations après deux doses du vaccin Pfizer/BioNTech et à 92 % pour Oxford/AstraZeneca.

Sur 14 019 personnes ayant contracté ce variant, seules 166 ont été hospitalisées, révèle l'étude menée entre le 12 avril et le 4 juin, soulignant qu'il s'agit « de résultats comparables à l'efficacité du vaccin pour éviter l'hospitalisation liée au variant Alpha », apparu fin 2020 dans le sud-est de l'Angleterre.

En complement (PHE) : Effectiveness of COVID-19 vaccines against hospital admission with the Delta (B.1.617.2) variant

Table 1: Estimated vaccine effectiveness against hospitalisation
<table><tr><th></th><th></th><th colspan="3">Alpha</th><th colspan="3">Delta</th></tr><tr><th>Vaccination status</th><th></th><th>OR vs symptomatic disease</th><th>HR vs hospitalisation</th><th>VE vs hospitalisation</th><th>OR vs symptomatic disease</th><th>HR vs hospitalisation</th><th>VE vs hospitalisation</th></tr><tr><td>Any vaccine</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr><tr><td></td><td>Dose 1</td><td>0.51 (0.48-0.55)</td><td>0.44 (0.28-0.70)</td><td>78% (65-86)</td><td>0.69 (0.64-0.75)</td><td>0.37 (0.22-0.63)</td><td>75% (57-85)</td></tr><tr><td></td><td>Dose 2</td><td>0.13 (0.1-0.15)</td><td>0.64 (0.24-1.72)</td><td>92% (78-97)</td><td>0.20 (0.18-0.23)</td><td>0.29 (0.11-0.72)</td><td>94% (85-98)</td></tr><tr><td>Pfizer</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr><tr><td></td><td>Dose 1</td><td>0.53 (0.47-0.58)</td><td>0.32 (0.14-0.73)</td><td>83% (62-93)</td><td>0.64 (0.54-0.77)</td><td>0.10 (0.01-0.76)</td><td>94% (46-99)</td></tr><tr><td></td><td>Dose 2</td><td>0.06 (0.05-0.08)</td><td>0.88 (0.21-3.77)</td><td>95% (78-99)</td><td>0.12 (0.1-0.15)</td><td>0.34 (0.10-1.18)</td><td>96% (86-99)</td></tr><tr><td>Astrazeneca</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr><tr><td></td><td>Dose 1</td><td>0.51 (0.48-0.55)</td><td>0.48 (0.30-0.77)</td><td>76% (61-85)</td><td>0.70 (0.65-0.76)</td><td>0.41 (0.24-0.70)</td><td>71% (51-83)</td></tr><tr><td></td><td>Dose 2</td><td>0.26 (0.21-0.32)</td><td>0.53 (0.15-1.80)</td><td>86% (53-96)</td><td>0.33 (0.28-0.39)</td><td>0.25 (0.08-0.78)</td><td>92% (75-97)</td></tr></table></td></tr>
<tr><td>14 juin
Covid-19 : le variant Delta, dit « indien », circule de plus en plus dans plusieurs pays d'Europe
https://www.lemonde.fr/planete/article/2021/06/14/covid-19-la-circulation-du-variant-delta-augmente-dans-plusieurs-pays-d-europe_6084063_3244.html</td><td>Depuis trois semaines, le nombre de cas de Covid-19 augmente en moyenne glissante sur sept jours en Angleterre, passant de 2 000 mi-mai à près de 6 000 début juin, et 8 000 cas quotidiens le 11 juin. Le variant Delta, dit « indien », y est désormais majoritaire, représentant près de 74 % des cas.

Au Portugal également, l'incidence augmente depuis la deuxième semaine de mai : environ 400 cas y étaient recensés le 8 mai, et 900 le 10 juin. Dans la semaine du 17 au 22 mai, les échantillons mis en ligne dans la base de données Gisaid étaient à presque 50 % des variants Delta (18 sur 38).

L'Allemagne dénombre, quant à elle, 50 % de séquences Delta supplémentaires en moins de deux semaines (517 cas au 11 juin) et la Belgique 60 % en plus (191 cas), quand la France compte 130 cas, contre 80 au 31 mai. Néanmoins, le variant Alpha reste dominant dans l'Hexagone : selon l'enquête Flash de Santé publique France datant du 25 mai, il représentait alors 87,8 % et le variant Delta 0,5 % des 800 séquences étudiées.</td></tr>
<tr><td>14 juin</td><td>Novavax a affirmé lundi que son vaccin anti-COVID-19 était efficace à plus de 90 %, y compris contre les variants, après une étude réalisée sur près de 30 000 personnes aux États-</td></tr>
</table>

<table>
<tr>
<td>Le vaccin de Novavax efficace à plus de 90 %, y compris contre les variants https://www.lapresse.ca/covid-19/2021-06-14/le-vaccin-de-novavax-efficace-a-plus-de-90-y-compris-contre-les-variants.php</td>
<td>Unis et au Mexique. Le vaccin « a montré une protection de 100 % contre les formes modérées et sévères de la maladie.

En complément (Novavax) : Novavax COVID-19 Vaccine Demonstrates 90% Overall Efficacy and 100% Protection Against Moderate and Severe Disease in PREVENT-19 Phase 3 Trial

• 93% efficacy against predominantly circulating Variants of Concern and Variants of Interest
• 91% efficacy in high-risk populations
• 100% efficacy against variants "not considered Variants of Concern/Interest"
• All COVID-19 hospitalizations/death occurred in the placebo group</td>
</tr>
<tr>
<td>11 juin
Royaume-Uni
Le variant Delta 60 % plus contagieux que l'Alpha https://www.lapresse.ca/international/europe/2021-06-11/royaume-uni/le-variant-delta-60-plus-contagieux-que-l-alpha.php</td>
<td>Le variant Delta du coronavirus, désormais dominant au Royaume-Uni, est environ 60 % plus contagieux que son prédécesseur et poursuit sa poussée dans le pays.

Selon cette étude des autorités sanitaires (Public Health England), 42 323 cas (29 892 de plus qu'il y a une semaine) de ce variant identifié en Inde et présent dans une cinquantaine de pays ont été détectés au Royaume-Uni. Il représente plus de 90 % des nouveaux cas. (….) Le nombre de cas sur sept jours est désormais en hausse de plus de 60 % et le nombre de patients hospitalisés vient de repasser au-dessus de 1000.

En complement (PHE) : SARS-CoV-2 variants of concern and variants under investigation in England: technical briefing 15

Table 17. Multivariate conditional logistic regression of odds of household transmission for Delta compared to Alpha
<table><tr><th></th><th>Unadjusted Odds Ratio (95% CI)</th><th>P value</th><th>Adjusted Odds* (95% CI)</th><th>P value</th></tr><tr><td>Delta household transmission</td><td>1.66(1.28-2.14)</td><td><0.001</td><td>1.64(1.26-2.13)</td><td><0.001</td></tr></table>*Adjusted for sex, age, ethnicity, deprivation of residence (IMD), vaccination status of index case</td>
</tr>
<tr>
<td>11 juin
SARS-CoV-2 variants of concern and variants under investigation in England: technical briefing 15 https://www.gov.uk/government/publications/investigation-of-novel-sars-cov-2-variant-variant-of-concern-20201201</td>
<td>For the first time this week, published figures include genotyping assay data, using a highly specific mutation as an indicator of a probable Delta variant case. The most recent data show 96% of sequenced and genotyped cases are Delta.

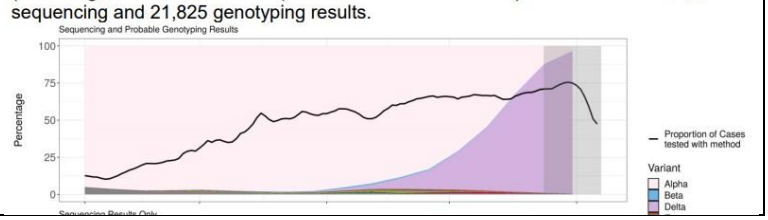
Figure 3. Variant prevalence for all England available case data from 1 February 2021 as of 7 June 2021
(excluding 50 cases where the specimen date was unknown). This includes 162,992 sequencing and 21,825 genotyping results.
 
</td>
</tr>
</table>

Table 3. Rules-based decision algorithm (RBDA) to identify variant and mutation (VAM) profiles from genotype assay mutation profiles. N501Y target was replaced by P681R in May 2021. Mutations are categorised black (must be present), orange (must not be confirmed absent), blue (may be present or absent), green (must not be confirmed present)

Variant	Public Health Manangement Level	Assay mutation profile				
		P681R	N501Y	E484K	K417N	K417T
Delta*#	3					
Beta	3					
Gamma	2					
Undetermined with E484K	2					
Undetermined	1	All other results				

*Genotyping assay for B.1.617 cannot distinguish between Kappa, Delta and B.1.617.3 and all results are treated as probable Delta given the current dominance of this lineage. #Delta with K417N will now also be reported. The clade currently present in the UK is AY.1.

10 juin

BNT162b2-elicited neutralization of B.1.617 and other SARS-CoV-2 variants https://www.nature.com/articles/s41586-021-03693-y

Here we report that 20 human sera, drawn 2 or 4 weeks after two doses of BNT162b2, neutralize engineered SARS-CoV-2 with a USA-WA1/2020 genetic background (a virus strain isolated in January 2020) and spike glycoproteins from the newly emerged B.1.617.1, B.1.617.2, B.1.618 (all first identified in India) or B.1.525 (first identified in Nigeria) lineages.

Geometric mean plaque reduction neutralization titers against the variant viruses, particularly the B.1.617.1 variant, appear lower than the titer against USA-WA1/2020 virus, but all sera tested neutralize the variant viruses at titers of at least 40.

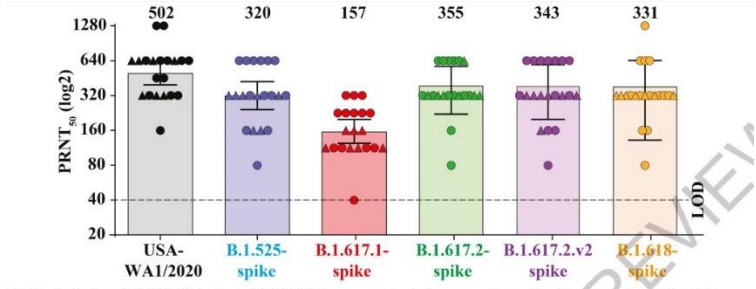


Fig. 1 | Neutralization of USA-WA1/2020 and variant SARS-CoV-2's by BNT162b2-immune sera. Neutralization of variant SARS-CoV-2's by BNT162b2 vaccine-elicited sera. The $PRNT_{50}$ results for USA-WA1/2020 and variant viruses are plotted. Individual $PRNT_{50}$ values are presented in Extended Data Table 1. Each data point represents the geometric mean $PRNT_{50}$ against the indicated virus obtained with a serum sample obtained 2 weeks (circles) or 4 weeks (triangles) after the second dose of vaccine. The $PRNT_{50}$'s were determined in duplicate assays, and the geometric means were calculated (n=20, pooled from two independent experiments). The heights of bars and the numbers over the bars indicate geometric mean titers. The horizontal bars indicate 95% confidence intervals. The dashed line indicates the limit of detection (LOD) at 1:40. Statistical analysis was performed using the two-tailed Wilcoxon matched-pairs signed-rank test. The statistical significance of the difference between geometric mean titers in the USA-WA1/2020 neutralization assay and in each variant virus neutralization assay with the same serum samples are as follows: $P = 0.002$ for B.1.525-spike, $P < 0.0001$ for B.1.617.1-spike, $P = 0.001$ for B.1.617.2-spike, $P = 0.004$ for B.1.617.2-v2-spike, $P = 0.001$ for B.1.618-spike.

10 juin

Public Health England - [10 June Risk assessment for SARS-CoV-2 variant Delta]

10 June 2021 Risk assessment for SARS-CoV-2 variant: Delta (VOC-21APR-02, B.1.617.2) Public Health England

Indicator	RAG*	Confidence	Assessment and rationale
Transmissibility between humans		**HIGH**	**Transmissibility appears greater than wild type (first wave) virus** Delta continues to demonstrate a substantially increased growth rate compared to Alpha, across multiple analyses. Delta cases are rising whilst Alpha cases are declining. Secondary attack rates are higher for Delta than for Alpha but have declined slightly over time; further analysis is being undertaken. There is in vitro evidence suggestive of increased replication in biological systems that model human airway. It is highly likely that Delta is more transmissible than Alpha.
Infection severity		**LOW**	**Increased severity (hospitalisation risk) when compared to Alpha** Early evidence from England and Scotland suggests there may be an increased risk of hospitalisation compared to contemporaneous Alpha cases. A large number of cases are still within the follow up period.
Immunity after natural infection		**LOW**	**Experimental evidence of functional evasion of natural immunity but insufficient epidemiological data** Pseudovirus and live virus neutralisation using convalescent sera from first wave and Alpha infections shows a reduction in neutralisation. There is currently insufficient evidence to assess whether the risk of reinfection differs between Delta and Alpha.
Vaccines		**HIGH**	**Epidemiological and laboratory evidence of reduced vaccine effectiveness** There are now analyses from England and Scotland supporting a reduction in vaccine effectiveness for Delta compared to Alpha. This is more pronounced after one dose (absolute reduction in vaccine effectiveness against symptomatic infection of approximately 15% to 20% after 1 dose). Iterated analysis continues to show vaccine effectiveness against Delta is higher after 2 doses but that there is a reduction for Delta compared to Alpha. There is uncertainty around the magnitude of the change in vaccine effectiveness after 2 doses of Oxford-AstraZeneca vaccine. Although this is observational data subject to some biases, it holds true across several analytic approaches and the same effect is seen in both English and Scottish data. It is strongly supported by pseudovirus and live virus neutralisation data from multiple laboratories. There are no data on whether prevention of transmission is affected. The analysis of vaccine effectiveness against hospitalisation is in process. The acquisition of the mutation K417N, which may be antigenically significant, in a small number of cases is noted.
Overall assessment			Delta is predominant and all analyses find that it has a very substantial growth advantage. The observed high growth rate is likely to be due to a combination of transmissibility and immune escape; there is still geographic heterogeneity and a probable contribution from place-based context. Iterated analyses this week continue to support our previous estimates of vaccine effectiveness and hospitalisation risk. The priority investigations are vaccine effectiveness against hospitalisation and death, further investigations of secondary attack rates, characterisation of the generation time, viral load and period of infectivity, and epidemiological studies of reinfections.

The therapeutics risk assessment is under review for all variants and is not included.

*refer to scale and confidence grading slide

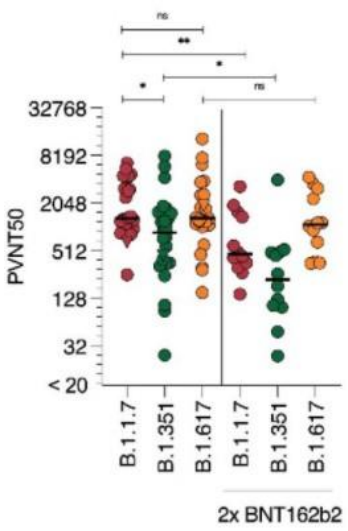
8 juin

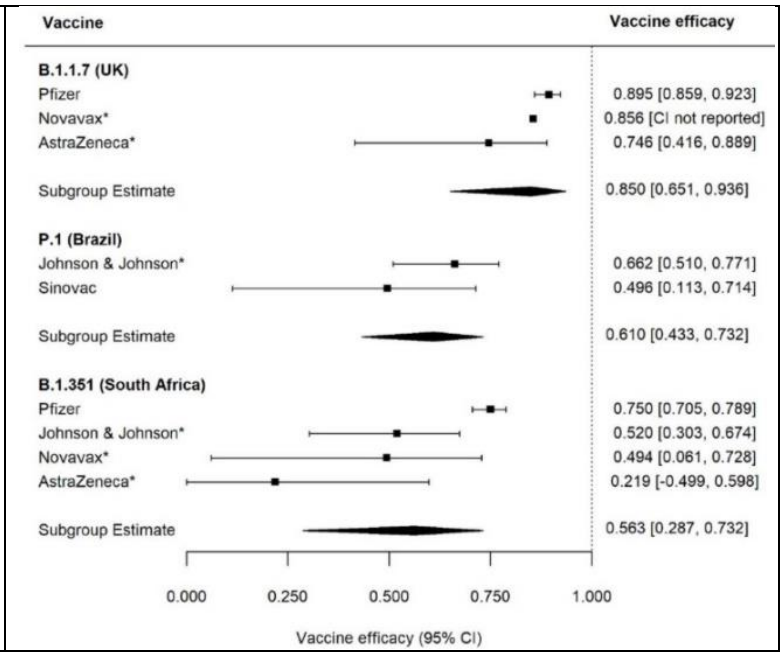
WHO –Weekly epidemiological update on COVID-19 - 8 June 2021
https://www.who.int/publications/m/item/weekly-epidemiological-update-on-covid-19---8-june-2021

Table 3: Summary of phenotypic impacts* of Variants of Concern (VOCs)

WHO label	Alpha	Beta	Gamma	Delta
Transmissibility	Increased transmissibility and secondary attack rate[1]	Increased transmissibility[2]	Increased transmissibility[1]	Increased transmissibility and secondary attack rate[3,4,5]
Disease severity	Not confirmed, possible increased risk of hospitalization[6], severity and mortality[7]	Not confirmed, possible increased risk of in-hospital mortality[8,9]	Not confirmed, possible increased risk of hospitalization[10]	Not confirmed, possible increased risk of hospitalization[5]
Risk of reinfection	Neutralizing activity retained,[11] risk of reinfection remain similar[12,13]	Reduction in neutralizing activity reported; T cell response elicited by D614G virus remains effective[14–17]	Moderate reduction in neutralizing activity reported[18,19]	Reduction in neutralizing activity reported[20]
Impacts on diagnostics	Limited impact – S gene target failure (SGTF); no impact on overall result from multiple target RT-PCR, No impact on Ag RDTs observed[21]	No impact on RT-PCR or Ag RDTs observed[16]	None reported to date	None reported to date
Impacts on vaccine efficacy/effectiveness	Protection retained against disease • Severe disease: No/minimal loss: Pfizer BioNTech-Comirnaty[22–27] • Symptomatic disease: No/minimal loss: AstraZeneca-Vaxzevria, Novavax-Covavax, PfizerBioNTech-Comirnaty[23,24,27–30] • Infection: No/minimal loss: Pfizer BioNTech-Comirnaty[31] • Asymptomatic infection: No/minimal loss: Pfizer BioNTech-Comirnaty.[23,32] Inconclusive/moderate-substantial loss, limited sample size: AstraZeneca-Vaxzevria[29]	Reduced protection against disease; limited evidence • Severe disease: No/minimal loss: Janssen Ad26.COV 2.5, PfizerBioNTech-Comirnaty[24,33] • Mild-moderate disease: No/minimal loss: Janssen-Ad26. COV 2.5.[33] Moderate loss: Novavax-Covavax.[34] Inconclusive/ substantial loss, limited sample size: AstraZeneca-Vaxzevria[35] • Infection: Moderate loss: PfizerBioNTech-Comirnaty[24] • Asymptomatic infection: No evidence	Protection likely against disease; very limited evidence, on only one vaccine • Symptomatic Disease: No/minimal loss: Sinovac-CoronaVac[36,37] • Infection: No/minimal loss: Sinovac-CoronaVac[37]	Protection likely against disease; very limited evidence on only two vaccines • Symptomatic Disease: No/minimal loss: Pfizer BioNTech-Comirnaty, AstraZeneca- Vaxzevria.[38] Minimal/modest loss: *single dose* of PfizerBioNTech-Comirnaty, AstraZeneca-Vaxzevria[38]
Impacts on neutralization by vaccine	• No/minimal loss: Bharat-Covaxin, Gamaleya-Sputnik V, Moderna-mRNA-1273, Novavax-Covavax, Pfizer BioNTech-Comirnaty, BeijingCNBG-BBIBP-CorV, Sinovac-CoronaVac[17,38–63] • Minimal/moderate loss: AstraZeneca-Vaxzevria[29,53]	• Minimal/modest loss: Beijing CNBG-BBIBP-CorV, Sinovac-CoronaVac, Anhui ZL - Recombinant[64–66] • Minimal to substantial loss: Moderna-mRNA-1273, Pfizer BioNTech-Comirnaty[17,40,44,46–48,50,52–54,60,62,63,67–73] • Moderate to substantial loss: AstraZeneca-Vaxzevria, Gamaleya- Sputnik V, Janssen-Ad26.COV 2.5, Novavax-Covavax[46,55,70,70,74]	• No/minimal loss:AstraZeneca-Vaxzevria,Sinovac-CoronaVac[53,75] • Minimal/moderate loss: Moderna-mRNA-1273, Pfizer BioNTech-Comirnaty[17,40,41,50,52,53,59,62,76,77]	• Modest/moderate loss: Pfizer BioNTech Comirnaty, Bharat-Covaxin[60,78,79] (Note: sublineage of B.1.617 not specified in Bharat-Covaxin study) • Substantial loss: *single dose* of AstraZeneca-Vaxzevria[78]

*Generalized findings as compared to previously/co-circulating variants. Based on emerging evidence, including non-peer-reviewed preprint articles and reports, all subject to ongoing investigation and revision.

1 juin Heterologous ChAdOx1 nCoV-19 and BNT162b2 prime-boost vaccination elicits potent neutralizing antibody responses and T cell reactivity https://www.medrxiv.org/content/10.1101/2021.05.30.21257971v1	We here analyzed a cohort of 26 individuals aged 25-46 (median 30.5) years that received a ChAdOx1 nCoV-19 prime followed by a BNT162b2 boost after an 8-week interval for reactogenicity, antibody responses and T cell reactivity. The heterologous ChAdOx1 nCoV-19 / BNT162b2 prime-boost vaccination regimen is not associated with serious adverse events and results in a potent humoral immune response and elicits T cell reactivity. Antibody titers increased significantly over time resulting in strong neutralization titers 2 weeks after the BNT162b2 boost. Neutralizing activity against the prevalent strain B.1.1.7 was 3.9-fold higher than in individuals receiving homologous BNT162b2 vaccination, only 2-fold reduced for variant of concern B.1.351, and similar for variant B.1.617. In addition, $CD4^+$ and $CD8^+$ T cells reacted to SARS-CoV-2 spike peptide stimulus 2 weeks after the full vaccination. F 
21 mai Efficacy Estimates for Various COVID-19 Vaccines: What we Know from the Literature and Reports https://www.medrxiv.org/content/10.1101/2021.05.20.21257461v1.full	We find that, on average, the efficacy against any disease with infection is 85% (95% CI: 71 - 93%) after a fully course of vaccination. The VE against severe disease, hospitalization or death averages close to 100%. The average VE against infection, regardless of symptoms, is 84% (95% CI: 70 - 91%). We also find that the average VE against transmission to others for infected vaccinated people is 54% (95% CI: 38 - 66%). For B.1.1.7, VE is 86% (95% CI: 65 - 84%), which is just somewhat reduced compared to the wild type virus, but this VOC does not have a mutation that affects immunity. In contrast, the two other variants B.1.1.28 (P1) and B.1.351 have summary estimates of VE's of 61% (95% CI: 43 - 73%) and 56% (95% CI: 29 - 73%), respectively, that is considerably lower than the VE's for the wild type viruses.


Vaccine
Vaccine efficacy
B.1.1.7 (UK)
Pfizer
0.895 [0.859, 0.923]
Novavax*
0.856 [CI not reported]
AstraZeneca*
0.746 [0.416, 0.889]
Subgroup Estimate
0.850 [0.651, 0.936]
P.1 (Brazil)
Johnson & Johnson*
0.662 [0.510, 0.771]
Sinovac
0.496 [0.113, 0.714]
Subgroup Estimate
0.610 [0.433, 0.732]
B.1.351 (South Africa)
Pfizer
0.750 [0.705, 0.789]
Johnson & Johnson*
0.520 [0.303, 0.674]
Novavax*
0.494 [0.061, 0.728]
AstraZeneca*
0.219 [-0.499, 0.598]
Subgroup Estimate
0.563 [0.287, 0.732]
0.000
0.250
0.500
0.750
1.000
Vaccine efficacy (95% CI)

7 juin 2021

Publications sélectionnées

Titre	Extrait pertinent
6 juin Royaume-Uni Le variant Delta 40 % plus transmissible, selon le ministre de la Santé https://www.lapresse.ca/international/europe/2021-06-06/royaume-uni/le-variant-delta-40-plus-transmissible-selon-le-ministre-de-la-sante.php	« La meilleure estimation de l'avantage de croissance, comme nous l'appelons […] est d'environ 40 % », a-t-il déclaré sur la BBC, citant les travaux du groupe de scientifiques qui conseillent le gouvernement. Malgré une augmentation de nombre de nouveaux cas de COVID-19 ces derniers jours, dépassant les 5000 voire 6000 cas recensés quotidiennement, le nombre d'hospitalisations reste stable, a ajouté Matt Hancock. La majorité des hospitalisations concerne des patients qui n'ont pas été vaccinés, a-t-il assuré.
5 juin Most labs in Canada not fully able to detect Delta COVID-19 variant, experts warn https://globalnews.ca/news/7922969/covid-19-delta-variant-testing-canada/	According to Dr. Laurence Pelletier, a researcher from the Lunenfeld-Tanenbaum Research Institute at Mount Sinai Hospital, public health units across the provinces are, for the most part, not equipped with testing equipment that can fully sequence or identify some COVID-19 variants. (…) According to them, a majority of public health labs are using "more conventional" PCR tests that are limited due to them being only able to look at one or two specific mutations. While those tests work well for variants of concern like the Alpha B.1.1.7, those with three or more mutations like the Delta variant can't be distinguished. (…) "The obvious answer to that is no, there's not enough variant testing across Canada and there's not even enough in Ontario, to be honest," said Pelletier, who worked alongside Wrana and Mount Sinai's Dr. Tony Mazzulli to screen over 11,000 positive cases from all across the Greater Toronto Area. (…) because of the difficulties in identifying variants with more mutations, public health units like the ones in Ontario and many other provinces are having difficulty in pinpointing which exact ones were spreading. According to Dr. Gerald A. Evans, the chair of infectious diseases at Queen's University, the Delta variant's lack of the N501Y mutation and inclusion of E484Q and L452R mutations made it harder for labs to screen. (…)
4 juin La 2e dose est vitale contre les variants, dit Dre Tam https://www.lapresse.ca/covid-19/2021-06-04/la-2e-dose-est-vitale-contre-les-variants-dit-dre-tam.php	Les données préliminaires publiées la semaine dernière par Public Health England laissent croire que les vaccins contre la COVID-19 de Pfizer-BioNTech et Oxford-AstraZeneca sont efficaces contre le nouveau variant après deux doses, mais une efficacité moindre a été montrée avec une seule dose. Vendredi, 65 % des Canadiens admissibles avaient reçu au moins une dose d'un vaccin contre la COVID-19, mais les

	traqueurs de vaccins montrent qu'environ seulement 7 % de la population admissible était entièrement vaccinée. (…) ». « Il est donc très important d'obtenir cette deuxième dose lorsque des variants comme le delta sont dans notre communauté. » Vendredi, les données sur le nombre de cas du variant delta détectés au Canada n'étaient pas disponibles sur le site web de l'Agence de la santé publique du Canada. (…) « L'impact du variant B.1617 et de ses sous-lignées est toujours en cours d'évaluation au Canada, où le variant a été détecté dans les dix provinces et dans un territoire », peut-on lire.
4 juin Delta variant may lead to higher rates of hospitalisation, PHE warns https://www.independent.co.uk/news/health/covid-delta-indian-variant-hospitals-b1859182.html	The Delta variant of coronavirus first identified in India may lead to an increased risk of hospitalisation compared to the UK's Alpha variant, Public Health England (PHE) has said. **En complement:** SARS-CoV-2 variants of concern and variants under investigation in England: technical briefing 14 • **Prevalence**: In the week commencing 17 May 2021, the most recent week where sequencing data are complete, 61% of sequenced cases are Delta (B.1.617.2) • **Transmissibility:** Secondary attack rates for contacts of cases with Delta (B.1.617.2) and no travel history are higher than those for contacts of non-travel cases with Alpha (B.1.1.7): 12.4% (11.7% - 13.2%) [993/7,987] compared to 8.2% (8.0% - 8.4%) [6,295/76,948]. • **Immunity and reinfection**: During the period of time that Delta (B.1.617.2) became prevalent, there has been no increase in PCR-positive participants in the SIREN cohort overall (30% seropositive on recruitment, and now 95% vaccinated) and reinfections remain at very low numbers in individuals previously either PCR positive or seropositive • **Severity PHEngland**: Using stratified Cox proportional hazard regression, there was a significantly increased risk of hospitalisation within 14 days of specimen date (HR 2.61, 95% CI 1.56-4.36, p<0.001), and emergency care attendance or hospitalisation within 14 days (HR 1.67, 1.25-2.23, p<0.001), for Delta (B.1.617.2) cases compared to Alpha (B.1.1.7) cases after adjustment for confounders (age, sex, ethnicity, area of residence, index of multiple deprivation, week of diagnosis and vaccination status). • **Severity PHScotland**: There was an increased hazard ratio of hospitalisation for those who were S-gene

	positive compared with those with S gene target failure (2.39, 95% 1.72 to 3.31).

En complement: Risk assessment for SARS-CoV-2 variant: VOC-21APR-02 (B.1.617.2)

3 June 2021 Risk assessment for SARS-CoV-2 variant: Delta (VOC-21APR-02, B.1.617.2) Public Health England

Indicator	RAG*	Confidence	Assessment and rationale
Transmissibility between humans		HIGH	**Transmissibility appears greater than wild type (first wave) SARS-CoV-2** Delta continues to demonstrate a substantially increased growth rate compared to Alpha, across multiple analyses. Delta cases are rising whilst Alpha cases are declining. Secondary attack rates, including household secondary attack rates, are higher for Delta, but these are not yet corrected for vaccination status. There is in vitro evidence suggestive of increased replication in biological systems that model human airway. It is highly likely that Delta is significantly more transmissible than Alpha.
Infection severity		LOW	**Increased severity (hospitalisation risk) when compared to Alpha** Early evidence from England and Scotland suggests there may be an increased risk of hospitalisation compared to contemporaneous Alpha cases. A large number of cases are still within the follow up period. In some areas, hospital admissions show early signs of increasing, but the national trend is not clear.
Immunity after natural infection		LOW	**Experimental evidence of functional evasion of natural immunity but insufficient epidemiological data** Pseudovirus and live virus neutralisation using convalescent sera from first wave and Alpha infections shows a reduction in neutralisation. National reinfection surveillance data are being analysed. There is no increase in numbers of reinfections in the SIREN national healthcare worker cohort.
Vaccines		HIGH	**Epidemiological and laboratory evidence of reduced vaccine effectiveness** There are now analyses from England and Scotland supporting a reduction in vaccine effectiveness for Delta compared to Alpha. This is more pronounced after one dose (absolute reduction in vaccine effectiveness against symptomatic infection of approximately 15-20% after 1 dose). Iterated analysis continues to show vaccine effectiveness against Delta is higher after 2 doses but that there is a reduction for Delta compared to Alpha. There is a high level of uncertainty around the magnitude of the change in vaccine effectiveness after 2 doses of Oxford-AstraZeneca vaccine. Although this is observational data subject to some biases, it holds true across several analytic approaches and the same effect is seen in both English and Scottish data. It is strongly supported by pseudovirus and live virus neutralisation data from multiple laboratories. There are no data on whether prevention of transmission is affected and insufficient data to assess vaccine effectiveness against severe disease. The acquisition of an additional mutation which may be antigenically significant in a small number of cases is noted.
Overall assessment			Delta is predominant and all analyses find that it has a very substantial growth advantage. The observed high growth rate is most likely to be due to a combination of place based context, transmissibility and immune escape. Both English and Scottish analyses continue to support the finding of reduced vaccine effectiveness which has increased to high confidence. New early data from England and Scotland suggest a possible increased risk of hospitalisation compared to Alpha. The priority investigations are vaccine effectiveness against hospitalisation and transmission, household secondary attack rate corrected for vaccination, characterisation of the generation time, viral load and period of infectivity, and epidemiological studies of reinfections.

The therapeutics risk assessment is under review for all variants and is not included.
*refer to scale and confidence grading slide

4 juin COVID-19: une seule dose de Pfizer moins efficace contre certains variants, selon une étude https://www.journaldemontreal.com/2021/06/04/covid-19-une-seule-dose-de-pfizer-moins-efficace-contre-certains-variants-selon-une-etude	Après une seule dose de vaccin Pfizer contre la COVID-19, on est moins susceptible de produire des anticorps protecteurs face aux variants initialement détectés en Inde et en Afrique du Sud que face à celui initialement repéré en Angleterre, selon une étude en laboratoire. Publiée dans la revue médicale The Lancet, l'étude évalue la production d'anticorps protecteurs (dits « neutralisants ») de personnes vaccinées avec Pfizer/BioNTech (n=250). « Après une seule dose de Pfizer/BioNTech, 79 % des personnes avaient une réponse anticorps détectable contre la souche originale (et D614G), mais cela tombait à 50 % pour le variant Alpha (B.1.1.7), 32 % pour le variant Delta (B.1.617.2) et 25 % pour le variant Beta (B.1.351) », selon le Francis Crick Institute. Par ailleurs, l'étude publiée dans *The Lancet* montre qu'après deux doses du vaccin Pfizer, le niveau d'anticorps protecteurs est moins important en présence du variant Delta que des autres variants. Ces résultats corroborent ceux d'autres études, dont l'une de l'Institut Pasteur en France. **En complément (3 juin)** : Neutralising antibody activity against SARS-CoV-2 VOCs B.1.617.2 and B.1.351 by BNT162b2 vaccination

3 juin Le danger posé par le variant B.1.617 https://ici.radio-canada.ca/nouvelle/1798376/covid-19-variant-indien-delta-dangers-ontario	Le variant delta, détecté au départ en Inde, risque de devenir « prédominant » dans le Grand Toronto d'ici quatre semaines, selon le médecin hygiéniste de la région de Peel. (…) Le premier ministre ontarien Doug Ford a évoqué mercredi le risque de flambée de cas de COVID-19 liée à ce variant pour justifier sa décision de garder les écoles fermées jusqu'en septembre prochain. Selon l'estimation du Groupe ontarien pour le consensus en matière de modélisation et de conseils scientifiques, le variant B.1.617 représente maintenant 23 % des nouveaux cas de COVID-19 en Ontario. Le mathématicien Troy Day de l'Université Queen's, qui fait partie de ce groupe d'experts qui conseillent la province, raconte que le B.1.617 est en train de remplacer le variant B.1.1.7 (identifié à l'origine en Grande-Bretagne) qui a mené à la troisième vague en Ontario. Le Dr Lawrence Loh, le médecin hygiéniste de la région de Peel en banlieue de Toronto, presse le gouvernement provincial d'offrir les deuxièmes doses le plus rapidement possible et de songer à distribuer plus de doses dans les points chauds comme sa région. **En complément (5 juin)** Aux prises avec le variant Delta, Peel veut être prioritaire pour la 2e dose https://ici.radio-canada.ca/nouvelle/1798918/peel-variant-delta-vaccin-deuxieme-dose-ontario
2 juin B.C. experts urge caution during reopening, warn of delta variant 'wild card' https://bc.ctvnews.ca/b-c-experts-urge-caution-during-reopening-warn-of-delta-variant-wild-card-1.5454093	In its latest bi-monthly report, the B.C. COVID-19 Modelling Group hopes its latest analysis encourages decision-makers to slow down and scrutinize the behaviour of the B.1.617 variant, now known as the "delta variant." "The good news is B.C. continues to see the case numbers decline, which his fantastic, but the wild card is B.1.617.2," said co-author and UBC biomathematics professor Sally Otto. "That variant is spreading in India and really wreaking havoc there." "With currently dominant strains (P.1 and B.1.1.7), cases are projected to increase briefly and then turn around later in June, as vaccination levels rise," write the B.C. report's authors. "Vaccine effectiveness with B.1.617.2 with dosing schedule used in B.C. is unclear. Current level of community spread in B.C. of B.1.617.2 is uncertain." En complement: BC COVID-19 Data
2 juin Variant indien Seule la sous-lignée Delta jugée « préoccupante » https://www.lapresse.ca/covid-19/2021-06-01/variant-indien/seule-la-sous-lignee-	Seule une sous-lignée Delta (B.1.617.2) du variant de la COVID-19, détecté pour la première fois en Inde, est encore considérée comme « préoccupante », tandis que deux autres ont été rétrogradées, a indiqué mardi l'Organisation mondiale de la santé (OMS).

delta-jugee-preoccupante.php	L'OMS avait classé le mois dernier la totalité du variant comme « préoccupant », mais a indiqué mardi que seule une sous-lignée doit à présent être considérée comme telle. « Il est devenu évident que davantage de risques pour le public sont associés au B.1617.2, tandis que des taux de transmission moindres ont été observés avec les autres sous-lignées », a indiqué l'OMS dans son point épidémiologique hebdomadaire sur la pandémie. La sous-lignée B.1617.1 a en revanche été rétrogradée à la catégorie de « variant d'intérêt », et baptisée Kappa. Quant au B.1617.3, il n'est plus considéré comme intéressant par l'OMS et ne s'est pas vu attribuer de lettre grecque en raison de sa relative faible occurrence. Un nouveau variant, signalé samedi par les autorités sanitaires du Vietnam, semble être une déclinaison de Delta, a indiqué mardi la Dr Maria Van Kerkhove, responsable technique de la lutte contre la COVID-19 au sein de l'agence.

Fait saillants de la veille scientifique (pour le rapport génomique hebdomadaire du 7 juin)

1 juin 2021. L'Organisation mondiale de la santé (OMS) a reclassifié certains variants jugés préoccupants ou d'intérêt à la lumière des connaissances scientifiques actuelles. Concernant le variant ayant émergés en Inde, la lignée B.1.617.1 a été rétrogradée à variant d'intérêt (alias Kappa) et la lignée B.1.617.3 n'est plus considéré comme un variant d'intérêt, alors que la lignée B.1.617.2 demeure un variant préoccupant (alias Delta). Concernant le variant de lignée B.1.616 ayant émergé en France, il n'est plus considéré comme un variant d'intérêt. Par ailleurs, un nouveau variant dit « hybride » signalé au Vietnam, semble être une déclinaison de la lignée B.1.617.2 (Delta). Depuis la fin avril, le Vietnam a signalé une forte augmentation des cas de COVID-19, mais il n'existe pas de preuve que ce nouveau variant en soit à l'origine.

31 mai 2021. L'Organisation mondiale de la santé (OMS) utilise désormais, et recommande aux autorités de santé publique, l'usage de l'aphabet grec pour toutes les communications publiques concernant les variants préoccupants et variants d'intérêt dans le monde. Entre autres, Alpha pour désigner B.1.1.7 (émergence du Royaume-Uni), Beta pour désigner B.1.351 (émergence d'Afrique du Sud), Gamma pour désigner P.1 (émergence du Brésil) et Delta pour désigner B.1.617.2 (émergence de l'Inde). Si les 24 lettres sont attribuées, d'autres noms seront annoncés par cette organisation.

31 mai 2021. Suite aux recommandations de l'Institut national de santé publique du Québec (INSPQ), la lignée B.1.617 (incluant ses trois sous lignées B.1.617.1, B.1.617.2 et B.1.617.3) est classée variant préoccupant au Québec.

27 mai 2021. Selon les autorités de santé publique d'Angleterre (Public Health England), le variant de lignée B.1.617.2 continue de gagner en importance (43% des nouveaux cas séquencés selon le briefing technique no. 13) et pourrait remplacer le variant de lignée B.1.1.7, qui est prédominant dans ce pays. Cette progression serait attribuable à une combinaison de facteurs, dont le contexte de transmission (taux de contact) et les caractéristiques biologique du variant B.1.617.2 connues à ce jour selon les données épidémiologiques : une transmissibilité accrue (jusqu'à 50 %) et une efficacité vacinale réduite, notamment après une dose (environ 33 % contre 50 %) comparativement à la lignée B.1.1.7. Des cas de réinfection avec le variant B.1.617.2 ont été détectés en Angleterre, mais sans preuve d'une augmentation du risque de réinfection, selon une étude de cohorte chez les travailleurs de la santé (95% vaccinés). Les impacts de la lignée B.1.617.2 sur la virulence de la COVID-19 sont encore à l'étude.

Références

La Presse. Variant indien, seule la sous-lignée Delta jugée « préoccupante », mis à jour le 2 juin 2021

Organisation mondiale de la santé (OMS). COVID-19 Weekly Epidemiological Update, 1 June 2021

Institut national de santé publique du Québec (INSPQ). État de situation sur le variant B.1.617 du SRAS-CoV-2 (émergent d'Inde) et recommandations pour en rehausser la surveillance au Québec

Public Health England. Risk assessment for SARS-CoV-2 variant: VOC-21APR-02 (B.1.617.2), 27 May 2021

Public Health England. SARS-CoV-2 variants of concern and variants under investigation in England: technical briefing 13, 27 May 2021

31 mai 2021

Webinaire à venir
1 juin à 12h - Vigie du virus SRAS-CoV-2 dans les eaux usées
Cliquez ici pour accéder au site Web du RÉESE et obtenir l'information

Publications sélectionnées

Titre	Extrait pertinent
31 mai L'OMS utilisera les lettres grecques pour nommer les variants https://www.journaldemontreal.com/2021/05/31/covid-19-loms-utilisera-les-lettres-grecques-pour-nommer-les-variants-oms	L'idée est d'avoir des noms « faciles à prononcer et à retenir », mais aussi d'éviter que le grand public et les médias utilisent des appellations « stigmatisantes et discriminatoires » faisant référence au lieu où les premiers cas de variant ont été détectés, a expliqué l'Organisation mondiale de la santé (OMS) dans un communiqué. Les noms scientifiques continueront d'exister car ils fournissent des données utiles aux experts, mais l'OMS ne les utilisera plus dans sa communication quotidienne. Et l'organisation encourage vivement les autorités nationales, les médias et autres à adopter les nouveaux noms. Ainsi, le variant B.1.1.7, d'abord identifié au Royaume-Uni, a été baptisé Alpha; le B.1.351, identifié pour la première fois en Afrique du Sud, devient Beta; et le variant P.1, détecté au Brésil, Gamma. L'OMS a donné deux noms différents aux sous-lignées distinctes du variant B.1.617, qui a ravagé l'Inde et s'est étendu à des dizaines de pays: B.1.617.2 devient ainsi Delta, et B.1.617.1 devient Kappa. **En complement - 31 mai** WHO announces simple, easy-to-say labels for SARS-CoV-2 Variants of Interest and Concern
29 mai Un nouveau variant découvert au Vietnam. https://www.lapresse.ca/international/asie-et-oceanie/2021-05-29/covid-19/un-nouveau-variant-decouvert-au-vietnam.php#	« Nous avons découvert un variant hybride combinant le virus indien et le britannique », a déclaré samedi le ministre de la Santé, Nguyen Thanh Long, lors d'une réunion nationale sur la pandémie. « La caractéristique principale de ce virus est qu'il se transmet rapidement dans l'air. La concentration de virus dans la gorge et la salive augmente rapidement, et il se répand très vite dans l'environnement proche », a-t-il expliqué. Il n'a pas précisé le nombre de cas attribuables à ce nouveau variant, dont les caractéristiques seront prochainement publiées, a-t-il déclaré, pour l'ajouter à la carte des variants dans le monde.
29 mai	Le vaccin Pfizer produit des anticorps qui sont capables de neutraliser le variant indien du coronavirus, avec cependant

Variant indien « Efficacité légèrement diminuée » pour le vaccin Pfizer https://www.lapresse.ca/covid-19/2021-05-29/variant-indien/efficacite-legerement-diminuee-pour-le-vaccin-pfizer.php	une « efficacité légèrement diminuée » en laboratoire, selon une étude de chercheurs de l'Institut Pasteur. Chez les personnes vaccinées avec deux doses du vaccin Pfizer, les anticorps présents dans leur sérum sanguin sont efficaces sur le variant anglais, mais légèrement moins efficaces contre le variant indien étudié, selon ces travaux parus sur le site de prépublication BioRxiv. « les sérums de patients ayant eu un COVID-19 et recueillis jusqu'à 12 mois après les symptômes ainsi que les personnes ayant reçu le vaccin Pfizer restent neutralisants, mais sont 3 à 6 fois moins puissants contre le (variant indien) B.1617.2 par rapport au B.1.1.7 » (variant anglais). Les résultats de l'étude, réalisée avec des hôpitaux universitaires français, montrent qu'une dose du vaccin AstraZeneca, un vaccin efficace contre le variant anglais, « fonctionne très peu contre les variants indiens et sud-africains ». **En complément - 27 mai** Reduced sensitivity of infectious SARS-CoV-2 variant B.1.617.2 to monoclonal antibodies and sera from convalescent and vaccinated individuals
28 mai 25 cas du variant indien confirmés au Québec https://www.tvanouvelles.ca/2021/05/28/covid-19-25-cas-de-variants-indien-confirmes-au-quebec	Selon des scénarios présentés vendredi par l'Institut national de santé publique du Québec (INSPQ), une adhésion faible de la population aux mesures sanitaires toujours en place malgré le déconfinement pourrait entraîner une recrudescence «importante» des hospitalisations d'ici l'été. Les personnes jeunes, puisqu'encore non vaccinées en majorité, seraient alors susceptibles d'être affectées par cette hausse des cas. Par ailleurs, la majorité des 25 cas de variant indien détectés au Québec sont issus de voyageurs ayant été testé à la frontière. « Nous n'avons pas de signe de circulation communautaire accélérée de ce variant », a expliqué la Dre Jocelyne Sauvé. Toujours selon madame Sauvé, près de 25 cas de ce variant sont confirmés sur le territoire québécois à ce jour. Les données sur les variants seront mis à jour officiellement lundi prochain. **En complément - 31 mai 2021** Données sur les variants du SRAS-CoV-2 au Québec INSPQ

27 mai
Risk assessment for SARS-CoV-2 variant: VOC-21APR-02 (B.1.617.2)
https://www.gov.uk/government/publications/investigation-of-sars-cov-2-variants-of-concern-variant-risk-assessments

27 May 2021 Risk assessment for SARS-CoV-2 variant: VOC-21APR-02 (B.1.617.2) **Public Health England**

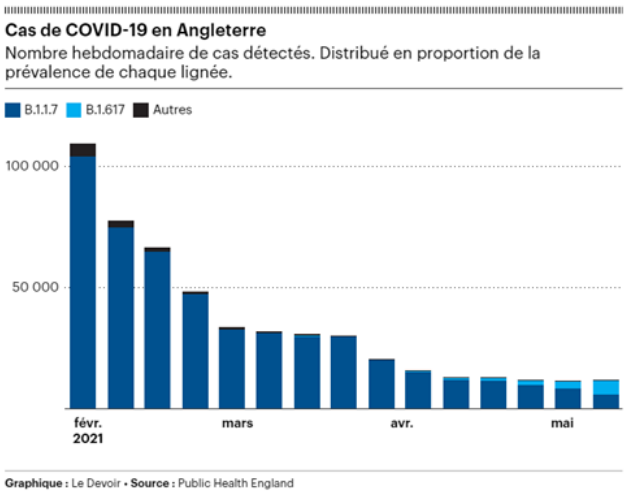
Indicator	RAG*	Confidence	Assessment and rationale
Transmissibility between humans		HIGH	**Transmissibility appears greater than wild type (first wave) SARS-CoV-2** There is an increased growth rate compared to B.1.1.7 in the current context. Secondary attack rates, including household secondary attack rates, are higher for B.1.617.2, but these are not yet corrected for vaccination status. There is in vitro evidence suggestive of increased replication in biological systems that model human airway. The observed epidemiological growth rate and replacement of B.1.1.7 are unlikely to be due entirely to immune escape, given the improved understanding of antigenic change; it is likely that B.1.617.2 is more transmissible than B.1.1.7. The magnitude of the change in transmissibility remains uncertain.
Infection severity			**Insufficient information** Most cases are recent and there has been insufficient follow up time to allow an assessment of severity. Early warning signals are being monitored with no evidence of increases in hospitalisation in national data.
Immunity after natural infection		LOW	**Experimental evidence of functional evasion of natural immunity but insufficient epidemiological data** Pseudovirus and live virus neutralisation using convalescent sera from first wave and B.1.1.7 infections shows a reduction in neutralisation. There are small numbers of reinfections detected through national surveillance which would be expected with a prevalent variant. These are being further investigated. There is no signal of an increase in reinfections in individuals in a national healthcare worker cohort study (95% vaccinated); monitoring continues.
Vaccines		MODERATE	**Epidemiological and laboratory evidence of reduced vaccine effectiveness** National vaccine effectiveness monitoring shows a reduction in vaccine effectiveness against symptomatic infection after 1 dose of vaccine for B.1.617.2 compared to B.1.1.7 (moderate confidence).Current data suggest this is an absolute reduction of approximately 20% after 1 dose. Iterated analysis continues to show vaccine effectiveness is higher after 2 doses with a small reduction for B.1.617.2 (moderate confidence). Although this is observational data subject to some biases, it holds true across several analytic approaches and is consistent with observed outbreaks. It is now strongly supported by pseudovirus and live virus neutralisation data from multiple laboratories. There are no data on whether prevention of transmission is affected and insufficient data to assess vaccine effectiveness against severe disease. The acquisition of an additional mutation which may be antigenically significant in a small number of cases is noted. Monitoring continues.
Overall assessment			B.1.617.2 has continued to replace B.1.1.7 and there are now clusters of areas with clearly growing incidence of B.1.617.2. There are also areas where there are limited S gene target data which may obscure the most recent expansion of the outbreak. The observed growth rate is most likely to be due to a combination of place based context, transmissibility and immune escape. The priority investigations are vaccine effectiveness against hospitalisation and transmission, household secondary attack rate corrected for vaccination, characterisation of the generation time, viral load and period of infectivity, epidemiological studies of reinfection and comparative severity analyses.

The therapeutics risk assessment is under review for all variants and is not included.
*refer to scale and confidence grading slide

En complement – 24 mai
Effectiveness of COVID-19 vaccines against the B.1.617.2 variant

26 mai
Le variant B.1.617 est responsable de la moitié des cas de COVID-19 en Angleterre.
https://www.ledevoir.com/societe/science/604493/le-variant-b-1-617-est-responsable-de-la-moitie-des-cas-de-covid-19-en-angleterre

Apparu en Inde, le variant B.1.617 n'y est pas cantonné. Il est responsable, selon les dernières données disponibles, d'environ la moitié de la transmission de la COVID-19 en Angleterre. Dans certaines régions de cette nation britannique, la progression de ce variant est très rapide. Toutefois, une précision s'impose : le nombre total de nouveaux cas dans ce pays ne suit pas une tendance à la hausse. Le variant B.1.1.7, largement dominant durant l'hiver et le début du printemps, est en train de perdre son hégémonie. Le variant B.1.617 (indien) gagne en importance depuis avril, mais n'a pas la même aisance à décoller que son cousin anglais, l'automne dernier, quand la campagne de vaccination n'était pas encore commencée.



