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RESEARCH ARTICLE

Household transmission of seasonal coronavirus infections: Results from the Flu Watch cohort study [version 1; peer review: 1 approved, 2 approved with reservations]

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v1 **First published:** 19 Jun 2020, **5**:145
https://doi.org/10.12688/wellcomeopenres.16055.1
Latest published: 19 Jun 2020, **5**:145
https://doi.org/10.12688/wellcomeopenres.16055.1

Abstract

Background: In the context of the current coronavirus disease 2019 (COVID-19) pandemic, understanding household transmission of seasonal coronaviruses may inform pandemic control. We aimed to investigate what proportion of seasonal coronavirus transmission occurred within households, measure the risk of transmission in households, and describe the impact of household-related factors of risk of transmission.
Methods: Using data from three winter seasons of the UK Flu Watch cohort study, we measured the proportion of symptomatic infections acquired outside and within the home, the household transmission risk and the household secondary attack risk for PCR-confirmed seasonal coronaviruses. We present transmission risk stratified by demographic features of households.
Results: We estimated that the proportion of cases acquired outside the home, weighted by age and region, was 90.7% (95% CI 84.6- 94.5, *n*=173/195) and within the home was 9.3% (5.5-15.4, 22/195). Following a symptomatic coronavirus index case, 14.9% (9.8 - 22.1, 20/134) of households experienced symptomatic transmission to at least one other household member. Onward transmission risk ranged from 11.90% (4.84-26.36, 5/42) to 19.44% (9.21-36.49, 7/36) by strain. The overall household secondary attack risk for symptomatic cases was 8.00% (5.31-11.88, 22/275), ranging across strains from 5.10 (2.11-11.84, 5/98) to 10.14 (4.82- 20.11, 7/69). Median clinical onset serial interval was 7 days (IQR= 6-9.5). Households including older adults, 3+ children, current smokers, contacts with chronic health conditions,

Open Peer Review

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	1	**2**	**3**
version 1 19 Jun 2020	? report	? report	✓ report

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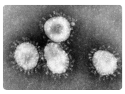
and those in relatively deprived areas had the highest transmission risks. Child index cases and male index cases demonstrated the highest transmission risks.
Conclusion: Most seasonal coronaviruses appear to be acquired outside the household, with relatively modest risk of onward transmission within households. Transmission risk following an index case appears to vary by demographic household features, with potential overlap between those demonstrating the highest point estimates for seasonal coronavirus transmission risk and COVID-19 susceptibility and poor illness outcomes.

Keywords
coronavirus, HCoV-NL63, HCoV-OC43, HCoV-229E, SARS-CoV-2, epidemiology



This article is included in the Coronavirus (COVID-19) collection.

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Author roles: Beale S: Conceptualization, Data Curation, Formal Analysis, Investigation, Methodology, Writing – Original Draft Preparation; **Lewer D**: Conceptualization, Investigation, Methodology, Writing – Review & Editing; **Aldridge RW**: Conceptualization, Investigation, Methodology, Supervision, Writing – Review & Editing; **Johnson AM**: Investigation, Methodology, Writing – Review & Editing; **Zambon M**: Conceptualization, Methodology, Resources, Writing – Review & Editing; **Hayward A**: Conceptualization, Funding Acquisition, Investigation, Methodology, Supervision, Writing – Review & Editing; **Fragaszy E**: Conceptualization, Data Curation, Funding Acquisition, Investigation, Methodology, Supervision, Writing – Review & Editing

Competing interests: AH serves on the UK New and Emerging Respiratory Virus Threats Advisory Group. AMJ was a Governor of Wellcome Trust from 2011-18 and is Chair of the Committee for Strategic Coordination for Health of the Public Research. The other authors declare no competing interests.

