Call Date

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Call Agenda

Welcome

Jasmine Chaitram, CDC Office of Laboratory Systems and Response (OLSR)

Measles Update

Sara Elizabeth Oliver and Jessica Prince Guerra, CDC Measles Response

Virtual Reality Training on Specimen Handling

Joseph Rothschild, CDC Division of Laboratory Systems (DLS)

Specimen Submission to CDC

Valerie Albrecht, CDC Office of Laboratory Systems and Response (OLSR)

Call Transcript

NOTE: Due to technical difficulty, the first 7 minutes 55 seconds did not record. Transcript shown in blue not based on recording.

Jasmine Chaitram: Good afternoon and thank you for joining us today. My name is Jasmine Chaitram, and I am in CDC's Office of Laboratory Systems and Response (OLSR).

(Lab Week Slide) I want to wish all the laboratory professionals out there a very happy lab week. Laboratory professionals play a critical role in clinical care, public health, and emergency response to protect the health of our nation. CDC is celebrating lab week and the Division of Laboratory Science (DLS) at CDC has developed a 2026 Lab Week theme "Laboratory Professionals Safeguard Health" because we want to celebrate your valuable role in testing with precision and applying rigorous quality and safety best practices to generate laboratory test results. Next slide.

OLSR is the CDC division that works to improve public health and patient outcomes by advancing laboratory systems both here at CDC and throughout the nation. We work closely with clinical and public health laboratories across the country to support laboratory emergency preparedness and response activities and have been hosting these calls since March 2020. Next slide.

We will be sharing slides from today's call, along with the audio and transcript, and we will post them online within the next week or two. You can find them on CDC's Laboratory Outreach Communication System (LOCS) page at the link shown here. Just a reminder that today's call will be recorded. I'd also like to remind everyone that the findings and conclusions in these slide decks are those of the authors and may not necessarily represent CDC's official position. Please keep that in mind when you go back and look at some of the slides that we post on our LOCS webpage.

(Next slide) All participants are muted and chat feature is disable. If you have a question, the Chat window will not be operational, so as before, please use the Question and Answer (Q&A)

function in Teams so that we can address it during the call. Also, please include your email so that we can follow it up if we're not able to answer it during the call.

If you have non-laboratory testing questions, please contact CDC-INFO at cdc-infostaff@cdc.gov
If you're from the media and have questions about the presentation or would like to follow up with a speaker, please contact CDC Media Relations at media@cdc.gov

I have one quick announcement.

(Announcement Slide) CDC's Division of Laboratory Systems (DLS) is pleased to offer laboratories access to the International Organization for Standardization (ISO) 35001:2019—*Biorisk Management for Laboratories and Other Related Organizations* standard (ISO 35001:2019). This initiative supports our ongoing efforts to strengthen biosafety and biosecurity and promote a culture of biorisk management.
If your institution is interested in receiving access to ISO 35001:2019, here's how the process will work:

1. You designate a point of contact (POC) responsible for biorisk management at your institution (e.g., laboratory director, biosafety officer, etc.).
2. Your POC emails the DLS Biosafety mailbox (DLSBiosafety@cdc.gov) expressing interest and including your institution's name and address.
3. DLS will review the request and notify your POC if your institution is approved. Your POC will then coordinate distribution using the names, email addresses, and job titles of individuals who should receive access.

We encourage your institution to take advantage of this opportunity to gain access to a vital resource that can help you enhance your biorisk management practices. If you have any questions or require further information, please don't hesitate to contact us at DLSBiosafety@cdc.gov.

And with that, I'd like to introduce our first speakers for today from CDC's Measles Response Team, Sara Elizabeth Oliver and Jessica Prince Guerra. They will provide an update on measles.

Sara Oliver:

Before routine vaccination, there were nearly half a million reported cases, 50,000 hospitalizations, and 500 deaths. Following vaccine licensure, cases fell precipitously and the US declared measles elimination in 2000.

Higher number of measles cases, notably before our last couple of years was in that 2018-2019 space. But if we look back in 2025, we obviously had a significant number of cases with over 2000. And then in 2026, through this month, we've had almost what we've had in all of 2025. So definitely on track to continue to have a significant number of measles cases through this year as well. Next slide.