En complément - 27 mai
SARS-CoV-2 variants of concern and variants under investigation in England: technical briefing 13

26 mai L'histoire «génétique» du variant P.1, très virulent au Brésil https://www.ledevoir.com/societe/science/604499/l-histoire-genetique-du-variant-p-1-tres-virulent-au-bresil	Une étude très fouillée parue ce lundi dans Nature Medicine raconte maintenant l'histoire « génétique » de ce variant. Les auteurs ont analysé en détail la signature génétique de 250 échantillons du virus prélevés chez des malades de l'Amazonas entre mars 2020 et janvier 2021. En observant l'apparition des différentes mutations, ils arrivent à reconstruire l'arbre évolutif menant au variant P.1. (…) un nouveau variant (B.1.1.28) a remplacé celui qui était en place (B.1.195), mais cela n'a pas modifié la dynamique de l'épidémie. Il pavait toutefois la voie au variant P.1, qui est apparu en novembre 2020. (…) Grâce à leurs nouvelles analyses, les chercheurs arrivent cependant à dire que le variant P.1 n'est pas apparu d'un coup chez un patient souffrant d'un très long épisode d'infection, mais plutôt à la faveur d'une accumulation de mutations chez des hôtes différents. **En complement - 25 mai** COVID-19 in Amazonas, Brazil, was driven by the persistence of endemic lineages and P.1 emergence E484K as an innovative phylogenetic event for viral evolution: Genomic analysis of the E484K spike mutation in SARS-CoV-2 lineages from Brazil
25 mai Le variant indien détecté dans au moins 53 territoires, selon l'OMS https://www.lapresse.ca/international/2021-05-25/covid-19/le-variant-indien-detecte-dans-au-moins-53-territoires-selon-l-oms.php	L'OMS a en outre reçu des informations, provenant de sources non officielles, selon lesquelles le variant B.1617 a été trouvé dans sept autres territoires, d'après les chiffres de la mise à jour épidémiologique hebdomadaire de l'agence de santé des Nations unies, portant le nombre total à 60. Selon le rapport, ce variant B.1617 manifeste une transmissibilité accrue tandis que la gravité des cas concernée est en cours d'étude.
25 mai Weekly epidemiological update on COVID-19 - 25 May 2021 WHO https://www.who.int/publications/m/item/weekly-epidemiological-update-on-covid-19---25-may-2021	In this edition, a special focus update is provided on SARS-CoV-2 Variants of Interest (VOIs) and Variants of Concern (VOCs) B.1.1.7, B.1.351, P.1, and B.1.617. **Table 3: Summary of phenotypic impacts* of Variants of Concern (VOCs), as of 25 May 2021** **VOC (lineage) / B.1.1.7 / B.1.351 / P.1 / B.1.617** **Transmissibility** — Increased transmissibility[1], Increased secondary attack rate[1] / Increased transmissibility[2] / Increased transmissibility[1] / Increased transmissibility[3,4] **Disease severity** — Not confirmed; possible increased risk of hospitalization[5], severity and mortality[6] / Not confirmed, possible increased risk of in-hospital mortality[7,8] / Not confirmed, possible increased risk of hospitalization[9] / Under investigation **Risk of reinfection** — Neutralizing activity retained[10], risk of reinfection remain similar[11,12] / Reduction in neutralizing activity reported. T cell response elicited by D614G prototype virus remains effective against B.1.351[13–15] / Moderate reduction in neutralizing activity reported[16,17] / Under investigation, possible modest reduction in neutralization activity (B.1.617.1)[4] **Impacts on diagnostics** — Limited impact – S gene target failure (SGTF; no impact on overall result from multiple target RT-PCR, No impact on Ag RDTs observed. [18] / No impact on RT-PCR or Ag RDTs observed[16] / None reported to date / None reported to date **Generalized findings as compared to wildtype/non-VOC viruses. Based on emerging evidence, including nonpeer-reviewed preprint articles and reports, all subject to ongoing investigation and revision.*

Table 4. Summary of vaccine performance against Variants of Concern (VOC) relative to previously circulating (non-VOC) variants

B.1.1.7	B.1.351	P.1	B.1.617
Efficacy/effectiveness against disease or infection			
Protection retained against disease Severe disease: No/minimal loss: Pfizer BioNTech-Comirnaty[21–25] Symptomatic Disease & Infection: No/minimal loss: AstraZeneca- Vaxzevria, Novavax-Covavax, Pfizer BioNTech-Comirnaty[6–15] Asymptomatic infection: No/minimal loss: Pfizer BioNTech-Comirnaty[22,36] Inconclusive/Moderate-substantial loss, limited sample size:AstraZeneca-Vaxzevria[27]	Reduced protection against disease,limited evidence Severe disease: No/minimal loss: Janssen Ad26.COV 2.5, PfizerBioNTech-Comirnaty[23,37] Mild-moderate disease: Moderate loss: Janssen-Ad26.COV 2.5,Novavax-Covavax[37,38] Inconclusive/substantial loss, limitedsample size: AstraZeneca-Vaxzevria[39] Infection: Moderate loss: PfizerBioNTech-Comirnaty[23] Asymptomatic infection: No evidence	Protection likely against disease, very limited evidence on only one vaccine Symptomatic Disease: No/minimal loss: Sinovac-CoronaVac[40,41] Infection: No/minimal loss: Sinovac-CoronaVac[41]	Protection likely against disease (for B.1.617.2), very limited evidence on only two vaccines Symptomatic Disease: B.1.617.2: No/minimal loss: AstraZeneca- Vaxzevria after one dose and Pfizer BioNTech-Comirnaty after two doses[42] Minimal/modest loss: AstraZeneca- Vaxzevria after two doses[42]
Neutralization			
No/minimal loss: Bharat-Covaxin, Gamaleya-Sputnik V, Moderna- mRNA-1273, Novavax-Covavax, Pfizer BioNTech-Comirnaty, BeijingCNBG-BBIBP-CorV, Sinovac-CoronaVac[43–64] Minimal/moderate loss: AstraZeneca-Vaxzevria[27,58]	Minimal/modest loss: Beijing CNBG-BBIBP-CorV, Sinovac-CoronaVac, Anhui ZL - Recombinant[65–67] Minimal to substantial loss: Moderna-mRNA-1273, Pfizer BioNTech-Comirnaty[44,48,50–55,57–59,68–73] Moderate to substantial loss: AstraZeneca-Vaxzevria, Gamaleya-Sputnik V, Novavax-Covavax[50,60,70,70]	No/minimal loss: AstraZeneca-Vaxzevria, Sinovac-CoronaVac [58,74] Minimal/moderate loss: Moderna-mRNA-1273, Pfizer BioNTech-Comirnaty[44,45,55,57,58,64,75,76]	B.1.617 (sublineage unspecified) Minimal/modest loss: Bharat-Covaxin[77] B.1.617.1: Minimal/modest loss: SII - Covishield[78] Modest/moderate loss: Moderna- mRNA-1273, Pfizer BioNTech-Comirnaty[73,79,80] B.1.617.2, B.1.617.3: No sublineage-specific evidence

24 mai

ECDC - SARS-CoV-2 variants of concern as of 24 May 2021 https://www.ecdc.europa.eu/en/covid-19/variants-concern

Variants of concern (VOC)

Lineage + additional mutations	Country first detected (community)	Spike mutations of interest	Year and month first detected	Evidence for impact on transmissibility	Evidence for impact on immunity	Evidence for impact on severity	Transmission in EU/EEA
B.1.1.7	United Kingdom	N501Y, D614G, P681H	September 2020	Yes (v) [1]	Unclear [2]	Yes (v) [3, 4]	Dominating
B.1.1.7+E484K	United Kingdom	E484K, N501Y, D614G, P681H	December 2020	Yes (v) [1]	Neutralisation (v) [2, 5]	Yes (v) [3]	Outbreaks
B.1.351	South Africa	K417N, E484K, N501Y, D614G, A701V	September 2020	Yes (v) [6]	Escape (v) [7, 8]	Yes (v) [4, 9]	Community
P.1	Brazil	K417T, E484K, N501Y, D614G, H655Y	December 2020	Yes (v) [10]	Neutralisation (v) [11]	Yes (v) [4]	Community
B.1.617.2	India	L452R, T478K, D614G, P681R	December 2020	Yes (v) [12-14]	Escape (v) [15]		Community

Variants of interest (VOI)

Lineage + additional mutations	Country first detected (community)	Spike mutations of interest	Year and month first detected	Evidence for impact on transmissibility	Evidence for impact on immunity	Evidence for impact on severity	Transmission in EU/EEA
B.1.525	Nigeria	E484K, D614G, Q677H	December 2020		Neutralisation (m) [5]		Community
B.1.427/B.1.429	USA	L452R, D614G	September 2020	Unclear [12]	Neutralisation (v) [12]		Sporadic/Travel
P.3	The Philippines	E484K, N501Y, D614G, P681H	January 2021	Yes (m) [1]	Neutralisation (m) [5]		Sporadic/Travel
B.1.616	France	V483A, D614G, H655Y, G669S	February 2021	Detection (c) [13]			Single outbreak
B.1.617.1	India	L452R, E484Q, D614G, P681R	December 2020	Yes (v) [14]	Neutralisation (v) [15, 17]		Outbreaks
B.1.617.3	India	L452R, E484Q, D614G, P681R	February 2021	Yes (m) [1]	Neutralisation (m) [5, 12]		Not detected
B.1.620	Unclear (b)	S477N, E484K, D614G, P681H	February 2021		Neutralisation (m) [5, 14]		Outbreaks
B.1.621	Colombia	R346K, E484K, N501Y, D614G, P681H	January 2021	Yes (m) [1]	Neutralisation (m) [5]		Sporadic/Travel

24 mai France - Avis du Conseil scientifique COVID-19 - les variants B.1.617 dits « Indiens » https://solidarites-sante.gouv.fr/IMG/pdf/avis_conseil_scientifique_24_mai_2021.pdf	a. Le variant B.1.617.2 est en expansion rapide au Royaume-Uni, en particulier dans la communauté d'origine indienne. Il a un niveau de transmission élevé mais demeure sensible aux vaccins. b. Le variant B.1.617.2 est déjà présent en France sous forme de clusters en nombre limité. Ceci rappelle la situation dans laquelle nous étions avec la variant UK dès fin décembre 2020. c. L'élément stratégique essentiel est d'avoir une stratégie de dépistage très active via le criblage et le séquençage en optimisant les données issues des laboratoires publics et privés (voir annexe). Cette stratégie permet également de détecter les autres VOCs. d. Dès la découverte de cas, la stratégie mise en œuvre par la CNAM de « Tracer-Isoler-Accompagner » doit être particulièrement réactive. J **Autres variants à surveiller** : A noter que le pourcentage de virus présentant une mutation en 484 est en augmentation régulière depuis plusieurs semaines, faisant anticiper une circulation majoritaire de virus avec ces mutations dans quelques mois.
23 mai COVID-19: pourquoi certaines personnes entièrement vaccinées sont quand même infectées https://www.lesoleil.com/actualite/science/covid-19-pourquoi-certaines-personnes-entierement-vaccinees-sont-quand-meme-infectees-6e67536b863d36823c19dc1044d6f408	Les vaccins ne sont pas efficaces à 100 % pour freiner la transmission ou l'infection. Le risque que certaines personnes entièrement vaccinées soient infectées est faible, mais il faut s'attendre à ce que cela se produise. Plusieurs raisons peuvent expliquer les infections post-vaccination. (…) L'efficacité de ces réponses (immunitaires) est également variable. Elle dépend de plusieurs facteurs, notamment l'état de santé, la prise de médicaments ou l'âge. Les infections post-vaccination peuvent aussi être causées par des variants du virus qui échappent à la détection immunitaire et se développent même chez les personnes vaccinées.

	Une étude réalisée sur les infections post-vaccinales par le SARS-CoV-2 en Californie, a montré que les risques d'infection n'étaient pas plus élevés en raison des variants dans cette région. **En complément – 24 avril** Post-vaccination SARS-CoV-2 infections and incidence of the B.1.427/B.1.429 variant among healthcare personnel at a northern California academic medical center Karen B. Jacobson

Faits saillants – 26 mai 2021

SPÉCIAL : variant B.1.617 (Inde)

Selon les autorités de santé publique d'Angleterre (Public Health England), les vaccins actuels se révèlent efficaces contre les infections symptomatiques causées par le variant préoccupant B.1.617.2 ayant émergé en Inde (respectivement, 88% pour Pfizer/BioNTech et 60% pour AstraZeneca/Oxford deux semaines après la deuxième dose).

Les résultats d'efficacité vaccinale pour le variant B.1.617.2 sont comparables à ceux observés contre les infections symptomatiques causées par le variant préoccupant B.1.1.7 ayant émergé au Royaume-Uni (respectivement, 93% pour Pfizer/BioNTech et 66% pour AstraZeneca/Oxford deux semaines après la deuxième dose).

Les données montrent toutefois une réduction de l'efficacité de ces vaccins après une seule dose contre les infections symptomatiques causées par le variant B.1.617.2 par rapport au variant B.1.1.7 (34% contre 51%, données combinées pour les deux vaccins).

Les données et périodes de suivi sont insuffisantes pour estimer l'efficacité de ces vaccins contre les infections sévères causées par le variant B.1.617.2.

La virulence des infections (risque d'hospitalisation ou de décès) associées au variant B.1.617.2 est en cours d'évaluation. Des cas de réinfection ont été détecté en Angleterre, mais sans preuve d'une augmentation du risque de réinfection selon une étude de cohorte chez les travailleurs de la santé (95% vaccinés).

Selon des analyses épidémiologiques en Angleterre, la transmissibilité du variant B.1.617.2 serait égale ou supérieure (jusqu'à 50%) à celle du variant préoccupant B.1.1.7.

Selon des analyses de laboratoire, la mutation L452R retrouvée dans la protéine de spicule du variant B.1.617.2 entrainerait une augmentation de l'infectivité du virus et une diminution de l'activité neutralisante des anticorps induits par une infection précédente ou la vaccination.

Le variant B.1.617.2 est maintenant retrouvé dans au moins 60 pays à travers le monde.

Références

Public Health England. Press release, Vaccines highly effective against B.1.617.2 variant after 2 doses, 22 May 2021

Public Health England. SARS-CoV-2 variants of concern and variants under investigation in England: technical briefing 12, 22 May 2021

Scientific Advisory Group for Emergencies. SAGE 89 minutes: Coronavirus (COVID-19) response, 13 May 2021

Deng, X., Garcia-Knight, M. A., Khalid, M. M., Servellita, V., Wang, C., Morris, M. K., et coll. (2021). Transmission, infectivity, and neutralization of a spike L452R SARS-CoV-2 variant. *Cell*.

World Health Organisation. Weekly epidemiological update on COVID-19, 25 May 2021

23 mai 2021

Article de presse	Extrait pertinent	Source scientifique
22 mai Vaccines highly effective against B.1.617.2 variant after 2 doses https://www.gov.uk/government/news/vaccines-highly-effective-against-b-1-617-2-variant-after-2-doses	Vaccine effectiveness against symptomatic disease from the B.1.617.2 variant is similar after 2 doses compared to the B.1.1.7 (Kent) variant dominant in the UK, and we expect to see even higher levels of effectiveness against hospitalisation and death. The study found that, for the period from 5 April to 16 May: • the Pfizer-BioNTech vaccine was 87.9% (95%CI: 78.2 to 93.2) effective against symptomatic disease from the B.1.617.2 variant 2 weeks after the second dose, compared to 93.4% (95%CI: 90.4 to 95.5) effectiveness against the B.1.1.7 variant • 2 doses of the AstraZeneca vaccine were 59.8% (95%CI: 28.9 to 77.3) effective against symptomatic disease from the B.1.617.2 variant compared to 66.1% (95% CI: 54.0 to 75.0) effectiveness against the B.1.1.7 variant • both vaccines were 33.5 (20.6 to 44.3) effective against symptomatic disease from B.1.617.2, 3 weeks after the first dose compared to around 50% effectiveness against the B.1.1.7 variant The analysis included data for all age groups from 5 April to cover the period since the B.1.617.2 variant emerged. It included 1,054 people confirmed as having the B.1.617.2 variant through genomic sequencing, including participants of several ethnicities. Data published on Thursday 20 May for vaccine effectiveness covered the period since December for those aged over 65. The difference in effectiveness between the vaccines after 2 doses may be explained by the fact that rollout of second doses of AstraZeneca was later than for the Pfizer-BioNTech vaccine, and other data on antibody profiles show it takes longer to reach maximum effectiveness with the AstraZeneca vaccine. As with other variants, even higher levels of effectiveness are expected against hospitalisation and death. There are currently insufficient cases and follow-up periods to estimate vaccine effectiveness against severe outcomes from the B.1.617.2 variant. PHE will continue to evaluate this over the coming weeks.	
21 mai Covid-19: UK cases of variant from India rise by 160% in a week	Failures in the government's test and trace system (between 17 April and 17 May) may have contributed to the spread of the B.1.617.2 variant in the UK, cases of which have risen by more than 160% in the past week. Cases of the B.1.617.2 variant, first detected in India, rose from 1313 to 3424 in the week to 19	

https://www.bmj.com/content/373/bmj.n1315	May, show data from Public Health England.1 The variant is still predominantly affecting the north west of England and London, but there are clusters across the country. A further variant, known as VUI-21MAY-01 or AV.1, has been designated by Public Health England as a "variant under investigation" on the basis of the mutation profile and apparent localised cluster in Yorkshire and Humber region (Spike: D80G, T95I, G142D, 144del, N439K, E484K, D614G, P681H, I1130V, D1139H) (Technical Briefing 12). There have been 49 cases of this variant across the country, mainly concentrated in Yorkshire and the Humber. It has been detected in the UK, Greece, and Chad, though its origin is unclear. Public Health England said that there was currently no evidence that covid-19 vaccines will be less effective in protecting people against either B.1.617.2 or AV.1. The government's Scientific Advisory Group for Emergencies (SAGE) has said it was a realistic possibility that the B.1.617.2 variant is as much as 50% more transmissible than the B.1.1.7 variant. SAGE 89 minutes: Coronavirus (COVID-19) response, 13 May 2021

We conducted a test-negative, case-control study of adults >=70 years of age from Sao Paulo State from January 17 to April 29, 2021, during which vaccination with a two-dose regimen of CoronaVac was implemented. We selected 7,950 matched pairs with a mean age of 76 years from 26,433 COVID-19 cases and 17,622 test-negative controls. Adjusted vaccine effectiveness was 18.2% (95% CI, 0.0 to 33.2) and 41.6% (95% CI, 26.9 to 53.3) in the period 0-13 and >=14 days, respectively, after the 2nd dose. Administration of a single vaccine dose was not associated with reduced odds of COVID-19. Vaccine effectiveness >=14 days after the 2nd dose declined with increasing age and was 61.8% (95% CI 34.8 to 77.7), 48.9% (95% CI 23.3 to 66.0) and 28.0% (95% CI 0.6 to 47.9) among individuals 70-74, 75-79 and >=80 years of age, respectively (p-interaction = 0.05). CoronaVac was 42% effective in the real-world setting of extensive P.1 transmission, but significant protection was not observed until completion of the two-dose regimen. These findings underscore the need to maintain non-pharmaceutical interventions when mass vaccination with CoronaVac is used as part of an epidemic response.	**21 mai** Effectiveness of the CoronaVac vaccine in the elderly population during a P.1 variant-associated epidemic of COVID-19 in Brazil: A test-negative case-control study Otavio T. Ranzani, https://www.medrxiv.org/content/10.1101/2021.05.19.21257472v1?rss=1%22

20 mai COVID-19 Les vaccins efficaces contre « tous les variants », dit l'OMS https://www.lapresse.ca/covid-19/2021-05-20/covid-19/les-vaccins-efficaces-	« Tous les variants du virus de la COVID-19 qui sont apparus jusqu'à présent répondent aux vaccins disponibles et approuvés » par l'OMS, a souligné Hans Kluge, le directeur de l'OMS Europe, au cours d'une conférence de presse en ligne. Interrogée sur l'efficacité du vaccin d'AstraZeneca sur le variant B.1351, identifié pour la première fois en Afrique du Sud, l'OMS estime que la vaccination avec ce sérum réduit les

contre-tous-les-variants-dit-l-oms.php	formes graves de COVID-19. « Bien qu'une confirmation dans des études de plus grande envergure soit nécessaire », l'AstraZeneca réduira toujours le nombre des hospitalisations et les morts liées au variant sud-africain, a déclaré jeudi l'OMS dans un courriel envoyé à l'AFP.
19 mai Erreur sur le premier cas de variant indien détecté au Québec https://www.journaldemontreal.com/2021/05/19/erreur-sur-le-premier-cas-de-variant-indien-detecte-au-quebec	L'Institut national de santé publique du Québec (INSPQ) a confirmé au *Journal* que le premier cas du variant B.1.617 (ou variant indien), détecté le 19 avril dernier sur le territoire Mauricie et du Centre-du-Québec, a fait l'objet d'une «classification erronée». Le Québec avait dépisté 11 cas de variant indien en date de vendredi dernier. Il nous a été impossible de savoir si la révision de ce cas avait une incidence sur ce bilan. (…) Selon l'INSPQ, cela s'explique par les ajustements du système international de classification de variants, surnommé le système «Pangolin». Celui-ci est mis à jour régulièrement pour affiner son efficacité. (…) Le virologue à la retraite Jacques Lapierre aimerait pour sa part que l'INSPQ, qui n'a pas dévoilé de nouveau bilan sur ce variant depuis vendredi dernier, dévoile plus d'informations. «Si ce n'est pas un cas de variant indien, il faudrait qu'ils nous disent c'est quoi. On aimerait avoir plus de détails sur ce variant-là étant donné qu'on soupçonne qu'il est plus dangereux que les autres.»
18 mai Le variant brésilien P.1 est bel et bien présent à Montréal https://www.ledevoir.com/societe/sante/602150/covid-19-le-variant-bresilien-prend-du-galon-a-montreal	Si rien n'indique que le variant indien B.1.617 est répandu à Montréal, ce n'est pas le cas des variants brésilien P.1 et sud-africain B.1.351, qui semblent désormais nourrir une transmission communautaire dans divers milieux de la métropole. C'est du moins ce que constate la Direction régionale de santé publique (DRSP) de Montréal, dont le dernier relevé rapporte un bond de 28 cas du variant brésilien P.1 dans la métropole en une semaine (de 60 à 88 cas). La province enregistre au total une hausse de plus de 30 % des cas de variant P.1 en sept jours (de 154 à 251), une augmentation concentrée dans la métropole, en Montérégie, dans les Laurentides et en Outaouais. Selon la Dre Sarah-Amélie Mercure, cheffe médicale par intérim du secteur Prévention et contrôle des maladies infectieuses à la DRSP de Montréal, il est clair que ce variant provoque des éclosions « atypiques », avec des taux de propagation élevés, notamment chez les gens vivant sous le même toit. Le variant P.1 a déjà fait irruption dans divers milieux de travail et de vie de la métropole, notamment à la résidence pour aînés Le Manoir Outremont, où on le soupçonne d'être en cause dans le décès de quatre résidents qui n'avaient toujours pas reçu leur 2e dose de vaccin anti-COVID. (…) Dès le début avril, la Colombie-Britannique affichait l'éclosion la plus importante du variant P.1 hors du Brésil, avec plus de 800 cas ; un mois plus tard, on en dénombre plus de 4400. L'Alberta suit avec plus de 2200 cas, puis l'Ontario, avec près

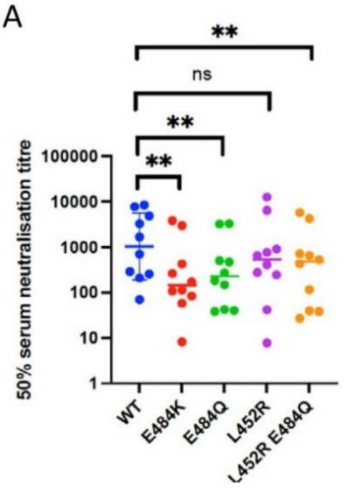
	de 2000 cas, indique le dernier relevé l'Agence de la santé publique du Canada.
17 mai Variant apparu en Inde - Les vaccins de Pfizer et Moderna devraient rester efficaces, selon des travaux préliminaires menés par des scientifiques américains https://www.lapresse.ca/covid-19/2021-05-17/variant-apparu-en-inde/les-vaccins-de-pfizer-et-moderna-devraient-rester-efficaces.php	**16 mai** The Spike Proteins of SARS-CoV-2 B.1.617 and B.1.618 Variants Identified in India Provide Partial Resistance to Vaccine-elicited and Therapeutic Monoclonal Antibodies Takuya Tada https://www.biorxiv.org/content/10.1101/2021.05.14.444076v1.full In this study, we addressed the questions of antibody resistance and variant spike protein affinity for ACE2 using lentiviruses pseudotyped by the B.1.617 (452R and E484Q mutations in the RBD in addition to D614G and the P681R) and B.1.618 (E484K in the RBD in addition to D614G and the N-terminal deletion Δ145-146) spike proteins. Analysis of the infectivity of each virus, normalized for particle number, on ACE2.293T cells showed that the B.1.617 spike protein (L452R/E484Q/P681R) was >2-fold increase in infectivity while B.1.618 was similar to wild-type D614G. Analysis of the individual mutations showed that the increased infectivity of the B.1.617 spike was attributed to L452R, which itself caused a 3.5-fold increase in infectivity and in combination with E484Q caused a 3-fold increase. The other individual point mutations had no significant effect on infectivity (Δ145-146, E484K, P681R) We found that the viruses with the B.1.617 and B.1.618 spike proteins were partially resistant to neutralization by convalescent serum antibody (2.3 and 2.5-fold) and vaccine-elicited antibodies (4 and 2.7-fold) (Pfizer and Moderna). The resistance was caused by the L452R, E484Q and E484K mutations. Δ145-146 and P681R had no significant effect on neutralization resistance. In addition, the neutralizing titer of the mixture of REGN10933 and REGN10987 was 4.7-fold decreased in neutralizing titer for virus with the B.1.617 spike while the neutralization of virus with the B.1.618 spike was unchanged
The outbreak of SARS-CoV-2 in minks has been observed recently, raising serious concerns over cross-species transmission and the emergence of variants capable of rendering antibody therapy and vaccines less effective. Here, the species tropism and antigenicity of the spike protein of ten variants were analyzed in pseudovirus-based assays involving 25 cell lines as well as 293T cells expressing ACE2 receptor from 14 species. No significant change in cellular tropisms was observed with the reported mink variants (compared to the currently	**17 mai** Cellular tropism and antigenicity of mink-derived SARS-CoV-2 variants Li Zhang https://www.nature.com/articles/s41392-021-00617-0

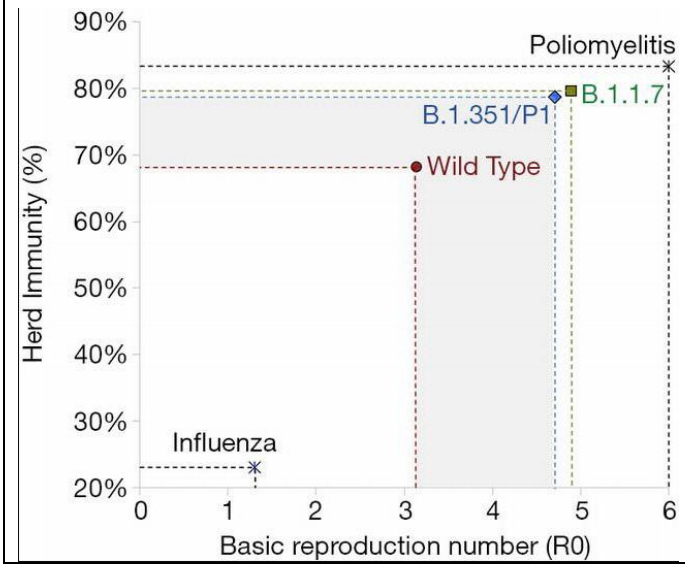
predominant D614G variant). We found 8 out of 25 cell lines from human or primates were susceptible to the infection by these variants. There was a slight increase of infectivity in 69-70del and A262S-containing variants, and significantly reduced infectivity of the cluster 5 variant. In neutralizing assays, variants bearing Y453F, F486L, and A262S demonstrated decreased reactivities to at least one monoclonal antibody (mAb). Notably, variants with F486L and other additional mutations were resistant to eight neutralizing mAbs in addition to some polyclonal antisera or convalescent plasma. Together, these findings indicate that these variants are similar to the human viral isolates in terms of infectivity and cellular tropisms, while decreased sensitivity of variants bearing F486L in conjunction with other mutations to neutralization by some mAbs and polyclonal antibody preparations warrants close monitoring of the ever-evolving viruses.	

17 mai 2021

Article de presse	Extrait pertinent	Source scientifique
16 mai Virus : Londres se dit confiant dans l'efficacité des vaccins contre le variant indien Londres se défend d'avoir traîné à agir face au variant indien https://www.lapresse.ca/international/europe/2021-05-16/virus-londres-se-dit-confiant-dans-l-efficacite-des-vaccins-contre-le-variant-indien-londres-se-defend-d-avoir-traine-a-agir-face-au-variant-indien.php **En complément** **13 mai** Coronavirus variant found in India may spread faster than type detected in Kent https://www.theguardian.com/world/2021/may/13/uk-covid-scientists-variant-found-in-india-variant-may-be-spreading-faster-than-kent-strain	Le nombre de cas attribués au variant indien dans le pays a plus que doublé en une semaine, grimpant à 1313 cette semaine, selon les autorités sanitaires. Ils se concentrent surtout dans le nord-ouest et à Londres. « Si les gens ont été vaccinés deux fois […] nous avons une certitude croissante, sur la base de premières données de laboratoire […], que les vaccins sont efficaces contre le variant indien », a souligné le ministre de la Santé, Matt Hancock, sur la BBC. Pour enrayer la propagation du variant B1.617.2, qui risque de devenir « dominant » selon les autorités sanitaires, l'intervalle entre les deux doses de vaccin (jusqu'à trois mois) est réduit à huit semaines pour les personnes de plus de 50 ans et les plus vulnérables, tandis que le dépistage a été renforcé dans les zones touchées. Malgré les appels à la prudence de scientifiques, le gouvernement a estimé qu'il n'y avait aucune raison de repousser l'assouplissement prévu lundi, avec le retour du service en salle dans les pubs et restaurants, la réouverture des lieux culturels et la reprise des voyages à l'étranger. Le comité scientifique conseillant le gouvernement (SAGE) a estimé qu'il existait une « possibilité réaliste » que le variant soit jusqu'à 50 % plus contagieux que celui apparu fin 2020 dans le sud-est en Angleterre (B.1.1.7).	
15 mai Le variant B.1.617 sous surveillance rehaussée https://www.ledevoir.com/societe/sante/601523/11-cas-de-variant-indien-confirmes-au-quebec	À l'instar du Canada, le Québec hissera cette souche sur la courte liste des variants sous surveillance rehaussée (VSSR) dès la semaine prochaine, selon l'Institut national de la santé publique du Québec (INSPQ). C'est le Laboratoire national de microbiologie (LNM) de Winnipeg qui a confirmé la détection de 11 cas de variant B.1.617 détectés au Québec, après le séquençage d'échantillons prélevés sur des voyageurs aux aéroports. (…) Le 22 avril dernier, un premier cas de variant B.1.617 avait été rapporté en Mauricie. (…) Jeudi, 26 travailleurs d'un chantier minier de l'île de Baffin au Nunavut ont été rapatriés par avion à Saint-Hubert en raison d'une éclosion, où l'on soupçonne des variants — dont le variant indien — d'être en cause, selon TVA. Ils ne font pas partie du décompte officiel des 11 cas de variant B.1.617 confirmés par séquençage.	
France - En date du 12 mai 2021, le lignage B.1.617 est désormais classé VOC. Cela concerne donc l'ensemble des		**12 mai**

trois sous-lignages B.1.617.1, B.1.617.2 et B.1.617.3, qui diffèrent légèrement en termes de mutations d'intérêt. (…) Ce lignage (…) a été classé comme VOC par l'OMS le 11 mai 20213 , et demeure à ce stade classé VOI par l'ECDC . Variants préoccupants (VOC) en France : • **20I/501Y.V1 (B.1.1.7)** 88,9% des séquences (Flash #7) • **20H/501Y.V2 (B.1.351)** 4,6% des séquences en métropole, 90% à la Réunion (Flash #7) • **20J/501Y.V3 (P.1)** 0,2% des séquences (Flash #7) 95% des séquences en Guyane (S16) • **20I/484K ou 484Q** (B.1.1.7 + E484K/Q) 0,9% des séquences (Flash #7) Diffusion communautaire en Bretagne (Finistère) et IDF • **20A/452R (B.1.617.1/2/3)*** Détections sporadiques et clusters familiaux. 24 épisodes impliquant au moins un cas de variant du lignage B.1.617 ont été rapportés.	Analyse de risque liée aux variants émergents de SARS-CoV-2 réalisée conjointement par le CNR des virus des infections respiratoires et Santé publique France Mise à jour partielle du 12/05/2021 concernant le lignage 20A/452R (B.1.617) https://www.santepubliquefrance.fr/media/files/01-maladies-et-traumatismes/maladies-et-infections-respiratoires/infection-a-coronavirus/analyse-de-risque-des-variants-emergents-de-sars-cov-2-12-05-21
12 mai Variant indien Les vaccins à ARN messager semblent efficaces https://www.lapresse.ca/covid-19/2021-05-12/variant-indien/les-vaccins-a-arn-messager-semblent-efficaces.php	Les vaccins anti-COVID-19 utilisant la technologie de l'ARN messager, comme ceux de BioNTech-Pfizer et Moderna, semblent efficaces contre le variant à l'origine d'une flambée des cas en Inde, a indiqué mercredi l'Agence européenne des médicaments (EMA). (…) L'agence s'est également montré optimiste concernant la capacité des vaccins fonctionnant sur la base d'un adénovirus, soit AstraZeneca/Oxford et Johnson & Johnson, à protéger contre ce variant. (…) attendre des données supplémentaires venant d'Inde où une version du vaccin AstraZeneca est administrée.
Covishield comprises the larger proportion in the vaccination program in India. (…) The neutralizing-antibody (NAb) titer against B.1.167.1 and prototype B.1 variant (D614G) was determined of the vaccine sera (4 weeks after second dose) of COVID-19 naïve subjects (n=43) . (…) A neutralization reduction factor of 1.94 (p-value <0.001) was observed between the B.1 (D614G) and B.1.617.1 variant.	**12 mai** Neutralization potential of Covishield vaccinated individuals against B.1.617.1 Pragya D. Yadav, https://www.biorxiv.org/content/10.1101/2021.05.12.443645v1?rss=1%22
In this study, using a live virus assay, we describe the neutralizing antibody response to the B.1.617.1 variant in serum from infected (n=24) and vaccinated (n=25) individuals. (…) We found that the B.1.617.1 variant is 6.5 to 7-fold (p-value <0.01) more resistant to neutralization by sera from COVID-19 convalescent and Moderna and Pfizer vaccinated individuals (reference virus : WA1/2020). Despite this, a majority of the sera from convalescent individuals (79%; 19/24 samples) and all sera from vaccinated individuals were still able to neutralize the B.1.617.1 variant.	**10 mai** Infection and vaccine-induced neutralizing antibody responses to the SARS-CoV-2 B.1.617.1 variant Venkata-Viswanadh Edara https://www.biorxiv.org/content/10.1101/2021.05.09.443299v1?rss=1%22
Three B.1.617 sub-lineages are characterised by L452R and P681R in spike. The number of sequenced isolates of B.1.617.1 and B.1.617.2 has been steadily increasing both	**9 mai**

globally and in India, though with the caveat of very low sequencing of prevalent cases. A high proportion of global sequences is from the UK where B.1.617.2 appears to be dominating imported cases and local transmissions. **Vaccine breakthrough in a Delhi health facility is dominated by B1.617.** During the wave of infections during March and April an outbreak of SARS-CoV-2 was confirmed in 33 vaccinated staff members at a single tertiary centre (age 27-77 years; AstraZeneca). Sequencing revealed the majority were B.1.617.2 with a range of other B lineage viruses including B.1.1.7. Importantly no severe cases were documented in this event. **B.1.617.1 Spike confers partial evasion of BNTl62b2 vaccine elicited antibodies.** We tested nine stored sera from Pfizer BNT162b2 vaccinees against a range of spike mutation bearing pseudotyped virus. As expected E484K conferred a ten-fold reduction in neutralisation by vaccine sera, and E484Q had a slightly milder yet significant impact. When E484Q and L452R were combined, there was a statistically significant loss of sensitivity as compared to wild type, but the fold change was similar to that observed with each mutation individually with no evidence for an additive effect. **P681R confers increased syncytium formation capability on B.1.617.1 spike.** B.1.617.1 spike bearing L452R, E484Q and P681R mediates entry into cells with slightly reduced efficiency compared to Wuhan-1. (…) Furthermore, we show that the P681R mutation significantly augments syncytium formation (cell-cell fusion activity) upon the B.1.617.1 spike protein, potentially contributing to increased pathogenesis observed in hamsters and infection growth rates observed in humans.	SARS-CoV-2 B.1.617 emergence and sensitivity to vaccine-elicited antibodies Isabella Ferreira (COG-UK) https://www.biorxiv.org/content/10.1101/2021.05.08.443253v1?rss=1%22 A 
B.1.617 was fully resistant against Bamlanivimab, a monoclonal antibody used for COVID-19 treatment. Both L452R and E484K are likely responsible. Bamlanivimab failed to inhibit entry driven by the S protein of variant B.1.351, as expected B.1.617 evaded, with moderate efficiency, antibodies induced by infection (~2-fold vs 6-fold for the B.1.351 variant) or vaccination with BNT162b2 vaccine (~ 3-fold reduction vs 11-fold for the B.1.351 variant). Collectively, our study reveals that antibody evasion of B.1.617 may contribute to the rapid spread of this variant.	**5 mai** SARS-CoV-2 variant B.1.617 is resistant to Bamlanivimab and evades antibodies induced by infection and vaccination Markus Hoffmann https://www.biorxiv.org/content/10.1101/2021.05.04.442663v1?rss=1%22
The threshold of herd immunity is substantially dependent on the R0 (i.e., the estimated number of subjects who could be infected by a single carrier in a vulnerable population), and could be estimated as: 1-1/R0.	**Avril 2021** How will emerging SARS-CoV-2 variants impact herd immunity? Giuseppe Lippi

• **Wild type**, R0 of approximately 3.14 • **B.1.1.7** : 56% increased transmission potential [95% credible interval (CrI), 50–74%] compared to the wild-type strain, (R0) of approximately 4.90 • **B.1.351** : 50% higher transmission potential (95% CrI, 20–113%), R0 of approximately 4.71 • **P.1** : ~50% increased transmissibility, and thereby by a predicted R0 comprised between 4.70–4.90 Owing to the fact that the R0 of the emerging SARS-CoV-2 variants B.1.1.7, B.1.351 and P1 (B.1.1.28.1) has been calculated at 50–56% higher than that of the wild type strain, this increased infective potential translates into the need for the herd immunity threshold to be further increased by around 10–12% without mitigating interventions, to achieve a new value approximating 80%.  	https://atm.amegroups.com/article/view/66312/html

10 mai 2021

Article de presse	Extrait pertinent	Source scientifique
10 mai Le variant découvert en Inde classé comme « préoccupant » par l'OMS https://www.lapresse.ca/covid-19/2021-05-10/le-variant-decouvert-en-inde-classe-comme-preoccupant-par-l-oms.php	« Il y a des informations selon lesquelles le B.1617 est plus contagieux », mais aussi des éléments qui permettent de penser qu'il atténue la réponse des anticorps qui permettent de combattre le virus, et « **par conséquent nous le classons en variant préoccupant au niveau mondial** », a déclaré la docteur Maria Van Kerkhove, responsable technique de la lutte contre la COVID-19 au sein de l'OMS. La scientifique a expliqué que plus de détails seraient publiés mardi dans le rapport épidémiologique hebdomadaire de l'agence onusienne, mais qu'il restait beaucoup de recherches à mener sur ce variant, notamment par le biais d'un séquençage accru, « pour savoir quelle quantité de ce virus circule », mais aussi le degré de « sévérité » avec lequel il atténue la réponse des anticorps. **En complément** PHE - SARS-CoV-2 variants of concern and variants under investigation in England: technical briefing 10 VUI-21APR-02 (B.1.617.2) was escalated to a **variant of concern** on 6 May 2021 (VOC21APR-02). There are insufficient data currently to assess the potential for immune escape. There has been a steep recent increase in the number of cases identified (N=509 genomically confirmed) of this variant of concern in the UK, which includes both imported (n=157 confirmed after travel) and domestically-acquired cases. CDC – SARS-CoV-2 Variant Classifications and Definitions The B.1.526, B.1.526.1, B.1.525, B.1.617, B.1.617.1, B.1.617.2, B.1.617.3, and P.2 variants circulating in the United States are classified as **variants of interest**. SPF - Classement des variants du SARS-CoV-2 en France, 05/05/2021 **Variant à suivre (VOI)** : 20A/452R (B.1.617.1/2/3)* Détections sporadiques chez des voyageurs revenant d'Inde	
8 mai Montréal - Une résidence happée par une éclosion liée à un variant https://www.lapresse.ca/covid-19/2021-05-08/montreal/une-residence-happee-par-une-eclosion-liee-a-un-variant.php	**Dix-huit personnes ont contracté la COVID-19 au Manoir Outremont à Montréal, aux prises avec une éclosion liée aux variants B.1.351 sud-africain ou P.1 brésilien.** Deux personnes âgées qui y habitaient en sont mortes. (…) Les premiers cas de COVID-19 ont été confirmés à la fin du mois d'avril au Manoir Outremont. (…) **Une première dose du vaccin avait été administrée le 12 février** dans cette résidence privée pour aînés qui possède plus de 350 chambres. La deuxième dose y a été administrée les 4 et 5 mai. (…) La Direction régionale de santé publique de Montréal n'a pas voulu donner de détails sur la source de l'éclosion pour des raisons de confidentialité.	
This is a preliminary evaluation of (Moderna) mRNA-1273 and mRNA-1273.351 given as boosters to individuals that had		**6 mai**

been vaccinated 6.2 to 6.7 months previously with mRNA-1273 in an amended phase 2 clinical trial of mRNA-1273. (…) Vaccination with both mRNA-1273 and mRNA-1273.351 boosters elicited higher neutralizing titers against the wild-type original strain and comparable titers against the B.1.351 and P.1 variants versus peak titers observed after the primary series vaccinations as measured against the wild-type virus (Figure 4E), suggesting that immune memory was induced by mRNA-1273 priming. Additionally, **the mRNA-1273.351 booster appeared to be more effective at increasing neutralization against the B.1.351 variant than a boost with mRNA-1273.**	Preliminary Analysis of Safety and Immunogenicity of a SARS-CoV-2 Variant Vaccine Booster https://www.medrxiv.org/content/10.1101/2021.05.05.21256716v1?rss=1%22
The BNT162b2 vaccine was effective against infection and disease in the population of Qatar, despite the B.1.1.7 and B.1.351 variants being predominant within the country; however, **vaccine effectiveness against the B.1.351 variant was approximately 20 percentage points lower (75.0% [95% CI, 70.5 to 78.9] than the effectiveness (>90%) reported in the clinical trial and in real-world conditions in Israel and the United States.** In Qatar, as of March 31, **breakthrough infections have been recorded in 6689 persons who had received one dose of the vaccine and in 1616 persons who had received two doses**. Seven deaths from Covid-19 have been also recorded among vaccinated persons: five after the first dose and two after the second dose. Nevertheless, the reduced protection against infection with the B.1.351 variant did not seem to translate into poor protection against the most severe forms of infection (i.e., those resulting in hospitalization or death), which was robust, at greater than 90%.	**5 mai** Effectiveness of the BNT162b2 Covid-19 Vaccine against the B.1.1.7 and B.1.351 Variants https://www.nejm.org/doi/full/10.1056/NEJMc2104974?af=R&rss=currentIssue
Of 6324 participants who underwent screening, 4387 received at least one injection of vaccine or placebo. Approximately 30% of the participants were seropositive for SARS-CoV-2 at baseline. Among 2684 baseline seronegative participants (94% HIV-negative and 6% HIV-positive), predominantly mild-to-moderate Covid-19 developed in 15 participants in the vaccine group and in 29 in the placebo group (vaccine efficacy, 49.4%; 95% confidence interval [CI], 6.1 to 72.8). Vaccine efficacy among HIV-negative participants was 60.1% (95% CI, 19.9 to 80.1). Of 41 sequenced isolates, 38 (92.7%) were the B.1.351 variant. **Post hoc vaccine efficacy against B.1.351 was 51.0% (95% CI, –0.6 to 76.2) among the HIV-negative participants.** Preliminary local and systemic reactogenicity events were more common in the vaccine group; serious adverse events were rare in both groups.	**5 mai** Efficacy of NVX-CoV2373 Covid-19 Vaccine against the B.1.351 Variant https://www.nejm.org/doi/full/10.1056/NEJMoa2103055?af=R&rss=currentIssue
Two doses of BNT162b2 are highly effective (≥92%; Israel, analysis period Jan 24 to April 3, 2021) across all age groups (≥16 years, including older adults aged ≥85 years) in	**5 mai** Impact and effectiveness of mRNA BNT162b2 vaccine

preventing symptomatic and asymptomatic SARS-CoV-2 infections and COVID-19-related hospitalisations, severe disease, and death, including those caused by the B.1.1.7 SARS-CoV-2 variant (estimated prevalence of the B.1.1.7 variant of 94·5% among SARS-CoV-2 infections). There were marked and sustained declines in SARS-CoV-2 incidence corresponding to increasing vaccine coverage. These findings suggest that COVID-19 vaccination can help to control the pandemic.	against SARS-CoV-2 infections and COVID-19 cases, hospitalisations, and deaths following a nationwide vaccination campaign in Israel: an observational study using national surveillance data https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(21)00947-8/fulltext
What is already known about this topic? B.1.526 emerged in November 2020 as a SARS-CoV-2 variant of interest in New York City (NYC). The presence of the E484K mutation is concerning because it has been shown to attenuate antibody neutralization in vitro. **What is added by this report?** The NYC Department of Health and Mental Hygiene analyzed laboratory and epidemiologic data to characterize cases of B.1.526 infection and the associated potential for breakthrough infection and reinfection. Preliminary evidence suggests that, to date, B.1.526 does not lead to more severe disease or increased risk for infection after vaccination. **What are the implications for public health practice?** Rapid integration of whole genome sequencing and population-based surveillance data is critical to characterizing new SARS-CoV-2 variants.	**5 mai** Rapid Emergence and Epidemiologic Characteristics of the SARS-CoV-2 B.1.526 Variant — New York City, New York, January 1–April 5, 2021 Corinne N. Thompson, https://www.cdc.gov/mmwr/volumes/70/wr/mm7019e1.htm?s_cid=mm7019e1_x
The recently reported “UK variant” (B.1.1.7) of SARS-CoV-2 is thought to be more infectious than previously circulating strains as a result of several changes, including the N501Y mutation. We present a 2.9-Å resolution cryo-electron microscopy (cryo-EM) structure of the complex between the ACE2 receptor and N501Y spike protein ectodomains that shows Y501 inserted into a cavity at the binding interface near Y41 of ACE2. **This additional interaction provides a structural explanation for the increased ACE2 affinity of the N501Y mutant, and likely contributes to its increased infectivity.** However, this mutation does not result in large structural changes, enabling important neutralization epitopes to be retained in the spike receptor binding domain. We confirmed this through biophysical assays and by determining cryo-EM structures of spike protein ectodomains bound to 2 representative potent neutralizing antibody fragments.	**29 avril** Cryo-electron microscopy structures of the N501Y SARS-CoV-2 spike protein in complex with ACE2 and 2 potent neutralizing antibodies https://journals.plos.org/plosbiology/article?id=10.1371/journal.pbio.3001237

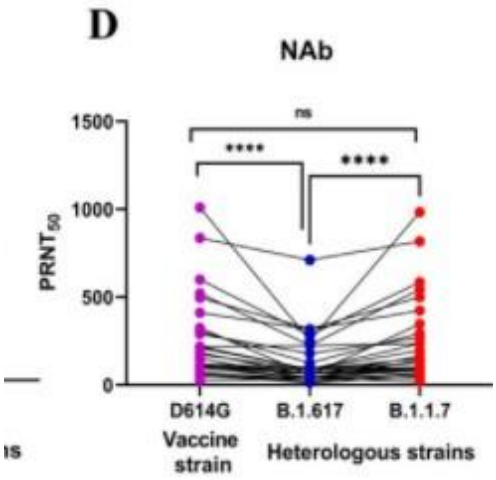
3 mai 2021

Article de presse	Extrait pertinent	Source scientifique
3 mai Peu d'infections à la COVID-19 chez les personnes vaccinées https://www.lapresse.ca/covid-19/2021-05-03/peu-d-infections-a-la-covid-19-chez-les-personnes-vaccinees.php	L'Agence de la santé publique du Canada (ASPC) a déclaré qu'en date du 26 avril, 2274 personnes avaient reçu un diagnostic de COVID-19 au moins deux semaines après avoir obtenu leur première dose de vaccin. À cette date, on estime qu'environ 7,1 millions de Canadiens avaient reçu au moins une première dose deux semaines plus tôt, ce qui signifie qu'il y a eu une infection chez environ 0,03 % des personnes vaccinées. Les personnes vaccinées représentent environ 1,3 % des infections à la COVID-19 depuis le début des vaccinations au Canada en décembre, indique l'agence. L'ASPC souligne que le nombre d'infections chez les personnes vaccinées est faible et que les données ne sont pas encore disponibles en détail pour bien comprendre les raisons de ces cas. **En complément** CDC - COVID-19 Breakthrough Case Investigations and Reporting. As of April 26, 2021, more than 95 million people in the United States had been fully vaccinated against COVID-19. During the same time, CDC received 9 245 reports of vaccine breakthrough infections from 46 U.S. states and territories.	
Here, we first analyze the prevalence of N440K variants within the sequences submitted from India and identify a rising trend of its spread across various clusters. We then compare the replicative fitness and infectivity of a prototype of this variant with two other previously prevalent strains. (…) A total of 1555 entries with N440K substitution could be identified from across the world. Interestingly, India contributed the largest proportion of N440K variants at 33%, followed by the USA and Germany (…) The N440K variant produced ten times higher infectious viral titers than a prevalent A2a strain.		**30 avril** N440K variant of SARS-CoV-2 has Higher Infectious Fitness Dixit Tandel https://www.biorxiv.org/content/10.1101/2021.04.30.441434v1?rss=1%22
LY-CoV1404 is a highly potent, neutralizing, SARS-CoV-2 spike glycoprotein receptor binding domain (RBD)-specific antibody identified from a convalescent COVID-19 patient approximately 60 days after symptom onset. In pseudovirus studies, LY-CoV1404 retains potent neutralizing activity against numerous variants including B.1.1.7, B.1.351, B.1.427/B.1.429, P.1, and B.1.526 and binds to these variants in the presence of their underlying RBD mutations (which include K417N, L452R, E484K, and N501Y).		**30 avril** LY-CoV1404 potently neutralizes SARS-CoV-2 variants Kathryn Westendorf https://www.biorxiv.org/content/10.1101/2021.04.30.442182v1.full
We investigated if single dose vaccination, with or without prior infection, confers cross protective immunity to variants. We analyzed T and B cell responses after first dose vaccination with the Pfizer/BioNTech mRNA vaccine BNT162b2 in healthcare workers (HCW) followed longitudinally, with or without prior Wuhan-Hu-1 SARS-CoV-2 infection. After one dose, individuals with prior infection		**30 avril** Prior SARS-CoV-2 infection rescues B and T cell responses to variants after first vaccine dose Catherine J. Reynolds

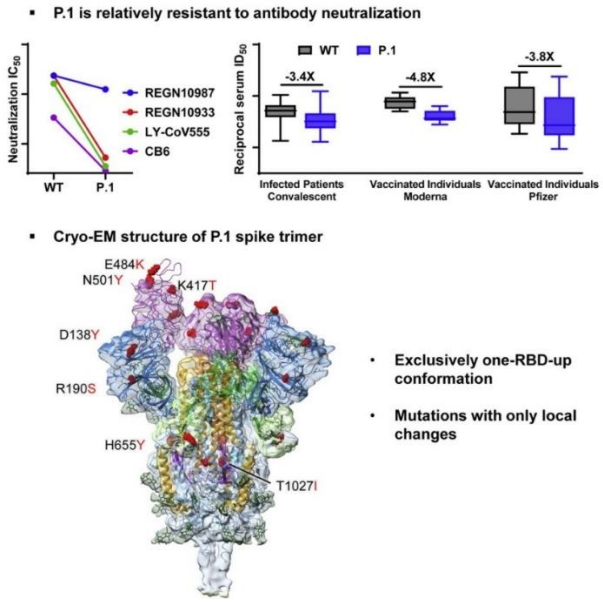
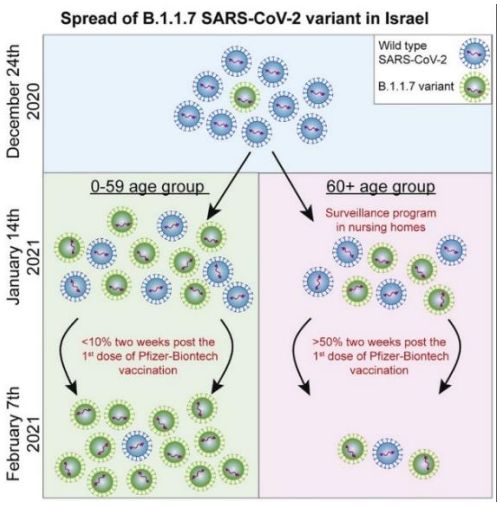
showed enhanced T cell immunity, antibody secreting memory B cell response to spike and neutralizing antibodies effective against B.1.1.7 and B.1.351. By comparison, HCW receiving one vaccine dose without prior infection showed reduced immunity against variants.	https://science.sciencemag.org/content/early/2021/04/29/science.abh1282
28 avril Hundreds of travellers tested positive for COVID-19 variants since mandatory hotel quarantines implemented https://nationalpost.com/news/hundreds-of-travellers-landing-in-canada-test-positive-for-covid-19-variants	More than 2,000 people returning to Canada since the federal government brought in mandatory hotel quarantines have tested positive for COVID-19 and more than a quarter of them were infected with a variant of concern. Data supplied to The Canadian Press by the Public Health Agency of Canada show that between Feb. 22 and April 22, 557 international air travellers tested positive for a variant of concern. Most of them, 518 cases, are the B.1.1.7 variant first identified in the United Kingdom, which is the dominant variant in Canada. Another 27 passengers tested positive for the B.1.351 variant first identified in South Africa, and 12 tested positive for the P.1 variant identified in Brazil.
28 avril L'Europe pourrait atteindre l'immunité collective d'ici août https://www.lapresse.ca/international/europe/2021-04-28/l-europe-pourrait-atteindre-l-immunite-collective-d-ici-aout.php	Alors que le seuil exact requis pour atteindre ce niveau critique de vaccination reste un sujet de débat, les experts estiment qu'un niveau supérieur à 70 % perturberait considérablement la transmission du virus au sein d'une population. Le patron du laboratoire BioNTech s'est dit mercredi « confiant » dans l'efficacité de son vaccin contre le variant indien de la COVID-19 qui suscite l'inquiétude au moment où l'Inde est débordée par une flambée épidémique. (…) Si des « tests » sont encore en cours, « le variant indien présente des mutations que nous avons déjà étudiées et contre lesquelles notre vaccin agit, ce qui nous rend confiants », a expliqué M. Sahin lors d'une conférence de presse en ligne.
27 avril Le variant indien détecté dans « au moins 17 pays », selon l'OMS https://www.lapresse.ca/covid-19/2021-04-27/le-variant-indien-detecte-dans-au-moins-17-pays-selon-l-oms.php	La modélisation préliminaire de l'OMS basée sur les séquences soumises au GISAID indique que « le B.1617 a un taux de croissance plus élevé que les autres variants en circulation en Inde, ce qui suggère une plus grande contagiosité ». L'OMS a récemment classifié ce variant comme un « variant d'intérêt » et non pas « un variant préoccupant ». Et ce variant suscite encore des interrogations. « D'autres conduites » peuvent aussi être à l'origine de la recrudescence des cas en Inde, avance l'OMS, comme le non-respect des restrictions sanitaires et les rassemblements de masse. L'Organisation souligne en outre que d'autres variants actuellement en circulation présentent également une grande contagiosité, mais que la combinaison de ces deux facteurs « pouvait jouer un rôle dans la résurgence des cas » en Inde.

