COVID-19 NATIONAL TESTING PROGRAMME SERVICE EVALUATION EVIDENCE REPORT

This report documents that a service evaluation was conducted on behalf of the Department of Health and Social Care, England (DHSC), intending to either support or refute the hypothesis detailed below in relation to the COVID-19 national testing programme. Details of the nature of the experiment, hypothesis, conducting labs, results and policy recommendation from the result are included below.

Experiment ID	COMBI021
Date Experiment Requested	21/05/20
Control used for experiment	Throat and nose swabs collected by individuals trained by clinical staff, qRT-PCR controls at [redacted]
Protocol version	1
Type of validation	Service Evaluation
Hypothesis	Alphalab SW1040 Swab is suitable for use in self-swabbing collection of samples for COVID-19 antigen test-based diagnosis.
What product being tested	COMBI021: E&O BM1673-M043-3 Vial + Medium, Alphalab SW1040 Swab
What time incubation	Up to 24 hours post swab collection
Objectives	To determine whether self-swabbing is as effective as swabs taken by trained individuals for diagnosing SARS-CoV-2 positive patients.

Details of the experiment including the conducting lab, time frames, results and additional observations of the experiment are detailed below.

Date Experiment Started	31/05/20
Experiment Conducting Lab	[redacted] and [redacted]
Date Experiment Completed	02/06/20
Inclusion criteria	• Subjects have agreed to take part in the self-swabbing exercise and are ≥18 years old • Subjects have read and understood the self-swabbing instructions. • Minimum of 50% of cohort to be composed of individuals who do not have experience of performing medical procedures
Summary of methods	1. Subject will swab their throat and nose according to the self-swabbing instructions. Swabbing will be monitored by a trained testing operator and technique will be noted in the case report form. The swab will be placed in the viral transport medium. 2. 4 identical barcodes will be produced and these should be: a. One attached to the tube with the self-swab b. One attached to the bag holding the self-swab tube c. One attached to the case report form d. One given to the subject 3. A trained testing operator will swab the patient's throat and nose according to standard diagnostic requirements and placed into the viral transport medium.

	4. 4 identical barcodes will be produced and these should be: a. One attached to the tube with the assisted-swab b. One attached to the bag holding the assisted-swab tube c. One attached to the case report form d. One given to the subject 5. The samples will be collated and sent to [redacted] with the case report forms at the end of the day for processing using the standard diagnostic workflow. Samples will be stored and transported together, and run together on the same qRT-PCR plate. [redacted] workers will be blinded to: a. Which samples belong to which subject b. The collection mode of the sample 6. qRT-PCR CT value data for the samples will be sent to Workstream 2 for unbinding, matching to electronic case report forms and analysis.
Results (high level summary report)	• A total of 492 subjects were successfully recruited into the Service Evaluation, 34 samples were filter out from analysis: o 10 subjects withdrew from the study o 18 samples did not have paired self-assisted samples o 6/464 (1.3%) samples that were reported as 'invalid' following qRT-PCR analysis (i.e. a non-concordant positive or negative result was obtained across the 3 SARS-CoV-19 genes assayed) for both self and assisted swabs. One was invalid with both self swabbing and assisted swabbing; 3 were invalid for self, with a one negative and two positive results for assisted; and two negative for self with both being void for assisted. No observational comments were made at the time of collection that would account for the sample being invalid • The remaining 458 pairs of samples were analysed, no duplicates were identified. • Overall 448 of 458 (97.8%%; 95% confidence interval: 96.5%-99.2%) subjects were concordant for positive or negative diagnosis. o 421 of these were diagnosed as COVID-19 negative o 27 of these were diagnosed as COVID-19 positive o 10 of 458 subjects had discordant results across both samples, of whom: ▪ 8 samples were diagnosed as COVID-19 negative in the self-collected samples and COVID-19 positive according to the assisted-test sample. Only one subject was reported to have previous experience of clinical procedures ▪ 2 was diagnosed as COVID-19 positive according to the self-collected sample, and as COVID-19 negative according to the assisted-test sample, no prior clinical experience reported. Only one subject was reported to have previous experience of clinical procedures

	▪ No observational comments were made during sample collection against these samples to account for the discordance ▪ Overall there was no evidence that the self swabbing was inferior to assisted swabbing (*P*=0.1) o Viral loads of the bacteriophage MS2 showed no significant difference between self (mean=22.9, sem 0.05) and assisted (mean=22.8, sem 0.05; CT difference mean 0.03; 95% ci: -0.06-0.11, *P*=0.5) swabbing. Lower CT values in the negative swabs (mean=22.8, sem 0.03) indicate a high quantity of DNA in MS2 values when compared to the positive swab (mean=23.2, sem 0.14; 95% ci: -0.68-(-0.11), *P*=0.01). o The results were divided (arbitrarily) into high viral load (CT<25), low viral load (CT>=25 & CT<35) and negative (C=0), which gave 11 discordant samples (Appendix 1). There were 9 samples in favour of assisted swabbing and 2 samples for self-swabbing, *P*=0.07) • Quantitative PCR assay was completed targeting the ORF1ab, N-gene and S-genes. Concordant positive samples were used to compare the cycle threshold (CT) values of self-swabbing and assisted swabbing. The results for the individual gene targets are shown in Appendix 2. o Average CT score for self-swabbing was 20.4 (sem 1.01), and for assisted-swabbing it was 20.6 (sem 1.00). o CT difference (self swab vs assisted-swab) mean -0.28; 95% ci: -1.4-0.88, *P*=0.62
Additional Observations	
Summary of conclusions	There was no material difference between self and assisted swabs, when looking at the concordant positive samples. In the discordant results there were more positive swabs in the assisted group, which is reflective of the TS/5-34A findings, but no significant difference was seen.
Supporting graphs / data (to attach in the appendix)	Appendix 1 Quantitative data analysis by viral load grouping Appendix 2 Quantitative data analysis across 3 genes Appendix 3 Average viral load comparison of self vs assisted swabs in COVID positive individuals Appendix 4 Validation Evidence Report SWTC008c