Grant information: This project was supported by the Wellcome Trust through funding to the Flu Watch Study [091011]. The Flu Watch study received funding from the Medical Research Council (MRC) and the Wellcome Trust [091011, G0600511, G0800767 and MC_U122785833]. SB is supported by an MRC doctoral studentship [MR/N013867/1]. The funders were not actively involved in the design, delivery, or analysis of this research. The views expressed in this publication are those of the authors and not necessarily of the MRC or the Wellcome Trust. AH is an NIHR Senior Investigator. The views expressed in this Article are those of the authors and not necessarily those of the NIHR, or the Department of Health and Social Care.
The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

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How to cite this article: Beale S, Lewer D, Aldridge RW *et al.* **Household transmission of seasonal coronavirus infections: Results from the Flu Watch cohort study [version 1; peer review: 1 approved, 2 approved with reservations]** Wellcome Open Research 2020, **5**:145 https://doi.org/10.12688/wellcomeopenres.16055.1

First published: 19 Jun 2020, **5**:145 https://doi.org/10.12688/wellcomeopenres.16055.1

Background

Understanding household transmission parameters is important for outbreak modelling and response as coronavirus disease 2019 (COVID-19) becomes established in communities worldwide. While studies are currently underway, developing robust estimates for household transmission parameters will take some time. Evidence from other human coronaviruses may therefore be useful, given similar routes of transmission[1,2].

Outbreaks of other emerging coronaviruses, i.e. severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS), appear to be primarily based in health care settings without substantial community transmission and household transmission studies are limited. Estimates of transmission risk to at least one other household member following a SARS index case range from 12.3%–13.5%, with estimated secondary household attack risks between 4.6%–10.2%[3–5]. In index cases, younger age and healthcare worker status were associated with lower risk of household transmission. A single study of MERS found that 44% of households with an index case experienced onwards transmission, with a secondary attack risk of 24% and risk factors for developing secondary infection in contacts including being adult, male, and having long-term conditions[6].

Seasonal coronavirus infections also appear to cluster within households[7], with proportions of onwards transmission to at least one household member following child index cases ranging between 8% and 33%[8,9]. A recent community cohort study based in Michigan[10] found secondary attack risks ranging from 7.2%–12.6% for circulating seasonal coronavirus strains and clinical-onset serial intervals between 3.2–3.6 days.

Here we aimed to report key characteristics of seasonal coronavirus household transmission in a population-based UK cohort, using data from the Flu Watch study[11]. We present the proportion of laboratory-confirmed seasonal coronavirus infections acquired within and outside the household, the household transmission risk and secondary attack risk for symptomatic cases, the clinical-onset serial interval, and transmission risk stratified by demographic household features.

Method

Study design and procedures

Data were drawn from the Flu Watch prospective cohort study of acute respiratory infections in English households[11]. We included the three winter seasons (2006–2007, 2007–2008, 2008–2009), during which all samples were systematically tested for coronaviruses. The Flu Watch study methodology and cohort profile are described in detail elsewhere[11,12].

Whole households were recruited annually to the study following random selection of a household member from GP practice lists. From 2008–2009, participants from the previous cohort were also re-invited to participate. Inclusion criteria were that all household members agreed to participate, and all members over 16 agreed to provide blood samples for other Flu Watch research. Exclusion criteria were household size >6 members, severely incapacitating or terminal illness in any household member, and heavy involvement in other research[12].

Participants provided demographic data at seasonal baseline following recruitment, and were followed-up weekly via telephone or online throughout each season to report any symptoms of acute respiratory infection. If participants experienced any symptoms, they were requested to provide a nasal swab on the second day of illness and to provide a daily diary of symptoms from the first day of illness until the symptoms resolved. Real-time PCR was carried out to screen nasal swabs for a panel of viruses, including three circulating seasonal coronavirus strains (229-E, NL63, and OC43)[11].

Definitions and analyses

Guided by an estimated incubation period of 2–5 days and further 2–18 days of symptomatic illness with viral shedding for seasonal coronaviruses[13,14], we defined index cases as the first PCR-confirmed infection in a household or >23-days following a prior case, co-primary cases as potential index cases of the same strain arising within ≤2 days, and secondary cases as infections with the same strain occurring >2 days and ≤23 days from exposure to the index case(s). We assumed that household transmission to any secondary cases had occurred if the strain was unknown, but criteria for transmission were otherwise met.