26 avril 2021

Article de presse	Extrait pertinent	Source scientifique
25 avril La chasse aux variants https://www.lapresse.ca/actualites/sciences/2021-04-25/la-chasse-aux-variants.php **En complément** **18 avril** SRAS-CoV-2 : l'évolution du virus en direct https://ici.radio-canada.ca/nouvelle/1785576/virus-mutations-evolution-variants-covid-avenir-science	« À l'INSPQ, on en a cinq (variants « préoccupants) : ceux du Brésil, de la Grande-Bretagne, de l'Afrique du Sud, du Nigeria et de l'Inde. Il y a aussi d'autres variants à l'étude qu'on va peut-être inclure sur cette liste à surveillance rehaussée. Ce sont des variants qui sont soit plus transmissibles, soit plus graves. » (…) Une autre catégorie s'appelle « variants d'intérêt ». New York : un variant (B.1.526) (…) Brésil : Un autre variant brésilien, P2 (…) Californie : ici aussi, il s'agit de deux variants (B.1.427/429). (…) Selon Benoît Mâsse, épidémiologiste à l'Université de Montréal, les variants seraient de 50 % à 100 % plus transmissibles que les souches de la première vague. « Alors le seuil d'immunité collective n'est plus de 70 %, mais de 90 % maintenant avec des variants plus contagieux. » Selon M. Mâsse, par contre, quand de 35 % à 40 % de la population sera vaccinée, la situation sanitaire devrait commencer à s'améliorer.	
24 avril Vitesse élevée de propagation et variants La Dre Tam se dit « raisonnablement optimiste » https://www.lapresse.ca/covid-19/2021-04-24/vitesse-elevee-de-propagation-et-variants/la-dre-tam-se-dit-raisonnablement-optimiste.php	Selon les données de la Dre Tam, l'ensemble des hôpitaux canadiens ont admis en moyenne 4167 patients du 16 au 22 avril, une augmentation de 22 % par rapport à la semaine précédente. (…) Les unités de soins intensifs ne sont pas épargnées par la sévérité de l'actuelle vague de COVID-19. En moyenne quotidienne, 1268 personnes y ont été traitées, une hausse de 21 % par rapport à la semaine précédente. (…) Quant aux décès, la Dre Tam signale une hausse de 11 % au cours de la dernière période de sept jours. (…) Selon elle, l'augmentation du variant brésilien est aussi une source d'inquiétude. « Les données préliminaires indiquent que les vaccins pourraient ne pas être aussi efficaces contre le variant P.1, ce qui rend le contrôle de sa propagation encore plus important », ajoute-t-elle.	
The SIREN study is a prospective cohort study among staff (aged ≥18 years) working in publicly-funded hospitals in the UK. (…) 23 324 participants from 104 sites (all in England) met the inclusion criteria for this analysis and were enrolled. (…) A single dose of BNT162b2 vaccine showed vaccine effectiveness of 70% (95% CI 55–85) 21 days after first dose and 85% (74–96) 7 days after two doses in the study population. (…) Our findings show that the BNT162b2 vaccine can prevent both symptomatic and asymptomatic infection in working-age adults. (…) Given the dominance of the B.1.1.7 variant in England during the study period, which accounted for 50% or more positive tests in Pillar 2 laboratories since the beginning of December, 2020, in the South East, London, and East of England, and in all regions by early January 2021 (with Yorkshire and the Humber the last region), our findings suggest that the BNT162b2 is effective against the B1.1.7.		**23 avril** COVID-19 vaccine coverage in health-care workers in England and effectiveness of BNT162b2 mRNA vaccine against infection (SIREN): a prospective, multicentre, cohort study Victoria Jane Hall https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(21)00790-X/fulltext

Here, we report the isolation of SARS-CoV-2 of new lineage B.1.617 with several spike mutations from Maharashtra state, India. Among 146 COVID-19 cases, 15 retrieved SARS-CoV-2 sequences demonstrated the presence of a combination of L452R and E484Q mutations. (…) None of the cases developed the severe disease during infection and recovered completely in due course. Further, we investigated the neutralization efficiency of convalescent sera (n=17) and the sera collected from BBV152 (Covaxin) vaccinated individuals (n=28) against the B1(D614G) and B.1.617 variants.  For D614G vs. B.1.617, the GMT ratio was 1.95, (95% CI:1.60 - 2.38 and p-value <0.0001) resulting in a statistically difference. Similarly, the GMT ratio comparison of B.1.1.7 was significantly higher than the GMT for B.1.617 (GMT ratio 1.84, 95% CI: 1.50 - 2.27, p value< 0.0001) and the CI was not within the equivalence interval (**Figure 1 C** and **1D**). The comparison of D614G and B.1.1.7 showed equivalent responses with a GMT ratio of 1.06 which is close to 1, and the 95% CI (1.02 to 1.10) was well within the statistical equivalence.	**23 avril** Neutralization of variant under investigation B.1.617 with sera of BBV152 vaccinees Pragya D. Yadav https://www.biorxiv.org/content/10.1101/2021.04.23.441101v1.full **En complement** **24 avril** Convergent evolution of SARS-CoV-2 spike mutations, L452R, E484Q and P681R, in the second wave of COVID-19 in Maharashtra, India Sarah Cherian https://www.biorxiv.org/content/10.1101/2021.04.22.440932v1?rss=1%22 **20 avril** What do we know about India's Covaxin vaccine? *BMJ* 2021; 373 doi: https://doi.org/10.1136/bmj.n997 (Published 20 April 2021)
We compared 19,207 cases of SARS-CoV-2 variant B.1.1.7/S gene target failure (SGTF), 436 B.1.351 and 352 P.1 to non-variant cases reported by seven European countries. COVID-19 cases with these variants had significantly higher adjusted odds ratios for hospitalisation (B.1.1.7/SGTF: **1.7**, 95% confidence interval (CI): 1.0–2.9; B.1.351: **3.6**, 95% CI: 2.1–6.2; P.1: **2.6**, 95% CI: 1.4–4.8) and B.1.1.7/SGTF and P.1 cases also for intensive care admission (B.1.1.7/SGTF: **2.3**, 95% CI: 1.4–3.5; P.1: **2.2**, 95% CI: 1.7–2.8). B.1.351: **3.3** (1.9–5.7).	**22 avril** Characteristics of SARS-CoV-2 variants of concern B.1.1.7, B.1.351 or P.1: data from seven EU/EEA countries, weeks 38/2020 to 10/2021 separator commenting unavailable Tjede Funk https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2021.26.16.2100348?TRACK=RSS

The Kentucky Department for Public Health (KDPH) and a local health department investigated a COVID-19 outbreak in a SNF that occurred after all residents and health care personnel (HCP) had been offered vaccination. Among 83 residents and 116 HCP, 75 (90.4%) and 61 (52.6%), respectively, received 2 vaccine doses. Twenty-six residents and 20 HCP received positive test results for SARS-CoV-2, the virus that causes COVID-19, including 18 residents and four HCP who had received their second vaccine dose >14 days before the outbreak began. An R.1 lineage variant was detected with whole genome sequencing (WGS). Although the R.1 variant has multiple spike protein mutations (S:E484K, S:D614G, S:G769V, S:W152L), vaccinated residents and HCP were 87% less likely to have symptomatic COVID-19 compared with those who were unvaccinated. **En complement** **15 avril** CDC Identifies Small Group of Covid-19 Infections Among Fully Vaccinated Patients. approximately 5,800 cases of Covid-19 infection among more than 66 million Americans who have completed a full course of vaccination.(…) Of the breakthrough cases identified by the CDC, more than 40% occurred in people older than 60, while 65% of the cases were in female patients, according to Tom Clark, leader of the vaccine evaluation team at the federal agency. The CDC found that 29% of breakthrough infections were asymptomatic and 7% of patients experiencing a breakthrough infection were hospitalized. So far, 74 people have died after experiencing breakthrough infections. The agency is expected to publish some of these findings next week.	**21 avril** COVID-19 Outbreak Associated with a SARS-CoV-2 R.1 Lineage Variant in a Skilled Nursing Facility After Vaccination Program — Kentucky, March 2021 https://www.cdc.gov/mmwr/volumes/70/wr/mm7017e2.htm
In a cohort of 417 persons (employees at the Rockefeller University campus) who had received the second dose of BNT162b2 (Pfizer–BioNTech) or mRNA-1273 (Moderna) vaccine at least 2 weeks previously, we identified 2 women with vaccine breakthrough infection. Despite evidence of vaccine efficacy in both women, symptoms of coronavirus disease 2019 developed, and they tested positive for SARS-CoV-2 by polymerase-chain-reaction testing. Viral sequencing revealed variants of likely clinical importance, including E484K in 1 woman and three mutations (T95I, del142–144, and D614G) in both. In the clade analysis for Patient 1, the closest match was between clades 20B and 20C. The SARS-CoV-2 variant first identified in the United Kingdom (B.1.1.7) is clade B, and the variant first identified in New York City (B.1.526) is clade 20C.	**21 avril** Vaccine Breakthrough Infections with SARS-CoV-2 Variants Ezgi Hacisuleyman https://www.nejm.org/doi/full/10.1056/NEJMoa2105000
Highlights	**18 avril**

• P.1 is refractory to multiple neutralizing mAbs, including three out of the four with EUA (Emergency Use Authorization) • P.1 is relatively resistant to neutralization by convalescent plasma and vaccinee sera • Cryo-EM structure of P.1 spike trimer reveals exclusively one-RBD-up conformation 	Increased resistance of SARS-CoV-2 variant P.1 to antibody neutralization PengfeiWang https://www.sciencedirect.com/science/article/pii/S1931312821001839?via%3Dihub
Munitz et al., demonstrate that despite a 45% increased transmission of the B.1.1.7 SARS-CoV-2 variant, the Israeli vaccination program curtails its spread in elderly populations. Furthermore, pro-active surveillance programs likely enable the containment of viral spread in nursing homes. Thus, combined programs are achievable, reduce severe illness and subsequent death. 	**17 avril** BNT162b2 Vaccination Effectively Prevents the Rapid Rise of SARS-CoV-2 Variant B.1.1.7 in high risk populations in Israel https://www.cell.com/cell-reports-medicine/fulltext/S2666-3791(21)00080-X
We assessed humoral and T cell responses against SARS-CoV-2 WT and VOC and endemic human coronaviruses	**16 avril**

(hCoV) that were induced after single and double vaccination with BNT162b2. Despite readily detectable IgG against the receptor-binding domain (RBD) of the SARS-CoV-2 S protein at day 14 after a single vaccination, inhibition of SARS-CoV-2 S-driven host cell entry was weak and particularly low for the B.1.351 variant. Frequencies of SARS-CoV-2 specific T cells were low in many vaccinees after application of a single dose and influenced by immunity against endemic hCoV. The second vaccination significantly boosted T cell frequencies reactive for WT, B.1.1.7 and B.1.351 variants. These results call into question whether neutralizing antibodies significantly contribute to protection against COVID-19 upon single vaccination and suggest that cellular immunity is central for the early defenses against COVID-19.	Humoral and cellular immune responses against SARS-CoV-2 variants and human coronaviruses after single BNT162b2 vaccination Metodi V. Stankov https://www.medrxiv.org/content/10.1101/2021.04.16.21255412v1
This analysis was performed as part of the prospective COVID-19 Health Action Response for Marines study (CHARM). CHARM included predominantly male US Marine recruits, aged 18–20 years, following a 2-week unsupervised quarantine at home (n=3168). Among 189 seropositive participants, 19 (10%) had at least one positive PCR test for SARS-CoV-2 during the 6-week follow-up (1·1 cases per person-year). In contrast, 1079 (48%) of 2247 seronegative participants tested positive (6·2 cases per person-year). The incidence rate ratio was 0·18 (95% CI 0·11–0·28; p<0·001). Seropositive young adults had about one-fifth the risk of subsequent infection compared with seronegative individuals. Although antibodies induced by initial infection are largely protective, they do not guarantee effective SARS-CoV-2 neutralisation activity or immunity against subsequent infection.	**15 avril** SARS-CoV-2 seropositivity and subsequent infection risk in healthy young adults: a prospective cohort study Andrew G Letizia https://www.thelancet.com/journals/lanres/article/PIIS2213-2600(21)00158-2/fulltext
We investigated SARS-CoV-2 infection clusters involving 95 HCP (health care personnel) and 137 possible patient contact sequences. The majority of HCP infections could not be linked to a patient or co-worker (55/95; 57.9%) and were genetically similar to viruses circulating concurrently in the community. We found 10.5% of infections could be traced to a coworker (10/95). Strikingly, only 4.2% of HCP infections could be traced to a patient source (4/95).	**15 avril** Viral sequencing reveals US healthcare personnel rarely become infected with SARS-CoV-2 through patient contact Katarina M Braun https://academic.oup.com/cid/advance-article/doi/10.1093/cid/ciab281/6226897

19 avril 2021

Article de presse	Extrait pertinent	Source scientifique
19 avril What do we know about the Indian coronavirus variant? https://www.theguardian.com/world/2021/apr/19/what-do-we-know-about-the-indian-coronavirus-variant	**How was the variant discovered?** Scientists in India drew attention to the new variant as it gained ground in the western state of Maharashtra between December 2020 and March this year. On 24 March, the Indian health ministry reported that 15%-20% of coronavirus sequenced in the region – an early hotspot of the country's second wave – carried two unusual mutations: E484Q and L425R (escape mutations : Greaney et al. (2020); Li et al. (2020); Liu et al. (2020); Wang et al. (2021)). The figure has reportedly risen to more than 60% in the region since then. The variant has been named B.1.617. **When did it arrive in the UK?** Genomic surveillance in the UK found the Indian variant among samples dating back to February. Public Health England (PHE) said last week that it was aware of 73 cases in England and four in Scotland, but on Monday the health secretary, Matt Hancock, revised the figure up to 103. Most are linked to travel from India, but some cases have come about through transmission of the virus in people's homes. **How dangerous is the variant?** It is hard to tell. Last week, PHE declared it a "variant under investigation", a label given to potentially worrisome new variants that are not well understood. Scientists are now working to confirm whether or not the variant is more dangerous than others in circulation, for example by spreading more quickly, causing more severe disease or evading immunity built up from previous infection or vaccination. If lab studies, epidemiological analyses and other work confirms it to be more problematic, it will be upgraded to a "variant of concern".(…) That said, the mutations in the Indian variant are highly unlikely to render vaccines completely ineffective, because the shots induce such broad immune defences. **Are scientists worried?** Jeffrey Barrett, leader of the Covid-19 genomics initiative at the Sanger Institute, said the Indian variant may not be as problematic as other variants of concern, such as those first seen in South Africa and Brazil. The variant existed at low levels for months in India, and has cropped up in other places, without taking off rapidly, suggesting that it may not be as transmissible as the Kent variant that is now dominant in the UK, he said. (…) The concern is bolstered by the most recent data from Health Canada, which shows that passengers infected with coronavirus were found on all 27 flights arriving in Canada from Delhi between 4 and 14 April.	
19 avril	The full length of the study will be 12 months, including a minimum of eight follow-up appointments after discharge. The first phase, which will start in April 2021, will establish the	

Human challenge trial launches to study immune response to COVID-19 https://www.ox.ac.uk/news/2021-04-19-human-challenge-trial-launches-study-immune-response-covid-19	lowest dose of virus which, in approximately 50% of people who have previously been naturally infected, can take hold and start replicating but produce little or no symptoms. Up to 64 healthy participants between the ages of 18 – 30 who have previously been naturally infected with COVID-19 will be re-exposed to the virus in carefully controlled conditions. The virus used in the study will be the original strain from Wuhan, China. In the second phase of the study, expected to start in summer 2021, all participants will be infected with the standardised dose of virus which was established in phase one. The participants will be quarantined in a specially designed hospital suite for a minimum of 17 days under the care of the research team. They will undergo numerous medical tests including CT scans of the lungs and MRI scans of the heart. Any participants who develop any symptoms will be given medical treatment with the Regeneron monoclonal antibody treatment.
17 avril Soins intensifs - Les admissions en hausse, l'âge des patients en baisse https://www.lapresse.ca/covid-19/2021-04-17/soins-intensifs/les-admissions-en-hausse-l-age-des-patients-en-baisse.php	L'arrivée des variants au Québec se fait surtout sentir aux soins intensifs, où l'on observe une hausse de 82 % des admissions depuis un mois (de 91 à 167 patients), contre à peine 12 % aux soins réguliers (de 442 à 497 patients). Un intensiviste attribue également cette pression à des hospitalisations plus longues et à l'admission de patients atteints de la COVID-19 nettement plus jeunes que durant les précédentes vagues. « On voit qu'il y a moins de patients qui partent. Et comme on est en plein milieu de la troisième vague, certains sont traités pendant plusieurs semaines. »
17 avril Propagation dans plusieurs régions - Les variants représentent la quasi-totalité des cas https://www.lapresse.ca/covid-19/2021-04-17/propagation-dans-plusieurs-regions/les-variants-representent-la-quasi-totalite-des-cas.php	Les variants à l'origine de la flambée des cas observée au Québec ont progressé plus vite que ne le projetaient initialement les analystes du gouvernement. Ils représentent désormais la quasi-totalité des nouvelles infections par la COVID-19 recensées au quotidien dans plusieurs régions, alors que la métropole et ses environs semblent avoir mieux résisté à leur progression. **Des seuils atteints plus tôt.** Les modélisateurs de l'Université McGill et de l'INSPQ prévoyaient dans une analyse datée du 26 mars que 75 % des nouveaux cas d'infection à l'échelle provinciale seraient imputables aux variants près du 22 avril, et 100 %, fin juin. **Québec discret.** Le gouvernement s'est fait discret jusqu'à maintenant sur le fait que les variants représentent maintenant près de 100 % des cas dans plusieurs régions. Le ministre de la Santé et des Services sociaux, Christian Dubé, y a fait indirectement référence il y a quelques jours en annonçant son intention de réduire les tests de criblage dans les zones de la province les plus touchées pour permettre officiellement d'intensifier les tests de dépistage.
17 avril Le variant nigérian détecté à Québec: ce qu'il faut savoir	Aux côtés du très répandu variant britannique et de ceux d'Afrique du Sud et du Brésil, la souche du Nigéria fait partie des variants placés sous surveillance rehaussée par l'Institut national de santé publique du Québec (INSPQ).

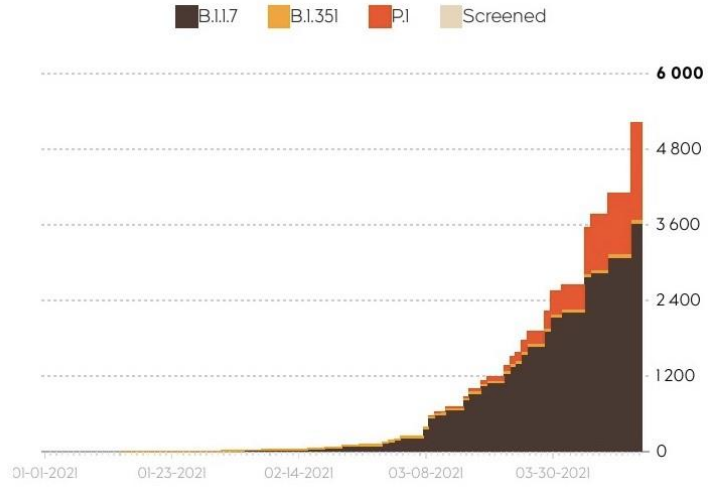
https://www.lesoleil.com/actualite/covid-19/le-variant-nigerian-detecte-a-quebec-ce-quil-faut-savoir-49aa35f99c4c5ea62b2116ab21640bc1

INSPQ

RÉGION SOCIOSANITAIRE (RSS)	B.1.1.7 ÉMERGENCE ROYAUME-UNI	B.1.351 ÉMERGENCE AFRIQUE DU SUD	P.1 ÉMERGENCE BRÉSIL	B.1.525 ÉMERGENCE NIGÉRIA	TOTAL
01 - Bas-Saint-Laurent	16				16
02 - Saguenay–Lac-Saint-Jean					
03 - Capitale-Nationale	153	2		3	158
04 - Mauricie et Centre-du-Québec	6				6
05 - Estrie	35				35
06 - Montréal	1 596	10	5	5	1 616
07 - Outaouais	174	2		5	181
08 - Abitibi-Témiscamingue		131			131
09 - Côte-Nord					
10 - Nord-du-Québec					
11 - Gaspésie–Îles-de-la-Madeleine					
12 - Chaudière-Appalaches	68				68
13 - Laval	133	3		4	140
14 - Lanaudière	112	5		1	118
15 - Laurentides	150	6	1		157
16 - Montérégie	98	3	2		103
Inconnu		1			1
Hors Québec	13			1	14
Ensemble du Québec	2 554	163	8	19	2 744

15 avril
Le variant brésilien en Colombie-Britannique
https://www.sciencepresse.qc.ca/actualite/2021/04/15/variant-bresilien-colombie-britannique

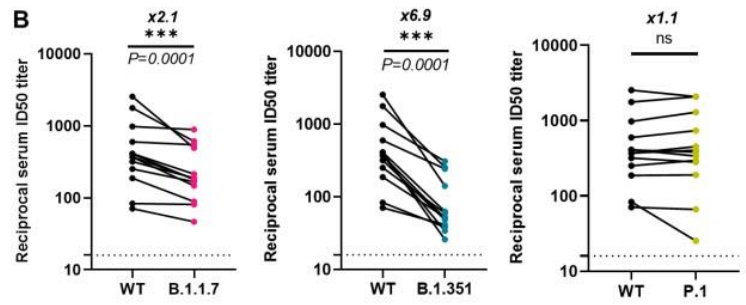
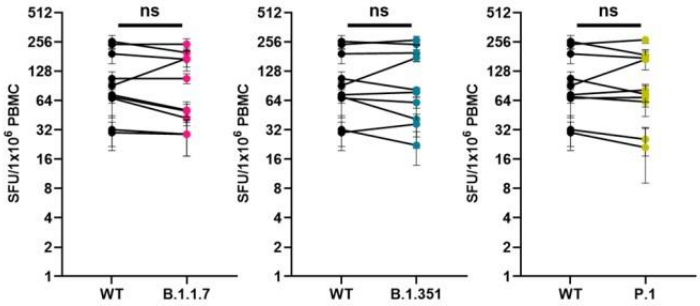
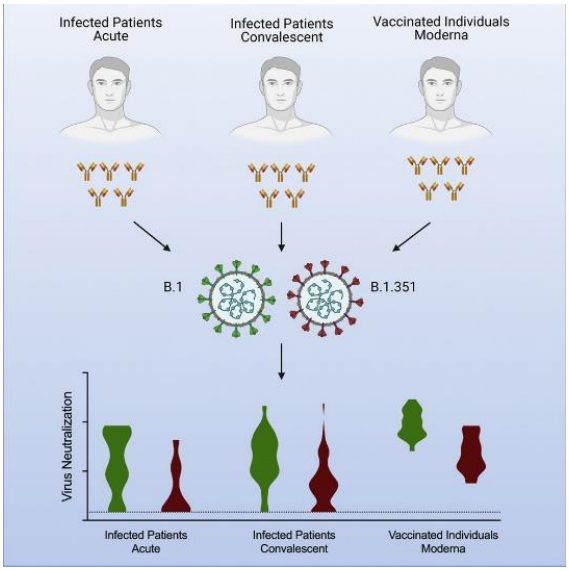
La Colombie-Britannique est à présent le lieu de la plus grande éclosion du variant brésilien… en-dehors du Brésil. Plus de 550 nouveaux cas du variant brésilien (P1) ont été identifiés depuis le 9 avril, soit à peu autant, pour cette période, que les nouveaux cas du variant britannique. Et la courbe est désormais à l'avantage du brésilien qui, avec un total de plus de 1500 cas en date du 15 avril, se rapprochait rapidement des 3600 cas du variant britannique (B117).



Here we compared humoral and cellular responses against SARS-CoV-2 VOC in subjects immunized with the DNA vaccine, INO-4800.

INO-4800 vaccination induced neutralizing antibodies against all variants tested, with reduced levels detected against B.1.351.

14 avril
INO-4800 DNA Vaccine Induces Neutralizing Antibodies and T cell Activity Against Global SARS-CoV-2 Variants
https://www.biorxiv.org/content/10.1101/2021.04.14.439719v1

 IFNγ T cell responses were fully maintained against all variants tested. **Figure 2: INO-4800 Cellular immune response against SARS-CoV-2 variants** 	
In this study, Edara et al. (2021) report that, despite reduced antibody binding to the B.1.351 RBD, sera from infected (acute and convalescent) and Moderna (mRNA-1273)-vaccinated individuals were still able to neutralize the SARSCoV- 2 B.1.351 variant, suggesting that protective humoral immunity may be retained against this variant. 	**14 avril** Infection- and vaccine-induced antibody binding and neutralization of the B.1.351 SARS-CoV-2 variant Venkata ViswanadhEdara https://www.sciencedirect.com/science/article/pii/S1931312821001372
The increasing prevalence and diversity of SARS-CoV-2 spike variants raises concerns for potential immune escape. Using a validated pseudovirus neutralization assay, Shen et al. show	**14 avril** SARS-CoV-2 variant B.1.1.7 is susceptible to neutralizing

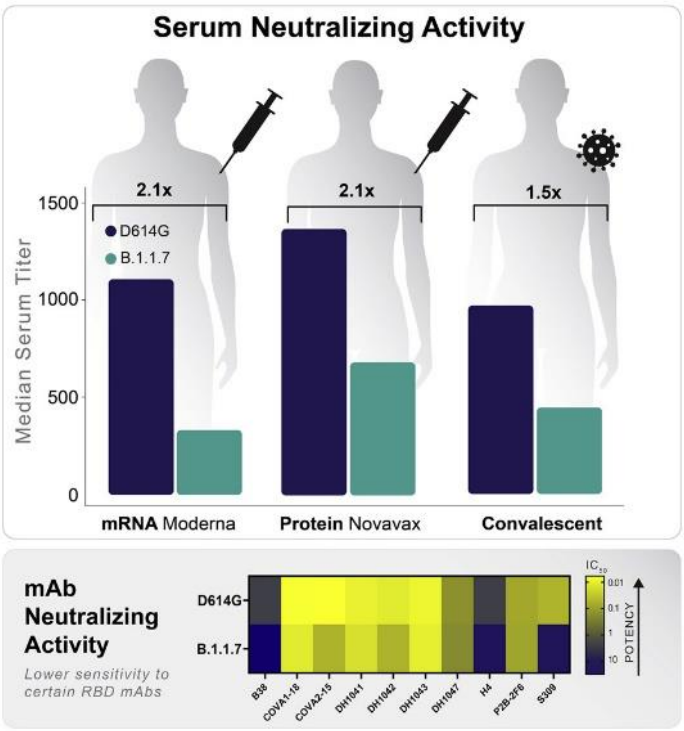
that the B.1.1.7 variant escapes a subset of monoclonal antibodies but remains susceptible to vaccine-elicited antibodies and serum samples from people who recovered from COVID-19.  	antibodies elicited by ancestral spike vaccines XiaoyingShen https://www.sciencedirect.com/science/article/pii/S1931312821001025
In the present study, we reviewed the major variants and the effects of existing variants on neutralizing antibodies and vaccine protection and propose new ideas for applying current vaccines against variants and developing next-generation vaccines.	**14 avril** Effects of SARS-CoV-2 variants on vaccine efficacy and response strategies Lianlian Bian https://www.tandfonline.com/doi/full/10.1080/14760584.2021.1903879

Table 1. Results of convalescent plasma against SARS-CoV-2 variants.

Virus type	Variant	Control strains	No. of sample	Reduction fold (control/variant)	Reference
pseudovirus	B.1.1.7	D614G	15	1.55	Shen et al. [36]
pseudovirus	B.1.1.7 B.1.351	WT	20	2.7–3.8 11.0–33.1	Wang et al. [33]
infectious cDNA clone	E484K mutation	WT	30	2.4–4.2	Jangra et al. [58]
live virus	B.1.1.7	WT	34	3.9	Gavin R. et al. [56]
live virus	B.1.351	WT	34	13.3	Gavin R. et al. [57]
mouse-adapted virus	N501Y MA-SARS-CoV-2	WT	30	*	Rathnasinghe et al. [59]

Annotation: WT = Wuhan reference strain; * No fold reduction in neutralization titers was mentioned in this study, although the results showed that N501Y did not mediate antibody escape.

Table 2. Results of vaccine-elicited sera against SARS-CoV-2 variants.

Vaccine	Type of vaccine	Gene	Sample No.	Type of virus	Control strain	Variant	Reduction fold (control/variant)	Reference
Moderna vaccine	RNA vaccine	S	/	pseudovirus	D614G	K417N-E484K-N501Y-D614G	2.7	Wu et al. [62]
						B.1.351	6.4	
Moderna vaccine	RNA vaccine	S	12	pseudovirus	WT	B.1.1.7	1.8	Wang et al. [33]
						B.1.351	8.6	
Pfizer/BioNTech vaccine	RNA vaccine	S	10			B.1.1.7	2	
						B.1.351	6.5	
Moderna vaccine	RNA vaccine	S	40	pseudovirus	D614G	B.1.1.7	2.11	Shen et al. [36]
NVX-CoV2373	protein nanoparticle	S	28				2.25	
Pfizer/BioNTech vaccine	RNA vaccine	S	40	pseudovirus	WT	B.1.1.7	1.25	Muik et al. [38]
Pfizer/BioNTech vaccine	RNA vaccine	S	23	pseudovirus	WT	B.1.1.7	3.85	Collier et al. [37]
Pfizer/BioNTech vaccine	RNA vaccine	S	20	infectious cDNA clone	WT	Mutant N501Y	0.68	Xie et al. [60]
						Mutant Δ69/70 + N501Y+D614G	0.71	
						Mutant E484K+N501Y +D614G	1.23	
Pfizer/BioNTech vaccine	RNA vaccine	S	5	infectious cDNA clone	WT	E484K mutation	3.4	Jangra et al. [58]
Pfizer/BioNTech vaccine	RNA vaccine	S	20	infectious cDNA clone	N501	Y501	1.46	Shi et al. [61]
Pfizer/BioNTech vaccine	RNA vaccine	S	25	live virus	WT	B.1.1.7	3.3	Gavin R. et al. [56]
AstraZeneca-Oxford vaccine	Adenovirus vector vaccine	S	25	live virus	WT	B.1.1.7	2.1 ~ 2.5	
Pfizer/BioNTech vaccine	RNA vaccine	S	25	live virus	WT	B.1.351	7.6	Gavin R. et al. [57]
AstraZeneca-Oxford vaccine	Adenovirus vector vaccine	S	25	live virus	WT	B.1.351	9	
BBIBP vaccine	Inactive vaccine	full length	12	live virus	WT & D614G	B.1.351	1.6	Gao et al. [63]
Zhifei vaccine	protein subunit vaccine	RBD	12	live virus	WT & D614G	B.1.351	1.6	
Pfizer/BioNTech vaccine	RNA vaccine	S	6	mouse-adapted virus	WT	N501Y MA-SARS-CoV-2	*	Rathnasinghe et al. [59]

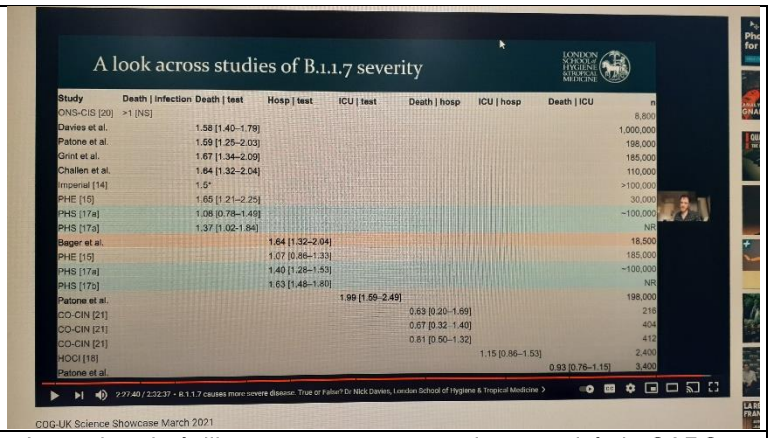
Annotation: S = spike; RBD = receptor binding domain; WT = Wuhan reference strain; * No fold reduction in geometric mean titers (GMT) was mentioned in this study, although the results showed that N501Y did not mediate antibody escape.

Lineage P.1, acquired 17 mutations, including a trio in the spike protein (K417T, E484K and N501Y) associated with increased binding to the human ACE2 receptor. Molecular clock analysis shows that P.1 emergence occurred around mid-November 2020 and was preceded by a period of faster molecular evolution. Using a two-category dynamical model that integrates genomic and mortality data, we estimate that P.1 may be 1.7–2.4-fold more transmissible, and that previous (non-P.1) infection provides 54–79% of the protection against infection with P.1 that it provides against non-P.1 lineages. Enhanced global genomic surveillance of variants of concern, which may exhibit increased transmissibility and/or immune evasion, is critical to accelerate pandemic responsiveness.	**14 avril** Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil Nuno R Faria https://science.sciencemag.org/content/early/2021/04/13/science.abh2644.long

12- 16 avril 2021

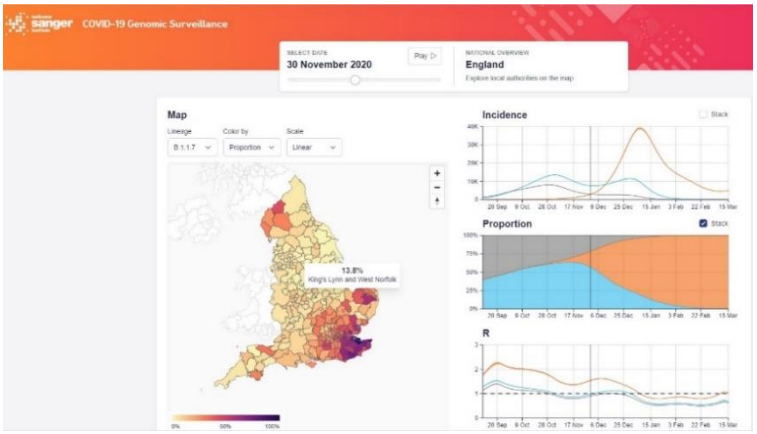
Article de presse	Extrait pertinent	Source scientifique
13 avril Le vaccin de Moderna efficace à 90 % selon un essai américain https://www.lapresse.ca/covid-19/2021-04-13/le-vaccin-de-moderna-efficace-a-90-selon-un-essai-americain.php	Le vaccin de Moderna est efficace à 90 % contre la COVID-19 et à 95 % contre les formes graves de la maladie, a annoncé la firme de biotechnologie américaine dans de nouveaux résultats publiés mardi, en légère baisse par rapport à un précédent essai clinique. Moderna ne précise pas dans son communiqué si cette baisse dans l'efficacité est attribuable à l'émergence de nouveaux variants. Mais la firme de biotechnologie travaille sur deux versions modifiées de son vaccin, spécifiques aux variants, dont les résultats sur des souris — pas encore évalués par des pairs — sont encourageants. « Les nouvelles données pré-cliniques sur nos vaccins candidats spécifiques aux variants nous donnent confiance dans notre capacité à anticiper l'émergence de nouveaux variants », a applaudi Stéphane Bancel, le patron de Moderna. Press release: Moderna Provides Clinical and Supply Updates on COVID-19 Vaccine Program Ahead of 2nd Annual Vaccines Day **Preclinical Data on Variant-Specific Booster Candidates** New preclinical data on the Company's variant-specific booster vaccine candidates have been submitted as a preprint to *bioRxiv* and will be submitted for peer-reviewed publication. These variant-specific vaccine candidates include mRNA-1273.351, which is more specifically targeted against the SARS-CoV-2 variant known as B.1.351 first identified in the Republic of South Africa, and a multivalent booster candidate, mRNA-1273.211, which combines mRNA-1273 (Moderna's authorized vaccine against ancestral strains) and mRNA-1273.351 in a single vaccine. Both mRNA-1273.351 and mRNA-1273.211 increase neutralizing titers against SARS-CoV-2 variants of concern in Balb/c mice. Specifically, this preclinical data confirms improved neutralizing titers with the mRNA-1273.351 vaccine primary series. The multi-valent vaccine provided the broadest level of immunity. A boost at 6 months with mRNA-1273.351 closed the neutralizing titer gap for the variants of concern. Following the mRNA-1273.351 boost, neutralizing titers were comparable between the ancestral strain (Wuhan) and the new B.1.351 variant. The Company's Phase 2 study to evaluate three approaches to boosting is ongoing.	
12 avril Le variant britannique n'entraînerait pas plus de formes graves https://www.lapresse.ca/covid-19/2021-04-12/covid-19/le-variant-britannique-n-	Genomic characteristics and clinical effect of the emergent SARS-CoV-2 B.1.1.7 lineage in London, UK: a whole-genome sequencing and hospital-based cohort study Dan Frampton, PhD Comment: Lack of detail in population-level data impedes analysis of SARS-CoV-2 variants of concern and clinical outcomes	

entrainerait-pas-plus-de-formes-graves.php	Les auteurs de la première étude, publiée dans *The Lancet Infectious Diseases*, ont analysé les données de 341 malades de la COVID-19 hospitalisés à Londres entre le 9 novembre et le 20 décembre, en pleine émergence du variant 501Y. V1, désormais dominant dans une grande partie de l'Europe. 58 % d'entre eux étaient infectés par ce variant, aussi connu par le nom de sa lignée, B.1.1.7, et 42 %, par d'autres souches. 36 % des patients du premier groupe sont tombés gravement malades ou sont décédés, contre 38 % dans le deuxième groupe, ce qui suggère que le B.1.1.7 n'est pas associé à une plus grande gravité. Les chercheurs ont en revanche montré que les échantillons provenant de patients infectés par le variant contenaient en moyenne une plus grande quantité de virus, indice d'une transmissibilité plus élevée. Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study Mark S Graham, PhD Comment: Monitoring differences between the SARS-CoV-2 B.1.1.7 variant and other lineages La seconde étude, parue dans *The Lancet Public Health*, a analysé les données de près de 37 000 utilisateurs britanniques d'une application mobile conçue pour signaler ses symptômes de la COVID-19, diagnostiqués positifs entre le 28 septembre et le 27 décembre. À partir du nombre de personnes ayant rapporté des symptômes chaque semaine dans une zone donnée, elle conclut que le variant « britannique » présentait un taux de reproduction 1,35 fois plus élevé, c'est-à-dire que chaque patient contaminé infectait en moyenne 35 % de personnes en plus qu'avec les souches du virus qui circulaient auparavant. En revanche le variant n'a pas entraîné de symptômes plus graves ou une plus grande probabilité d'avoir des symptômes prolongés (« COVID-19 long ») **31 Mars** Second COG-UK Showcase Event - Mars 2021 Nicholas G. Davis

	
12 avril Brésil Malgré l'hécatombe, une lueur d'espoir face au variant https://www.lapresse.ca/international/amerique-latine/2021-04-12/bresil/malgre-l-hecatombe-une-lueur-d-espoir-face-au-variant.php	« Le variant brésilien augmente un peu la capacité du SARS-CoV-2 à échapper à l'immunité donnée par une première infection », explique Michael Busch, virologue à l'Université de Californie à San Francisco. Il est le coauteur de toutes les études sur la COVID-19 à Manaus, notamment celle publiée dans *Science,* en décembre, qui a conclu que 75 % des habitants de la ville avaient été touchés par la première vague de la pandémie. Une autre étude publiée fin février par M. Busch et ses collègues brésiliens a montré que le variant brésilien est de 25 % à 60 % plus susceptible d'échapper à l'immunité contre le SARS-CoV-2 que la souche de Wuhan qui a fait le tour du monde à la fin de l'hiver 2020. Le variant brésilien peut donc échapper à l'immunité conférée par une première dose dans 12,5 % à 16 % des cas, selon le virologue californien. Cela signifie aussi que les vaccins demeureront probablement efficaces, selon lui.
11 avril Vaccin Pfizer-BioNTech Moins efficace contre le variant sud-africain https://www.lapresse.ca/covid-19/2021-04-11/vaccin-pfizer-biontech/moins-efficace-contre-le-variant-sud-africain.php	Evidence for increased breakthrough rates of SARS-CoV-2 variants of concern in BNT162b2 mRNA vaccinated individuals Talia Kustin Une équipe de l'Université de Tel Aviv et de l'organisation de soins de santé Clalit a séquencé les prélèvements de 150 Israéliens qui ont été déclarés positifs à la COVID-19 alors qu'ils avaient reçu les deux doses du vaccin. Parmi ceux-ci, le taux de prévalence du variant sud-africain était huit fois plus élevé que chez les personnes non vaccinées (5.4% versus 0.7%). (…) Les chercheurs préviennent toutefois que l'étude a été menée sur un très petit échantillon et que des recherches supplémentaires seront nécessaires pour confirmer ces chiffres (The study, released on Saturday, compared almost 400 people who had tested positive for COVID-19, 14 days or more after they received one or two doses of the vaccine, against the same number of unvaccinated patients with the disease.).

	L'étude israélienne a également démontré une protection plus faible au variant B.1.1,7, d'origine britannique, dans les semaines suivant la première dose du vaccin.(…) Les résultats démontrent que le taux de prévalence du variant britannique était 2,6 fois plus élevé chez les personnes vaccinées avec seulement une dose que chez les personnes non vaccinées.
10 avril La troisième vague déferle d'un océan à l'autre https://www.lapresse.ca/covid-19/2021-04-10/la-troisieme-vague-deferle-d-un-ocean-a-l-autre.php	La troisième vague se fait durement sentir au Canada où, malgré une tendance à la hausse, le Québec semble pour l'instant mieux s'en tirer que plusieurs autres provinces, particulièrement l'Ontario et l'Alberta. Tour d'horizon du pays, où les cas sont en hausse de 29 % depuis une semaine. • Le reconfinement de l'Ontario • En Alberta, le resserrement des règles • Fin du séquençage systématique en Colombie-Britannique • Vaccination élargie en Saskatchewan
9 avril Chinese COVID-19 vaccine maintains protection in variant-plagued Brazil https://www.sciencemag.org/news/2021/04/chinese-covid-19-vaccine-maintains-protection-variant-plagued-brazil	Matt D.T. Hitchings et coll. (7 avril): Effectiveness of CoronaVac in the setting of high SARS-CoV-2 P.1 variant transmission in Brazil: A test-negative case-control study Preliminary results from a large study of health care workers now suggest one dose of CoronaVac, a vaccine developed by a Chinese company (Sinovac Biotech), is still about 50% effective against symptomatic COVID-19 in a Brazilian city where more than three-fourths of new cases are caused by the highly transmissible variant known as P.1. (…) CoronaVac likely offers far greater protection against severe disease, hospitalization, and death than against milder cases of COVID-19. That was seen in two dose efficacy trials conducted in Brazil and other countries and is typical of COVID-19 vaccines. But the new study has not yet collected enough severe cases to calculate effectiveness, Croda says. (…) The CoronaVac study involved medical data from 67,718 health care workers from Manaus, a city in the Amazon region that is the epicenter of the P.1 variant. The mutant virus now accounts for 75% of all positive test results in the city, where the health system is collapsing because of COVID-19. (…)The 49.6% real-world effectiveness is similar to the **vaccine's efficacy of 50.34% against symptomatic COVID-19 after both doses**, found in a phase 3 clinical trial conducted in Brazil by the Butantan Institute, a state-owned research institute and vaccinemaker.
7 avril Wellcome Sanger Institute COVID–19 Genomic Surveillance https://covid19.sanger.ac.uk/	**Lineages in space and time** v0.2.0 updated 7 April 2021 This website shows how SARS-CoV-2 lineages have changed in frequency over time across England. It is a collaboration between the Wellcome Sanger Institute, the European Bioinformatics Institute, Public Health England, and the COVID-19 Genomics UK (COG-UK) Consortium. The model underlying these data is updated from lineage-specific growth of SARS-CoV-2 B.1.1.7 during the English national lockdown. The sequence data come from

Sanger's COVID–19 Genomic Surveillance Initiative. Lineages are assigned using the pangolin tool.

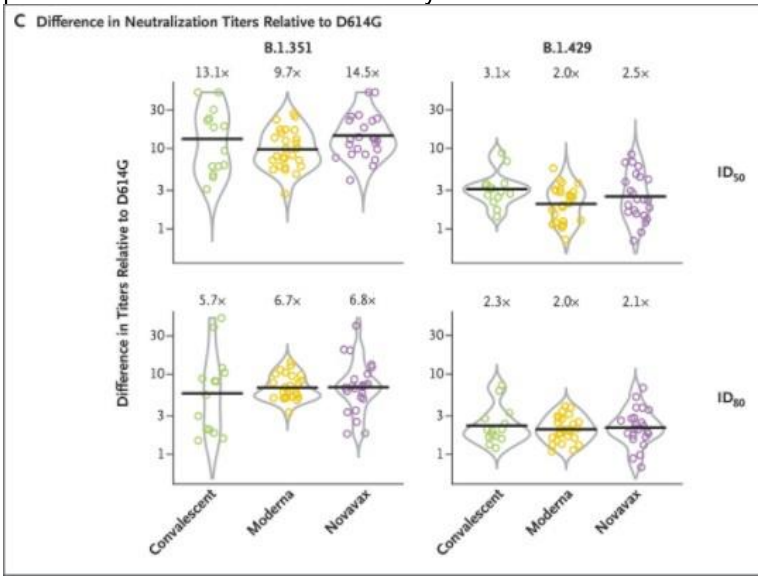


En complement:

COG-UK/ME

The COG-UK / Mutation Explorer (COG-UK/ME) provides information and structural context on mutations and associated variants in the genes encoding SARS-COV-2 proteins that have been identified from sequence data generated by the COVID-19 Genomics (COG-UK) Consortium by Monday 12 April 2021. We focus on SARS-CoV-2 spike gene mutations of potential or known importance based on epidemiological, clinical and/or experimental observations. The Mutation Explorer comprises of:

1. high frequency individual amino acid replacements (Table 1), a subset of which may be important
2. mutations of potential or known clinical and public health importance based on current evidence (Table 2)
3. the designated global variants of concern and their structural context (Table 3)
4. frequency plots for mutations at specific residue in SARS-CoV-2 ORFs (Visualiser)
5. mutations of potential antigenic significance as indicated by experimental studies: shown to lead to weaker neutralisation of the virus by convalescent plasma from people who have been infected with

	SARS-CoV-2 and/or demonstrated escape from some monoclonal antibodies (mAbs) that may be given to patients with COVID-19 (Antigenic Information: Antibody Sites) 6. mutations in T cell epitopes as indicated by experimental studies (Antigenic Information: T Cell Epitopes).
We measured the neutralizing activity of serum specimens obtained from 14 convalescent persons and from 49 recipients of one of two different vaccines based on the ancestral spike: an mRNA vaccine (mRNA-1273 [Moderna]; 26 recipients)[2] and a protein nanoparticle vaccine (NVX-CoV2373 [Novavax]; 23 recipients).[3] We selected mRNA-1273 samples that represented high, medium, and low neutralization titers. NVX-CoV2373 samples were randomly selected and were not preselected on the basis of antibody titers.  As compared with the D614G variant, we found that B.1.429 (S13I, W152C, and L452R) was approximately 2 to 3 times less sensitive to neutralization by convalescent serum and by serum samples obtained from vaccinated persons, whereas B.1.351 (L18F, D80A, D215G, Δ242–244, R246I, K417N, E484K, N501Y, and A701V) was approximately 9 to 14 times less sensitive to neutralization.These results, and the high efficacy shown by these vaccines, suggest that vaccine-elicited neutralizing antibodies are likely to remain effective against the B.1.429 variant.	**7 avril** Neutralization of SARS-CoV-2 Variants B.1.429 and B.1.351 https://www.nejm.org/doi/full/10.1056/NEJMc2103740
At the end of 2020, a variant named 20I/501Y.V1 (lineage B.1.1.7) emerged and replaced other circulating strains in several regions. This phenomenon has been poorly associated to biological evidence that this variant and original strain exhibit different phenotypic characteristics. Here, we analyse the replication ability of this new variant in different cellular models using for comparison an ancestral D614G European strain (lineage B1). Results from comparative replication kinetics experiments *in vitro* and in a human reconstituted	**22 mars** Replicative fitness SARS-CoV-2 20I/501Y.V1 variant in a human reconstituted bronchial epithelium Franck Touret https://www.biorxiv.org/content/10.1101/2021.03.22.436427v1

bronchial epithelium showed no difference. However, when both viruses were put in competition in a human reconstituted bronchial epithelium, the 20I/501Y.V1 variant outcompeted the ancestral strain. Altogether, these findings demonstrate that this new variant replicates more efficiently and could contribute to better understand the progressive replacement of circulating strains by the SARS-CoV-2 20I/501Y.V1 variant.	

