Our study is necessarily limited by its single-center, retrospective design and small cohort size. Although the patients who were and were not receiving antifibrotic therapy at the time of transplant were largely similar regarding disease severity and clinical characteristics, the rationale for treatment differences were not captured and may introduce possible bias.

In conclusion, we found that pretransplant antifibrotic therapy in our cohort is safe and associated with improved resolution of PGD as well as decreased incidence of airway stenosis and LB. Randomized prospective studies should establish if antifibrotic therapy has a role in the peri–lung-transplant period. ■

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Presence of SARS-CoV-2 Aerosol in Residences of Adults with COVID-19

To the Editor:

Although vaccines are effective at preventing coronavirus disease (COVID-19), uncertainty remains about practical public health responses to vaccine-resistant variants or future novel respiratory viruses. Reducing attack rates in households, estimated to be as high as 54% in the United States, is a key strategy (1). In addition to close physical contact, emerging opinion suggests that airborne transmission is linked to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spread, particularly in lower-socioeconomic-status households with greater crowding, even if isolation and personal protective equipment minimize large particle transmission (2–5).

The size-dependent airborne behavior of particles originating from the respiratory tract has a continuous distribution from tens of nanometers to tens of microns. Recognizing this continuity, there are two primary pathways, requiring different control strategies, by which respiratory viral infections spread through air to others. First, larger respiratory droplets that rapidly settle onto surfaces, typically within 1–2 meters of the source, are amenable to hand hygiene, social distancing, and face masks. Second, albeit with more limited direct evidence, is aerosolization and spread of smaller respiratory droplets, or droplet nuclei, primarily <0.5 micrometers in final size, capable of staying suspended in air

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Author Contributions: R.J.L., G.M., K.B.G., and H.M.K. conceived of the study, trained and supervised field staff, and drafted the manuscript. S.A. oversaw air sampling. N.T.M., P.O.-S., and F.T.L. assisted with data analysis and interpretation. A.L., A.d.R., and L.C. performed air sampling and assisted with data handling. S.H. assisted with recruitment of subjects and writing.

Table 1. Participant demographics, saliva C_T counts on day of sampling, whether the index participant had a cough, the number of individuals residing in the home, and whether any were reported to have been positive

Home	Age (*yr*)	Sex	N Gene	ORF1-AB Gene	S Gene	Household Members (*n*)	Other Reported Positive*	Participant Cough
1	40	Male	24.3	23.7	23.6	2	Yes	Yes
2	46	Female	16.9	16.7	16.7	4	Yes	Yes
3	31	Male	25.0	24.7	25.0	1	N/A	No
4	47	Female	23.9	22.2	24.0	4	Yes	Yes
5	61	Female	33.7	30.9	ND	2	No	No
6	65	Female	25.5	26.3	26.8	5	No	Yes
7	30	Female	27.5	27.7	27.4	1	N/A	Yes
8	64	Male	26.3	27.9	27.4	2	No	No
9	37	Male	17.7	17.3	17.0	3	No	Yes
10	47	Male	28.1	27.5	27.7	4	Yes	No
11	62	Female	25.1	25.0	25.0	2	No	Yes

Definition of abbreviations: COVID-19 = coronavirus disease; C_T = cycle threshold; N/A = not applicable; ND = not detected.
*Based on participant response to the question: "Do any of the other people staying in your home during this study have a recent positive COVID-19 test (within the past week) or current COVID-19 symptoms?"

Table 2. The presence of SARS-CoV-2 RNA in air samples in 11 homes with subjects testing newly positive for COVID-19

	Isolation Room				Common Room			
Home	N Gene	ORF1-AB Gene	S Gene	Subject Present (*h*)*	N Gene	ORF1-AB Gene	S Gene	Subject Present (*h*)*
1†	ND	ND	ND	16	—	—	—	0
2†	**34.3**	ND	**36.6**	24	—	—	—	0
3	ND	ND	ND	22.5	ND	ND	ND	0
4	**31.4**	**28.5**	**28.8**	10	ND	**34.5**	**36.4**	14
5	**35.8**	**32.8**	**33.1**	17	**32.0**	**30.9**	**31.6**	7
6	ND	**34.4**	ND	23.5	ND	ND	ND	0.5
7	ND	ND	ND	17	ND	**33.7**	**36.8**	7
8	ND	ND	ND	22	ND	**35.8**	ND	2
9	**32.1**	**31.3**	ND	12	**32.2**	**31.6**	**32.0**	4
10	ND	ND	ND	13	ND	ND	ND	10
11	ND	**34.7**	**36.2**	14	ND	**34.9**	ND	8
Homes detected	4	5	4	—	2	6	4	—

Definition of abbreviations: COVID-19 = coronavirus disease; C_T = cycle threshold; ND = not detected; SARS-CoV-2 = severe acute respiratory syndrome coronavirus 2.
Bolded C_T counts represent positive (<37) samples for each gene in each room.
*Number of hours out of 24 that participants reported being in each room. Total hours may be less than 24 because of time spent in other rooms.
†Common room air samples for homes 1 and 2 were invalid for technical reasons.

for hours and requiring filtering or ventilation for interdiction (2–4). We report the first naturalistic observations of household air contamination with SARS-CoV-2 RNA. We know of no prior reports of air sampling for SARS-CoV-2 RNA in homes without manipulation of the behavior or activity of participants.

