20171107\_LabUSrealm\_Notes

Attendees: Maggie (allscripts), Lisa, Kathy, Freida, Riki, Dan, Andrea, Diego,

LRI236/LRI237:

OBX-30 values:

* MCS - Micro Culture Status (e.g., Normal Flora, No Growth, Not Isolated)
* MSQ - Micro Specimen Quality (White Blood Cell)
* MOD - Micro Other Descriptor (anything else that does not fit but is not at the isolate level)
* MIN - Micro Isolate Name (species, genus)
* MIGQ - Micro Isolate Growth Quantity (numbers, <10, 100<>300)
* MIGC - Micro Isolate Growth Category (Moderate, Many, Few)
* MIA - Micro Isolate Attributes (Gramstain, Enzyme Functions)
* MID - Micro Isolate Descriptor (anything else that does not fit the other isolate level categories)

MSQ – what does that mean? Would it be better to be under MOD?

Is there a workflow in the lab where these are called out separately? Often it is just a statement under the culture result; required to report that may impact patient results – if you have cells that are contaminants – that may affect if doc may want to re-order – this is what that was aimed at

Before culture you do gram stain or another stain – this is a judgment call – drop MSQ and use MOD instead – add note to include observations on specimen quality (epithelial cells) – compare this to the LOINC manual for micro reporting! – would it have a LOINC vs stick it in an NTE?

How would you handle PCR results? Suppose just using RSLT in OBX-29 and unspecified, if OBX-30 MUST be specified.

Gram stain results on sample vs isolate:

Few gram negative rods

Moderate gram positive cocci in clusters

Idea was to cover all gramstains under MIA

Also supply the example for few vs moderate – in EPIC it is often just a sentence for text mining

What is

Just adding observations under culture for the different steps in the micro workflow, or creating a separate test that is then linked to the culture as “reflex”

LIMS set up example:

Analyte – similar to chemistry set up like NA+ etc

In micro have 1: many observations

Culture = many organism

Isolate = individual ID / biochem / susceptibility = all under the LOINC of the culture

Can support up to 5 isolates from single culture

So that is why the OBX-30 would be really helpful to properly place the information into the right results (outbound and inbound from reference labs)

Most results are text. less often structured

Sometimes gram negative rod could be identified as proteus species – that would make MIN vs MIA? And how to deal with the many or moderate

But will have to also keep in mind that the gram stain result is what will change to the fuller id to species with the next updated result, so should be in the same “location”

Important to use the OBX-30 for identification in decision support – for the doc worklist vs the infection control officer – speciated organism will most often have susceptibility

When you use non-culture based tests like PCR for species identification – despite the ordinal results but from infection disease control also important

Presumptive Salmonella in culture – then you keep going to speciate in more detail and that will impact the final organism ID = confirmed organism

Quantification – why separated out?

May be because the quality and how to store in dB is different – depends more on datatype

Most of the <10,000 etc codes are related to urine culture and possibly for M tb cultures – it is still relative similar to few, many, etc.

* May be combine MIGQ - Micro Isolate Growth Quantity (numbers, <10, 100<>300)
* MIGC - Micro Isolate Growth Category (Moderate, Many, Few)

Into MIG = Micro isolate growth (can be either numbers, <10, 100, >10,000 or many, moderate)

Moderate growth etc

Isolate identification – generic = alpha strep up to genus / species

sensitivities

Biochems don’t get reported out

Everything else is a comment

So for that split we are down to:

* MCS - Micro Culture Status (e.g., Normal Flora, No Growth, Not Isolated)
* MOD - Micro Other Descriptor (anything else that does not fit but is not at the isolate level)
* MIN - Micro Isolate Name (species, genus – include gram stain on isolate here – like presumptive proteus etc)
* MIG - Micro Isolate Growth Quantity (numbers, <10, 100<>300, Moderate, Many, Few)
* MID - Micro Isolate Descriptor (anything else that does not fit the other isolate level categories

VS what we currently have:

MIRM Micro Isolate Related Modifier = quantification

MNIR Micro Non-Isolate Related = normal flora and anything else?

MIR Micro Isolate Related = organism name at any level

Still missing where the gram stain on the sample goes – but smears and gram stain on samples has different LOINC, so OBX-30 may not be as needed as for these – so just use the OBX-29 RSLT and no OBX-30?

But in some cases the LOINC may be methodless – for example Microbacteria Identified LOINCs

When Regenstrief’s new proposal is adopted, then the need for OBX-30 is less relevant

Micro results are updated over time – blood culture first report the gram negative rod to help with starting the ABx treatment and then get more specialized later

* MCS - Micro Culture Status (e.g., Normal Flora, No Growth, Not Isolated)
* MOD - Micro Other Descriptor (anything else that does not fit but is not at the isolate level)
* MSS - Micro Sample Stain (gram stain on samples)
* MIN - Micro Isolate Name (species, genus – include gram stain on isolate here – like presumptive proteus etc)
* MIG - Micro Isolate Growth Quantity (numbers, <10, 100<>300, Moderate, Many, Few)
* MID - Micro Isolate Descriptor (anything else that does not fit the other isolate level categories

If we are keeping the PCRs out, so we want to also pull out the organism specific cultures with ordinal results from this list – create a new code for PCRs and organism specific culture = we need to look at the OBX-3 here to understand what we are looking for?

Keep separate from MIN; we are currently identifying micro vs non-micro in OBR-47 by lab section, but the PCRs may still be in micro section, but not following the micro set up.

Separate set up for micro vs additional info compared to data structure for non-micro.

If PCR is used for identification should we use the MIN here – there are PCRs where the organism name is in OBX-5 also.

For PH call – when using PHD wants to know what mechanism you used – you are detecting the part of a organism while in the culture you determine that there is a viable organism there

Also may not be the organism, but a toxin that is pathogenic and is being looked for.

Send email to PH people asking about the need for PCR / organism specific culture to have OBX-30 specific values.

LRI#237: Motion to adopt the following terms instead of MIRM, MNIR and MIR - Maggie Wright, Dan Rutz - further discussion: may be add more examples in the () and fix the example message snippets

• MCS - Micro Culture Status (e.g., Normal Flora, No Growth)

• MOD - Micro Other Descriptor (anything else that does not fit but is not at the isolate level)

• MSS - Micro Sample Stain (gram stain on samples)

• MIN - Micro Isolate Name (species, genus – include gram stain on isolate here – like presumptive proteus species)

• MIG - Micro Isolate Growth Quantity (numbers, <10,000 CFU, >100,000 CFU, Few, Moderate, Many)

• MID - Micro Isolate Descriptor (anything else that does not fit the other isolate level categories)

Against: 0, abstain: 1, in favor: 6

Riki to send email with this motion to PH to get input.

Call adjourned 4:31 PM ET