

Meeting: CSTE Data Standardization – Identifiers -Data Element-Specific Team Meeting

Date: July 19, 2024

Attendees: 69

CSTE (3)	PHAs (30)	CDC (31)
Becky Lampkins Gillian Haney Meredith Eddy	<u>DSWG Co-Chairs</u> Laura Erhart AZ Molly Crockett MA	Luis Hernandez GDIT Myrna del Mar González GDIT Angie Agunloye Ellen Martinson Erin Miller Fatima Saifi Hailey Vest John Gerstle Julie Vanderkolk Katherine DeBord Kerry Souza Kristen Delea Lauren Korhonen Laurie Barker Lesliann Helmus Marion Rice Melissa Pagaoa Meeyoung Park Nicki Roth Nicole Gallaway Noreen Kloc Peter Boersma Rachelle Oseni Renee Boehmert Robert Pratt Samantha Retzlöff Sara Johnston Shelby Lyons
JMC (4)	<u>DEST Members</u>	
Grace Mallard Natalie Raketich Sam Spoto Sara Sanford	Morrow Toomey AK Melissa Kealey CA Sequoia Rent DE Kayleigh Nerhood GA John Satre IA Luis Vela ID Ryan Burke MA Judie Hyun MD Ed Hartwick MI Mario Beltran MI Elizabeth Lando-King MN Elizabeth Shiffman MN Hanna Chakoian MN Nwanne Onumah MS Kristen Merrell MT Erin Doyle NJ Stella Tsai NJ Elizabeth Kessler NV Theron Huntamer NV EJ Klingler NYC	

	Eman Addish PHILA Kacee Redden SD Steve Eichner TX Alina Paegle UT Brianna Rossi VA Cher Levenson WA Sophia Cantor WA Misty Johnson WI	Tricia Aden Van Tong Yuritzy Glez Pena <u>OTHER (1)</u> Salomon Compaore FHI 360
--	---	---

**SOME INDIVIDUALS DIALED IN; THE NAMES ARE UNKNOWN, AND THEY ARE LEFT OFF OF THE ATTENDANCE*

HIGH-LEVEL MEETING NOTES (REFER TO MEETING SLIDES FOR MORE DETAIL AS NEEDED):

DEST Opportunities for Participation

- DEST sign-ups are ongoing.
- **[Action Requested]** Please sign up for upcoming data elements on the [DEST Sign-Up here](#).
- Upcoming data elements
 - Laboratory – first call 8/9
 - Reporting Source – first call is 8/16
 - Race/Ethnicity/Tribal Affiliation
 - Social Determinants of Health
- DEST member expectations—members are not expected to write documents, lead meetings, or prepare slides. The goal is to keep members engaged in conversations about content during and between meetings.
- Active participation in polling, document review, discussion, and other input during and between meetings is expected.

DSWG Reminders

- DSWG members will soon receive draft recommendations for feedback, including
 - Exposures, Risk Factors, and Underlying Conditions
 - Signs, Symptoms, and Clinical Manifestations
 - Disability

Meeting Ground Rules

- We welcome everyone's opinions and active participation from jurisdictions, CDC programs, CSTE membership, etc.
- As we work through data elements/classes, we strive for 80/20 consensus.

In-Scope vs Out-of-Scope

- Focus on core data for surveillance and transmission to the CDC within selected data classes.
- We will work to identify standard definitions and value sets within that definition of core data.
- This is not a discussion of how to collect this data, frame questions in surveys or interviews, or implement these data standards. This is also not meant to impose limitations on how jurisdictions collect data.

Identifiers Structure

What does it mean for an identifier to be core?

- As I started our May call, I'd like us to all be on the same page about what it means when we call an identifier a core data element. A core identifier should be something that would be capable of being transmitted across conditions when needed. For instance, it's very clear that each case requires a unique ID to be identified as a unique case, so this value will always be present. However, something like an "outbreak ID" would rarely be present, as most cases are not part of an outbreak, but if core then a jurisdiction should be capable of capturing/sending that field across conditions. When we define an identifier as core, we are saying that jurisdictions and CDC will be prepared to transmit and receive that identifier across conditions when applicable. We can think about what we're defining as a minimum value set, or minimum set of identifiers, for what jurisdictions are prepared to send.
- There may be additional identifiers that are needed on a condition specific basis, and our minimum set of identifiers would not prevent the potential repeating group structure from including those identifiers. The conversation today though is going to focus on what should be consistently implemented across many conditions.

