Evaluation of Sample Pooling for SARS-CoV-2 Detection in Nasopharyngeal Swab and Saliva Samples with the Idylla SARS-CoV-2 Test

Paul Hofman,a,b,c Maryline Allegra,b Myriam Salah,a Jonathan Benzaquen,d Virginie Tanga,a,b Olivier Bordone,a,b Julien Fayada,b Elodie Long-Mira,a Sandra Lassalle,a Elisabeth Lanteri,a Virginie Lespinet-Fabre,a,b Patrick Brest,c Baharia Mograbi,c Charlotte Maniel,d Jacques Boutros,d Sylvie Leroy,d Simon Heeke,d Véronique Hofman,a,b,c Charles-Hugo Marquette,c,d Marius Iliéa,b,c

aLaboratory of Clinical and Experimental Pathology, Centre Hospitalier Universitaire de Nice, FHU OncoAge, Université Côte d’Azur, Nice, France
bHospital-Related Biobank (BB-0033-00025), Centre Hospitalier Universitaire de Nice, FHU OncoAge, Université Côte d’Azur, Nice, France
cTeam 4, Institute of Research on Cancer and Aging, CNRS INSERM, Centre Antoine-Lacassagne, Université Côte d’Azur, Nice, France
dDepartment of Pulmonary Medicine and Oncology, Centre Hospitalier Universitaire de Nice, FHU OncoAge, Université Côte d’Azur, Nice, France
eDepartment of Thoracic/Head and Neck Medical Oncology, The University of Texas MD Anderson Cancer Center, Houston, Texas, USA

ABSTRACT Due to increased demand for testing, as well as restricted supply chain resources, testing for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection continues to face many hurdles. Pooling several samples has been proposed as an alternative approach to address these issues. We investigated the feasibility of pooling nasopharyngeal swab (NPS) or saliva samples for SARS-CoV-2 testing with a commercial assay (Idylla SARS-CoV-2 test; Biocartis). We evaluated the 10-pool and 20-pool approaches for 149 subjects, with 30 positive samples and 119 negative samples. The 10-pool approach had sensitivity of 78.95% (95% confidence interval [CI], 54.43% to 93.95%) and specificity of 100% (95% CI, 71.51% to 100%), whereas the 20-pool approach had sensitivity of 55.56% (95% CI, 21.20% to 86.30%) and specificity of 100% (95% CI, 25% to 100%). No significant difference was observed between the results obtained with pooled NPS and saliva samples. Given the rapidity, full automation, and practical advantages of the Idylla SARS-CoV-2 assay, pooling of 10 samples has the potential to significantly increase testing capacity for both NPS and saliva samples, with good sensitivity.

IMPORTANCE To control outbreaks of coronavirus disease 2019 (COVID-19) and to avoid reagent shortages, testing strategies must be adapted and maintained for the foreseeable future. We analyzed the feasibility of pooling NPS and saliva samples for SARS-CoV-2 testing with the Idylla SARS-CoV-2 test, and we found that sensitivity was dependent on the pool size. The SARS-CoV-2 testing capacity with both NPS and saliva samples could be significantly expanded by pooling 10 samples; however, pooling 20 samples resulted in lower sensitivity.

KEYWORDS COVID-19, pooling, SARS-CoV-2, Idylla test

The control of the coronavirus disease 2019 (COVID-19) pandemic requires huge efforts to allow widespread screening for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in the general population and to enable testing and contact tracing. In addition, these measures must include the ability to detect known virus variants of SARS-CoV-2 promptly and in large numbers, as well as immediately identifying the emergence of novel variants that emerge throughout the pandemic (1).

