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Detection of long SARS-CoV-2 nucleocapsid sequences in peripheral blood monocytes collected soon after hospital admission.

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ABSTRACT

Many different viruses infect circulating mononuclear cells to disseminate infection to diverse organs. Blood mononuclear cells (PBMC) are being intensively studied as immunologic and pathologic responders to the new pandemic SARS-CoV-2 virus (CoV19) but direct evidence showing CoV19 in these cells has not been published. PBMC myeloid cells that take up residence in various organs can harbor viral genomes for many years in lymphatic tissues, skin and brain, and act as a source for re-infection and/or post-viral organ pathology. To test if PBMC from acutely ill hospitalized patients contain viral nucleic acids, we first analyzed a standard short CoV19 nucleocapsid (NC) 72bp sequence. Because NC proteins protect the viral genome, we further analyzed longer (301nt) adjacent NC stretches by RNA/qPCR. In 2 of 11 patient PBMC, but no uninfected controls, longer NC sequences were positive as early as 2-6 days after hospital admission and were validated by sequencing. The presence of longer NC sequences indicates pathogenic fragments, or possibly the complete infectious virus, are carried by a rare population of monocytes, probably a subset of myeloid migratory cells. Predictably, such cells carried CoV19 to heart and brain with consequent late post-viral immune pathologies that are now evident.

INTRODUCTION

Some acute lytic viral infections release free viral particles into the bloodstream where they are easily assayed with modern molecular techniques. However, a large variety of viruses travel within white blood cells such as retroviruses, e.g., HIV (*1, 2*) and flaviviruses, e.g., Dengue (*3*). Some viruses carried in white blood cells are associated with chronic disease. Poliovirus, a "neurotropic" enterovirus originally thought to spread directly through nerves, instead transits from gut to white blood cells to spleen, and only later infects brain (*4*). There are at least 13 different classes of DNA and RNA viruses that infect peripheral blood mononuclear cells (PBMC) that can be a reservoir for persistence (*5*), in addition to the infectious Creutzfeldt-Jakob Disease (CJD) agent (*6*). Like HTLV1, a retrovirus that can be sequestered in brain myeloid microglia, the CJD agent in white blood cells progressively increases after primary infection of gut dendritic (myeloid lineage) cells to later show up in highly infectious myeloid microglia in brain (*7, 8*). Experimentally, the CJD agent requires cell-to-cell contact for infection (*9*), probably via viral synapses, the same mechanism or conduit used for T to myeloid cell transmission of HIV (*1*). Moreover, chronic HIV infection of brain microglia is linked to neurocognitive disorders and dementia, as is the very different ~20-25nm CJD infectious particle (*10, 11*). These observations emphasize the general principle that infected migrating myeloid cells can take up residence in and perpetuate infection and chronic pathology in the brain and other organs. The presence of nucleocapsid CoV19 RNA, especially in migrating myeloid cells, might explain some of the ensuing brain and heart pathologies that were predictable and that have become increasingly evident during this pandemic Coronavirus 2019 Disease (COVID-19).

We were aware that PBMC could contain extremely low CoV19 RNA due to the presence of the virus possibly limited to rare myeloid cell types. Those cell types can be less abundant than the 1-2% dendritic cells in a PBMC population typically dominated by lymphocytes (70-90%). Many different myeloid cell-types are increasingly appreciated and classified, and many of them show wide phenotypic flexibility (*12*). Moreover, total cellular RNA is very low in PBMC, ~1/40th of that produced by epithelial and cultured tumor cells such as HeLa cells and NIH/3T3 cells. Nevertheless, there were three additional reasons to pursue this study. First, coronaviruses are complex, and can elicit autoimmune responses that damage brain. For example, the mouse hepatitis coronavirus (MHV) induces a post-viral autoimmune demyelinating disease that is a model of Multiple Sclerosis, and other coronavirus strains, such as CoV19, might elicit a different type of post-viral brain pathology. Indeed, respiratory coronaviruses, prior to the CoV19 strain,

that cause human colds have been neuroinvasive, with viral RNA demonstrated in brain parenchyma as well as in myeloid microglia in culture (*13*).

We proposed to study CoV19 in PBMC in April 2020 because first, little was known about potential immediate viral or late immunologic CoV19 effects on the brain. We suspected that a subset of blood monocytes, not just neural olfactory spread, might be a conduit for CoV19 into brain with subsequent development of neuropsychiatric symptoms. A wide variety of neurologic complications and neuropathology have now been published, e.g., thromboemboli, infarction, radiologic changes consistent with an autoimmune encephalitis (*14)* and even the presence of CoV19 in neurons (*15*). Second, coronaviruses are but one group of many different viruses including influenza, rhinoviruses and adenoviruses that commonly infect the population. Infrequent lethal sudden deaths from uncharacterized winter "viral" infections on routine autopsy can show classical acute lymphocytic and myeloid infiltrates in an otherwise normal heart. Some of these might be due to a coronavirus strain. The recent collapse of healthy young athletes may be caused by CoV19 PBMC dissemination leading to vascular microthrombi in the heart and brain. Third, the long-standing Yale-China relationship gave LM the opportunity to attend a zoom meeting with doctors from Wuhan who shared their data and experience with us early in 2020. In one slide, a striking feature was the pathology of an interstitial pneumonia dominated by many large cells that were most consistent with a myeloid lineage. This further elicited the impetus to find if PBMC CoV19 infection could be a source of multiorgan spread. We found over 300nt of CoV19 nucleocapsid RNA in PBMC indicating these cells can be a conduit for spread of the virus, or viral elements, to other organs.