Potential Identifier Structure

- On our May call we talked about utilizing a repeating group structure for Identifiers. Last month 64% of our group preferred the repeating group structure for identifiers versus 36% preferred sending as discrete data elements, and this month we would like to finalize the data elements within this structure and their minimum value set.
- Last month this repeating group had data elements that captured the type of identifier, the unique value, and the assigner. After discussion on the last call, and given what is included in our current minimum value set for identifiers, the proposed structure for the identifiers repeating group has been simplified to only include the Identifier Type and Identifier Value. The removed element of "Identifier assigner" was a way to denote who assigned the ID, however, this could potentially create the "parent-child-grandchild" structure scenario in some use cases, may be complex to implement with a structured data type like an OID, and may have limited utility for analysis if free text.
- So now in this version of the structure:
 - Identifier Type would have a defined value set. For core, this would include our "Minimum Value Set" for identifiers.
 - The second element called "Identifier value" captures the actual ID value.

- A reminder that this approach would exclude local record ID and local subject ID, or as we renamed them on the June DSWG call the Case ID and Person ID, as those are already required to be included in every message in their own specified HL7 fields.
- In practice, this could look like the example presented here. The first OBX segment transmits the identifier type of NORS ID (or CDC's National Outbreak Reporting System), the second transmits the identifier value of EIP123456.
- With this change from the last call, is the simplification of this repeating group to two data elements beneficial? Does anyone have any questions or comments here?
- Discussion
 - No comments

Minimum Set of Identifiers

- In May we polled on these identifiers as our minimum set of identifiers. We had 54% of our group vote that yes these are core, and 43% vote that only some are core. The one identifier that came up in discussion as problematic for that group is the Legacy case identifier. Now that we're solidifying the identifier structure on this call, we'd also like to re-poll on our minimum set of identifiers with the Legacy Case ID removed. That ID will be noted as something that CDC needs to support as it's important for jurisdictions undergoing a surveillance system transition, but otherwise it is not core for all jurisdictions or conditions. Does anyone have any questions or comments here?
- Discussion
 - Sara Johnston: To clarify what we're talking about here, we have this identifier type data element that would have a value set that would have at the minimum these 3 values available. And the discussion is that legacy case identifier would not be included in this minimum value set, but could be included in the value set because it could still be used in this way where it's applicable?
 - Sam Spoto: Yes it could still be used in the repeating group. I do agree that it's hard to like visualize what this means when we don't entirely know how this will be implemented in the end. And I'm not sure if this is true, but at least in my mind how I've started to think of it is, I know we've said when we're voting for this, what, for instance, would you like to see in some kind of Gen. V, 3, type, mmg? and that gets a little murky when you talk about, "Well, here's the minimum values that are core." But you still want to be able to use that structure for something that's not core. And so I've started to think of core as the things in that Gen. V. 3 that are prioritized, as you really need to send this thing. What we're agreeing on is the minimum set of identifiers are the things that are important across all conditions. This legacy case ID is not important for a jurisdiction that's not changing from one surveillance system to another.
 - Gillian Haney: Would this legacy identifier be defined as a legacy identifier for something that came from an STLT? CDC would need to have a legacy identifier if the case was de-duped.
 - Sam Spoto: The way this currently being used is if a jurisdiction has one surveillance system that they have been using and reporting cases under with case IDs from that surveillance system, and they are undergoing a change to a new surveillance

system that's going to assign all of those cases a new case ID. This legacy case ID would say, "Here's the case ID from our old surveillance system," so you can link these 2 cases together and know that they are the same person.

- Gillian: Got it, so on CDC's side as they're receiving the information, if receiving the information, they would need to do something separate to be able to manage that.
- Sam: Yes

Polling process

- As usual, each poll question today will have its own slide, and today the answer choices are really going to vary by question. For the polls where we are asking if something is core or not, the goal is to reach 80% or more agreement, and ideally have additional discussion when not quite there.
- Data elements that receive at least 80% agreement are considered resolved with "strong support". If for any questions we can't reach the target agreement of 80%, but still more than half the group is in agreement, these points have been included in previous recommendations as having "weak support".

