20170803\_LabUSRealm\_Notes

Attendees: Craig Newman, Kathy Walsh, Riki Merrick, Freida Hall, Rhonda , Walter Kemper, Brendan Reilly, John Roberts, Dan Rutz, Nell Lapres (only 5 min)

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LOI Block Vote: 101, 112, 120, 125

PULL #112 for further discussion

No motion on the remaining items, so remove Block ID and review one at a time:

LOI#120: Comment about how to convey unknown name – this datatype is used in places, where name is known – can also send ID number and not send name as alternative, but In the case where there is no ID number there MUST be a name for the fields where this datatype is used – motion to find not persuasive – John R, Kathy, no further discussion, against: 0, abstain: 0, in favor: 7

LOI#101: Review NK1-30 and NK1-32 are for contact person information, when NK1-13 is valued (organization as Next of kin - Motion to make NDBS component usage O in both LOI and LRI for NK1-30 and NK1-32 – Freida, John, no further discussion, against: 0, abstain:0, in favor: 7

LOI#112: SPM-2 usage RE – change usage to R for NDBS profile – have to have the placerID (state printed ID on the paper card) as well as collection date time, before sending the order – so that will always be known at time of order – this requirement means that the EHR-S must be able to enter the ID from the card (often a barcode) into their system AND associated it with the SPM-2.1 field – currently this element is sent as OBX using a LOINC;

SpecimenID of the bloodspot card is also now required to be recorded in birth registries in several states – exampels are VA and TX – it is the primary ID – there is a note that it is not sent in message as OBX with that LOINC, but rather in SPM segment – do we need to allow for both?

LOI#104: requirement for ordering provider name - CLIA is specific that it is either a person or the lab – where the lab director is used as default – it is not good to hardcode that, because there is turn over

The reason to have this name is so if there is a question about the test / sample there is a person that can be reached – follow yup for new samples is usually with the discharge provider, not the submitting facility, because by the time the lab has questions or needs another sample, the patient has been discharged

but in NDBS labs that is NOT collected from the message – they have a look up table with all that information on the submitting facility based on the facility name or ID – so may be we can make OBR-16/ORC-12 C(R/RE when NDBS profile is used (based on MSH-21?) – we have NOT made that kind of condition in the past – it is like a standing order. If the common component is R we cannot make NDBS RE using the varies notation

Could we change the data type used for NDBS and figure out how to populate one field here? – more research on this one

Receiver side is where the problem lies – can take message, but NOT store and send back in result, or we can decide to have NDBS system be non-conformant to the guide – not a good idea – will need to have more conversation here

Epic joins, so switching to LRI

LRI:

The use of the result subtype codes is not well described – need better definitions in the value set as well as a whole set of examples – wonder if it would be better to have categories like culture and related observations vs PCR and other detection tests, that don’t result in isolation of organism

LRI#234: email from Dan (EPIC):  
**Observation Subcomponents**

Green – Example in guide

Blue – Suggested example to add to guide

Red- Example is guide, suggested removal

**MIR**( Isolate Related) – Seems to be identified organisms.

         Named Organism – e.x. Staphylococcus aureus

         Gram Stains with organism information – e.x. Gram Positive Cocci in clusters (page 191)

         Organism groups – e.x. Shigella Species

         General organism observations – e.x. Normal Flora - if not accompanying another named organism (Page 191, 256) Should probably be MNIR because it does not refer to a specific isolate. See Normal Flora Section

         Non organisms – ex. WBCS - (Page 191) Should probably be MNIR because it is a cell not an organism

**MIRM**(Isolate Related Modifier) – These seem like the any other OBX segments that modify the organism

         Colony Counts -  Many, Heavy Growth

         Numeric Colony Counts

o   ex. OBX|1|SN|624-7^Bacteria Spt Resp Cul^LN^...|^6^1|>^10000|CFU/mL|

o   ex. OBX|1|SN|624-7^Bacteria Spt Resp Cul^LN^...|^6^1|60,000-100,000|CFU/mL|

         General organism observations – e.x. Normal Flora Normal Flora with accompanying isolate (no example)

**MNIR**(Non Isolate related) – Anything not specific to an organism, or modifying an organism

         General organism observations – e.x. Normal Flora Normal Flora with no accompanying isolate (Page 259)