RESULTS

PBMC from 7 male and 7 female patients ranging from 24-82 years and 4 random uninfected control volunteer were initially studied. The 14 patient PBMC were taken 2-6 days after hospital admission with positive CoV19 swab test. To avoid RNA extraction losses in low RNA PBMC, exhaustive DNA removal was not pursued. PBMC recovery can vary, especially in patients with other underlying illnesses. Thus, all PBMC RNA extracts (from 4 control asymptomatic volunteer CoV19 swab-negative and 14 CoV19 positive patients), were tested for GAPDH by RT/qPCR to assess amounts of RNA in each; 11 patient samples were adequate for nucleocapsid (NC) RT/qPCR tests, and showed a mean of 69% ($\pm$35%SD) of the "normal" controls. The other 3 patients yielded only 1/10th the control RNAs and were inadequate for NC analyses. CoV19 NC RNA was initially evaluated with the CDC:N1 primer pair/probe reagent performed in triplicate in the diagnostic lab of NDG. For reference, the N1 primer pair amplifies a

72bp product that begins 14nt downstream from the nucleocapsid start codon as shown in red (see Table I, Methods). None of the normal samples or water controls were positive for this 72bp product whereas positive RNA controls from the complete RNA nucleocapsid genome (designated G), complete viral RNA copies (e3), and CoV19 infected Vero cell RNA (designated V+) produced their expected threshold cycles (Ct) and dilution curves. One patient's PBMC (18*) was unambiguously positive with Cts of 35.37, 34.02 and 34.91. These Cts were equivalent to 114, 264 and 152 viral copies respectively (mean of 177) in a nominal estimate of 5e4 PBMC. This indicated this 72nt NC RNA was present in a low percentage of cells. One other patient sample tested in parallel (14*) was ambiguous in this test with a Ct of 37.19 in one of three replicates. All other patient samples were negative for the 72nt RNA. We repeated these 72bp RT/qPCRs in our lab in duplicate, and found only patient 18* was comparably positive with Cts of 34.2 and 34.7. The variability in Cts of patient 18* in the triplicate samples was likely due to unevenly dispersed residual DNA.

The 4 control normal samples (designated 1n-4n), and the 11 patient samples (all designated by an *), were subsequently tested for longer adjacent stretches of the NC that covered an additional 301bp as detailed in Table I (see Methods). A single forward primer (F3) was used to generate both a shorter 251bp sequence (with primer R5) as well as a longer 301bp sequence (with primer R3). This allowed sequencing from two different PCR reactions for validation.

Melting profiles RT/qPCR reactions with these primer pairs, using serial dilutions of positive controls along with H_2O negative controls, revealed significantly different melting temperatures (Tm) for each primer pair products. Fig. 1 shows the Tm profiles from the 72bp versus the 251 and 301bp amplifications. The CDC:N1 primers melted at 81.45ºC ($\pm$0.07 SD) and had a broad profile. In contrast, the 251bp F3/R5 product gave a significantly higher and sharper Tm of 83.7ºC ($\pm$ 0.06 SD). As expected, the longest 301bp product had the highest Tm (84.19ºC $\pm$ 0.13 SD) with a very sharp and unambiguous curve. This allowed clear distinction of real positives from background primer-dimers and other artefacts with very different Tms. In the CDC:N1 and F3/R3 graphs of standards, the water negative control shows no true melt and only a single profile was obtained. However, in less purified samples, Tm peak artefacts were sometimes seen and these typically occurred in PBMC RNA extracts that contained DNA. These non-specific and variable peaks sometimes precluded simple and valid digital Cts since a single threshold could not be used for all the different samples in a run. We therefore used the following criteria to validate CoV19-specific peaks: 1) a Tm or peak profile of the PBMC RT/qPCR that matched the positive controls, 2) a minimum of both a positive Tm peak and positive gel band of correct length that was verified

in ≥2 separate aliquots of each patient RNA sample, and 3) sequencing of patient gel bands that matched those from bands of parallel controls including the nucleocapsid genome (G), the e3 reference virus, and the CoV19 infected Vero cell (V+) RNA. Uninfected Vero cell RNA (V-) was also used as a negative total cell RNA control.

Fig. 2 shows representative gel runs of RT/qPCR bands for the 251bp (**A**) and 301bp (**B**) NC products. For clarity, gel images were inverted. Lanes with control and patient samples are indicated, and the dot marks 300bp in 100bp marker lanes. In Fig. 2A only the + lanes show the predicted band, i.e., the nucleocapsid genome control (lane G), the infected Vero cells (V+), and patient extracts 14* and 18*. The second 18* band shown is also positive, and from a different aliquot that was run with it's H_2O (w) control (lanes 13-14). The 14* band at 251bp is weak but visible, and shows a smear of background that is consistent with non-specific DNA. Higher loads of this sample on another gel showed a very strong 251bp band (data not shown). Moreover, the RT/qPCR peak profile of the 14* amplified product shown above also revealed an overwhelmingly dominant peak with a Tm matching the other positive controls (see Fig. 3A). Faint smears near the top of the gel in other PBMC samples (lanes 7-10) also indicate high molecular weight non-specific genomic DNA products. The control normal PBMC (n1, n4), uninfected Vero cells (V-), water (w) and other patient samples (11*, 12*, 22*, 23*) are all negative without such non-specific smears. However, some show primer-dimers.