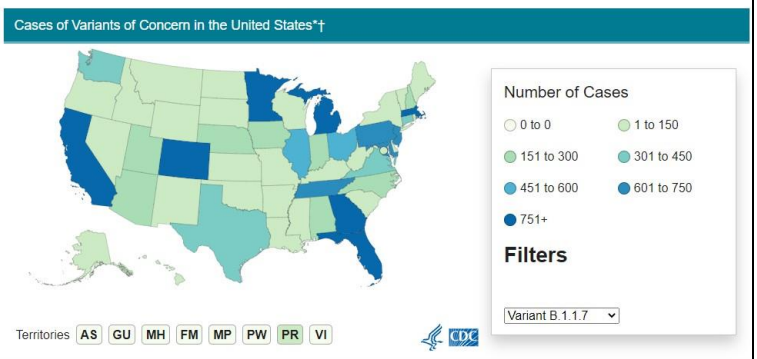
5- 9 avril 2021

Article de presse	Extrait pertinent	Source scientifique
8 avril Des patients plus jeunes hospitalisés https://www.lapresse.ca/covid-19/2021-04-08/des-patients-plus-jeunes-hospitalises.php	Le chef de service des soins intensifs à l'Hôpital Maisonneuve-Rosemont, le Dr Francois Marquis, affirme qu'au cours des quelque deux dernières semaines, l'âge moyen des personnes infectées par la COVID-19 admises à l'hôpital a reculé de 10 ou 15 ans. Contrairement à la première vague de la pandémie, l'an dernier, le Dr Marquis voit maintenant plusieurs patients âgés de 30 ou 40 ans qui n'ont pas d'antécédents médicaux. Ils ne prennent pas de médicaments et ne soufrent pas de maladies telles l'hypertension artérielle et le diabète. Le Dr De Serres prétend que davantage de jeunes sont malades parce que les variants du coronavirus se transmettent plus facilement entre les personnes et provoquent des conditions médicales plus aiguës.	
7 avril More Contagious Virus Variant Is Now Dominant in U.S., C.D.C. Chief Says https://www.nytimes.com/2021/04/07/us/politics/coronavirus-variants-cdc.html	The B.1.1.7 variant, first identified in Britain, is now the source of most new coronavirus infections in the United States, the director of the Centers for Disease Control and Prevention said.	

US COVID-19 Cases Caused by Variants

Updated Apr. 8, 2021 Languages Print

Variant	Reported Cases in US	Number of Jurisdictions Reporting
B.1.1.7	19,554	52
B.1.351	424	36
P.1	434	28



Autre nouvelle connexe

CDC: SARS-CoV-2 Variant Classifications and Definitions (24 mars)

- A US government interagency group developed a Variant Classification scheme that defines three classes of SARS-CoV-2 variants:
  - Variant of Interest
  - Variant of Concern
  - Variant of High Consequence
- The B.1.1.7, B.1.351, P.1, B.1.427, and B.1.429 variants circulating in the United States are classified as variants of concern

USA Today: In the race to stay ahead of COVID-19 variants, US lags globally (7 avril)
The CDC tries to sequence at least 7,000 positive test samples a week, about 2% of new cases. Some say it needs to do more; a 2% rate could mean not catching new variants early enough.

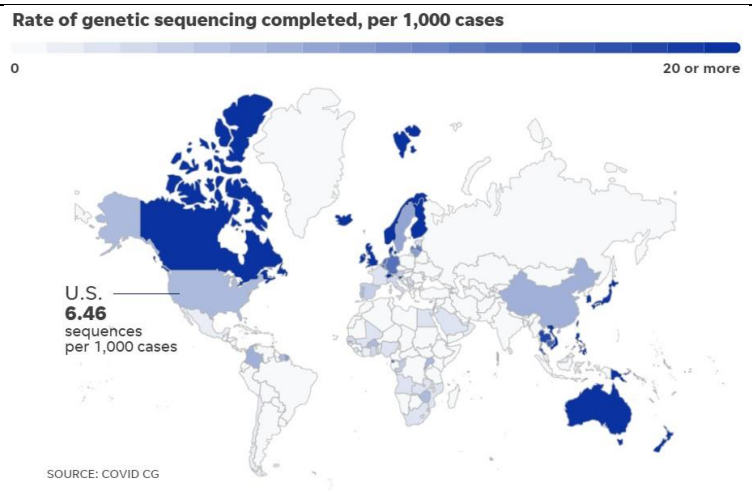
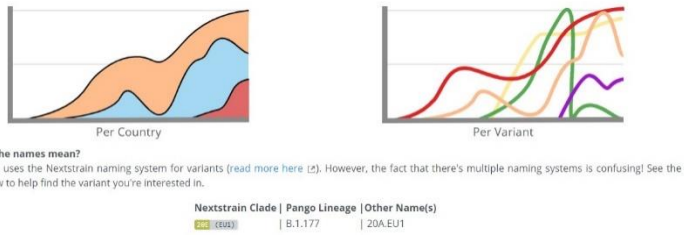
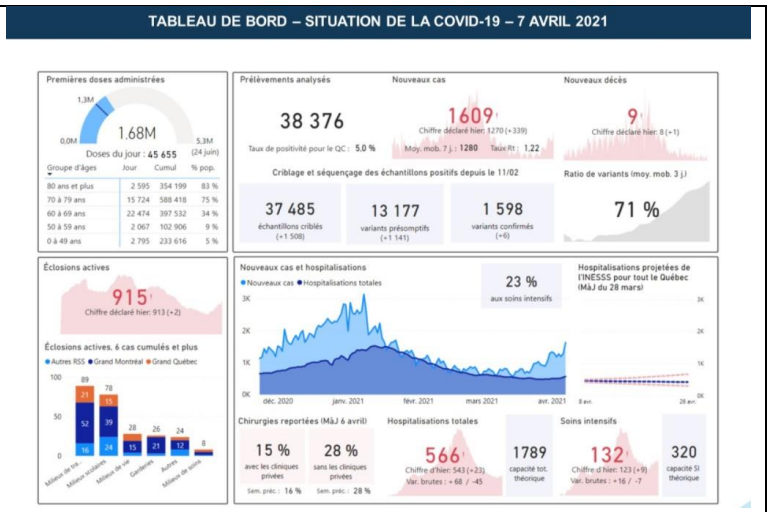
	 Last week, it (B.1.1.7) made up an estimated 32% of new cases. Another fast-spreading variant, B.1.526 – which was first detected in New York – reached 36%, according to CoVariants.org (outil développé par Emma Hodcroft et coll.). • Browse Variants • Explore Per-country distribution • Explore Per-variant distribution • View Shared mutations  **Access to data limited for most scientists**: GISAID has strict rules that make it hard to access and share data on gene sequences. the data in GISAID is not random, so without a fuller understanding of how it was collected, the results of any analysis could be biased. That's one reason the CDC created its own database in February called National SARS-CoV-2 Strain Surveillance.
6 avril Variant first found in Brazil newest COVID-19 challenge in B.C. https://www.cbc.ca/player/play/1881856067992	The P1 COVID-19 variant, first seen in Brazil, is creating a big problem for health officials because of how quickly it spreads. Currently concentrated in the Vancouver area, modelling shows it could spread out of control by late April.

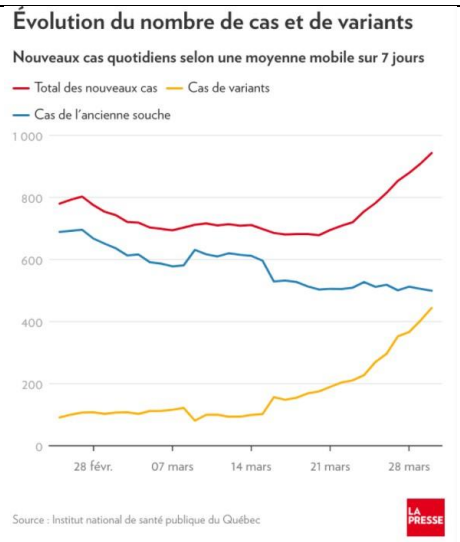
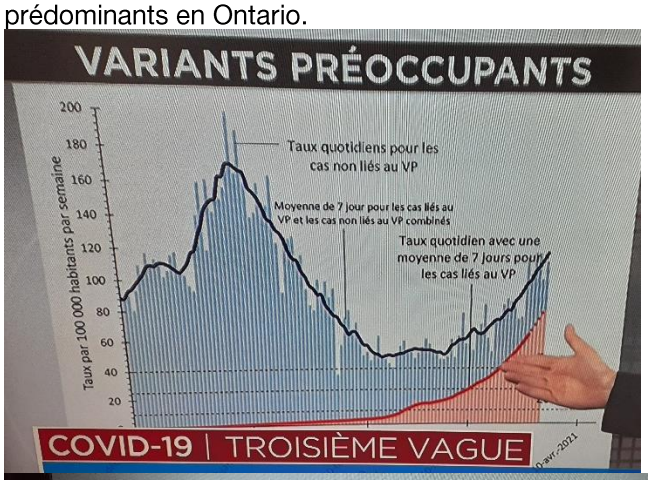
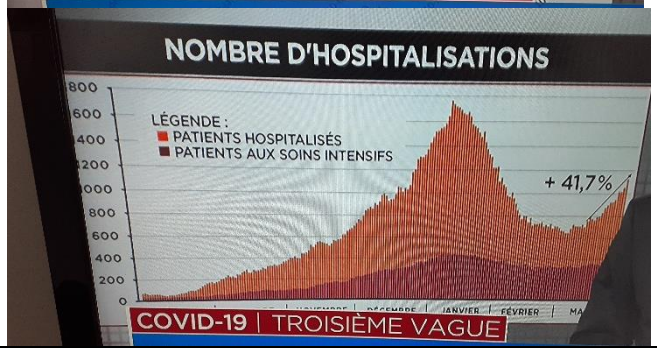
	Table 2. Cumulative number of cases involving variants of concern (VOC) publicly reported, as of April 8, 2021 7:00 PM EST **Location** / **B.1.1.7 variant** / **B.1.351 variant** / **P.1 variant** **Canada** / **23,611** / **345** / **1,039** British Columbia / 2,842 / 51 / 883 Alberta / 8,229 / 26 / 23 Saskatchewan / 943 / 8 / 0 Manitoba / 298 / 20 / 0 Ontario / 9,632 / 75 / 131 Quebec / 1,430 / 154 / 2 Newfoundland and Labrador / 178 / 1 / 0 New Brunswick / 28 / 0 / 0 Nova Scotia / 23 / 10 / 0 Prince Edward Island / 6 / 0 / 0 Yukon / 1 / 0 / 0 Northwest Territories / 1 / 0 / 0 Nunavut / 0 / 0 / 0
6 avril Avec la COVID-19 aussi, tous les variants mènent au même virus https://www.ledevoir.com/societe/sante/598193/tous-les-chemins-menent-au-meme-virus	Fin janvier, deux laboratoires américains — l'un en Louisiane, l'autre au Nouveau-Mexique — comprennent qu'une certaine mutation du coronavirus gagne en fréquence dans les échantillons analysés. (…) La mutation qui fait l'objet d'un récent article scientifique de Vaughn Cooper et ses collègues est nommée Q677H. (…) La mutation 677H serait l'une des dix mutations qui, selon M. Cooper, sont véritablement capables d'accroître la transmission du virus dans une population non immunisée. (…) « C'est clair qu'il y a de l'évolution convergente, observe également Jesse Shapiro, spécialiste de l'évolution des populations microbiennes à l'Université McGill. (…) On constate aussi au Québec certains signes d'une évolution convergente du SRAS-CoV-2. Sandrine Moreira, la responsable de la génomique et de la bio-informatique au Laboratoire de santé publique du Québec, indique que la mutation 677H est maintenant présente dans différentes lignées québécoises. Difficile de dire, cependant, si cette mutation a été importée au Québec par des voyageurs ou si elle est apparue spontanément dans la province. (…) Une autre des mutations cruciales et récurrentes est E484K. (…) Au Québec, on a aussi trouvé « une poignée » de variants britanniques qui en étaient munis.
5 avril COVID-19 Tous les indicateurs en hausse https://www.lapresse.ca/covid-19/2021-04-05/covid-19/tous-les-indicateurs-en-hausse.php	Le nombre de personnes hospitalisées et de celles succombant à la COVID-19 ne cesse de croître, deux semaines après le début d'une troisième vague alimentée par les variants.

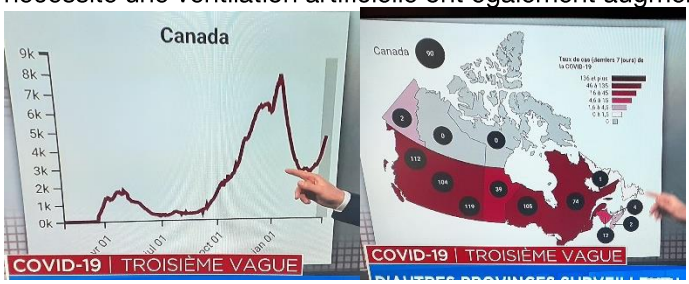
	 Source : quebec.ca
Nine short talks on the themes of massive sequencing, molecular testing, variant distribution/detection/prioritization and the implications for patients and prevention. If you missed the live event, you can watch the full recording here.	**31 Mars** Watch the second COG-UK Showcase Event COG-UK
This study examined whether CD8+ T-cell responses from COVID-19 convalescent individuals (n=30) potentially maintain recognition of the major SARS-CoV-2 variants (n=45 mutations assessed). Only one mutation found in B.1.351-Spike overlapped with a previously identified epitope (1/52), suggesting that virtually all anti-SARS-CoV-2 CD8+ T-cell responses should recognize these newly described variants.	**30 mars** CD8+ T cell responses in COVID-19 convalescent individuals target conserved epitopes from multiple prominent SARS-CoV-2 circulating variants Andrew D Redd https://academic.oup.com/ofid/advance-article/doi/10.1093/ofid/ofab143/6189113?searchresult=1
To address the potential threat posed by VOC, we sampled a SARS-CoV-2 uninfected UK cohort recently vaccinated with BNT162b2 (Pfizer-BioNTech, two doses delivered 18-28 days apart), alongside a cohort sampled in the early convalescent stages after natural infection in the first wave of the pandemic in Spring 2020. We tested antibody and T cell responses against a reference isolate of the original circulating lineage, B, and the impact of sequence variation in the B.1.1.7 and B.1.351 VOC. Neutralization of the VOC compared to B isolate was reduced, and this was most evident for the B.1.351 isolate. This reduction in antibody neutralization was less marked in post-boost vaccine-induced responses compared to naturally induced immune responses and could be largely explained by the potency of the homotypic antibody response. After a single vaccination, which induced only modestly neutralizing homotypic antibody titres, neutralization against the VOC was completely abrogated in the majority of	**29 mars** Two doses of SARS-CoV-2 vaccination induce more robust immune responses to emerging SARS-CoV-2 variants of concern than does natural infection. Donal T. Skelly https://www.researchsquare.com/article/rs-226857/v2

vaccinees. Importantly, high magnitude T cell responses were generated after two vaccine doses, with the majority of the T cell response directed against epitopes that are conserved between the prototype isolate B and the VOC. These data indicate that VOC may evade protective neutralizing responses induced by prior infection, and to a lesser extent by immunization, particularly after a single vaccine dose, but the impact of the VOC on T cell responses appears less marked.	
Here we performed a comprehensive analysis of SARS-CoV-2-specific CD4+ and CD8+ T cell responses from COVID-19 convalescent subjects recognizing the ancestral strain, compared to variant lineages B.1.1.7, B.1.351, P.1, and CAL.20C as well as recipients of the Moderna (mRNA-1273) or Pfizer/BioNTech (BNT162b2) COVID-19 vaccines. Similarly, we demonstrate that the sequences of the vast majority of SARS-CoV-2 T cell epitopes are not affected by the mutations found in the variants analyzed. Overall, the results demonstrate that CD4+ and CD8+ T cell responses in convalescent COVID-19 subjects or COVID-19 mRNA vaccinees are not substantially affected by mutations found in the SARS-CoV-2 variants.	**1 mars** Negligible impact of SARS-CoV-2 variants on $CD4^+$ and $CD8^+$ T cell reactivity in COVID-19 exposed donors and vaccinees Alison Tarke https://www.biorxiv.org/content/10.1101/2021.02.27.433180v1

29 - 2 avril 2021

Article de presse	Extrait pertinent	Source scientifique
1 avril Le vaccin Pfizer-BioNTech efficace contre le variant sud-africain https://www.lapresse.ca/covid-19/2021-04-01/le-vaccin-pfizer-biontech-efficace-contre-le-variant-sud-africain.php	Dans ce pays, « 800 participants ont été recrutés, neuf cas de COVID-19 ont été observés, tous dans le groupe placebo, ce qui indique une efficacité du vaccin de 100 % », explique l'alliance Pfizer-BioNTech. Sur l'ensemble des 46 307 participants aux essais de phase 3 dans plusieurs pays, le vaccin a démontré une efficacité de 91,3 %, selon la même source. Sur les 927 cas symptomatiques de COVID-19 dans l'étude, 850 cas concernaient des patients du groupe placebo et 77 cas se trouvaient dans le groupe vacciné. Press relase	
1 avril Progression des variants - Des statistiques incomplètes https://www.lapresse.ca/covid-19/2021-04-01/progression-des-variants/des-statistiques-incompletes.php	L'Institut national de santé publique du Québec (INSPQ), qui publie depuis un an un graphique montrant la progression quotidienne du nombre de cas sans égard à la souche, n'a pas repris l'exercice pour les variants, se limitant à publier chaque jour quelques chiffres détaillant le nombre cumulé de cas de ce type et la fluctuation observée par rapport à la veille. M. Lamarre affirme que cette approche « manque de transparence » et ne permet pas d'appréhender facilement la propagation des variants	

	
31 mars Un nouveau confinement de quatre semaines en vue en Ontario https://www.lapresse.ca/covid-19/2021-03-31/un-nouveau-confinement-de-quatre-semaines-en-vue-en-ontario.php	Le gouvernement de Doug Ford devrait à son tour annoncer ce jeudi de nouvelles mesures de confinement. Au contraire du Québec, toutefois, celles-ci s'appliqueraient partout en Ontario, pour une durée d'au moins quatre semaines. L'objectif serait de mettre un « frein d'urgence » à la croissance des nouvelles infections des variants, qui sont prédominants en Ontario.  
30 mars Augmentation des cas de COVID-19 à travers le Canada	Propagation rapide des variants, hausse des hospitalisations chez les plus jeunes, resserrement des mesures. D'un océan à l'autre, le bilan canadien de la COVID-19 n'est pas encourageant.

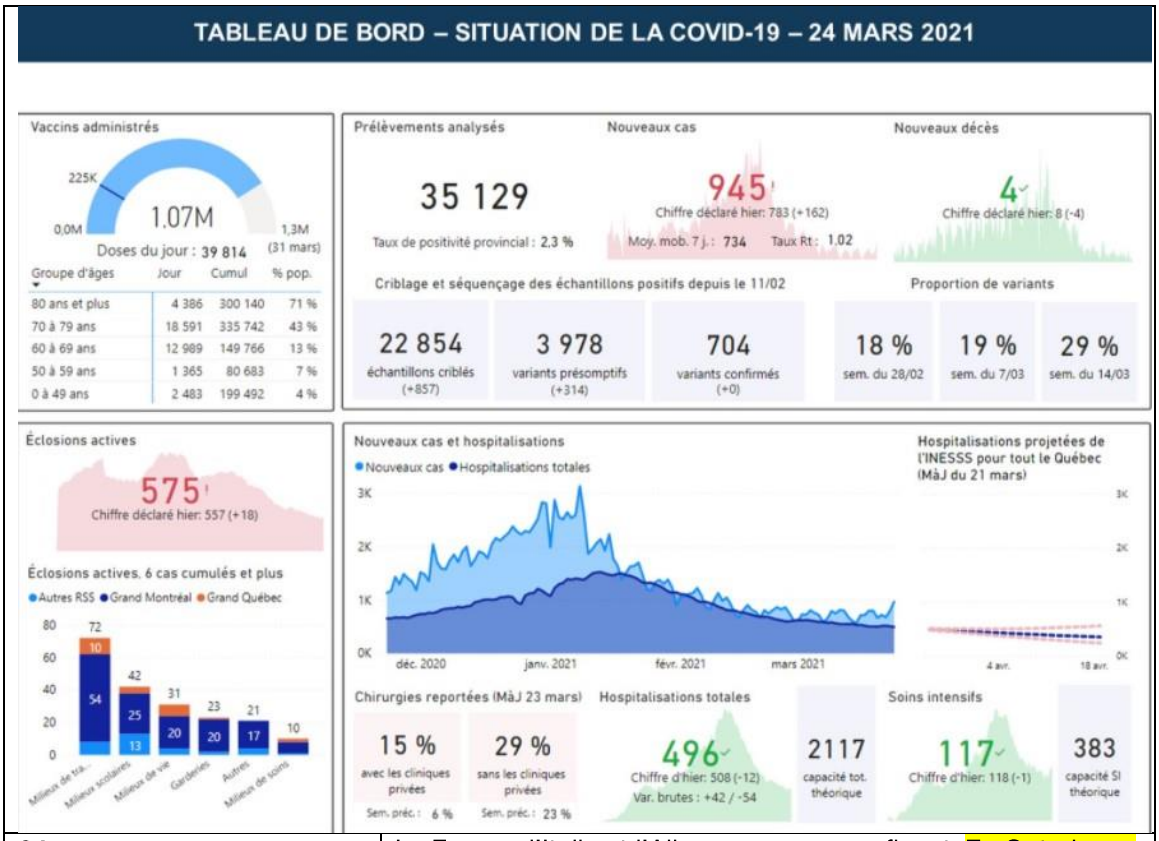
https://www.lapresse.ca/covid-19/2021-03-30/augmentation-des-cas-de-covid-19-a-travers-le-canada.php	**Forte propagation des variants :** Jusqu'à présent, 9009 cas de variants ont été détectés au Canada. Plus de 90 % d'entre eux sont des cas de variant britannique. **Hausse des hospitalisations… chez les jeunes :** Au cours de la dernière semaine, le nombre de lits d'hôpital occupés par des patients de la COVID-19 au Canada a augmenté de 1629 à 1778. Les patients aux soins intensifs et ceux qui ont nécessité une ventilation artificielle ont également augmenté. 
501Y.V2 virus was effectively neutralized by plasma from second wave infections and first wave virus was effectively neutralized by first wave plasma. In cross-neutralization, 501Y.V2 virus was poorly neutralized by first wave plasma, with a 15.1-fold drop relative to 501Y.V2 neutralization by second wave plasma across participants. In contrast, second wave plasma cross-neutralization of first wave virus was more effective, showing only a 2.3-fold decline relative to first wave plasma neutralization of first wave virus. While we only tested one plasma elicited by E484K alone, this potently neutralized both variants. The observed effective neutralization of first wave virus by 501Y.V2 infection elicited plasma provides preliminary evidence that vaccines based on VOC sequences could retain activity against other circulating SARS-CoV-2 lineages.	**29 mars** Escape of SARS-CoV-2 501Y.V2 from neutralization by convalescent plasma • Sandile Cele https://www.nature.com/articles/s41586-021-03471-w
FINDINGS: The average proportion of 20I/501Y.V1 variant (B.1.1.7) was found to be a significant predictor of cumulative number of COVID-19 deaths within two months before the deaths peak and between 1 January - 25 February 2021, as well as of the deaths peak height when calculating the proportion during the second wave and the pre-peak period. The average proportion of 20A.EU2 variant (S:477N) was a significant predictor of cumulative COVID-19 deaths in the pre-peak period. INTERPRETATION: Our findings suggest that the spread of a new variant of concern 20I/501Y.V1 had a significant impact on the mortality during the second wave of COVID-19 pandemic in Europe and that proportions of 20A.EU2 and 20I/501Y.V1 variants were associated with increased mortality in the initial phase of that wave.	**28 mars** On the association between SARS-COV-2 variants and COVID-19 mortality during the second wave of the pandemic in Europe View ORCID ProfileKatarzyna Jablonska https://www.medrxiv.org/content/10.1101/2021.03.25.21254289v1?rss=1%22
27 mars Les jeunes, « nouveaux vulnérables » https://www.lapresse.ca/covid-19/2021-03-27/covid-19/les-jeunes-nouveaux-vulnerables.php	Ils sont les « nouveaux vulnérables ». Si le Québec connaît le même scénario que l'Europe, les jeunes seront les plus durement touchés par la troisième vague de la COVID-19. Une catastrophe annoncée pour le système de santé, mettent en garde des experts. Plus il y aura de jeunes infectés, plus, nécessairement, dans le lot, il y aura des cas de maladie extrêmement sévères. Le

	Dr François Marquis, chef des soins intensifs de l'hôpital Maisonneuve-Rosemont. Le cas de la France lui donne raison. Ces dernières semaines, une hausse inquiétante des jeunes dans les lits des soins intensifs y a été signalée, de même qu'en Belgique et, plus près, en Ontario. Pour la Dre Amélie Boisclair, ce n'est qu'une question de temps avant que la vague frappe son unité des soins intensifs à l'hôpital Pierre-Le Gardeur, à Terrebonne. En quelques jours, tous ses lits se sont remplis. Par des patients plus jeunes et très malades.
In our earlier study on virus shedding using VOC 202012/01(UK variant) and D614G variant in hamster model, we observed significantly higher viral RNA shedding through nasal wash in case of UK variant. Hence, we compared the transmission of both the UK and D614G variant by various routes in Syrian hamsters to understand whether the high viral RNA shedding could enhance the transmission efficiency of the variant. The current study demonstrated comparable transmission efficiency of both UK and D614G variants of SARS-CoV-2 in Syrian hamsters.	**26 mars** Comparison of SARS-CoV-2 VOC 202012/01 (UK variant) and D614G variant transmission by different routes in Syrian hamsters Sreelekshmy Mohandas https://www.biorxiv.org/content/10.1101/2021.03.26.437153v1?rss=1%22
In this investigation, we analyzed coronavirus disease 2019 (COVID-19) public health data from Parana, the largest state in southern half of Brazil, between September 1, 2020 and March 17, 2021, to evaluate recent trends in case fatality rates in different age groups. A total of 553,518 cases of SARS-CoV-2, 8,853 currently registered as fatal, were finally included in our analysis. . Patients aged 20-29 years experienced a tripling of their CFR, from 0.04% to 0.13%, while those aged 30-39, 40-49, 50-59 experienced approximate CFR doubling. Individuals between 20 and 29 years of age whose diagnosis was made in February 2021 had an over 3-fold higher risk of death compared to those diagnosed in January 2021 (Risk Ratio (RR): 3.15 [95%CI: 1.52-6.53], p<0.01), while those aged 30-39, 40-49, 50-59 years experienced 93% (1.93 [95%CI:1.31-2.85], p<0.01), 110% (RR: 2.10 [95%CI:1.62-2.72], p<0.01), and 80% (RR: 1.80 [95%CI:1.50-2.16], p<0.01) increases in risk of death, respectively. Notably, the observed CFR increase coincided with the second consecutive month of declining number of diagnosed SARS-CoV-2 cases. Taken together, these preliminary findings suggest significant increases in CFR in young and middle-aged adults after identification of a novel SARS-CoV-2 strain circulating in Brazil,	**26 mars** Sudden rise in COVID-19 case fatality among young and middle-aged adults in the south of Brazil after identification of the novel B.1.1.28.1 (P.1) SARS-CoV-2 strain: analysis of data from the state of Parana Maria Helena Santos de Oliveira, https://www.medrxiv.org/content/10.1101/2021.03.24.21254046v1?rss=1%22
Sera from 58 convalescent individuals collected up to 9 months after symptoms, similarly neutralized B.1.1.7 and D614G. In contrast, after 9 months, convalescent sera had a mean sixfold reduction in neutralizing titers, and 40% of the samples lacked any activity against B.1.351. Sera from 19 individuals vaccinated twice with Pfizer Cominarty, longitudinally tested up to 6 weeks after vaccination, were similarly potent against B.1.1.7 but less efficacious against B.1.351, when compared to D614G. Neutralizing titers increased after the second vaccine dose, but remained 14-	**26 mars** Sensitivity of infectious SARS-CoV-2 B.1.1.7 and B.1.351 variants to neutralizing antibodies • Delphine Planas https://www.nature.com/articles/s41591-021-01318-5

fold lower against B.1.351. In contrast, sera from convalescent or vaccinated individuals similarly bound the three spike proteins in a flow cytometry-based serological assay. Neutralizing antibodies were rarely detected in nasal swabs from vaccinees. Thus, faster-spreading SARS-CoV-2 variants acquired a partial resistance to neutralizing antibodies generated by natural infection or vaccination, which was most frequently detected in individuals with low antibody levels. Our results indicate that B1.351, but not B.1.1.7, may increase the risk of infection in immunized individuals.	
Initial COVID-19 vaccine candidates were based on the original sequence of SARS-CoV-2. However, the virus has since accumulated mutations, among which the spike D614G is dominant in circulating virus, raising questions about potential virus escape from vaccine-elicited immunity. Here, we report that the D614G mutation modestly reduced (1.7–2.4-fold) SARS-CoV-2 neutralization by BNT162b2 vaccine-elicited mouse, rhesus, and human sera, concurring with the 95% vaccine efficacy observed in clinical trial.	**25 mars** The effect of SARS-CoV-2 D614G mutation on BNT162b2 vaccine-elicited neutralization Jing Zou https://www.nature.com/articles/s41541-021-00313-8

22 - 26 mars 2021

Article de presse	**Extrait pertinent**	**Source scientifique**
25 mars Coronavirus: 'Double mutant' Covid variant found in India https://www.bbc.com/news/world-asia-india-56507988	The government said that an analysis of the samples collected from India's western Maharashtra state showed "an increase in the fraction of samples with the E484Q and L452R mutations" compared with December last year. "Such [double] mutations confer immune escape and increased infectivity," the health ministry said in a statement. Dr Jameel added that "there may be a separate lineage developing in India with the L452R and E484Q mutations coming together".	
The best supported models did not indicate a substantial difference in VOC transmissibility among different age groups. There is a consensus among all analyses that the VOC has a substantial transmission advantage with a 50% to 100% higher reproduction number. • We estimated the ratio of reproduction numbers between 25 October and 16 January to be 1.89 (95% CrI: 1.43-2.65) • By mid-January, the ratio fell from 1.89 to 1.54 (95%CI: 1.34-1.82)		**25 mars** Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England Erik Volz https://www.nature.com/articles/s41586-021-03470-x
https://www.quebec.ca/sante/problemes-de-sante/a-z/coronavirus-2019/situation-coronavirus-quebec/		

24 mars COVID-19 Des signaux rouges en zone orange https://www.lapresse.ca/debats/editoriaux/2021-03-24/covid-19/des-signaux-rouges-en-zone-orange.php		La France, l'Italie et l'Allemagne se reconfinent. En Ontario, en Colombie-Britannique et en Alberta, les cas et les hospitalisations sont repartis à la hausse. En Ontario et en France, où les taux de vaccination sont similaires à chez nous (entre 10 et 13 %), les admissions aux soins intensifs connaissent des hausses préoccupantes. Il faut regarder du côté du Royaume-Uni (45 % de la population vaccinée) pour trouver un exemple de pays où les hôpitaux connaissent un véritable répit. Au Michigan, dans un pays où trois fois plus de citoyens sont vaccinés qu'au Québec, le nombre de cas a doublé en deux semaines. Le New Jersey compte 315 cas par 100 000 habitants, quatre fois plus qu'au Québec. Les voyants qui clignotent ne viennent plus seulement de l'extérieur. Ils sont maintenant chez nous. Au Saguenay–Lac-Saint-Jean, en Outaouais et même dans le Bas-du-Fleuve, le passage en zone orange s'est accompagné d'une hausse rapide des cas. Contrairement à l'Ontario et à bien des pays européens, le Québec a encore une marge de manœuvre. Les variants finiront par devenir dominants, mais ils ne comptent actuellement que pour 30 % des cas. Cela nous donne une fenêtre pour vacciner à toute allure et tenter de les prendre de vitesse.

21 mars Vaccins contre la COVID-19 - De bonnes nouvelles sur les variants https://www.lapresse.ca/covid-19/2021-03-21/vaccins-contre-la-covid-19/de-bonnes-nouvelles-sur-les-variants.php	La plupart des études sur l'efficacité des vaccins se penchent sur la capacité des anticorps qu'ils génèrent à « neutraliser » le SARS-CoV-2, le coronavirus responsable de la COVID-19. Mais les anticorps ne font pas qu'attaquer directement les pathogènes. « Ils peuvent aussi appeler à l'aide d'autres mécanismes du système immunitaire », explique Andrés Finzi, du Centre de recherche du CHUM, qui est l'auteur principal de l'étude mise en ligne jeudi sur le site de prépublication scientifique BioRxiv. « On appelle cela la réponse effectrice médiée par les anticorps. Nous observons qu'un des types de réponses effectrices, ADCC [cytotoxicité cellulaire dépendante des anticorps], survient dès la première dose. » Cette « cytotoxicité » implique d'autres cellules que les anticorps, qui attaquent les pathogènes que leur désignent ces derniers. **18 mars** A single BNT162b2 mRNA dose elicits antibodies with Fc-mediated effector functions and boost pre-existing humoral and T cell responses https://www.biorxiv.org/content/10.1101/2021.03.18.435972v1 *Our results suggest that while the neutralization potency of vaccine-elicited antibodies is being developed, other antibody functions such as Fc-mediated effector functions could contribute to vaccine efficacy early on. Accordingly, three weeks after a single dose we observed strong ADCC but no neutralization activity (Figure 3). Strikingly, vaccination of previously-infected individuals induced a very significant increase of pre-existing humoral immunity including ADCC and neutralization. Neutralization potency was increased enabling neutralization of several variants including the B.1.1.7 variant, Spikes with the E484K mutation and even the phylogenetically more distant SARS-CoV-1. (…) These results give support to the consideration by various jurisdictions of a widened interval between the first and second dose in the context of vaccine shortage to protect a larger proportion of the population* **10 mars** The great escape? SARS-CoV-2 variants evading neutralizing responses https://www.cell.com/cell-host-microbe/pdf/S1931-3128(21)00089-5.pdf
Existing vaccines may protect against the Brazilian coronavirus variant. In the pre-print publication, available on bioRxiv, the authors report on the neutralization of these strains when using blood samples from both people who have natural antibodies generated from a COVID-19 infection and from those with antibodies generated from the ChAdOx1 nCoV-19 Oxford-AstraZeneca and BNT162b2 Pfizer-BioNTech vaccines. These data show a nearly three-fold reduction in the level of virus neutralisation by the antibodies generated by the	**19 mars** Antibody evasion by the Brazilian P.1 strain of SARS-CoV-2 https://www.biorxiv.org/content/10.1101/2021.03.12.435194v2

ChAdOx1 nCoV-19 and BNT162b2 vaccines for the B.1.1.7 (Kent) and P.1 (Brazil) variants when compared to the original 'Victoria' strain, and a 9-fold and 7.6-fold reduction respectively against the B.1.351 'South Africa' strain.

The authors comment that as P.1 and B.1.351 contain very similar changes in the receptor binding domain, it was assumed that the neutralizing antibodies would be similarly affected, meaning that vaccination will likely still provide some protection against P.1. They believe that the drop in vaccine efficacy against mild to moderate disease against B.1.351 is likely a reflection of the mutations occurring outside the receptor binding domain.

They further highlight that given the large reductions in neutralization tires, developing vaccine constructs to B.1.351 should be the greatest priority for vaccine developers globally. https://www.ox.ac.uk/news/2021-03-18-existing-vaccines-may-protect-against-brazilian-coronavirus-variant

19 mars

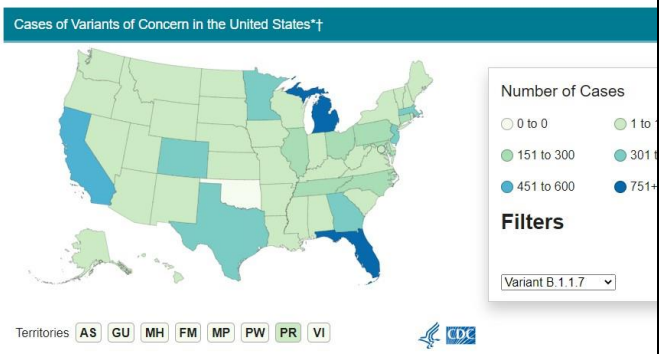
Fauci says the variant from the U.K. likely accounts for up to 30% of Covid infections in U.S. https://www.cnbc.com/2021/03/19/covid-fauci-says-the-variant-from-the-uk-likely-accounts-for-up-to-30percent-of-infections-in-us.html

- The highly contagious variant first identified in the U.K. likely accounts for up to 30% of Covid-19 infections in the United States, White House Chief Medical Advisor Dr. Anthony Fauci said.
- The variant, called B.1.1.7, has been reported in at least 94 countries and detected in 50 jurisdictions in the U.S., Fauci said.
- U.S. health officials say the variant could become the dominant strain in the U.S. by the end of this month or in early April.

US COVID-19 Cases Caused by Variants

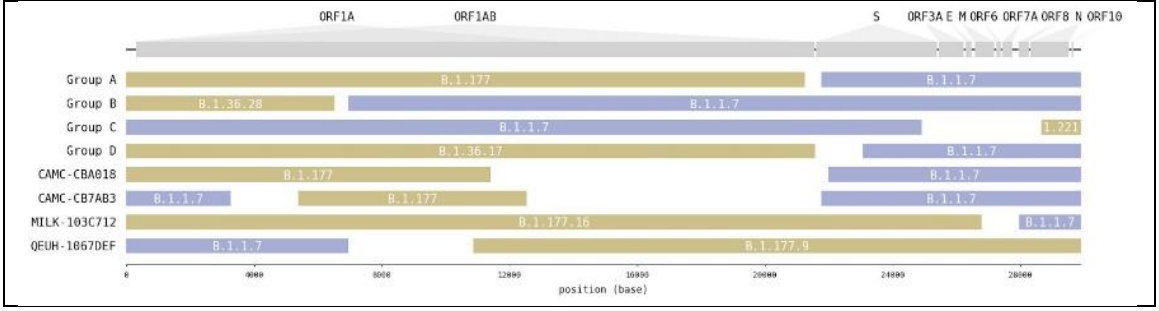
Updated Mar. 23, 2021 Languages Print

Variant	Reported Cases in US	Number of Jurisdictions Reporting
B.1.1.7	7501	51
B.1.351	219	27
P.1	61	18



A survey of SARS-CoV-2 genome sequences from the UK has detected a number of variants that had been assigned to the B.1.1.7 lineage but which do not contain the full set of

18 mars

B.1.1.7 'lineage defining' mutations [1]. Examination of these sequences revealed that some genome sections carry mutations characteristic of B.1.1.7, whilst other sections carry mutations specific to another lineage (Figure1; Table 1). Long runs of mutations along the SARS-CoV-2 that match different lineages are strongly indicative of virus recombination.	Recombinant SARS-CoV-2 genomes involving lineage B.1.1.7 in the UK https://virological.org/t/recombinant-sars-cov-2-genomes-involving-lineage-b-1-1-7-in-the-uk/658?fbclid=IwAR0hcJ1vurOmeQ9N0UJjNk8iBWpDcPeZb6-U2OfmOCrwUonKnd4ILKlHpZw
	

15 - 19 mars 2021

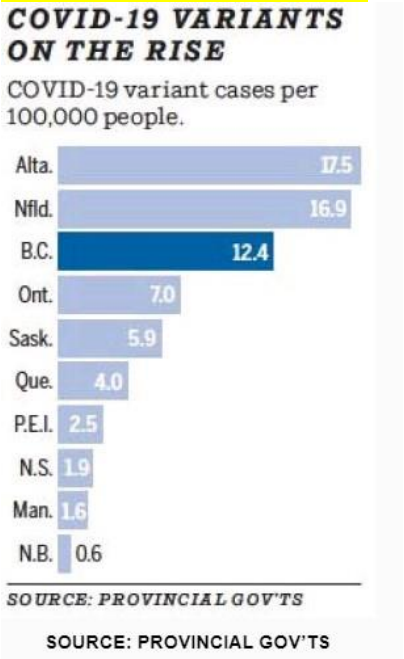
Article de presse	Extrait pertinent	Source scientifique
18 mars Troisième vague Paris et d'autres régions de France en confinement pour un mois dès samedi https://www.lapresse.ca/international/europe/2021-03-18/troisieme-vague/paris-et-d-autres-regions-de-france-en-confinement-pour-un-mois-des-samedi.php	Confinement, épisode 3 pour près d'un tiers des Français. La progression de l'épidémie s'accélère nettement » et elle « s'apparente de plus en plus clairement à une troisième vague » de COVID-19 avec les variants, a déclaré le premier ministre Jean Castex au cours d'une conférence de presse. La pression sur les services de réanimation, accueillant les malades les plus graves, est repartie à la hausse, avec 4246 malades, contre 4219 la veille, un nouveau plus haut depuis fin novembre. Plus d'un quart de ces patients (1201) sont hospitalisés en Île-de-France.	
18 mars Le vaccin d'AstraZeneca ne sera pas administré en Abitibi-Témiscamingue pour le moment https://ici.radio-canada.ca/nouvelle/1778324/vaccin-astrazeneca-variant-sudafricain-abitibi-temiscamingue	En raison de l'importante présence du variant du coronavirus sud-africain, la santé publique de l'Abitibi-Témiscamingue n'administrera pas le vaccin d'AstraZeneca, moins efficace contre les variants, du moins tant que le variant sera la souche prédominante dans la région. En quelques semaines, 100 cas du variant sud-africain ont été confirmés dans la région, et pas seulement dans la MRC d'Abitibi. La santé publique est en attente de résultats de criblage de 58 autres cas suspectés. On ne sent pas encore une stabilité au niveau de nos cas, et c'est important de continuer la vigilance, de limiter nos contacts; et les prochaines semaines seront déterminantes, notamment avec l'avancement de la vaccination, affirme la Dre Landry.	

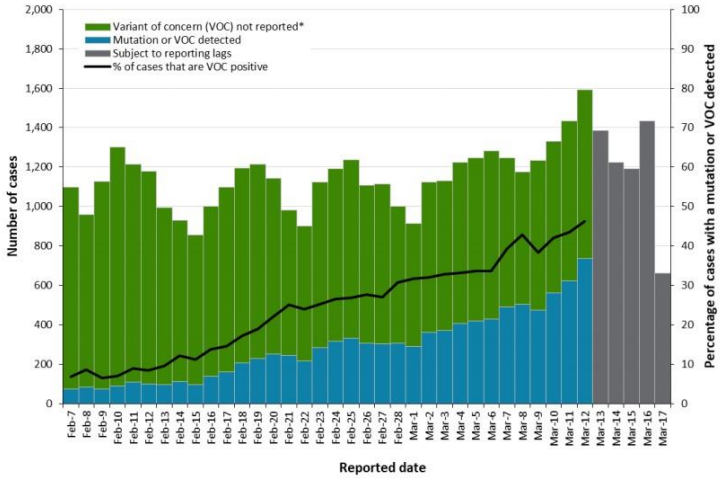
Tableau 2. Nombre cumulatif de variants préoccupants rapporté publiquement par lieu au Canada en date du 18 mars 2021

Lieu	Variant B.1.1.7	Variant B.1.351	Variant P.1
Canada	**4 169**	**241**	**89**
Colombie-Britannique	1 040	41	51
Alberta	1 169	17	2
Saskatchewan	129	6	0
Manitoba	63	13	0
Ontario	1 136	47	35
Québec	431	107	1
Terre-Neuve-et-Labrador	178	0	0
Nouveau-Brunswick	6	0	0
Nouvelle-Écosse	13	10	0
Île-du-Prince-Édouard	4	0	0
Yukon	0	0	0
Territoires du Nord-Ouest	0	0	0
Nunavut	0	0	0

18 mars
Nombre cumulatif de variants préoccupants rapporté publiquement par lieu au Canada en date du 18 mars 2021
https://sante-infobase.canada.ca/covid-19/resume-epidemiologique-cas-covid-19.html#VOC

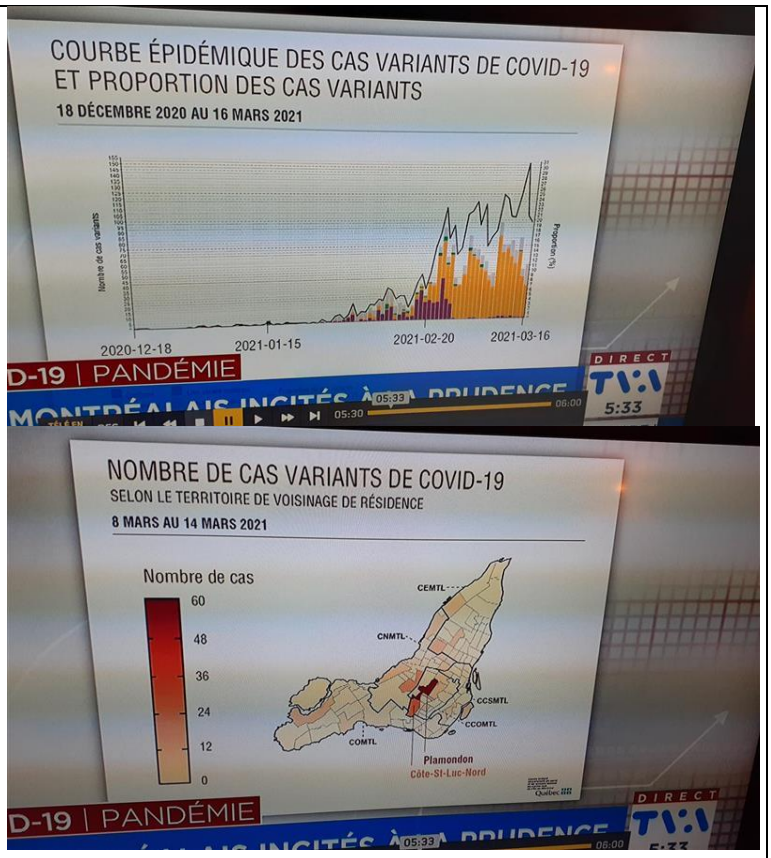
Vancouver Sun 12 mars 2021



<table>
<tr>
<td>Figure 5. Number of confirmed COVID-19 cases and percent positive for mutations or VOCs: Ontario, February 07, 2021 to March 17, 2021
Note: Data used to calculate the number of cases tested
 
</td>
<td>18 mars
SURVEILLANCE REPORT
COVID-19 Daily Epidemiological Summary
This daily report provides an epidemiological summary of COVID-19 activity in Ontario to date.</td>
</tr>
<tr>
<td>18 mars
Des parents de Côte-Saint-Luc bientôt vaccinés pour freiner les variants
https://www.ledevoir.com/societe/sante/597153/covid-19-des-parents-de-cote-saint-luc-bientot-vaccines-pour-freiner-les-variants</td>
<td>Afin de bloquer la propagation des variants de la COVID-19, la Direction régionale de santé publique (DRSP) de Montréal lancera vendredi un projet-pilote de vaccination auprès de milliers de parents d’enfants fréquentant des garderies et des écoles des secteurs de Plamondon et de Côte-Saint-Luc.

26 % des cas de variants détectés dans la métropole sont actuellement concentrés dans ces quartiers, a indiqué la DRSP jeudi midi, et l’on craint que ces formes plus agressives du SRAS-CoV-2 ne se propagent ailleurs, notamment dans des quartiers défavorisés où la forme originale du virus est déjà très présente.

Pas moins de 86 % des cas de variants recensés à ce jour dans ces quartiers proviennent des garderies et des écoles.</td>
</tr>
</table>

	
17 mars La relâche n'a pas happé Montréal https://www.lapresse.ca/covid-19/2021-03-17/covid-19/la-relache-n-a-pas-happe-montreal.php	Depuis février, 20 % des nouveaux cas de COVID-19 sont liés au variant britannique. En Ontario, où on vient de déclarer qu'une troisième vague était en cours, près de 50 % des nouveaux cas sont liés au variant. Dre Drouin, qui souligne qu'une troisième vague de COVID-19 est inévitable. Cette troisième vague « sera associée au variant britannique » et ce variant « cause jusqu'à 64 % plus de formes sévères de la maladie et de décès »
17 mars Les réinfections sont rares, mais un peu plus fréquentes chez les plus de 65 ans https://www.lapresse.ca/covid-19/2021-03-17/covid-19/les-reinfections-sont-rares-mais-un-peu-plus-frequentes-chez-les-plus-de-65-ans.php	C. H. Hansen *et al*. Assessment of protection against reinfection with SARS-CoV-2 among 4 million PCR-tested individuals in Denmark in 2020: a population-level observational study. *The Lancet*. Published online March 17, 2021. doi: 10.1016/S0140-6736(21)00575-4. En 2020, dans le cadre de la stratégie de tests PCR gratuites du Danemark, environ 4 millions d'individus (69 % de la population) ont subi 10,6 millions de tests L'évaluation à grande échelle des taux de réinfection confirme que seule une petite proportion de personnes (0,65 %) a eu un test PCR positif à deux reprises.