Several challenges continue to hamper the testing for SARS-CoV-2 infection promptly, accurately, and in large numbers, due in part to the rapid increase in cases and the complexity of the testing procedure but also to the limited resources in the...
Therefore, limited laboratory capacity worldwide, particularly in Africa, South America, and some parts of Asia (3, 4), has hindered access to testing for SARS-CoV-2 and has delayed results. In order to overcome these issues and to increase testing throughput, pooling of multiple samples has been proposed as a strategy (5). The pooling strategy is considered a practical and effective method to analyze large quantities of samples without significantly loss of performance, especially when it comes to centralized testing models with automated systems. Several teams have recently reported successful pooling of SARS-CoV-2 samples (6–11). However, those reports were limited to geographic areas such as the United States or South Korea. In addition, in the United States an emergency use authorization was required by the Food and Drug Administration for testing pooled samples for asymptomatic screening, offering a regulatory basis for the selection of the testing methods and strategies that is lacking in other countries. Some of the methods used were laboratory-developed real-time (RT)-PCR tests, often requiring up to hundreds of samples to be grouped in batches to be tested in parallel. One of the consequences was a prolonged delay for the results to be obtained, i.e., 6 to 24 h after nasopharyngeal swab (NPS) specimen collection but possibly even longer, depending on the local conditions and the organization of sample workflows and technologies. We previously validated a fast and accurate ready-to-use RT-PCR assay using the Idylla platform (Biocartis, Mechelen, Belgium) (12), which had 100% positive and negative agreement with standard-of-care RT-PCR tests. However, data are still limited regarding the best strategy for detecting SARS-CoV-2 cases by pooling samples and assessing how they influence the analytical precision of the RT-PCR analysis (2, 8, 11, 13–20). Therefore, it is necessary to continue assessing the potential of pooling NPS and saliva samples to increase SARS-CoV-2 testing capacity in clinical laboratories, especially with commercially available assays. In this study, we aimed to investigate the feasibility of two strategies for pooling NPS and saliva samples for SARS-CoV-2 testing with the Idylla commercial assay.

RESULTS

Subjects. NPS and saliva samples were collected from 149 subjects referred (i) by their attending physician because of recent (≤2 weeks) symptoms of COVID-19 or (ii) by the contact-tracing staff of the French public health insurance, since they were considered close contacts of a laboratory-confirmed COVID-19 case.

Pools of 10 samples. There was a contingency between the variables, with a significant correlation between the SARS-CoV-2 individual results and the results obtained with the pooled samples (P < 0.0001) (Table 1). In our study, the analytical sensitivity and specificity for pools of 10 samples were equal to 78.95% (95% confidence interval [CI], 54.43% to 93.95%) and 100% (95% CI, 71.51% to 100%), respectively. The estimated accuracy was 98.11% (95% CI, 85.08% to 100%). The absolute percentage of agreement between the two groups was 86.66%. There was substantial agreement between the two groups (k = 0.733).

The median N cycle threshold (C_t) value for the individual positive samples was 37.52 (range, 23.48 to 42.00; interquartile range [IQR], 9.41 [95% CI, 34.42 to 38.58]),

| Individual assay result | No. (%) with pooled assay result of: | Total |
|--------------------------|-------------------------------------|-------|
|                          | Negative 11 (36.7) 0 (0) 11 (36.7)  |
|                          | Positive 4 (13.3) 15 (50) 19 (63.3) |
|                          | Total 15 (50) 15 (50) 30 (100)     |
whereas the median N Ct value for the pooled samples was 41.50 (range, 28.22 to 45; IQR, 34 [95% CI, 37.67 to 40.87]). The median open reading frame 1b (Orf1b) Ct value for the individual positive samples was 39.31 (range, 27.79 to 42.51; IQR, 7.43 [95% CI, 36.26 to 39.53]), while it was equal to 41.50 for the pooled samples (range, 30.22 to 45; IQR, 3.87 [95% CI, 38.47 to 41.15]). There was a strong positive linear correlation between the Ct values for the N gene ($r = 0.874$, $P < 10^{-4}$) (Fig. 1a) or the Orf1b gene ($r = 0.824$, $P < 10^{-4}$) (Fig. 1b) for individual and pooled samples.

No significant difference was observed between the results obtained with pooled NPS or saliva samples ($P = 0.202$). However, the comparison between the Ct values (N or Orf1b) for the NPS and saliva samples showed significantly higher values in saliva samples than in NPS samples (median ± standard deviation [SD] N Ct values: NPS, 35.33 ± 4.92; saliva, 40.94 ± 3.05 [$P = 0.0034$]; median ± SD Orf1b Ct values: NPS, 36.36 ± 4.23; saliva, 41.25 ± 2.35 [$P = 0.0021$]).