The two positive patient extracts 14*and 18* that reproducibly yielded the 251bp gel band were also positive for the 301bp band as shown in Fig. 2B. This further supported the presence of longer stretches of CoV19 NC RNA. Each of the positive patient 14* and 18* samples shown in Fig. 2B were also taken from different sample aliquots than those in Fig. 2A. These longer 301bp NC reactions were run in parallel RT/qPCR tubes, with the representative positive and negative controls shown. The CoV19 standards e, G and V+ all gave relatively clean profiles with only primer-dimer type bands under 100bp. All the control normal PBMC RNAs (n3, n4, and the negative patient samples 15*, 22*and 19*) gave some higher molecular weight smears with a few non-specific bands under 200bp. Additionally, an ~ 360bp band is seen in both the stronger 14* sample and the 18* sample (lanes 11 and 14 respectively). This might signify cross-contamination. However, this artefactual peak's Tm and profile was clearly different in each of these two aliquots.

Fig. 3 shows individual samples with the same non-specific gel band can be discriminated from each other by their Tm peaks. The peak profiles of the 251bp (**A**) and 301bp (**B**) RT/qPCR products are representative and from the MyGo mini and Stratasys qPCR machines respectively. Duplicates run on both machines also gave comparable results. In Fig. 3A, H_2O gave a flat

negative (blue) line with no peaks whereas all three positives gave the same sharp high fluorescent peak (e+ in black, 14* in purple and 18* in red). The Tm of this peak was the same (83.71±0.6) as previously shown for other positive controls in Fig. 1. Note that although patient 14* showed a weak 251 gel band in Fig. 2A (lane 9), it showed a strongly dominant Tm peak as the nucleocapsid genome (G) and the Tm peak was clearly much stronger than the non-specific background. The small artefactual peaks of patient 23* were clearly non-specific by their Tms, and were easily thresholded for more reliable Cts.

Limitations of thresholding for Cts, especially with the longer NC primers in PBMC extracts with residual DNA, are shown in Fig. 3B. In this profile, H_2O displays an artefactual broad peak starting at ~80ºC and this is clearly an artefact due to a primer dimer of ~50bp. This dimer artefact also is seen ion patient samples 14* (purple) and 18* (red) beneath the largest H_2O peak. The positive 14* sample's 301bp fluorescent peak lies under the other positive peaks, including the NC control (in green), and has an indistinguishable Tm of 84.19±0.13SD as shown for other positive controls in Fig. 1. The same large non-specific gel band of ~350bp was seen in both the 14* and 18* samples (Fig. 2, lanes 11 and 14,), yet surprisingly, these higher melting peaks were clearly different from each other as shown at arrows. This confirmed that the 14* and 18* artefactual long peaks were different from each other in sequence, making cross-contamination of the two samples unlikely. This was borne out by independent sequencing of individual amplified samples both of the 251 and 301bp products in each.

For sequencing confirmation, each of the RT/qPCR bands from positive controls (e, G, V+) as well as both of the bands from the positive patients above (14* and 18*) was determined. All 10 eluted band samples (5 of 251bp and 5 of 301bp) were reamplified, and the bands again gel purified for sequencing. Band eluates run on gels before sequencing showed no other visible bands or primer contamination (data not shown), and all sequences unambiguously confirmed their identity with the NC sequence as detailed in methods. Sequences were confirmed using both strands except DNA close to the F3 and R3 primer ends were read only on one strand. Inspection of run peaks in each confirmed the sequence shown Table I (Methods).

DISCUSSION

In summary, the use of NC primers adjacent to the 72bp NC RNA revealed strong evidence that long CoV19 NC sequences were present in patient PBMC. The two positive patient samples (14* and 18*) were validated by sequencing and completely matched our 3 positive internal controls as well as the CoV19 NC sequences in the database. While we were limited to a small

sample of PBMC, nominally ~6e4 cell RNA for 2-3 repeat replicate studies of each of two longer NC, it is clear that only a few select cells (probably ≤1/100) carry these sequences.

The fact that no one else has reported direct reproducible detection of CoV19 RNA sequences in PBMC indicates spread via these cells has not been widely considered even though they are a common route for the dissemination of many viruses to other organs. More remarkably, coronavirus studies using mouse hepatitis virus (MHV), were previously presumed to spread by blood because lesions and antigens were distributed in a vascular pattern akin to the vascular pathology now reproducibly seen in COVID-19 patients. After MHV intranasal infection, an infectious viremia with a significant titer was demonstrated by a colleague here in 1991. The virus was present in whole blood, plasma and buffy coat (white blood) cells 3 days post infection (4.1-4.8 logs, LD_{50}/ml, by a sensitive infant mouse titration assay). Moreover, by 5 days post infection this titer was maintained only in buffy coat cells (*14*). A biphasic clearance from plasma was also noted during the first 5 days post nasal inoculation, and importantly, the MHV viremia was intermittent. Many infectious agents are known to enter the bloodstream in spikes that coincide with intermittent fevers, and we suspect that patients with COVID-19 may not have a constant detectable level of viremia. The patients here were sampled only at one time point in disease and this could explain why only 20% of our patients were positive.

