CENTERS FOR DISEASE CONTROL AND PREVENTION
Moderator: Chris Motsek
March 23, 2017
2:00 pm EDT

Coordinator: Good afternoon and thank you for standing by. For the duration of today's conference all participants' lines are on a listen-only mode until the question and answer session. At that time, if you would like to ask a question press star 1. Today's call is being recorded. If you have any objections, you may disconnect at this time. It is my pleasure to introduce Mr. Chris Motsek, Deputy for CDC's Zika State Coordination Task Force. Thank you sir, you may begin.

Chris Motsek: Thank you, Holly. Good afternoon, good morning depending on your time zone. This is Chris Motsek, the State Coordination Task Force Deputy. Welcome to the Sustaining Zika Response in 2017 - Epidemiology and Surveillance National Webinar. We understand this is a communication focused webinar. Invited participants include state health officers; state, local, and territorial preparedness directors; epidemiologists; laboratory staff; and anyone who participates in Zika-related activities within their jurisdictions and other staff with Zika-related expertise within their jurisdictions.

We are aware that the invite has been shared with your constituents or other appropriate parties of interest. However, if you represent the media, press - we are going to ask that you please disconnect at this time. Today's discussion has been structured for public health participation. The intent of today's webinar is to provide a brief overview session on epidemiology and surveillance, Zika preparedness, and response activities. A functional two-way discussion will follow.

Following today's webinar, there will be 5 remaining subsequent sessions on the following functional areas: vector issues, public and private partnerships, pregnancy and birth defects, blood safety and medical investigations. Please keep in mind, we will continue to update our guidance as we learn more through research. Following today's presentation and question and answer segment, if you have additional questions, please feel free to email us at preparedness@cdc.gov again that's preparedness@cdc.gov.

Today: Dr. Carolyn Gould, who is the Clinical Epidemiology team lead for the CDC Zika Response, and Michael Johansson from the Zika Modeling Team. He's the Zika Modeling team lead - in the biology and the Dengue Branch - will be a subject matter experts representing the Epidemiology and Surveillance Task Force. So I will turn it over to the subject matter experts, and we wish you a good webinar.

Dr. Carolyn Gould: Thank you. Thank you to the State Coordination Task Force for inviting our task force to present today, and thank you all for joining the webinar. So, I will be first presenting an update on the epidemiology of Zika virus - going into a little more detail than I did on the first general webinar - if any of you attended that. And then Michael Johannson will present some results of the modeling work that he and his team have been doing to assess different surveillance strategies for detecting local transmission of Zika virus.

We hope this will be informative for jurisdictions that might be considered different enhanced or sentinel surveillance strategies as we move into the next mosquito season. Michael will then present some surveillance data from Zika, dengue, and chikungunya viruses in the Americas, and how that information can inform what we might expect to see for Zika virus in the coming season. Stacey Martin, who is the lead for the Epidemiology and Surveillance Task Force, will join us for the Q&A portion of the webinar.

Next slide please? Next slide. So Zika virus was first isolated from a sentinel rhesus macaque monkey in Uganda in 1947. Before 2007, only sporadic human disease cases were reported from Africa and Southeast Asia. In 2007, the first Zika outbreak was reported on Yap Island in the Federated States of Micronesia. In 2013 to 2015, more than 30,000 suspected cases were reported from French Polynesia and other Pacific islands.

Next slide. These are data from the World Health Organization showing the cumulative number of countries reporting local mosquito-borne transmission of Zika virus since 2007 by WHO region. You can see the dramatic rise in the number of countries reporting cases beginning in late 2015 and the Pan-American region followed by the Western Pacific region and African and Southeast Asian regions.

Next slide. In May of 2015, the first locally acquired cases of Zika virus in the Americas were reported in Brazil. The virus then spread rapidly throughout the Americas with local transmission of Zika virus reported in a total of 49 countries and territories in the Americas to date. The only countries that have not reported local transmission are Bermuda, Canada, and Uruguay. Chile is also on this list, but Easter Island - a territory of Chile - reported Zika virus prior to 2015.

Next slide. These are data from PAHO showing the numbers of reported suspected and laboratory confirmed cases of locally transmitted Zika virus by country in the Americas. As of March 9, over 750,000 cases have been reported. Shown here are the countries reporting the largest numbers of cases. The largest number of cases have been reported from Brazil, followed by Colombia, and Venezuela. Overall, of - about 1/3 of the cases in these reports

are laboratory confirmed. You can find more specific information on each country on the PAHO website.

Next slide. This is a pie chart showing the breakdown of suspected and laboratory-confirmed locally acquired cases of Zika virus disease in the Americas by region. South America accounts for 70% of cases, followed by the Caribbean with 21%, and Central America with 8%. North America, which includes Mexico, accounts for only 1% of reported cases.

Next slide. Narrowing down our focus to the United States, prior to the outbreak in the Americas between 2007 and 2014 only 14 Zika virus disease cases were identified among US travelers. Cases among travelers have increased substantially since then. Local transmission in the US has only been identified in South Florida and Southern Texas. Outbreaks have occurred in 3 US territories: Puerto Rico, US Virgin Islands, and American Samoa.

Next slide. These are laboratory-confirmed Zika virus disease cases reported to ArboNET by US states and territories as of March 8. You can refer to the CDC website for the most recent numbers. As of March 22, which should be posted today, there were 5,109 cases reported from US states, most of which were travel associated cases.