	Le taux d'infection (3,3 %) était cinq fois plus élevé chez les personnes déclarées positives au cours de la deuxième vague après avoir eu un test négatif lors de la 1re. Mais en prenant en compte l'âge, l'étude montre que 0,60 % (55/9137) des moins de 65 ans qui avaient eu la COVID-19 lors de la première vague, ont été déclarées à nouveau positives pendant la 2e vague, contre 0,88 % (17/1931) parmi les 65 ans ou plus. La protection contre une réinfection, conférée par l'infection naturelle, n'était donc que de 47 % parmi les personnes âgées de 65 ans ou plus, contre 80 % chez les plus jeunes, selon leur étude parue dans The Lancet. Les chercheurs se sont également penchés sur la protection contre la réinfection des agents de santé, en raison de leur risque élevé d'exposition au virus, et ont estimé qu'elle atteignait 81,1 %. Ils indiquent n'avoir « trouvé aucune différence » dans la protection estimée contre les infections répétées entre les deux sexes, ni preuve d'une diminution de la protection pendant les six à sept mois observés. Leur analyse s'est concentrée sur la souche COVID-19 historique et ne comporte aucune évaluation concernant des variants.
16 mars Retour en classe au secondaire: l'INSPQ s'inquiète de la multiplication des contacts https://www.lenouvelliste.ca/actualites/covid-19/retour-en-classe-au-secondaire-linspq-sinquiete-de-la-multiplication-des-contacts-f7017309c196eb7001309b959742bb1b	Finis les cours à distance une journée sur deux, les élèves de 3e à 5e secondaire seront bientôt de retour en classe à temps plein dans les zones orange. Une mesure non recommandée par l'INSPQ, qui privilégie toujours la diminution des contacts pour freiner la transmission du virus, surtout dans un contexte de multiplication des variants.

We analyse a dataset linking 2,245,263 positive SARS-CoV-2 community tests and 17,452 COVID-19 deaths in England from 1 September 2020 to 14 February 2021. For 1,146,534 (51%) of these tests, the presence or absence of B.1.1.7 can be identified because of mutations in this lineage preventing PCR amplification of the spike gene target (S gene target failure, SGTF[1]). Based on 4,945 deaths with known SGTF status, we estimate that the hazard of death associated with SGTF is 55% (95% CI 39–72%) higher after adjustment for age, sex, ethnicity, deprivation, care home residence, local authority of residence and test date. This corresponds to the absolute risk of death for a 55–69-year-old male increasing from 0.6% to 0.9% (95% CI 0.8–	**15 mars** Increased mortality in community-tested cases of SARS-CoV-2 lineage B.1.1.7 Nicholas G. Davies https://www.nature.com/articles/s41586-021-03426-1

1.0%) within 28 days after a positive test in the community. Correcting for misclassification of SGTF and missingness in SGTF status, we estimate a 61% (42–82%) higher hazard of death associated with B.1.1.7.	
14 mars COVID-19: les cas de variants se multiplient dans les écoles montréalaises https://www.journaldemontreal.com/2021/03/14/covid-19-les-cas-de-variants-se-multiplient-dans-les-ecoles-montrealaises	De nombreuses écoles montréalaises sont aux prises avec des éclosions de variants de la COVID-19 dans leurs établissements, ce qui a engendré des fermetures.

8 - 12 mars 2021

Article de presse	Extrait pertinent	Source scientifique
12 mars Variants et vaccination « Il faut accélérer la cadence » https://www.lapresse.ca/actualites/2021-03-12/variants-et-vaccination/il-faut-accelerer-la-cadence.php	Pour contrer la propagation des variants, « il faudrait que le taux de croissance des personnes vaccinées soit supérieur au taux de croissance du variant », En **Ontario**, de 30 % à 40 % des nouveaux cas de COVID-19 sont liés aux variants. Au **Québec**, 18 % des nouveaux cas enregistrés dans la dernière semaine sont liés aux variants, contre 13 % la semaine précédente. À **Montréal**, c'est 20 % des nouveaux cas qui sont liés au variant du Royaume-Uni. Et en **Abitibi-Témiscamingue**, 80 % des 36 nouveaux cas constatés dans la dernière semaine sont des cas suspectés du variant sud-africain.	
12 mars COVID-19 Une grande partie de l'Italie reconfinée à partir de lundi https://www.lapresse.ca/international/europe/2021-03-12/covid-19/une-grande-partie-de-l-italie-reconfinee-a-partir-de-lundi.php	Le gouvernement italien devrait annoncer vendredi le reconfinement d'une grande partie du pays à partir de lundi, entraînant la fermeture des écoles, bars et restaurants afin d'endiguer une troisième vague épidémique menaçant de saturer les hôpitaux. L'Italie, qui a passé cette semaine la barre des 100 000 morts dus à la pandémie, enregistre une forte hausse des contaminations et des décès, due en grande partie au variant britannique. Jeudi, les autorités ont fait état de 26 000 nouveaux cas et 373 morts en 24 heures.	
11 mars Novavax L'entreprise confirme l'efficacité de son vaccin contre la COVID-19 https://www.lapresse.ca/covid-19/2021-03-11/novavax/l-entreprise-confirme-l-	Les essais cliniques de phase 3 ont été conduits au Royaume-Uni sur plus de 15 000 personnes de 18 à 84 ans, dont 27 % avaient plus de 65 ans. L'efficacité était de 89,7 % contre les formes symptomatiques de la maladie, avec 96 cas de COVID-19 dans le groupe ayant reçu un placebo, contre 10 cas dans le groupe vacciné.	

efficacite-de-son-vaccin-contre-la-covid-19.php	Dans le détail, son efficacité était de 96,4 % contre la souche initiale du virus, et de 86,3 % contre le variant britannique (B.1.1.7), selon les résultats communiqués par l'entreprise. Un autre essai de plus petite ampleur (phase 2b) a par ailleurs été conduit sur 2665 participants en Afrique du Sud, où un autre variant (B.1351) s'est largement répandu. Là, l'efficacité du vaccin est tombée à 48,6 %. Preprint (3 mars) https://www.medrxiv.org/content/10.1101/2021.02.25.21252477v1
11 mars **Montréal Pas de retour à la normale avant septembre** **https://www.lapresse.ca/covid-19/2021-03-11/montreal/pas-de-retour-a-la-normale-avant-septembre.php**	La directrice régionale de santé publique de Montréal, la Dre Mylène Drouin, a indiqué qu'il est prévu que le variant britannique du coronavirus, qui représente actuellement 20 % des nouveaux cas dans la métropole, devienne la souche prioritaire vers la fin du mois de mars ou au début du mois d'avril.
11 mars **France : Situation sanitaire inquiétante, particulièrement en IDF, dit Véran** **https://www.latribune.fr/depeches/reuters/KBN2B32KQ/france-situation-sanitaire-inquietante-particulierement-en-idf-dit-veran.html**	"Le nombre de patients COVID en soins critiques réanimatoires a nettement augmenté cette dernière semaine (...) La pression sur les capacités de réanimation devrait encore s'accentuer dans les semaines à venir", a-t-il ajouté. Les variants plus contagieux du virus, qui sont désormais "la norme en France", a dit Olivier Véran, sont responsables de davantage d'admissions en unités de soins intensifs que ne l'était la version initiale du coronavirus.
11 mars Variants of concern cause more than 40% of new COVID-19 cases in Ontario, experts say **https://www.cbc.ca/news/canada/toronto/covid-19-ontario-march-11-2021-variants-of-concern-1.5945381?cmp=rss**	Variants of concern are currently responsible for about 42 per cent of new daily cases of COVID-19 in Ontario, the province's science advisory table said Thursday. The group, made up of health experts and professionals, launched a new online dashboard focused on the variants of concern (VOCs). It shows that the variants continue to spread. The data is more or less right on track with what was predicted in models released by the table in late February. As of yesterday, however, 6,513 test samples had screened positive for the tell-tale mutation that indicates the presence of a VOC. Labs are still trying to pinpoint specific variants in the vast majority of those samples.

View Count: **3809**

Current Status

Latest Reproduction Number R(t)	
New Variants of Concern	1.24
Early Variants	0.90
Estimated Number of Cases per Day (7-Day Average)	
New Variants of Concern	451
Early Variants	620
Estimated Incidence per 100,000 per Week (7-Day Average)	
New Variants of Concern	21.7
Early Variants	29.8
Estimated Percentage of Cases	
New Variants of Concern	42%
Early Variants	58%

Status Report, 11-Mar-2021

Note that the new variants of concern (VOC) are the more transmissible variants with N501Y mutations originally identified in the United Kingdom (B.1.1.7), South Africa (B.1.351) and Brazil (P.1); B.1.1.7 is currently the dominating VOC. Early variants include all the non-VOC SARS-CoV-2 viruses without N501Y mutation.

Tableau 2. Nombre cumulatif de variants préoccupants rapporté publiquement par lieu au Canada en date du 10 mars 2021

Lieu	Variant B.1.1.7	Variant B.1.351	Variant P.1
Canada	**2 641**	**207**	**32**
Terre-Neuve-et-Labrador	88	0	0
Île-du-Prince-Édouard	4	0	0
Nouvelle-Écosse	11	8	0
Nouveau-Brunswick	6	0	0
Québec	235	97	1
Ontario	921	39	17
Manitoba	11	11	0
Saskatchewan	64	6	0
Alberta	721	13	0
Colombie-Britannique	580	33	14
Yukon	0	0	0
Territoires du Nord-Ouest	0	0	0
Nunavut	0	0	0

Remarque : Données en date du 10 mars 2021. Le tableau présente les données rapportées publiquement par les

Figure 5. Number of confirmed COVID-19 cases and percent positive for mutations or VOCs: Ontario, February 07, 2021 to March 10, 2021

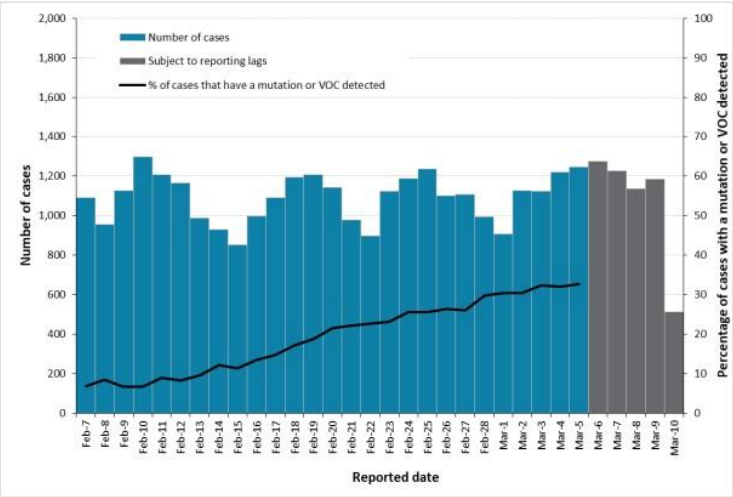
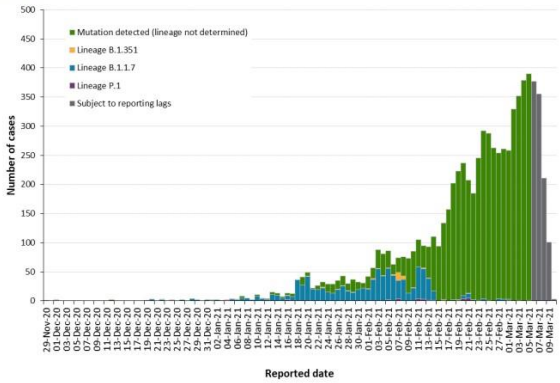


Figure 6. Confirmed COVID-19 cases with a mutation or VOC detected by public health unit reported date: Ontario, November 29, 2020 to March 10, 2021



[COVID-19 in Ontario: January 15, 2020 to March 10, 2021]

Table 8. Summary of confirmed COVID-19 cases with a mutation or VOC detected by age group and gender: Ontario

	Lineage B.1.1.7	Lineage B.1.351	Lineage P.1	Mutation detected (lineage not determined)	Cumulative case count as of March 10, 2021
Gender: Male	469	21	19	3,345	3,854
Gender: Female	485	20	9	3,094	3,608
Ages: 19 and under	128	2	3	1,134	1,267
Ages: 20-39	358	17	11	2,521	2,907
Ages: 40-59	260	12	10	1,881	2,163
Ages: 60-79	145	9	4	833	991
Ages: 80 and over	65	1	0	144	210

Note: Not all cases have a reported age or gender reported. Data corrections or updates can result in

Table 9. Summary of confirmed COVID-19 cases with a mutation or VOC detected by likely source of acquisition: Ontario

	Lineage B.1.1.7	%	Lineage B.1.351	%	Lineage P.1	%	Mutation detected (lineage not determined)	%	Cumulative case count up to March 10, 2021	Cumulative percentage
Travel	50	5.2%	8	19.5%	1	3.6%	187	2.9%	246	3.3%
Outbreak-associated or close contact of a confirmed case	703	73.5%	30	73.2%	17	60.7%	4,273	65.6%	5,023	66.6%
Epidemiological link – type unspecified	0	0.0%	0	0.0%	0	0.0%	0	0.0%	0	0.0%
No known epidemiological link	196	20.5%	3	7.3%	10	35.7%	1,558	23.9%	1,767	23.4%
Information missing or unknown	7	0.7%	0	0.0%	0	0.0%	495	7.6%	502	6.7%
Total	**956**		**41**		**28**		**6,513**		**7,538**	

Note: Information for how cases are grouped within each category is available in the technical notes. Data for cases with a B.1.1.7, B.1.351, and

11 mars Virus: hausse des contaminations en Allemagne, confrontée à une «troisième vague» https://www.journaldemontreal.com/2021/03/11/virus-hausse-des-contaminations-en-allemagne-confrontee-a-une-troisieme-vague	Le taux d'incidence a bondi à 69,1, contre 65,4 mercredi. Sur les sept derniers jours, 61 005 personnes sont tombées malades, contre 57 255 la semaine dernière. Cette hausse des infections, après plusieurs semaines de baisse, puis de stagnation, inquiète les autorités sanitaires. D'autant que le variant britannique du coronavirus, considéré comme plus contagieux, s'impose rapidement dans le pays: il représente désormais 55 % des cas diagnostiqués, contre 46 % début mars, selon l'institut Robert Koch.
10 mars COVID-19 variant has overwhelmed Brazil's healthcare system, expert says https://globalnews.ca/news/7688699/brazil-hospital-coronavirus7688699/	New COVID-19 cases continue to decline in North America, but in Latin America infections are still rising, particularly in Brazil where a resurgence has caused record daily deaths, the Pan American Health Organization (PAHO) warned on Wednesday. A new variant first discovered late last year has led to a surge in new infections there that have overwhelmed the health care system, which continues to experience widespread shortages of medical supplies, including oxygen, she said.

10 mars COVID-19: le variant anglais est 64 % plus mortel, selon une étude **https://www.journaldemontreal.com/2021/03/10/covid-19-le-variant-anglais-est-64--plus-mortel-selon-une-etude**	Ses auteurs se sont basés sur les données de 110 000 personnes testées positives hors hôpital entre octobre et janvier, qu'ils ont suivies durant 28 jours. La moitié avait été infectée par le coronavirus classique, l'autre par le variant anglais (appelé VOC 202012/01 ou B.1.1.7, du nom de sa «lignée», c'est-à-dire sa famille génétique). Les chercheurs ont comparé la mortalité dans l'un et l'autre des deux groupes (141 décès contre 227), en prenant en compte certains facteurs comme l'âge, le sexe ou l'origine ethnique, et ont estimé que le variant anglais était 64 % plus mortel. *BMJ* 2021; 372 doi: https://doi.org/10.1136/bmj.n579
10 mars Two variants may account for half of New York City's virus cases, analysis finds. https://www.nytimes.com/2021/03/10/nyregion/virus-variants-nyc.html	One of the so-called variants, first detected in the city, now accounts for nearly 40 percent of all cases analyzed in local laboratories. The increase in the variant, B.1.526, was so striking that officials said they believed it was more infectious than the original form of the coronavirus. He and his colleagues have found two subtypes of the B.1.526 variant: one with the E484K mutation seen in South Africa and Brazil, which is thought to help the virus partially dodge the vaccines; and another with a mutation called S477N, which may affect how tightly the virus binds to human cells. "Our preliminary analysis does not show that this new strain causes more severe illness or reduces the effectiveness of vaccines," said Dr. Jay Varma, an adviser to Mr. de Blasio. Another more contagious variant, B.1.1.7, first discovered in Britain, also is spreading steadily in the city, accounting for 12 percent of cases analyzed in the last week of February, up from 8 percent the prior week. B.1.1.7 may be more lethal than earlier versions of the virus.
Here, data from the national healthsurveillance of hospitalized individuals and frequency of the P.1 variant were analysed using a model-based approach to estimate P.1 parameters of transmissibility and reinfection by maximum likelihood. The new variant transmissibility was found to be about 2.5 times higher (Confidence Interval (95%CI): 2.3-2.8) compared to the previous variant in Manaus. A low probability of reinfection by the new variant (6.4%, 95%CI: 5.7-7.1%).) was estimated, even under initial high prevalence (68%, 95%CI: 63-74%), by the time P.1 emerged.	**9 mars** **Renato M. Coutinho et coll. (Brésil)** Model-based estimation of transmissibility and reinfection of SARS-CoV-2 P.1 variant https://www.medrxiv.org/content/10.1101/2021.03.03.21252706v2
8 mars Les Américains vaccinés peuvent se réunir sans masque https://www.lapresse.ca/international/etats-unis/2021-03-08/les-americains-vaccines-	**Directrice des Centres pour le contrôle et la prévention des maladies (CDC).** La vaccination rapide aux États-Unis (…) une proportion six fois plus grande de la population qu'au Canada a reçu deux doses de vaccin. « Les gens qui sont vaccinés sont moins susceptibles d'avoir une infection asymptomatique et potentiellement moins susceptibles de transmettre à d'autres

peuvent-se-reunir-sans-masque.php	le SARS-CoV-2 », Les CDC ne recommandent toutefois pas aux personnes complètement vaccinées de voyager d'un État à l'autre, pour éviter de stimuler la circulation des variants **Cédric Yansouni, microbiologiste-infectiologue au Centre universitaire de santé McGill (CUSM).** Il faut aussi prendre en compte la possibilité de dissémination de variants qui pourraient être moins résistants aux vaccins actuels. Dès que 25 % d'une population est protégée, il y a une pression de sélection qui favoriserait les variants moins susceptibles aux vaccins. Alors il y a une course contre la montre. » « Même si les vaccins sont très efficaces, le risque de transmission du virus par une personne vaccinée n'est certainement pas réduit à zéro, dit le Dr Yansouni. Il est probablement réduit des deux tiers. Dans un contexte de circulation des variants, ça demeure problématique. »

1 - 5 mars 2021

Article de presse	Extrait pertinent	Source scientifique
4 mars Le variant britannique pourrait être la souche dominante ce printemps https://www.lapresse.ca/covid-19/2021-03-04/covid-19-au-quebec/le-variant-britannique-pourrait-etre-la-souche-dominante-ce-printemps.php	INSPQ Épidémiologie et modélisation de l'évolution de la COVID-19 : projections du 4 mars 2021 https://www.inspq.qc.ca/covid-19/donnees/projections/4-mars-2021 • Les projections incluent la vaccination des résidents de Résidences pour ainés (RPA) et des personnes de 70 ans et plus vivant à domicile, selon le calendrier actuel du gouvernement (incluant un retard possible de deux semaines). L'impact de la vaccination est modélisé avec 75-85 % d'efficacité, trois semaines après la première dose. L'efficacité vaccinale est la même pour la souche initiale et le variant. • Les projections incluent l'arrivée d'un variant plus transmissible dans le Grand Montréal et dans les Autres régions. Les projections sont basées sur l'hypothèse que le variant est 1,4 à 1,9 fois plus transmissible par contact et 1,1 à 1,5 fois plus sévère (risque d'hospitalisation ou de décès par cas) que la souche initiale.	
4 mars Le « cocktail variants et semaine de relâche » tenu à l'œil https://www.lapresse.ca/covid-19/2021-03-04/montreal-reste-en-zone-rouge/le-cocktail-variants-et-semaine-de-relache-tenu-a-l-oeil.php	« Le portrait épidémiologique de Montréal a atteint un certain plateau », (…) Mais « clairement, nos indicateurs sont encore au palier rouge selon les seuils indiqués », a-t-elle poursuivi. Et les variants, qui étaient responsables de 12 % des nouveaux cas à Montréal la semaine dernière, en représentent maintenant 15 % à 16 %. Les milieux scolaires sont en effet les plus touchés à Montréal, avec 43 éclosions associées à des variants, contre une vingtaine en milieux de travail, sept dans les services de garde, une en CHSLD et une autre dans une résidence pour	

<table>
<tr><td></td><td>aînés. Plus de la moitié des éclosions détectées dans des écoles, soit 26, ne comptaient cependant qu'un seul cas.

De plus, on ne recense aucun décès associé à un variant, et très peu d'hospitalisations. « Ça se compte sur doigts d'une main », a indiqué la Dre Drouin

Dre Drouin en conférence de presse</td></tr>
<tr><td>4 mars
Nombre cumulatif de variants préoccupants rapporté publiquement par lieu au Canada
https://sante-infobase.canada.ca/covid-19/resume-epidemiologique-cas-covid-19.html#VOC</td><td>
<table>
<tr><th>Lieu</th><th>Variant B.1.1.7</th><th>Variant B.1.351</th><th>Variant P.1</th></tr>
<tr><td>Canada</td><td>1 552</td><td>114</td><td>3</td></tr>
<tr><td>Terre-Neuve-et-Labrador</td><td>19</td><td>0</td><td>0</td></tr>
<tr><td>Île-du-Prince-Édouard</td><td>3</td><td>0</td><td>0</td></tr>
<tr><td>Nouvelle-Écosse</td><td>6</td><td>1</td><td>0</td></tr>
<tr><td>Nouveau-Brunswick</td><td>6</td><td>0</td><td>0</td></tr>
<tr><td>Québec</td><td>94</td><td>41</td><td>0</td></tr>
<tr><td>Ontario</td><td>664</td><td>31</td><td>3</td></tr>
<tr><td>Manitoba</td><td>6</td><td>2</td><td>0</td></tr>
<tr><td>Saskatchewan</td><td>5</td><td>1</td><td>0</td></tr>
<tr><td>Alberta</td><td>531</td><td>10</td><td>0</td></tr>
<tr><td>Colombie-Britannique</td><td>218</td><td>28</td><td>0</td></tr>
<tr><td>Yukon</td><td>0</td><td>0</td><td>0</td></tr>
<tr><td>Territoires du Nord-Ouest</td><td>0</td><td>0</td><td>0</td></tr>
<tr><td>Nunavut</td><td>0</td><td>0</td><td>0</td></tr>
</table>
</td></tr>
<tr><td>3 mars
Un vaccin anti-variant sud-africain pourrait immuniser contre d'autres variants
https://www.lapresse.ca/covid-19/2021-03-03/un-vaccin-anti-variant-sud-africain-pourrait-immuniser-contre-d-autres-variants.php</td><td>Une étude préliminaire réalisée en Afrique du Sud tend à montrer que les personnes contaminées par le variant sud-africain du nouveau coronavirus possèdent une meilleure immunité face aux autres mutations du virus, ont annoncé mercredi des experts.

Selon les données de cette étude, présentées par un groupe de scientifique du Réseau de Surveillance génomique de l'Afrique du Sud, seuls 4 % des 55 sujets déjà infectés par le 501Y.V2 n'ont pu venir à bout d'une contamination à la souche originale du nouveau coronavirus.

Selon cette étude, les anticorps générés par le variant sud-africain se sont également avérés efficaces à 100 % contre le variant brésilien, sur un échantillon toutefois très faible, de sept patients.

Le laboratoire américain Moderna a récemment annoncé qu'il commencerait mi-mars un essai clinique d'une version de son vaccin spécialement adaptée au variant sud-africain.</td></tr>
<tr><td>2 mars
Brazil variant evaded up to 61% of immunity in previous Covid cases, study finds
https://www.theguardian.com/world/2021/mar/02/brazil-variant-evaded-immunity-previous-covid-cases</td><td>The coronavirus variant originally found in Manaus in Brazil and detected in six cases in the UK was able to infect 25% to 61% of the people in the Amazonian city who might have expected to be immune after a first bout of Covid, researchers say. (…) The variant, called P1, not only has potential to evade the immune protection of previous illness or vaccines, but is more transmissible than the original coronavirus. The study in Manaus, which has not yet been published in peer-reviewed form, found it was about 1.4 to 2.2 times more transmissible than the original virus.(…) Manaus,</td></tr>
</table>

	the largest city in the Amazon basin, suffered a first wave of Covid in April/May. Studies of blood donors suggested 66% of people had antibodies against the virus in July and 76% by October, which would have been expected to give them immunity. But the city suffered a serious second wave. There could have been various explanations, including the possibility that the data on previous infection was wrong, but the team of researchers identified the P1 variant on 6 December. It spread rapidly: within eight weeks, it was implicated in 87% of cases.
1 mars Abitibi-Témiscamingue Le variant de l'Afrique du Sud encore « bien présent » https://www.lapresse.ca/covid-19/2021-03-01/abitibi-temiscamingue/le-variant-de-l-afrique-du-sud-encore-bien-present.php	La région compte un total de 40 cas confirmés du variant de l'Afrique du Sud, selon le site de l'INSPQ qui effectue une surveillance des variants au Québec. En point de presse lundi, les autorités régionales ont indiqué que 28 des cas remontaient cependant à l'éclosion survenue en janvier, qui est maintenant terminée. (…) Douze cas positifs au variant sud-africain sont donc liés à l'éclosion à l'école Notre-Dame-de-Fatima de Landrienne (…) Dix-huit personnes ont été déclarées positives à la COVID-19 dans cette école, dont 16 élèves et deux enseignants.(…) « On constate que la transmission se fait plus rapidement et plus facilement », assure-t-elle. Par exemple, dans les foyers où une personne est contaminée presque tout le monde va l'avoir ce qui n'était pas nécessairement le cas avec la souche initiale du coronavirus, a vulgarisé Dre Sobanjo. (…)Les autorités régionales ignorent toujours comment le variant de l'Afrique du Sud a pu s'introduire en Abitibi-Témiscamingue. Toutes les personnes interrogées dans le cadre des enquêtes épidémiologiques n'ont pas voyagé à l'étranger (…)Il ne semble pas avoir de « lien direct » entre l'éclosion survenue en janvier et celle de la mi-février à Landrienne.
1 mars Dépistage de masse Des tests automatisés bloqués par une exigence de dernière minute https://www.lapresse.ca/covid-19/2021-03-01/depistage-de-masse/des-tests-automatises-bloques-par-une-exigence-de-derniere-minute.php	La sensibilité des tests de Diagnostiques Lilium, 100 fois plus élevée que celle des machines Cobas 8800 récemment acquises par le gouvernement, est aussi la clé pour venir à bout de la pandémie, dit M. Ahlfors, ajoutant que sa plateforme de tests RT-PCR peut simultanément détecter les variants spécifiques du Royaume-Uni, d'Afrique du Sud et du Brésil, ce qu'aucune autre plateforme de PCR au Canada ne peut faire pour le moment.
SURVEILLANCE REPORT **24 février** Enhanced Epidemiological Summary COVID-19 Variants of Concern in Ontario: December 1, 2020 to February 15, 2021 https://www.publichealthontario.ca/-/media/documents/ncov/epi/covid-19-variant-epi-summary.pdf?la=en • Laboratory Data	**Page Web - PHO** COVID-19 Variants of Concern (VOCs) https://www.publichealthontario.ca/en/diseases-and-conditions/infectious-diseases/respiratory-diseases/novel-coronavirus/variants

<table>
<tr><td colspan="2">

- Case Characteristics
- Geography
- Cases Over Time
- Severity and Outcome
- Likely Source of Acquisition
- Technical Notes
- References

Mise à jour du 4 mars
Daily Epidemiologic Summary COVID-19 in Ontario: January 15, 2020 to March 01, 2021
https://www.publichealthontario.ca/-/media/documents/ncov/epi/covid-19-daily-epi-summary-report.pdf?la=en

- Summary of confirmed variant of concern (VOC) cases: Ontario
- Confirmed COVID-19 variants of concern (VOC) cases by public health unit reported date
- Summary of confirmed variant of concern (VOC) cases by age group and gender: Ontario
- Summary of confirmed variant of concern (VOC) cases likely source of acquisition
- Technical Notes: Data Sources, Data Caveats

</td></tr>
<tr><td>New research shows California coronavirus variant is more transmissible
https://www.washingtonpost.com/health/california-covid-variant/2021/02/24/0fb75550-76a3-11eb-948d-19472e683521_story.html</td><td>A separate study from scientists at the University of Washington, posted Monday to the preprint server BioRxiv and not yet peer-reviewed, found that a mutation known as L452R in the California variant gives the virus an advantage in binding to receptors in human cells. The authors write that “the positive selection for this mutation became particularly strong only recently, possibly reflecting viral adaptation to the containment measures or increasing population immunity.</td></tr>
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New COVID-19 variants found in New York, California
https://www.cidrap.umn.edu/news-perspective/2021/02/new-covid-19-variants-found-new-york-california

In New York, a new variant that carries a mutation that may weaken the effectiveness of COVID-19 vaccines has been identified as the B.1.526 variant. In a paper published today from Columbia University, the authors noted a steady increase in the detection rate of B.1.526 cases from late December to mid-February, with a rise of 12.3% in the past 2 weeks.

In California, variant B.1.427/B.1429 now makes up more than 50% of cases in 44 counties, according to the Washington Post. Researchers believe that strain is more transmissible because of a mutation that enables the virus to more easily bind to human receptor cells.

25 février
Annavajhala et al. (USA)
A Novel SARS-CoV-2 Variant of Concern, B.1.526, Identified in New York
https://www.medrxiv.org/content/10.1101/2021.02.23.21252259v1

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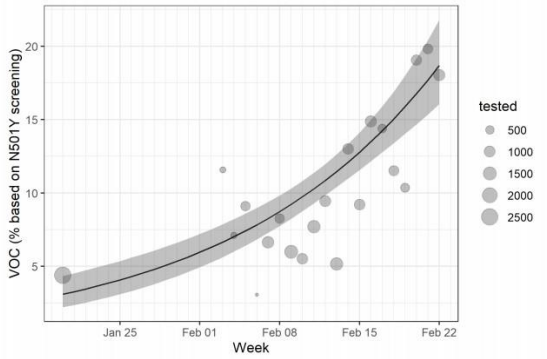
</table>

Article de presse	Extrait pertinent	Source scientifique
25 février Variants will likely make up 40% of Ontario's COVID-19 cases by mid-March, modelling predicts https://www.cbc.ca/news/canada/toronto/covid-19-ontario-february-25-2021-1.5927580?cmp=rss	Le groupe d'experts qui conseille le gouvernement affirme que des variants plus contagieux représenteront probablement 40 % de tous les cas dans cette province d'ici la deuxième semaine de mars province's latest projections Variants of Concern (VOC) continue to spread quickly in Ontario (likely 40% of cases in second week of March)  	
25 février Hausse des cas de COVID-19 La Finlande serre la vis https://www.lapresse.ca/international/europe/2021-02-25/hausse-des-cas-de-covid-19/la-finlande-serre-la-vis.php	Selon la première ministre Sanna Marin, « **nos précédents outils ne sont plus suffisants pour contrôler la situation** ». Le variant britannique du coronavirus « a rapidement aggravé la situation », a-t-elle déclaré. Mi-février, le pays a vu la hausse du nombre de nouveaux cas s'accélérer, passant de 46 par 100 000 personnes à 62 en une semaine. À ce jour, 690 cas de variants au coronavirus ont été détectés en Finlande – sur un total de plus de 55 000 cas. Parmi eux, 660 sont issus du variant britannique, selon les chiffres publiés mercredi par le gouvernement.	
25 février Plus de 2,5 millions de décès de la COVID-19 https://www.lapresse.ca/covid-19/2021-02-25/plus-de-2-5-millions-de-deces-de-la-covid-19.php	Les dirigeants européens réunis en visioconférence ont appelé à « maintenir des restrictions fermes ». En France, le variant anglais, plus contagieux, « concerne désormais à peu près **la moitié des personnes** » contaminées par la COVID-19, (…) vingt départements étaient placés sous « surveillance renforcée » en raison d'une circulation accrue de l'épidémie, et pourront faire l'objet de mesures de confinements locaux à partir du week-end du 6 mars si la situation continuait à se dégrader. Au Royaume-Uni en revanche, **la situation s'améliore**. Les autorités sanitaires britanniques ont décidé jeudi d'abaisser le niveau d'alerte relatif à la pandémie de COVID-19, le risque de saturation des hôpitaux ayant « reculé » dans ce pays, soumis à un sévère confinement depuis début janvier.	
25 février	L'alliance **Pfizer-BioNTech** va proposer une troisième dose de son vaccin contre la COVID-19 aux participants de leur	

Pfizer testera l'efficacité d'une troisième dose de son vaccin https://www.lapresse.ca/covid-19/2021-02-25/variants/pfizer-testera-l-efficacite-d-une-troisieme-dose-de-son-vaccin.php	essai clinique initial, afin d'évaluer son effet possible sur un renforcement immunitaire face aux variants du virus, ont annoncé les deux entreprises jeudi. Les participants de la phase 1 de leur essai clinique aux États-Unis se verront ainsi offrir une troisième dose « 6 à 12 mois » après avoir reçu les deux premières, « dans le cadre de la stratégie de développement clinique des deux entreprises pour évaluer l'efficacité d'une troisième dose contre les variants » en circulation ou futurs. Pfizer et BioNTech précisent également être en « discussions avec les autorités de régulation » pour soumettre une version modifiée de leur vaccin « avec une séquence spécifique aux variants ». La société de biotechnologie américaine **Moderna** – à l'origine de l'autre vaccin autorisé aux États-Unis –, a de son côté annoncé mercredi qu'une version modifiée de son vaccin, développée spécifiquement contre le variant sud-africain, était prête à être testée sur des humains dans le cadre d'essais cliniques. L'Agence américaine des médicaments (FDA) avait indiqué lundi que les fabricants n'auraient pas à conduire de nouveau les longs essais cliniques pour les versions modifiées de leurs vaccins déjà autorisés,
24 février New research shows California coronavirus variant is more transmissible https://www.washingtonpost.com/health/california-covid-variant/2021/02/24/0fb75550-76a3-11eb-948d-19472e683521_story.html	The new California research contends that the variant, which goes by two names, B.1.427 and B.1.429, has spread widely because it is more transmissible. • In laboratory experiments, researchers created a version of the virus and found that it was **more efficient at infecting cells and lung tissue** growing in a dish. • They also found that **the amount of virus in people's noses was significantly higher** for people infected with the variant than for others. A separate study from scientists at the University of Washington, posted Monday to the preprint server BioRxiv and not yet peer-reviewed, found that a **mutation known as L452R in the California variant gives the virus an advantage in binding to receptors in human cells**. Separately, researchers have identified a mutation in a spot on the virus called Q677, which initially was detected in variants in Louisiana and New Mexico. It has popped up independently in seven variants in what appears to be a case of "convergent evolution." Scientists worry when a specific mutation keeps appearing in scattered locations, because it suggests that this genetic change reliably gives the virus an advantage.
24 février	Plus de 300 cas du nouveau variant du Royaume-Uni sont actuellement suspectés à Montréal. **Et les trois quarts des**

Les élèves du primaire en zone rouge devront porter le masque médical https://www.lapresse.ca/covid-19/2021-02-24/les-eleves-du-primaire-en-zone-rouge-devront-porter-le-masque-medical.php	**22 éclosions liées à cette souche sont dans des écoles primaires.** Des 300 cas suspectés, 40 % touchent des jeunes de moins de 18 ans. Et 20 %, des adultes de 35 à 44 ans, souvent leurs parents. « La distribution est beaucoup chez les moins de 50 ans. On a très peu de cas chez la population aînée actuellement Actuellement, environ de 8 % à 10 % des nouveaux cas sont liés aux variants. « Il faut continuer de maintenir les mesures populationnelles et réduire les contacts »
23 février Des écoles sur le pied d'alerte https://www.lapresse.ca/covid-19/2021-02-23/variants/des-ecoles-sur-le-pied-d-alerte.php	Malgré la baisse sensible du nombre de nouveaux cas de COVID-19, **12 écoles ont été fermées entièrement ou partiellement au Québec,** en raison d'une possible contamination aux variants. La grande majorité de ces établissements se trouvent dans la région de Montréal.
22 février Études britanniques Les vaccins contre la COVID-19 diminuent les hospitalisations https://www.lapresse.ca/covid-19/2021-02-22/etudes-britanniques/les-vaccins-contre-la-covid-19-diminuent-les-hospitalisations.php	Les résultats préliminaires d'une étude en Écosse ont révélé que le vaccin Pfizer-BioNTech réduisait les admissions à l'hôpital jusqu'à 85 % quatre semaines après la première dose, tandis que le vaccin Oxford-AstraZeneca réduisait les admissions jusqu'à 94 %. En Angleterre, les données préliminaires d'une étude sur les **travailleurs de la santé** suggèrent que le vaccin de Pfizer diminue le risque d'attraper la COVID-19 de 70 % après une dose, un chiffre qui est passé à 85 % après la seconde. L'agence de santé publique anglaise Public Health England a réalisé une étude sur les **travailleurs de la santé**, qui laisse croire que le vaccin peut aider à prévenir la transmission du virus, « car vous ne pouvez pas propager le virus si vous n'avez pas d'infection ». Les résultats sont basés sur des tests de COVID-19 effectués toutes les deux semaines qui détectent les infections, que quelqu'un présente ou non des symptômes.
20 février La vigilance reste de mise, affirme la Dre Theresa Tam https://www.lapresse.ca/covid-19/2021-02-20/700-cas-des-differents-variants/la-vigilance-reste-de-mise-affirme-la-dre-theresa-tam.php	Les autorités sanitaires du pays ont identifié, en date du 18 février, **plus de 700 cas des différents variants** de la COVID-19 dans l'ensemble du pays En date de jeudi, • 664 cas du variant britannique, • 39 du variant sud-africain et • 1 du variant brésilien ont été identifié au pays.

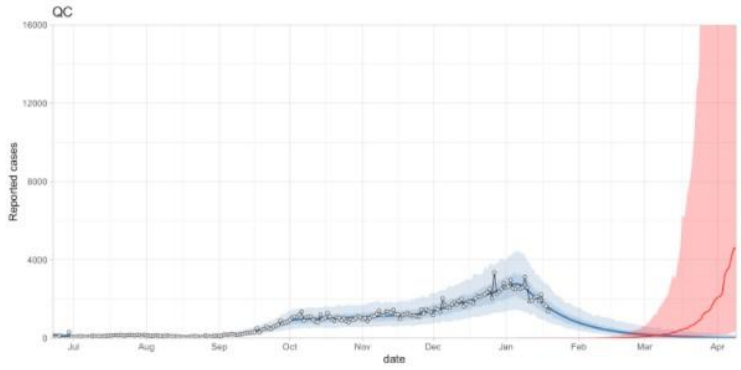
Introduction of **the E484K** mutation in a B.1.1.7 background to reflect newly emerging viruses in the UK led to a more substantial loss of neutralising activity by vaccine-elicited antibodies and mAbs (19 out of 31) over that conferred by the B.1.1.7 mutations alone. E484K emergence on a B.1.1.7 background represents a threat to the **vaccine BNT162b**.	**15 février** **Collier et al. (UK)** SARS-CoV-2 B.1.1.7 sensitivity to mRNA vaccine-elicited, convalescent and monoclonal antibodies

	https://www.medrxiv.org/content/10.1101/2021.01.19.21249840v4
Action Plan 1. Assess the impact of new variants on viral detection with existing platforms. 2. Develop approaches for variant screening. 3. Actively monitor for emergence of variants in the clinical laboratory. 4. Consider enhanced retrospective testing for special populations with prolonged COVID-19 positivity (e.g., multiple strong positive nucleic acid test results over at least a month; patients with prior documented COVID-19 that have a new positive SARS-CoV-2 test results after a period of negativity (re-infection), or >90 days after their first documented positive)	**30 janvier** **Filkins et al. (USA)** Laboratory action plan for emerging SARS-CoV-2 variants https://academic.oup.com/clinchem/advance-article/doi/10.1093/clinchem/hvab020/6124354

15 - 19 février 2021

Article de presse	Extrait pertinent	Source scientifique
To test whether acute infection with B.1.1.7 is associated with higher or more sustained nasopharyngeal viral concentrations, we assessed longitudinal PCR tests performed in a **cohort of 65 individuals infected with SARS-CoV-2 undergoing daily surveillance testing**, including **seven infected with B.1.1.7**. For individuals infected with B.1.1.7, the **mean duration of the proliferation phase was 5.3 days (90% credible interval [2.7, 7.8]), the mean duration of the clearance phase was 8.0 days [6.1, 9.9], and the mean overall duration of infection (proliferation plus clearance) was 13.3 days [10.1, 16.5].** These compare to a mean proliferation phase of 2.0 days [0.7, 3.3], a mean clearance phase of 6.2 days [5.1, 7.1], and a mean duration of infection of 8.2 days [6.5, 9.7] for non-B.1.1.7 virus. The **peak viral concentration for B.1.1.7 was 19.0 Ct** [15.8, 22.0] compared to 20.2 Ct [19.0, 21.4] for non-B.1.1.7. This converts to 8.5 log10 RNA copies/ml [7.6, 9.4] for B.1.1.7 and 8.2 log10 RNA copies/ml [7.8, 8.5] for non-B.1.1.7. https://www.amazon.ca/s?k=qgeem&__mk_fr_CA=%C3%85M%C3%85%C5%BD%C3%95%C3%91&crid=TZ7QMM1Q2T1P&sprefix=qjeem%2Caps%2C188&ref=nb_sb_ss_sc_1_5z These data offer evidence that SARS-CoV-2 variant B.1.1.7 may cause longer infections with similar peak viral concentration compared to non-B.1.1.7 SARS-CoV-2. This extended duration may contribute to B.1.1.7 SARS CoV-2's increased transmissibility.		**Février** **Kissler et coll. (USA)** Densely sampled viral trajectories suggest longer duration of acute infection with B.1.1.7 variant relative to non-B.1.1.7 SARS-CoV-2 https://dash.harvard.edu/handle/1/37366884

Février New variant found in UK with South Africa mutation https://www.pressreader.com/article/281487869058691	New variant B.1.525 has been linked to **33 infections in Britain** (…) carries the same E484K mutation present within the worrying South Africain and Brazilian variants. **Voir aussi Lineage of note – PANGOLIN global report** B.1.525 report: International lineage (13 countries) with variants of biological significance E484K, Q677H, F888L and a similar suite of deletions to B.1.1.7 A.23.1 report : International lineage (17 countries) with variants of biological significance (Spike F157L, V367F, Q613H and P681R), described fully in the preprint: Bugembe et al 2021. Q613H is predicted to be functionally equivalent to the D614G mutation that arose early in 2020.
17 février Two variants merge to form first recorded 'recombinant' virus https://www.ctvnews.ca/health/coronavirus/two-variants-merge-to-form-first-recorded-recombinant-virus-1.5312679	Researchers in New Mexico recently discovered what is **believed to be the first recorded "recombination event"** of **the COVID-19 pandemic between a variant of SARS-CoV-2 that originated in the U.K. and another from California.** Earlier this month, computational biologist and HIV researcher Dr. **Bette Korber** of the Los Alamos National Laboratory in New Mexico briefed researchers on the recombination evidence at a webinar hosted by the New York Academy of Sciences. She reportedly said that her lab has **identified just a single genome among thousands, but the discovery is still important**.
16 février Vaccins : l'UE veut se préparer aux mutations de la COVID-19 https://www.lapresse.ca/international/europe/2021-02-16/nouveaux-variants/vaccins-l-ue-veut-se-preparer-aux-mutations-de-la-covid-19.php	L'UE veut s'organiser face aux mutations du nouveau coronavirus, qui pourraient exiger des versions modifiées des vaccins actuels, a indiqué mardi la Commission, à la veille du **lancement d'un programme européen d'étude de ces variants**. Dans ce cadre, l'UE lancera un programme consacré à l'étude des mutations du virus responsable de la COVID-19, a annoncé la présidente de la Commission européenne Ursula von der Leyen, dans un entretien mardi au quotidien français Les Échos paru mardi. **Baptisée « Incubateur HERA », l'initiative réunira compagnies pharmaceutiques, autorités sanitaires, scientifiques et la Commission européenne « avec d'importants fonds dédiés », a-t-elle affirmé,** ajoutant que l'UE aiderait les fabricants à augmenter leurs capacités de production de vaccins « de deuxième génération ». En outre, l'Agence européenne des médicaments (EMA) **adaptera ses règles pour accélérer l'approbation de nouvelles versions de vaccins déjà autorisés** dans l'UE, a indiqué dimanche la Commissaire à la Santé, Stella Kyriakides.



- The time of introduction of the new variant is the same in all the provinces -- random, uniform in Jan 5 - Jan 25, 2021.
- In this modelling, the control measures currently in place continue indefinitely.
- We have modelled a mean 40% increase in the transmission rate, compared to the COVID-19 circulating in Canada today
- The new variant's trajectory does not reflect a build-up of immunity due vaccination. However, current vaccination strategies are not targeting transmission and we have limited natural immunity, so in the time frame of now to March, this is not an unrealistic assumption.

SFU - High-transmission variants in Canada
February 17, 2021
https://www.sfu.ca/magpie/blog/high-transmission-variant-modelling.html

Voir aussi
INSPQ - Épidémiologie et modélisation de l'évolution de la COVID-19 : projections du 17 février 2021
https://www.inspq.qc.ca/covid-19/donnees/projections/17-fevrier-2021

There are 4 variants of concern:

Variant surveillance overview UK

Data on variants of concern is updated twice weekly online. Total case numbers per VOC as of 10 February 2021 are shown in Table 1.

Table 1. Total case numbers England per VOC as of 10 February 2021

		England genomic cases 10 February 2021		
Variant	**Pangolin lineage**	**confirmed**	**probable**	**total confirmed and probable**
VOC 202012/01	B1.1.7	50,148	5,774	55,922
VOC 202102/02	B.1.1.7 with E484K cluster	23	0	23
VOC 202012/02	B.1.351	126	56	182
VOC 202101/02	P1	0	0	0

Hospitalisations
Of 23 cases, data are available for 18, of which are none were hospitalised following their infection.

Deaths
Of 23 cases, data are available for 18, of which none have died.

Cases in individuals who have been vaccinated
Of 23 cases, data are available for 18, of which 1 was known to be vaccinated before the onset of infection (5 days prior).

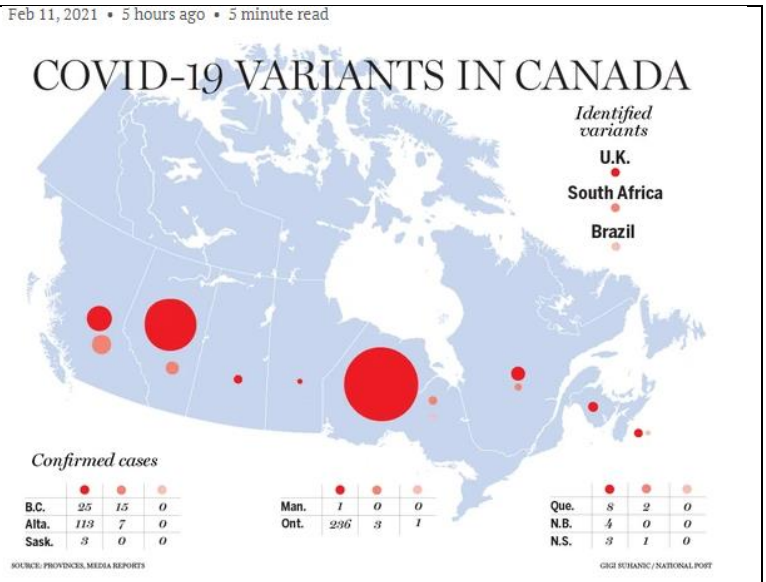
International Epidemiology
International cases have not been reported

13 February 2021
Investigation of SARS-CoV-2 variants of concern in England - Technical briefing 6 -
https://www.gov.uk/government/publications/investigation-of-novel-sars-cov-2-variant-variant-of-concern-20201201

12 février Gare à une troisième vague, prévient la Dre Theresa Tam https://www.lapresse.ca/covid-19/2021-02-12/variants/gare-a-une-troisieme-vague-previent-la-dre-theresa-tam.php	Les grands responsables fédéraux de la santé publique préviennent que si les infections à la COVID-19 semblent suivre une tendance à la baisse, des variants inquiétants représentent toujours une menace croissante pour la mitigation de la pandémie au Canada. La docteure Tam a souligné **qu'au moins trois provinces observaient des preuves de transmission communautaire des nouveaux variants, plus contagieux.** On signale actuellement dans huit provinces plus de 429 cas du variant identifié pour la première fois au Royaume-Uni et 28 cas de celui identifié pour la première fois en Afrique du Sud, a déclaré Mme Tam. Le variant trouvé pour la première fois au Brésil n'a été signalé qu'une seule fois jusqu'ici au Canada. **Selon mon tableur, environ 688 cas au Canada (total), dans la semaine du 14 février :** • B.1.1.7 = 648 • B.1.351 = 39 • P.1 = 1

8 - 12 février 2021

Article de presse	Extrait pertinent	Source scientifique
12 février Criblage des échantillons du Grand Montréal Une mesure qui arrive trop tard, selon des experts https://www.lapresse.ca/covid-19/2021-02-12/criblage-des-echantillons-du-grand-montreal/une-mesure-qui-arrive-trop-tard-selon-des-experts.php	« C'est très bien d'avoir confirmé le criblage de tous les échantillons de la grande région de Montréal, parce que c'est là qu'on a le plus de transmission communautaire et de cas, mais j'aurais préféré que ces mesures soient mises en place plus tôt », indique Roxane Borgès Da Silva, professeure à l'École de santé publique de l'Université de Montréal. Pour Benoît Mâsse, professeur de santé publique à l'Université de Montréal, le Québec doit accélérer le processus de criblage. « C'est comme si on avait deux semaines de retard. Ça fait longtemps qu'on sait que l'Ontario le fait. » M. Mâsse précise toutefois que le criblage ne permet pas d'identifier de nouveaux variants. « Il faut absolument faire du séquençage pour voir l'évolution du virus, ses mutations et les nouveaux variants. » Les États-Unis ont annoncé que le variant britannique serait la souche dominante dans quelques semaines. On risque d'avoir la même chose au Québec. C'est inquiétant pour nos hospitalisations, les décès et tout le reste.	