The MHV studies have relevance for the minor proportion of positives in CoV19 PBMC found here based on two factors. First, our samples were taken 2-6 days after symptomatic admission, and these patients were probably infected at least 5 days before admission, a time when viremia may not be as high as during the asymptomatic phase. Second, the known clearance of MHV from blood during the initial infection could also lower the number of PBMC positives in patients evaluated here. In this context the study of plasma and PBMC at earlier phases of CoV19 exposure seems warranted. Such temporal evaluations could be useful diagnostically and also lead to antibody and other new strategies to prevent progressive spread to other organs. Assessing PBMC during later progressive disease with more severe organ dysfunction, or in more susceptible populations such as the elderly, may also be informative for understanding CoV19 viremic clearance or lack thereof. Notably, patient 18* was 78 years old and her PBMC was taken 6 days after her symptoms had already developed along with a positive swab admission test.

The longer NC sequences analyzed here and the RT/qPCR products amplified encompass a substantial (33%) portion of the entire nucleocapsid that codes for a genome-protective protein of 455aa. For future studies, several technical changes can minimize the nucleocapsid RT/qPCR artefacts we encountered in PBMC. First, we had only ~2e6 PBMC, optimally yielding a total of

0.6μg RNA for all our repeated RT/qPCR tests with the longer NC primers. This level is not sufficient for robust reproducible determinations. Our patient PBMC also had an average of 70% of normal PBMC by GAPHD levels further limiting positive detection. Second, by not rigorously removing genomic DNA, we found more artefact bands and background than in the purer positive RNA cell controls such as the V+ samples. These controls rarely showed anything other than a low melt dimer of ~50bp that could be thresholded. Third, to establish reproducible positives we sampled aliquots using very small samples (1-3ul per reaction with nominally 2.5e4 cell RNA/μl) and a much higher level of input should uncover more positive patients. Finally, more quantitative NC RT/qPCR Cts should start with ≥ 5e7 PBMC per individual. This number of PBMC would also allow for sorting of PBMC subsets that concentrate CoV19 sequences.

The positive results here emphasize the importance of further studies to determine which PBMC cell type concentrates CoV19 sequences. The present small sample study shows a relatively low amount of CoV19 NC copies in total PBMC RNA, probably limited to a select cell type. Unfortunately, we could not obtain more of our positive patient samples to assess combined CoV19 antigen and cell-type specific antibody tests. It is also important to determine if the subset of positive cells carry fully infectious CoV19, and not just the NC sequence, as for example by culture or animal inoculation. Electron microscopy for viral particles in selected cell types isolated by sorting, in addition to in-situ viral hybridization with antigenic cell-type specific markers, can be effectively performed on low numbers of subset cells. We suspect that a circulating myeloid cell type probably carries CoV19 sequences or products, especially because these cells can take up residence in tissues and act as a latent source for infection and/or chronic immune stimulation. As antigen presenting cells, they are capable of stimulating immune responses that are detrimental to the host. Myeloid cells with CoV19 are also a likely viral conduit because of their known ability to attach and enter tissues via the vascular endothelium. New hamster and mouse transgenic angiotensin converting enzyme 2 receptor models of COVID-19 may be the most sensitive way to assay infectivity in such PBMC subsets. Identifying the positive cell subtype will also facilitate therapeutic approaches that specifically target these cells to prevent early dissemination of Cov19, in part or whole, to other organs.

MATERIALS AND METHODS

***Samples*:** Collection of de-identified control ("uninfected normal") blood samples and those from patients with positive CoV19 nasopharyngeal swab tests, first assayed by the US CDC 2019-nCoV_N1 primer–probe set at the Yale-New Haven Hospital (YNHH), were approved by the Institutional Review Board of the Yale Human Research Protection Program (no. FWA00002571,

Protocol ID 2000027690). This PBMC project submitted by LM ("Is COVID-19 virus detectable in white blood cells") was approved by the Yale Biorepository Board of Governors. LM also has HIC approval to study de-identified pathological blood and tissues (HIC# 8810003391) as well as BSL3 certification.

A total of 18 YNHH peripheral blood monocytes (PBMC) samples were studied. The PBMC were collected and prepared by YNHH nurses, technicians and the Yale IMPACT Research Team from fresh blood and PBMC were separated using standard Ficoll-Paque™ methods, then then frozen at -80°C in DMSO-human serum; they had a nominal estimate of 5e6 cells/ml/sample. We selected PBMC samples taken as close to admission as possible to avoid unknown effects of any hospital treatments or progressive disease on viral replication or spread. All patient PBMC samples here were taken within the first week after admission and age range, gender and predisposing risk factors were broadly represented. Patients who subsequently were admitted to the ICU or intubated were excluded.

***Isolation of PBMC RNA*:** Individual 1ml PBMC in DMSO-human serum samples were thawed briefly in a 37°C water bath in the neuropathology biohazard hood BSL2+ lab, mixed gently by pipetting using 1ml pipettor tips, and transferred to 8ml MEM at 22°C with only 4-6 samples processed per day. The diluted samples were centrifuged at 700g x 10min at 22°C. The NEB Total Miniprep kit was then used as suggested with the following modifications. First, lysis of cells was carefully monitored to minimize breaking large chromatin strands. After discarding each diluted serum-DMSO supernatant, the pellet was tapped to suspend it in residual MEM, 700µl lysis buffer was added and cells allowed to lyse for ~30" followed by gentle up/down pipetting as needed to disperse lysates using a 1ml tip. Second, only the first "g" column that removes large genomic DNA was used and further DNAse treatment and column purification was avoided because total yields of PBMC RNA could be ≤1µg in 5e6 cells. The g column supernatant then bound to the RNA binding column and eluted in ~90µl H_2O; the top ~65µl away from any residual silica fines or molecular aggregates that were collected and this supernatant recentrifuged. Half (30µl) was used for GAPDH quantification and anti-viral response studies (ML-R and JC-CH) as well as for a standard analysis in triplicate of the CDC 72nt NC primer-reporter assay by the Grubaugh lab (*15*). The other half was divided into subaliquots and frozen for further nucleocapsid (NC) tests. PBMC RNA extracts represented maximally 2.5e4 cells/µl assuming a 100% recovery.

