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Transcript

„Avian influenza – a devastating pandemic for birds and a threat for global health?“

Panelists

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Recording

- ▶ You can find the recording here: <https://www.sciencemediacenter.de/alle-angebote/pressbriefing/details/news/antibiotika-einsatz-resistenzen-und-alternativen/>
- ▶ If you need an audio file or a speaker's view of the recording, you can contact redaktion@sciencemediacenter.de.



Transcript

Host [00:00:00]

Welcome everyone to this press briefing on avian influenza. My name is Annegret Burkert, and I work here at the Science Media Center Germany as an editor for medicine and life science. I have to say, I'm very excited about today's briefing because it's a collaboration of the three SMCs: the SMC in Spain, in UK and in Germany. And I'm very happy that we could bring together three top experts on avian influenza, which have an excellent overview about this topic and who will answer your questions today. The media coverage so far has a strong focus on the zoonotic potential of the virus, and for sure this seems to be the most concerning issue. However, the dimension of this panzootic event is much broader. The virus has now arrived in North and South America and so far only Antarctica and Australia have been spared. Millions and millions of birds have died and other species are affected as well. Like now, the colony of sea lions in Peru, where almost 600 animals were killed by the virus. So what does this also mean for biodiversity? Are there any measures that can be taken to contain further spread? How much does the scientific community already know about this highly pathogenic avian influenza variant and what can be expected and translated from previous research on other variants? Those, and of course your questions, we would like to answer in the following 50 minutes. You can already put your questions in the question and answer tool that you find below. Please do not use the chat. My colleague will collect the questions and forward them to me. So please type them in the question answer tool. Now, I would like to introduce the three experts. Here with us today is Ursula Höfle. She is a contract professor at the National Game and Wildlife Research Institute in Spain. Her scientific interest is focussed on infectious diseases in wild birds, especially those of importance for conservation and for transmission at the Wildlife-livestock interface. Being located in Spain, she has a good insight into the outbreak at the Galician mink farm. Also with us today is Ian Brown. He is a professor for avian virology, pathobiology and population science in the UK. His specific research interests include the epidemiology, pathogenicity, transmission and infection dynamics in relation to the control of influenza in animal hosts, including zoonotic threat. He is also the director of the International Reference Laboratories for Avian Influenza of the World Organisation of Animal Health and the Food and Agriculture Organisation. He has led the science response for the avian influenza outbreak in 2021/22 and is functioning as an advisor in poultry health. Hello Mr. Brown. The third expert I'd like to introduce is Martin Beer. He is the head of the Institute for Diagnostic Virology at the Federal Research Institute for Animal Health in Germany. Together with his colleagues, he is responsible for the surveillance and analysis of avian influenza cases in Germany. Furthermore, he is coordinating the Delta Flu Consortium: an EU Horizon 2020 project that aims to improve prevention and control of avian influenza. Welcome all three of you. And thanks for being here. I would like to start with the questions to you, Martin. Could you please give us an overview of the current zoonotic event situation? And what is the difference or the contrast to former epidemics was avian influenza?

Martin Beer [00:03:39]

You have to go back a little bit. This story with H5 high pass viruses started in 1996 when this Goose Guangdong virus developed and was spreading from poultry to wild birds, from wild birds to poultry. And after some years, this virus was able to travel with migratory birds. And then a group of this viruses, mainly H5N1, came to Europe and to other countries and this was the major strain further developing until 2014. Then, other clades came in, also reaching northern America. This is then the 2.3.4.4. clade. First [2.3.4.4]a and then from 2016 on 2.3.4.4b H5 viruses – and this is the clade which is currently doing all this panzootics – which started mainly with H5N8. And this virus was much more reassorting [...]. And this virus was much more re-assorting, this low-pass viruses, we saw more a kind of a cloud of viruses and it further developed. And we think it was further adapting to wild birds. And in the last two years, it's now mainly again H5N1 – it is



a subtype – which is the same clade related to this H5N8 viruses. And there is much more wild birds infected. Many wild bird infection means many poultry infections, also poultry to poultry infection and some spill-over, especially to carnivores. So that is the situation. So the main thing what changed is the virus seems much better adapted to wild birds, and it's also better adapted to situations like somewhere in Europe or even in Northern Europe or in other parts of the world. So, this seasonality is a little bit lost, so from 2021 on and especially last year. And I look to Ian in UK, for example, and also in Germany on the coastline, we had a lot of birds, wild birds, colony breeding birds dying of this H5N1 viruses, which is still – and I think this is important – not a single type of virus. Those are still reassortants which have the same subtype and we know it's more than 30 genotypes worldwide now and also in Europe. And I think the situation is worrying mainly in the wild birds and the poultry. And there is some risk of this spill-over infections to the mammals.

