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**From:** Jeremy Farrar [J.Farrar@I&S]  
**Sent:** 21/01/2020 08:27:31  
**To:** WOOLHOUSE Mark [mark.woolhouse@I&S]  
**Subject:** Re: novel coronavirus

It will

It probably already has

So many asymptomatic, very mild infectious individuals who can transmit – sort of worst hybrid of flu+SARS!

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**From:** WOOLHOUSE Mark <Mark.Woolhouse@I&S>  
**Date:** Tuesday, 21 January 2020 at 09:25  
**To:** Jeremy Farrar <J.Farrar@I&S>  
**Subject:** RE: novel coronavirus

Thanks. Just to be clear. You DON'T think it will go global? Or that it will? My money's on the latter but of course I hope to be wrong. mw

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**From:** Jeremy Farrar <J.Farrar@I&S>  
**Sent:** 21 January 2020 08:18  
**To:** WOOLHOUSE Mark <Mark.Woolhouse@I&S>  
**Subject:** Re: novel coronavirus

Long story as you would imagine!

I would disagree on one point – I think inevitable there will be cases beyond Asia in the coming days and weeks – suspected cases (or which there will of course be many) in Australia and France today. At this time of year – probably will prove negative but given what we know, seems inevitable to me. Will forward the updates I have shared within Wellcome – don't judge the science too harshly, some a lay audience, all personal views!

In confidence – of course! Email if any questions

**JF INTERNAL AT WELLCOME**

Yes of course – suspected cases in Australia and France this morning, as one would expect and at this time of year with so many other respiratory infections there will be lots of suspected cases, many or most will prove not to be true cases but I think inevitable there will be cases beyond Asia in the coming days and weeks.

Let me know if you will forward or easier for me to

Best wishes Jeremy

On 20 Jan 2020, at 20:54, Mike Ferguson <M.Ferguson@I&S> wrote:

thank you for the update

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**From:** Jeremy Farrar <J.Farrar@I&S>  
**Sent:** 20 January 2020 20:27  
**To:** Mike Ferguson <M.Ferguson@I&S>  
**Cc:** Eliza Manningham-Buller <emb@I&S>  
**Subject:** Family cluster with Wuhan coronavirus infection

Quick update

- Major increase in number of cases over last 24 hours
- Now reported from many cities in China - Beijing, Shanghai, Shenzhen, Guangdong etc
- Reports of cases in Japan, Korea, Thailand
- Health Care Workers getting infected - >16 from a single exposure patient
- Very wide range of illness - Asymptomatic, Very Mild, Very Severe
- Emergency Cttee of WHO on Wednesday. Apparently China requested it - suggests they do want to declare it a PHEIC
- RCT started in Wuhan - using ISARIC protocols & treatment randomisation from the MERS protocol in Saudi
- CEPI redeploying their MERS programmes to n-CoV and activating the Disease X platform with some additional funds.

We are

- Chairing WHO Cttee on R&D
- In touch daily with China CDC
- ISARIC is helping coordinate the RCT in Wuhan - possible to adapt design if mAbs available in weeks to come Mike
- CEPI linked with NIH, EU etc
- Keeping UKG updated through Chris Whitty and Patrick Vallance and through other parts of UKG. Public Health England on the WHO calls.
- NR just texted to ask me to stand in for him at Davos so he can stay in Geneva and chair the Emergency Cttee considering a PHEIC

All in hand.

No need for any funding from Wellcome

Having the Epidemic Team in place extraordinary helpful.

Will get considerably worse over the Chinese New Year - prediction 2 below playing out - I assume cases in EU/Americas as some point.

Not forgetting Ebola! And making sure WHO do not forget Ebola - which remains in a worrying state in DRC

All in hand. All Calm. No need for panic!

On 20 Jan 2020, at 12:52, Mike Ferguson <M.Ferguson@I&S> wrote:

a terrific primer and analysis

Jeremy - I remember reports about neutralising antibodies in MERS (in some slaughterhouse workers, I think) - if some asymptomatic and/or mild symptom patients have them for this new virus (?) [Q has anyone set up plaque assays yet?] maybe Regeneron (or Kymab or UCB) could make a therapeutic antibody. Regeneron may already be on it. I am good friends with Neil Stahl (Executive VP for R+D, Regeneron) who oversaw the Ebola therapeutic Ab development - they had the MAb within weeks of getting the B-cells. I may make a discreet enquiry. But my question for you is, if the incubating asymptomatic patients are infectious - would a symptom-triggered therapeutic intervention stand any chance of curtailing an epidemic?