RNA Standards: A CoV19 nucleocapsid (NC) RNA, a full length CoV19 viral control at e3 from UTMB, and mock infected and CoV19 infected total cell RNA were used as controls. The

CoV19 RNA standard for the NC segment was generated as described (*15*) from full-length SARS-CoV-2 RNA (WA1_USA strain of UTMB; GenBank: MN985325) using RT/qPCR followed by T7 transcription from the complementary DNA strand. The FAM dye and BHQ1 quencher were from IDT. This NC RNA, as well as the full length viral RNA, was used for standard dilution comparisons of different real-time qPCR machines used here i.e., BioRad, Stratagene and MyGo mini S (Azura Genomics). Additionally, total cellular RNA from mock-infected and CoV19 infected Vero cells were prepared as described previously by ML-R and JC-CH (*16*). For infection, high-titer stocks of SARS-CoV-2 virus (isolate USA-WA1/2020, CoV-2 WA1) from the BEI reagent repository were obtained by passaging in Vero E6 cells with viral titers determined by plaque assay on Vero E6 cells (ATCC). Virus was cultured exclusively in a biosafety level 3 facility. Cells were infected with virus at a multiplicity of infection (MOI) of 5, and 24 hours post infection were harvested for RNA extraction using the Direct-Trizol RNA kit according to the manufacturer's instructions (Zymo Research). Mock-infected Vero cell RNA (V-) and CoV19 infected (V+) RNAs were used as paired total cellular RNA controls.

RT/qPCR: All 18 control and patient PBMC samples were initially tested in triplicate RT/qPCR in the Grubaugh lab (*15*) using the CDC primer/reporter pairs as described and compared to dilutions of the NC RNA and viral e3 RNA as standards. These standards were also used for assays done in duplicate on both Stratasys and MyGo mini qPCR machines. In addition, control mock-infected (V-) and infected (V+) Vero cell RNAs were used as paired standards with longer NC primer pairs. In these, as well as GAPDH RT/qPCR, we used the Luna Universal One-Step RT/qPCR Kit, NEB. The primers GAPDH-F: ACAACTTTGGTATCGTGGAAGG and GAPDH-R: GCCATCACGCCACAGTTTC had a thermal cycle of 55ºC for 10 minutes for RT, with denaturation at 95ºC x 1', then 45 cycles of 95ºC x 10" and 60ºC x 30" followed by a standard polishing and melting curve generation at 95ºC 1', 55ºC and 95ºC x 30". Relative RNA amounts from patients were normalized to GAPDH of the negative uninfected control PBMC.

The reference sequence for the full NC transcribed segment used for longer NC primer design (LM) was NCBI Reference Sequence: NC_045512.2 from 28274 (ATG) to 29533 with primers F3: TCTTGGTTCACCGC (orange underlined below) and R5: GCAACCATATGCCGTCT yielding a 251bp product. The F3 primer was also used with R3: GATTGCGGGTGCCAATGTG to yield a 301bp sequence reconfirmed the internal sequence of controls and positive patient samples. The relevant portion of the NC is shown with the short 72bp primers and probe in red. The new NC primers and products are shown in other colors starting with the F3 primer (underlined in orange).

Table I: NC Amplification Sequences

5'ATGTCTGATAATGGACCCCAAAATCAGCGAAATGCACCCCGCATTACGTTTGGTGGACCCTCAGATTCA
ACTGGCAGTAACCAGAATGGAGAACGCAGTGGGGCGCGATCAAAACAACGTCGGCCCCAAGGTTTACCC
AATAATACTGCGTCTTGGTTCACCGCTCTCACTCAACATGGCAAGGAAGACCTTAAATTCCCTCGAGGAC
AAGGCGTTCCAATTAACACCAATAGCAGTCCAGATGACCAAATTGGCTACTACCGAAGAGCTACCAGAC
GAATTCGTGGTGGTGACGGTAAAATGAAAGATCTCAGTCCAAGATGGTATTTCTACTACCTAGGAACTGG
GCCAGAAGCTGGACTTCCCTATGGTGCTAACAAAGACGGCATCATATGGGTTGCAACTGAGGGAGCCTTG
AATACACCAAAAGATCACATTGGCACCCGCAATC

Tests of standards with different RT/qPCR temperatures and times gave positive results with the most consistent for the 251bp F3/R5 primer pair at 360nM each was 1) RT at 56ºC x 15", 2) 95ºC x 60" and 3) 45 cycles at 95ºC x 10", 58ºC x10" annealing and 64ºC x 30" for extension with polishing and melt as for GAPDH above, again using the NEB LUNA One-step RT/PCR kit. The longer 301bp reverse R3 primer with a lower Tm was the same except the 45 cycle phase used 57ºC x 10" for annealing followed by a 59ºC x 30" extension. These reactions typically were done in a total of 14µl with 2-3µl PBMC extract to conserve sample for repeat confirmations.

