

Pivoting from Cancer to COVID-19 in a global pandemic

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The COVID-19 crisis in Nice, France, and the impact in a pathology lab

SARS-CoV-2 diagnosis set-up in a pathology lab: experience of the LPCE

Current development using the NGS approach for SARS-CoV-2 assessment

Perspective



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COVID-19 Dashboard by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins



Walk of the SARS CoV 2 on the « promenade des Anglais »

Higher incidence of the virus in France (March 2021)













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Evolution of COVID-19 cases in Nice, France

October 1, 2020 to April 19, 2021







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ORIGINAL RESEARCH

Clinical and molecular practice of European thoracic pathology laboratories during the COVID-19 pandemic. The past and the near future

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Pathology laboratories participating to the survey



Molecular Biology activity from March to May 2019 and from March to May 2020



p.value Log[OR] (SD)

Activity of thoracic cancer surgeries in the South Region, France

Between 2019 and 2020







ORIGINAL RESEARCH

Clinical and molecular practice of European thoracic pathology laboratories during the COVID-19 pandemic. The past and the near future





Specimen to report in a single day with only two user touchpoints

Ion Torrent Genexus System

- Lysate from FFPE
 tissue
- Plasma
- Whole blood
- Peripheral blood
 lymphocyte (PBL)
- Lysate from freshfrozen tissue
- Lysate form bone
 marrow



2 hour turnaround time 12 FFPE (DNA and RNA) 6 Plasma

- Genexus S	Software	
Library variant	Library preparation to variant interpretation	
lon Torrent [™]	Ion Torrent [™] Gen Integrated Sequencer (No	nexus ™ vember 2019)
GX5 th Chip: 12–15M reads/lane		

14 hours for a single-lane run (approx. 24 to 30 hours for full chip) Up to 32 Samples per run



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Setting up a collection of SARS-CoV-2 positive NSP samples and storage in an accredited biobank (BB-0033-00025)





Hofman et al, Ann Transl Med 2021, in press

Setting up a collection of SARS-CoV-2 positive oral samples and storage in an accredited biobank (BB-0033-00025)



The sponge is put into the mouth

After screwing the top cap back on, the tube is shaken to bring the sponge into the middle of the tube



After unscrewing th cap, the sponge is by squeezing the bo tube to drop 3 drop. viral transport micro



Second Period Ν p < 0.001 p < 0.00150 -40 30 5 20 10-05 Synlab 05 laylla

All-in-on saliva sampling technique with a sponge. Usefulness of a double-capped plastic

Viral load of NasoPharyngeal and oral samples assessed by the Ct for the Orf1b and N genes

Manuscript submitted, 2021



FIG. 1. Facilities of the COVID-19 Nice Louis Pasteur Hospital Biobank. LPCE, Laboratory of Clinical and Experimental Pathology.



BIOPRESERVATION AND BIOBANKING Volume 00, Number 00, 2020 © Mary Ann Liebert, Inc. DOI: 10.1089/bio.2020.0055

Establishment of a Collection of Blood-Derived Products from COVID-19 Patients for Translational Research: Experience of the LPCE Biobank (Nice, France)

Virginie Tanga,^{1,2} Sylvie Leroy,³ Julien Fayada,¹ Marame Hamila,¹ Maryline Allegra,¹ Zeineb Messaoudi,¹ Christelle Bonnetaud,¹ Virgine Lespinet,¹ Olivier Bordone,¹ Kevin Washetine,¹ Jennifer Griffonnet,³ Charlotte Maniel,³ Lorène Philibert,³ Eric Selva,¹ Jonathan Benzaquen,³ Marius Ilie,^{1,2} Elodie Long,^{1,2} Sandra Lassalle,^{1,2} Elisabeth Lantéri,^{1,2} Charles-Hugo Marquette,^{2,3} Véronique Hofman,^{1,2} and Paul Hofman^{1,2}



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London

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NEWS BRIEFING

Covid-19: New coronavirus variant is identified in UK

England's health secretary, Matt Hancock, has told parliament that a new variant of covid-19 has been identified and may be driving infections in the south east, leading to headlines about "mutant covid." **Jacqui Wise** answers some common questions

Jacqui Wise



The 501.V2 and B.1.1.7 variants of coronavirus disease 2019 (COVID-19): A new time-bomb in the making?

Taha Bin Arif MBBS 💿

Department of Medicine, Dow Medical College, Dow University of Health Sciences, Karachi, Pakistan



Could it be that the B.1.1.7 lineage is more deadly?