Rutgers Institutional Review Board approved this study, and participants provided informed consent.

Methods

Recruitment occurred in fall and winter of 2020–2021 through an e-mail flyer at the time of notification of test positivity. Adults testing positive within the prior 7 days were eligible to participate. Saliva screening at the first home visit verified continued positivity (Table 1).

Air samples were collected for 24 hours on polytetrafluoroethylene (PTFE) filters (SKC Inc.) in two separate rooms (if available) in each participant's home using an open-face filter holder and Leland Legacy pump (SKC Inc.) operated at 10 L/min. Samples were eluted in RNA-grade water and analyzed by reverse-transcriptase polymerase chain reaction (RT-PCR) for the presence of three SARS-CoV-2–specific genes. There is no universal protocol for RT-PCR testing of SARS-CoV-2, let alone for its analysis in environmental samples (6). Our selected laboratory (Infinite BiologiX) used a U.S. Food and Drug Administration–approved procedure developed at Rutgers to target three genomic regions of SARS-CoV-2: nucleocapsid (N) gene, spike (S) gene, and open reading frame-AB (ORF1-AB) region. To maximize detection sensitivity, we assessed presence (cycle threshold [C_T] < 37) or absence of each gene in our air samples (7). The selected rooms were defined as the isolation room (the room used primarily, but not exclusively, by the subject) and the common room (a separate but adjacent room). Participants recorded hours spent in both rooms during

sampling, but instructions for self-isolation were not provided. Samplers were placed 1 meter away from the nearest wall and away from vents, windows, traffic flow, and obstructing furniture where possible. Samplers faced downward to avoid large droplets. The study included 11 homes (Table 1) with 20 air samples (60 individual SARS-CoV-2 gene RT-PCR tests) collected from 11 isolation rooms and 9 common rooms (Table 2).

Results

In addition to the primary case, one or more known or suspected recently positive individuals were reported to be present in 4 of 11 (36%) homes at the time of sampling. During sampling, participants reported spending between 10 and 24 hours in the isolation room. Seventy-three percent of participants reported spending some time in the common room (range 0–14 h) and 45% of participants reported time in other areas of the home (range 0–8 h).

For each of the three genes, the percentage of homes with a positive air sample ranged from 36% to 45% in the isolation room and from 22% to 67% in the common room. Eight homes out of 11 (73%) had at least one gene detected, and 5 of 11 isolation room samples had at least two genes detected. Six of nine homes with sampling in both the isolation room and common room had at least one gene detected in the common room (Table 2), and four of these common rooms had two genes detected. Seven of these nine homes reported no other cases in the household (Table 1), including the two living alone, and in five of these homes, the common room was positive for viral aerosols. An additional occupant who recently tested positive or had symptoms consistent with COVID-19 was present in only two of seven (29%) homes with multiple occupants and a valid common room test.

Discussion

Our results provide strong empirical support that aerosols of small respiratory droplets and nuclei containing airborne SARS-CoV-2 RNA are present both within and outside of home isolation rooms, presenting infection risk beyond close contact with other occupants.

Our indoor air sampling data clearly demonstrate that measurable airborne SARS-CoV-2 RNA is present in home air of most infected individuals. We found SARS-CoV-2 viral RNA, likely as both free virus and bound to other particulate matter (PM), not only in the isolation room but, importantly, elsewhere in the home (common room), consistent with high risk of home airborne transmission. Previously, detection of airborne SARS-CoV-2, likely as part of PM, has been limited to the hospital or clinic setting (8–12), an automobile cabin (13), and two reports identifying it in outdoor PM samples (14, 15).

Further buttressing our findings is a study of viral aerosols measured only in isolation rooms of apartments at a specified distance of 2 meters from the participant, using a 20-minute scripted (nonnaturalistic) air sampling protocol (16). Our novel empirical findings support the hypothesis that exposure to airborne small droplets and/or droplet nuclei is a pathway for COVID-19 transmission and a candidate explanation for high household attack rates (1).

Despite models, laboratory experiments, and theory-based discussions, previous field data have not empirically addressed or clarified the relative importance of real-world exposure pathways that must be interdicted to prevent transmission of COVID-19. Studies are needed with adequate power and definitive assessment of infection status of all household members, their locations within the household, clear discrimination between aerosols and larger droplets by size-selective sampling, and assessment of aerosolized virus viability (12). ■

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