There were 221 cases acquired through presumed local mosquito-borne transmission, 215 in Florida and 6 in Texas. Seventy-five cases were acquired through other routes including sexual transmission, congenital infection, laboratory transmission for one case, and an unknown probably person-to-person route for 1 case. In the territories there were 38,099 cases reported, most of which were locally acquired.

Next slide. This is the map of the US showing the numbers of reported Zika virus disease cases by state and territory as of March 8. The darker colors represent higher numbers of cases reported. This map is also on the website.

Next slide. This table shows the state of residence for reported Zika virus disease and presumptive viremic donor cases as of March 8. Shown here are states with the highest number of reported cases. The symptomatic disease cases for Florida and Texas include both the travel-associated and locally acquired cases, as you can see in the footnote.

The presumptive viremic donors are those whose blood tested positive, when screened upon donation, for Zika virus RNA by the blood collection agency and who meet the laboratory criteria for confirmation, as outlined in Appendix E of the ArboNET reporting instructions. Reported presumptive viremic donor cases were recently added to the website. Because some presumptive viremic donors might develop symptoms after their donation or might have had symptoms in the past, they may be reported as both Zika virus disease cases and presumptive viremic donors.

Next slide. So, moving to the states reporting local transmission. In Florida, sporadic locally acquired cases began to be reported from several South Florida counties beginning in July 2016. Active mosquito-borne transmission was later identified in three small areas of Miami-Dade County. This led to designated red zones being applied to those areas with recommendations for pregnant women to avoid travel to these areas, and for testing, and follow-up of pregnant women with exposure to those areas. Florida led an intensive public health response including aerial adulticide and larvacide applications, which helped control the outbreaks. There's currently no evidence of ongoing sustained local transmission in Florida, although Miami-Dade County remains a Zika cautionary or yellow area.

Next slide. This is the current map of Miami-Dade County on our website showing the previous active Zika virus transmission areas and the ongoing yellow area in Miami-Dade County with the recommendation that pregnant women should consider postponing travel to the area.

Next slide. Moving to Texas. The first case of local mosquito-borne Zika virus infection was reported in Brownsville in November 2016. This area borders Mexico - very close to areas where Mexico has reported active Zika virus transmission. Because of additional local cases identified in Brownsville, most of whom lived in very close proximity to the index case, Brownsville was designated a yellow cautionary area in December of 2016 leading to recommendations for pregnant women to avoid travel to that area and for testing and follow-up of pregnant women. To date, there have been 6 cases of local transmission reported in Brownsville.

Next slide. And this is a map on our website showing Brownsville with the yellow area designation. And just note the proximity of Brownsville to the US-Mexico border.

Next slide. So moving to some data from the territories, these are the reported Zika virus disease and presumptive viremic donor cases from the territories as of March 8. Puerto Rico reported the majority of the cases, followed by US Virgin Islands, and American Samoa. Of note, data from the enhanced Zika virus surveillance system in American Samoa have indicated that Zika virus transmission has been interrupted there. And this will be described in an MMWR report to be published tomorrow.

Next slide. And this is a map from the Puerto Rico Department of Health website showing the municipality of residence for reported Zika virus disease

cases in Puerto Rico - as of January - showing widespread Zika virus transmission on the island.

Next slide. And here you can see the age distribution for reported Zika virus disease cases in the US states and territories, as of January 25. The higher numbers of cases in the 20 to 39 year age group and the 40- to 59-year-old age group may reflect, in part, the additional testing occurring in pregnant women as well as exposure among travelers in these age groups.

Next slide. And finally this is the epi curve showing month of illness onset for Zika virus disease cases reported in US states and territories with a peak of the outbreak occurring in late summer with a steep decline occurring in the fall and winter. I'm now going to turn it over to Michael Johannson to discuss the modeling analysis to inform strategies for detecting local transmission as well as projections for the upcoming season. Thank you very much for your attention.

Michael Johansson: Thank you Carolyn. So I'll get started here. What we set out to look at here is, in the absence of known local transmission what are different ways that we could detect transmission should it be occurring, and specifically trying to look at what the effectiveness of different approaches would be. So I want to be clear from the beginning that we looked at three general strategies. And these are not going to be strategies that are necessarily applicable everywhere, and there may be additional strategies that should be considered. But they're general strategies to help us compare different types of approaches that we could take.

So, the first strategy is to test all pregnant women twice during pregnancy akin to what the recommendations are for areas with local transmission. And this testing, in this case, would use the IgM MAC-ELISA assay. Another option is

to just use blood donor data. So, testing all blood bank donors using the NAT assay. And then the third option is using emergency department patients.

And in order to do those, we need to consider the chief complaints that emergency department patients expressed that might be related to Zika so use data from BioSense surveillance across the US. And then we also need to consider what proportion of symptomatic people with Zika might actually seek care. So we used data from Puerto Rico to understand what proportion of actual infections might end up in symptoms and might end up with/in people with symptoms who are seeking care and then might get detected. And we assume that the assay used for detection there would be RT-PCR. Again, these are just three different approaches. But I think, as you'll see, there's some broad insights to be gained just from looking at these.

So, go to the next slide. Here - this is probably the most complicated slide. So I'll take a couple minutes to go over this. What we're looking at here is the probability of detection given different surveillance systems under different scenarios. So there's three different plots here. These plots are for three different population sizes - a population of 10,000 people, 100,000 people, and a million people.