**Pools of 20 samples.** The frequency distribution of the variables was independent, as there was no significant association between the individual SARS-CoV-2 results and the results obtained with the pooled samples ($P = 1$) (Table 2). In our study, the analytical sensitivity and specificity for pools of 20 samples were equal to 55.56% (95% CI, 21.20% to 86.30%) and 100% (95% CI, 25% to 100%), respectively. The estimated accuracy was 96% (95% CI, 63.24% to 100%). The absolute percentage of agreement between the two groups was 60%. There was a slight agreement between the two groups ($k = 0.2$).

The median N Ct value for the individual positive samples was 35.44 (range, 23.48 to 41.29; IQR, 6.04 [95% CI, 31.16 to 38.56]), whereas the median N Ct value for the pooled samples was 40.48 (range, 30.16 to 46.05; IQR, 8.74 [95% CI, 35.69 to 43.11]). The median Orf1b Ct value for the individual positive samples was 37.51 (range, 29.79 to 40.63; IQR,
4.22 [95% CI, 34.24 to 39.36]), whereas that for the pooled samples was equal to 42.06 (range, 32.10 to 45; IQR, 4.44 [95% CI, 37.92 to 43.85]). There was a strong positive linear correlation between the \( \text{CT} \) values for the N gene \( (r = 0.800, P < 10^{-4}) \) (Fig. 2a) or the Orf1b gene \( (r = 0.891, P < 10^{-4}) \) (Fig. 2b) for individual and pooled samples.

No significant difference was observed between the results obtained for pooled NPS or saliva samples \( (P = 0.206) \). In addition, the comparison between the \( \text{CT} \) values (N or Orf1b) for the NPS and saliva samples showed higher values in saliva samples than in NPS samples (median \( \pm \) SD N \( \text{CT} \) values: NPS, 36.13 \( \pm \) 4.12; saliva, 42.68 \( \pm \) 3.91 \( [P = 0.296] \); median \( \pm \) SD Orf1b \( \text{CT} \) values: NPS, 38.14 \( \pm \) 3.99; saliva, 43.64 \( \pm \) 1.77 \( [P = 0.210] \)).

**DISCUSSION**

These preliminary results demonstrated that the 10-pool approach was sensitive and accurate for the detection of SARS-CoV-2 infection in both NPS and saliva pooled samples from symptomatic and asymptomatic individuals, while the pooling of 20 samples showed a drastic decrease in sensitivity. In this setting, the prevalence of the disease was low, \( \sim 1\% \).

Since the beginning of the COVID-19 pandemic, various pooling strategies have been developed (6–11). The effect of pooling on sensitivity varied among previous studies and was dependent on the pool size, platform, and assay employed (6–11). Prior studies found that, as the pool size increased (range, 2 to 20 samples), sensitivity decreased and \( \text{CT} \) values for target genes increased (6–11).

In our study, the approach of pooling 20 samples (1 positive sample/20 samples) showed a loss of sensitivity within a 1% positive rate, while the approach of pooling 10 samples (1 positive sample/10 samples) showed sensitivity and specificity values similar to those in prior studies (2). Currently, there are limited data on assessment of the optimal pool size (21). The pool size should be selected according to the disease prevalence to save tests and thus to be cost- and time-effective. In addition, some studies did not include samples with \( \text{CT} \) values above 35, which could have had an impact on the reported overall excellent sensitivity (7). The strength of our study resides in the fact that we analyzed consecutive pools of samples, which simulated the real-life situation, including positive samples with low viral loads.

In each pooling approach in our study, false-negative results occurred, all in saliva samples with \( \text{CT} \) values of \( >35 \), suggesting a potential decrease in sensitivity for low viral loads, as reported previously (8, 9). False-negative results are of concern because
infected individuals might not be isolated and could infect others (22). Although special precautions should be taken with RT-PCR false-negative results (22), it is also known that the majority of positive results obtained with just one targeted gene and with Ct values of >35 correspond to nonviable/noninfectious particles that are nonetheless detected by RT-PCR (23). In addition, we did not observe false-positive results in our study, even for samples with Ct values of >35.