11 février The state of COVID-19 variants in Canada: Ontario has more than half the cases https://nationalpost.com/news/canada/the-state-of-covid-19-variants-in-canada-ontario-has-more-than-half-the-cases	
11 février Legault envisage de prolonger les mesures en zone rouge https://www.lapresse.ca/covid-19/2021-02-11/covid-19-au-quebec/legault-envisage-de-prolonger-les-mesures-en-zone-rouge.php	Il juge « très, très inquiétante » la présence des variants du coronavirus. « On ne prend pas ça à la légère », s'est défendu le premier ministre, soutenant que 8,5 % des échantillons positifs font l'objet d'un séquençage génomique pour déceler les variants. « On veut doubler ça », a-t-il ajouté. **« Je pense qu'au total, en tout cas, ce que me dit le Dr Arruda, c'est qu'on en fait plus que n'importe quelle autre province, [du] séquençage [et du] criblage. Puis, moi, j'ai demandé qu'on en fasse encore plus. »** L'Ontario prévoyait la semaine dernière le criblage sur 100 % des tests positifs pour détecter les variants et visait à séquencer au moins 10%. **L'Alberta utilise le criblage sur 100% des tests positifs; et environ 20% font l'objet d'un séquençage**.
10 février COVID-19 à Montréal Jusqu'à 44 cas potentiels de variants dont un dans une école https://www.lapresse.ca/covid-19/2021-02-10/covid-19-a-montreal/jusqu-a-44-cas-potentiels-de-variants-dont-un-dans-une-ecole.php	D'autant plus que 44 cas potentiels de variants sont sous le radar des autorités, dont 1 à l'école primaire Stanislas.(…) En tout, **neuf cas confirmés de variants ont été confirmés jusqu'à maintenant par séquençage à Montréal.** La majorité est de variants britanniques. S'ajoutent **23 cas suspects et 12 cas confirmés par liens épidémiologiques pour un total éventuel de 44 cas de variants.**
9 février Nouveaux variants Déconfiner dans le brouillard https://www.lapresse.ca/debats/editoriaux/2021-02-09/nouveaux-variants/deconfiner-dans-le-brouillard.php	Vous avez déjà essayé de conduire en dégivrant exactement 8,5 % de votre pare-brise avant de prendre le volant ? 😊 Depuis la semaine dernière, l'Ontario fait du criblage sur 100 % de ses virus. **Le Québec dit vouloir lui emboîter le pas. Mais il nous a été impossible de savoir où en était l'opération ni d'obtenir d'échéancier précis.**
9 février	L'Afrique du Sud a suspendu en fin de semaine l'administration du vaccin d'AstraZeneca, parce qu'il ne serait

Que valent les vaccins contre les variants ? https://www.lapresse.ca/covid-19/2021-02-09/que-valent-les-vaccins-contre-les-variants.php	pas efficace contre le principal variant du pays. Puis, lundi, une autre enquête a affirmé que celui de Pfizer reste efficace contre les variants anglais et sud-africain. Une étude menée par l'Université du Texas et **Pfizer, publiée lundi dans Nature Medicine,** a permis au géant pharmaceutique d'affirmer que son vaccin n'est que **« légèrement moins efficace »** contre l'une des mutations du variant sud-africain de la COVID-19. **Des tests en laboratoire** sur des versions synthétiques du virus, dotées des trois principales mutations des variants britannique et sud-africain, ont révélé que **le pouvoir de neutralisation du vaccin contre le virus baisse de 19 %** en présence de l'une des mutations sud-africaines, relève Pei-Yong Shi, auteur principal de l'étude à l'Université du Texas. Nous publions la semaine prochaine dans le **New England Journal of Medicine une étude sur l'efficacité du vaccin de Pfizer** contre le **variant sud-africain** en entier, pas une version synthétique, et je suis optimiste, même si je ne peux pas en dévoiler les conclusions. » Les tests de l'étude de **Nature Medicine** ont été faits sur les sérums de **20 patients** ayant reçu les **deux doses du vaccin Pfizer**. Les chercheurs de l'Université du Texas ont aussi testé **deux autres mutations qui, à l'inverse, permettent d'augmenter la neutralisation du coronavirus par le vaccin de plus de 40 %.** Ces **deux mutations sont présentes dans les variants anglais, sud-africain et brésilien.** Mais encore là, il n'est pas clair qu'un changement de neutralisation se traduise en un changement clinique, avec moins de risques d'avoir une COVID-19 avec des symptômes. La fin de semaine dernière, **l'Afrique du Sud** a annoncé la suspension de l'administration du vaccin **d'AstraZeneca sur la base d'une étude non encore publiée, qui montrait une efficacité réduite de 78 %.** Il s'agit d'un petit groupe de 2000 jeunes patients, d'une moyenne d'âge de 31 ans, dont la moitié ont reçu une seule des deux doses du vaccin selon AstraZeneca, d'après le site médical Statnews. Dans le groupe ayant reçu le vaccin, 19 personnes ont eu la COVID-19 avec des symptômes légers contre 23 dans le groupe placebo. Aucun des cobayes n'a eu des symptômes graves. Deux autres vaccins ont annoncé des données préliminaires inquiétantes pour la COVID-19, selon Statnews : **Johnson & Johnson a rapporté une chute de 66 % à 57 %** pour l'efficacité contre les formes « modérée à sévère » de la maladie, et **Novavax, une chute de 89 % à 50 %** pour les formes « légère à modérée ». Moderna a indiqué travailler à une troisième dose du vaccin comme « rappel » (boost) contre le variant sud-africain. « Un élément important de réponse viendra quand on aura les données complètes des essais cliniques dans les pays touchés par le variant sud-africain et celui du Brésil », dit M. Shi, de l'Université du Texas.

8 février La France surveille avec inquiétude les trois variants https://www.lapresse.ca/international/europe/2021-02-08/covid-19/la-france-surveille-avec-inquietude-les-trois-variants.php	**La France surveille la montée du variant anglais qui pourrait à terme nécessiter un nouveau confinement, et renforce ses mesures contre le sud-africain et le brésilien moins répandus mais potentiellement encore plus problématiques**. « Un renforcement spécifique est prévu » pour ces deux variants, explique la Direction générale de la santé (DGS), (…) ils « présentent un risque d'échappement immunitaire et vaccinal ». **Selon la DGS, l'isolement des personnes contaminées par le variant sud-africain ou brésilien va passer à 10 jours, contre 7 d'ordinaire, et un test PCR négatif sera nécessaire pour en sortir.** La part des cas suspectés d'être des variants (essentiellement anglais, mais aussi sud-africain ou brésilien) s'élevait à **14 % de tous les cas détectés en France le 27 janvier,** selon des résultats préliminaires rendus publics jeudi. C'est nettement plus que les 3,3 % de cas positifs attribués au variant anglais les 7 et 8 janvier. **À ce rythme, les spécialistes s'attendent à ce que le variant anglais devienne majoritaire en France d'ici à début mars.**
8 février Le variant britannique se propage rapidement aux États-Unis https://www.lapresse.ca/international/etats-unis/2021-02-08/covid-19/le-variant-britannique-se-propage-rapidement-aux-etats-unis.php	Une équipe de scientifiques menée par des chercheurs de l'institut de recherche Scripps a analysé **un demi-million d'échantillons** de tests collectés à travers le pays depuis l'été dernier. Plutôt que d'effectuer un séquençage pour chacun d'entre eux, ils ont réussi à identifier une anomalie particulière qui était un signe « fiable (d'identification) par procuration » pour le variant. **L'équipe a ajouté que le taux de transmission était au moins 35 à 45 % plus haut que les variants plus communs, et que la prévalence doublait tous les 10 jours.**
8 février South Africa suspends use of AstraZeneca's COVID-19 vaccine after it fails to clearly stop virus variant https://www.sciencemag.org/news/2021/02/south-africa-suspends-use-astrazenecas-covid-19-vaccine-after-it-fails-clearly-stop	Yet the South African trial of the vaccine, conducted in about 2000 people, found such a **low efficacy against mild and moderate disease, under 25%**, that it would not meet minimal international standards for emergency use. But scientists are hopeful it might still prevent severe disease and death—arguably the most important job for any COVID-19 vaccine. That was impossible to tell from this placebo-controlled trial because it was small and recruited relatively healthy, young people—their average age was only 31. None of the subjects in either arm of the study developed severe disease or required hospitalization.

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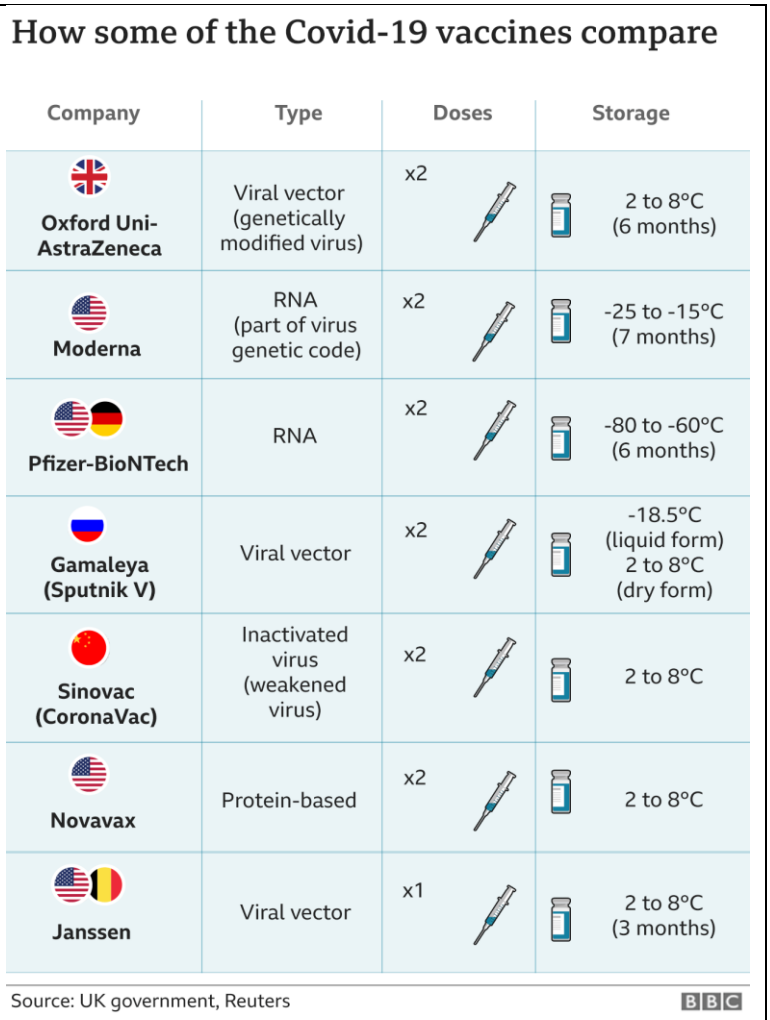

https://www.bbc.com/news/world-africa-55975052

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7 février
COVID-19 : un premier cas du variant brésilien est signalé au Canada
https://ici.radio-canada.ca/nouvelle/1769079/variant-mutation-bresil-cas-coronavirus-toronto

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Un premier cas du variant brésilien de la COVID-19 a été signalé à Toronto. Il s'agit aussi du premier cas détecté au Canada. Le patient, qui a récemment **voyagé au Brésil, est actuellement hospitalisé**. Par ailleurs, elle indique **aussi qu'un second cas du variant sud-africain a été détecté à Toronto. Ce cas n'a pas d'historique de voyage récent et n'a eu aucun contact connu avec quiconque est un voyageur de retour**, peut-on aussi lire dans le communiqué. Jusqu'à présent, l'Ontario recense 174 cas du variant identifié tout d'abord au Royaume-Uni.

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6 février
Variants : les experts retiennent leur souffle
https://www.lapresse.ca/covid-19/2021-02-06/covid-19/variants-les-experts-retiennent-leur-souffle.php

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Pour faire face à l'arrivée de variants plus contagieux au **Québec**, le gouvernement Legault a annoncé deux mesures vendredi : **augmenter le séquençage du virus détecté dans des tests positifs de 8,5 % à 10 % et avoir davantage recours à des tests PCR dits de criblage.**

L'Ontario rapportait jeudi que pour la journée du **20 janvier, 5,5 % des nouveaux cas étaient associés au variant**

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	britannique. La province compte 152 cas de ce variant et un cas du variant sud-africain.	
5 février AstraZeneca Covid-19 Vaccine Effective Against U.K. Variant in Trial https://www.wsj.com/articles/astrazeneca-vaccine-effective-against-u-k-covid-19-variant-in-study-11612530912	Oxford study finds the vaccine to be **75% (74,6%) effective against the U.K. variant** and 84 % against other lineages	
Using longitudinal symptom and test reports of 36,920 users of the Covid Symptom Study app testing positive for COVID-19 between 28 September and 27 December 2020, we examined the association between the regional proportion of B.1.1.7 and reported symptoms, disease course, rates of reinfection, and transmissibility. **We found no evidence for changes in reported symptoms, disease severity and disease duration associated with B.1.1.7.** We found a **likely reinfection rate of around 0.7%** (95% CI 0.6-0.8), but no evidence that this was higher compared to older strains. We found an **increase in R(t) by a factor of 1.35 (95% CI 1.02-1.69).** Despite this, we found that regional and national lockdowns have reduced R(t) below 1 in regions with very high proportions of B.1.1.7.	**29 janvier** **Graham et al. (UK)** The effect of SARS-CoV-2 variant B.1.1.7 on symptomatology, re-infection and transmissibility https://www.medrxiv.org/content/10.1101/2021.01.28.21250680v1?rss=1%22	

1 - 5 février 2021

Article de presse	Extrait pertinent	Source scientifique
4 février Quatre premiers cas de variant brésilien en France https://www.lapresse.ca/international/europe/2021-02-04/covid-19/quatre-premiers-cas-de-variant-bresilien-en-france.php	L'un de ces cas est « une femme qui revenait de Manaus au Brésil » et a transité par Sao Paulo, Francfort, Paris et Marseille, dans le sud de la France. Manaus est une des villes brésiliennes les plus durement touchées par la pandémie. M. Castex et M. Véran ont indiqué que les variants représentaient environ 14 % de l'ensemble des tests positifs à la COVID-19 selon une enquête menée sur la journée du 27 janvier, contre 3,3 % les 7 et 8 janvier.	
4 février Identification des variants L'Ontario se dote d'une stratégie plus rapide et moins coûteuse https://www.lapresse.ca/covid-19/2021-02-04/identification-des-variants/l-ontario-se-dote-d-une-strategie-plus-rapide-et-moins-couteuse.php	**Québec** 8 cas variants UK **Ontario** L'Ontario est la province canadienne qui a recensé le plus grand nombre de contaminations aux nouveaux variants, avec **69 cas du variant britannique et 1 cas du variant sud-africain.** (…) En plus d'effectuer le séquençage, la province utilisera donc un nouveau procédé, **le criblage, sur 100 % des cas positifs**. Pour ce faire, le service de santé publique d'Ontario utilisera un test PCR qui amplifie uniquement les mutations	

	des trois variants préoccupants. (…) L'Ontario a développé un test qui cible précisément cette mutation, ce qui permet d'attraper les trois variants », explique Mme Moreira. (…) Si le test est positif, les autorités sanitaires effectueront un séquençage complet pour déterminer précisément de quel variant il s'agit **Alberta** Face à la menace des variants au pays, l'Alberta, qui compte **51 cas d'infection aux nouveaux variants, a choisi d'augmenter la période de quarantaine obligatoire à 24 jours,** plutôt que 14, pour les personnes qui vivent avec une personne qui a été déclarée positive pour un variant de la COVID-19. (…) L'Alberta a doublé sa capacité de séquençage ces deux dernières semaines. La province examine maintenant environ 300 échantillons positifs par jour, soit près de cinq fois plus d'échantillons par habitant que l'Ontario. (…) **Source** https://www.cp24.com/ Chief medical health officer Dr. Deena Hinshaw says there are **50 cases of the variant first found in the United Kingdom and 7 originating in South Africa**, for a total rise of six cases in the last 24 hours. **Colombie-Britannique** 18 cas d'infection aux nouveaux variants ont été détectés en Colombie-Britannique, soit **14 du variant du Royaume-Uni et 4 de celui d'Afrique du Sud**. **Nouveau-Brunswick** La province a confirmé mardi **3 cas du variant britannique** **Nouvelle-Écosse** 1 cas pour chacun des deux variants. **Saskatchewan, le Manitoba et l'Île-du-Prince-Édouard** Aucun nouveau variant sur leur territoire. The London Free Press, Canada (3 février) Total Canada: > 135 cas variant UK, et ≥ 30 cas variant Sud-Africain
3 février OMS - Webinar: SARS-CoV-2 virus mutations and variants https://www.who.int/news-room/events/detail/2021/02/03/default-calendar/sars-cov-2-virus-mutations-and-variants	The latest on the COVID-19 global situation and the emergence of new mutations and variants Join this webinar to learn about the new SARS-CoV-2 variants that have emerged; the implications of these variants; and what is being done to monitor and respond to the emergence of SARs-CoV-2 variants. Speaker: Dr Sylvie Briand, Director Global Infectious Hazards Preparedness WHO Watch the video recording here
3 février	**338 cas en 2 semaines (TVA nouvelles du midi, 4 février)**

« Hausse soudaine » des cas de COVID-19 Situation préoccupante à Saint-Jean-sur-Richelieu https://www.lapresse.ca/covid-19/2021-02-03/hausse-soudaine-des-cas-de-covid-19/situation-preoccupante-a-saint-jean-sur-richelieu.php La Montérégie resserre les mailles du filet https://www.lapresse.ca/covid-19/2021-02-03/hausse-soudaine-des-cas-a-saint-jean-sur-richelieu/la-monteregie-resserre-les-mailles-du-filet.php	Alors que le nombre de cas diminue en Montérégie depuis le 17 janvier, Saint-Jean-sur-Richelieu affiche la tendance contraire. « On a vu une **hausse soudaine des cas dans la semaine du 17 janvier, où on a vu presque 200 nouveaux cas »**, a déclaré la Dre Julie Loslier, directrice de santé publique de la Montérégie, en conférence de presse mercredi. Résultat, cette ville qui représente seulement 7 % de la population de la Montérégie est actuellement responsable **d'environ 10 % des cas actifs de la région,** une situation jugée « préoccupante ». « Dans la ville de Saint-Jean, on a quand même 25 éclosions actives qui cumulent plusieurs cas, a souligné la directrice de santé publique. Ça circule dans tous les milieux et ça touche tous les groupes d'âge. » Cela ne permet pas de conclure qu'ils sont attribuables à un nouveau variant plus contagieux, dit-elle. La Montérégie travaille toutefois avec le Laboratoire de santé publique du Québec pour faire séquencer des échantillons de Saint-Jean et d'ailleurs dans la région « comme on le ferait dans d'autres éclosions d'envergure ».
3 février Vaccin d'AstraZeneca La transmission du virus réduite de 67 % après une dose https://www.lapresse.ca/covid-19/2021-02-03/vaccin-d-astrazeneca/la-transmission-du-virus-reduite-de-67-apres-une-dose.php	Le chef du projet, Andrew Pollard, a expliqué à la BBC mercredi que ce vaccin pourrait avoir un « impact énorme » en terme de transmission tout en précisant que ces tests avaient été réalisés avant l'apparition des variants, or « ce virus essaye à tout prix de trouver des façons de continuer à se transmettre ». Contre les infections, l'étude montre une **efficacité de 76 % après une première dose**, qui se maintient pendant trois mois. L'efficacité **grimpe à 82 %** après une deuxième dose injectée **trois mois plus tard.**
2 février Variants Le Canada traverse « une période très délicate », affirme la Dre Tam https://www.lapresse.ca/covid-19/2021-02-02/variants/le-canada-traverse-une-periode-tres-delicate-affirme-la-dre-tam.php	Au moins **148 cas des variants** qui sont d'abord apparus au Royaume-Uni (connu scientifiquement sous le nom de B.1.1.7) et en Afrique du Sud (connu sous le nom de B.1351) ont été **confirmés dans tout le pays, a déclaré la Dre Tam mardi.** Les autorités sanitaires de **l'Ontario, de l'Alberta et de la Colombie-Britannique** ont identifié les deux mutations, 135 de la souche B.1.1.7 et 13 de la souche B.1351. Les quatre cas du variant B.1351 confirmés en Colombie-Britannique et le seul cas signalé dans la région de Peel en Ontario n'ont aucun lien connu avec les voyages internationaux, ce qui fait craindre une propagation communautaire.
1 février Variant sud-africain Opération de dépistage massif en Angleterre	Les autorités sanitaires britanniques ont lancé lundi une opération de **dépistage massif dans huit zones de l'Angleterre après la découverte de 11 cas du variant sud-africain sans lien établi avec un quelconque voyage.**

https://www.lapresse.ca/international/europe/2021-02-01/variant-sud-africain/operation-de-depistage-massif-en-angleterre.php	Les autorités ont comme objectif de tester **80 000 personnes** dans les régions concernées (certaines zones de Londres, des West Midlands, de l'Est, du Sud-Est et du Nord-Ouest). **Depuis le 22 décembre, 105 cas de ce variant susceptible d'être plus contagieux, contre lesquels certains des vaccins actuels semblent moins efficaces**, ont été détectés, selon le ministère britannique de la Santé.
29 janvier Ontario Takes Immediate Action to Stop the Spread of COVID-19 Variants https://news.ontario.ca/en/release/60176/ontario-takes-immediate-action-to-stop-the-spread-of-covid-19-variants-1	Recent evidence shows Ontarians' efforts to contain COVID-19 are working, with provincial trends in most key public health indicators trending down. **However, recent modelling suggests that the UK variant and other new variants remain a significant threat to controlling the pandemic and could become the dominant strain of the virus in the province by March 2021,** posing an increased threat to public health and hospital capacity. **As of January 29, 2021, the number of UK variant COVID-19 cases in Ontario will be posted daily on covid-19.ontario.ca/,** with a breakdown of how many cases per public health unit included in the provincial epidemiologic summary.
29 janvier Les variants, une menace au contrôle de la pandémie https://www.lapresse.ca/covid-19/2021-01-29/les-variants-une-menace-au-controle-de-la-pandemie.php	**Depuis la dernière semaine, le Rt, soit le taux de reproduction des cas, est estimé à 0,79 au Québec, selon les données de l'INSPQ.** C'est la première fois depuis la mi-novembre que le Rt de la province est inférieur à 1. **En conservant toutes les mesures sanitaires mises en place dans la province et en ayant un variant 50 % plus contagieux, on pourrait passer d'un Rt de 0,79 à un Rt de 1,2**. On se retrouvait à nouveau avec une augmentation du nombre de cas M. Maheu-Giroux explique que pour maîtriser le nouveau variant britannique, il faudrait avoir un Rt de 0,65. Il indique que ce nombre n'a été atteint qu'une seule fois depuis le début de la pandémie, à la fin du mois de mai. Selon M. Mâsse, il serait très difficile de retourner à des niveaux aussi bas.
29 janvier À 85 % contre les formes plus graves Le vaccin Johnson & Johnson efficace à 66 % https://www.lapresse.ca/covid-19/2021-01-29/a-85-contre-les-formes-plus-graves/le-vaccin-johnson-johnson-efficace-a-66.php#	Le vaccin, qui ne nécessite qu'une seule injection, est efficace à 85 % pour prévenir les formes graves de la maladie, selon un essai clinique majeur, qui comptait près de 44 000 personnes dans 8 pays. Contrairement aux remèdes de Pfizer et Moderna, qui utilisent la technique innovante de l'ARN messager, le vaccin de « J & J » est un vaccin à « vecteur viral ». (…) Un procédé aussi employé pour les vaccins d'AstraZeneca et de Sputnik. **https://www.jnj.com/johnson-johnson-announces-single-shot-janssen-covid-19-vaccine-candidate-met-primary-**

	endpoints-in-interim-analysis-of-its-phase-3-ensemble-trial#_ftn1 Among all participants from different geographies and including those infected with an emerging viral variant, Janssen's COVID-19 vaccine candidate was 66% effective overall in preventing moderate to severe COVID-19, 28 days after vaccination. The onset of protection was observed as early as day 14. **The level of protection against moderate to severe COVID-19 infection was 72% in the United States, 66% in Latin America and 57% in South Africa, 28 days post-vaccination.** The trial, conducted in eight countries across three continents, includes a diverse and broad population including 34% (N= 14,672) of participants over age 60. The study enrolled 44% (N=19,302) of participants in the United States, 41% (N=17,905) in Central and South America (Argentina, Brazil, Chile, Colombia, Mexico, Peru) and 15% (N=6,576) in South Africa. Forty-five percent of participants are female, 55% male.
ECDC assesses the probability of the introduction and community spread of variants of concern in the EU/EEA as **very high due to their increased transmissibility.** Such an increased transmissibility is likely to lead to an increased number of infections. This, in turn, is likely to lead to higher hospitalisation and death rates across all age-groups, but particularly for those in older age groups or with co-morbidities. Consequently, stricter NPIs are needed to reduce transmission and relieve the pressure on healthcare systems. Therefore, **the impact of introduction and community spread is considered to be high.** The overall risk associated with the introduction and community spread of variants of concern is therefore assessed as being **high/very high**.	**21 janvier** Risk related to the spread of new SARS-CoV-2 variants of concern in the EU/EEA – first update https://www.ecdc.europa.eu/en/publications-data/covid-19-risk-assessment-spread-new-variants-concern-eueea-first-update
The modeled trajectory of this variant in the U.S. exhibits rapid growth in early 2021, becoming the **predominant variant in March**. **Aussi** TABLE. Characteristics of SARS-CoV-2 variants of concern — worldwide, September 2020–January 2021	**15 janvier** **Emergence of SARS-CoV-2 B.1.1.7 Lineage — United States, December 29, 2020–January 12, 2021** Weekly / January 22, 2021 / 70(3);95–99 https://www.cdc.gov/mmwr/volumes/70/wr/mm7003e2.htm?s_cid=mm7003e2_w#suggestedcitation

Article de presse	Extrait pertinent	Source scientifique
The receptor-binding motif (RBM) is a highly variable region of SARS-CoV-2 spike RBM mutation N439K has emerged independently in multiple lineages (30+ countries, europe) N439K increases spike affinity for hACE2; viral fitness and disease are unchanged N439K confers resistance to several mAbs and escapes some polyclonal responses		**28 janvier** Thomson et al. (UK) Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity https://www.cell.com/cell/fulltext/S0092-8674(21)00080-5?rss=yes
28 janvier Novavax's Vaccine Works Well — Except on Variant First Found in South Africa https://www.nytimes.com/2021/01/28/health/covid-vaccine-novavax-south-africa.html	An early analysis in Britain found that the vaccine had an efficacy rate of nearly 90 percent. But in a small South Africa trial, the efficacy rate dropped to just under 50 percent. Novavax, which makes one of six vaccine candidates supported by Operation Warp Speed last summer, has been running trials in Britain, South Africa, the United States and Mexico. It said Thursday that an early analysis of its 15,000-person trial in Britain revealed that the two-dose vaccine had an efficacy rate of nearly 90 percent there. But in a small trial in South Africa (4,400 volunteers), the efficacy rate dropped to just under 50 percent. Almost all the cases that scientists have analyzed there so far were caused by the variant, known as B.1.351. The data also showed that many trial participants were infected with the variant even after they had already had Covid. The fact that three vaccines all appeared to show lowered effectiveness against the variant from South Africa is not encouraging, and the results Novavax announced Thursday were the first to occur outside of a laboratory, testing how well a vaccine worked in people infected with a new variant. Johnson & Johnson is also on the cusp of announcing results of its Covid-19 vaccine trials, and has also tested its candidate in South Africa.	
28 janvier Détection du variant britannique Le Québec pressé d'accélérer le rythme https://www.lapresse.ca/covid-19/2021-01-28/detection-du-variant-britannique/le-quebec-presse-d-accelerer-le-rythme.php	Le Danemark a notamment décidé il y a quelques semaines de séquencer plus de 75 % des nouveaux échantillons positifs, contre 11 % avant Noël. Les chercheurs ont mis en relief du même coup le fait que le variant britannique, plus contagieux, se propageait activement dans le pays, une réalité « cachée » par le fait que le nombre total de cas d'infection, tous variants confondus, est en baisse. Camilla Holten Møller, spécialiste en modélisation épidémiologique du Statens Serum Institut, à Copenhague, a indiqué mardi que la proportion de nouvelles infections imputées au variant britannique par les autorités danoises depuis l'intensification du séquençage au début de l'année était passée, sur une période de trois semaines, de 2 à 12 %. Et les autorités s'attendent à ce que ce variant devienne la souche dominante d'ici le début du mois de mars.	

	Le taux d'échantillons positifs faisant l'objet d'un séquençage génomique varie largement d'un pays à l'autre. Il atteint près de 60 % en Australie, 50 % en Nouvelle-Zélande, où le virus est largement sous contrôle, et tombe à seulement 0,3 % aux États-Unis, selon une récente compilation du Washington Post. La majorité des pays sont sous la barre de 15 %.
27 janvier Le traitement de Regeneron reste efficace contre les variants britannique et sud-africain https://www.lapresse.ca/actualites/sciences/2021-01-27/covid-19/le-traitement-de-regeneron-reste-efficace-contre-les-variants-britannique-et-sud-africain.php	Le REGEN-COV, constitué « des deux anticorps neutralisants » appelés imdevimab et casirivimab, « a gardé sa puissante capacité de neutralisation contre le variant B.1.1.7 » britannique ainsi que « contre le variant B.1351 » sud-africain, a déclaré la société dans un communiqué. Concernant le variant sud-africain toutefois, l'un des deux anticorps, le casirivimab, a vu sa « puissance réduite ». Des scientifiques de l'Université de Columbia sont parvenus aux mêmes conclusions, et leur étude a été soumise à l'évaluation des pairs. Cette « pré-publication » présente en revanche des résultats plus inquiétants concernant d'autres anticorps de synthèse, le bamlanivimab : il est « inactif » contre le variant sud-africain, selon les chercheurs. Or c'est ce qui est utilisé dans le traitement de l'entreprise Eli Lilly, qui bénéficie lui aussi d'une autorisation en urgence aux États-Unis. Le bamlanivimab devrait également être inefficace face au variant brésilien, puisque ce dernier présente des mutations similaires au sud-africain, précisent les scientifiques.
26 janvier Le variant anglais représente un cas sur dix dans la région parisienne https://www.lapresse.ca/international/europe/2021-01-26/covid-19/le-variant-anglais-represente-un-cas-sur-dix-dans-la-region-parisienne.php	L'analyse de 1080 tests PCR positifs, réalisés entre le 11 et le 21 janvier dans huit sites de dépistage de la grande région parisienne, a conclu que 9,4 % correspondent au variant anglais Un taux de 2,5 % au niveau national avait été constaté après une première « enquête flash » nationale sur plus de 10 000 PCR positives les 7 et 8 janvier. Une deuxième doit débuter mercredi. L'étude « intermédiaire » menée en Île-de-France « correspond assez bien aux modélisations qui ont été faites par l'Institut Pasteur », a souligné Mme Marcelin, rappelant que l'organisme tablait sur une fourchette de 2 à 12 % début février, puis 12 à 64 % début mars. « On est à un point d'inflexion », a constaté le Pr Frédéric Batteux, chef du service d'immunologie de l'hôpital Cochin, observant que le taux de reproduction de la COVID-19 « est passé au-dessus de 1,2 » et continue de monter.
25 janvier La France inquiète des variants de la COVID-19 https://www.lapresse.ca/international/europe/2021-01-	Le variant VOC 202 012/01, qui a provoqué une flambée épidémique au Royaume-Uni, où plus de 1000 malades de la COVID-19 sont morts chaque jour la semaine dernière, était présent « plutôt à des niveaux de 7, 8 ou 9 % dans certaines

25/troisieme-confinement-en-vue/la-france-inquiete-des-variants-de-la-covid-19.php	régions françaises », alors qu'une première enquête l'a mesuré à 1,4 % au niveau national les 7 et 8 janvier. Santé publique France doit lancer une nouvelle étude cette semaine, pour évaluer la circulation des variants anglais et sud-africain, plus contagieux.	
25 janvier Une explosion de cas en mars, craignent des chercheurs https://www.lapresse.ca/covid-19/2021-01-25/une-explosion-de-cas-en-mars-craignent-des-chercheurs.php	selon les modélisations faites par des experts de l'Université Simon Fraser, en Colombie-Britannique, le Canada pourrait atteindre 15 000 cas par jour à la mi-mars et 20 000 cas quelques jours plus tard si un variant au taux de transmission 40 % plus élevé s'établit au Canada.	
25 janvier Une baisse de protection contre le variant sud-africain constatée https://www.lapresse.ca/covid-19/2021-01-25/vaccin-de-moderna/une-baisse-de-protection-contre-le-variant-sud-africain-constatee.php	« L'étude n'a **pas montré d'impact significatif** sur les titres (niveaux, NDLR) d'anticorps contre le variant B.1.1.7 par rapport à de précédents variants », a expliqué Moderna à propos du variant britannique. En revanche, « **une réduction par six » des niveaux d'anticorps** contre le variant sud-africain (B.1351) a été observée. Mais « malgré cette réduction », les niveaux d'anticorps « restent au-dessus de ce qui est attendu comme nécessaire pour procurer une protection », écrit Moderna. Pour étudier l'impact de son vaccin, appelé mRNA-1273, Moderna a réalisé des prélèvements de sang sur huit personnes ayant reçu les deux doses de son remède, et plusieurs primates également immunisés.	**25 janvier** **Wu et al. (Moderna)** mRNA-1273 vaccine induces neutralizing antibodies against spike mutants from global SARS-CoV-2 variants https://www.biorxiv.org/content/10.1101/2021.01.25.427948v1
23 janvier Un variant plus mortel, un autre plus résistant https://www.lapresse.ca/actualites/sciences/2021-01-23/covid-19/un-variant-plus-mortel-un-autre-plus-resistant.php	**La mortalité du variant britannique** Un rapport publié vendredi par un groupe de surveillance des virus respiratoires du ministère de la Santé du Royaume-Uni a sonné l'alarme : « Il pourrait y avoir une augmentation de la sévérité de la maladie » avec le variant britannique, B117, apparu en septembre. Les études initiales, avec des groupes contrôles similaires, ne montraient pas d'augmentation de la mortalité chez les personnes l'ayant contracté, dit le rapport. Mais d'autres rapports plus récents, sur quelques centaines	

	de patients, semblent indiquer un risque de mourir jusqu'à 30 % supérieur, particulièrement chez certaines personnes ayant des vulnérabilités génétiques. **Le variant sud-africain résistant** Le variant sud-africain du SARS-CoV-2, le coronavirus responsable de la COVID-19, résiste aux anticorps produits par la souche première du SARS-CoV-2 et peut-être aux vaccins. Telle est la conclusion d'une étude sud-africaine publiée mercredi sur le site de prépublication scientifique medRxiv. (…) on doit noter que l'étude porte sur de petits groupes de patients, 14 et 30,(…) **Ralentir l'entrée au Québec** J'aimerais avoir beaucoup plus d'informations sur le séquençage et les résultats du séquençage au Québec. Cela dit, le labo de la Santé publique est peut-être "on top of it", mais ça serait réconfortant de savoir qu'on suit l'évolution des variants au Québec de très près. » **Le problème des masques en tissu** Jeudi, la France a demandé à la population de ne plus porter le masque artisanal en tissu, jugé inefficace contre les nouveaux variants, et a recommandé le port du masque chirurgical. (…) Vendredi, l'Organisation mondiale de la Santé (OMS) a toutefois indiqué qu'elle ne prévoyait pas changer ses recommandations et qu'elle considérait toujours que les masques en tissu étaient efficaces, et ce, même contre les nouveaux variants.	
22 janvier Ottawa déploie deux unités mobiles à Toronto pour soulager les hôpitaux https://www.lapresse.ca/covid-19/2021-01-22/covid-19-en-ontario/ottawa-deploie-deux-unites-mobiles-a-toronto-pour-soulager-les-hopitaux.php	La province signale également au moins 15 cas du « variant britannique », dont quatre n'avaient pas d'antécédents de voyage, ce qui laisse croire à une transmission communautaire de cette souche plus contagieuse. « Nous nous attendons certainement à en voir davantage au fur et à mesure que nos laboratoires testent ces variants », a expliqué la docteure Yaffe.	
22 janvier Le variant britannique associé à une plus forte mortalité https://www.lapresse.ca/international/europe/2021-01-22/covid-19/le-variant-britannique-associe-a-une-plus-forte-mortalite.php	Pour les hommes âgés d'une soixantaine d'années, le risque de mortalité est de 10 sur 1000 avec le virus, un chiffre qui atteint 13 à 14 sur 1000 avec le nouveau variant « Je tiens à souligner qu'il y a beaucoup d'incertitude autour de ces chiffres », a déclaré M. Vallance, soulignant une « inquiétude qu'il y ait eu une	**22 janvier** **NERVTAG paper on COVID-19 variant of concern B.1.1.7** https://www.gov.uk/government/publications/nervtag-paper-on-covid-19-variant-of-concern-b117

	augmentation de la mortalité ainsi qu'une augmentation de la transmissibilité ».	
Most current cases in the catchment population in LA fall into two distinct subclades: 1) 20G (24% of total) is the predominant subclade currently in the United States 2) a relatively novel strain in **clade 20C, CAL.20C strain (~36% of total)** is defined by five concurrent mutations. After an analysis of all of the publicly available data and a comparison to our recent sequences, we see a dramatic growth in the relative percentage of the CAL.20C strain beginning in November of 2020. The predominance of this strain coincides with the increased positivity rate seen in this region. Unlike 20G, this novel strain CAL.20C is defined by multiple mutations in the S protein: S13I; W152C; **L452R**		**20 janvier** **Zhang et al. (USA)** Emergence of a novel SARS-CoV-2 strain in Southern California, USA https://www.medrxiv.org/content/10.1101/2021.01.18.21249786v1
Une étude in vitro a testé le plasma d'individus vaccinés par les vaccins de Moderna (n=14) ou Pfizer-BioNTech (n=6) contre un panel de pseudovirus contenant, notamment, N501Y (signature variant UK), K417N, E484K et la combinaison de ces 3 mutations (signature variant sud-africain). Parmi les plasmas testés, une faible diminution (statistiquement significative) de l'activité de neutralisation anticorps a été observée pour N501Y (1.3 à 2.5 fois), E484K (1 à 3 fois) et la combinaison K417N:E484K:N501Y (1.1 à 3 fois)		**19 janvier** **Wang et al. (USA)** mRNA vaccine-elicited antibodies to SARS-CoV-2 and circulating variants https://www.biorxiv.org/content/10.1101/2021.01.15.426911v1
Here we show that 501Y.V2 lineage exhibits **complete escape from three classes of therapeutically relevant monoclonal** antibodies. Furthermore 501Y.V2 shows substantial or complete **escape from neutralizing antibodies in COVID-19 convalescent plasma.** These data highlight the prospect of reinfection with antigenically distinct variants and may foreshadow reduced efficacy of current spike-based vaccines.		**19 janvier** **Wibmer et al. (Afriq. du S.)** SARS-CoV-2 501Y.V2 escapes neutralization by South African COVID-19 donor plasma https://www.biorxiv.org/content/10.1101/2021.01.18.427166v1

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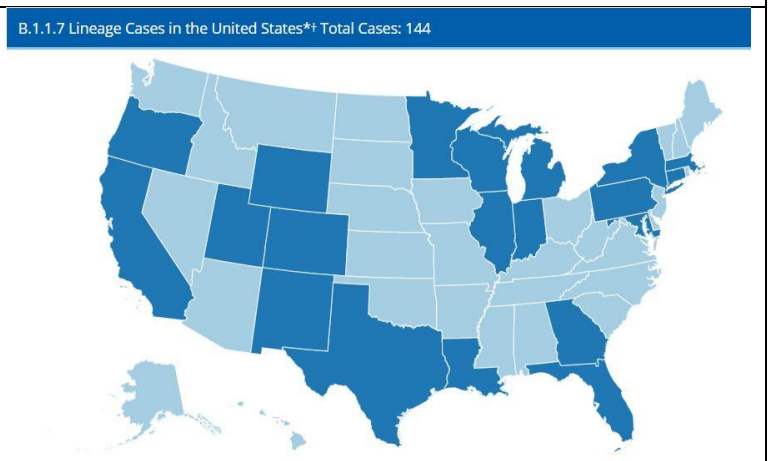
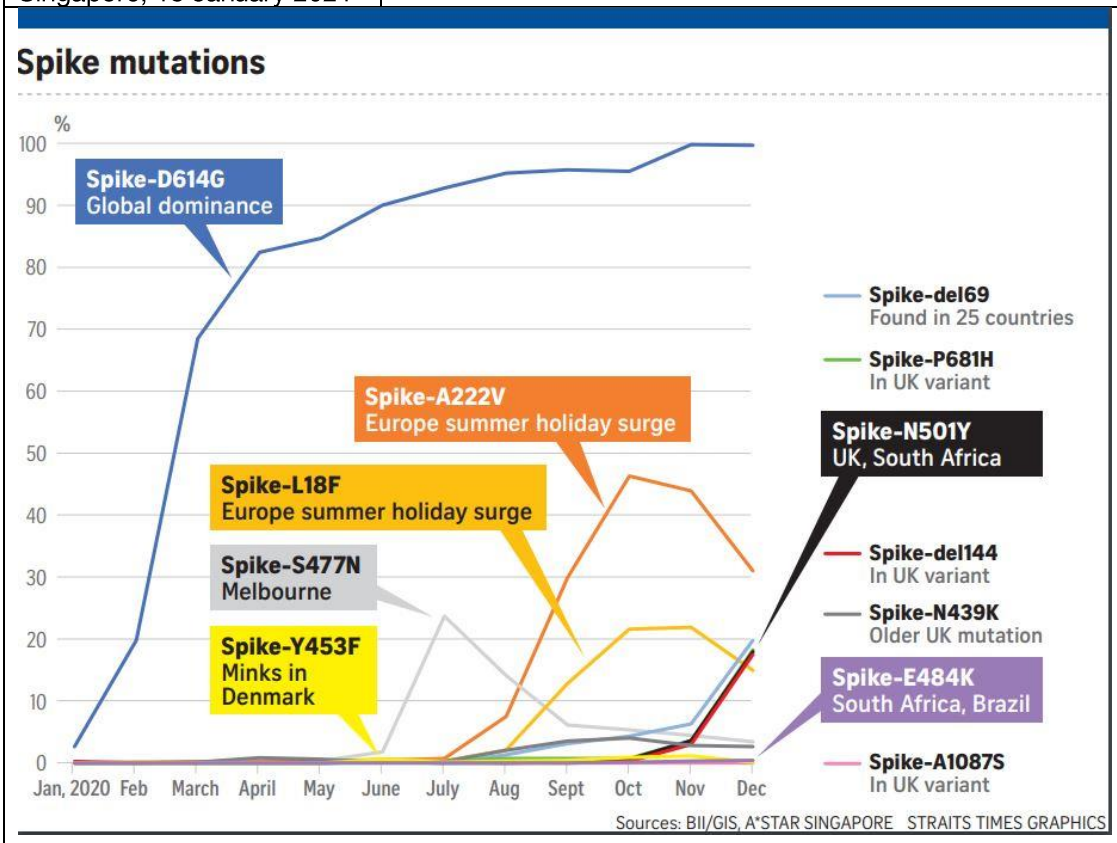
Article de presse	Extrait pertinent	Source scientifique
21 janvier Nouveaux variants - La situation se dégrade en Europe, les autorités appelées à agir https://www.lapresse.ca/international/europe/2021-01-21/nouveaux-variants/la-situation-se-degrade-en-europe-les-autorites-appelees-a-agir.php	**L'agence européenne chargée des épidémies**, *« Le message essentiel est de se préparer à une escalade rapide de la rigueur des mesures (pour contrer le virus) dans les semaines à venir afin de préserver les capacités de soins, ainsi que d'accélérer les campagnes de vaccination. »*. **Le Centre de prévention et de contrôle des maladies (ECDC),** qui regroupe les 27 pays de l'UE ainsi que le Royaume-Uni, la Norvège et l'Islande, a également relevé à « élevé/très élevé » son évaluation des risques sanitaires liés aux nouveaux variants.	

20 janvier **Courriel de Sandrine :** *J'ai demandé à l'équipe de J. Shapiro et J Hussin de jeter un œil sur la situation des isolats québécois avec le S477N. Résumé de nos discussions* - Bien que la mutation S477N soit aussi présente dans l'éclosion australienne, les souches québécoises sont dans un cluster différent (B.1.160 pour Québec et D2 pour l'Australie) - B.1.160 est également présente en Europe - Certaines souches québécoises de B.1.160 montrent un « saut » de 5 mutations. Comme ceci est en lien avec une éclosion dans un CHSLD (St Eusèbe, Lanaudière), l'hypothèse que la souche ait touché un individu affaiblit au niveau immunitaire est possible - Nous avons trop peu de séquences reliées aux souches B.1.160 québécoises pour identifier s'il augmente en nombre. Nous suggérons un séquençage ciblé (à discuter vendredi) en plus du séquençage aléatoire de routine o des contacts des cas de l'éclosions de St Eusèbe o d'un échantillon de cas associés à des éclosions en Lanaudière Voir ppt 20200118situation préoccupante	
20 janvier **Courriel: URGENT - DEMANDE pour 11h / Questions du premier ministre** *A-t-on plus d'information sur les nouveaux variants?* *Est-ce vrai qu'il s'attaque davantage aux enfants?* ***DGSP- Marlène/Yves*** Réponse : voir document le point sur les nouveaux variants	
20 janvier US COVID-19 Cases Caused by Variants CDC B.1.1.7 (variant UK) Total 144 cases • Florida 46 • California 40 • New York 17	
19 janvier Washington s'attaque à la pandémie, le variant britannique se propage https://www.lapresse.ca/international/2021-01-19/covid-19/washington-s-attaque-a-	Le variant anglais du coronavirus continue de se propager dans le monde, touchant au moins **60 pays et territoires**, Le variant sud-africain du coronavirus se diffuse lui plus lentement et est présent dans **23 pays et territoires**, soit 3 de plus qu'au 12 janvier, a précisé l'OMS.

la-pandemie-le-variant-britannique-se-propage.php	À Manaus, dans l'État de l'Amazonas, les médecins sont frappés par la virulence de la deuxième vague, qui a débordé les hôpitaux, confrontés à une pénurie dramatique d'oxygène. **En complément** New variant report - Global Report Investigating Novel Coronavirus Haplotypes	
19 janvier **The new SARS-CoV-2 variant and other mutations under review by COG-UK**	A brief summary of the latest COG-UK mutational surveillance report, which explores SARS-CoV-2 spike gene mutations of potential or known importance. The report is structured in four parts: 1) a **list of high frequency** individual mutations, a subset of which may be important; 2) highlighted mutations of potential or known **clinical and public health importance** based on current evidence; 3) a list of mutations known to lead to **weaker neutralisation** of the virus by convalescent plasma from people who have been infected with SARS-CoV-2, and/or some monoclonal antibodies (mAbs) that may be given to patients with COVID-19; 4) **structural analyses** of mutations and variants described in 2) above.	
18 janvier Afrique du Sud Le nouveau variant du virus pas plus mortel, mais 50 % plus contagieux https://www.lapresse.ca/international/afrique/2021-01-18/afrique-du-sud/le-nouveau-variant-du-virus-pas-plus-mortel-mais-50-plus-contagieux.php	Baptisée 510Y. V2, cette mutation « est 50 % plus transmissible », mais « rien n'indique que le nouveau variant est plus sévère », a déclaré le Pr Salim Abdool Karim, épidémiologiste et coprésident du comité scientifique au ministère de la Santé sud-africain.	**Pearson et al. (UK).** Estimates of severity and transmissibility of novel South Africa SARS-CoV-2 variant 501Y.V2 https://cmmid.github.io/topics/covid19/sa-novel-variant.html
18 janvier News -Covid-19: What new variants are emerging and how are they being investigated? *BMJ* 2021; 372 doi: https://doi.org/10.1136/bmj.n158	The G2P-UK National Virology Consortium has been launched to work with COG-UK to study how mutations may affect key outcomes, • the transmissibility of variants, • the severity of illness they cause, and • their response to vaccines and treatments.	
18 janvier Experts divided on effect of new strains on effort to curb virus	Source: The Bioinformatics Institute (BII), by the Agency for Science, Technology and Research (A*STAR)	

The Straits Times, Singapore, 18 January 2021	



In order to enact more aggressive public health measures to minimize the spread of such strains, genomic surveillance needs to be of sufficient scale to **detect early emergence and expansion in the broader virus population**. By modeling common performance characteristics of available diagnostic and sequencing tests, we developed a model that assesses the sampling required to detect emerging strains when they are less than 1% of all strains in a population. This model demonstrates that **5% sampling of all positive tests allows the detection of emerging strains when they are a prevalence of 0.1% to 1.0%.**	**15 janvier** **Vavrek et al. (USA)** Genomic surveillance at scale is required to detect newly emerging strains at an early timepoint https://www.medrxiv.org/content/10.1101/2021.01.12.21249613v1
Some variants (e.g., S477N) were resistant to neutralization by multiple mAbs, whereas others (e.g., E484K) escaped neutralization by convalescent sera, suggesting some humans induce a narrow repertoire of neutralizing antibodies.	**11 janvier** **Liu et al. 2021** Landscape analysis of escape variants identifies SARS-CoV-2 spike mutations that attenuate monoclonal and serum antibody neutralization https://www.biorxiv.org/content/10.1101/2020.11.06.372037v2

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Article de presse	Extrait pertinent	Source scientifique
14 janvier COVID reinfections are unusual — but could still help the virus to spread https://www.nature.com/articles/d41586-021-00071-6 Voir aussi **14 janvier** Expert reaction to a preprint from the SIREN study looking at SARS-CoV-2 infection rates in antibody positive healthcare workers https://www.sciencemediacentre.org/expert-reaction-to-a-preprint-from-the-siren-study-looking-at-sars-cov-2-infection-rates-in-antibody-positive-healthcare-workers/	Immune responses from past infection **reduce the risk** of catching the virus again by **83% for at least five months**. (compared to participants that had not been previously infected) **Repeat infections are rare — they occurred in fewer than 1% of about 6,600 participants who had already been ill with COVID-19 (n=44 possible reinfection over 5 months**); only 30% of the people with possible reinfections reported any symptoms) people who become re-infected can **carry high levels of the virus in their nose and throat, even when they do not show symptoms**. Such viral loads have been associated with a high risk of transmitting the virus to others	**18 décembre** **Wallace et al. (UK)** SIREN protocol: Impact of detectable anti-SARS-CoV-2 on the subsequent incidence of COVID-19 in 100,000 healthcare workers: do antibody positive healthcare workers have less reinfection than antibody negative healthcare workers? https://www.medrxiv.org/content/10.1101/2020.12.15.20247981v1
11 janvier La France surveille avec appréhension le rebond des Fêtes et le variant https://www.lapresse.ca/international/europe/2021-01-11/covid-19/la-france-surveille-avec-apprehension-le-rebond-des-fetes-et-le-variant.php	À quel point le variant « VOC 202 012/01 », qui a provoqué une flambée épidémique au Royaume-Uni, s'est-il installé en France ? Pour essayer d'y répondre, et face à l'apparition de premières éclosions potentielles, une enquête nationale a été lancée pour faire une « **première cartographie » de ce variant, en analysant tous les tests positifs de jeudi et vendredi derniers.** « En milieu de semaine on saura quelle est la taille de l'ennemi et là il faudra prendre les mesures appropriées », a expliqué à RMC/BFM-TV, l'épidémiologiste Arnaud	**11 janvier** **Bal et al. (France)** Two-step strategy for the identification of SARS-CoV-2 variant of concern 202012/01 and other variants with spike deletion H69-V70, France, August to December 2020 https://www.medrxiv.org/content/10.1101/2020.11.10.20228528v3 From August 3rd to December 20th (…) 59/9,266 **(0.6%) of positive tests** had no amplification of the S gene.