And on the x-axis is different incidences of infection. So we want to - sorry I think it just got advanced there. Can you go back one more? Yes that's the one, thank you. So, looking at different instances - incidences of infection and different populations sizes, we have different probabilities of detecting cases should they occur.

Now if we look at the center plot here, we can look just at the right side and where we have one infection per 1000 people in the population per week. And then look at one of the bars here so we can look at the blue bar. And that

represents an uncertainty interval - a 50% uncertainty interval of how likely we are to detect transmission should an infection be occurring at that level using that particular surveillance system, which in this case is looking at emergency department patients exhibiting rash. So in that case, what we're saying is that we think it's most likely that we will detect 60% to 90%, or that we have a 60% to 90% probability of detecting cases. So we're more likely to detect the cases if there's a live level of transmission in the population size and we're using the ED patient surveillance system.

So if you look across these three graphs you can see that with a population of 10,000 people you're unlikely to detect transmission given any of the systems. If you look at the population of 100,000 people you can see that we're most likely to detect infections, if we're doing surveillance among ED patients with rash followed by ED patients with headache and rash. And we use headache and rash because out of the five symptoms we looked at that was the symptom combination that was most common among Zika virus infections. If we look at pregnant women, we have a slightly lower probability to detection. And if we look at the - just using the blood bank donor assays - then we have a lower detection probability of detection.

If we then look to a population of a million people on the right, we can see that all those properties are higher. And that's because when we have a larger population at the same incidence rate, we have a higher number of cases. So we're more likely to detect those cases because there's just more of them. And you can see that if we had a high incidence in a large population, even with the blood bank donor surveillance system, we're likely to detect cases. So really, we're trying to look at the distribution of how likely we are to detect transmission here.

Next slide. There's also other components of this. So on the left here is the number of tests that you would have to do per week. And remember that these are different tests. So for pregnant women is the ELISA, for blood bank donors it's the NAT assay, and for ED patients it's RT-PCR. So we can see that we have to do the most tests with - for the blood bank donors, followed by pregnancy - pregnant women, followed by ED patients with rash. And really, we have to do quite a lot less testing, If you're only testing ED patients that have headache and rash. And that's because a relatively low number of those present at emergency departments each week.

If we look to the second - oh yes - so all of these numbers are considering a population of 100,000. The ones on the far right, of which I'll get to in a minute, are not dependent on the population size, but a number of them are and all of those are just they just scale directly with a population. So if we had a million people, it would be ten times as many number of tests per week and ten times as many false positives per week. And we'll use that 100,000 for the rest of the slides moving forward.

So, this middle plot is the number of false positives. And so specificity is lower with the ELISA than the other assays. So, we get more false positives if we're only testing pregnant women. And of course that's important because among pregnant women, we were particularly concerned about infection, and that would require follow-up on those cases. So we want to avoid doing too many tests, and we also want to avoid false positives when we can.

The third component of the slide on the right is just showing the proportion of overall infections that are detected. So on the top is .05 on the y-axis. So that means that none of these systems would even detect 5% of all of the infections that occur. And that's because a lot of the infections are asymptomatic or mild, and people don't seek care, or that you're testing a relatively small

proportion of the population in the case of the pregnant women and blood donors. So, it's important to sort of keep that in mind, in the background, that we're trying to maximize our probability of detection knowing that we're only going to be able to detect a small proportion of the infections that will actually occur.

Next slide. So what we saw especially looking at the - in terms of the ED patients - that we were doing less tests and we had the highest probability of detection. So we looked at all the different possible symptom combinations they're because we really want to balance symptoms that are uncommon in ED patients. So we want to limit the number of tests that are being done on people who might not be infected. But we also want to maximize the symptoms that are common among Zika virus infection, so that we can maintain a high probability of detection.

So as we look across here, we can see that some of the symptoms on their own are quite common. But when we start looking at the combination of symptoms which is expressed in a number of tests - so on top is a number of tests that you would need. So those are the number of people in a population of 100,000 who would likely be presenting at emergency departments each week with those symptoms that it quickly becomes very low, as you start combining symptoms. However when you get to the end where we have two or more symptoms, three or more symptoms, and rash plus any other symptom, we have a certain number of tests there. So we're back up around ten test per week in a population of 100,000.

And then we go down to the bottom side. When we're looking at the probability of detection, we can see that using just rash has the highest probability. But when we go down to those on the far right again with two or more symptoms, and three or more symptoms, or rash plus any other symptom

which are akin to many of the case definitions that are currently being used, we maintain a relatively high probability of detection. So we don't lose a lot of probability of detection, but we drastically decrease the number of tests that need to be done.

Next slide. But here is just comparing those three case definitions with just using rash. And again, you can see that all the different incidences of infection looking in a population of 100,000 people. We have relatively comparable probabilities of detection with the three or more symptoms being slightly more restrictive and a slightly lower probability of detection than the more inclusive definitions.

If we look on the right we can see how that compares to the number of tests, which also then relates to the number of false positives, which is low with these assays anyways because were using RT-PCR. But you can see that by moving away from just rash to symptom definitions that or case definitions that include multiple symptoms, you can drastically reduce the number of tests that are needed.