We also evaluated pooling of saliva samples. There was no significant difference between the results obtained with pooled NSP samples and saliva samples. We and others previously showed that saliva samples were acceptable samples for SARS-CoV-2 detection, with the added advantages of allowing for self-collection and not requiring trained nursing staff members, sialagogic drugs, or particular constraints (such as fasting); their acceptability makes them ideal for institutionalized elderly people or for children (24–26). While studies on the subject are scarce, the approach of combining pooling with saliva collection could further expand the availability of testing (11, 19). However, variations in Ct values between individual and pooled saliva samples appeared to be more evident than with NPS samples, as shown previously (6, 11). This could be attributed to possible inhibition in saliva samples with greater mucus content (11). Further studies using a larger sample set will be needed to determine the effect of pooling on saliva virus loads.

The main limitations of our study were the retrospective design and the inclusion of a smaller sample size for cases. However, even with this design, our results proved that the approach of pooling 10 samples is sensitive and concordant with the individual RT-PCR results for both NPS and saliva samples. In conclusion, we demonstrated that the approach of pooling 10 samples has the potential to significantly increase SARS-CoV-2 testing capacity with both NPS and saliva samples with good sensitivity, whereas pooling of 20 samples shows significantly lower sensitivity.

MATERIALS AND METHODS

**Patients and samples.** This retrospective study was performed with a cohort of 149 consecutive subjects who were enrolled in a large prospective study (ClinicalTrial.gov registration no. NCT04418206) conducted at the University Côte d’Azur COVID-19 Biobank (BB-0033-00025, Pasteur Hospital, Nice, France) (27). The subjects volunteered at the Nice-Côte d’Azur Metropolis community-based COVID-19 center (Nice, France), which was accessible to the general population for screening for a period of 22 weeks (21 September 2020 to 23 March 2021) (25, 26). The mean age ± SD was 43 ± 15 years; 83 subjects were female and 66 were male, as described previously (25, 26).

NPS or saliva samples were collected randomly from the subjects. The interval between symptom onset and testing was 3.6 ± 2.6 days, and most participants (107/149 subjects [72%]) were sampled in the early stage of the disease, i.e., within 4 days after symptom onset. Of those subjects, 30 (20%) had positive RT-PCR results with one of the sampling techniques and thus were diagnosed as having COVID-19. Informed consent was obtained from all subjects involved in the study.

For SARS-CoV-2 detection, the Idylla SARS-CoV-2 kit was used on the Idylla platform (Biocartis), as reported previously (12). A positive or negative result was determined according to the instructions for use of the Idylla SARS-CoV-2 test. Pool screening was performed using this assay and targeting the same target as for individual samples. All samples were stored at −80°C at the University Côte d’Azur COVID-19 Biobank (BB-0033-00025, Louis Pasteur Hospital, Nice, France) prior to analysis (27). The sponsor of the study was Nice University Hospital. The study was conducted according to the guidelines of the Declaration of Helsinki and was approved by the Institutional Review Board Sud Méditerranée V of Centre Hospitalier Universitaire de Nice (registration no. 20.04014.35208 [date of approval, 22 April 2020]), with SHAM liability insurance (no. 159087).

**Sample pooling.** Samples were combined into pools of 10 samples (n = 30 pools) or 20 samples (n = 10 pools) (Fig. 3). Before use, samples were eluted with 200 μl phosphate-buffered saline (PBS) (0.9% NaCl; Verselyne Fresenius) and stored at −80°C within the Biobank.

Each pool contained equal amounts of one SARS-CoV-2-positive sample (as determined by the Idylla SARS-CoV-2 test; 30 positive samples) and the number of individual SARS-CoV-2-negative samples required to complete the target pool size. RNA extraction from pooled samples and SARS-CoV-2 detection were performed from a total input volume of 200 μl, as recommended by the manufacturer. Thus, 20 μl of each sample was mixed in an Eppendorf tube for a pool of 10 samples, and 10 μl of each sample was mixed for a pool of 20 samples.

**Statistical analysis.** The two-tailed Fisher’s exact test for categorical data was used to analyze associations between variables. The Mann-Whitney nonparametric test was used to analyze the unpaired samples. The kappa agreement test was used for categorical variables. The Pearson product-moment correlation coefficient was used to assess linear dependence between the Ct values. Correlation was judged as follows: very strong, 1 to 0.8; strong, 0.8 to 0.5; fair, 0.5 to 0.2; poor, 0.2 to 0. The normality of
data was not tested. The alpha risk was set to 5% ($\alpha = 0.05$). Statistical analysis was performed with the online software EasyMedStat (version 3.8; EasyMedStat, Neuilly-Sur-Seine; France).