We estimated the proportions of total PCR-confirmed coronavirus cases in the study likely acquired in the community (i.e. index, co-primary, or single-person household cases) and acquired in the household (i.e. secondary cases). The proportions were weighted to the English national structure of age and region[11].

For households in which secondary transmission was possible (i.e. excluding single-person households and episodes of co-primary infection affecting all household members), we calculated the symptomatic household transmission risk– the proportion of households that experienced at least one secondary case – and the household secondary attack risk – the proportion of total exposed participants who became secondary cases. To avoid multiple inclusions of the same episode where there were co-primary cases, transmission risk and secondary attack risk were estimated based on a randomly-selected single index case. Due to the testing protocol, it was not possible to detect asymptomatic primary or secondary cases. We calculated the clinical-onset serial interval as the time in days from onset of reported symptoms in the index case(s) to onset of reported symptoms of the secondary case(s). All co-primary or multiple secondary cases in this cohort reported symptom onset on the same day.

We stratified the household symptomatic transmission risk by the following household features potentially relevant to transmission: the age structure of the household (adults between 16–64 only, older adult(s), adult(s) and children), age of index case (child <16, adult 16-64, older adult 65+) for households with children (not stratified for other household structures due to

limited variation), the number of people and number of children in the household, whether the household contained current smoker(s), index of multiple deprivation, long-term health conditions in household contact(s), and the index sex, index healthcare worker status and index transmission-preventive hygiene behaviour. Index case hygiene behaviour was classified as a binary variable according to adherence to prevention guidelines[15,16] i.e. covering the mouth while coughing or sneezing, using a single-use tissue, and washing the hands habitually after coughing or sneezing and at least moderately-frequently throughout the day (>=5 times according to median split and previous literature[17]). Due to the small number of household transmissions, we present descriptive stratified analyses only and do not describe by strain sub-groups. Where features of the index case or index-exposed dyads were investigated, we included only those households where there was a clear index case rather than co-primary cases. Any instances of missing demographic data are noted in Table 1.

Table 1. Household transmission risk stratified by demographic features of household.

	Transmission Risk % (95% CI)	Transmission Occurred *n* (column %)	
		Yes	No
Household structure			
Adults only	9.09 (3.38, 22.21)	4 (20.00)	40 (35.09)
Older adult(s)	25.00 (10.47, 48.73)	5 (25.00)	15 (13.16)
Adult(s) and child(ren)	15.71 (8.84, 26.40)	11 (55.00)	59 (51.75)
Number of children			
0	14.06 (7.40, 25.10)	9 (45.00)	55 (48.25)
1	0.00 (n/a)	0 (0.00)	27 (23.68)
2	21.88 (10.60, 39.80)	7 (35.00)	25 (21.93)
3+	36.36 (13.47, 67.71)	4 (20.00)	7 (6.14)
Smoker(s) in household[a]			
Yes	28.57 (10.61, 57.42)	4 (22.22)	10 (9.52)
No	12.84 (7.70, 20.66)	14 (77.78)	95 (90.48)
IMD			
1-2 (lower)	23.08 (10.50, 43.41)	6 (30.00)	20 (17.55)
3	12.20 (5.07, 26.53)	5 (25.00)	36 (31.58)
4	13.89 (5.78, 29.78)	5 (25.00)	31 (27.19)
5 (higher)	12.90 (4.80, 30.32)	4 (20.00)	27 (23.68)
Contact(s) with chronic condition[b]			
Yes	16.67 (7.54, 32.92)	6 (33.33)	30 (27.03)
No	12.90 (7.41, 21.51)	12 (66.67)	81 (72.97)
Index age* **(households with children)**			
Adult	12.90 (4.75, 30.58)	4 (44.44)	27 (52.94)
Child	17.24 (7.11, 36.10)	5 (55.56)	24 (47.06)
Index healthcare worker*			
Yes	0.00 (n/a)	0 (0.00)	7 (6.60)
No	15.38 (9.85, 23.23)	18 (100.00)	99 (93.40)
Index hygiene* [c]			
Yes (all recommendations)	0 (n/a)	0 (0.00)	13 (12.87)
No	16.98 (10.89, 25.50)	18 (100.00)	88 (87.13)
Index sex*			
Male	18.46 (10.69, 29.99)	12 (66.67)	53 (50.00)
Female	10.17 (4.57, 21.11)	6 (33.33)	53 (50.00)