Next slide. So there's limitations to the model, as I mentioned before. First, there's many variables. Each one of them has uncertain and also variability across jurisdictions. So we have and present a lot of those details today. We have all those details. And we're working on writing them up so that we can share them later. The analysis was also just limited to the surveillance strategies, though many other strategies are possible.

We've limited the syndromic surveillance to ED visits because that was the data that we were able to obtain. But there's certainly other places that you could try to capture syndromic illness. And then the cost of the analyzing these - implementing these systems - was not something that we specifically

analyzed here. And that's something that would likely vary by - substantially by jurisdiction depending on the infrastructure and other considerations that are in place there.

Next slide. So the conclusions for this are that the probability of detection for any surveillance strategy depends on the incidence of infection and the population size. So I think those things are important things to consider for the – from the beginning - when trying to decide what surveillance system will be most appropriate, and how likely you are to detect transmission when it's occurring.

Second, the expected proportion of the infection detected by any system is low. So we know that there's going to be a lot of infections that are not going to be detected by any of these systems. Third, assay specificity is important. So we want to avoid false positives that are going to – we're going to require follow-up. Fourth is that, testing ED patients with Zika symptoms is likely more effective than testing pregnant women or blood donors because we have a higher probability of detection, and we also have fewer false positive results.

And then among ED patients, case definitions are ideally capture symptoms that are common among Zika virus infections and uncommon among ED patients who are not necessarily Zika virus infected. So that when there's no Zika virus transmission, there's not a lot of testing being done on people who don't have Zika. Of course we need some of that testing in order to be able to detect it, should it occur. So it is really - balancing those trade-offs is key in terms of making case definitions and deciding on a surveillance strategy.

Okay next slide. So now I'm going to shift themes a bit here and just speak briefly about what we expect in terms of epidemiology in 2017 on kind of a broad scale. So next slide. There's three tiers, I think, to think about in terms

of risk. One is what are the epidemics in the tropical areas? What's going to happen there? Are we going to have big epidemics in 2017 like what we saw in 2016?

Those of course pose risks to travelers, which can lead to infected travelers as we've seen many arrive in 2016. And then that can then lead to risk of local transmission in CONUS and Hawaii. So, I'm going to use some evidence from Zika, chikungunya, and dengue to talk briefly about each of those. And I'll just go one slide quickly on each of them, and then we can discuss more later as needed.

So the next slide please. So looking first at Puerto Rico and other tropical areas, the plot on the right here is specific estimates that we've made for Puerto Rico. So, we've used three different surveillance systems, one on suspect Zika cases, another on Guillain-Barré cases, and another using blood bank data to then estimate the total number of infections that are occurring. And this was the number of infections, not the number of symptomatic ill people seeking care but the total number of infections.

You can see that the estimates from each of these vary quite a bit both compared to each other and over time, and that there's quite a bit of uncertainty in them. But you can also see that there's agreement among them. So, we're fairly certain that a - I mean it's clear that a large outbreak occurred. And these - all of these estimates come together to suggest that 20% to 30% of all people in Puerto Rico were infected in 2016. Now I show this example for Puerto Rico in particular because we have done a lot of work here, and there is very solid surveillance data. Modeling estimates for other locations suggest that similarly large outbreaks have occurred. So many places have experienced large outbreaks over the past year and in some cases, in Brazil in particular, over the past two years.

Nonetheless, this level of exposure is not enough to engender herd immunity on a population level. So the fact that there has been these huge epidemics does not prevent future transmission from occurring. So we think that local transmission is likely to continue. And in fact, we see that for chikungunya. So we had the big epidemic of chikungunya in Puerto Rico - what three years ago now - and we are still seeing cases almost every week of chikungunya. That continues to happen, although it's not as common as it was in in that first year when the major epidemic happened.

So which gets to the next point is that another large epidemic is not likely. So, while we expect to continue seeing transmission in Puerto Rico and other areas is there, we're much less likely to have large epidemics in the near future because so much of the population is now immune. And that does reduce the transmission among other people. That also in turn means that large scare geographic spread is likely to be more restrictive than what we've seen in the past. So because there's less transmission in these areas, there's also less likely to be less exposure to travelers.

Next slide. And this is really looking at, sort of, what that might look like. So on the top on the right, we can see the number of imported cases of chikungunya in the United States over the last nine years. So you can see before the introduction - so introduction in the America happened in the end of 2013. And you could see that there were travelers - infected travelers - arriving in every year before that but that's really when the spike happened. And the big epidemics happened in 2014 and then into 2015. And that's really when most of the infected travelers were arriving. Since then, they continue to arrive, but it's decreased substantially.

Chikungunya has a lifelong immunity for most people, as we expect that Zika does. So we expect that this trend will be similar because there's been a decrease and a lot of people have already been infected. So now there'll be a decrease in transmission in these areas, which means less transmission to travelers and a fewer number of travelers arriving in the US infected with Zika. But we don't expect that to go away.

On the bottom, we can see that both chikungunya and Zika. And so the Zika data that Carolyn showed earlier is the same data and then we just superimpose chikungunya upon that - that we see seasonality among travelers. And that's because a lot of travelers are coming from the Caribbean, Mexico, and Central America, where the dengue transmission season really corresponds to the Northern Hemisphere summer into the late summer and early fall. So we expect this seasonality to also continue to be the case for Zika although cases can clearly happen in other times of the year - likely due to exposure in other locations.