Policy recommendation from this data (to be completed by DHSC)	The current approach of self and assisted swabbing should continue. The slight difference in performance is within reasonable tolerances. Return of results messaging should include mitigations for false negatives. In conjunction with the separate evidence of length of time in which swab samples remain viable for up to 10 days on the swab (see Validation Evidence Report SWTC008c, Appendix 4) it is appropriate that this swab/medium combination is used for home testing The data from this service evaluation should be used to support the MHRA derogation for use in home swabbing

The signatures below confirm that requesting authority is satisfied that the experiment was conducted was conducted successfully (regardless of outcome) and that the above details are complete and correct.

[redacted]

Requesting authority (11/07/2020)

[redacted]

[redacted]

Department of Health and Social Care

[redacted]

Conducting Authority (14/07/2020)

[redacted]

University of Oxford

Appendix 1

Quantitative data analysis by viral load grouping

The results were divided (arbitrarily) into high viral load (CT<25); low viral load (CT>=25 & CT<35) and negative (CT=0). There were 9 samples in favour of assisted swabbing (blue) and 2 samples in favour of self-swabbing (green), which was a significant difference *P*=0.2.

		Assisted Swabbing groups			
Self Swabbing groups		**High (<25)**	**Low (25-35)**	**Negative**	**Total**
	High (<25)	22	0	1	23
	Low (25-35)	1	4	1	6
	Negative	3	5	421	429
	Total	26	9	423	458

Appendix 2

Quantitative data analysis across 3 gene

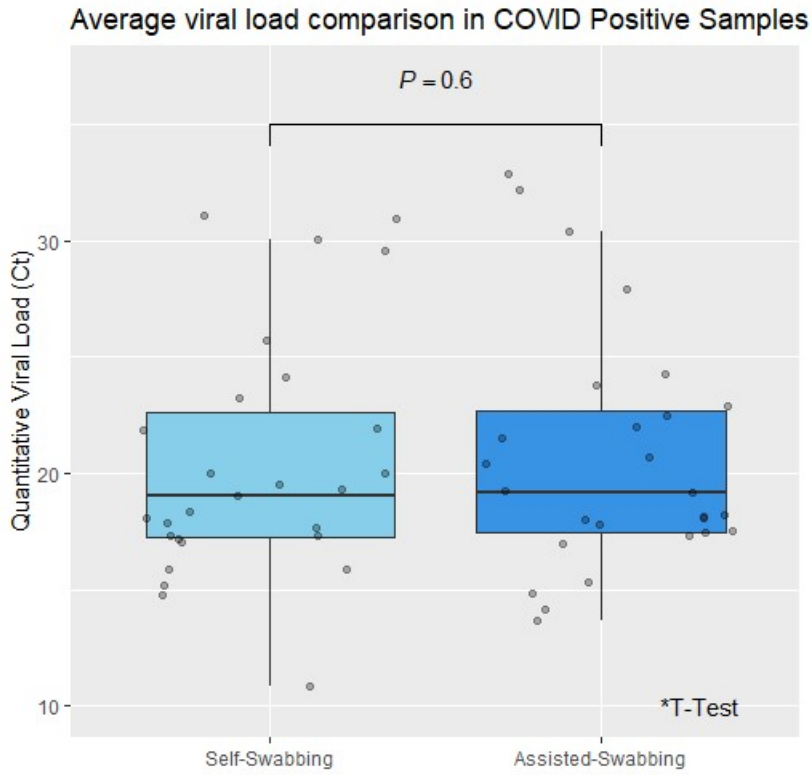
The average and standard error of mean for CT values of the three target genes in 27 subjects who were diagnosed as concordant COVID-19 positive.

Method	ORF1ab	N-gene	S-gene	Total Average
Self-swabbing	19.6 (SEM: 1.25)	21.2 (SEM: 1.02)	20.3 (SEM: 1.20)	20.4 (SEM: 1.01)
Assisted-swabbing	19.3 (SEM: 1.25)	21.1 (SEM: 1.10)	21.6 (SEM: 1.10)	20.6 (SEM: 1.00)

Appendix 3

Average viral load comparison of self vs assisted swabs in COVID positive individuals

The average CT value was taken across the three genes in all 27 concordant COVID positive individuals, the boxplot below shows a comparison between the self-swabbing and assisted swabbing samples. No significant difference was seen, CT difference (self swab vs assisted-swab) mean -0.28; 95% ci: -1.4-0.88, *P*=0.62.



SWTC008c - Appendix 4

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