So I won't go into in-depth detail over our numbers. I'll highlight that the website is updated every Friday with the real-time case counts as we get them from states, so it's updated weekly. As of this last week, we've had over 1700 confirmed measles cases throughout. There is a map there so you can see where the cases have been occurring.
Many of them are associated with some large outbreaks that have been in the media, but we have had cases throughout 33 jurisdictions in the U.S. Next slide.

Thanks. Yeah. And then again this table is straight from the website, so it's publicly available as well. It walks through the cases we had in 2025 and then 2026. If we look at the overall comparison, I won't go through each row, but you can see the vast majority of these are in unvaccinated individuals. An interesting point, it used to be previously that a lot of our cases were in that under 5 population. We're seeing more in that 5 to 19, child to adolescent young adult population. Over half of the cases this year have been in that 5- to 19-year-old population. So we're watching that. Thankfully, we've not had any reported deaths from measles in 2026 so far. Next slide.

And then also CDC counts a large outbreak as more than 50 cases, and many or nearly all of those have occurred in close-knit communities with low vaccination coverage.
So this is highlighting a lot of the large outbreaks that we've had again since elimination and most of these are in those close-knit communities, again with low vaccination coverage.
So we know that's the population where the most susceptible again to these large outbreaks. Next slide.

So pivoting to some specific clinical testing for measles. Overall when you're thinking through to establish a measles diagnosis, it's really thinking through what the clinical case definition is, what the vaccination history and then if there's been a traveler exposure history in the prior 21 days. So not every rash is measles, but it is important to make sure that people are thinking of measles, especially if they see somebody who is unvaccinated and has had potentially traveled or, you know, a potential exposure history up to about 21 days previously. Next slide.

Then as a reminder for the diagnostic evaluation of measles, we really combined PCR plus serology. So it's a RT-PCR from an NP/OP swab as well as an IG M serologic test.
If the testing is more than three days after rash onset, consider getting NP/OP and urine for a PCR to improve sensitivity. Obviously the specificity is incredibly high for a PCR test, but we do know that the further time wise out you get from rash onset, the NP/OP swab may be a little less sensitive. And then consulting with public health authorities early when measles is suspected can help ensure the right tests are done and that the specimens are routed appropriately. Next slide.

So again, measles testing with PCR is preferred, either that NP or OP swab as soon as possible upon suspicion of measles. Again, it's the most, both sensitive and specific in that zero to three days after rash onset, but you can use it up to 10 days. And again the urine if you're getting it in that day three to day 10 can, especially towards the end of that PCR window, help improve your sensitivity. Next slide.

An IgM antibody has limitations and really should be used paired with a PCR. It can be detected for six to eight weeks after acute measles. So it can be helpful in a larger time frame. However, the next slide really walks us through some of the limitations when it comes to IgM. If you want to go on to that next slide.

IgM testing alone can really pose challenges and settings with low measles incidence, and I will say that while the U.S has overall seen an increase in measles cases over the last two years, most people still live in an incident with low measles. So we do know that for IgM, we've had cross-reactivity with other causes of febrile rash illness, and that can sometimes make test interpretation difficult. We also have false positive results that are more common when the likelihood of measles is low. So if there isn't local active transmission, if a patient hasn't traveled, if it's not really in a setting where measles is suspected, or if you have a patient, you know that's been fully vaccinated, that doesn't have a known exposure, that's when we worry

about having false positives and again that it can be really difficult to know what to do with that test. So really recommend pairing the IgM with the PCR. Next slide.

Then we know that after MMR vaccination, some people can develop a fever and a rash that can appear similar to measles infection. It's not common, it's again that 1-5% of persons, but we do know that it can happen. It can be confusing to know what to do. Next slide.

So we have a MeVA assay or a measles vaccine assay and that helps determine between vaccine strain measles virus and the wild-type measles virus. Next slide.

So we use those when there's an epi risk of measles infection and a recent vaccine recipient. Really the time that we need this most acutely is if you're in the setting of an outbreak, you know, somebody's been exposed to measles, they get vaccinated as a part of that post-exposure prophylaxis, the MMR vaccine can be effective for post exposure prophylaxis if given in the first couple of days after exposure. But if you have somebody in the week after that, that develops a rash, it can sometimes be really difficult to distinguish,
is this a vaccine rash from the vaccine they got, or are they developing measles from the exposure that they had. So that's when doing this MeVA testing can really help distinguish if there's an epi risk and a recent vaccination history. Then MeVA should be performed if that standard PCR is positive. Next slide.