* outbreaks with clear index case only (*n*=10 outbreaks with co-primaries excluded); [a] unavailable for *n*=11 outbreaks; [b] unavailable for *n*=5 outbreaks; [c] unavailable for *n*=5 outbreaks; abbreviations: CI = confidence interval, IMD = indices of multiple deprivation.

To estimate potential non-detection of household transmissions due to non-adherence to swabbing protocol, we measured the proportion of exposed participants who reported symptoms within one month of an index case but did not submit a nasal swab. Analyses were performed in Stata Version 15.

Results

Proportion of infections acquired in the households and features of transmission

Table 2 reports the proportion of infections acquired within and outside of the household and the symptomatic transmission risk, secondary attack risk, and clinical-onset serial interval by strain and overall.

There were a total of 195 coronavirus cases during the three seasons in households in which transmission was possible, of which a weighted proportion of 90.66% (95% CI 84.60-94.49, 173/195) were index or co-primary cases presumably acquired in the community, and 9.34% (5.51-15.40, 22/195) were in exposed household members and presumed to be acquired through household transmission. The proportion of presumed household-acquired infections ranged across strains from 6.18% (1.92-18.12, 5/60) for NL63, to 10.59% (4.71-22.09, 10/80) for OC43, and 12.15% (5.01-26.60, 7/52) for 229E. Strain data was unavailable for three cases.

There were 134 potential household outbreaks with a coronavirus index case or co-primary cases. All 22 co-primary cases from 10 households occurred on the same day. Of the 134 potential outbreaks, 22 had transmission to at least one other household member giving an overall household transmission risk of 14.93% (95% CI: 9.78-22.11). Across strains, household transmission risk ranged from 11.90% (4.84-26.36, 5/42) for NL63, 13.21% (6.27-25.72, 7/53) for OC43, and 19.44% (9.21-36.49, 7/36) for 229E.

A total of 22 exposed participants contracted a coronavirus infection, out of 275 participants at risk (excluding index and co-primary cases), yielding a household secondary attack risk of 8.00% (95% CI: 5.31-11.88, 22/275) overall. Secondary attack risks by strain were 5.10% (2.11-11.84, 5/98) for NL63, 8.73% (4.56-16.10, 9/103) for OC43, and 10.14% (4.82-20.11, 7/69) for 229E. Due to unknown index strain, outbreak strain was unavailable for five exposed participants.

The median clinical-onset serial interval was 7 days (IQR = 6-9.5 days, range 5-21 days). This median value was consistent for 229E and NL63, with some between-strain variation in range, and similar to the OC43 median serial interval of 6.5 days. There were two households for which the exact date of symptom onset of the exposed case could not be traced (only the beginning date of the week of illness), which were excluded from the serial interval calculation.

Demographic features and transmission Risk

Table 1 reports household symptomatic transmission risk stratified by demographic features of households. Transmission risks were highest for households containing older adults (25.00%, 95% CI 10.47, 48.73), households with children (15.71%; 8.84, 26.40), then adult-only households (9.09%; 3.38, 22.21). Households with 3+ children (36.36%; 13.34, 67.96), those with smokers (28.57%; 10.61, 57.42), those in deprived areas (23.08%; 10.50, 43.41), and those in which 1+ household contact had a chronic health condition (16.67%; 7.54, 21.51) had the highest transmission risks within their categories. In households with children, child index cases demonstrated higher transmission risk (17.24%; 7.11, 36.10) than adult index cases (12.90%; 4.75, 30.58). Male index cases also demonstrated higher transmission risk (18.46; 10.69, 29.99) than female index cases (10.17%; 4.57, 21.11). There was no evidence of onward transmission if the index case was a healthcare worker or if they practiced good hand and respiratory hygiene, though the number of index cases in these categories were low (n= 7 and 13 respectively).