Host [00:06:32]

Thank you, Martin, for this first overview. I would like to address an entry question to you, Ian. Are there any tools or any measurements that can be taken to contain the spread?

Ian H. Brown [00:06:45]

Well, first the important principle worldwide is to do active monitoring and surveillance and tracking: where is the virus? What populations is it in? So there's a lot we can do in tracking and monitoring in wild birds, but of course, the key focus is that poultry-wild bird interface. There are a lot of things we can do in poultry. We can have good detection systems so that we can find disease quickly. If we find disease in a poultry or kept-bird flock quickly, then we can take action to eliminate that. Depending on where you are in the world, there are different systems that are used because it will depend on the amount of veterinary infrastructure. But the traditional method is to detect infected flocks, kill the birds quickly because it will only spread and kill them in time and make sure that the virus doesn't spread from that farm or setting to another one. So, you do that through a form of what we call movement restrictions. You effectively lock down the area that's infected. Now, if you do that in an effective way, you can absolutely stop the spread of infection, going from one group of kept birds to another. Ultimately, if we can control the disease more effectively in poultry, we reduce the interface between poultry and wild birds. And as Martin has said, this virus is evolving quite happily in wild birds, but you do still occasionally get spill back. So, we need to cut that source off because ultimately the virus probably will become more benign or die out in wild bird populations. And then, of course, the last tool which is being now increasingly used around the world is vaccination. There's a lot of interest in vaccination. It has been practiced in some parts of the world now for probably 15 years. Other areas such as Europe and the Americas, are now considering whether vaccination can be a complementary tool to all of those other measures.

Host [00:08:36]

I think to this vaccination point, I will definitely come back. But first I also would like to raise an entry question to Ursula. There was already mentioned the spill over. Now there was a spill over to a mink farm and the Galician region in Spain. [...] What is known so far about that, is there anything new known about this outbreak? Is it known how the minks were actually infected? And is there already evidence how the virus was transmitted between the animals?

Ursula Höfle [00:09:15]

Not really or not much that has really transcended. What's currently underway is sequencing of all the viruses that have been detected in wild birds in the same region where the mink farm is located – whole genome



sequencing to try and compare the sequences and the gene structure of the viruses, because there was or there is some evidence from from what is known until now that potentially the infection of the mink was through wild birds and specifically gulls, because they have direct access to these farms and they are very often drawn to these farms, because they are open buildings and the food is provided on top of the cages. So it's really accessible for wild animals, both mammals, rodents and wild birds. So this is the likely route of infection. And there is some molecular evidence for this because of the similarity of this virus to gull-viruses that have been detected early on in the region. But this is being further tested. So it's not really absolutely conclusive. And so far, the sequences that are around – there's still not enough data. So they're working on it. But [...] even if enough sequences are around, it's not absolutely sure that we will definitely know if this was the route of infection, but it's definitely the most likely one. And on the other hand, the epidemiology of the outbreak, that's the first way the virus is spreading through this farm was like blotchy spot like outbreaks with a few animals and a few neighbouring cages in different barns and in different locations in the barn, and then more sustained spread through the populations and through different barns. That also suggest mink to mink transmission in this outbreak. And this is again supported by genomic data, which is the mutation of PB2protein (*part of the viral polymerase; editors note*), the change of threonin to alanin, which enhances protease activity of the viruses in mammalian cells – so facilitates transmission. So – again, these two facts are circumstantial evidence. You would really have to prove this experimentally, which is something that will take much more time. But there is also some experimental evidence from studies that are not linked to this outbreak that are actually previous to this outbreak from researchers in China that were already concerned about this, that have shown that it's fairly easy for these viruses that mink are very susceptible to both avian and human influenza viruses and they quite easily adapt to spread between individuals. So, we don't really have hard information for this, but a lot of the circumstantial evidence.

Host [00:12:48]

How likely is it that the mammal to mammal transmission at the Mink farm was an isolated event?