So really just highlighting that that CDC partners with the VPD reference centers or these vaccine preventable disease reference centers that provide diagnostic testing as well as the genetic characterizations for these VPD's, that really do support the jurisdictions as well as CDC. So many states are in the process of onboarding a variety of different tests and assays as well, but we do know that the VPD reference centers all have access to MeVA, as well as if we're going to start seeing potentially increasing vaccine preventable diseases overall, know that for mumps, for varicella, adeno and enterovirus, as well as just some overall genetic characterizations, these VPD reference centers are an amazing resource. Next slide.

So each state is assigned what their regional or specific reference center is. All of this is available on the internet and each state health department would know which lab they've been assigned to as well. So the state health departments can really be the primary conduit, especially for measles testing, to make sure that everything's going appropriately and going to the reference center if it's needed. Next slide.

Then I'll end my section before I turn it over to Jessica to just highlight that we do have on CDC's website about measles lab testing. There's a lot of resources that are hopefully helpful.
Let us know if there's additional information that would be helpful to include, but it goes through overall lab testing for measles and then the next slide.

This is all information that is tied to that, that primary website going through like what specimens to submit, how you would ship the specimens to CDC if that's what is needed, as well as some decision, support and tools for what type of testing is recommended for clinicians. So really walking through when you would get a PCR and when you would get the Ig M and then what specimens. We have a PDF handout that can be used as people are trying to make those determinations. Next slide.

Yes, I think this is where I end on the general stuff and hand it over to Jessica for the more specific stuff. Thanks.

Jessica Guerra:

Great. Thanks so much, Dr. Oliver. So my name is Jessica Prince Guerra and I am the team lead for the Molecular Virology team in the viral vaccine preventable disease branch. But I'm also a Senior Science Advisor for the laboratory Task force on the measles response. And so I wanted to take some time to go over genetic characterization for measles viruses and both from a historical perspective, but also in terms of newer technologies such as full genome sequencing. And so I'll start off by saying that since 2000, measles molecular data, including sequencing data, has been a critical component of our surveillance system, but also in terms of our elimination analysis and in our reports to the Regional Verification Committee. But I wanted to go over a few of the characteristics of measles viruses that maybe make it a little bit more different than other viruses. So measles is a more conserved virus than other RNA viruses, meaning that we don't see the rapid change that we do, that is common for flu or HIV.
We have a sequencing window called the N450 sequencing window, which is within the N gene that is really the global standard for both genotyping and determining what's called a distinct sequence ID (DSId). And over time, as measles cases have been decreasing, also the genetic diversity of the virus has also been decreasing. And as of 2021, only B3 and D8 wild type genotypes are circulating and have been detected. Next slide please.

So as I was mentioning the global standard for genotyping is this N450 region, and in the past, we've really been able to rely on the diversity within this region to discern between different transmission chains. And as I mentioned, you're able to get a distinct sequence ID or a DSId that's assigned to each unique sequence of the N450 region, in order to determine the genetic diversity between different strains. However, because there's been an overall consolidation of measles genotypes over time, using this specific region has been a little bit more challenging and I'll go through why this is also the case, as we've been seeing in U.S cases within 2025 and now into 2026. Next slide please.

So between 2025 and 2026, a majority, around 76% of the specimens that have been genotyped thus far using that N450 region, all have the same N450 sequence and they were genotype D8 with a distinct sequence ID of 9171. This was also the primary genotype and distinct sequence ID that has been circulating wildly in both Canada and Mexico and other countries within the Americas. And because of this, this has made it particularly challenging to determine when outbreaks in the United States, in which the sequence were detected, were linked or resulted from domestic spread, or resulted from new international importations. And so this has really been in contrast to prior years where we have historically seen sort of different sequences in the N450 region over time, with different outbreaks linked to separate importation events from different regions linked with different sequences. And so because of this, this is why we're really moving towards investigating whole genome sequencing as another important tool for our molecular surveillance for measles than in the past. Next slide please.

