Twitter Thread by Marion Koopmans



Marion Koopmans
@MarionKoopmans

Ok, see if I can save some time later in the week with this ongoing nonsense: there is a group that claims that the original PCR assay developed by Victor Corman and Christian Drosten and validated by a collaboration of expert labs does not detect a new virus at all.

> >> vanuit NL (naast Borger zelf) de lasterneuroloog Jan Bonte, een huisarts en een klinisch chemicus/antroposofe.
>
> — Pepijn van Erp (@pjvanerp) November 29, 2020

They argue that this is because the PCR primers also detect SARS https://t.co/cidvDcSJWD

Fortunately, virologists know this ……viruses do indeed have parts in their genetic code that are conserved. That is actually used to classify them, and it can come in handy when designing a test to pick up all variants of a family of viruses. https://t.co/OBiCqPriXl

See an example where this knowledge is used for design of a test that can pick up ALL coronaviruses https://t.co/NCoN3sMR14 . This type of test was also used when this virus first emerged.

So yes, when designing a test, selection of primers is key (as anyone involved in diagnostic virology knows) https://t.co/6p8sKCft7W In the paper, the sequence conservation among a highly selected sublineage of SARS-like viruses was used for primer selection.

There are many SARS-like viruses in nature, say bats. So if we would use the current PCR assays in bats, yes, we would pick up other SARS-like viruses. Why then use it in humans, does that mean these tests pick up something entirely different?

Nope. We have a fairly good understanding of human coronaviruses. SARS was a big outbreak in 2003, but has not been found in humans since. Okok…I hear someone say: but how can you be sure?

Well, you never are 100% sure of that, so that is why we do another step, with any novel disease: sequencing. You have a person that tests positive, then you sequence the entire genome of the virus in that person.

This has been done quite a bit, all over the world. See this for instance https://t.co/nBocdNcEoy And if you want to dig down: here is the platform where scientists from all over the world share their data. https://t.co/Jnw78r4ssw

You can even go in and design your own PCR primers, that is one of the great advantages for this type of sharing. As the Chinese colleagues did early January, thanks for that.

sequencing also helps us understand how these viruses change, as viruses do when they replicate a lot. This introduces mutations, so over time, you start to see lineages. Therefore, with time, there may be subtle differences between the viruses in different parts of the world.

This is something to track when you are in diagnostics, working with PCR. So scientists use software programs to make sure that the new viruses found still would be detected with the PCR tests that they use.

With an outbreak of this size, that becomes quite a load of work, so thanks for bioinformaticians: they help develop tools to do this automatically.

Here is one developed by a guy in my lab. He did not think much of it, because this is really considered good diagnostic practice, but hey. https://t.co/63YsGgmdZL And https://t.co/rCm8KIXhcs is another platform where people into virus genomic analysis share and discuss work

And I hear some people ask: but was the virus ever cultured? Yes, it was. Over and over and over again. Look at some of the blogs by Ian Mackay to explain the whole thing (again) https://t.co/CIH5GKRG65 @MackayIM

So finally: why did we do the PCR design this way? Because it was January 6th, we were hearing of a new SARS like virus, and there were no samples, viruses outside of China, yet we needed to make sure to be ready for testing (and were asked to do so in travellers).

The labs on this paper all had worked with SARS, had samples from SARS patients in their freezers. So that made it possible to do a first check of how this would work. A valid choice in an emerging disease outbreak, where you are in the blind phase.

And also because SARS was eliminated. So, yes, these tests are positive in people with SARS COV 2. And now back to real work.