	Fontanet, membre du Conseil scientifique, qui guide les choix du gouvernement.	
10 janvier Un troisième variant détecté au Japon https://www.lapresse.ca/international/asie-et-oceanie/2021-01-10/covid-19/un-troisieme-variant-detecte-au-japon.php	Un nouveau variant de la COVID-19, différent de ceux de la Grande-Bretagne et de l'Afrique du Sud, a été détecté chez quatre voyageurs brésiliens (2 adultes dont 1 hospitalisé, et 2 enfants dont 1 asymptomatique), a annoncé dimanche le ministère japonais de la Santé.(…) **le nouveau variant contenait 12 mutations, dont l'une est également présente dans les variants trouvés au Royaume-Uni et en Afrique du Sud.** Le vaccin de Pfizer-BioNTech contre la COVID-19 protégerait efficacement contre la mutation N501Y de ces deux variants.(…) Le vaccin n'a toutefois pas encore été testé pour la mutation supplémentaire E484K présente sur le variant repéré en Afrique du Sud.	
UK - We have detected a confirmed case of reinfection (78 years old man with no history of immunosuppression) with SARS-CoV-2 with the second episode due to the 'new variant' VOC-202012/01 of lineage B.1.1.7. The initial infection occurred in the first wave of the pandemic in the UK and was a mild illness. **8 months later,** during the second wave of the pandemic in the UK reinfection with the '**new variant' VOC-202012/01** was confirmed and caused a **critical illness**.		**9 janvier** **Harrington et al. (UK)** Confirmed Reinfection with SARS-CoV-2 Variant VOC-202012/01 https://academic.oup.com/cid/advance-article/doi/10.1093/cid/ciab014/6076528
8 janvier Pfizer Says Its Vaccine Works Against Key Mutation in Contagious Variants https://www.nytimes.com/2021/01/08/health/pfizer-covid-vaccine-variant-mutation.html	Pfizer and BioNTech announced on Friday that their Covid vaccine is effective against **one (N501Y) of the mutations** present in the new contagious variants identified in Britain and South Africa. In the new study, which was posted online Thursday and has not yet gone through formal scientific review, (...) **the mutant virus could not infect human cells mixed with antibodies from vaccinated people**. B.1.1.7 (Britain) has turned up in 45 countries. B.1.351 (South Africa) has spread to a dozen other countries so far. On Friday, Public Health England released a new study (Technical briefing 3) of B.1.1.7 in which researchers estimated that the variant is 30 to 50 percent more transmissible than other forms of the virus.	
A 45-year-old female healthcare executive, (…) with no comorbidities. In the first episode, the patient presented diarrhea, myalgia, asthenia and odynophagia for approximately 7 days. (…) In the second episode,		**6 janvier** Nonaka et al. (Brazil) Genomic Evidence of a Sars-Cov-2 Reinfection Case With

symptomatically **more severe**,(…) separated by a **147-day interval** **Cycle threshold values (Cts)** of N, E and RdRp targets were 25, 26, and 27 in the first episode and **21, 12 and 17 in the second episode**. Four weeks after testing positive by RTPCR in the second episode, an IgG test was performed and showed a positive result (index value: 2.15 on 11/23/2020). Sample A was identified as B.1.1.33 lineage and sample B as B.1.1.248, a lineage derived from B.1.1.28. (…) In the first infection, the retrieved genome presented the S:G1219C, while in the **second infection, S:E484K and S:V1176F** were observed. In both samples, we found ORF1ab:P4715L, S:D614G, N:R203K, and N:G204R mutations.	E484K Spike Mutation in Brazil https://www.preprints.org/manuscript/202101.0132/v1

30 décembre New Covid variant linked to higher viral load in respiratory samples https://www.theguardian.com/world/2020/dec/30/new-covid-variant-linked-to-higher-viral-load-in-respiratory-samples	**27 décembre** **Kidd et al. (UK)** S-variant SARS-CoV-2 is associated with significantly higher viral loads in samples tested by ThermoFisher TaqPath RT-QPCR https://www.medrxiv.org/content/10.1101/2020.12.24.20248834v1 • a **high proportion of S-gene negative** samples; note the number having an S-gene undetectable profile (178 of 641; **27.7%**) at far right, compared with ORF and N-gene undetectable positive profiles (both 13 of 641; 2.0%). • Although S-negative samples occurred across the range of Ct values for ORF and N genes, clustering of S-negative results around **very low Ct values of ORF and N** can be clearly seen, and probably accounts for the lowering of the median Ct (ORF1ab: 18 vs 22 pour les S-positive); N: 19 vs 23 pour les S-positive) • approximately 35% of S-dropout samples had **high viral loads** (between 10 and 10,000-fold greater than 1 x 10^6), compared to 10% of S-positive samples.

Labo - We analyze 2 million RT-PCR SARS-CoV-2 tests performed at Helix to identify the rate of S gene dropout We observe a rise in S gene dropout in the US starting in early October, with **0.25%** of our daily SARS-CoV-2-positive tests (…) with last week (december) exhibiting the highest level yet, at **0.5%.**	**30 décembre** **Wahshington et al. (USA)** S gene dropout patterns in SARS-CoV-2 tests suggest spread of the H69del/V70del mutation in the US https://www.medrxiv.org/content/10.1101/2020.12.24.20248814v1
We downloaded 155,958 severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) genomes from GISAID and evaluated • whether variants improved prediction of reported severity beyond age and region.	**3 décembre** **Voss et al. (USA)** Variants in SARS-CoV-2 Associated with Mild or Severe Outcome

<table>
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- specific variants to determine the magnitude of association with severity and the frequency of these variants among the genomes. (…).

From 3,637 sequences with clear severity indications, we generated two classes: “Mild” and “Severe” (n= 2,870 hospitalized, ICU, pneumonia or deceased). (…) 85% of these genomes had at least one variant associated with patient outcome. Viral sequences were obtained from the **six major geographical regions in GISAID between January and October 2020.**

Among individual variants, we found **17 single nucleotide variants** in SARS-CoV-2 have more than **two-fold greater odds** of being associated with higher severity (hospitalized and deceased).

Supplementary Table 2. Summary of Variants and Association with Severe Outcome.

Variant_Name	Odds_Ratio	Amino Acid	Mutation_Type	Variant_Frequency
A23403G	1.71	D614G	Missense	0.6118
T28144C	1.73	L84S	Missense	0.0425
G21255C	1.75	A6997A	Silent	0.0012
C8782T	1.79	S2839S	Silent	0.0437
C26750T	1.80	I76I	Silent	0.0065
C9438T	1.81	T3058I	Missense	0.0027
C4543T	1.82	T1426T	Silent	0.0030
G26730T	1.88	V70F	Missense	0.0024
C6040T	1.93	F1925F	Silent	0.0048
C26735T	2.01	Y71Y	Silent	0.0844
T29148C	2.61	I292T	Missense	0.0276
C28076T	2.62	C61C	Silent	0.0009
C28657T	2.67	D128D	Silent	0.0166
G29616T	2.70	R20I	Missense	0.0116
C29870A	2.73		Non-coding	0.0059
C8139T	2.92	S2625F	Missense	0.0027
C10319T	3.02	L3352F	Missense	0.0042
T27299C	3.21	I33T	Missense	0.0271
C10188T	3.36	T3308I	Missense	0.0033
G29711T	3.58		Non-coding	0.0009
C23185T	3.98	F541F	Silent	0.0152
C6310A	4.25	S2015R	Missense	0.0488
G26144T	4.27	G251V	Missense	0.0294
C25549T	5.18	L53F	Missense	0.0051
C13620T	5.86	D4452D	Silent	0.0071
G25088T	74.64	V1176F	Missense	0.0369

Including genomic viral variants can substantially improve classification of COVID-19 patient outcomes as compared with models using only age and region.

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<td>https://www.medrxiv.org/content/10.1101/2020.12.01.20242149v1</td>
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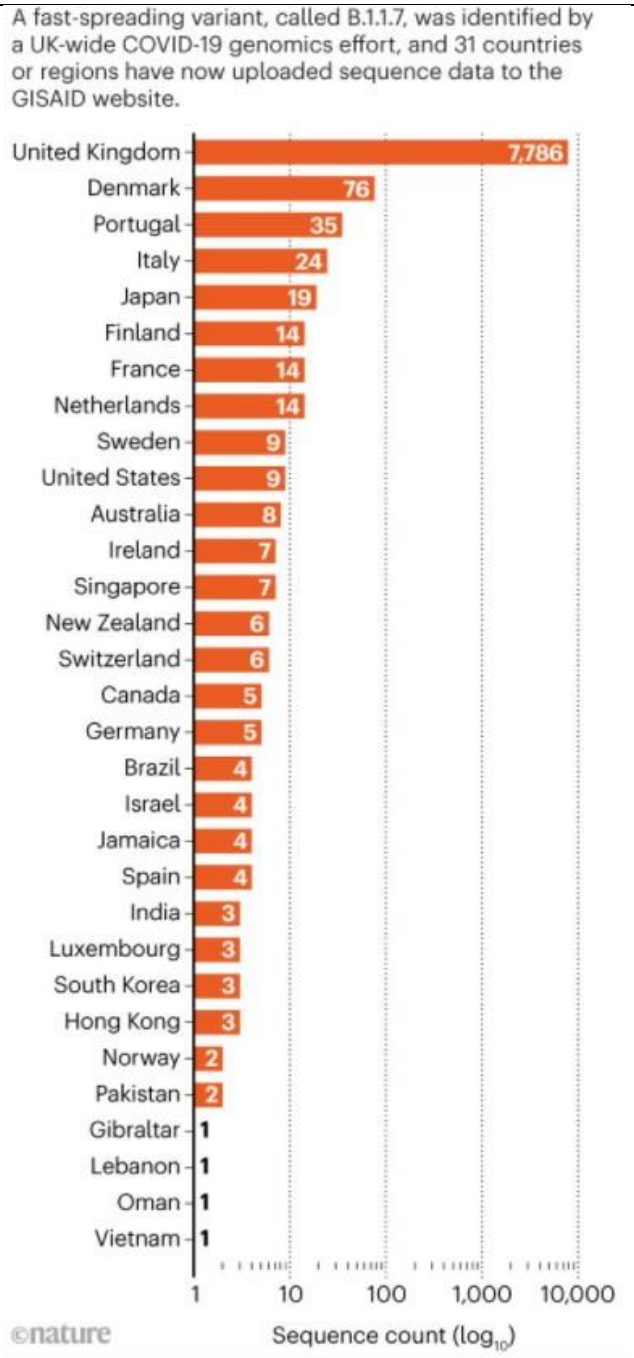
3 - 8 janvier 2021

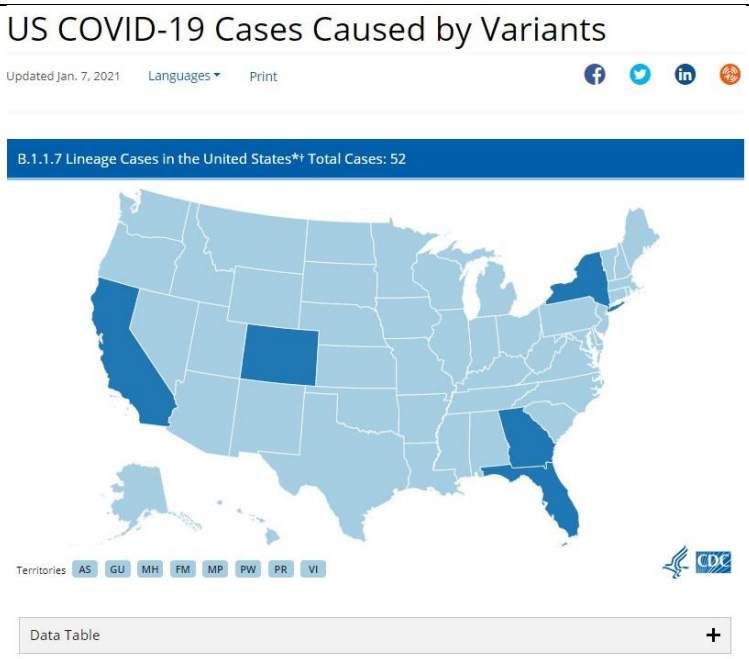
Article de presse	Extrait pertinent	Source scientifique

7 janvier
Could new COVID variants undermine vaccines? Labs scramble to find out
https://www.nature.com/articles/d41586-021-00031-0



The B.1.1.7 variant carries 8 changes that affect the spike protein, and several more in other genes (REF : Spike 69-70 del; 144 del, N501Y, A570D, P681H, T716I, S982A, D1118H));

South African 501Y.V2 variant carry up to 9 changes to the spike protein (REF: Spike D614G, D80A, D215G, E484K, N501Y, A701V, L18F, R246I, K417N).

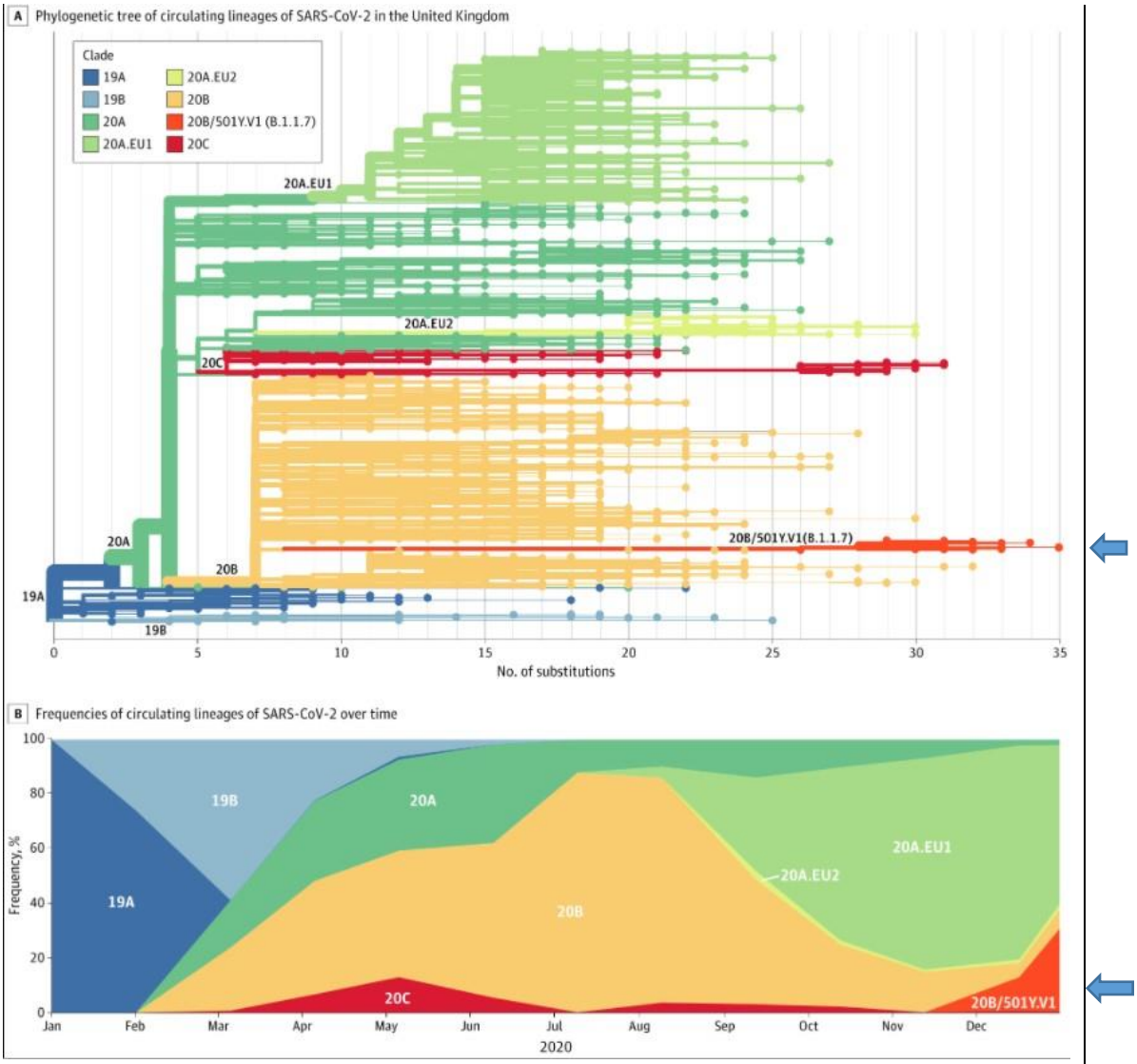
	Much of the focus is centred on a change to the spike protein (receptor binding domain) that is shared by both lineages, called N501Y. **One hypothesis hinted at in previous studies is that the N501Y change allows the virus to attach to cells more strongly, making infection easier.** **A report published in late December supports that hypothesis:** it found more SARS-CoV-2 genetic material in the swabs of people infected with the B.1.1.7 variant, compared with those infected with viruses lacking the N501Y change. **The N501Y mutation is one of several that Menachery's team is preparing to test in hamsters, a model for SARS-CoV-2 transmission.** A team led by his colleague Menachery found that the 501Y mutation, at least, did not drastically affect the activity of neutralizing antibodies in convalescent serum – (…) but **there is emerging evidence that the E484K mutation (identified in the 501Y.V2 variant) can enable the virus to escape some people's immune responses** (December preprint4,) (…) In a 4 January preprint5 E484K and several other mutations can escape recognition by antibodies in peoples' convalescent sera to varying degrees.
7 janvier CDC reports over 50 cases of UK coronavirus strain in US https://www.foxnews.com/health/cdc-lists-52-cases-of-mutated-uk-coronavirus-strain-in-us	 In an update Wednesday, the **CDC listed 26 cases** in California, two in Colorado, 22 in Florida, one in Georgia and an additional case in New York, for a total of 52 cases. On Thursday, Pennsylvania's Department of Health said that it had a confirmed case of the variant as well. **The CDC noted that the figures are an underestimate**, writing: "The cases identified above are based on a sampling of SARS-CoV-2-positive specimens and do not represent the total number of B.1.1.7 lineage cases that may be circulating

	in the United States and may not match numbers reported by states, territories, tribes, and local officials." **The CDC plans to update the page biweekly as more reported cases of the variant strain arise.**

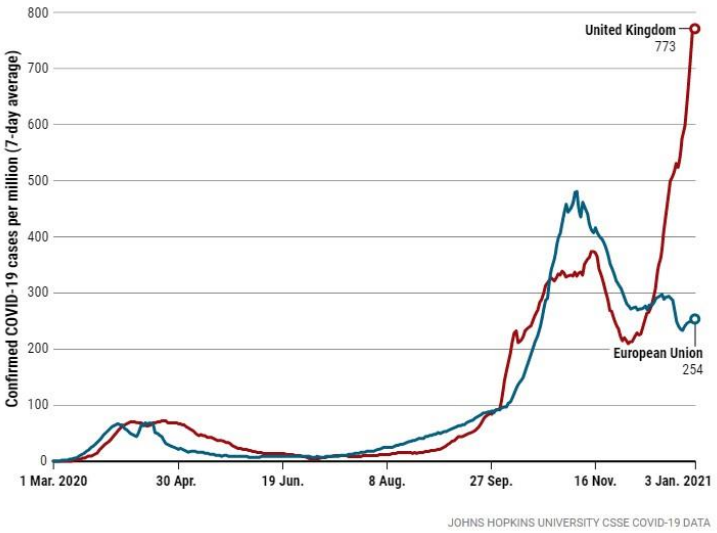
Strictly speaking, a variant is a strain when it has a demonstrably different phenotype (eg, a difference in antigenicity, transmissibility, or virulence). Evaluation of a new SARS-CoV-2 variant should include assessment of the following questions: • Did the variant achieve prominence through natural selection or chance events? • If the evidence suggests natural selection, which mutation(s) are being selected? • What is the adaptive benefit of these mutations? • What effect do these mutations have on transmissibility and spread, antigenicity, or virulence? **Spike D614G** **Spike N453Y and Mink** **Lineage B.1.1.7 and N501Y** As of December 28, 2020, this variant accounted for approximately 28% of cases of SARS-CoV-2 infection in England, and population genetic models suggest that it is spreading 56% more quickly than other lineages. Unlike D614G, which could plausibly have benefited from early chance events, lineage B.1.1.7 expanded when SARS-CoV-2 cases were widespread and has seemingly achieved dominance by outcompeting an existing population of circulating variants. This is strongly suggestive of natural selection of a virus that is more transmissible at a population level.	**6 janvier 2021** **Lauring et Hodcroft** Genetic Variants of SARS-CoV-2—What Do They Mean? https://jamanetwork.com/journals/jama/fullarticle/2775006

Figure: Spread of a New SARS-CoV-2 Variant
A, Phylogenetic tree showing the relationship of lineage B.1.1.7 (20B/501Y.V1, orange branch and tips) to other circulating lineages. The long branch length for this lineage reflects the fact that it accumulated a significant number of mutations prior to being discovered.

B, Frequencies of circulating lineages over time. Lineages are colored as in the tree, with lineage B.1.1.7 (20B/501Y.V1) shown in orange.



Antigenicity and Vaccine Effectiveness
At this point, strong selection of a variant at the population level is probably not driven by host antibody because there are not sufficient numbers of immune individuals to systematically push the virus in a given direction. (…) Because current vaccines provoke an immune response to the entire spike protein, it is hoped that effective protection may still occur despite a few changes at antigenic sites in SARS-CoV-2 variants.

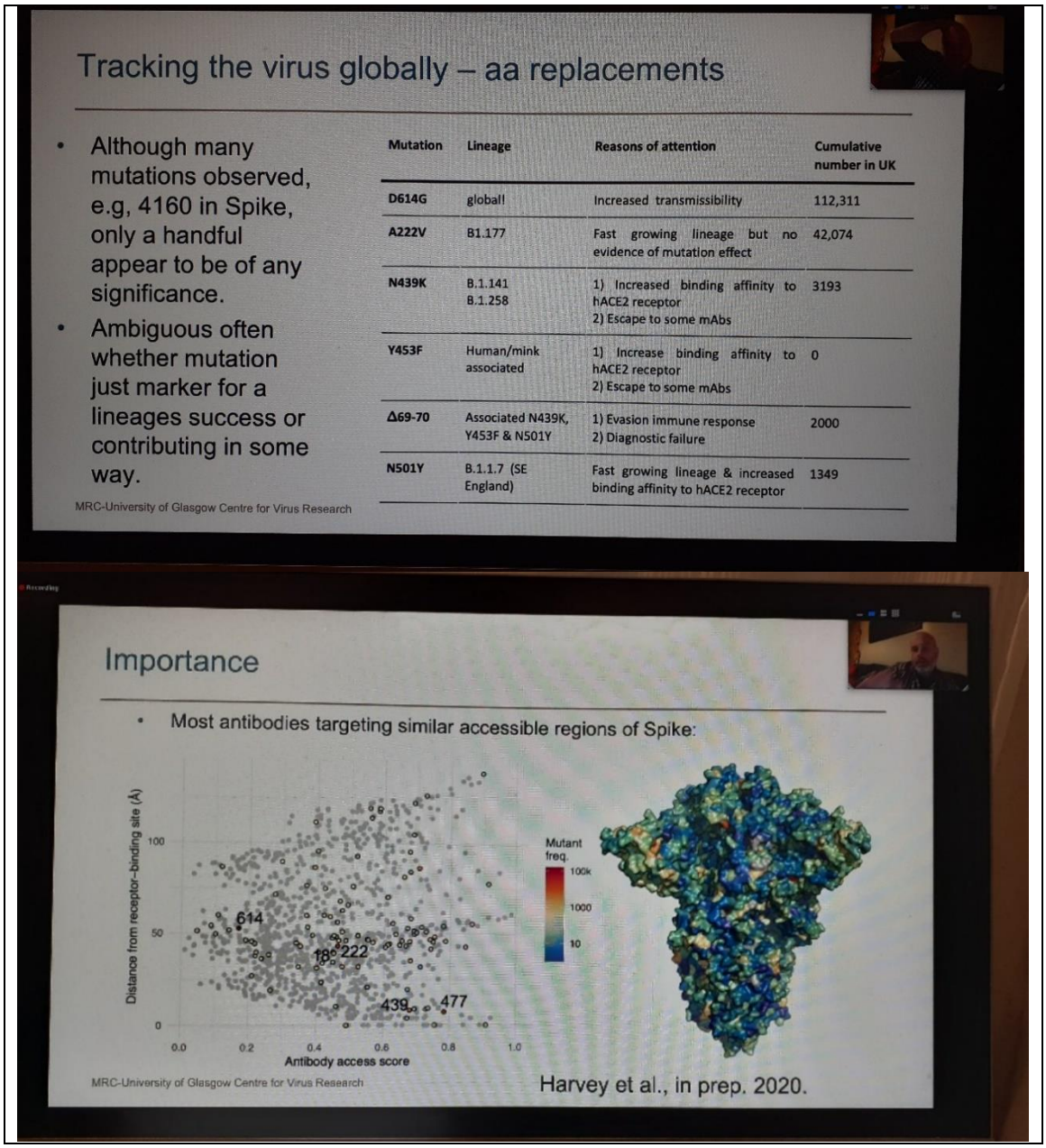
5 janvier Viral mutations may cause another 'very, very bad' COVID-19 wave, scientists warn https://www.sciencemag.org/news/2021/01/viral-mutations-may-cause-another-very-very-bad-covid-19-wave-scientists-warn	 **Figure: Confirmed COVID-19 cases per million - UK and European Union (7-day average)** One concern is that B.1.1.7 will now become the dominant global variant with its higher transmission and it will drive another very, very bad wave And data from Denmark, which leads the European Union in the sequencing of SARS-CoV-2, aren't reassuring either. Routine surveillance there has picked up the variant dozens of times; its frequency went from 0.2% of sequenced genomes in early December to 2.3% 3 weeks later. If the **U.K. estimates of a 50% to 75% increase in the virus' reproduction number**, or R, hold true, "keeping the virus from spreading has become a lot harder,"
31 décembre 2020 OMS - SARS-CoV-2 Variants Disease Outbreak News https://www.who.int/csr/don/31-december-2020-sars-cov2-variants/en/	**SARS-CoV-2 Variants**. • In late January or early February 2020, a variant of SARS-CoV-2 with a **D614G substitution** in the gene encoding the spike protein emerged. (…) became the dominant form of the virus circulating globally (…) increased infectivity and transmission (…) The SARS-CoV-2 virus with the D614G substitution does not cause more severe illness or alter the effectiveness of existing laboratory diagnostics, therapeutics, vaccines, or public health preventive measures. • In August and September 2020, a SARS-CoV-2 variant **("Cluster 5" variant** in Denmark consisting of four mutations, defined by a two amino acids deletion (69-70) and three amino acid replacements in position 453, 692 and 1229 (Y453F, I692V and M1229I)) linked to infection among farmed mink and subsequently transmitted to humans, was identified in North Jutland, Denmark. (…) Due preliminary studies conducted in Denmark, there is **concern that this**

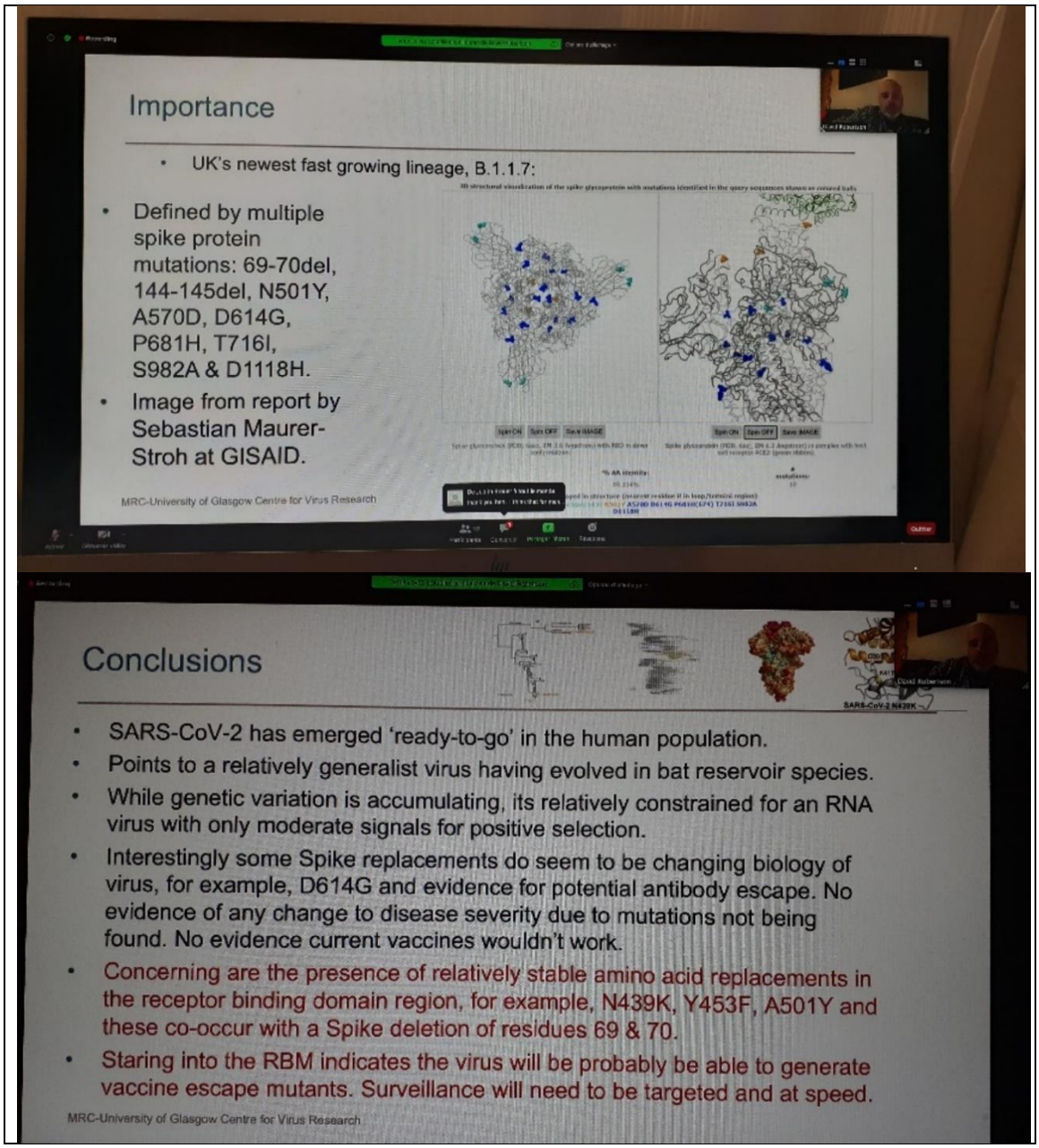
	variant has may result in reduced virus neutralization in humans. (…) To date, following extensive investigation and surveillance, Danish authorities have identified only 12 human cases of the Cluster 5 variant in September 2020, and it does not appear to have spread widely. • On 14 December 2020, authorities of the United Kingdom reported to WHO a variant referred to by the United Kingdom as **SARS-CoV-2 VOC 202012/01** (…) This variant contains 23 nucleotide substitutions and is not phylogenetically related to the SARS-CoV-2 virus circulating in the United Kingdom at the time the variant was detected. How and where SARS-CoV-2 VOC 202012/01 originated is unclear. (…) Preliminary epidemiologic, modelling, phylogenetic and clinical findings suggest that S**ARS-CoV-2 VOC 202012/01 has increased transmissibility**. However, preliminary analyses also indicate that there is **no change in disease severity** (as measured by length of hospitalization and 28-day case fatality), or occurrence of reinfection between variant cases compared to other SARS-CoV-2 viruses circulating in the United Kingdom. (Technical briefing of 21/12/2020) Another of the mutations in the VOC 202012/01 variant, the deletion at position **69/70del was found to affect the performance of some diagnostic PCR assays with an S gene target**. • On 18 December, national authorities in South Africa announced the detection of a new variant of SARS-CoV-2 that is rapidly spreading in three provinces of South Africa. South Africa has named this variant **501Y.V2**, because of a N501Y mutation.(…) **preliminary studies suggest the variant is associated with a higher viral load**, which may suggest potential for increased transmissibility (…) there is no clear evidence of the new variant being associated with more severe disease or worse outcomes.(…) As of 30 December, the 501Y.V2 variant from South Africa has been reported from four other countries to date. **WHO risk assessment** While initial assessment suggests that 202012/01 and 501Y.V2 do not cause changes in clinical presentation or severity, if they result in a higher case incidence, this would lead to an increase in COVID-19 hospitalizations and deaths. **WHO advice** WHO further advises countries, where feasible, to increase routine systematic sequencing of SARS-CoV-2 viruses to better understand SARS-CoV-2 transmission and to monitor for the emergence of variants.

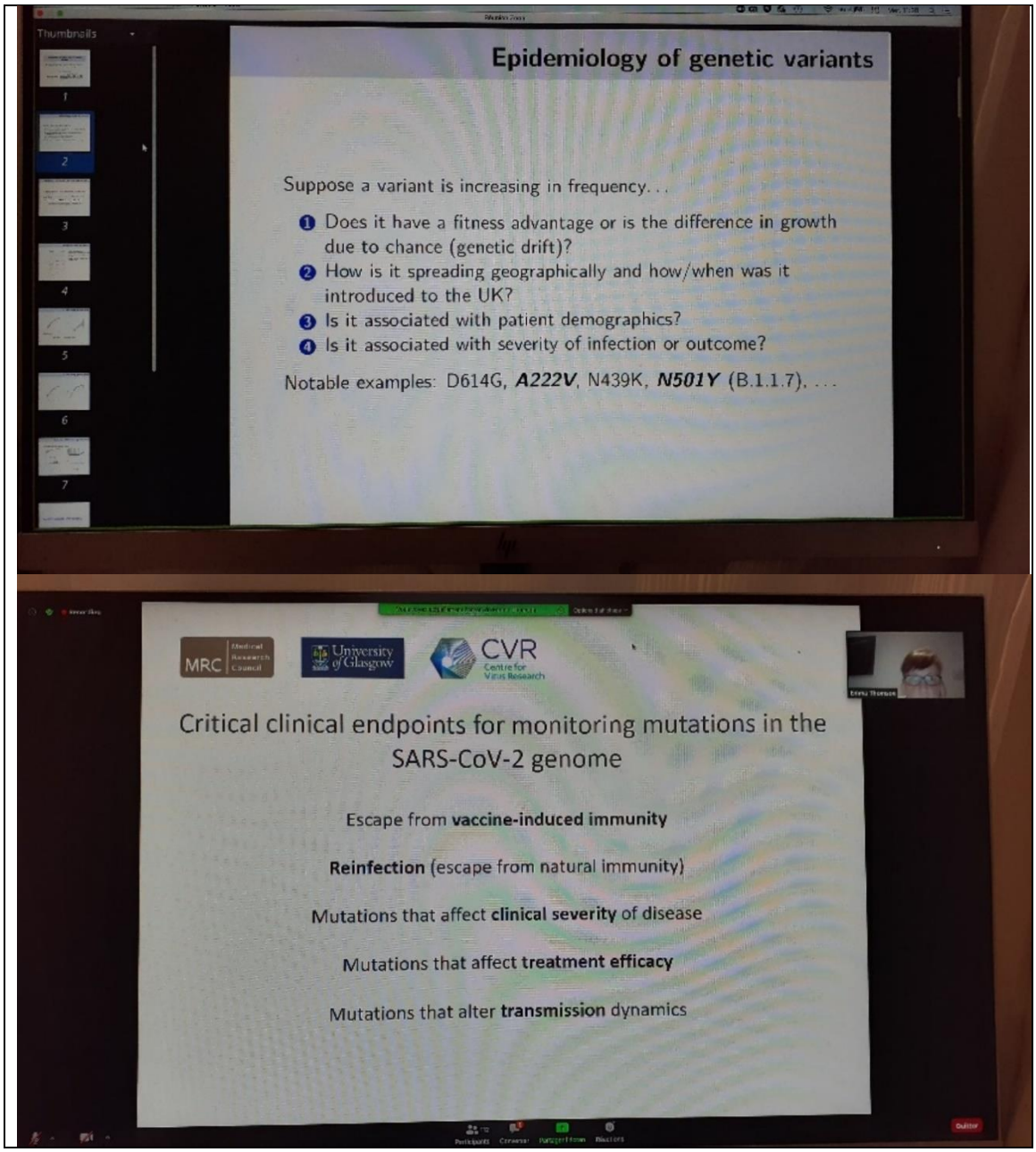
The SARS-CoV-2 lineage B.1.1.7, now designated Variant of Concern 202012/01 (VOC). (…) We examine epidemiological evidence for this VOC having a transmission advantage from several perspectives: • Phylodynamic modelling indicates that genetic diversity of this lineage has changed in a manner consistent with **exponential growth**; • Chang in VOC frequency correspond closely to changes inferred by **S-gene target failures** (SGTF); • growth trends in SGTF and non-SGTF case numbers at local area level across England show that the VOC has **higher transmissibility** than non-VOC lineages; • SGTF data indicate a shift in the age composition of reported cases, with a **larger share of under 20 year olds** among reported VOC than non-VOC cases; • There is a consensus among all analyses that the VOC has a substantial transmission advantage (…) the **ratio of reproduction numbers varying between 1.4 and 1.8.**	**30 décembre 2020** **Volz et al. (UK)** Transmission of SARS-CoV-2 Lineage B.1.1.7 in England: Insights from linking epidemiological and genetic data https://www.medrxiv.org/content/10.1101/2020.12.30.20249034v2

14 - 18 décembre 2020

Article de presse	Extrait pertinent	Source scientifique
16 décembre COG-UK First Showcase Event – 16th Dec 2020 • 2e vague = des lignées différentes de la 1re (importation), dont la nouvelle B.1.1.7 • Mutation Spike- 69-70 (nt 21764) = non détection du gène par RT-PCR • Surveillance sentinelle (8 000 séquences/semaine) • Aucune information sur les possibles cas de réinfections, ni définition		


Tracking the virus globally – aa replacements
Although many mutations observed, e.g, 4160 in Spike, only a handful appear to be of any significance.
Ambiguous often whether mutation just marker for a lineages success or contributing in some way.
MRC-University of Glasgow Centre for Virus Research
Mutation | Lineage | Reasons of attention | Cumulative number in UK
D614G | global! | Increased transmissibility | 112,311
A222V | B1.177 | Fast growing lineage but no evidence of mutation effect | 42,074
N439K | B.1.141 B.1.258 | 1) Increased binding affinity to hACE2 receptor 2) Escape to some mAbs | 3193
Y453F | Human/mink associated | 1) Increase binding affinity to hACE2 receptor 2) Escape to some mAbs | 0
Δ69-70 | Associated N439K, Y453F & N501Y | 1) Evasion immune response 2) Diagnostic failure | 2000
N501Y | B.1.1.7 (SE England) | Fast growing lineage & increased binding affinity to hACE2 receptor | 1349
Importance
Most antibodies targeting similar accessible regions of Spike:
Distance from receptor–binding site (Å)
Antibody access score
Mutant freq.
614
222
439
477
MRC-University of Glasgow Centre for Virus Research
Harvey et al., in prep. 2020.


Importance
UK's newest fast growing lineage, B.1.1.7:
Defined by multiple spike protein mutations: 69-70del, 144-145del, N501Y, A570D, D614G, P681H, T716I, S982A & D1118H.
Image from report by Sebastian Maurer-Stroh at GISAID.
MRC-University of Glasgow Centre for Virus Research
Conclusions
SARS-CoV-2 has emerged 'ready-to-go' in the human population.
Points to a relatively generalist virus having evolved in bat reservoir species.
While genetic variation is accumulating, its relatively constrained for an RNA virus with only moderate signals for positive selection.
Interestingly some Spike replacements do seem to be changing biology of virus, for example, D614G and evidence for potential antibody escape. No evidence of any change to disease severity due to mutations not being found. No evidence current vaccines wouldn't work.
Concerning are the presence of relatively stable amino acid replacements in the receptor binding domain region, for example, N439K, Y453F, A501Y and these co-occur with a Spike deletion of residues 69 & 70.
Staring into the RBM indicates the virus will be probably be able to generate vaccine escape mutants. Surveillance will need to be targeted and at speed.
MRC-University of Glasgow Centre for Virus Research


Thumbnails
Epidemiology of genetic variants
Suppose a variant is increasing in frequency...
1 Does it have a fitness advantage or is the difference in growth due to chance (genetic drift)?
2 How is it spreading geographically and how/when was it introduced to the UK?
3 Is it associated with patient demographics?
4 Is it associated with severity of infection or outcome?
Notable examples: D614G, A222V, N439K, N501Y (B.1.1.7), ...
MRC Medical Research Council
University of Glasgow
CVR Centre for Virus Research
Critical clinical endpoints for monitoring mutations in the SARS-CoV-2 genome
Escape from vaccine-induced immunity
Reinfection (escape from natural immunity)
Mutations that affect clinical severity of disease
Mutations that affect treatment efficacy
Mutations that alter transmission dynamics

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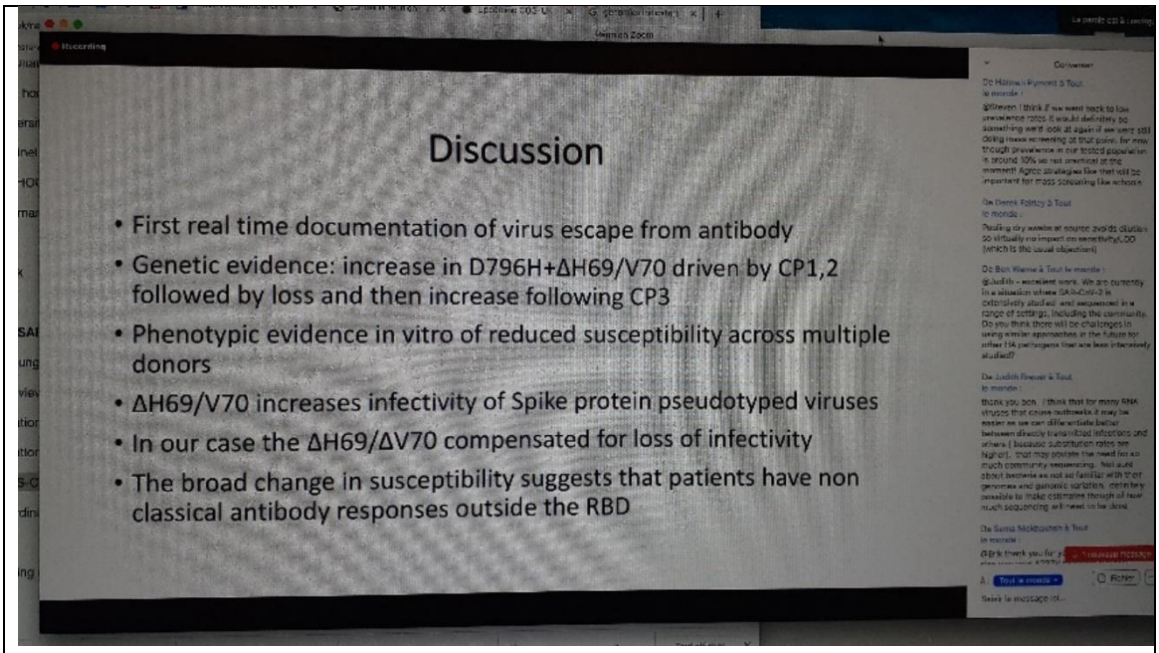
<tr><td colspan="2"> 
</td></tr>
<tr><td>The variant described today in the House of Commons contains a novel set of mutations associated with a lineage spreading rapidly in the South East of England (and more widely) (…). This variant carries a set of mutations including an N501Y mutation in the receptor binding motif of the Spike protein that the virus uses to bind to the human ACE2 receptor.

Efforts are under way to confirm whether or not any of these mutations are contributing to increased transmission. There is currently no evidence that this variant (or any other studied to date) has any impact on disease severity, or that it will render vaccines less effective, although both questions require further studies performed at pace. We will provide further updates as our investigations proceed.</td><td>14 décembre
Update on new SARS-CoV-2 variant and how COG-UK tracks emerging mutations
https://www.cogconsortium.uk/news_item/update-on-new-sars-cov-2-variant-and-how-cog-uk-tracks-emerging-mutations/</td></tr>
<tr><td>14 décembre
News story
PHE investigating a novel strain of COVID-19
https://www.gov.uk/government/news/phe-investigating-a-novel-strain-of-covid-19</td><td>The strain was identified due to Public Health England’s (PHE) proactive and enhanced monitoring following the increase in cases seen in Kent and London. The variant has been named ‘VUI – 202012/01’ (the first Variant Under Investigation in December 2020).

As of 13 December, 1,108 cases with this variant have been identified, predominantly in the South and East of England.</td></tr>
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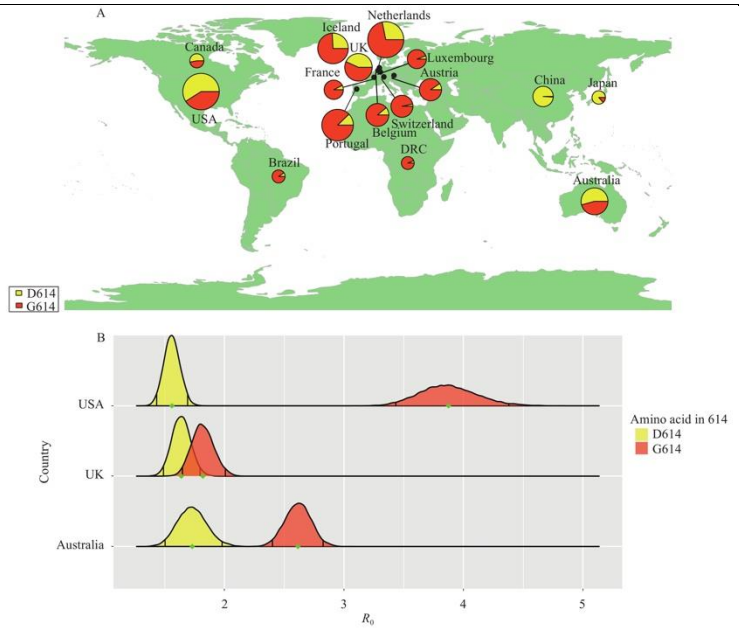
7 - 11 décembre

Article de presse	Extrait pertinent	Source scientifique
Question: What effect did the lockdown have on the SARS-CoV-2 lineages introduced into and then transmitted within Scotland and Wales since the start of the pandemic?		**9 décembre** Two new reports to SAGE (Scientific Advisory Group for Emergencies) on the genomic

The two reports (…) tell a tale of **repeated introductions of the virus** (…), after which some of the viruses undergo very extensive spread through the population. (…) **In Scotland**, the analysis confirmed about **300 independent introductions** of the virus into the country, defined based on new lineages being seen for the first time.(…) **Only around a quarter of these 'new' lineages appeared to become established** (defined as being detected more than five times). (…) A striking observation was that **following the first lockdown, the majority of virus lineages that had been circulating in the population in Scotland appeared to become extinguished**. Very few lineages persisted over the summer. This supports the idea that it is possible to eradicate the virus from a country when stringent public health measures are in place. What was then observed going into **the second wave is that disease was caused by new lineages that has been introduced into the country,** many of which could be traced to introductions from countries outside of the UK.(…) **In Wales**, the analysis identified that the **current population of circulating SARS-CoV-2 is also different t**o the lineages that were present in March and April 2020. (…) The Welsh analysis also **examined transmission on a more local level**, identifying that cases in areas of **high population density** (cities) were more likely to result from local chains of transmission, whereas those in **less urban areas** were more likely to be associated with imports from elsewhere and rarely led to local onward transmission.	analysis of epidemic waves of COVID-19 in Scotland and Wales https://www.cogconsortium.uk/news_item/two-new-reports-to-sage-on-the-genomic-analysis-of-epidemic-waves-of-covid-19-in-scotland-and-wales/
it was still unclear if COVID-19 virus strains with G614 were more transmissible than those with D614 We reconstructed several transmission chains of COVID-19 during the **early epidemic phase for 3 countries** (Australia, the UK, and USA) based on genomic data from GISAID (7) and Bayesian inference under an epidemiological model for strains with D614 and G614 due to the similar amount of genomes within each country (Figure 1A). Then we inferred the R0 in those transmission chains to compare the difference of transmissibility among humans between D614 and G614. Our findings demonstrated that the **G614 mutation accelerated the transmission of the COVID-19 virus and also had higher spatial transmissibility,** indicating that strains with G614, which were the dominant strains around the world, could spread on a larger scale and be more difficult to control.	**Liang Wang et al. (China)** Epidemiological Model Suggests D614G Spike Protein Mutation Accelerates Transmission of COVID-19 — Worldwide, 2020[J]. China CDC Weekly, 2020, 2(49): 946-947. http://weekly.chinacdc.cn/en/article/doi/10.46234/ccdcw2020.247

 FIGURE 1. The statistics and transmissibility of the COVID-19 virus with D614 and G614 during the early phases of the pandemic within each country. (A) The number of publicly available genomes with D614 and G614 during the **first two months after the first confirmed case in each country.** The size of the pie chart is associated with the number of genomes. (B) The distribution of R0 for D614 and G614 during the first two months after the first confirmed case in each country. The **mean of R0 is represented by a green point.** The black line within the distribution represents the 95% confidence interval (CI).	

30 - 3 décembre

Article de presse	Extrait pertinent	Source scientifique
3 décembre Largest Genetic Study on Children with COVID-19 Takes a Closer Look at Mutations https://www.verywellhealth.com/covid-19-children-largest-study-mutations-severity-5089761	We analyze the relationships between viral genetic variants and clinical characteristics in children (n=141). The D614G mutation in the spike protein was present in 99.3% of the isolates. **Phylogenetic clade 20C (61.0%, 86/141 isolates) was associated with severe cases of COVID-19** (p=0.0467, OR=6.95), but small sample size precludes a definitive conclusion.	**13 novembre** **Pandey et al. (USA)** High Prevalence of SARS-CoV-2 Genetic Variation and D614G Mutation in Pediatric Patients with COVID-19 https://academic.oup.com/ofid/advance-article/doi/10.1093/ofid/ofaa551/5981353

Genomic surveillance **identified a COVID-19 case with SARS-CoV-2 lineage B.1.177 from an individual in eastern Ontario in late September, 2020 (3 SNPs : C22227T, C28932T, G29645T).** The individual had recently returned from Europe. Genomic analysis with publicly available data indicate the most closely related genomes to this specimen were from Southern Europe. Genomic surveillance did not identify further cases with this lineage (…) we cannot rule out onward transmission		**2 décembre** **Guthrie et al. (Public Health Ontario)** Detection of the Novel SARS-CoV-2 European Lineage B.1.177 in Ontario, Canada https://www.medrxiv.org/content/10.1101/2020.11.30.20241265v2?rss=1%22
There is concern regarding whether an individual exposed to one variant of a virus will have cross-reactive memory to the second. Accordingly, we analyzed the serologic reactivity of both variants, and found that **antibodies (IgG, IgM and IgA) from 88 donors from a high-incidence population reacted toward both the original D614 spike and the G614 spike variant**. These data suggest patients who are exposed to either variant have cross-responsive humoral immunity.		**1 décembre** **Klumpp-Thomas et al. (USA)** D614G Spike Variant Does Not Alter IgG, IgM, or IgA Spike Seroassay Performance https://academic.oup.com/jid/advance-article/doi/10.1093/infdis/jiaa743/6013009
1 décembre Upcoming COG-UK First Showcase Event – 16th Dec 2020 https://www.cogconsortium.uk/news_item/upcoming-cog-uk-showcase-event-16th-dec-2020/	**SARS-CoV-2 sequencing to inform clinical care, public health interventions and policy decisions** Session 1 – Overview of the Four Nations Experience: lineage introduction and transmission (Scotland, Wales, Northern Ireland and England) Session 2 – Overview of Genomic-Informed Evidence on Transmission in Specific Environments (Hospitals, Care homes and Universities) Session 3 – SARS-CoV-2 Mutations – Implications for Transmission, Disease Severity, Therapeutics and Vaccines	
27 novembre SARS-CoV-2 : que sait-on de la dynamique de la charge virale, des durées d'excrétion et de contagiosité du virus ? https://www.lemonde.fr/blog/realitesbiomedicales/2020/11/27/sars-cov-2-que-sait-on-de-la-dynamique-de-la-charge-virale-des-durees-dexcretion-et-de-contagiosite-du-virus/	79 studies (5340 individuals) on SARS-CoV-2 (…) Mean duration of SARS-CoV-2 RNA shedding was 17·0 days (95% CI 15·5–18·6; 43 studies, 3229 individuals) in upper respiratory tract (…) Maximum shedding duration was 83 days in the upper respiratory tract (…) No study detected live virus beyond day 9 of illness, despite persistently high viral	**19 novembre** **Cevik et al. (UK)** SARS-CoV-2, SARS-CoV, and MERS-CoV viral load dynamics, duration of viral shedding, and infectiousness: a systematic review and meta-analysis. https://www.thelancet.com/journals/lanmic/article/PIIS2666-5247(20)30172-5/fulltext#%20

	loads, which were inferred from cycle threshold values. SARS-CoV-2 viral load in the upper respiratory tract appeared to peak in the 1st week of illness	
14 studies of 2568 individuals were included. The incidence of recurrent SARS-CoV-2 positivity was 14.8% (95% confidence interval [CI] 11.44-18.19%). The pooled estimate of the interval from disease onset to recurrence was 35.4 days (95% CI 32.65-38.24 days), and from the last negative to the recurrent positive result was 9.8 days (95% CI 7.31-12.22 days).		**26 novembre** **Azam et al. (Indonesia)** Recurrent SARS-CoV-2 RNA positivity after COVID-19: a systematic review and meta-analysis https://pubmed.ncbi.nlm.nih.gov/33244060/
We review how the D614G variant was identified and discuss recent evidence about the effect of the mutation on the characteristics of the virus, clinical outcome of infection and host immune response.		**5 novembre** **Groves et al. (UK)** The D614G mutations in the SARS-CoV-2 spike protein: Implications for viral infectivity, disease severity and vaccine design https://www.sciencedirect.com/science/article/pii/S0006291X20320386?via%3Dihub#!