Poll 1 – Identifier Structure

- The first poll today is on identifier structure, with the repeating group of two data elements. Identifier type would be limited to a value set that would include our minimum set of core identifiers, and identifier type would be whatever the unique ID is. Does anyone have any questions before we launch the poll?
- Discussion
 - Sarah Johnston: Sorry you just said would be limited to that value set or the value?
 - Sam: it would be limited to a value set that would include our minimum set of core identifiers
- Poll Question: Do you support the repeating group structure for identifiers as shown below? (Yes, I can live with it/No, prefer discrete data elements)

DSWG_7.19.24_Q1

1. Do you support the repeating group structure for identifiers as shown below? (Single Choice)

Yes, I can live with it. 100%

No, prefer discrete data elements. 0%

You did not answer this question

Poll 2 – Minimum Value Set

- Ok this second poll is to get a more concrete on this minimum value set that we talked about last month. This removes the legacy case ID and keeps a CDC-assigned case id (kind of like DCIPHER ID), a jurisdiction assigned outbreak ID, and the CDC NORS ID. Does anyone have any questions before we launch this poll?
- Discussion
 - Gillian Haney: On that CDC assigned case ID, are there any more descriptors associated with that? Is it coming from a CDC lab, is it assigned to decipher? Is there anything else that we might need to know
 - Peter: Right now it's pretty broad. The benefit of this value set is that we can add additional values with more specificity. So it's kind of a catch all right now, in its current state. But we would have the potential to add things down the line with specificity, as I've seen in the NORS ID description.
 - Lesliann: I think this kind of thing would be really helpful when we have the next COVID outbreak and the CDC starts assigning case IDs at the beginning when they're getting calls, and if we can make those connections because there's a way for the case report that comes in to have that or the case notification that comes in to have that ID in it. It's going to save CDC and the jurisdictions a whole lot of time going back and forth. I would think that that ID would not just be a number, but might be COVID something, or would have something they would tell you like which event it was related to as part of the ID. So something would be identified. But I think there's a lot of utility and would save everyone a lot of headaches.
 - Gillian: I completely agree. I'm just trying to figure if there would be multiple IDs that we might need to distinguish from in that particular CDC assigned case ID type
 - John Satre: So is this a new concept or does it exist already? The CDC assigned case ID.
 - Peter: This is a new concept to include in an MMG like this. CDC's assigned case IDs in the past there hasn't been an effective way of capturing it in an MMG.
 - John: Ok, I'm just thinking how do we manage this on our side? This seems like it would be a manually entered, error-prone approach potentially.
 - Peter: Yeah and welcome others to comment on this. The use of it would be pretty specific, so it wouldn't be a general use case, for all cases. It would be used particularly in the start of a response when there's CDC Assigning IDs and it's kind of inherently a messy process, but as opposed as not having a place to capture it.
 - John: So this wouldn't be like manually entering a value for every COVID case.
 - Peter: Right, you could think of this like the early days of MPOX response.
 - Robert Pratt: Peter, since you have been supporting our TB onboarding of the new MMG, you are aware that we do have a state assigned jurisdiction ID, not for outbreak purposes but just as an identifier, but based on CDC format and guidelines this here is outside that realm?
 - Peter: right, so that has the potential to move into a repeating structure like this if we wanted to do it but that wouldn't be plugged into this field. This one is for situations such as an emergency response.