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**JF INTERNAL AT WELLCOME**

**LAY SUMMARY**

**Subject:** Re: Family cluster with Wuhan coronavirus infection

Coronavirus – a family of viruses that infect a wide range of mammals (bats, civet cats, rodents, camels) including humans

Cause of the common cold, SARS, MERS and others

Rarely an animal coronavirus crosses the species barrier and a novel infection is caused in humans

This is what led to SARS (Bats-Civet Cats-Humans) and MERS (Unknown-camels-humans)

Coronavirus are RNA viruses so can evolve and adapt to new species quickly once they cross the species barrier – makes the trajectory of a new epidemic impossible to predict

Usually cause a upper respiratory infection and pneumonia – SARS had ~8% mortality rate, MERS about the same.

No specific treatment, no vaccine for any coronavirus – CEPI has >1 vaccine in development for MERS/SARS

Cluster of pneumonia cases identified in Wuhan China between 12 December – 4<sup>th</sup> January

Caused by a coronavirus not previously known to cause infection in humans

Linked with a live animal market – initially ~40 patients, 2 died, mostly mild

Increasingly clear that not all cases linked with the market

Human-2-Human transmission

Family clusters but some patients with no known links

Cases now identified in Shenzhen, Beijing and in Thailand, Japan, Korea – can assume will be across China

Confirmed cases now >200 but guesstimates from travel data and known clusters would suggest 1500-2000 cases – which would seem reasonable

**So**

A novel human infection with a coronavirus

Causes an upper respiratory infection and pneumonia

Human-2-human transmission – from the Lancet paper over the weekend 3 transmission cycles – Family in Wuhan, Family from Shenzhen, Family in Shenzhen – suggestions quite high transmission

Spectrum of illness – asymptomatic, mild illness to severe illness

Seems that people are infectious before symptoms (unlike SARS) which increases transmission to others, and unlike SARS quarantine of people with symptoms will not stop the spread.

Now circulating in multiple cities in China and regionally

Chinese New Year – 25<sup>th</sup> January – 400M people move mostly city-rural in China and holidays in the region and around the world

**Many gaps in knowledge remain – including but not limited to -**

Origin of the infection – which animal and where that is seen across China

Propensity for transmission between humans – the infamous R0 – how many people does on infected person pass it on to

Who transmits to who – role of asymptomatic and mild cases in transmission – if they play a role then difficult/impossible to contain

Evolution of the coronavirus

Incubation period – time from infection to illness and transmission potential in that period – the longer the incubation period the worse to control

Clinical spectrum of disease – who is at greater risk of severe disease, age, multi-morbidity

Work on – Prevention, Diagnostics, Treatment, Vaccines

Extent of human infection

Possibility of

- It is contained by preventative measures and it stops over next few days/weeks
- It spreads extensively as humans have no immunity, mostly a mild infection, some patients with other conditions have severe disease
- It evolves and becomes more severe – more SARS or MERS like.

My guess for what it is worth would be the second of these.

Hope that helps.

**From:** Eliza Manningham-Buller <[emb@wellcome.ac.uk](mailto:emb@wellcome.ac.uk)> I&S

**Date:** Sunday, 19 January 2020 at 18:24

**To:** Mike Ferguson <[M.Ferguson@wellcome.ac.uk](mailto:M.Ferguson@wellcome.ac.uk)> I&S, Jeremy Farrar <[J.Farrar@wellcome.ac.uk](mailto:J.Farrar@wellcome.ac.uk)> I&S

**Subject:** RE: Family cluster with Wuhan coronavirus infection

Please may I have a short tutorial next week on the importance of this ? Thanks !

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**From:** Mike Ferguson

**Sent:** 19 January 2020 17:55

**To:** Jeremy Farrar <J.Farrar@I&S> Eliza Manningham-Buller <emb@I&S>

**Subject:** Re: Family cluster with Wuhan coronavirus infection

Thanks Jeremy

Very pleased you are there to bring sanity - as you say, info must be released asap, could make a massive difference in China re New Year travel policies etc (great timing, as ever) or at the very least alerts for health-care systems.

fingers crossed

Mike

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**From:** Jeremy Farrar <J.Farrar@I&S>

**Sent:** 19 January 2020 09:59

**To:** Eliza Manningham-Buller <emb@I&S> Mike Ferguson <M.Ferguson@I&S>

**Subject:** FW: Family cluster with Wuhan coronavirus infection

Quick update

I had a series of phone calls last night with XYZ who had been reviewing the manuscript, with China and lastly with WHO.