Next slide. Lastly, what does that mean for our autochthonous transmission risk? So we can look at dengue, chikungunya, and Zika for this. For dengue, we had introductions over the years. So we've had, you know, travel-associated cases every year for quite some time now. And occasionally we see sporadic transmission. The plot here makes it look a little bit like this is increasing, but we really don't have strong evidence to support that. But the bulk of the cases at the end are due to the one outbreak in Hawaii that was relatively large.

With chikungunya, we saw in the first year - I think there was a total of 12 travel, 12 autochthonous cases reported in the US followed by one case in 2015. So again, there was increased risk in the first year and then probably decreased risk after that. But there's still risk of it occurring. With Zika we've

already seen over 200 locally acquired cases in the US. And in terms of the relative numbers here, there's been a lot more effort in terms of increasing surveillance activities, which makes us think that detecting higher numbers of cases of Zika is likely, even if the risk is not substantially different from what we've seen with these other diseases.

So while this risk continues and continues to be associated with travel-associated travel - imported cases associated with travel - we expect that that risk of introduction is going to be going down. And that these local transmission events could continue to occur but will probably be less likely to occur as there are fewer introductions.

Next slide. So just to kind of summarize that if we looked at Puerto Rico and other dengue epidemic areas, there's herd immunity is growing but it's not likely high enough to prevent future transmission. So it's going to reduce future transmission but not eliminate it. For US travelers that means risk will continue, but it's likely going to decrease. And it will likely show seasonality as we've seen with chikungunya.

In the US states limited, local transmission could occur as we've seen before with both dengue and chicken now Zika, but it's likely to be sporadic and small clusters again as we've seen before. And we might also see more of it in terms of the that we're actually detecting more of it through surveillance as improved surveillance and testing is implemented across the US compared to what we had previously with dengue and chikungunya.

So the take-home message is that we don't expect Zika to be the same in 2017 as it was in 2016, but it is likely to continue to occur on all of these levels. That we will have more local transmission in endemic areas that will lead to infected travelers. And that may lead to small local outbreaks within the US.

So with this, I think, that's the end of our presentation there, and I will turn it back to the moderator.

Chris Motsek This is Chris. I just want to say thank you. Right now, what we would like to do, Holly, is get a question and answer session going with Dr. Gould, Michael and Stacey, if possible.

Coordinator: Thank you. To ask a question unmute your phone press star followed by the number 1. And when prompted, record your name clearly so I may introduce you. To withdraw your question press star 2. Again, to ask a question press star 1. It will take a few moments for questions to come in. Please stand by. Our first question comes from Brad. Your line is open.

Woman 1: (Unintelligible) me?

Coordinator: Yes. Your line is open. Dr. Randy Culpepper your line is open.

Randy Culpepper: Thank you so much. I have two questions regarding to better pinpoint where we should direct our communication efforts. Do you have data on the proportion of cases by ethnicity or race? And the second question is, do we have data on where our US travelers are primarily getting infected? Which countries they're traveling to? Thank you.

Dr. Carolyn Gould: I don't. We don't have that offhand in terms of the cases by ethnicity. I would have to check and see if - what level of demographic data we're getting in ArboNET to be able to answer that question. So that's something we can look into. So that would be dependent upon what the states are entering into ArboNET. And then, as far as the travel associated cases, we have looked at that. And there was data published in a previous MMWR, of - about the most frequent areas that travelers coming back with Zika virus disease went to. But

in general, the highest number of travel associated cases we have, have come from the Caribbean, followed by Central and South America, I believe. But that's other data. Again it's – there is an MMWR that sort of laid out the regions for travel associated cases.

Randy Culpepper: Thank you very much.

Coordinator: Our next question comes from Mr. (Drocheck) with the South Carolina Department of Health. Your line is open.

(Drocheck): Thanks for taking my question. With regards to the section on the modeling and surveillance strategies, I appreciate the information regarding laboratory testing to detect Zika transmission. One of the criteria that is often used along with some presentations is travel history. Did you – have you looked at that in the model to see how it increases or decreases the false positive rates or such because, I think, when you look at just laboratory testing in the population - that's only in my opinion - that's just part of the picture?

Michael Johansson: Yes. So we were. The modeling exercise was specifically to look at people who didn't necessarily have a travel history. So we're looking for local transmission in the absence of other information that would lead you to believe that it's travel associated. So there is guidance for testing among travelers already that I think would capture those people. So we weren't as concerned about that component with this model. This is more about how to detect cases among people who have not necessarily been traveling.

(Drocheck): Thanks.

Coordinator: Our next question comes from James Watt with the California Department of Public Health. Your line is open.

James Watt: Thank you very much. I have a question of - about your projections for disease incidence in the US-Mexico border region. In California, most of our travel-associated cases have traveled to Mexico. And it's our understanding that in Mexico, disease last year was initially higher in southern states and then kind of moved north later in the season. And I'm just wondering what we might expect along the border based on your modeling given that disease levels were relatively low in northern Mexico in 2016?

Michael Johansson: So I think it's a great question, and I'm not going to have a satisfactory answer for you. I think the, you know, what you've said - I haven't looked specifically at Mexico in terms of any detailed modeling. What you said in general about the epidemiology is correct in terms of what the data has shown us.