Ursula Höfle [00:12:58]

At this point, it looks like it was, at least for this particular virus, an isolated event. And the actual mink to mink transmissibility developed de novo in this mink farm, because this was a farm that's about 50.000 animals, more than 50.000. It's a bit like a situation in the poultry farm where you have poultry, chicken to chicken transmission and a lot of mutations arise that finally give rise to different viruses in this population. And this is probably something that's happened in the mink farm. So this particular mutation and this particular change in this virus probably happened there, because this specific virus has only been detected once before in a polecat, so this is the only mammal detection. But on the other hand, there are a few other outbreaks like the Caspian Seals and in Russia or the sea lions in Peru, that although there's no data on this so far, but they suggest that that could also be mammal to mammal transmission be happening somewhere else. But this could be a completely different virus or different strain and different mutations. So we don't really know. But there's definitely increasing evidence for bird to mammal, mammal to mammal transmission. But these are probably completely isolated events.

Host [00:14:31]

So maybe [...] thank you. This is maybe also a question to all three of you. Looking at this 600 animals, sea lions infected in Peru or the ones in the Caspian Sea. What is your feeling? Are those single events that all those lions infected themself individually, or does this look like there was transmission among the sea lions?



Ian H. Brown [00:15:01]

I can go first and I'm sure Martin will have a viewpoint. I think we have to be quite careful before we jump to conclusions here. So, one thing that's important to understand is, if there is an awful lot of wild birds infected and sick and dying from this virus. So, there's a lot of birds in the environment. We know animals like sea lions and indeed these other mammals that have been detected, they either share habitat and have close contact with these populations or they actually scavenge and predate them. So, although there's a lot of sea lions, there's also an awful lot of wild birds dying. There's a lot of brown pelicans dying along that coast. So, we can't exclude the possibility that the sea lions are having a feast on the dead Sea birds. It's important with the number infected like that, though that the work is done fast, and the viruses are recovered from these sea lions, and they're compared. And the genetics is looked at very carefully. Because if you look at the genetics of the virus, as Ursula explained, if it starts transmitting from one sea lion to the other, when you look at the genetic sequences, you can work that out. Rather than they're just acquiring the infection directly from wild birds. So, I think before we assume, because there's a lot, we need to actually wait for that analysis to be done. It's really important. And I think a sustain mammalian transmission is absolutely not proven for these viruses. Now, normally the sort of populations that have been reported in getting exposed, you know, grizzly bears, porpoises, otters, foxes, they don't tend to live in large colonial groups. They tend to be more smaller population groups. So, we say their contact structure is different. So that doesn't...it's not quite the same as the mink farm. So, we have to be aware of that as well. So, we have to be watchful. But absolutely, I think we...we need to be cautious before we assume the virus is transmitting between the sea lions.

Martin Beer [00:17:04]

Maybe to add to the Sea lion and Seal story, because we had a H5N8 found in three seals in Germany. So that was one of the earliest events and we could sequence them. And there was some adaptation, but we could also show that this was single events, because the strains in the three Seals were different. So that was most likely a wild bird, infected wild bird, which was taken up by these animals, and then they got infected. I think the pure number that you have, 500 or so, this is something which is concerning or as Ian said, we have to look at the sequences because then there should be adaptation. If there is also a different kind of sequences, we would see a completely different situation if that would be uptake - all in all cases, uptake from dead wild birds - so therefore we have to wait here. But it's something we have to be aware of and we have to follow it very closely because especially the species like mink or sea lions or seals, they are highly susceptible. So, it's easier for the virus to jump over this hurdle. So, it does not mean that they immediately now are able to go further into mammals because this is very special mammals. Also, the minks, if you look at ferrets, this is our main model for influenza. So, the minks have a special specialty which makes it easier for the virus. And the same as for this in group living sea mammals. So, it's...We have to be careful to not draw too many conclusions and wait for the data we have, but we need the awareness. And I think it is important, therefore, that all these dead mammals, especially carnivores, are collected, tested and the viruses have to be sequenced to follow. Is there some of the many genotypes we have, which is easier transmitted? Because that's one of the problems we see. And there was a question I saw, that [asked] what is a subtype and what is a genotype? So, the Subtype is the HA and NA type. But there are six other segments. So, the virus can still be different, and it is most likely different between the Peru-virus and the one in the minks and the virus we see in some cases in wild birds. So, we have to follow this very closely.

Host [00:19:37]

But do we know how the new mutations in clade 2.3.4.4b influence the fitness of the virus?



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Martin Beer [00:19:47]

It's so many different viruses, if I can say that, that we try to follow that, but the virus is faster changing than we can characterize it. To be honest, that is the case, and we have to concentrate and therefore this awareness is so important. We have to collect these cases in the field and then select the ones where the situation, like in the minks, the sea lions or other die offs where we say: this is the viruses we characterize. And then are some of this virus is characterized in ferrets and we still see that this is not the level of infection and zoonotic potential as we saw with the original H5N1. I think this is an important message from my side.