Adherence to swabbing protocol during household outbreaks

Among the 275 exposed household members, there were 75 distinct episodes of respiratory symptoms within 23 days of a household coronavirus index case. For 4 of these episodes

Table 2. Community and household-acquired infections and features of household transmission.

	229E	NL63	OC43	All*
Infections acquired in community: % (95% CI, n/N)	87.85 (73.40-94.99, 45/52)	93.82 (81.88-98.08, 55/60)	89.41 (77.91-95.29, 70/80)	90.66 (84.60- 94.49, 173/195)
Infections acquired in household: % (95% CI, n/N)	12.15 (5.01-26.60, 7/52)	6.18 (1.92-18.12, 5/60)	10.59 (4.71-22.09, 10/80)	9.34 (5.51-15.40, 22/195)
Household transmission risk: % (95% CI, n/N)	19.44 (9.21-36.49, 7/36)	11.90 (4.84-26.36, 5/42)	13.21 (6.27-25.72, 7/53)	14.93 (9.78-22.11, 20/134)
Secondary attack risk: % (95% CI, n/N)	10.14 (4.82- 20.11, 7/69)	5.10 (2.11-11.84, 5/98)	8.73 (4.56-16.10, 9/103)	8.00 (5.31-11.88, 22/275)**
Serial interval (days): Mdn (IQR, range)	7.0 (6.0-21.0, 5.0-21.0)	7.0 (6.0-7.5, 6.0-8.0)	6.5 (6-8.75, 6.0-14.0)	7.0 (6.0-9.5, 5.0-21.0)

*All strains include cases where strain was unknown (n=3); **due to unknown index strain, n=5 exposed contacts were included with no outbreak strain recorded.

(5.33%), the participant did not provide a swab at any point during their illness.

Discussion

The study describes a range of important characteristics of seasonal coronavirus transmission that have not previously been reported. The great majority of infections (91%) were acquired outside the household. Following a symptomatic index case within the household, onward transmission to at least one other household member occurred in 14.9% of households, with a secondary attack risk of 8.0%. Risk of onwards household transmission fell within previous estimates for seasonal coronaviruses[8,9] and were higher than the limited literature suggests for SARS[3–5], but lower than for MERS[6]. The secondary attack risk fell within the range identified for seasonal coronavirus strains in a recent US-based longitudinal cohort study[10] and was somewhat lower than preliminary estimates of the household secondary attack risk for COVID-19 - ranging between 10.5% in USA[18], 13.6% in Taiwan[19]; 14.9% in Shenzen, China[20], and 31.6% in Zhejiang Province, China[21]. Our estimate for the median clinical-onset serial interval (7 days) was larger than Monto *et al.*'s (2020) estimate[10] (3.2-3.6 days), though this may reflect different handling of potentially co-primary cases, as only an upper-bound distance between cases was specified in the latter study.

Since the virus causing COVID-19 is a recently emerged pathogen there is likely to be minimal population immunity, this contrasts with seasonal coronaviruses, where results from the Flu Watch study show a protective effect of recent infection[22]. This may contribute to higher household secondary attack risk in COVID-19 than in seasonal coronavirus. Given emerging evidence that some individuals with asymptomatic or pre-symptomatic SARS-CoV-2 infections may be capable of transmitting the virus to others[23–26], preventing household transmission of SARS-CoV-2 may be notably challenging. Recent COVID-19 household transmission studies have also occurred during periods when there have been stringent measures to control transmission. Intensified hand and respiratory and environmental cleaning during a pandemic may decrease household transmission. Measures that ensure families stay at home together may increase household secondary attack risk by increasing the level of contact in the home. In the current study the majority of infections were acquired outside the household. The proportion of infections acquired outside the household is likely to be lower during periods of social distancing[27]. We have previously shown that conducting a wide range of activities outside the household, including visiting supermarkets, shops, restaurants, places of worship and using public transport, increase the risk of acquiring acute respiratory infection[28].