ACKNOWLEDGMENTS

This work was supported by Agence Régionale de Santé Provence-Alpes-Côte d’Azur, Conseil Départemental 06 des Alpes Maritimes, Ville de Nice, Métropole Nice Côte d’Azur, Fonds de Dotation AVENI.

Author contributions were as follows: conceptualization, P. Hofman, C.-H. Marquette, and M. Ilié; formal analysis, P. Hofman, S. Heeke, and M. Ilié; funding acquisition, P. Hofman; investigation, C.-H. Marquette and M. Ilié; methodology, P. Hofman, M. Allegra, M. Salah, J. Benzaquen, V. Tanga, O. Bordon, J. Fayada, E. Long-Mira, S. Lassalle, E. Lantéri, V. Lespinet-Fabre, P. Brest, B. Mograbi, C. Maniel, J. Boutros, S. Leroy, S. Heeke, V. Hofman, C.-H. Marquette, and M. Ilié; project administration, P. Hofman, C.-H. Marquette, and M. Ilié; resources, P. Hofman and C.-H. Marquette; software, M. Ilié; supervision, S. Heeke; validation, C.-H. Marquette and M. Ilié; writing of original draft, P. Hofman, C.-H. Marquette, and M. Ilié; writing review and editing, P. Hofman and M. Ilié. All authors have read and agreed to the published version of the manuscript.

We declare no conflicts of interest.

REFERENCES

1. Oude Munnink BB, Nieuwenhuijse DF, Stein M, O’Toole Á, Haverkate M, Möllers M, Kamga SK, Schapendonk C, Pronk M, Lexmond P, van der Linden A, Bestebroer T, Chestakova I, Overmars RJ, van Nieuwkoop S, Molenkamp R, van der Eijk AA, GeurtsvanKessel C, Vennema H, Meijer A, Rambaut A, van Dissel J, Sikkema RS, Timen A, Koopmans M, Dutch-Covid-19 Response Team. 2020. Rapid SARS-CoV-2 whole-genome sequencing and analysis for informed public health decision-making in the Netherlands. Nat Med 26:1405–1410. https://doi.org/10.1038/s41591-020-0997-y.

2. de Salazar A, Aguilera A, Trastoy R, Fuentes A, Alados JC, Causse M, Galán JC, Moreno A, Trigo M, Pérez-Ruiz M, Roldán C, Pena MJ, Bernal S, Serrano-Conde E, Barbeito G, Torres E, Riazzo C, Cortes-Cuevas JL, Chueca N, Coira A, Sanchez-Calvo JM, Marfil E, Becerra F, Gude MJ, Pallarés Á, Pérez Del Molino ML, García F. 2020. Sample pooling for SARS-CoV-2 RT-PCR screening. Clin Microbiol Infect 26:1687.e1–e5. https://doi.org/10.1016/j.cmi.2020.09.008.

3. Maeda JM, Nkengasong JN. 2021. The puzzle of the COVID-19 pandemic in Africa. Science 371:27–28. https://doi.org/10.1126/science.abf8832.

4. Khadka RB, Gyawali R. 2020. Estimating PCR testing in Nepal for Covid-19: challenges and opportunities. Kathmandu Univ Med J (KUMJ) 18:309–312.

5. Nguyen NT, Brahmachari H, Bish EK, Bish DR. 2019. A methodology for deriving the sensitivity of pooled testing, based on viral load progression and pooling dilution. J Transl Med 17:252. https://doi.org/10.1186/s12967-019-1992-2.

6. Barat B, Das S, De Giorgi V, Henderson DK, Kopka S, Lau AF, Miller T, Moriarty T, Palmore TN, Sawney S, Spalding C, Tanjutco P, Wortmann G, Zelazny AM, Frank KM. 2021. Pooled saliva specimens for SARS-CoV-2 testing. J Clin Microbiol 59:e02486-20. https://doi.org/10.1128/JCM.02486-20.

7. Kim SY, Lee J, Sung H, Lee H, Han MG, Yoo CK, Lee SW, Hong KH. 2020. Pooling upper respiratory specimens for rapid mass screening of COVID-19 by real-time RT-PCR. Emerg Infect Dis 26:2469–2472. https://doi.org/10.3201/eid2610.201955.

