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Microbiology Spectrum

Detection of SARS-COV-2 in saliva and naso-pharyngeal swab according to viral variants

Maud Salmona, Marie-Laure Chaix, Linda Feghoul, Nadia Mahjoub, Sarah MAYLIN, Nathalie Schnepf, Hervé Jacquier, Eve-Marie Walle, Marion Helary, Guillaume Mellon, Nathalie Osinski, Widad Zebiche, Yacine Achili, Rishma Amarsy, Veronique Mahé, Jérôme Le Goff, and Constance Delaugerre

Corresponding Author(s): Maud Salmona, APHP Hospital Saint Louis

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Reviewer(s): Disclosure of reviewer identity is with reference to reviewer comments included in decision letter(s). The following individuals involved in review of your submission have agreed to reveal their identity: Diana Hardie (Reviewer #1)

Transaction Report:

(Note: With the exception of the correction of typographical or spelling errors that could be a source of ambiguity, letters and reports are not edited. The original formatting of letters and referee reports may not be reflected in this compilation.)

DOI: <https://doi.org/10.1128/spectrum.02133-22>

August 12, 2022

Dr. Maud Salmona
APHP Hospital Saint Louis
1 av Claude Vellefaux
Paris 75010
France

Re: Spectrum02133-22 (Detection of SARS-COV-2 in saliva and naso-pharyngeal swab according to viral variants)

Dear Dr. Maud Salmona:

Thank you for submitting your manuscript to Microbiology Spectrum. Please note that in order to speed up the review process and in an attempt to avoid further delays, I am relying on the review of single reviewer and my own assessment. When submitting the revised version of your paper, please provide (1) point-by-point responses to the issues raised by the reviewers as file type "Response to Reviewers," not in your cover letter, and (2) a PDF file that indicates the changes from the original submission (by highlighting or underlining the changes) as file type "Marked Up Manuscript - For Review Only". Please use this link to submit your revised manuscript - we strongly recommend that you submit your paper within the next 60 days or reach out to me. Detailed instructions on submitting your revised paper are below.

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Daniel Perez

Editor, Microbiology Spectrum

Journals Department
American Society for Microbiology
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Washington, DC 20036
E-mail: spectrum@asmusa.org

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3. Line 56: evade, not elute
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Staff Comments:

Preparing Revision Guidelines

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Response to Reviewers

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Thanks to the reviewer to highlight this issue. Among the 134 samples analyzed in WGS, we retrieved the following lineages: 29 wuhan, 19 Alpha (including 4 Alpha+484K), 11 Beta, 33 Delta and 42 Omicrons (21J)). These results were consistent with the screening results for all samples (the 29 Wuhan were determined to be "Other" by the PCR screening). We are sorry for the reference which was indeed not correct, we have removed it from the manuscript. We have modified the paragraph in the following way : « *Whole-genome sequencing was performed for 134 samples with RT-PCR variant-specific screening test results. Briefly, Qiaseq SARS-Cov-2 Prime Panel (Qiagen, Hilden, Germany) was used to create tiled amplicon across the SARS-Cov-2 genome. DNA libraries were prepared using Nextera XT and sequenced using Illumina Miseq with a 300 v2 cartridge (Illumina, San Diego, CA USA). Among the 134 samples sequenced with WGS, Nextclade (<https://clades.nextstrain.org/>) retrieved the following lineage: 29 Wuhan (no VOC), 19 Alpha (including 4 Alpha+484K), 11 Beta, 33 Delta and 42 Omicron VOCs. These results were consistent with RT-PCR variant-specific screening test results for all samples.* »

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We are sorry, our sentence was not clear. Indeed, it is the absence of E484K/Q and the presence of 452R which allowed to define Delta VOC. To clarify, we have modified the sentence in the following way: " The presence of L452R without E484K/Q was assigned to Delta VOC" (line 99/100)

3. Line 56: evade, not elute

4. Line 139: "...performed for 909 (71%) and 380 (29%) cases, respectively. The RT-PCR were done..."

We have made the changes requested by the reviewer.

September 19, 2022

Dr. Maud Salmona
APHP Hospital Saint Louis
1 av Claude Vellefaux
Paris 75010
France

Re: Spectrum02133-22R1 (Detection of SARS-COV-2 in saliva and naso-pharyngeal swab according to viral variants)

Dear Dr. Maud Salmona:

Thank you for submitting your manuscript to Microbiology Spectrum. Please address the minor comments of the reviewer and send back. The ms will be considered accepted after those minor changes are addressed. When submitting the revised version of your paper, please provide (1) point-by-point responses to the issues raised by the reviewers as file type "Response to Reviewers," not in your cover letter, and (2) a PDF file that indicates the changes from the original submission (by highlighting or underlining the changes) as file type "Marked Up Manuscript - For Review Only". Please use this link to submit your revised manuscript - we strongly recommend that you submit your paper within the next 60 days or reach out to me. Detailed instructions on submitting your revised paper are below.

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Washington, DC 20036
E-mail: spectrum@asmusa.org

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Spectrum review August 2022

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4. Line 139: "...performed for 909 (71%) and 380 (29%) cases, respectively. The RT-PCR were done..."

Review of the revised manuscript: 19 September 2022

I am satisfied that the points raised in the original review have been addressed. I have the following minor issues to resolve:

1. Lines 121-124: move to results. For the 42 omicron samples that underwent whole genome sequencing, what was the predominant sub genotype? i.e indicate whether these were BA.1 or 2 (or other).
2. Figure 1 (a and b): add to the colour code key that grey dot/triangle reflects un-genotyped samples.

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I have the following minor issues to resolve:

1. Lines 121-124: move to results. For the 42 omicron samples that underwent whole genome sequencing, what was the predominant sub genotype? i.e indicate whether these were BA.1 or 2 (or other).

We have moved the paragraph to the results section as requested by the reviewer.

Concerning the 42 Omicrons, 40 were BA.1 and 2 were BA.2, we have added this information in the paragraph.

2. Figure 1 (a and b): add to the colour code key that grey dot/triangle reflects un-genotyped samples

We have made the changes requested by the reviewer.

October 12, 2022

Dr. Maud Salmona
APHP Hospital Saint Louis
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Paris 75010
France

Re: Spectrum02133-22R2 (Detection of SARS-COV-2 in saliva and naso-pharyngeal swab according to viral variants)

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We add the following paragraph lines 148- 150

“Data Availability Statement:

SARS-Cov-2 whole genome sequences can be found in the GISAID database (<https://gisaid.org/>) , GISAID Virus name numbers are detailed in the supplementary material.”

We also add GISAID Virus name numbers in the Supplementary Mat.

hCov-19/France/IDF-SLS-762111069335/2021 ; hCov-19/France/IDF-SLS-762111068761/2021 ;
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October 19, 2022

Dr. Maud Salmona
APHP Hospital Saint Louis
1 av Claude Vellefaux
Paris 75010
France

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