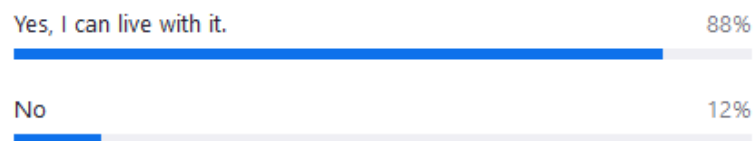
- Elizabeth Shiffman: So my member is based on my experiences with the Zika outbreak and I know that it was a really crazy time in terms of CDC assigned Case IDs for cases because people were getting multiple ID, and I guess my only concern is, if something like this is a repeating field...it's great to have a spot for it for outbreaks, but I know that in that situation people had so many different IDs and multiple CDC case IDs to link things together...It makes be a little nervous with CDC assigned case IDs but I understand why they're needed.
 - Gillian: I think that's really valid, is there any way to put some guardrails around how we would want to define this? Like the 1st assigned ID from a positive case or something? Because the situation I'm thinking of is you know what happened in Mpox, or when there's an emerging infection, when the CDC is actually doing the lab testing. I recall we were having to send data down through Decipher, and CDC assigned laboratory result was the Id that was trying to link some of the data that was being sent through Gen V2. And if we had that ID in our surveillance systems and been able to send that element through Gen V2 to link on the Decipher end, it would have been so much less painful.
 - Lesliann: Based on what you mentioned, where a case is in Decipher twice and the jurisdiction realizes, 'hey, no wait, that's the same person.' We want to merge it and just count it once, there might be a need to be 2 CDC assigned case IDs for the same event in that record. So that we can that "yeah that's the same person who is in Decipher twice. Don't come back asking us about it again." So it sounds like we need some flexibility in how this would be used. And certainly where we've got things that need to be matched. It's going to be really critical. This has been one of the handicaps that we've had, they just cost a lot of people a lot of time. So we're really trying to figure out how do we put something in there. And if people have suggestions for it, and maybe it's a repeating ID that you can use multiple times that just has different values in it. And we have to recognize that there might be multiple values for it.
- Sam: I do want to point out that in that case of the CDC laboratory results, we will be talking about Specimen ID as a way of linking the case to the CDC specimen from the CDC lab which is not this field here. So the CDC assigned case ID is focused on when CDC has assigned an ID to that case specifically, not to a person and not to a lab result but to a case of a disease.
 - Gillian: Yeah in situations past it's been the laboratory ID from the LIMS system on the CDC end that was used
 - Lesliann: Then do we need another one for once that aren't for emergency response?
 - Sam: Has CDC ever assigned case IDs not in an emergency response?
 - Lesliann: I'm sure we have, I feel that I don't think it's valuable to narrow it because I think it just means we're going to have to create another value. I would rather leave it open. I think the "such as" gives us a good example, but if we limit it, we're going to have to create another one right off, so I don't think there's value in limiting.
 - Sam: That's helpful. I do agree when you're thinking about this, we're thinking about all the different IDs that might go in here in a different situations, but has there ever been a situation where CDC has assigned multiple case IDs to the same case?
 - Lesliann: Even when you have the same case that gets reported to CDC multiple times or it's reported as separate cases, and then it gets merged into one case, that in itself means there are potentially going to be multiple CDC IDs that belong to the same case and I can see where there might be something in hepatitis B. It's in the perinatal system that the vaccine preventable disease people are looking at and another one that's in the hepatitis program system that they're looking at as an adult with

hepatitis. So I think keep our minds open to the fact that there may well be more than one ID assigned to a case and just plan for that level of flexibility unless it adds such complexity we have to avoid it.

- EJ Klinger: I have a question about having multiple CDC case assigned IDs or any multiple of these. Does this structure work with having 2 identifier types of the same thing with different data in the data element description?
 - Lesliann: As a repeating ID or not. If it's a repeating element, you can have multiples. That's structure, is it not?
 - Peter: That's the thought it would be a repeating block within whatever generic core and so you could send multiple instances with distinct separate ID of the same ID type if that's necessary.
- Chat
 - Katherine DeBord: like if another outbreak starts while the mpox one continues... can it hold 2 IDs for the two events?
 - Lesliann Helmus: I think the ID should be specific to the event, so it might start with MPOX
 - Misty Johnson: I think often the CDC-ID would be empty, but in the time when it's needed, it's like an open slot.
 - Gillian: Agree
 - Ed Hartwick: So we would expect the CDC ID to be blank frequently?
 - Sarah Johnston: Yes, mostly empty
 - Katherine DeBord: thank you- that's really helpful
 - Renee Boehmert: So maybe change the definition for CDC-assigned-Case-ID then? it think the operative words that is causing ambiguity is "for use in situations such as....", just a thought
 - Renee Boehmert: I just think emergency response should have its own distinct ID
 - Sophia Cantor: Would this be additional or somehow adjacent to outbreak?
 - Ed Hartwick: I think leaving it open but emphasizing that it should be a case and not a specimen or a person
 - Renee Boehmert: like a if-then- else deal?
 - Ed: More like it should be unique to a case if possible
 - Gillian: Perhaps CDC just needs to have a clear protocol for what populates this field
 - Sophia Cantor: maybe an "emerging" ID concept
- Poll Question: Do you support the below identifiers as our "minimum value set" for identifiers? (Yes, I can live with it/No)