16- 26 novembre

Article de presse	Extrait pertinent	Source scientifique
25 novembre Dallas woman was reinfected with COVID after 4 months. https://www.star-telegram.com/news/coronavirus/article247414100.html	three confirmed cases in the U.S. and 26 worldwide, according to an unofficial COVID-19 **reinfection tracker** published by BNO News. The tracker, which bases its finding on case studies and news reports, showed an **additional 599 suspected cases**, including 28 in South Dakota and 100 in Washington state as of Nov. 21.	**23 novembre** **Prado-Vivar *et al.* (Ecuador)** A case of SARS-CoV-2 reinfection in Ecuador https://www.thelancet.com/journals/lancet/article/PIIS1473-3099(20)30910-5/fulltext#%20 **21 novembre** **Lee et al. (South Korea)** Evidence of Severe Acute Respiratory Syndrome Coronavirus 2 Reinfection After Recovery from Mild Coronavirus Disease 2019 https://academic.oup.com/cid/advance-article/doi/10.1093/cid/ciaa1421/5997517 **15 novembre** **Colson *et al.* (France)** Evidence of SARS-CoV-2 re-infection with a different genotype https://www.journalofinfection.com/article/S0163-4453(20)30706-4/fulltext
24 novembre COVID-19 in care homes — what have we learned from genome sequencing? https://www.cogconsortium.uk/news_item/covid-19-in-care-homes-what-have-we-learned-from-genome-sequencing/	In a recent preprint, researchers from across the COVID-19 Genomics UK (COG-UK) Consortium have looked at all the studies worldwide which have used genome sequencing to better understand outbreaks in care homes. Only a small amount of work has been done on this area, with 11 studies in total from the UK, USA and The Netherlands. So, what have we learned from genome sequencing in care homes? • The majority of infections in care homes have not come from hospitals but from the local community • As a result, when infections are high in a community you will find there are more care home outbreaks • A high percentage of cases without symptoms (asymptomatic) is common • Once the virus is established in care homes it tends to be of one dominant lineage (identical or nearly identical virus) found in both residents and staff • Once the virus has entered a care home it spreads rapidly despite infection control measures	

	• To date there is no difference in the mortality rate between different lineages in care homes which have outbreaks. The mortality rates are high.	
20 novembre Priority Research Questions for COG-UK https://www.cogconsortium.uk/news_item/priority-research-questions-for-cog-uk/	67 questions/statements, which we grouped into 7 categories (+ priority, urgency, expected timelines, and notes for each question). The full list can be downloaded here. 1. SARS-CoV-2 transmission; 2. Disease pathogenesis; 3. SARS-CoV-2 evolution, including within-host diversity; 4. Reinfection and coinfection; 5. Host response; 6. Metadata; 7. Technology and surveillance.	**Re(co)infection (priority)** How common are reinfections? (very high) Are there specific genetic changes associated with reinfecting viral lineages? (useful) Which other respiratory pathogens are co-circulating and are these the basis for symptomatic negative test results? (high) Is there any evidence for super infection? (high) Can we use rapid, real-time metagenomic sequencing (on e.g. Oxford Nanopore MinION) to detect SARS-CoV-2 and other respiratory viruses, bacteria and fungi in a single test with high specificity and sensitivity? (high)
20 novembre Immune responses to coronavirus persist beyond 6 months https://www.nature.com/articles/d41586-020-00502-w	Dan et al. found that participants' immune responses varied widely. But several components of immune memory of SARS-CoV-2 tended to persist for at least 6 months. Among the persistent immune defenders were **memory B cells**, which jump-start antibody production when a pathogen is re-encountered, and two important classes of T cell: **memory CD4+ and memory CD8+ T cells.** The results have not yet been peer-reviewed.	**20 novembre** **Hartley et al. (Autralia)** Rapid and lasting generation of B-cell memory to SARS-CoV-2 spike and nucleocapsid proteins in COVID-19 disease and convalescence https://www.medrxiv.org/content/10.1101/2020.11.17.20233544v1.full **16 novembre** **Dan et al. (USA)** Immunological memory to SARS-CoV-2 assessed for greater than six months after infection https://www.biorxiv.org/content/10.1101/2020.11.15.383323v1

		12 novembre **Schulien et al. (Allemagne)** Characterization of pre-existing and induced SARS-CoV-2-specific CD8⁺ T cells https://www.nature.com/articles/s41591-020-01143-2 **15 aout** **Rodda et al. (USA)** Functional SARS-CoV-2-specific immune memory persists after mild COVID-19 https://www.medrxiv.org/content/10.1101/2020.08.11.20171843v2

2- 13 novembre

Article de presse	Extrait pertinent	Source scientifique
11 novembre A coronavirus mutation could weaken antibodies' power https://www.nature.com/articles/d41586-020-00502-w	A widespread variant (Spike:N439K mutation in the receptor binding motif RBM) of the new coronavirus has the potential to evade the immune response that some people mount after infection.(…) N439K S protein has enhanced binding affinity to the hACE2 receptor, and that N439K virus has similar clinical outcomes and *in vitro* replication fitness as compared to wild- type. (…) N439K mutation resulted in immune escape from a panel of neutralizing monoclonal antibodies, including one in clinical trials, as well as from polyclonal sera from a sizeable fraction of persons recovered from infection.	**5 novembre** **Thomson *et al*. (UK-USA)** The circulating SARS-CoV-2 spike variant N439K maintains fitness while evading antibody-mediated immunity https://www.biorxiv.org/content/10.1101/2020.11.04.355842v1
10 novembre COG-UK passes 100K genomes https://www.cogconsortium.uk/news_item/cog-uk-passes-100k-genomes/	This week saw COG-UK pass an important milestone, having now sequenced more than 100K SARS-CoV-2 genomes in 8 months (…) Prior to SARS-CoV-2, the largest previous dataset for real-time genomic viral epidemiology during an epidemic was ~1500 genomes from the West African Ebola outbreak, which were sequenced over the course of 2014-2016. By comparison, COG-UK surpassed this total within the first month	

	With the impending roll out of national vaccination programmes, which will begin to apply a new selective pressure to SARS-CoV-2 as it continues to spread, COG-UK researchers are working with others to monitor changes in the evolution of the virus, to identify mutations that may impact on the efficacy of particular vaccines (as potentially seen with the recent SARS-CoV-2 mink outbreak) and prioritise them for further investigation, and to inform national and local policy for vaccine choices and non-pharmaceutical interventions going forward.	
9 novembre EXPLAINER: SARS-CoV-2 mutations, the science behind the mink case. What do we know about the Danish 'Cluster 5'? https://www.cogconsortium.uk/news_item/explainer-sars-cov-2-mutations-the-science-behind-the-mink-case/	The Danish government will cull 17 million farmed mink in the country after detecting variants of the SARS-CoV-2 in these animals with mutations that have been transmitted back to humans (…) presence of a cluster of variants, 'cluster 5', consisting of four mutations, defined by a two amino acids deletion (69-70) and three amino acid replacements in position 453, 692 and 1229 (Y453F, I692V and M1229I) in the Spike protein, which are now spreading among farmed mink and small numbers of people in Denmark (…) Phylogenetic analyses by the COVID-19 Genomics UK (COG-UK) consortium show that the 69-70 deletion can also be associated with the N439K mutation at the spike receptor binding motif (RBM)	**Welkers et al. (The Netherlands)** Possible host-adaptation of SARS-CoV-2 due to improved ACE2 receptor binding in mink **Lien Teams**
6 novembre EXPLAINER: SARS-CoV-2 mutations, what we have learned from new fast-growing lineages and the Spike N439K variant https://www.cogconsortium.uk/news_item/explainer-sars-cov-2-mutations-what-we-have-learned-from-new-fast-growing-lineages-and-the-spike-n439k-variant/	Hodcroft *et al.* speculated, with appropriate caution, that the 'success' of the B.1.177 lineage may be associated with the presence of the (spike) A222V (…) Severe cases of COVID-19 infection are strongly associated with age and certain comorbidities, so there is no expectation that this variant will have an impact on disease severity (as shown for the previously studied spike protein variants such as D614G Thomson *et al.* (…) investigated another variant with a mutation in the spike protein (N439K) originating from lineage B.1, observed in March 2020 in Scotland, extinct in June, and now circulating in multiple countries including Europe as another large lineage and again independently in the USA (…). Based on a comparison of all of the Scottish lineages, the authors found no evidence for a faster rate of growth for the N439K variant beyond that already determined for the D614G mutation which is also found in all variants	

	carrying N439K. However, Thomson *et al.* demonstrated in the laboratory that N439K enhances binding affinity to the hACE2 receptor and is able to escape the neutralising activity of some monoclonal antibodies (mAbs), including one in clinical trials, and from antibodies present in sera from a sizeable fraction of people recovered from infection. In a large comparison of Scottish patients **no increased disease severity was observed**. It will be important to assess whether viruses carrying N439K have the potential to be resistant to the natural immune response, which may make them more likely to be associated with reinfections.

26- 30 octobre

Article de presse	Extrait pertinent	Source scientifique
	Two emergent variants: **V1176F** in co-occurrence with D614G mutation in the viral Spike protein, and **S477N**, located in the Receptor Binding Domain (RBD) of the Spike protein, are associated with high fatality rates and are increasingly spreading throughout the world (n=7634 genomes).	**23 octobre** **Farkas et al. (Canada)** Large-scale population analysis of SARS-CoV-2 whole genome sequences reveals host-mediated viral evolution with emergence of mutations in the viral Spike protein associated with elevated mortality rates https://www.medrxiv.org/content/10.1101/2020.10.23.20218511v1.full.pdf
29 octobre Mutant COVID-19 strain in Spanish farm workers sparked Europe's second wave: scientists https://nationalpost.com/news/world/mutant-covid-19-strain-in-spanish-farm-workers-sparked-europes-second-wave-scientists	A novel SARS-CoV-2 variant 20A.EU1 (**Spike : A222V**) that emerged in early summer 2020, presumably in Spain, (…) and a second variant 20A.EU2 with mutation **Spike : S477N** (…) account for the majority of recent sequences in Europe • No direct evidence that it spreads faster. • There are currently no data to evaluate whether this variant affects the severity of the disease. • diverse variants of SARS-CoV-2 continue to circulate across Europe.	**25 octobre** **Hodcroft et al. (Switzerland)** Emergence and spread of a SARS-CoV-2 variant through Europe in the summer of 2020 https://www.medrxiv.org/content/10.1101/2020.10.25.20219063v1.full.pdf
	E-mail survey: COG-UK genome sequence data and tools have been used in more than 120 retrospective and live public health outbreak	**16 octobre** Report 12: 15th October 2020 – COVID-19 Genomics UK (COG-UK) Consortium

	investigations in the UK since March 2020. • 61-75 hospital • 24-43 surveillance programmes • 23-32 defined outbreaks (e.g. in a workplace) • 12-16 community As the transition to a new operational phase continues, COG-UK will provide large scale genomic surveillance service to support the investigation of a growing proportion of live outbreaks in the UK. A viral lineage carrying a mutation, Spike: **N439K**, (…) in the receptor binding motif of the SARS-CoV-2 spike protein, is now spreading in Europe (including 500+ infections in the UK). (…) Investigation of clinical outcomes from >1600 Scottish patients infected with either the lineage defined by 439K versus the wild-type lineage (439N) showed no significant difference in disease severity. This variant (**N439K**) (…) does highlight the need to establish a systematic approach for monitoring the appearance and spread of all variants and prioritising mutations of interest for further characterisation, in particular when selective pressure from mass vaccination programmes begins. - other mutations are being observed in the spike receptor binding motif: S477N (>300 UK sequences), T478I (>100), S494P (>20), E484Q (>10), S477I (>10), E484Q (>10) and others at lower frequencies	https://www.cogconsortium.uk/news_item/report-12-15th-october-2020/

19- 23 octobre

Article de presse	Extrait pertinent	Source scientifique
21 octobre Australia may have recorded first case of Covid-19 reinfection https://www.theguardian.com/world/2020/oct/21/australia-may-have-recorded-first-case-of-covid-19-re-infection	Genomic sequencing has not yet been completed, but the premier Daniel Andrews said the man first tested positive to the virus in July. He tested positive again in October. In many cases it is unclear whether a second positive test is truly a reinfection or merely dead virus being shed.	ND
22 octobre SARS-CoV-2 mutations dictate severity of COVID-19 disease https://www.news-medical.net/news/20201022/SARS-CoV-2-mutations-dictate-severity-of-COVID-19-disease.aspx	Obj: identifying viral mutations that were associated with different outcomes in the patient.(…) Of the over 72,000 complete sequences available (GISAID), clinical data were available in only just over 5,000 sequences and follow-up data in ~3,200 patients.(…) The limited proportion of sequences included in this study may have caused sampling bias. The majority of samples came from Asia, while ~27% were from Europe, ~9% were from Central America, ~6-7% from the Americas, and ~5% from Africa. The severity break-up was as follows: 625 with mild (non-hospit), ~2,300 moderate (hospit), and ~220 severe (ICU, death). Looking only at mutations observed in 2% or more of the samples (clinical relevance): • 6 mutations related to **mild disease**: in ORF8, ORF3a, nsp4, nsp6, and N • 5 mutations related to **moderate disease**: in spike (L54F), ORF3a, N, exonuclease, NSP2	**Nagy et al. (Hungary)** **20 octobre** Different mutations in SARS-CoV-2 associate with severe and mild outcome https://www.medrxiv.org/content/10.1101/2020.10.16.20213710v1

	• 8 mutations related to **severe disease**: in spike (D614G), polymerase, ORF3a, N, exonuclease, NSP7 associated with severe disease	
20 octobre Genomics ties university COVID cases to care-home deaths https://www.nature.com/articles/d41586-020-00502-w	An explosive outbreak of COVID-19 among young people in a US university town (2,002 cases in September 2020) spilt into the surrounding community, leading to the deaths of two people in local care homes.(…) the "overwhelming majority" of those cases was caused by only two viral variants	**Richmond et al. (USA)** **14 octobre** SARS-CoV-2 sequencing reveals rapid transmission from college student clusters resulting in morbidity and deaths in vulnerable populations https://www.medrxiv.org/content/10.1101/2020.10.12.20210294v1
15 octobre Genome-wide association study identifies ABO blood protein https://www.physiciansweekly.com/genetic-variants-linked-to-severe-covid-19/	835 patients and 1255 control participants from Italy and 775 patients and 950 control participants from Spain were included in the final analysis. We identified a 3p21.31 gene cluster (SLC6A20, LZTFL1, CCR9, FYCO1, CXCR6 and XCR1) as a genetic susceptibility locus in patients with Covid-19 with respiratory failure and confirmed a potential involvement of the ABO blood-group system (at locus 9q34.2).	**Ellinghaus et al. (Germany)** **14 octobre** Genomewide Association Study of Severe Covid-19 with Respiratory Failure https://www.nejm.org/doi/full/10.1056/NEJMoa2020283?query=recirc_curatedRelated_article The group's findings were originally reported online in June.

12- 16 octobre

Article de presse	Extrait pertinent	Source scientifique
15 octobre Une Québécoise de 37 ans attrape la COVID-19 une deuxième fois https://ici.radio-canada.ca/nouvelle/1741166/quebecoise-attrape-covid-19-deuxieme-fois-reinfection-immunite	La femme de 37 ans, originaire de Québec mais aujourd'hui résidente de Montréal (…) Pour une deuxième fois en cinq mois, (…) Ses symptoms ont été moins intenses que lors de sa première infection. (…) La première fois, ç'a été un peu plus sérieux.	ND

	(…)première infection, qu'elle a contractée en travaillant dans un CHSLD en éclosion en mai dernier	
14 octobre Dutch woman dies after catching COVID-19 twice, the first reported reinfection death https://www.ctvnews.ca/health/coronavirus/dutch-woman-dies-after-catching-covid-19-twice-the-first-reported-reinfection-death-1.5144351	The woman, 89, suffered from a rare type of bone marrow cancer (…). Her immune system was compromised due to the cell-depleting therapy she received (…) However, the researchers said her natural immune response could still have been "sufficient" to fight-off COVID-19. (…) But two days into chemotherapy treatment -- 59 days after the start of the first (symptomatic) COVID-19 episode -- the woman developed fever, cough and difficulty breathing.(…) She once again tested positive for coronavirus, and no antibodies were detected in her blood system when tested on days four and six. Her condition deteriorated on day eight.(…) The woman was not tested between infections, so researchers have no confirmed negative tests.(…) they found the genetic makeup of the two viruses to be different	**Mulder et al. (Netherlands)** Reinfection of SARS-CoV-2 in an immunocompromised patient: a case report https://www.dutchnews.nl/wpcms/wp-content/uploads/2020/10/ciaa1538.pdf **(accepted for publication in the journal Clinical Infectious Diseases)**
12 octobre Un Américain devient le cinquième cas de réinfection à la COVID-19 https://ici.radio-canada.ca/nouvelle/1740629/coronavirus-reinfection-immunite-covid-19-nevada-lancet-etats-unis	Un Américain a attrapé deux fois la COVID-19 à un mois et demi d'intervalle et la deuxième infection était plus sévère que la première (…) Selon cette revue médicale, cinq cas ont été confirmés jusque-là : à Hong Kong (il s'agissait du premier, annoncé le 24 août), en Belgique, aux Pays-Bas, en Équateur et dans l'État américain du Nevada	**12 octobre** **Tillett et al. (USA)** Genomic evidence for reinfection with SARS-CoV-2: a case study https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30764-7/fulltext ****Note de breffage**** **21 septembre** **ECDC** *Threat Assessment Brief: Reinfection with SARS-CoV-2: considerations for public health response*

		• How can a SARS-CoV-2 reinfection be identified? • How common are SARS-CoV-2 reinfections? • What is known about the role of reinfection in onward transmission? • What do these observations mean for acquired immunity? • options for public health response are proposed. https://www.ecdc.europa.eu/en/publications-data/threat-assessment-brief-reinfection-sars-cov-2
13 octobre Found: genes that sway the course of the coronavirus https://www.sciencemag.org/news/2020/10/found-genes-sway-course-coronavirus	Genome-wide association study (GWAS) in 2244 critically-ill Covid-19 patients from 208 UK intensive care units (…) has identified gene variants that put people at greater risk of severe disease.(…) Our findings reveal that critical illness in Covid-19 is related to at two biological mechanisms: innate antiviral defences, which are known to be important early in disease (IFNAR2 and OAS genes), and host-driven inflammatory lung injury, which is a key mechanism of late, life-threatening Covid-19 (DPP9, TYK2 and CCR2)	**25 septembre** **Pairo-Castineira et al. (UK)** Genetic mechanisms of critical illness in Covid-19 https://www.medrxiv.org/content/10.1101/2020.09.24.20200048v2 ***Pour information*** **GenOMICC (Genetics Of Mortality In Critical Care)**, is a global collaborative study to understand the genetic basis of critical illness. https://genomicc.org/
12 octobre COVID-19 vaccines should not be affected by SARS-CoV-2 mutations, researchers say https://www.drugtargetreview.com/news/74149/covid-19-vaccines-should-not-be-affected-by-sars-cov-2-mutations-researchers-say/	(…) most vaccines under development worldwide have been modelled on the original 'D-strain' of the virus (…) The study tested blood samples from ferrets given a candidate vaccine against virus strains that either possessed or lacked this mutation – known as 'D614G'.(…) We confirmed through experiments (neutralisation assay) and (molecular) modelling that vaccine candidates are still effective. We have also found the G-strain is unlikely to require frequent 'vaccine matching'	**8 octobre** **McAuley et al. (Australia)** Experimental and in silico evidence suggests vaccines are unlikely to be affected by D614G mutation in SARS-CoV-2 spike protein https://www.nature.com/articles/s41541-020-00246-8

5- 9 octobre

Article de presse	Extrait pertinent	Source scientifique
	In this pilot-study, we investigate the expression pattern and level of SARS-CoV-2 host invasion genes (ACE2, TMPRSS2, PCSK3, EMILIN1, EMILIN2, MMRN1, MMRN2, DPP4) in (…) 28 negative subjects and 35 severely affected COVID-19 patients (n=63). ACE2 and DPP4 (CD26) genes showed a significant overexpression in COVID-19 patients (…) their expression levels had a good performance in distinguishing COVID-19 patients from negative subjects. A coordinated expression pattern of these genes is crucial for SARS-CoV-2 infection and these expression patterns may be useful for predictive diagnosis, prognosis and pathophysiology of COVID-19	**6 octobre** **Amati et al. (Italy)** Expression profiles of the SARS-CoV-2 host invasion genes in nasopharyngeal and oropharyngeal swabs of COVID-19 patients. https://www.cell.com/heliyon/fulltext/S2405-8440(20)31986-1?_returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS2405844020319861%3Fshowall%3Dtrue
	We compared SARS-COV-2 genetic diversity in 19 mild and 27 severe cases (n = 46 samples). With respect to the reference sequence, in-depth sequence analysis revealed a total number of 236 variants with frequency >10% in all SARS-CoV-2 genomes. Severe cases exhibited significantly higher within-host variants (5 to 44; mean = 16) compared to mild cases (4 to 10; mean = 6).	**6 octobre** **Khatib et al. (Qatar)** Within-Host Diversity of SARS-CoV-2 in COVID-19 Patients With Variable Disease Severities https://www.frontiersin.org/articles/10.3389/fcimb.2020.575613/full

	In patients with severe symptoms, in-depth analysis of the protein coding regions revealed the dominance of non-synonymous variants that resulted in amino acid substitutions (mean = 11) over synonymous variants (mean = 5). These results suggest that SARS-CoV-2 exists as a complex and dynamic distribution of variants within infected patients, rather than a single genomic sequence, in particular, among patients with severe symptoms. Within-host diversity might play a role in the development of severe disease outcomes in COVID-19 patients	
	Based on available evidence, reinfections seem rare (…) It is unclear if this is because of post-infection immunity or because (…) whole genome sequencing is not performed frequently on paired positive samples and correlated to clinical presentation. This study reports four WGS confirmed reinfections (…) Findings demonstrate that HCWs can get reinfected with SARS-CoV-2 with increased clinical severity in the second episode.	**21 septembre** **Shastri et al. (India)** Whole Genome Sequencing Confirmed SARS-CoV-2 Reinfections Among Healthcare Workers in India with Increased Severity in the Second Episode https://papers.ssrn.com/sol3/papers.cfm?abstract_id=3688220

28 septembre - 2 octobre

Article de presse	Extrait pertinent	Source scientifique
1 octobre A fast-spreading viral variety shows higher infectiousness https://www.nature.com/articles/d41586-020-00502-w	Both teams found that, compared with forms of the virus that lack the mutation, D614G variants replicated more efficiently in cells from human airway tissues. Baric's team also found that D614G variants spread faster	**28 septembre** **Hou et al. (USA)** SARS-CoV-2 D614G Variant Exhibits Enhanced Replication *ex vivo* and Earlier Transmission *in vivo*

	between hamsters, which are used to study SARS-CoV-2 transmission. Neither finding has been peer reviewed yet.	https://www.biorxiv.org/content/10.1101/2020.09.28.317685v1 **1 septembre 2020** **Plante et al. (USA)** Spike mutation D614G alters SARS-CoV-2 fitness and neutralization susceptibility https://www.biorxiv.org/content/10.1101/2020.09.01.278689v1
1 octobre Large scale COVID-19 genome sequencing in Norfolk helps manage outbreaks https://medicalxpress.com/news/2020-10-large-scale-covid-genome-sequencing.html	Over 1,500 COVID-19 genomes representing 42% of positive cases during the first wave (…) positive coronavirus cases came from the region's hospitals, community care organizations (food processing facility). • Stable evolutionary rate of 2 SNPs per month. • D614G mutation is the dominant genotype and associated with increased transmission. • No evidence of reinfection in 42 cases • WGS identified a sublineage associated with 6 care facilities (not detected in community testing) • WGS ruled out nosocomial outbreaks (HCWs to patients) • Rapid WGS confirmed the relatedness of cases (not found in the general community) from an outbreak at a food processing facility	**28 septembre** **The COVID-19 Genomics UK (COG-UK) consortium** Large scale sequencing of SARS-CoV-2 genomes from one region allows detailed epidemiology and enables local outbreak management https://www.medrxiv.org/content/10.1101/2020.09.28.20201475v1?rss=1%22
30 septembre COVID-19 update: World-leading research paper released into air travel transmission https://ww2.health.wa.gov.au/Media-releases/2020/COVID19-	(…) among the first studies worldwide to use whole genome sequencing to support epidemiological findings in a flight transmission investigation (March 21). (…) leading to the infection of at least eight	**29 septembre** **Speale et al. (Australia)** Flight-Associated Transmission of Severe Acute Respiratory Syndrome Coronavirus 2 Corroborated by Whole-Genome Sequencing

update-World-leading-research-paper-released-into-air-travel-transmission	other passengers (…) The circumstances of this outbreak were relatively unique (18 passengers were classified as primary cases, including 11 infectious during the flight) and the overall risk of acquiring COVID-19 related to air travel is likely to be low.	https://wwwnc.cdc.gov/eid/article/26/12/20-3910_article
	• 3940 SARS-CoV-2 viral genomes from Washington State • evidence of higher viral loads in patients infected with the 614G variant • do not find any evidence that the 614G variant impacts clinical severity or patient outcomes. • the behavior of individuals has been more important in shaping the course of the pandemic than changes in the virus (D614G).	**30 septembe** **Mueller et al. (USA)** Viral genomes reveal patterns of the SARS-CoV-2 outbreak in Washington State https://www.medrxiv.org/content/10.1101/2020.09.30.20204230v1?rss=1%22
28 septembre Tests reveal silent reinfections in hospital workers https://www.nature.com/articles/d41586-020-00502-w	Two staff members at a hospital in India who tested positive for the new coronavirus became reinfected several months later — and had no symptoms in either instance. After testing negative, they returned to work. Both tested positive again roughly three-and-a-half months after the first positive test. Neither had symptoms, but both had higher levels of virus than in May. Genomic analysis (…) showed that the SARS-CoV-2 that infected the workers the second time was genetically different from the first virus that infected them (…)	**23 septembre** **Gupta et al. (India)** Asymptomatic reinfection in two healthcare workers from India with genetically distinct SARS-CoV-2 https://academic.oup.com/cid/advance-article/doi/10.1093/cid/ciaa1451/5910388
25 septembre	Près de 15 % des formes graves de la COVID-19 s'expliqueraient par des	**24 septembre** **Zhang et al. (France-USA)**

COVID-19 : 15 % des formes graves dues à des anomalies génétiques et immunitaires https://ici.radio-canada.ca/nouvelle/1736560/covid-19-formes-graves-anomalies-genetiques-immunitaires	anomalies génétiques et immunitaires (…) chez certains patients des anomalies génétiques (mutations de 13 gènes) qui diminuent la production des IFN de type I (3-4 % des formes graves) (…) chez d'autres (…) la présence à des taux très élevés dans le sang d'anticorps (…) neutralisent l'action antivirale des IFN de type 1 (chez au moins 10 % des formes graves de la COVID) au lieu de s'attaquer au virus.	Inborn errors of type I IFN immunity in patients with life-threatening COVID-19 **https://science.sciencemag.org/content/early/2020/09/25/science.abd4570** **24 septembre** **Bastard et al. (France-USA)** Auto-antibodies against type I IFNs in patients with life-threatening COVID-19 **https://science.sciencemag.org/content/early/2020/09/23/science.abd4585**

21 - 25 septembre

Article de presse	Extrait pertinent	Source scientifique
23 septembre Houston methodist (hospital) covid-19 study shows rapid spread and potential for mutant viruses https://www.houstonmethodist.org/newsroom/houston-methodist-covid-19-study-shows-rapid-spread-and-potential-for-mutant-viruses/	Houston's second wave (May 12 through July 7) hit significantly younger patients who had fewer underlying conditions and were more likely to be Hispanic/Latino living in lower income neighborhoods. In addition, virtually all (99.9% vs 82% first wave) COVID-19 strains studied during the second wave displayed a Gly614 amino acid replacement in spike protein (…). While this mutation has been linked with increased transmission and infectivity, as well as a higher virus load in the nasopharynx, which connects the nasal cavity with the throat, the mutation did not increase disease severity, researchers said.	**23 septembre** **Long et al. (USA)** Molecular Architecture of Early Dissemination and Massive Second Wave of the SARS-CoV-2 Virus in a Major Metropolitan Area https://www.medrxiv.org/content/10.1101/2020.09.22.20199125v1 We examined the association between virus clades and disease severity based on overall mortality, highest level of required care (intensive care unit, inpatient or outpatient), need for mechanical ventilation, and length of stay. There was no simple relationship between virus clades and disease severity using these four indicators.
23 septembre 247 voyageurs à l'origine de l'épidémie au Québec https://www.ledevoir.com/societe/sante/586477/la-covid-comme-souvenir-de-voyage	Ce sont 247 personnes ayant voyagé en Europe, aux États-Unis, dans les Caraïbes et en Amérique latine durant la semaine de relâche scolaire qui sont à l'origine de	**18 septembre** **Murall et al. (Canada)** Genomic epidemiology of early introductions of SARS-CoV-2 into the Canadian province of Québec

	l'épidémie de COVID-19 qui a déferlé sur le Québec et qui a engendré plus de 66 000 cas à ce jour	https://virological.org/t/genomic-epidemiology-of-early-introductions-of-sars-cov-2-into-the-canadian-province-of-quebec/553
22 septembre Coronavirus mutations: what we've learned so far https://theconversation.com/coronavirus-mutations-what-weve-learned-so-far-145864	Sars-CoV-2 mutates fairly slowly for a virus, with any lineage acquiring a couple of changes every month; two to six-fold lower than the number of mutations acquired by influenza viruses over the same period. The challenge with D614G, as with other mutations, is disentangling whether they have risen in frequency because they happened to be present in viruses responsible for seeding early successful outbreaks, or whether they truly confer an advantage to their carriers.	**19 août** **Dorp et al. (UK)** No evidence for increased transmissibility from recurrent mutations in SARS-CoV-2 https://www.biorxiv.org/content/10.1101/2020.05.21.108506v5 « we conversely find that D614G does not associate with significantly increased viral transmission »
21 septembre Warning About Growing Prevalence Of New SARS-CoV-2 mutant strain V483A that is antibody resistant and even more infectious https://www.thailandmedical.news/news/v483g-mutation-warning-about-growing-prevalence-of-new-sars-cov-2-mutant-strain-v483g-that-is-antibody-resistant-and-even-more-infectious	Evidences coming from different researchers worldwide show that it is the next emerging mutation after D614G that can severely enhance the infection rate. V483A is not directly related with the virus-host cell interaction, but it has the ability to enhance the binding stability and binding capacity of the protein-protein complex. It is also assumed that this mutation can be one of the key factors for the higher death rate in the USA.	**17 septembre** **Ashwaq et al. (Saudi Arabia)** V483a – an Emerging Mutation Hotspot of Sars-Cov-2 https://www.preprints.org/manuscript/202009.0395/v1

14 - 18 septembre

Article de presse	Extrait pertinent	Source scientifique
18 septembre Oui, le SARS-CoV-2 mute (et c'est normal) https://www.ledevoir.com/societe/sante/586230/oui-le-	Le SARS-CoV-2 mute deux fois moins vite que la grippe et quatre fois moins vite que le VIH.	Références multiples et connues (ci-dessous)

sars-cov-2-mute-et-c-est-normal	« Le problème » est de savoir si ces « mutations changent la virulence ou pas ? Pour l'heure, « on n'a aucune donnée » en ce sens. La conclusion la plus stricte est donc que si cette souche (D614G) est sans doute plus « infectieuse », elle n'est pas forcément plus « transmissible » entre humains. Quant à l'hypothèse, formulée notamment en août par un scientifique de Singapour, que le virus deviendrait moins virulent, elle n'a pas été étayée scientifiquement. « Donc pour le moment, il ne semble pas que ces mutations, bien réelles, nous amènent à dire qu'il faudra faire comme pour la grippe un vaccin différent chaque année »	
15 septembre A groundbreaking guide to making 'cocktails' to treat COVID-19 https://www.nature.com/articles/d41586-020-00502-w	James Crowe (…) and colleagues created the most detailed map so far of the spike-protein mutations that could prevent binding by ten human antibodies. The team then used that information to design three antibody cocktails, each consisting of two antibodies.	**10 septembre** **Greaney et al. (USA)** Complete mapping of mutations to the SARS-CoV-2 spike receptor-binding domain that escape antibody recognition https://www.biorxiv.org/content/10.1101/2020.09.10.292078v1
14 septembre Early SARS-CoV-2 Transmission Reconstructed Using Genomics https://www.genengnews.com/news/early-sars-cov-2-transmission-reconstructed-using-genomics/	By analyzing the genomic sequences of SARS-CoV-2 samples from infected patients in Washington State, they suggest that most early SARS-CoV-2 infections derive from a single introduction in late January or early February, sparking rapid community transmission of the virus that went undetected for several weeks before this community spread became evident.	**10 septembre** **Bedford et al. (USA)** Cryptic transmission of SARS-CoV-2 in Washington state https://science.sciencemag.org/content/early/2020/09/09/science.abc0523.full

14 septembre Tweeter - GISAID Initiative https://twitter.com/GISAID/status/1305394976147140609	In a silver lining to this historic public health crisis, researchers from 117 nations have shared via GISAID #coronavirus genomes and associated data from 100,000 cases of #COVID-19.	N/A

7 - 11 septembre

Article de presse	Extrait pertinent	Source scientifique
10 septembre Surprise! A host of tantalizing new SARS-CoV-2 proteins is unveiled https://www.nature.com/articles/d41586-020-00502-w	Until now, SARS-CoV-2's RNA genome was known to hold the instructions for making 29 proteins…This scan turned up 23 previously unknown proteins, including some that are entirely new and others that are shortened or extended versions of known proteins.	**9 septembre** **Finkel et al. (Israel)** The coding capacity of SARS-CoV-2 https://www.nature.com/articles/s41586-020-2739-1
10 septembre How coronavirus took hold in North America and in Europe https://www.sciencedaily.com/releases/2020/09/200910150245.htm	Combining virus genomics with epidemiologic simulations and travel records, …, the results suggest an extended period of missed opportunity when intensive testing and contact tracing might have prevented SARS-CoV-2 from becoming established in North America and Europe.	**10 septembre** **Worobey et al. (USA)** The emergence of SARS-CoV-2 in Europe and North America https://science.sciencemag.org/content/early/2020/09/09/science.abc8169
9 septembre New tool outsmarts COVID-19 virus to help vaccine development https://www.eurekalert.org/pub_releases/2020-09/uom-nto090920.php	To develop COVID-3D, Professor Ascher's team analysed the genome sequencing data of over 120,000 SARS-CoV-2 samples from infected people globally, …, to identify mutations within each of the virus' proteins. They tested and analysed the mutations' effects on their protein structure using computer simulations.	**9 septembre** **Portelli et al. (Austalia)** Exploring the structural distribution of genetic variation in SARS-CoV-2 with the COVID-3D online resource https://www.nature.com/articles/s41588-020-0693-3
8 septembre The coronavirus is mutating — does it matter? https://www.nature.com/articles/d41586-020-02544-6	Note : Un article qui relativise l'impact des mutations du virus sur la pandémie, notamment le variant D614G.	Références multiples et connues (ci-dessous)

31 août - 4 septembre

Article de presse	Extrait pertinent	Source scientifique
4 septembre D614G spike mutation increases infectivity of SARS-CoV-2 and neutralization susceptibility https://www.news-medical.net/news/20200904/D614G-spike-mutation-increases-infectivity-of-SARS-CoV-2-and-neutralization-susceptibility.aspx	Spike substitution D614G enhances viral replication in the upper respiratory tract (but not lung) and increases neutralization susceptibility in infected hamsters	**1 septembre 2020** **Plante et al. (USA)** Spike mutation D614G alters SARS-CoV-2 fitness and neutralization susceptibility https://www.biorxiv.org/content/10.1101/2020.09.01.278689v1
1 septembre Minimal SARS-CoV-2 diversity suggests a global vaccine is feasible https://www.eurekalert.org/pub_releases/2020-09/wrai-msd090120.php	Genetic analysis of (18,514 SARS-CoV-2) sequences from more than 27,000 individuals infected with the coronavirus that causes COVID-19 reveals that the virus has mutated minimally since December 2019, suggesting one vaccine would be sufficient to combat global infections.	**31 août** **Dearlove et al. (USA)** A SARS-CoV-2 vaccine candidate would likely match all currently circulating variants https://www.pnas.org/content/early/2020/08/28/2008281117 En lien avec ce complément **21 septembre** Low genetic diversity may be an Achilles heel of SARS-CoV-2 https://www.pnas.org/content/early/2020/09/18/2017726117.long
30 août Mutated coronavirus strain found in Indonesia (Jakarta) as cases jump https://www.reuters.com/article/us-health-coronavirus-indonesia-cases-idUSKBN25Q08V	The “infectious but milder” D614G mutation of the virus has been found in (40%) genome sequencing data from samples collected by the institute, (…), adding that more study is required to determine whether that was behind the recent rise in cases.	**Aucun rapport/étude cité. Article relié** **31 juillet** **Volz et al. (UK)** Evaluating the effects of SARS-CoV-2 Spike mutation D614G on transmissibility and pathogenicity https://www.medrxiv.org/content/10.1101/2020.07.31.20166082v1 **2 juillet** **Korber et al. (USA)**

		Tracking changes in SARS-CoV-2 Spike: evidence that D614G increases infectivity of the COVID-19 virus https://www.cell.com/cell/fulltext/S0092-8674(20)30820-5
28 août Lab confirms first case of coronavirus reinfection in the US https://www.livescience.com/coronavirus-reinfection-case-confirmed-us.html	A young adult in Nevada was confirmed to have been infected with the coronavirus twice, marking the first confirmed case of reinfection in the U.S., and the fourth in the world. But according to the new case study, the 25-year-old Nevada patient developed more severe symptoms the second time he was infected.	**Peprint non disponible** **27 août** **Nouvelle U. of Nevada** Nevada State Public Health Lab-led team studying COVID-19 reinfection https://www.unr.edu/nevada-today/news/2020/covid-reinfection-study Forty-eight (48) days after testing positive for SARS-CoV-2 in April 2020 and after testing negative consecutively twice, a Washoe County, Nevada patient tested positive again, in June. The patient had tested negative on two separate occasions in the interim. The genomes of the patient's virus samples were sequenced in April and June, displaying significant genetic discordance between the two cases, implying the patient was infected twice.
25 août Two people in Europe reinfected with coronavirus months after 1st illness https://globalnews.ca/news/7296828/coronavirus-reinfected-europe-cases/	The Belgian case was a (50 years old) woman who had contracted COVID-19 for the first time in March and then again in June (…) the Belgian woman's in which symptoms were relatively mild, the body may not have created enough antibodies to prevent a re-infection, although they might have helped limit the sickness. The National Institute for Public Health in the Netherlands said it had also observed a Dutch case of re-infection (…) the patient was an older person with a weakened immune system.	**Aucun rapport/étude cité.** Pas encore de confirmation si variants génétiques entre deux épisodes infectieux

24 - 28 août

Article de presse	Extrait pertinent	Source scientifique
26 août Tracking SARS-CoV-2 evolution: notable mutations and potential targets https://www.drugtargetreview.com/news/69618/tracking-sars-cov-2-evolution-notable-mutations-and-potential-targets/	Researchers report that while the spike protein and RNA polymerase proteins have stabilised, other regions of the SARS-CoV-2 genome are becoming increasingly variable (nucleocapside protein and viron protein 3a = packaging and virus release, respectively).	**31 juillet** **Tomaszewski et al. (USA)** New Pathways of Mutational Change in SARS-CoV-2 Proteomes Involve Regions of Intrinsic Disorder Important for Virus Replication and Release https://www.biorxiv.org/content/10.1101/2020.07.31.231472v1.full
25 août Genetic data show how a single superspreading event sent coronavirus across Massachusetts — and the nation https://www.washingtonpost.com/climate-environment/2020/08/25/boston-coronavirus-superspreading-event/	A study of nearly 800 coronavirus genomes has found that viruses carrying the conference's characteristic mutation infected hundreds of people in the Boston area, as well as victims from Alaska to Senegal to Luxembourg. As of mid-July, the variant had been found in about one-third of the cases sequenced in Massachusetts and 3 percent of all genomes studied thus far in the United States.	**23 août** **Lemieux et al. (USA)** Phylogenetic analysis of SARS-CoV-2 in the Boston area highlights the role of recurrent importation and superspreading events https://www.medrxiv.org/content/10.1101/2020.08.23.20178236v1
24 août Hong Kong team reports first documented coronavirus reinfection in patient https://www.cbc.ca/news/health/covid19-re-infection-hong-kong-1.5697725	A Hong Kong man who recovered from the COVID-19 illness caused by the coronavirus was infected again four-and-a-half months later in the first documented instance of human reinfection	**25 août** **Kai-Wang To et al. (China)** COVID-19 re-infection by a phylogenetically distinct SARS-coronavirus-2 strain confirmed by whole genome sequencing https://academic.oup.com/cid/advance-article/doi/10.1093/cid/ciaa1275/5897019
21 août Scientists find COVID-19 coronavirus variant linked to milder infections **https://www.cbc.ca/news/health/milder-coronavirus-1.5694855**	The study showed that COVID-19 patients infected with a new variant of SARS-CoV-2 (382-nucleotide deletion in the ORF8 region) had better clinical outcomes, including a lower proportion developing low blood oxygen or requiring intensive care. The study also showed the variant, which has a large	**18 août** **Young et al. (Singapore)** Effects of a major deletion in the SARS-CoV-2 genome on the severity of infection and the inflammatory response: an observational cohort study https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(20)31757-8/fulltext

	deletion in a part of its genome, elicited a more robust immune response.	

3 - 7 août

Article de presse	Extrait pertinent	Source scientifique
5 août Study reveals changes in transmissibility of SARS-CoV-2 due to D614G spike mutation https://www.news-medical.net/news/20200805/Study-reveals-changes-in-transmissibility-of-SARS-CoV-2-due-to-D614G-spike-mutation.aspx	A recent research endeavor from the UK, currently available on the medRxiv* preprint server, indicates that spike 614G variant of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) increases in frequency relative to 614D variant in a selective advantage manner – but without higher coronavirus disease (COVID-19) mortality rates.	**31 juillet** **Volz et al. (UK)** Evaluating the effects of SARS-CoV-2 Spike mutation D614G on transmissibility and pathogenicity https://www.medrxiv.org/content/10.1101/2020.07.31.20166082v1
4 août Novel mutation identified in SARS-CoV-2 spike protein from Sweden https://www.news-medical.net/news/20200804/Novel-mutation-identified-in-SARS-CoV-2-spike-protein-from-Sweden.aspx	The mutation is located at the surface of the S1 subunit of the SARS-CoV-2 spike protein, the main surface structure the virus uses to gain entry to host cells. The S1 subunit contains the binding domain for the host cell membrane receptor angiotensin-converting enzyme 2 (ACE2).	**3 août** **Soratto et al. (Sweden)** SARS-CoV-2 genome sequences from late April in Stockholm, Sweden reveal a novel mutation in the spike protein https://www.biorxiv.org/content/10.1101/2020.08.03.233866v1

27-31 juillet

Article de presse	Extrait pertinent	Source scientifique
31 juillet As SARS-CoV-2 Virus Evolves, Genomic Data Should Be Collected Alongside Patient and Public Health Data https://www.nationalacademies.org/news/2020/07/as-sars-cov-2-virus-evolves-genomic-data-should-be-collected-alongside-patient-and-public-health-data-says-new-report	To better understand the evolution, transmission patterns, and disease progression of SARS-CoV-2 — the virus that causes COVID-19 — genome sequence data should be integrated with patient clinical data and epidemiological data, says a new report from the National Academies of Sciences, Engineering, and Medicine.	**31 juillet** **National Academies of Sciences, Engineering, and Medicine (USA)** Genomic Epidemiology Data Infrastructure Needs for SARS-CoV-2 https://www.nap.edu/catalog/25879/genomic-epidemiology-data-infrastructure-needs-for-sars-cov-2-modernizing

31 juillet The origin of SARS-CoV-2 traced https://www.weforum.org/agenda/2020/07/covid-19-coronavirus-science-stories-breakthroughs/	An international team of researchers from China, Europe and the U.S. have reconstructed the evolutionary history of SARS-CoV-2, the virus that causes COVID-19. Their findings, published this week in Nature Microbiology, suggest that the virus has been in circulation in bats for decades, having diverged from other bat viruses as long ago as 1948.	**28 juillet** **Boni et al. (USA)** Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic https://www.nature.com/articles/s41564-020-0771-4
29 juillet Antibody-resistant Coronavirus strain could throw a spanner in global efforts to beat pandemic https://www.financialexpress.com/opinion/covid-19-mutation-antibody-resistant-coronavirus-strain-could-throw-a-spanner-in-global-efforts-to-beat-pandemic/2038104/	Viruses engineered to produce the SARS-CoV-2's spike protein developed mutations that changed the spike protein in a way that allows it to evade neutralising antibodies. Similar mutations have been reported in patient samples from around the world, though these make for a minuscule fraction of the genomic variants being reported.	**21 juillet** **Weisblum et al. (USA)** Escape from neutralizing antibodies by SARS-CoV-2 spike protein variants https://www.biorxiv.org/content/10.1101/2020.07.21.214759v1
28 juillet Mutation that made coronavirus more infectious may make it vulnerable to vaccines: study https://globalnews.ca/news/7225793/coronavirus-mutation-vaccine-research/	"The gain in infectivity provided by D614G came at the cost of making the virus more vulnerable to neutralizing antibodies," wrote the authors.	**22 juillet** **Weissman et al. (USA)** D614G Spike Mutation Increases SARS CoV-2 Susceptibility to Neutralization. https://www.medrxiv.org/content/10.1101/2020.07.22.20159905v1
28 juillet Un seul passager serait à l'origine de l'épidémie sur le Diamond Princess https://www.lapresse.ca/international/2020-07-28/un-seul-passager-serait-a-l-origine-de-l-epidemie-sur-le-diamond-princess.php	La nouvelle analyse génétique montre que tous les virus partageaient une même mutation, ce qui suggère que « la dissémination de SARS-CoV-2 à bord du Diamond Princess a comme origine un seul évènement d'introduction, avant le début de la quarantaine », concluent les scientifiques japonais.	**2 Juillet** **Sekizuka et al. (Japan)** Haplotype networks of SARS-CoV-2 infections in the Diamond Princess cruise ship outbreak https://www.pnas.org/content/early/2020/07/27/2006824117
27 juillet Six souches de coronavirus découvertes: la contribution de l'Université de Bologne https://emergency-live.com/fr/la-sant%C3%A9-	48,635 SRQS-CoV-2 génomes de coronavirus ont été isolés dans des laboratoires du monde entier. Les chercheurs ont retracé la répartition géographique et la	**22 juillet** Mercatelli **et al. (Italy)** Geographic and Genomic Distribution of SARS-CoV-2 Mutations

et-la-s%C3%A9curit%C3%A9/six-souches-de-coronavirus-ont-d%C3%A9couvert-la-contribution-de-l%27universit%C3%A9-de-Bologne/	fréquence des différentes mutations du virus lors de sa propagation.	https://www.frontiersin.org/articles/10.3389/fmicb.2020.01800/full
27 juillet COVID-19 : Une vulnérabilité génétique aussi https://www.santelog.com/actualites/covid-19-une-vulnerabilite-genetique-aussi	Plusieurs études ont documenté les principaux facteurs de risque de complications et de décès de COVID-19, dont l'âge avancé, le sexe masculin et les comorbidités préexistantes dont principalement l'obésité, le diabète et l'hypertension artérielle. Le tabagisme est également documenté comme un facteur de forme plus sévère de la maladie. Ces scientifiques de l'Université de Radboud (Pays-Bas) sont les premiers à suggérer et préciser des facteurs de risque génétiques. Leurs analyses, présentées dans le JAMA Open Network identifient le rôle clé d'un gène particulier, TLR7, qui en cas de mutation, laisse libre cours aux complications.	**24 juillet** **Van der Made et al. (Netherlands)** Présence of Genetic Variants Among Young Men With Severe COVID-19 https://jamanetwork.com/journals/jama/fullarticle/2768926 **Voir aussi** **6 mai** **The OpenSAFELY Collaborative (UK)** Factors associated with COVID-19-related hospital death in the linked electronic health records of 17 million adult NHS patients https://opensafely.org/outputs/2020/05/covid-risk-factors/

Scan rapide littérature pour variant D614G (14 juillet)

14 juillet The pandemic virus is slowly mutating. But is it getting more dangerous? https://www.sciencemag.org/news/2020/07/pandemic-virus-slowly-mutating-it-getting-more-dangerous	The United Kingdom's COVID-19 Genomics Consortium has sequenced 30,000 SARS-CoV-2 genomes, allowing scientists to compare how fast 43 lineages carrying the G614 mutation and 20 with D614 spread.	**25 juin** **COVID-19 Genomics UK (COG-UK) Consortium** https://www.cogconsortium.uk/wp-content/uploads/2020/07/25th-June-2020-Report-COVID-19-Genomics-UK-COG-UK-Consortium.pdf
2 juillet Le coronavirus actuel est plus infectieux que la version originale, selon une étude https://www.journaldemontreal.com/2020/07/02/le-coronavirus-actuel-est-plus-	La variante du SARS-CoV-2 qui domine aujourd'hui dans le monde infecte plus facilement les cellules que celle qui est apparue à l'origine en Chine, ce qui la rend probablement plus contagieuse entre humains,	**2 juillet** **Korber et al. (USA)** Tracking changes in SARS-CoV-2 Spike: evidence that D614G increases infectivity of the COVID-19 virus https://www.cell.com/cell/fulltext/S0092-8674(20)30820-5

infectieux-que-la-version-originale-selon-une-etude-1	bien que cela reste à confirmer	
5 mai Une nouvelle souche du virus plus contagieuse: des chercheurs sonnent l'alerte https://www.journaldemontreal.com/2020/05/05/une-nouvelle-souche-du-virus-plus-contagieuse-des-chercheurs-sonnent-lalerte	Une nouvelle souche du coronavirus serait devenue dominante dans le monde, apparemment plus contagieuse que les versions qui se sont propagées aux premiers jours de la pandémie de COVID-19, selon une nouvelle étude menée par des scientifiques du Los Alamos National Laboratory.	**29 Avril** **Korber et al. (USA)** Spike mutation pipeline reveals the emergence of a more transmissible form of SARS-CoV-2 https://www.biorxiv.org/content/10.1101/2020.04.29.069054v1