The only question is, is some of the new reassortant then different or not? So this is a continuous follow up of the strains.

Host [00:20:42]

Do you think it's likely that the virus will spread even further, for instance, to Antarctica or Australia? And what species are particularly susceptible or in danger? Who would like to answer this question?

Ian H. Brown [00:21:01] Let

Ursula have a go.

Host [00:21:03] Okay,

Ursula?

Ursula Höfle [00:21:04]

Well, I'll have a step, but probably Ian should complete because I'm probably not all around. So, it's very likely. This is a period when migratory birds are on the move. Many of the birds that have been in wintering areas are returning to the breeding grounds. There's a lot of mingling at stopover points. And we have cold spells that also drives birds probably in Europe further south and other reasons further north. So, there is likely to be a lot of contact and birds that are susceptible are likely to get into contact with the virus. So, this on one hand and on the other hand, with [...] susceptible species and risks, we've seen so many surprising things with this virus, we can expect anything. And that's the thing at least for me, this is the real drama with this virus. It's been affecting species that we haven't seen before affected like large scavengers, like vultures. It's a very, very endangered species. And it's been wiping out entire colonies of some species. We expect to see a huge impact on biodiversity from this on some populations. So, this is apart from the obvious risk and worry about human infections or mammal to mammal transmission. This is the real serious part of this zoonotic.

Host [00:22:59]

Ian, you want to add on to this?

Ian H. Brown [00:23:00]

Well, I think it's to emphasize the point Martin made. We've got a virus or a group of viruses now that are very promiscuous. They seem to be able to extend the number and range of wild bird species they can infect. So, this is really is a relatively new development. So, the maintenance of this virus in Europe through the whole year, as Martin said, is a facet of the fact that this virus has been able to jump into other populations of birds that it previously wasn't found in. And that's quite a worrying development. So, if I look at what's



happening in South America, I've seen reports in things like kelp gulls. Well, we know in Europe and North America the gulls seem to have acquired this virus has quite a strong tropism for gulls which probably didn't have five years ago. So that's quite worrying because gulls are pretty ubiquitous. They move between populations, they shed the virus and of course we know it's getting into all sorts of populations. So, I think it is really quite a worry that the virus has already reached so far down into South America and we have to consider that there are definitely risks for biodiversity in terms of Antarctica. I mean, it really is a concern to think that it could end up in a place like Antarctica. Australasia has always been an interesting one. The Australians always looked very hard and wish to remain free of this virus and that has always been considered because the sort of wild bird populations that migrate distances into the Australasia are not the sort that necessarily carry this virus. But we have to rethink all of this now because this virus seems to have an ability to infect just about any bird population it comes across. So, we have to consider potentially all species of birds could have some level of susceptibility, which of course is a new dimension.

Martin Beer [00:24:53]

Maybe to add here. This means this new populations, also new continents like South America – this is a new number of birds, and all these birds carry low pass viruses. And since this virus is so promiscuous to switch segments, this means there is now a continuous change of this virus. And then you have spill-overs. And the question is: Is one of this better replicating or not? And it's for sure: in the bird selecting an even better one probably. And maybe there is then regional optimize for this bird species viruses. And one of the crucial questions of the future on the other hand will be there will be immunity in birds which survives: So, what does it mean for the future? Is the virus then driving away from immunity or is that stopping spread a little bit so that are now many, many questions we never had before because the virus was never before spreading like this.

Host [00:25:57]

Martin, maybe a short question. What is a low pass virus?

Martin Beer [00:26:02]

A low pass virus is a virus which we normally see in mainly waterfowl, but all kinds of birds. And this is if we talk again about subtypes from H1 to H16 and N1 to N9. So, a lot of different viruses which are not so harmful to the birds and only two types, the H5 and the H7. If they come into chicken or turkey, they can change to this high pass by a mutation in the hemagglutinin. And then they are a deadly virus, especially for chicken, turkey, but also some types of ducks. And this happened many years ago for one H5 type and this one is a success story for the virus. So, in 1996, it's developing further and the more it can spread, the better it can optimize.

Host [00:26:54]

Maybe a very short question, but I think it's quite interesting. Have there been historic examples of such a widespread of a zoonotic disease or is this unprecedented?

