Message

From: Rob.Orford@gov.wales [Rob.Orford@gov.wales]
Sent: 01/04/2020 09:18:24
To: Christopher.Williams25@wales.nhs.uk; ConnorTR@cardiff.ac.uk; Giri.Shankar@wales.nhs.uk; Robin.Howe@wales.nhs.uk
CC: HSSG.TAC@gov.wales; andrew.jones10@wales.nhs.uk; Fliss.Bennee@gov.wales; NR @gov.wales
Subject: RE: SAGE Paper on AB Outbreak

Thanks Chris, As Tom suggests a sequential approach to testing HCWs such that essential front line staff (in the current policy) are staggered across the week might be more sensitive to pick up outbreaks. We can ask HEIW for numbers of staff in the current policy if that sounds like a sensible approach?

I wondered also if a random sampling approach to vulnerable group carers would help track the incidence of COVID-19 infection in the community? We have the names and addresses of shielded individuals so we could send out swab tests that could be given to main carers?

With regard to an Amazon front end to 'triage and test' for key workers. I wonder if the following fields would help reduce unnecessary testing from circa 3K/d to something more manageable.

1. Digital Signature – *confirming that you understand the terms of service*
2. If you are symptomatic (*or a minor in your care*) – *enter symptoms from symptom tracker (possible additional triage layer)*
3. Do you work with vulnerable people or patients (Y/N)
4. If you are a key worker will your workplace absence cause negative impacts on critical services or infrastructure (Y/N)

5. Name of your Line Manager/Occupation Health Lead
6. Email Details of your Line Manager of Occupational Health Lead

7. If you work with a vulnerable person, you may have been given this swab test to help us understand the spread of SARS-CoV2 in the community

8. Enter postcode of vulnerable persons residence

9. Are you are completing this test for a minor in your household and you have answered yes to question 3 or 4 (Y)

Keen to pull the 'key worker testing' paper together today and circulate to TAC and the testing sub-group, before sending to CMO and the Minister ahead of tomorrow's Cabinet.

I hope we can discuss in TAC in a short while

Best wishes
Rob

From: Christopher Williams (Public Health Wales - No. 2 Capital Quarter, Health Protection) <Christopher.Williams25@wales.nhs.uk>
Sent: 01 April 2020 08:38

To: Thomas Connor <ConnorTR@cardiff.ac.uk>; Orford, Rob (HSS - Primary Care & Health Science) <Rob.Orford@gov.wales>; Giri Shankar (Public Health Wales - No. 2 Capital Quarter) <Giri.Shankar@wales.nhs.uk>; Robin Howe (Public Health Wales - Microbiology) <Robin.Howe@wales.nhs.uk>
Cc: HSSG.TAC <HSSG.TAC@gov.wales>; Andrew Jones (Public Health Wales) <andrew.jones10@wales.nhs.uk>; Bennee, Fliss (HSS-Technology, Digital & Transformation Directorate) <Fliss.Bennee@gov.wales>
Subject: RE: SAGE Paper on AB Outbreak

Thanks Tom
I'd agree with most of this- it was bad luck, as occurred in other sporadic cases in the UK found before the case definition changed, and the control of the outbreak through testing, isolation and PPE shows the importance of these measures in COVID control in hospitals. The social contacts may have been infected on a visit or possibly at home- but from my recollection of the notes they weren't visiting whilst symptomatic, so less likely to contribute to spread.
On regular testing I was thinking of a different scenario, whereby healthcare workers could be infected at home rather than the ward. Agree that only daily testing would be secure, but weekly testing would help to give routine reassurance and also set up a rhythym and acceptance of testing and self-consideration of symptoms. Of course you can be unlucky with this too and miss awhole week, but I think it could work and I think have seen that it's been used elsewhere (will check).
Many thanks
Bw chris