But I think one of the things that I also wanted to go over was, you know, while whole genome sequencing might be able to provide more genetic information, in terms ofbeing able to interpret how sequences are related between different specimens of cases, there are some important limitations that should be noted. So whole genome sequencing will allow for better resolution of the relatedness between sequences and transmission chains than just the N 450 alone. And highly distinct sequences provide support for ruling out transmission links. It's very hard when identical sequences are found because they may suggest a possible link, but it's really important to have epidemiological data for these cases, because it's possible that these identical sequences may have come from different sources because it's not been given enough

time to evolve over time. And this is particularly true in the case that we're seeing now, where we're having repeated introductions of the same lineage from different countries, but also domestic spread of a very similar sequence. Next slide please.

And again, going through some more methodological considerations for whole genome sequencing. While we know that it will be able to potentially improve the resolution by acquiring different base pair changes, one of the challenges of using whole genome sequencing for measles, in this context, is that because measles has such a slow rate of evolution and we don't expect to have a lot of differences. But even within a whole genome sequence, it's incredibly important that the methods that are used are highly accurate. And so one of the challenges is that there's no current standard or standardized approach for whole genome sequencing, both sort of on the wet lab side but also on the informatics side. And so it's really important that we're using methods that we understand the error rates for, because any error that's accidentally introduced in by the sequencing method or by the bioinformatic pipeline, may result in sort of differences in how the sequences are analyzed and the interpretation of those results. Another important thing to note is that the MF-NCR which is the non-coding region between the M and F genes, is a known variable region within the genome. However, it's technically difficult to sequence and assemble. And so we're sort of in this conundrum of, it's really important to get this region of the genome, but it's technically difficult to do so. And so different methods may capture that region better than others but just knowing that could be one of the caveats of a potential analysis if there's not good coverage within the MF-NCR region. And finally, once you have a whole genome sequence or a group of whole genome sequences that you're wanting to sort of analyze using phylogenetics, it's also very important to note that those types of analysis are sensitive to sampling bias and so as more sequences are added, the resolution of that analysis is going to increase because you've added more sequences to it. But you also need to ensure that there's good coverage across geographic and temporal sampling and to really understand that those sampling biases can influence your phylogenetic tree topology and again, your interpretation of the results. And so it's best to have a comprehensive and holistic analysis as the way to most accurately analyze sequences from outbreaks. And so with that, I'll pause there and just thank everybody for giving us the opportunity to present here today. Thanks.

Jasmine Chaitram: Sara and Jessica, thank you both. So very much for joining us and giving that very informative update. I don't see any questions in the Q&A section. If you're able to stay on and if questions pop up and you can answer them in the Q&A feature there, that would be great. If you have to run, that's OK too. We understand you guys have a lot to do but appreciate your time and thanks for joining us. OK, I'm going to move forward in the agenda. Our next topic is “Virtual Reality Training on Specimen Handling” and Joe Rothschild from the Division of Laboratory Systems at CDC will provide that quick update.

Joseph Rosthschild: Yeah. Thank you, Jasmine. So hello. My name is Joe Rothschild. I lead the activity of virtual reality laboratory training, here in DLS. So yeah, I'd like to announce we have released 3 new virtual reality training scenarios within onelabVR. These three scenarios are all based around specimen handling: handling blood specimens, urine specimens and respiratory specimens. And really, we did this because we were hearing that the laboratory community as a whole wanted some help in being able to sort of train up some of their laboratory professionals on ways to do this safely and efficiently. OnelabVR is available for free. You could get it for the meta quest or really any open XR compliant headsets. That's virtually every headset out there.

There's a QR code on the screen that you could scan with your phone if you want more information as well as you could go to reach.cdc.gov/onelabvr and learn everything that you could possibly want to know about one lab VR and what we're doing here at CDC.
And that's about it. Thank you.

Jasmine Chaitram: Thank you so much, Joe. All right. We are going to move to our last scheduled topic for this afternoon, which is specimen submission to CDC and that's going to be covered by Valerie Albrecht. And she was on our call in January. In case you missed it, she'll be repeating a little bit of information, but also giving you some new information about an important change that's coming. Thanks Val.

Valerie Albrecht: Great. Thank you, Jasmine. Good afternoon all. As mentioned, I'm Val Albrecht, and I'm going to provide some updates regarding the CDC specimen submission process. Next slide.

OK. So first something new I'd like to announce that we plan to retire the CDC specimen submission form. This is also known as the 50.34 form, and we'll do it this October.
We will be decommissioning the desktop application that is used by our submitters to access this form. So after October, specimen testing requests will need to be submitted through CSTOR, which is our online web portal. Next slide.