Ian H. Brown [00:27:08]

We have to be clear: This is not currently a zoonoses. There is occasional spill-over. And of course, indeed, there have been quite a significant number of human cases since 1996. So as Martin said that virus emerged in Southeast Asia and in the early years there were quite a lot of human infections with quite a high case



fatality rate. But the key thing was that virus wasn't able to transmit from one human to another. Now, that still remains the situation – although we have to obviously be in revision – that although there's a very large population of birds now around the globe infected with these viruses, we're still seeing that spill over into humans is a very, very rare event. So I think for us to talk about zoonoses, we're not at that point. We have to be mindful that this virus, of course, is got the ability to change. And could it change in a way that makes it more infectious to humans and that spill-over into mammals is why there is more concern and vigilance. But in terms of other viruses, well, of course, if you go back to 2009, that virus had its origins, we believe in pigs and spilled over into humans, although it was a pretty benign virus in the end. In terms of pandemic threat, it was pretty mild. But of course, we believe that the origin of pandemic viruses has animal reservoirs. The precise pathway and mechanism could be multiple. So, any animal virus that starts establishing in other populations is one of concern. But we should stress that this virus doesn't seem to be able to enter livestock mammalian species. So even though it's been circulating for over 20 years and Martins groups done some very nice work in this space recently, this virus actually doesn't really want to be in those hosts. So, the wildlife scavenging is a new dimension.

Martin Beer [00:29:06]

I really want to support this, that we have really to talk mainly on a bird panzootic. So, the virus is improving in birds and accidentally we have the spill-over and looking at the number of infected birds, this is still not a lot, but it also means more birds, more spill-overs and more mixture. So, I think we need the awareness, but it's not the right time to say we are very close to a H5 pandemic, so it's a panzootic and we have to be careful. We have to look at it and the zoonotic aspect is fortunately less than with the original one. So, and we can see this in some countries like Egypt, when the H5N1 went into Egypt, the number of human cases with H5N1 went down to zero. So, one virus, which was less zoonotic, it was better spreading in birds and then the cases went down. But we have to follow the situation and it's really difficult to predict what the virus is able to do.

Host [00:30:15]

From the immunity perspective, Martin, what is a barrier that keeps humans [being] infected by this virus?

Martin Beer [00:30:25]

So, the major hurdles are on one hand receptors, receptor optimization, optimization for replication. This is where we see the first adaptation in mammals like this 627K (*a point mutation in the PB2 gene; editors note*) or this mutation in the minks. But there are further hurdles: antigenic differences – okay, we have no H5 antibodies, but there is also innate immunity. So, our MxA is a very big hurdle for the virus. And there are some studies showing that it's not easy for H5 to overcome this. And this is probably one of the reasons why, for example, the minks are species where it can overcome because there this innate immunity is not very strong, so not comparable to humans. And therefore, Ian mentioned it, the pig...their Mx is closer to the functions we have in humans. So, if a virus is adapted to pigs, then we come closer to viruses which can easily jump to humans. So, a H5 high pass virus adapted to pigs would be a very high concern, much higher than the minks.

Host [00:31:35]

Could you quickly explain what Mx is?



Martin Beer [00:31:39]

That's a protein which is directly fighting the influenza virus, and it's replicating. It's an innate immunity [protein] which is directed very much against influenza viruses and all pandemic viruses. The viruses have normally a nuclear protein, so one protein which is able to escape this Mx gene. And during the 1918 (*influenza virus H1N1 causing a pandemic 1918; editors note*) and [another pandemic] it remained in all pandemics until the 2009. And then this swine flu virus developed a new nucleoprotein. And this nucleoprotein is not present up to now or this type in any of the H5 viruses. So, this is also something we have to remember: There is a lot of hurdles for these viruses, and this is probably the reason that it's up to now not going into really a pandemic situation. The virus has been spreading in birds since 1996 so many, many years, but it's now better than ever and we still have to follow it and be careful.

Host [00:32:45]

Yeah, maybe a question that also is fitting quite well: The head of the W.H.O. says we must prepare for a potential H5N1 human bird pandemic, if the science is uncertain about the potential for human spread, what is driving this remark?