8. Perchetti GA, Sullivan K-W, Pepper G, Huang M-L, Breit N, Mathias P, Jerome KR, Greninger AL. 2020. Pooling of SARS-CoV-2 samples to increase molecular testing throughput. J Clin Virol 131:e02486-20. https://doi.org/10.1016/j.jcv.2020.104570. https://doi.org/10.1016/j.jcv.2020.104570.

9. Wang H, Hoggan CA, Miller JA, Sahoo MK, Huang C, Mfuh KO, Sibai M, Zehnder J, Hickey B, Sinnott-Armstrong N, Pinsky BA. 2021. Performance of nucleic acid amplification tests for detection of severe acute respiratory syndrome coronavirus 2 in prospectively pooled specimens. Emerg Infect Dis 27:92–103. https://doi.org/10.3201/eid2701.203379.

10. Wyllie AL, Fournier J, Casanovas-Massana A, Campbell M, Tokuyama M, Vijayakumar P, Warren JL, Geng B, Muenker MC, Moore AJ, Vogels CB, Petrone ME, Ott IM, Lu P, Venkataraman A, Lu-Culligan A, Klein J, Earnest R, Simonov M, Datta R, Handoko R, Naushad N, Sewanan LR, Valdez J, White EB, Lapidus S, Kalinich CC, Jiang X, Kim DJ, Kudo E, Linehan M, Mao T, Moriyama M, Oh JE, Park A, Silva J, Song E, Takahashi T, Taura M,
Sample Pooling for SARS-CoV-2 Detection

Weizman O-E, Wong P, Yang Y, Bermejo S, Odiyo CD, Omer SB, Dela Cruz CS, Farhadian S, Martinello RA, Iwasaki A, Grubaugh ND, Ko Al. 2020. Saliva or nasopharyngeal swab specimens for detection of SARS-CoV-2. N Engl J Med 383:1283–1286. https://doi.org/10.1056/NEJMct2016359.

11. McMillen T, Jani K, Babady NE. 2021. Evaluation of sample pooling for SARS-CoV-2 RNA detection in nasopharyngeal swabs and salivas on the Roche Cobas 6800. J Clin Virol 138:104790. https://doi.org/10.1016/j.jcv.2021.104790.

12. Hofman P, Boutros J, Bencherit D, Benzaquen J, Leroy S, Tanga V, Bordone O, Allegre M, Lespinet V, Fayada J, Maniel C, Griffonnet J, Selva E, Troncone G, Portella G, Lavrut T, Chemla R, Carles M, Ilie M, Marquette C. 2021. A rapid near-patient RT-PCR test for suspected COVID-19: a study of the diagnostic accuracy. Ann Transl Med 9:921. https://doi.org/10.21037/atm-21-690.

13. Abdalhamid B, Bilder CR, McCutchen EL, Hinrichs SH, Koepsell SA, Iwen PC. 2020. Assessment of specimen pooling to conserve SARS-CoV-2 testing resources. Am J Clin Pathol 153:715–718. https://doi.org/10.1093/ajcp/aqaa064.

14. Deckert A, Barnighausen T, Kyei NN. 2020. Simulation of pooled-sample analysis strategies for COVID-19 mass testing. Bull World Health Organ 98:590–598. https://doi.org/10.2471/BLT.20.257188.

15. Hogan CA, Sahoo MK, Pinsky BA. 2020. Sample pooling as a strategy to detect community transmission of SARS-CoV-2. JAMA 323:1967–1969. https://doi.org/10.1001/jama.2020.5445.

16. Torres I, Albert E, Navarro D. 2020. Pooling of nasopharyngeal swab specimens for detection of SARS-CoV-2. J Med Virol 92:2193–2307. https://doi.org/10.1002/jmv.25971.

17. Wacharapluesadee S, Kaewpom T, Ampoot W, Ghai S, Khamhang W, Torres I, Albert E, Navarro D. 2020. Pooling of nasopharyngeal swab specimens for detection of SARS-CoV-2. J Med Virol 92:2306–2307. https://doi.org/10.1002/jmv.25971.