Demographic and health-related characteristics with the highest point estimates for symptomatic transmission risk overlapped with risk groups for susceptibility and/or poor outcomes in COVID-19, namely households comprising older adults, current smokers, exposed members with chronic illness, and those in deprived areas[29–31]. Although children had a higher point estimate for transmission risk, index cases were distributed relatively evenly across age groups, in contrast with a Michigan community cohort study in which children comprised the majority of index cases for most strains[10]. Good hand and respiratory hygiene by index cases may be helpful for disrupting transmission, possibly overlapping with the lack onwards transmission from healthcare workers. The findings should be interpreted with caution given relatively small numbers of positive transmissions and, related, wide confidence intervals for transmission risk estimates. We were underpowered to conduct multivariate analysis required to disentangle the interrelationships between potential demographic and health-related risk factors and this is a relevant area for further research concerning seasonal and pandemic coronaviruses.

This study had a number of limitations. Data were limited to winter seasons. Only symptomatic cases were swabbed and detected. While there appeared to be good adherence to the swabbing protocol among household members exposed to an index case, five percent of those who developed symptoms following exposure failing to provide a swab so secondary transmission may be underestimated. It is possible that the nasal swabbing protocol, which was developed primarily for influenza detection, did not provide ideal sensitivity for these strains of coronavirus. We also cannot exclude that index cases in the initial weeks of the study could have acquired the case through undetected household transmission. The analyses did not account for background rate of infection in the community and consequently some apparent secondary cases may have been acquired incidentally outside of the household. All risk factor analyses were limited by a relatively small number of onward transmissions.

To our knowledge, this study presents the first investigation into household transmission in seasonal coronaviruses in a population-based UK sample. In typical winter seasons with individuals freely able to continue typical activities and social contacts, household transmission appears to be lower than in COVID-19. However, this difference may reflect different levels of population immunity and behaviours rather than intrinsic differences in the transmissibility of seasonal coronaviruses and the pandemic strain. The high proportion of infections acquired outside the household reinforces Stay at Home messages. Corresponding population-based studies investigating COVID-19 household transmission - such as the UK Virus Watch study, modelled on the Flu Watch study used here - are warranted to inform transmission models and public health interventions.

Ethics statement

The protocol was approved by the Oxford Multi-Centre Research Ethics Committee (06/Q1604/103).

Data availability

Underlying data

University College London: Household Transmission of Seasonal Coronavirus Infections: Results from the Flu Watch cohort study. https://doi.org/10.5522/04/12383873.v1

This project contains the following underlying data:

- Household_CoV_acquired.csv (data required to compute the proportion of cases presumably acquired outside of the household versus and the proportion acquired from household transmission. Each row represents an anonymised PCR-confirmed seasonal coronavirus case)
- Household_CoV_acquired.dta (above data file in .dta format)
- Household_CoV_TransmissionRisk.csv (data required to compute the risk of symptomatic onward household transmission following a seasonal coronavirus index case, and perform stratified descriptive analyses)
- Household_CoV_TransmissionRisk.csv (above data file in .dta format)
- Household_CoV_SAR.csv (data required to compute the seasonal coronavirus secondary attack risk overall and by strain. Each row represents an anonymised exposed-index pair from a given outbreak)
- Household_CoV_SAR.dta (above data file in .dta format)
- HH Transmission Serial Interval.csv (presents available, anonymised data required to compute the median clinical-onset serial interval overall and by strain for each household outbreak)

Data are available under the terms of the Creative Commons Attribution 4.0 International license (CC-BY 4.0).