Purification and sequencing of the NC 251bp and 301bp bands: Each RT/qPCR (0.5 or 1 µl sample) was resolved on mini 2.5% agarose TAE gels, the DNA stained with SYBR gold and the fluorescence imaged digitally in color using a blue emission transilluminator box with an orange barrier filter. Band purification was done as described (*17*). Briefly, the 251bp and 301bp RT/qPCR bands were cut from 2.5% preparative gels (~5µl sample load), crushed in individual mini weigh boats under parafilm and transferred to 1.5ml polypropylene tubes. Then 200-300µl H_2O added prior to freeze-thawing and centrifugation at 13,000g for 10'. Eluted supernatants were collected with a 10µl tip to avoid small gel fragments. H_2O elution/freezing was repeated two more times and SYBR gold stained DNA was followed. More than 70% of the starting band fluorescence appeared in the supernatants while the final residual agarose fluorescence was weak. An aliquot of each eluate was taken for PCR amplification and sequencing using the above NC primers, followed by a second round of band purification. SYBR gold did not interfere with sequencing; some eluates concentrated by lyophilization were washed with 70% EtOH before suspending in 50 µl H_2O. These had no fluorescence and yielded the identical sequences.

FIGURE and TABLE LEGENDS

FIG. 1: Melt temperature (Tm) of RT/qPCR nucleocapsid (NC) products using different NC primer pairs. Note the short CDC:N1 product of 72bp has the lowest Tm while the longest F3/R3 pair (301bp) has the highest Tm. Each primer pair Tm product is significantly different (see text).

FIG. 2: A 2.5% agarose gel showing RT/qPCR products from **A**) the F3/R5 primer synthesized 251bp band and **B**) the 301bp band produced using the F3/R3 primer pair. Positive controls include full length nucleocapsid RNA genome (lanes G) a viral RNA control (lane e), total RNA from CoV19 infected Vero cells (V+ lanes). Negative controls include uninfected Vero cell RNA (V-) and water (w). PBMC from control uninfected "normal" (n1-4 lanes) and admitted patients with representative samples numbered with an asterisk (*) are compared. The duplicate 18* lane is from a different aliquot of that patient's PBMC in another RT/qPCR run (lanes 14-15). A dot is at 300bp in the 100bp ladder marker lanes. SYBR Gold fluorescent DNA is inverted for publication. Patient extracts show some additional artefactual products and smears most consistent with DNA in these samples. Some artefactual bands are sample specific, e.g., patient 12* has a strong sample-specific ~150bp gel band in A, and B shows an ~360bp band in lanes 11 and 14. Each duplicate in B is also from a different run with a different aliquot of that extract.

FIG. 3: Tm of representative peaks from above gel where **A)** shows the 251bp product. A few smaller peaks with different Tms than the 251bp band are seen and could be thresholded. Note the consistency of all NC positive band peaks. The low fluorescent dimer at a Tm at ~81°C is seen in 2 samples (longer black arrow) and a longer faint product, visible on the gel ($\geq$300bp) in 23* is also apparent (short orange arrow) at a Tm of ~89°C. **B**) demonstrates background and non-specific primer dimer peaks, including in the H_2O control (aqua) that interfered with Ct in contrast to the melts in A. The higher Tm peaks in 14* and 18* on gels looked the same, but had big Tm differences indicating they were sample specific artefact bands.

Table I: NC amplified sequences in color downstream from the MET start codon. The 72, 251 and 301bp products sequences are colored with respective primer pairs underlined in different colors. R3 is in green and R5 in orange. The 251bp product is in aqua and the 301bp longer product ends at R5. These amplified RT/qPCR products encompass a substantial (33%) portion of the entire NC RNA that codes for the 455aa nucleocapsid protein.