I think it's - and it's quite likely that there's been a lot of - a lot more transmission in different parts of Mexico than what we can necessarily read out of the surveillance data. And, I think exactly when outbreaks are happening in different populations can certainly vary, and I don't think we have a particularly good read on that, I think. As in all other places that once epidemics - well at least in like the dengue endemic areas where we know that there's been substantial dengue transmission in the past which is not all of Mexico but many parts of Mexico - we'd expect that once cases are reported there that big outbreaks are happening whether or not we have like full reports of all the data there. And then after those big outbreaks occur, we'd expect transmission to go down as well as the risk among travelers. I hope that at least helps sort of orient the answer even though I don't have a particularly clear one.

James Watt: Thank you.

Coordinator: Our next question comes from Mark Durand with the Pacific Island Health Officers' Association. Your line is open.

Mark Durand: Yes thank you. I have two questions. First of all, I'm wondering if there's any new information on the duration of IgM positivity for Zika virus? It's number one. Number two, the modeling presented today looks like in smaller populations the chance of detecting active transmission is a lot lower than we would like. And I'm wondering how that would affect. Usually we used two or three incubation periods during active surveillance with no new cases to sort of be our benchmark for declaring an end to transmission. I'm wondering if there are any specific guidelines that may be coming out for Zika for smaller populations? Thank you.

Dr. Carolyn Gould: Yes. We don't -- this is Carolyn -- not a lot of new data on duration of IgM positivity. It's obviously a question of great interest. There have been reports of cases, you know, that have had long, you know, up to seven months of IgM positivity for Zika virus. So but, you know, after three months, it does tend to wane in some people. And so that's why the guidance still recommends to - for the testing to be performed within 12 weeks of symptom onset because having a negative test after the time period wouldn't necessarily rule out infection.

And I think that that's a question we can also direct to the lab task force. As far as guidance for end of transmission - so you're right. It's, you know, unique situations where you have small populations, like I've referenced the America Samoa situation before, you know, relatively stable population with likely high population and immunity following widespread Zika virus transmission. There is a potential for interruption of transmission. And we've used, you know, as you referenced, three mosquito incubation periods as sort

of a conservative window - with no new cases - to indicate interruption of transmission as long as there is, you know, a good enhanced surveillance system occurring so that, you know, cases that are symptomatic are being tested.

So that is a unique situation to certain areas that have very small populations. I think in other areas where the population isn't so stable, and there's a larger population as Michael showed with Puerto Rico where 20% to 30% of the population was likely infected, we're - you know - the potential for interruption hasn't happened yet. So it's likely that those areas will continue to see cases but maybe not to the degree that we saw this past season.

Michael Johansson: Maybe I'll just add briefly to that - that in the case of local transmission and the enhanced surveillance activities that are happening, there's also enhanced awareness. And I think there's, you know, an opportunity to capture a larger percent of the symptomatic individuals that are there, so that you would have a better opportunity of capturing cases should they be occurring. And you're also looking over an extended period of time. so the numbers that I presented were a weekly probability of detection given a weekly infection rate. And if you had sustained transmission over multiple weeks, your probabilities increase because you're continuing to do surveillance, and you'll then have a chance of detecting it.

Mark Durand: Okay thanks. No specific guidance. But just sort of bear in mind that it may take more weeks of active surveillance to be sure there's no transmission in smaller populations.

Michael Johansson: Yes. So in the absence of known transmission, it's been like an ongoing challenge to detect transmission, should it occur. But in the presence of known transmission then that's when the other like the three-week guideline comes

into play, and enhanced surveillance activities are usually undertaken as well. So that kind of changes that equation a bit.

Mark Durand: Okay, thanks.

Coordinator: Our next question comes from (Allison Romano). Go ahead, your line is open.

(Allison Romano): Yes, thank you. I wanted to thank you all for going over all of this information, and I had a question. Regarding your rigorous detection strategies, I just wanted to be clear that even with those strategies outlined that they would probably only reveal 5% or less of the cases? I wanted to confirm that. And then also to ask if you had any idea of the 5100 cases that we are seeing here in the US - do you have any idea what percentage that may be of the total cases that might be out there based upon your estimation given some of the other data that you've revealed?

Michael Johansson: Yes. So I'll address the second one first. I don't think we have a good number on that. There's clearly, you know, different degrees of surveillance happening among travelers in different locations, and we don't have a good sense of what that means relative to the overall infection rate. So we haven't tried to make estimates of that.

And on your first point, the probability of detecting and its infections being less than 5% is - that is the right interpretation. If you, you know, I'm just saying this to be specific that, you know, sometimes we call a case symptomatic infection, but in this case, we're looking at all infections. So out of all of the people - symptomatic, asymptomatic, mild symptoms, more pronounced symptoms - where we're detecting less than 5% of all those infections. And that less than 5% is, in part, because with pregnant women

and blood donors we're only sampling a part of the population. So the best we can do is detect all infections among those people.

And in that case, we are looking that includes asymptomatic people or mild people because they would get tested in that case. And then when we're looking at ED patients or symptomatic people that by nature limited to people who are symptomatic and seeking care. And then in our case, we use seeking care in an emergency department, but you could use seeking care in any facility and probably increase that percentage to some degree. But it's still only going to be capturing a small fraction of the cases that actually - of the infections - that actually occur.

(Allison Romano): Got you. Thank you very much.