18. Hofman P, Boutros J, Bencherit D, Benzaquen J, Leroy S, Tanga V, Bordone O, Allegre M, Lespinet V, Fayada J, Maniel C, Griffonnet J, Selva E, Troncone G, Portella G, Lavrut T, Chemla R, Carles M, Ilie M, Marquette C. 2021. A rapid near-patient RT-PCR test for suspected COVID-19: a study of the diagnostic accuracy. Ann Transl Med 9:921. https://doi.org/10.21037/atm-21-690.

19. Pasomsub E, Watcharananan SP, Watcharanackchai T, Rakmanee K, Tassaneetrithep B, Kiertiburanakul S, Phuphakrat A. 2021. Saliva sample pooling for the detection of SARS-CoV-2. J Med Virol 93:1506–1511. https://doi.org/10.1002/jmv.26460.

20. Watkins AE, Fenichel EP, Weinberger DM, Vogels CBF, Brackney DE, Casanovas-Massana A, Campbell M, Fournier J, Bermejo S, Datta R, Dela Cruz CS, Farhadian SF, Iwasaki A, Ko Al, Grubaugh ND, Wyllie AL. 2021. Increased SARS-CoV-2 testing capacity with pooled saliva samples. Emerg Infect Dis. https://doi.org/10.3201/eid2704.204200.

21. Barak N, Ben-Ami R, Sido T, Perri A, Shtoyher A, Rivkin M, Licht T, Perez A, Magenhein J, Fogel J, Livneh A, Datch Y, Oknine-Djian E, Benedek G, Dor Y, Wolf DG, Yassour M, Hebrew University-Haddasah COVID-19 Diagnosis Team. 2021. Lessons from applied large-scale pooling of 133,816 SARS-CoV-2 RT-PCR tests. Sci Transl Med 13:eabf2823. https://doi.org/10.1126/scitranslmed.abf2823.

22. Woloshin S, Patel N, Kesselheim AS. 2020. False negative tests for SARS-CoV-2 infection: challenges and implications. N Engl J Med 383:e38. https://doi.org/10.1056/NEJMp2015897.

23. Bullard J, Dust K, Funk D, Strong JE, Alexander D, Garnett L, Boodman C, Bello A, Hedley A, Schifffman Z, Doan K, Bastien N, Li Y, Van Caeseele PG, Poliquin G. 2020. Predicting infectious severe acute respiratory syndrome coronavirus 2 from diagnostic samples. Clin Infect Dis 71:2663–2666. https://doi.org/10.1093/cid/ciaa638.

24. Chen JH, Yip CC, Poon RW, Chan KH, Cheng VC, Hung IF, Chan JF, Yuen KY, To KK. 2020. Evaluating the use of posterior oropharyngeal saliva in a point-of-care assay for the detection of SARS-CoV-2. Emerg Microbes Infect 9:1356–1359. https://doi.org/10.1080/22221751.2020.1775133.

25. Marquette CH, Boutros J, Benzaquen J, Ilie M, Labaky M, Bencherit D, Lavrut T, Leroy S, Chemla R, Carles M, Tanga V, Maniel C, Bordone O, Allegre M, Lespinet V, Fayada J, Griffonnet J, Hofman V, Hofman P. 2021. Salivary detection of COVID-19: clinical performance of oral sponge sampling for SARS-CoV-2 testing. medRxiv 2021.02.17.21251556. 2021.02.17.21251556.

26. Boutros J, Benzaquen J, Marquette CH, Ilie M, Labaky M, Bencherit D, Lavrut T, Leroy S, Chemla R, Carles M, Tanga V, Maniel C, Bordone O, Allegre M, Lespinet V, Fayada J, Griffonnet J, Hofman V, Hofman P. 2021. Salivary detection of COVID-19: clinical performance of oral sponge sampling for SARS-CoV-2 testing. ERJ Open Res https://doi.org/10.1183/23120541.00396-2021.

27. Tanga V, Leroy S, Fayada J, Hamila M, Allegre M, Messaoudi Z, Nouri S, Ilie M, Maniel C, Beldar O, Hadjadj S, Allegre M, Lespinet V, Fayada J, Griffonnet J, Hofman V, Hofman P. 2021. Salivary detection of COVID-19: clinical performance of oral sponge sampling for SARS-CoV-2 testing. medRxiv 2021.02.17.21251556. 2021.02.17.21251556.