Ian H. Brown [00:33:07]

Any spill-over event on the scale that we're seeing, as Martin says, it's a numbers game increases the risk, doesn't it? And we know from COVID, the pandemic preparedness takes time to get vaccines, antivirals, therapeutics. So, we have things on the shelves. We don't have H5 vaccines ready to vaccinate people. We do have, W.H.O have what they call candidate vaccine viruses. So, they survey all of these changes in the H5 viruses, and they put down what they call a seed vaccine strain. So, they can stop, they can start the process. So, to make a vaccine is quite a long process, as we know. So, they can do the preparatory steps. But it would be foolhardy to make a vaccine to H5 because which strain of H5, which one's going to give the best immunity in people? So, which is the one that's going to jump? We don't actually know if one is going to jump and which it is. You want to make sure you got the best vaccine, so you can do certain things. In terms of the preparedness, I think the W.H.O. was signaling it's really important that globally we work together, we do the tracking, we do the monitoring. We talked about the sea lion case. It's really important that that information is gathered quickly, and the data is shared with the international community to inform global pandemic preparedness. So, I think that's really the signaling that we're seeing a change, a bit of a step change in the spread of this infection. And we shouldn't say idle because obviously we know what happened with COVID.

Host [00:34:40]

There's also another question fitting this quite well: Is there a good enough surveillance going on in terms of genomics and are there gaps or which gaps are the biggest? Maybe this also goes again to you, Ian.

Ian H. Brown [00:34:56]

I'm sure Martin's just as qualified as I am, but I'll have a first go and I'm sure Martin will quit it. Look, we have come a long way from the emergence of H5 many years ago now, when that virus first emerged, data was quite slow. We didn't have the technology to generate genomes. We can generate genomes incredibly fast now, in hours. Then it probably took days and weeks. The ability to share data, there's an awful lot being done in the international space to generate free and easy opportunities to share data. In fact, encouraging that we have repositories where we can deposit these genomes and so they're available to the scientific community. So, the whole mind shift is changed, we have to be respectful, though, that those invest money and time to do the surveillance, the scientists, all the stakeholders, that they need to have value out of that work and that



needs to be respected. But I think the genome sharing now in influenza is better than it's ever been. There's always room for improvement. And I think the challenge will be as we move forward, as this virus finds its way into new populations and new parts of the world that may not have been experienced in doing this work in the past, they may need assistance and encouragement and support to make sure that we get the genomic data. So, we talked about the sea lions – keep going back to them, but it's an interesting point – have the right samples been taken? Is there a system where there are the resources to be able to generate this genomic data quickly and then share that with the international community? And the feedback is obviously the international community can provide advice and support to those countries in regions that are suffering these problems. So, you know, that is possibly the gap, these areas that are less used to doing this, but it's much better than it was, sure.

Martin Beer [00:36:54]

I also think we have to improve that, there is always room for improvement. But I would say, especially if there are events where we think something is special, like the outbreak with sea lions or some other die offs, than we need the sequencing as soon as possible and we need the sharing of the genomic sequences and finally also sharing the strengths on how to characterize the event if you are not having it in hand. This takes some time. We saw this also in the extremely busy times of the SARS-CoV-2 pandemic, where characterization and sharing of the origin strain early was also very important.

Host [00:37:35]

I got a bunch of questions that could somehow relate together, and I think fit your expertise. How high is the mortality in birds? And can you elaborate on bird species populations that you think are of special concern because they are affected predominantly?

Ursula Höfle [00:37:57]

So, bird mortality, that's a huge question. It depends very much on the species, there are bird species with very high mortality rates. Species that we knew are highly susceptible, such as pelicans. Right now, in South America, the brown pelican, the mortality is very high, but this bird is also very abundant. Just sticking with pelicans, last spring there was huge mortality in another pelican's species that in contrast to brown pelicans was very, very endangered, which is the Dalmatian pelican in Greece. So, in this case due to infection, they lost one of basically the largest colony in the world of the species and the population went down from more than a thousand birds to just 60. So, mortality depends very much on species, but depending on species, the mortality can be very high, especially in colony breeding birds. That's something Ian and Martin have already talked about. If the birds are close together, viral spread is far easier. So, this is the situation where we definitely get these high mortality events. Then on the other hand, there are a lot of species in which mortality is probably much more sporadic, which, for example, birds of prey. But on the other hand, among these species with very reduced, very fragmented populations, such as the bearded vulture or peregrine falcons, which are highly endangered: In those species just one of these stochastic events can be really, really harmful. So, it's the question that maybe Ian and Martin can add some more, but the general question is difficult to answer straightforwardly.