OK. Just a quick background though, but for you those of you not familiar with CSTOR, this is a web portal that helps to streamline the process to request test orders as well as submit specimen information as well as securely receive results from the CDC. It was originally created as an online alternative to the 50.34 form, and since going live, it's really become the preferred method for submitting specimens, since it does provide a centralized repository of test order approvals, specimen data, shipment status as well as CDC reports. Next slide.

All right, so instead of filling out the 50.34 form, from the electronic app, submitters will use the submit specimens module in CSTOR to provide the exact same data elements that were currently captured in the 50.34 form. Next slide.

OK. So just as a reminder, all SPHLs are currently onboarded to CSTOR. After doing that, our next step was to open the web portal to allow original submitters to onboard. Next slide.

So we started this effort in the summer of 2024 and these were some of our goals for original submitter onboarding. So essentially it was to support higher quality, more secure data submissions, allow more visibility into submissions and assist with report distribution and more or less a faster, smoother workflow to submit to CDC and access reports. Next slide.

So one of the features in CSTOR, SPHLs can configure direct submission permissions at the test order level. So here we have a screenshot of the module in CSTOR where SPHLs can manage the organizations in their jurisdictions and set permissions based on each test order. So as you can see in the bottom grid there, each test order in the CDC directory is listed and the SPHL can toggle either auto approved, pre-approval or even auto rejected if that test order should not ever be requested for direct submission to CDC. Next slide.

OK. So a list like that might seem a bit overwhelming to navigate as an original submitter trying to request test orders. So I just wanted to highlight an enhancement that we recently implemented in CSTOR, which is a tabular list of test orders with SPHL status. So, as an original

submitter at the create test order request page in CSTOR, there will be a link that you can click on to access this table for greater visibility into a specific SPHL submission status at each test order. Next slide, OK.

Another benefit I want to mention is that if an original submitter is onboarded to CSTOR, the SPHL has the ability to release reports through the web portal. So this option will display via a blue box, that you can see there, that can be clicked to then initiate secure and efficient report delivery to the onboarded original submitter. Next slide.

There's the blue box. OK. So what is the process for an original submitter to onboard to CSTOR? So first, as an original submitter, they will request CSTOR access via a REDCap form, which is found on the Internet site. There will be an initial review done by the CSTOR Help desk just to validate some of the submitter information. Then SPHL CSTOR lab admins will review and approve the onboarding request. The original submitter, CSTOR lab admin, will then onboard via SAMS which, is the secure access management services. Once that is completed, the original submitter CSTOR lab admins will then get access to CSTOR. Next slide.

Once all that has been completed, they can proceed to the submission workflow. So as I mentioned, the SPHL setup which test orders require SPHL review or approval. So the original submitters will go into CSTOR, they will create this test order request, fill out the specimen submission forms. Now if that test order requires SPHL pre-approval, then the SPHL will be prompted in CSTOR to review and approve that request. And then also if the test order requires CDC pre-approval in our own ELIM system, the CDC will review and approve that test order. Once all that has been completed, the original submitter will finalize their specimen forms and then be able to electronically ship the package. They will then be able to track the testing progress via CSTOR as well as view the final patient report once it's been released. Next slide.

All right. Thanks for your time. Hope this was a helpful overview and as always, if you have any questions, please reach out to cstor@cdc.gov for training or any additional information. Thanks Jasmine.

Jasmine Chaitram: Thank you so much Val for that update on things happening at CDC with specimen submission and that wraps up our agenda for today. There were a lot of emails provided in the slides here. Reminder that we will post the slides, the transcript and the audio. It was recorded a little bit late, but we did record it, so that will be available on the LOCS website. And these calls happen quarterly, so July 20th is our next scheduled call at 3:00 PM. We did not get any questions today, which is kind of unusual for this crowd, but I do want to remind you that there is an opportunity to ask questions. You can put them in the Q&A section. If you have a question and if you weren't able to get to submit it today or you think about it later after the call, please e-mail us at locs@cdc.gov and we will help you get that question answered and just again Happy Lab Week! Hope you all can use your free time here at the end of this call, since we ended early, to enjoy lab week. And please join us again for the next call. Thank you all.