DSWG_7.19.24_Q2

1. Do you support the below identifiers as our "minimum value set" for identifiers? (Single Choice)



You did not answer this question

Specimen ID

CDC Laboratory Results

- Jurisdictions currently send specimens to CDC labs for testing and submit case notifications for disease surveillance. Linking CDC lab results to their associated cases is valuable for CDC programs but is challenging due to the lack of consistent identifiers across specimens and case notifications. This siloing of information means:
 - CDC cannot easily determine how many cases are associated with the specimens it receives.
 - CDC cannot use this information analytically to better understand the cases.
- **A high-level overview of how CDC receives these two sets of information is shown on this slide:**
 - Specimens are sent to CDC from various sources, primarily public health labs and commercial labs.
 - After CDC conducts the testing, results are always sent back to the jurisdictions, regardless of who submitted the specimen. The results may be sent to the epidemiology program, the public health lab, or both, and they may be delivered through different routes and in different formats.
 - The CDC lab also provides the test results to the related program at CDC.
 - If the tested condition is notifiable and meets a surveillance case definition, the jurisdiction then sends a case notification to CDC.
- When the CDC program receives the test result from the CDC lab and the case notification from the jurisdiction, they often have difficulty matching the test result to the case notification due to differing identifiers. Many programs struggle with this issue. During the mpox response, the team used fuzzy matching, but a more straightforward strategy would be helpful.
- Next we will look at identifiers that get shared at each of these steps.

Case notification – Specimen linkage

- Specimens that are sent to CDC, either from public health labs or commercial labs, are accompanied by either a 50.34 form, a Global File Accessioning Template form, or a CDC Specimen Test Order and Reporting (CSTOR) entry.
- The fields across all of these forms are consistent and typically include the patient's name and some demographic information. Depending on the source of the specimen, these forms may also have:
- Public health patient ID and public health specimen ID if the specimen is from a public health lab.
- Original submitter patient and specimen ID if the specimen is from a commercial lab, or if a commercial lab first processed the sample and passed it to a public health lab.
- Intermediate submitter information if the specimen was handled by another entity before reaching CDC.

Example: CDC Laboratory Result (PDF)

- Regardless of who sends the specimen, CDC receives and tests the specimen and then returns results to jurisdictions in one of two ways – as an ELR message or as a PDF that can be accessed in CSTOR. Again, these results may go to the jurisdictional epi program, the public health lab, or both.
- Despite the different methods of specimen submission to CDC, both the ELR and PDF contain the same information.
- The results will always include the CDC specimen ID, a unique 10-digit identifier assigned by CDC. If the specimen was sent with a public health lab specimen ID, that ID will also be included in the results.
- In the PDF, the IDs the sample was sent with are found on the first page (which is not shown here), and the CDC specimen ID is found in the second box shown on this screen.
- In the ELR, the CDC specimen ID and public health specimen ID can be each found in multiple HL7 fields. Specimen IDs from commercial labs or intermediate labs will not be returned in the ELR.

Case Notifications to CDC

- On the case notification side, all notifications sent to CDC via MMG contain person-level and case-level identifiers.
- Some condition-specific message mapping guides request additional information to aid in matching, but there is inconsistency in what is requested and whether it is requested at all.
- For example:
 - The Malaria MMG asks if a specimen was sent to CDC and, if so, requests the type of specimen and the CDC Specimen ID.
 - The Mumps, Pertussis, RIBD, Varicella, and FDD MMGs all inquire if a specimen was sent to CDC for testing, and that question precedes the epi lab repeating block.
- As a result, typically, the case notification cannot be matched to the specimen:
- NNDSS cannot receive Personally Identifiable Information, so it cannot match on the name, even if the name was submitted with the specimen.
- Specimen IDs are not consistently received in case notifications, preventing matching on the CDC specimen ID.