FIG. 1

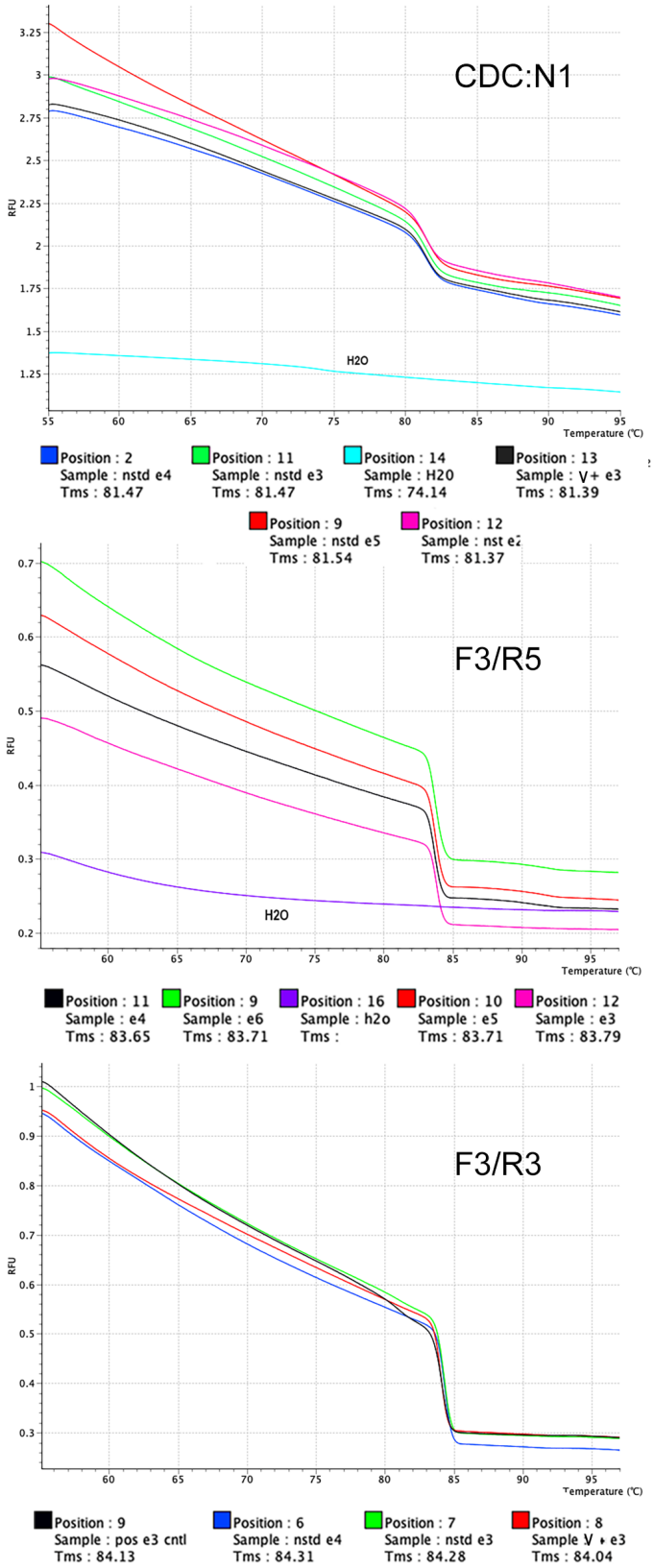

CDC:N1
RFU
Temperature (°C)
H2O
Position : 2
Sample : nstd e4
Tms : 81.47
Position : 11
Sample : nstd e3
Tms : 81.47
Position : 14
Sample : H20
Tms : 74.14
Position : 13
Sample : V+ e3
Tms : 81.39
Position : 9
Sample : nstd e5
Tms : 81.54
Position : 12
Sample : nst e2
Tms : 81.37
F3/R5
RFU
Temperature (°C)
H2O
Position : 11
Sample : e4
Tms : 83.65
Position : 9
Sample : e6
Tms : 83.71
Position : 16
Sample : h2o
Tms :
Position : 10
Sample : e5
Tms : 83.71
Position : 12
Sample : e3
Tms : 83.79
F3/R3
RFU
Temperature (°C)
Position : 9
Sample : pos e3 cntl
Tms : 84.13
Position : 6
Sample : nstd e4
Tms : 84.31
Position : 7
Sample : nstd e3
Tms : 84.28
Position : 8
Sample V + e3
Tms : 84.04

