**Orders & Observations Conference Call**

**9 September 2015**

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**WebURL:** [**https://join.me/vernetzt.us**](https://join.me/vernetzt.us)

**Recording (no audio): sorry forgot to hit record….**

**Attendees:**

|  |  |  |
| --- | --- | --- |
|  | Name | Organization |
| 1 | Kathy Walsh  | LabCorp |
| 2 | Carolyn Knapik | CAP |
| 3 | Ron van Duyne | CDC |
| 4 | Riki Merrick | Vernetzt, LLC / APHL |
| 5 | Wendy VerHoef | Samvit Solutions / NCI |
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 Regrets: Rob Hausam

**Co-Chair**: Riki Merrick

**Scribe:** Riki Merrick

Agenda/Minutes:

1. Agenda Review
2. Approve minutes from the last few calls: **- sorry I goofed: - NO quorum – so will need to re-approve minutes when we do have quorum – skipped over this this call**
	1. July 1, 2015 <http://wiki.hl7.org/index.php?title=File:SPM_Minutes_20150701_ConCallv1.docx>
	2. July 29, 2015 <http://wiki.hl7.org/index.php?title=File:SPM_Minutes_20150729_ConCall.docx>
	3. August 26, 2015 <http://wiki.hl7.org/index.php?title=File:SPM_Minutes_20150826_ConCallv1.docx>
3. Compare Specimen DAM to biologic specimen model in BRIDG - map specification source is BRIDG and the map to is specimen – stored here: <http://www.hl7.org/documentcenter/public/wg/bridg/BRIDG%20to%20Specimen%20DAM%20Mapping%20Spreadsheet%2020150826.xls>
	1. Link to BRIDG model: <http://bridgmodel.nci.nih.gov/files/BRIDG_Model_4.0_html/index.htm> - chose VIEW:BSP - biospecimen
	2. Link to Specimen DAM: <http://wiki.hl7.org/index.php?title=Specimen> – scroll to bottom for image

Discussion:

Last call we discussed PerformedSpecimenMove – in DAM there is a note about adding a container processing step – that is similar to specimen processing step – that would be equivalent to the PerformedMove / PerformedMaterialStorage step – agree, that we should probably split move from storage

Specimen – BRDIG decided that some attributes are at the material level, and the material can play a role of a specimen in more than one case, and some attributes are related to the role as specimen, while others are ONLY applicable to the material

The DAM collected the attributes more in a denormalized fashion and did not yet consider proper modeling rules – if we make a clear statement to that effect AND ensure that we can trace each of the DAM attributes to the BRDIG attributes, that should work out

Accession number – in DAM did not specifically call out, as several different uses of accession number exist – thought was this was covered by specimenIdentifier, which is 1..\*. in BRIDG accession is defined as grouper at time of collection – could potentially cover this, if the identifier datatype adds a type code (currently support the ID as string with assigning authority)

In BRIDG where would the AP specimenID be traced? – example organ resection, block, section, slide etc… - that would be materialID – not currently represented in the biospecimen subdomain diagram – the processingActivity would cover the details of creating the sub-specimen – that matches in DAM

Grouped / pooled specimen not currently represented in BRDIG – most likely would be a processing step

Dam might consider re-distributing some of the attributes to proper classes to further align with BRIDG

BRDIG is working on how to model by reference and how to deal with different level of normalization between the referenced model and BRIDG

What about original specimen amount / current specimen amount0 those would be observations on the specimen as it changes over time (at least the current).

Specimen condition – is really also an observation on the specimen – need to make explicit, that DAM allows repeats

SpecimenTypeCode – currently mapped to specimenTypeCode in BRIDG, which is deprecated – changed column H to implementation specific – the concept in DAM actually matches the materialTypeCode in BRIDG – these are not currently part of the mapping (base elements rather than domain specific elements)

Spreadsheet at end of call: <http://www.hl7.org/documentcenter/public/wg/bridg/BRIDG%20to%20Specimen%20DAM%20Mapping%20Spreadsheet%2020150909.xls>

To Dos:

Wendy will add MaterialIdentifier and MaterialProcessing to the biospecimen subclass diagram – and review if there are other base classes that should be added, to account for the different granularity in DAM / BRDIG – completed: <http://www.hl7.org/documentcenter/public/wg/bridg/BRIDG%204.0Plus%20Biospecimen%20Sub-Domain%20Diagram%20-%2020150909.png>

Riki will see, if she can find MS Office 2013 in order to avoid the protected mode / macro issue

Wendy will see, if she can get approval to take time to map additional classes, like material

1. Next Steps:
	1. Compare Specimen DAM to biologic specimen model in BRIDG = Identify issues, if any find resolution
	2. IHE AP domain is working on structured AP report in CDA and has some requirements, we might not yet have considered – have added the concerns identified to the spreadsheet above - Identify issues, if any find resolution
2. Action Items:

**Next Call September 23, 2015 10 AM EDT = 21:00 UTC**