- The person-level ID in a case notification usually differs from the person ID sent with a specimen, as the case notification is sent by a surveillance system while the specimen was sent to CDC from a lab system.
- On this call we will consider capturing information more consistently to support this matching process.

Specimen ID

- One method of capturing the CDC Specimen ID could be to include the specimen ID as a data element in case notifications, both in the lab template and in any epi lab block. While the specimen ID is already present in the laboratory template and in some epi lab repeating groups, the Lab DEST will talk about including it consistently. The goal of this is to leverage existing workflows rather than create new ones. However, like I said, this will be discussed in more detail during the Lab DEST in August. Our call right now is about identifiers and will not vote about the lab template or epi lab block, but I wanted to provide everyone with the context that this Specimen ID is being discussed in more than one data class.

Specimen ID, 2

- Separate from the lab template and epi lab block, the CDC Specimen ID and Public Health Specimen ID may also have a place in our identifiers value set, and that is what we'd like to talk about today. This wouldn't be taking advantage of existing lab workflows, but would be a place for someone to type in a CDC specimen ID if they're holding a paper lab, or if a jurisdiction can't send specimen ID from their automated workflow.
- My questions for this group are: Are there times when this would need to be sent, but lab data would not be sent, so it would be beneficial for this to function more as a stand-alone ID as part of the identifiers repeating group rather than the lab template and epi lab block? Would we prefer for these IDs to exist in both places, as core potentially, but not be required to fill out the same information in both places?
- Discussion
 - Ed Hartwick: I was thinking when you were talking about the idea of maybe it being sent as an identifier on its own and not necessarily part of a lab block, and I could see that if it was say its own question in a form, or in the message mapping guide like that, where it would be "what specimen IDs are involved in this case." I don't know if we have anything currently, but I could see that as a potential, especially with sites that may not have the lab block being filled in from the labs themselves but maybe having it as part of an Epi or Lab section inside of a MMG that might be outside of a lab. So I could see it being its own thing.
 - Sara Johnston: This is more of a question for discussion, but I wonder what jurisdictions thoughts are on specimens that would not necessarily end up in the lab repeat because they are genotyping specimens, or for something like that we'd still want to be able to create that linkage, but you may not have it in your lab repeat, specifically genotyping or like the lineage results.

- Ed Hartwick: Would those be a CDC ID or more of GSA ID or something like that?
- Sara: A good question. I think there's room for both but if CDC does the testing then you would have a CDC ID when it's uploaded into another system. You may also have an ID associated with that sequence that you would also want to include so you may have multiple actually.
- Gillian: Could jurisdictions comment about how they're currently capturing genomic data now and how that's working?
- Ed Hartwick: I think my guess is that probably everybody's experience is a little bit different.
- Gillian: Right, I'm curious to know if there are things that are working really well and I'm aware that some jurisdictions may be capturing the genomic data independently of the actual way that they're capturing all of the lab data.
- Ed: At least from Michigan standpoint, I think it's varied even by the condition. A lot of our genomic stuff ends up going to our Bureau of Laboratories first, then it gets passed on to us, us being the folks in Epi and surveillance. So maybe not directly from CDC. So a lot of times they've been working to capture more of the public identifiers for those and send those with it but I think for the most part we deal with specimen IDs that are laboratory-based at the bureau labs or like Michigan based rather than CDC lab IDs, because of trace back ability over here. So I don't think I've seen a lot of them, especially involving genomic stuff
- Sara: So, Ed, did you say you'd have your stat lab ID for that specimen, but not the CDC ID?
- Ed: Yeah, inside of our surveillance systems. A lot of times we'd end up with stat lab ID for it, not the CDC one, but the state lab one would likely in the LIMS system hold the CDC one. So it's hard to say. One specimen ends up with 6 IDs, gets confusing sometimes.
- Sara: Yeah but you'd at least have them, the second of these IDs the public health spec ID.
- Ed: Yes
- Gillian: I believe in Massachusetts before I left they were capturing the genomic related data separately within the lab and I don't think there's currently a standard for how to do that. Are there LOINC and SNOMED associate with the genomic data?
 - Ed: Well from our experience we know there's links associated with the public IDs for them, we've found one to use. And then SNOMED, I think it really depends on the condition because sometimes we'd be likely to see that kind of thing for a serotyping off of a salmonella but for typing for hepatitis, maybe not so much.
 - Misty Johnson: What we see in WI is very similar to what Ed was sharing for Michigan. Lab stuff comes in via ELRs, but anything for genomic sequencing I've been told that that's something they receive separately, not ELR. So that's something that our Epis normally have to type in manually into the case. And same as the CDC specimen ID, I don't think that stuff is ever received electronically. It's something that I don't know if they get it emailed or faxed or what. And then they'll type it in so it's not separate, it's not too numerous and I understand.