FIG. 2

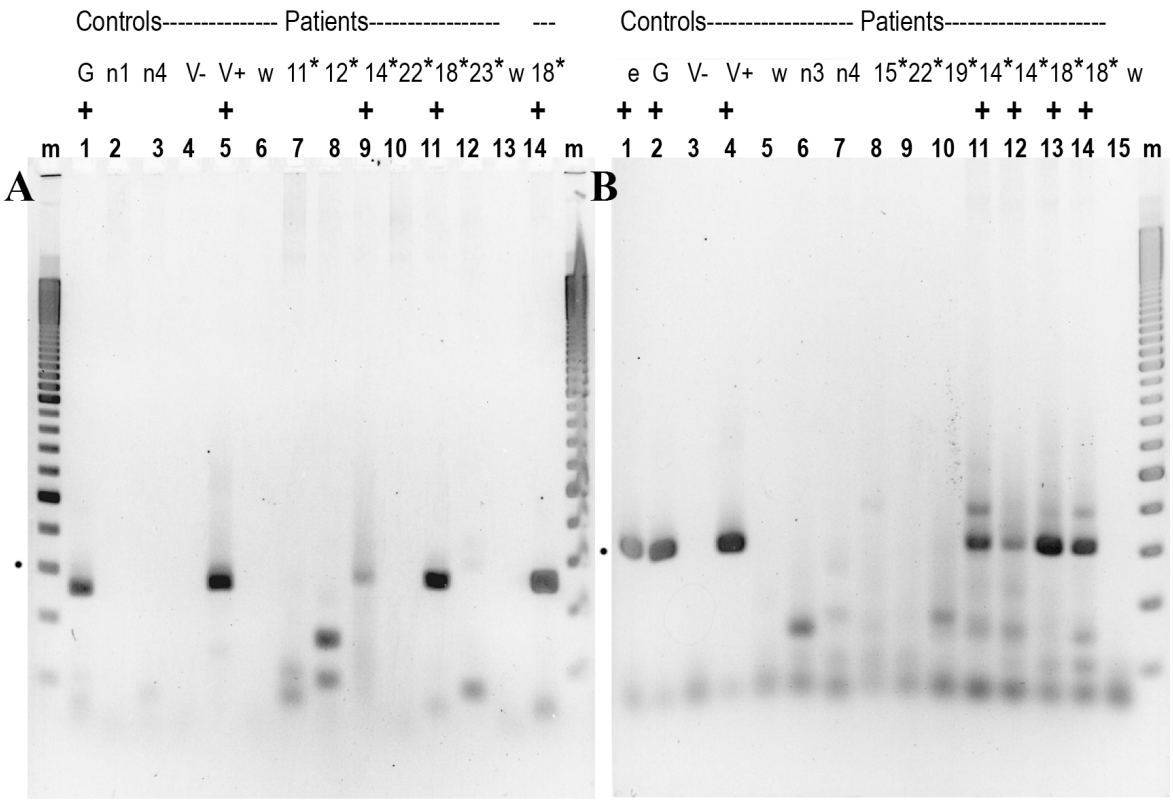
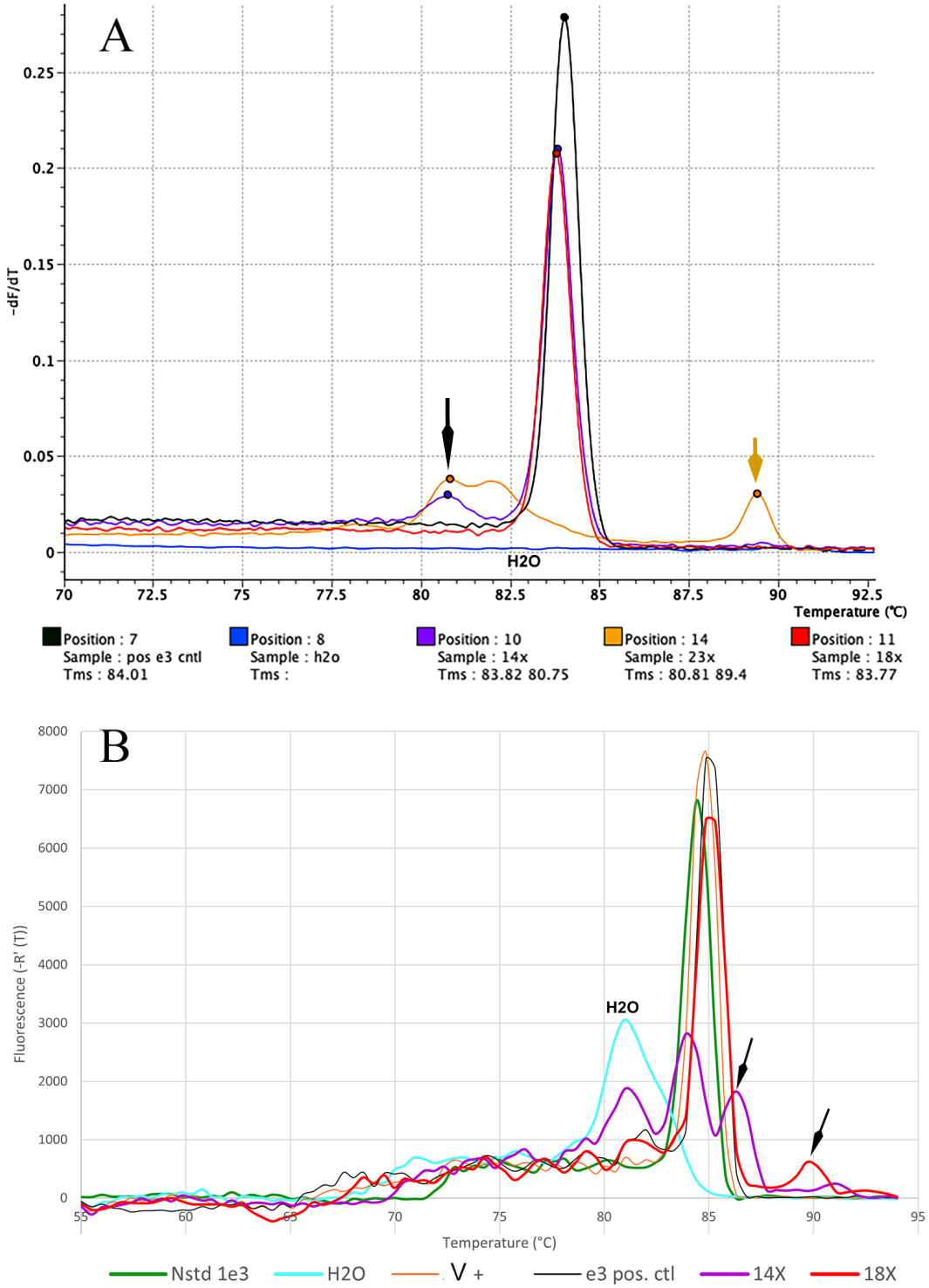

A
Controls---------- Patients---------- ---
G n1 n4 V- V+ w 11* 12* 14* 22* 18* 23* w 18*
+ + + + +
m 1 2 3 4 5 6 7 8 9 10 11 12 13 14 m
B
Controls---------- Patients----------
e G V- V+ w n3 n4 15* 22* 19* 14* 14* 18* 18* w
+ + + + + + + +
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 m

FIG. 3


A
-dF/dT
0.25
0.2
0.15
0.1
0.05
0
H2O
70
72.5
75
77.5
80
82.5
85
87.5
90
92.5
Temperature (°C)
Position : 7
Sample : pos e3 cntl
Tms : 84.01
Position : 8
Sample : h2o
Tms :
Position : 10
Sample : 14x
Tms : 83.82 80.75
Position : 14
Sample : 23x
Tms : 80.81 89.4
Position : 11
Sample : 18x
Tms : 83.77
B
Fluorescence (-R' (T))
8000
7000
6000
5000
4000
3000
2000
1000
0
H2O
55
60
65
70
75
80
85
90
95
Temperature (°C)
Nstd 1e3
H2O
V +
e3 pos. ctl
14X
18X

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