Host [00:40:14]

We only have eight minutes left, so I would like to come to another point. The vaccinations, how do you assess the role of vaccinations for poultry farming? I think this question goes again to Ian.



press briefing

Ian H. Brown [00:40:35]

Vaccination has been used in poultry for quite some time now against lots of diseases, in fact. And some diseases have been successfully controlled in poultry. So, this is quite possible. We now have new technologies, new generation vaccines, so we can do vaccination in a much more effective way. And some countries have been vaccinating for some time, but they've had variable success. So normally, where vaccination alone is used as the only frontline tool to defend against the virus, it will probably fail. I think it is recognized that it needs to be in combination with good surveillance, the ability to update the vaccines, the ability to monitor the efficacy of the vaccination program. And if you detect infective flocks, you still have to take action to remove infection. So, where vaccination is part of a control program, it can be highly successful. And obviously with this global threat now and with the benefits of advancement in vaccinology from COVID, there's a great opportunity here to develop more potent and efficacious vaccines. You've still got to be able to deliver those vaccines to large numbers of birds. That has to be practical. So, you know, how do you vaccinate a house full of 100,000 chickens easily and ensure that all of those birds have received vaccine? So that's a big challenge. And how do you then try to make sure that the virus that's in the environment in the wild bird population doesn't still spill over into those flocks? And, you know, as Martin touched on earlier, that these viruses are evolving so they could potentially, in time, escape vaccine immunity. So, you also need to have the potential to update the vaccine formulation. So, there are a lot of challenges before vaccinations make sense. Well, but we have the tools and there is an awful lot of work going on around the world now, particularly in Europe, which will be really moving this forward. Vaccination is a real possibility and ultimately probably able to reduce this very large 'fire' that's burning in avian populations. Vaccination is going to have an important role globally in trying to suppress this increasing problem.

Host [00:42:47]

Martin, do you want to add something?

Martin Beer [00:42:49]

Only a few additions. On one hand, for poultry, this is an option. We have to think [about this] now, also in the U.S., in Europe, where vaccination was not allowed before because we come into an endemic situation. So, if you have this now continuously, the pressure on the poultry farms is pretty high and vaccination is one part in stopping this. But we need the vaccine. So hopefully they will be available and will be tested and licensed. What it will not change a lot is the wild bird situation. So, this is still ongoing. But even there is some discussion about vaccinating, especially protected species, etc. But this will not be a big thing. So, I think we have three different parts: the wild birds, which we cannot change the situation very much. We have the poultry where we have all the hygienic measures and in the future in more parts, maybe vaccination. And then we have the spill-over infections which we have to follow.

Host [00:43:56]

Is there a risk that if you have infected poultry, that they seem to be healthy, but then they can also infect wild birds again? Is there also a risk of vaccinations for wild birds?

Martin Beer [00:44:09]

So, [concerning the question] that poultry is infected but you don't see it. That is always an argument which is against vaccination. And therefore, what Ian mentioned, we need this monitoring and surveillance systems to be sure that no virus is spreading in the background of vaccination. We don't recognize it and the virus might be changing, drifting away from the vaccine. But those are all things you can get under control by testing



measures and things like that. And I think in Europe it was not a major problem of the spillback from poultry to wild birds. But I think in Asia and Africa this is a major issue. So, there you have much more contact and not the same hygienic measures and I think this was the beginning of the whole story that this ping pong system was allowed for many years. And this could also not be stopped like in Egypt and other countries, Indonesia, by vaccination, but you could reduce it and you could also reduce human cases if you have a more zoonotic virus.

Host [00:45:16]

There was another question that I would like to forward to you in terms of prevention and looking at cases of COVID outbreaks, too: Would it be wise to close mink farms in general? Who wants to answer this question? Martin, go ahead.

Martin Beer [00:45:40]

I go ahead. So, I think we have to be careful overall in having animals in large numbers under suboptimal conditions and these highly susceptible animals. There are areas in the world where we are talking about millions and millions of these animals. And there I would say this is a continuous risk and we should have a very close eye on it. And if possible, this should be reduced as much as possible and should be controlled as much as possible. If you stop it totally, I think in Germany it's not possible also for welfare reasons. This comes in addition, and I think this is good, but other countries still also in Europe do it. And I hope that if they still have this kind of fur production, that it is under highly controlled conditions to avoid these kinds of adaptations.

Host [00:46:42]

Would the other two like to add something to that?

Ian H. Brown [00:46:47]

No, I just second what Martin has said. It's banned in some countries in the UK. We don't farm mink for the same reasons that Martin outlined. I think it's a recognition that there is a risk and not just for flu here. We're talking about any infectious disease [that] has the ability to invade these host populations. And we know that it's not such a big jump to people from such populations. So, is there inborn that they were controlled and the hygiene improved? If they have to be raised, then they have to be raised under better hygiene and very good monitoring. So, I know some rigorous systems were put in during COVID to routinely monitor. Monitoring in this sector probably wasn't something that happened before COVID. Then "Kirby" told us that we need to check them very regularly, and if we do that and we apply the proper hygiene, then obviously we can reduce the risk.