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Open Peer Review

Current Peer Review Status: ? ? ✓

Version 1

Reviewer Report 29 January 2021

https://doi.org/10.21956/wellcomeopenres.17611.r41693

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✓ **Melisa Shah**
COVID-19 Response Team, Centers for Disease Control and Prevention, Atlanta, GA, USA

Hannah Kirking
COVID-19 Response Team, Centers for Disease Control and Prevention, Atlanta, GA, USA

Brief Summary:
This is a well-written and timely article on household transmission of seasonal coronaviruses with implications for the current pandemic. This presents original work using a population-based cohort in England which has previously been described. This prospective cohort was contacted weekly during the winter season, which is when seasonal coronaviruses circulate. Symptomatic participants in each household kept a daily log of symptoms allowing for granular data collection. PCR and strain level characterization of coronavirus diagnoses were included which was a major strength. Household transmission risk is presented and stratified by relevant characteristics including household structure, number of children, smoking, and hygiene. The findings include description of clinical serial interval, secondary attack risk, and household transmission risk stratified by strain type. The comparison of this study's household attack rates to other coronaviruses (including SARS and MERS) is very valuable and adds to the cogwheel of data informing household transmission of COVID-19. The authors do a good job of noting caution in interpretation of results given that the risk factor section is underpowered with overlapping confidence intervals.

Major Concerns:
A particularly interesting result is the increased risk of transmission among males, households with older adults, smokers, and chronic illnesses which is also seen as risk factors for severe disease in COVID-19. But looking at Table 1, it is difficult to know if these trends are statistically significant given the overlapping confidence intervals. Additionally, for "older adults in the household" it is unclear whether this may simply be a proxy for more individuals in a household or for having children in the household (such as a multigenerational family). The limitation of wide confidence intervals is raised in the discussion section, but this potential relationship also appears in the abstract conclusion as a major finding. Given that there are so many caveats and need for further work in this area, I suggest removing the finding from the abstract and keep it described

with all the caveats in the discussion section. The fact that there were no household transmission when the index case followed hand and respiratory hygiene protocols seems to be a really important data point and finding of the study to highlight.

Minor Concerns:

1. Please define “deprived areas” or IMD (indices of multiple deprivation) used in Table 1 and comments in the discussion (bottom left paragraph) in the methods section.

2. In the methods section, the inability to identify asymptomatic primary or secondary cases is raised. It would be helpful to include this limitation in the discussion section and provide any underlying literature on asymptomatic transmission of seasonal coronaviruses. This is an important piece in how such data is linked to transmission of the current pandemic strain.

3. One of the strengths of the paper is the description of strains, but the discussion does not include any background on known differences or comments/hypotheses regarding whether strain type may play a role in household transmission risk.

4. When discussing “households with older adults”, does this also include children and could this simply be a proxy for more people in the household?

5. It may be valuable to discuss possible background immunity to common hCoVs a bit more in the discussion, and its possible impact on household transmission findings. This is where there is also a big difference between the common hCoVs and SARS-CoV-2. Authors allude to this throughout, but it may benefit from some attention in the discussion section.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Partly

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Respiratory virus transmission, SARS-CoV-2, household transmission

investigations.

We confirm that we have read this submission and believe that we have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 25 January 2021

https://doi.org/10.21956/wellcomeopenres.17611.r41764

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Melissa Rolfes
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The authors provide a report on seasonal coronavirus infections detected in the Flu Watch cohort in the UK and examine household and demographic features associated with subsequent infection in other household members. In general, the rationale and implications of the study are clearly described and further elaboration of the methods and results would strengthen the manuscript overall. This is important work for the public health community, grappling with the ongoing SARS-CoV-2 pandemic; however, one limitation of the Flu Watch study, and its conclusions and relevance for the current pandemic, are that all detected infections were symptomatic because only symptomatic participants contributed nasal swab specimens for PCR testing. I look forward to further studies that can build on this study design to innovatively capture asymptomatic seasonal respiratory virus infections to better understand the drivers behind onward transmission.

Specific comments that I hope the authors can address in the next version are below.

Major comments

- Please include further description of the weekly telephone/internet survey, including the list of symptoms that were asked about. The description should include enough detail to answer the following questions: Was the question addressed to one member of the household or did each member have to respond about symptoms? Was the list of symptoms different if the participant was a young child (and below what age were these different symptoms solicited)?