- Sara Johnston: Another question for jurisdictions, for those of you who are receiving ELR from CDC: Do you incorporate or display the CDC specimen ID as part of that? Or do you base off of your public health specimen ID? Are you capturing and have available the CDC specimen ID as part of that lab observation from the CDC ELR message?
 - Ed Hartwick: We're still onboarding ELR from CDC, our standard is whatever is mapped into SPM 2.2 would be what ends up being the specimen ID for it. So if the CDC put their ID for that when the lab comes in, that's what would be mapped in the system.
- Sam Spoto: Maybe we've learned that perhaps the CDC specimen ID could be useful there if the genomic testing is being done at CDC. If it's being done at the public health lab, the public health lab specimen Identifier here could be useful for that value. But I think also, if we're talking about maybe making a specific ID for genomic results, that seems like maybe an identifier that could be added to this repeating group if needed. And as Gillian said, getting more information on how we're receiving and capturing genomic data is important. But I'm also curious how many condition that affects and is that at the level of core yet? Or is that something that should just be standardized for the conditions where it's applicable in the future? So I'd like to bring us back to thinking about our core data elements here.
- Chat
 - Gillian Haney: I'd recommend getting some more info on how STLT are receiving and capturing the genomic data
 - Gillian Haney: I think it's ever increasing...
 - Ed Hartwick: I could support a separate Public ID that would be for those genomic ids

Poll 3 – Specimen ID

- Before we launch any poll, I want to take a minute to discuss if these are in identifiers what should they look like. In the proposal for the lab group it's really proposed as one data element of "specimen id" to use those existing lab workflows. However in identifiers we have a little more flexibility to have two more specific options in our value set rather than one. Where we're going next with this is "is this core, does it belong in our minimum value set". So before we get to that point, I'm not asking yet if this belongs in identifiers, I'm just asking "if it were to be there, should it have separate identifier types or one identifier type". Does anyone have any thoughts on this before we do any polling?
- Discussion
 - Elizabeth Shiffman: yeah from my perspective as a program that does a lot of sending out to CDC, I would prefer those to be separate because you need both for different things and so I'd hate for the local public health lab specimen ID to be subsumed or overwritten by the CDC specimen ID because I think they both have a role. So I would definitely advocate for them being 2.
- Chat
 - Sara Johnston: I think we should consider the genomic data concerns as core. Many conditions have genomic testing but they are doing different things for identifiers.
 - Misty Johnson: Agee

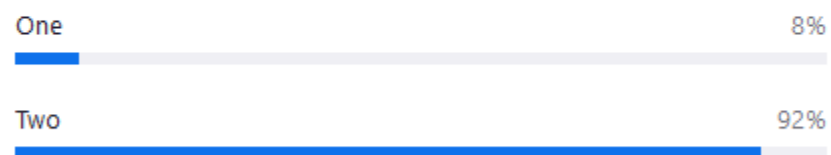
- Tricia Aden: I agree with Elizabeth.