Host [00:47:47]

Thank you so much. Looking at the time, I need to come to a close now. I know we could not answer all the questions that you raised. I'm sorry for that. However, I would like to ask a final question. I will ask each one of you. Which aspect of the recent avian flu strains does concern you the most? If you were the journalist, which aspect would you address or stress in your reporting? I would like to start with Ursula, please.



Ursula Höfle [00:48:26]

For me particularly, I think I've stressed this several times, I think the wild bird component of this is really the key – it's a wild birds and poultry panzootic really. But it's the change in the epidemiology of this virus, the adaptation to wild birds and the impact it has on a lot of different wild bird populations and biodiversity that for me is something really serious. And then the second part is – what Martin has stressed – with increased numbers of individuals and increased circulation the opportunity for the virus to adapt to a lot of different situations increases, also to different species. So, the risk is the many opportunities the virus gets through this really widespread and wide circulation. And one of the things that Martin mentioned and Ian spoke to earlier, are the huge change we've seen in this virus and that makes it so interesting. On one hand, the danger of potentially dangerous variants and on the other hand that the virus changed completely in from what we've been seeing early during limited circulation, spreads and outbreaks generally during winter. Now not only the viruses adapted more to wild birds, and it has gathered force in violence and in spread between wild birds but it's also able to persist longer. We have outbreaks in summer even in regions for example, such as the Iberian Peninsula, where we've actually had very, very sporadic outbreaks, even in the early panzootics and other years. Because we used to have a lot of UV light, we have a very high temperatures and now we're seeing outbreaks in August in Spain, which is something really, really unprecedented. And this shows that this virus is changing in many ways that we don't have a handle on. And this is what I would like to stress.

Host [00:50:43]

Thank you. Ian, what would you stress when you were a reporter?

Ian H. Brown [00:50:48]

I touched on this earlier, I think the expansion of the virus' and it's ability to infect other host populations. On several occasions now we see the extent of wild birds that take the virus into places, nations and ecosystems that he's not been in before that increase his exposure to other populations. So that's a whole new dynamic, transforming and evolving quite fast on a global scale. And as that gets into those places, have we got good surveillance systems that are globally set up to track and monitor those concerning events fast? So that's the thing to me that, you know, if you have a risk and if this virus was there, heaven forbid, it jumped in a certain place to humans, we need to have done that basic work in the animal and birds' sector fast. So, it is again about global responsiveness here and working together globally to make sure that we can track this virus very fast and understand what it's doing next. So, I think that's my biggest concern, have we got that global structure to ensure that we're communicating? Have we learned all the lessons from COVID.

Host [00:52:08]

Martin, what do you want to add?

Martin Beer [00:52:11]

I would add, the major point is still it's a global panzootic in birds and it's reaching more areas now. And this is a point which is also worrying me the most at the moment that it's reaching areas where this type of virus has never been seen. And we are talking about a whole continent with a lot of different bird species which never had contact to this kind of virus. We even don't know what kind of other influenza viruses are there, how the whole population, the biosystem in south America will react. And there is also a lot of poultry farming in some of these countries. So, I think this is a new mixture we have to follow up very closely. And then as a next step, this spill-overs. So, to really be aware that this can happen to non-bird species. And finally, the genetic variability, so that this virus is changing a lot even if it goes under the same public name. So, one H5N1 is not



the same in all regions and this is something which means it's a highly dynamic situation which we have to follow closely, as Ian said. Sequencing at the moment and surveillance monitoring is the measures we really need all over the globe. And this is hurdle in some countries and we have to work on this to get this done even better in more countries. To be informed early enough if something crucial changes.

Host [00:53:48]

A big thank you to all three being with us here today, for answering all the questions. I would like to thank all the attending journalists for all your questions. I know it's a huge complex topic and we could probably continue this press briefing for another two hours. We will prepare a transcript and provide it on our website as soon as possible. You will find a recording of this virtual press briefing at the website of the German Science Media Center in about one to two hours, and also you can also send us an email redaktion@sciencemediacenter.de if you need a technical transcript rapidly without further editing. Thank you so much for joining. Thank you for your time and I wish you a nice weekend.



press briefing

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