- The methods section did not include a definition of the indices of multiple deprivation. A short description of what the indices are based on would be important for re-creating this work and analysis. Additionally, a reference to the index would be helpful for readers.

- Please include the method you used to estimate the confidence intervals for the household transmission risk, the symptomatic secondary transmission risk, and the community infection risk...well, all really.

- The results section could be elaborated with more information about the cohort size. How many people (and how many households) participated in each season? What were the

demographic, household, geographic, and socioeconomic characteristics of the participants?

- In the 3rd paragraph of the results section, the authors state that 22 households had transmission (out of a possible 134) = 16.42% household transmission risk. But in Table 2, the number is 20 out of a possible 134 = 14.93%. Please make the appropriate corrections in the table and text.

- The literature on household transmission of SARS-CoV-2 is moving quickly, but it'd be useful to update the Discussion section and references to include more recent estimates of household secondary transmission risk for SARS-CoV-2.

Minor comments

- The authors appropriately use the term "symptomatic transmission risk", but perhaps the authors could consider modifying their title to further remind readers. Something like "Household transmission of symptomatic coronavirus infections: …"

- To avoid including both co-primary cases in the analysis, the authors chose a randomly-selected case to serve as the "primary"/index case. Can you include in the discussion whether or not your findings (particularly the risk %s in Table 1) were sensitive to this random draw? Effectively what you're doing is imputing who the primary case was in the household, but you've done the imputation once in the current analysis. You could do the imputation multiple times (10-15 times, for example) and then summarize the transmission risks that you get in each of those iterations (just like you would in a multiple imputation). This approach might be more robust to chance findings, especially since there were quite a few co-primary cases.

- I appreciate the importance of weighting the infection proportions for your sampling scheme and to the underlying population. In Table 1 and 2, though, it would have been helpful to have a reminder of which proportions were weighted to the underlying population and which ones were not. I believe you'd be able to weight the first two rows, but not the others; however, you'd know best. A footnote would suffice to me.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Partly

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?

Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Epidemiologic methods, epidemiology of influenza and other respiratory viruses, household transmission.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Reviewer Report 29 October 2020

https://doi.org/10.21956/wellcomeopenres.17611.r40663

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Eben Kenah
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This is a fascinating study of the household transmission of seasonal coronavirus infections in a well-described and well-run cohort study. The associations between transmission risk and the age of household members, number of children, male primary cases, primary case hygiene, smoking, and deprivation are all plausible and may be useful for thinking about the transmission of COVID-19. There are far too few studies of this kind, so this one is useful both for its own results and as an example for others. The paper is clearly written, and the data analyses are simple but thoughtful. My major comments are

- The methods used to calculate confidence intervals should be described more clearly, and confidence intervals (e.g., exact confidence intervals) should be given even when no onward transmission was observed.

- The limitations are adequately discussed with one exception: the methods implicitly assume that all secondary cases are infected by the primary case. Because it neglects multiple generations of transmission within the household.

Additional minor comments are listed below:

1. I appreciate the consistent use of "secondary attack risk''.

2. In line with the usage recommended by Giesecke (2014)[1], it might be better to use "primary case'' instead of "index case'' for the first person infected in the household. This would also be more consistent with the use of "co-primary'' throughout the manuscript.

3. (page~4, Table~1) Exact confidence intervals can be given for household groups in which there were no observed transmissions.

4. (page~5, bottom or right column) It would be more accurate to say that no observed

onward transmission if the primary case was a healthcare worker or if they practiced good hand and respiratory hygiene.

5. The methods used to calculate confidence intervals need to be explained more clearly. When I try to replicate them, I get similar results but not exact matches.

6. Given the uncertainty in the point and interval estimates, a single decimal point in the percentages is probably sufficient.

7. One other limitation needs to be mentioned: The method of calculating the secondary attack risk implicitly assumes that all secondary cases are infected by the primary case, ignoring the possibility of multiple generations of transmission within the household.

References

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Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Partly

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Statistical methods for infectious disease epidemiology, epidemiologic methods, survival analysis, causal inference.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.