Coordinator: I show no additional questions at this time. But if you would like to ask a question, unmute your phone, press star followed by the number 1 and record your name clearly, so I may introduce you. Again, to ask a question it is star 1. Again, one moment please for incoming questions. Our next question comes from Katherine Feldman. Go ahead. Your line is open.

Katherine Feldman: Yes hi, its Katherine Feldman in Maryland. In light of the projections that you presented, is there going to be any revised guidance specifically regarding the vector control guidance? Thanks.

Dr. Carolyn Gould: So not based on any of the data that has been presented here, as far as we know. But that would be a question for the Vector Issues Task Force. So we can pass that to them.

Katherine Feldman: That's great. Thanks

Dr. Carolyn Gould: Thanks.

Woman 2: We should add though that we are using the data that was presented to revise the CONUS plan, and we're the final stages of doing that. I suspect that that will be available probably in the next week or so, and expect a presentation of that at a future date.

Katherine Feldman: And does that CONUS plan - it's Katherine in Maryland again - does that CONUS plan include the vector?

Woman 2: It – briefly - it's not a vector plan, though - it's primarily epi response.

Katherine Feldman: Okay. And so, since I have the line still -Katherine here - I'll just again - something I've been speaking to some of you folks about; recognizing that the risk and certainly looking at historical evidence - looks like the risk of local transmission varies across CONUS, so that Florida and Texas are not the same as Maryland. And if there's any way to have like a tiered approach to vector control or if that's indicated given the historic data and projections? Thank you.

Woman 2: We'll make sure that the vector team gets that comment.

Coordinator: Our next question comes from Mr. Bailey with the Florida Department of Health. Go ahead your line is open.

Danielle Stanek: Yes this is Danielle Stanek. Can you hear me? Hello.

Coordinator: Yes. Your line is open.

Dr. Carolyn Gould: I can hardly hear you, Danielle.

Danielle Stanek: Can you hear me now?

Woman 2: Somewhat, go ahead.

Danielle Stanek: Okay. The question I have is, what duration for Dr. Johannson's modeling - what was the duration of time that the tests were assumed to be positive for, particularly for the NAT and the PCR? We had an imported case that was confirmed PCR-positive, and they were picked up on the NAT more than 60 days after the original – with the original illness in the sample. And that was confirmed initially at our labs and then the NAT was run two - more than two months later and was positive. And on the PCR was this run with the urine serum combo for the model as well? That's my other question.

Michael Johansson: Yes. So there's clearly uncertainty and a high degree of variability around these. So we really looked at what might happen on average because that's sort of more important than what happens in extreme cases, in terms of detection. So that said, for the - for IgM detection among pregnant women, which we don't have great data on. We went with a range of two to four months that it would be detectable.

For the NAAT assay, we assumed it would be detectable within two weeks. And there was some variability around that too - which I don't have off the top of my head in terms of uncertainty - that we incorporated. And, that again, that's- a mean - so we know that some will be detectable longer and some are likely detectable shorter amounts of time. And then for the PCR, we just – we assumed that it was going to be detectable because we were capturing symptomatic patients. So we assume that, you know, they're presenting at the same week of onset, and they're likely to be PCR positive at that point.

Danielle Stanek: And that was serum or serum and urine?

Michael Johansson: Serum. So yes, so serum for pregnant women.

Danielle Stanek: Okay…

Michael Johansson: And then…

Danielle Stanek: …because we have about a 40 60% positives on serum compared to if you looked at 100% of the positive urine.

Michael Johansson: Yes. So I guess we didn't look at urine specifically because I think most of the PCR has been done on serum. We did incorporate limited assay sensitivity as well. So that there is, you know, it's not that everyone's necessarily PCR- positive. It's that they're likely viremic at that time and could be detected by PCR, but there's also limits to the assay.

Danielle Stanek: Thanks.

Coordinator: Our next question comes from (Sherry Jin) with Parish County. Go ahead, your line is open.

(Sherry Jin): Yes. My question is on slide number 7. And this notation says number 7 of the cases are live confirmed. So my question is, how do you determine the case for the rest or 77% - just by clinical or by age link? Because, you know, Zika - the symptoms of Zika are very similar to dengue, to West Nile, and chikungunya. So, and that - like in Puerto Rico, in Honduras (unintelligible) - in those countries, they have all the disease together. So how do you determine this is Zika - not other disease?

Dr. Carolyn Gould: Yes. That's, Carolyn, that's a really good question. I think these are data that PAHO collects from the various countries. And, you know, there's varying degrees of laboratory testing depending on the area. And so that's why that sort of caveat was put in there because there are a large number of suspected cases that are included in these numbers, based on what's reported by the countries to PAHO. So it is a limitation of this data for sure.

(Sherry Jin): Okay. Okay, thank you.

Dr. Carolyn Gould: Thanks.

Michael Johansson: It's also – maybe. I'll just quickly - that it's a limitation of assays in some cases too because in a lot of these locations where dengue is endemic, the IgM test that would often be used are not necessarily as useful in terms of picking up cases. So there's limits in what they can detect in that way too.

(Sherry Jin): Okay.

Dr. Carolyn Gould: And add the variability and case definitions that are used as well across the various countries.

(Sherry Jin): Thank you.

Coordinator: Our next question is from (Kim Porter) with Field Services Branch. Your line is open.