He and I came to the conclusion overnight that the only option was to share the paper with the WHO, talk with China, and put pressure on the Lancet.

The information was too important to not share – the XYZ Journal should never have put the reviewer in such a distressing position.

**JF TO WHO and REVIEWER**

**Subject:** Re: Family cluster with Wuhan coronavirus infection

Thank you

DEAR XYZ – I am totally supportive of your decision as you know, a very distressing dilemma to be put in. But this is incredibly important information which has to be shared with WHO to inform their advice and be in the public domain as soon as practical. Your decision is both honourable and in the right spirit of public good. I am honoured that you reached out and I hope it was helpful to be able to share the challenge. Absolute full support now and in the future as needed.

**NR** – thank you for your understanding.

Available all day if helpful to discuss.

Very best wishes Jeremy

**WHO TO REVIEWER and JF**

Dear XYZ,

Yes, this is exactly what I meant, thank you.

The information that is included in this paper is very important and provides evidence for our working hypotheses (possibility of cases in other parts of China, limited H2H, broad spectrum of respiratory symptoms, including possibility of asymptomatic infections, GI symptoms, incubation period >14 days) from the very beginning.

Given the sensitivities the authors highlight, I would encourage the journal to publish as soon as possible (before and after the author respond to reasonable comments from reviewers). This way the information is available and the sequence can be uploaded for others to analyse.

It is very much appreciated that you have shared this with me so that we can include this information in our discussions about our guidance to member states and actions required by the organization.

If possible, please let me know when it will be published.

Happy to talk further if that would help,  
WHO

**REVIEWER TO JF and WHO**

Dear WHO,

I am not 100% clear what you mean by the journal's position.

The journal's editor strongly encouraged the authors to make the information public, but--as far as I know--did not take any action himself to make the information public. The journal's editor also confirmed to the authors that making the information public would not make any difference in the journal's decision whether or not to publish the manuscript. The journal's editor has responded rapidly to my emails and telephone calls, and is understanding about my dilemma, without making any judgement about what I should do.

I did indicate to the journal's editor that I would provide key information about the manuscript to a contact person at the WHO if the information had not been made public by this morning. As far as I know, this was not the case, so I have passed on the information to you.

Is this what you mean?

Best wishes, XYZ

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**WHO TO REVIEWER and JF**

INQ000103349\_0006

Dear XYZ,

Thank you for your email. I understand and appreciate your dilemma and I thank you reaching out.

I will review and discuss with my Sr Management, but i will not distribute. What is the journal's position?

Thank you,  
WHO

**REVIEWER to WHO and JF**

As you know, I have been in contact with Jeremy Farrar regarding information I have about a family cluster of Wuhan coronavirus infection. I am in a dilemma about this, because I received this information as a reviewer last Thursday and am bound to confidentiality. On the other hand, I think this information should be shared immediately with the public health community to improve control of the outbreak.

I did discuss this with the editor on Friday and again Saturday night, who had encouraged the authors to make the information public. The authors informed him that the reason that they had not yet made the information public, not because they were concerned that it would be more difficult to have it published in a scientific journal, but because under mainland Chinese law, any individual or institution that makes any sensitive information related to this ongoing epidemic publicly available may face very serious legal consequences. The lead author wrote (on Friday or Saturday) that he was flying to Wuhan to meet the officials and to explain to them the urgent need to make the information public. He hoped that they would be convinced to do this immediately, or at least within the next 48 hours.

The information is still not public as far as I can tell from internet (Sunday ,0730), so I feel obliged to share it with you. In the end, I cannot bring myself to send you the actual manuscript, but I have summarized the data that I think are important for you as best I can. I leave it to your discretion how to use this information.

If you wish to contact me, I am available, on Sunday as well as the days after that, at the following telephone number: Irrelevant & Sensitive

Yours sincerely,

XYZ

Family of five people from Shenzhen (P1, mother of 65; P2, father of 66; P3, daughter of 35; P4, son-in-law of 36; P5, grandson of 10; P6, granddaughter of ?) went to Wuhan by airplane on 29 December 2019, stayed together at the same hotel, and visited relatives there: R1, 1-year-old son of R2; R2 (cousin of P3); R3 (mother of R2; R4 (sister of R3); R5 (sister-in-law of P1). P1 to P6 returned to Shenzhen by airplane on 4 January 2020.

R1 was hospitalized in a Wuhan hospital with febrile pneumonia from 27 to 30 December 2019. R2 stayed in same hospital from 27 to 30 December and developed fever, cough and weakness on 4 January; R3 visited same hospital from 27 to 30 December and developed fever, cough, and weakness on 4 January and was hospitalized on 10 January; R4 developed fever, cough, and weakness on 4 January and was hospitalized on 5 January; R5 developed fever, cough and weakness on 4 January and hospitalised on 10 January. History of R1 to R5 provided by P3.