- Poll Question: In identifiers, should these specimen IDs be represented by one or two "Identifier Type" options? (One/Two)

N=26

DSWG_7.19.24_Q3

1. In Identifiers, should these specimen IDs be represented by one or two "Identifier Type" options? (Single Choice)



You did not answer this question

Poll 4 – Specimen ID Core

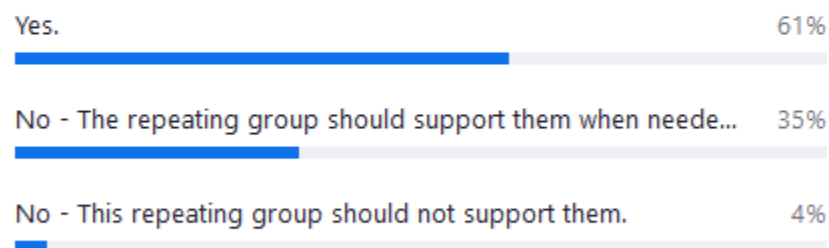
- Now we will get into "are these core". Because we've already talked about this some, I'd like to poll first and then if the group is not at 80% we can have some discussion. We are voting on adding the [one or two?] identifier types of As core identifiers.
- The answers here are "yes", meaning we should add them into our minimum value set as core identifiers, and then two options for No. The first option for No means that this repeating group should be able to support CDC specimen ID, but it's not core and shouldn't be in our minimum value set. The second option for "No" is that it's not core and this identifiers repeating group should not be used to transmit this information. Does anyone have any questions before this poll?
- Chat
 - Katherine DeBord: would it be possible to enter multiple specimen IDs (i.e., multiple CSIDs or multiple PHL IDs) per case?
- Discussion
 - Sara Johnston: I was a little bit thrown off with the question of making it core versus the way that I had been thinking about using these data elements, which is, we need a better way of linking the epi and the lab data. And so we talked about the case ID from CDC and being able to link to that and it seems really obvious when there's a CDC created case ID we need to be able to link to the lab data and the Epi date, the case data. This being the corollary of the way we can link the lab data and the case data, and sometimes that also means, as Gillian was pointing out, CDC might be using the lab ID to track the case initially. This is just another kind of component of

- that linkage and epi lab linkage is difficult so every jurisdiction having the ability to send the CDC specimen ID or their public health lab specimen ID would be really helpful. It's not going to be need in every scenario, but having that ability is helpful for that live linkage.
- Elizabeth Schiffman: I voted for the No, they should be supported when needed but not core. Justing thinking of my own conditions that I work on in the vector born world, there are some of our disease where we would just never have these because testing is all done commercially, and then we have other diseases where it's more of a mix or some diseases where things are kind of solely tested at public health labs or CDC, so for some of these things like Lyme disease, you'd never have that for any of these, because no one tests that except for commercial labs. So to me that means it doesn't need to be core. I think there are conditions it works well with and others where it's like if its always going to be blank, should it be there?
 - Poll question: Should these specimen ID value(s) be part of the minimum value set for Identifiers? (Yes/No – The repeating group should support them when needed, not core for all conditions/No – This repeating group should not support them)

First poll image (n=24)

DSWG_7.19.24_Q4

1. Should these specimen ID value(s) be part of the minimum value set for Identifiers? (Single Choice)

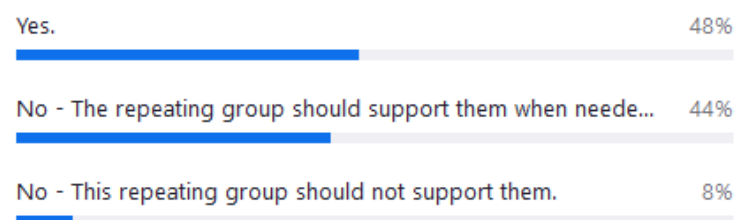


You did not answer this question

Second Poll Image (n=25)

DSWG_7.19.24_Q4

1. Should these specimen ID value(s) be part of the minimum value set for Identifiers? (Single Choice)



You did not answer this question

Next steps

- Upcoming team meetings
 - 8/9 1-2pm ET – Laboratory
 - 8/16 1-2pm ET – Reporting Source
- Next full DSWG call will be August 30th, 1-2pm ET
 - Medication/Treatment discussion
- ERU, SSCM, and Disability documents will go out to the wider DSWG soon