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From: Thomas Connor <ConnorTR@cardiff.ac.uk>
Sent: 31 March 2020 22:41
To: Rob.Orford@gov.wales; Christopher Williams (Public Health Wales - No. 2 Capital Quarter, Health Protection) <Christopher.Williams25@wales.nhs.uk>; Giri Shankar (Public Health Wales - No. 2 Capital Quarter) <Giri.Shankar@wales.nhs.uk>; Robin Howe (Public Health Wales - Microbiology) <Robin.Howe@wales.nhs.uk>
Cc: HSSG.TAC@gov.wales; Andrew Jones (Public Health Wales) <andrew.jones10@wales.nhs.uk>; Fliss Bennee <fliss.bennee@gov.wales>
Subject: Re: SAGE Paper on AB Outbreak

Thanks Rob,

In terms of the specific questions, I expect Robin/Giri/ NR will correct me if I get anything wrong or that they disagree with (not a medic so this is very much my perspective as a genomic epidemiologist – so expect they will correct me ☺), and Chris has more specific details of the supposed index case which may shed additional light on this. The questions of PPE and testing are a little outside of my area/expertise, but I think that some of the genomic/epi data does point in a certain direction.

- "The question of how to reduce nosocomial outbreaks is under consideration by SAGE. Does the genomic data tell us anything about possible control measures? From my reading of this it would suggest this event was fairly swift – would have enhanced testing of HCWs (e.g. weekly swab PCR testing) mitigated the outbreak"

So my gut feeling, looking at the timescales and the genome data is that the key issue was that here is a case who I think did not initially meet the case definition for testing, was missed and had an extended opportunity to transmit to HCWs and other patients. I also don't know what the situation was with visitors, given that household contacts also flagged positive. If the presumed index case was allowed visitors, then they may have contributed to spread within the ward/hospital as well. It would be good if we had, or could get, that data, and that may have compounded the issue and provided an additional route for transmission within the hospital.

I guess Robin can comment on how not having a diagnosis/suspecting COVID-19 in a patient might have affected staff use of PPE or handling of the patient early on, and how that could have contributed to the transmission that is observed.

In terms of enhanced testing of HCWs, again, Robin/Giri, NR may have a different view, but my feeling is that the missed patient/familial contacts diagnosis is the real issue here, but that the speed of spread is a salient piece of information for designing a routine testing scheme.

Just thinking in terms of timescales the potential for routine testing to have picked this up is very contingent on how that testing regimen is designed. In this case we have a cluster of 50-70 cases who all flagged positive within ~7 days of the suspected index case. That to me suggests that how one implemented something like weekly testing would be critical in catching something like this early. I would think that if a portion of staff tested every day then detection that there is a problem on a ward might be possible. But, say, testing everyone once a week could conceivably have missed basically all of the transmission here. So to me the message is to design routine testing well, taking into account the observed timescales in AB and understanding that such testing has to be rapid to be useful.

The other problem with HCW testing is if, say, the paramedic had flagged positive as part of routine screening, what would the next step be to work out where that has come from? I think that would need some serious thought.

- "Does the fact that there are not multiple variants in this outbreak suggest that actually PPE and infection control is actually good and that the AB outbreak was more bad luck than anything?"

So my feeling looking at the genomic data and the epi that I have seen so far is that this is a case of bad luck, and that it may be a one off, because of the timing.

The speed and extent of rapid spread suggests a lot of local transmission within the hospital over a short space of time, probably before anyone was aware of it. If the PPE, IPC and isolation processes are working, what we should see is a drop in cases in this cluster as we move along and hopefully IPC measures have reduced the chance for transmission. We may see diversification/accumulation of mutation as transmission chains lengthen as well (as each transmission event is an opportunity for a mutation to be fixed), which could imply that control measures are having an effect.

There is also a risk that this cluster has moved into the community, and spread may be occurring there now, but hopefully if that transition has occurred, that should be evident from the genomics and the metadata as well. I think that the next few sequencing runs will give us further information, and we can see what has happened with regards to this cluster. I am also hoping we might get some sequence data from Bristol as well, to see if there is any evidence of this cluster being linked with earlier English samples/clusters.

Hope this all makes sense, and am sure that Robin/Giri/Chris can comment on my non-medic assumptions above, and clarify any elements that I have wrong.

BW,

Tom.

Dr Thomas R Connor

Dr Thomas R Connor