(Kim Porter): Hi. Thanks very much. I actually have two quick questions, if time allows. One is, do all the viremic blood donors that you reported have travel history? And then also, do you have some new, any updated data on the role of sexual transmission in these outbreaks? Thanks.

Woman 2: So, it. Not necessarily for the first question. For the presumptive viremic donors and some -particularly in Florida - some of them may have not had a travel history. But I don't have that information off the top of my head, but that isn't - most of them do. Most of them are travel-associated cases , of - just like the disease cases are. And I'm sorry, can you repeat your second question?

(Kim Porter): Oh sure. I just wondered if there were any new data available or any, you know, additional analyses of - that indicate kind of the role of sexual transmission in Zika. We still have trouble sometimes talking about that too much in our state. And I just wondered, if you had any estimates on how big a role that's playing?

Woman 2: We don't have estimates on how big a role it's playing. It's also difficult to determine that, particularly in the territories and other areas, where there's active Zika virus mosquito-borne transmission because it's impossible to really distinguish between the two. And that's one of the reasons why we don't include that other route of transmission in the case classifications on the website for the territories. There is a lot of interest in this topic though. There was just recently a large international meeting in Geneva to discuss sexual transmission. So there's a lot of interest in research in that area. But we believe that it plays an important role in transmission.

(Kim Porter): Thanks.

Coordinator: Our next question comes from (Hannah Beringer) with Virginia Beach Department of Public Health. Your line is open.

Anna (Beringer): Thank you. It's Anna A-N-N-A. I'm with the Virginia Beach Department of Public Health. My question is, with the data that was shared today about detecting locally transmitted cases, were these individuals tested through public health state laboratories, through the CDC, or private laboratories, or was it a combination of all of the above?

Woman 2: So you're talking about the cases that were detected in Florida and Texas?

Anna (Beringer): Just the models that they share. That - how they would expect to detect a certain percentage of cases to detect local transmission.

Woman 2: Okay.

Anna (Beringer): And I wondered what means of testing these individuals either have or would go through?

Michael Johansson: Yes. So those aren't actual testing numbers. So we - the modeling part is that we simulated what that would look like given those different surveillance approaches. So if we had a population that had a certain infection rate, and we wanted to implement one of these approaches -you know – what, like on average, how many pregnant women are there at any given time? How many blood donors are there per week?

And figuring out the numbers of tests that you would then need to test those people and a likelihood of detecting transmission at different infection incidences, should that occur. So these are not actual test numbers that have been run but rather an analysis of what these different approaches would look like, and the way that you might actually implement them in different places would probably vary substantially.

Anna (Beringer): Okay, thank you. So I guess the answer is that it could be a variety of testing means - not all through public health - not all through private laboratories, but from various sources.

Michael Johansson: Yes. I think there would be different ways to accomplish those strategies. And it's more like overall guidelines on what kind of strategy might be most effective.

Anna (Beringer): Thank you.

Woman 2: Are there any more questions?

Coordinator: We do have a question from (Waldo Lopez). Go ahead, your line is open.

(Waldo Lopez): Yes good afternoon from the City of (Regal) Health Department. Is Zika associated with heart disease as we have read an article from the Mayo Clinic that's doing some research in Venezuela and found some associations? But is it significant enough?

Dr. Carolyn Gould: I think, at this point, the data really are too limited to draw conclusions about the potential impact of Zika virus on heart and cardiovascular disease. So I don't think we have enough data yet.

(Waldo Lopez): I have another question, ma'am. Once you have Zika, can you get Zika again?

Dr. Carolyn Gould: We believe that Zika infection confers lifelong immunity. That may not be the case in all situations, particularly for immunocompromised individuals, so - but generally, based on other arboviruses, we believe that it should confer lifelong immunity.

(Waldo Lopez): Thank you, ma'am.

Coordinator: I show no additional questions at this time. But as a reminder. If you would like to ask a question, press star 1.

Chris Motsek: And this is Chris with the SCTF. Unfortunately we're going to have to conclude the call today. We just want to say thank you to the Epidemiology and Surveillance Task Force for giving us the information.

Just a few quick notes. Just remember, we do have five task force specific webinars scheduled for next week. And the - there was some questions on vector. Vector's is actually our next one, and it's on Tuesday from 2:00 pm to 3:00 pm Eastern. Also please remember that the webinar slides, the transcripts, and the audio recordings are going to be posted to our Zika webpage. It's going to be on a rolling basis. So we hope to have this one posted a week out after the presentation. So hopefully by next Thursday or next Friday, we'll have it up on the Zika webpage.

Also just remember, you know, these are great resources. If any of your stakeholders are people that couldn't attend this, go ahead and please share the information. The link to access the previous webinars will also be provided to our awardees in the Division State of Local Readiness - DSLR - in our Friday updates and also to our partners within the SCTF partner share functional mailbox.

Again, I just want to say thank you for participating in today's webinar. And also - just as a reminder to increase our outreach efforts, please feel free to forward emails to additional parties you think should attend moving forward. Also remember, if you do have additional questions, please send them to preparedness@cdc.gov, and we will forward them to the applicable people

and try to get you an answer. So thank you, and have a good morning, afternoon, evening - wherever you are. And we look forward to providing these and continuing this sustainment strategy sessions next week. Thank you.

Coordinator: This concludes today's conference. Thank you for participating. You may disconnect at this time. Speakers please stand by for the post-conference.

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