P1 to P6 met with R2 to R5 every morning during their stay in Wuhan. P1 (without mask) and P3 visited R1 in the hospital on 29 December. None of the family (P1 to P6) had contact with animals, visited markets (including Huanan seafood wholesale market), or ate game meat in restaurants. R4 frequently visited wet market(s), but not the Huanan seafood market.

P1 developed fever, cough and generalized weakness on 3 January and went to hospital for persistent symptoms on 10 January. P2 developed fever and generalized weakness on 4 January and went to hospital for persistent symptoms on 10 January. P3 developed fever and diarrhoea on 2 January and went to hospital for investigation on 11 January. P4 developed fever and diarrhoea on 1 January and went to hospital for investigation on 11 January. P5 did not show symptoms, but went to hospital for investigation on 11 January. P6 did not show symptoms. Comorbidities were hypertension and treated benign intracranial tumour (P1), hypertension (P2), and chronic sinusitis (P4). At the time of writing, P1 to P5 were hospitalized under isolation in Shenzhen and were stable.

RT-PCR for RdRp and/or Spike genes of the Wuhan coronavirus at time of investigation in hospital were positive for nasopharyngeal swabs (P1, P2, P4, P5), throat swabs (P4, P5), and serum (P2). Samples from urine and stool (taken at 9 days after onset of diarrhoea from P3, and 10 days after onset of diarrhoea from P4) were negative. Real-time RT-PCR for the spike gene of the Wuhan coronavirus gave the following Ct values for nasopharyngeal swabs (P1, 32; P2, 28; P4, 33), throat swabs (P5, 39), and serum (P2, 40). Full virus genome from P2 showed



almost complete identity with Wuhan IVDC-HB-01/2019 and Wuhan-Hu-1, with only 3 base pair differences from the reference virus genomes.

Multiplex PCR of respiratory specimens for common respiratory viruses and bacteria, and multiplex PCR of faecal specimens for common diarrheal viruses, bacteria, and parasites were negative. No virological findings available from R1 to R5. Clinically, P1 to P5 had multi-focal ground glass opacities, especially around the peripheral parts of the lungs on CT scans.

#### Summary of important results:

-Likely human-to-human transmission, 4 out of 6 family members with confirmed Wuhan coronavirus infection in absence of contact with wet market, game animals, or game animal meat.

-Possible sources of infection according to authors: 1, P1 acquired infection from Wuhan hospital while visiting R1 and spread it to P2, P4, and P5; 2, P1 to P5 acquired infection directly from relatives R2 to R5; or 3, P1 to P5 acquired infection from an unknown common source in the community in Wuhan.

-Incubation period of 3 to 6 days according to authors.

-Infection associated with diarrhoea in two patients (P3 and P4)

-One patient (P5) asymptomatic, but virus-positive and clear chest x-ray changes, suggesting patients could be infectious before onset of symptoms.

-High rate of infection (5 out of 6 family members, based on CT scan changes)

-Full virus genome available from P2, but not yet in the public domain.

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**From:** WOOLHOUSE Mark <[Mark.Woolhouse](mailto:Mark.Woolhouse)> I&S

**Date:** Tuesday, 21 January 2020 at 08:59

**To:** Jeremy Farrar <[J.Farrar](mailto:J.Farrar)> I&S

**Subject:** re: novel coronavirus

Morning Jeremy,

I hope all is well with you and yours.

Am I right to be increasingly concerned about the slow drip feed of epidemiological information on the Wuhan coronavirus?

By now I'd have expected a raft of data on the course of clinical symptoms, incubation period, latent period, infectious period and so on. Even the first sequences took some time to be released. Some of this information may (or may not, I'm not in a position to say) be provided in publications in the pipeline. Nature tells me (somewhat crossly) that they are

working “behind the scenes” to make sure that information of public health value is made available quickly. Even if that is correct (whatever it means) then much of the public health community, and certainly the press and wider public, are still largely in the dark.

This makes it almost impossible to give sensible comment or advice to the health agencies, as I and many others are already being asked to do.

My own position is that there is a very significant likelihood of this going global (I’ve thought that for a while, but the likelihood is increasing daily at the moment). In which case, it would be prudent to start planning for that eventuality.

I am sure that you are very much engaged with this, and that alone would be somewhat reassuring.

Kind regards,

Mark

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