Chia Siang Kow¹ and Syed Shahzad Hasan^{2,3}

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SARS COV 2 variants of concerns present in France

- B.1.17 (UK): 82% of variants in France April 21, 2021
- 20H/501Y.V2 (South of Africa) and 20J/501Y.V3 (Brazil): 4.2% of variants in France April 21, 2021
- B.1.616 (ou 20C/655Y) (Britain, France): Not detected using SARS-CoV-2 RT-PCR from NSP swabs

Covid variants spread



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April 21, 2021, % of 20H/501Y.V2 and 20J/501Y.V3 variants among SARS-CoV-2 positive tests

B.1.617 (India)

April 29, 2021

Covid-19 dans le monde : le variant indien détecté en Belgique, chez des étudiants passés par Roissy

Vingt étudiants indiens ont été testés positifs à ce mutant du SARS-CoV-2. Ils ont été placés en quarantaine dans les villes flamandes d'Alost et de Louvain, où ils étaient arrivés mi-avril.

Le Monde

Key Questions around the new Coronavirus Strains

- How can we detect new strains?
- What is the origin of the new strain and how prevalent is it?
- Will current molecular or antigen-based tests miss detecting this strain?
- Does this strain spread more quickly?
- Does this strain lead to higher disease severity?
- What is the vaccine efficacy against the new strain?

There are still currently many unknowns. Ongoing research is needed to better understand virus strain evolution and spread.





Key questions on the new Coronavirus strains







Projects started in 2021 at the LPCE (Nice, France)



Ion AmpliSeq SARS-CoV-2 Research Panel

One assay surveying complete SARS-CoV-2 genome for epidemiological investigation



>99% coverage of SARS-CoV-2 genome (~30kb)

- World leading amplification technology: AmpliSeq[™]
- Amplicon length range: 125-275 bp
- 237 amplicons specific to SARS-CoV-2 + 5 human expression controls
- All potential serotypes covered
- 2250 manual-preped, 600 Chef-automated libraries or 240 Genexusautomated libraries

	*	Pool	No. Total Amplicons
LUB		1	
Mille !	-27278 (N=1-	2	247 (242 unique)*

Data analyses for SARS COV 2 variants



Identified variants in a retrospective analysis

Ongoing study conducted on the Ion Torrent Genexus system *total, 102 samples*

<u>Variants</u>

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B.1.160 (European)	64
B.1.1.77 (UK)	17
B.1.1.7 (UK)	8
B.1.241 (European)	3
B.23 (UK): 5 (4%)	2
B.1.1.2.41 (European)	1
B.1.1.2.21 (European)	1
B.1.596 (USA)	1
B.1.160.8 (Denmark)	1
A.19 (Burkina Faso)	1
B.1.411 (Sri Lanka)	1





Variant classification



• VOC (variants of concern)

- B.1.1.7(UK)
- B.1.351(South Africa)
- B.1.1.28.1 (Brazil)
- B.1.617 (India)
- VOI (variants under investigation)
- VUM (variant under monitoring)

Comparative analyses obtained from matched nasopharyngeal swabs (NSP) and saliva samples

Samples	NSP	Saliva
1	B.1.160	B.1.160
2	B.1.1.7	B.1.1.7
3	B.1.160	B.1.160
4	B.1.1.2.41	B.1.1.2.41
5	A.19	A.19
6	B.1.411	B.1.411
7	B.1.596	B.1.596
8	B.1.177	B.1.177
9	B.1.160	B.1.160
10	B.1.160	failed
11	B.1.160	B.1.160
12	B.1.1.7	B.1.1.7
13	B.1.160	B.1.160
14	B.1.160	B.1.160





GENEXUS: More advantages, less constraints during the COVID-19 crisis

- Less contact between the health care workers during the manipulation (better biosafety)
- Easy to use
- Easy to analyse data
- Short turnaround time (24h)
- Workflow automation
- Flexible (integration of different workflows for genomic assessment of solid tumors too)
- High number of analyses (until 112 samples per week)
- High **sensitivity** of detection (able to detect variants even with a low viral load/high Ct)
- Panel design improvement Ion AmpliSeq[™] SARS-CoV-2 Insight Research Panel just launched







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➤ @ ↓ ① Genomic evidence for reinfection with SARS-CoV-2: a case study

Richard L Tillett, Joel R Sevinsky, Paul D Hartley, Heather Kerwin, Natalie Crawford, Andrew Gorzalski, Chris Laverdure, Subhash C Verma, Cyprian C Rossetto, David Jackson, Megan J Farrell, Stephanie Van Hooser, Mark Pandori



Figure 1: Timeline of symptom onset, molecular diagnosis, and sequencing of specimens TMA=transcription-mediated amplification. *Sequenced specimens.





ORF1a and ORF1b encode replicase proteins. The other ORFs encode assembly proteins. ORF=open reading frame. S=spike. E=envelope. M=membrane. N=nucleocapsid. *Identifies variant 14 407 in specimen A and variants 14 407 and 14 408 in specimen B.



The world this week

Emerging variants to be permanently detected

News in focus

Nature | Vol 589 | 14 January 2021 | 177



Researchers race to determine why lineages identified in Britain and South Africa spread so quickly, and whether vaccines will be less effective against them.



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Acknowledgments