         Non organisms – ex. WBCs - (Page 191) Should probably be MNIR because it is a cell not an organism

         No Growth – ex. No Growth, No Staphylococcus aureus seen. Does not refer to an organism. No examples in guide

         Gram stains with organism information – ex. Gram Positive Rods. (page 258) Should be MIR (e.g. is MIR on p. 191)

**Normal Flora**

**Variance in guide**

**Page 251**

OBX|11|CWE|624-7^Bacteria Spt Resp Cul^LN^...|^6^1|263812008^Moderate growth^SCT^...|...||RSLT|MIRM

OBX|12|CWE|624-7^Bacteria Spt Resp Cul^LN^...|^6^2|23506009^Normal flora^SCT^...|...||RSLT|MIRM

**Page 256**

OBX|11|CWE|624-7^Bacteria Spt Resp Cul^LN^...|^6^1|263812008^Moderate growth^SCT^...|...||RSLT|MIRM

OBX|12|CWE|624-7^Bacteria Spt Resp Cul^LN^...|^6^2|23506009^Normal flora^SCT^...|...||RSLT|MIR

**Page 259**

OBX|11|CWE|624-7^Bacteria Spt Resp Cul^LN^...|^6^1|263812008^Moderate growth^SCT^...|...||RSLT|MNIR

OBX|12|CWE|624-7^Bacteria Spt Resp Cul^LN^...|^6^2|23506009^Normal flora^SCT^...|...||RSLT|MNIR

**Page 191**

OBX|11|CWE|624-7^Bacteria Spt Resp Cul^LN^...|**^6^1**|263812008^Moderate growth^SCT^...|RSLT|MNIR|

OBX|12|CWE|624-7^Bacteria Spt Resp Cul^LN^...|**^6^2**|23506009^Normal flora^SCT^...|RSLT|MIR|

**Suggested structure**

**No identified Organism**

OBX|11|CWE|624-7^Bacteria Spt Resp Cul^LN^...|^6^1|263812008^Moderate growth^SCT^...|...||RSLT|MNIR

OBX|12|CWE|624-7^Bacteria Spt Resp Cul^LN^...|^6^2|23506009^Normal flora^SCT^...|...||RSLT|MNIR

**Modifiying Identified organism**

OBX|11|CWE|624-7^Bacteria Spt Resp Cul^LN^...|^6^1|263812008^Moderate growth^SCT^...|...||RSLT|MIRM

OBX|12|CWE|624-7^Bacteria Spt Resp Cul^LN^...|^6^2|23506009^Normal flora^SCT^...|...||RSLT|MIRM

OBX|12|CWE|624-7^Bacteria Spt Resp Cul^LN^...|^6^2|60875001^Staphylococcus Epidermis^SCT^...|...||RSLT||MIR

**Comments**

If MNIR can contain a non-growth value, it would be more difficult to identify the growth. It may be useful to be able to write rules based on whether an organism had Heavy Growth or Moderate Growth.  Instead, things like “no growth” or “identification to follow” or “communicated to physician” should be in an NTE.

Need to include an example of how organism comments should be included.  At the very least we need more OBX-30 values (which are really taking the place of more discrete OBX-3 values, but yet matching the same OBX-3s is necessary to group all the different ~3 OBXs for the same observation together since OBX-4 is ONLY a function of OBX-3, unfortunately).

Good:

OBX|13|ST|624-7^Bacteria Spt Resp Cul^LN^...|^7^1^1|60,000-100,000|CFU/mL...|RSLT|MIRM|

OBX|14|CWE|624-7^Bacteria Spt Resp Cul^LN^...|^7^2^1|56415008^Klebsiella pneumonia^SCT^...|RSLT|MIR|

NTE|||Culture Identification to follow|

Bad:

OBX|13|ST|624-7^Bacteria Spt Resp Cul^LN^...|^7^1^1|60,000-100,000|CFU/mL...|RSLT|MIRM|

OBX|14|CWE|624-7^Bacteria Spt Resp Cul^LN^...|^7^2^1|56415008^Klebsiella pneumonia^SCT^...|RSLT|MIR|

OBX|14|ST|624-7^Bacteria Spt Resp Cul^LN^...|^7^3^1|Culture Identification to follow...|RSLT|MIRM|