

Minutes
Laboratory LOINC Committee Meeting
Indianapolis IN
June 13, 2006

Conference Call participants:

Michael Montgomery (Kaiser Permanente)
Georgina Kurtovich (Kaiser Permanente)
Sue Korsak (Partners), Elizabeth King (Partners)
Eric Haas (UC Davis)
Riki Merrick (UC Davis)

1. Announcements/News

- 1.1 NPRM for attachments – Roughly 50 comments out of 600 related to LOINC – but most were asking for more codes and more features – not hostile. We will add the terms and provide the functions that the comments requested. HL7 has a fair amount of work to do to address all of the ballot questions *and* upgrade the ASIG formats to version 2 of the CDRA. HL7 will also need to re-ballot.
- 1.2 International connections
 - 1.2.1 Met with Dr. Li the head of the Chinese Medical informatics organization that is the Chinese equivalent of HIMSS and Dr. Yu – from Health Ministry of Peoples Republic of China. Also met Forest Lin who translated LOINC to Simplified Chinese. They loved the LOINC pigs in China.
 - 1.2.2 Paris Hospital system (Assistance Publique – Hôpitaux de Paris, 42 hospitals) – 1 million admissions per year (23,000 beds) – will use LOINC.
- 1.3 Senate Bill 1418 – which passed the Senate – defines a new committee and requires adoption of CHI standards – which includes LOINC passed the senate. The house bill is HR4157 – is much less ambitious.
- 1.4 RELMA enhancements (brief Demo) ([Handout A](#))
 - 1.4.1 Don't forget – for easier mapping use common tests button as restriction and pay attention to squiggly line which like a spell checker indicates that the entered word is not known to LOINC.
 - 1.4.2 New approach to showing details about sets and panels.
 - 1.4.2.1 Keep existing structured view – add local browser view.
 - More buttons on the mapping screen.
 - Print – export.
 - Cut and paste (CTL C).
 - Font size change (switch at bottom).
 - Search (CTL F).
 - See “everything we know – when available.
 - Existing structured view can still be useful for panels.
 - Handouts.
 - Sample screen shots – Print out of CBC and diff panels ([Handout B](#))
 - print out of Glasgow coma score showing answers ([Handout C](#))

- 1.4.2.2 Demonstration of new HTML version of the ‘view details’ function. This view displays “everything” that we have stored for a given term in one HTML display including the fields required to define a full questionnaire/survey instrument such as CMS’s Minimum Data Set (see below). Three alternate displays are available: HTML, Structured and HTML w/details. The ‘structured’ view is what we have always provided; the HTML w/details shows attributes of children of a panel not just the attributes and structure of the panel. This structure will have much use going forward.
- 1.4.2.3 New structures to accommodate Panels and survey instruments more completely (Developed in collaboration with Thomas White and Stan Huff).
- It will carry everything that is needed to define a full input form including:
 - Structure
 - Structured Answer lists
 - Computational logic – initially using Thomas White’s “Pidgen C” (needs discussion)
 - Help (content we had is not yet ready for prime time).
 - We have implemented CMS’s Minimum Data Set (MDS) for nursing homes in this structure.
 - Tom White is developing software for capturing data per these definitions and delivering HL7 as output.
 - Sample 36 page MDS full form sample produced by the HTML details option described above. ([Handout D](#), [Handout E](#))
 - MDS Full assessment form as printed from details.
 - Six more variants
- 1.4.2.4 Clem mentioned goal of producing an interim release (late August or early September) to address comments in the NPRM and further improve the hierarchy.
- 1.4.2.5 New and improved Component hierarchy structure
- Pick “hierarchy & limits” button
 - See screen shots
 - Sample print outs ([Handout F](#), [Handout G](#))
 - Discussion
 - Shift click – gives the listing of all the LOINC codes under that particular node. This is a response to a long set of requests for a hierarchy. Default sort is component, system, property, and timing. This view reveals some areas where our naming conventions need some more work, and we welcome feedback.
 - Jim Case asked about how to submit comments: Clem responds with any method – editing into the PDF (highlighting, etc. – which may be a very easy way to deliver) notes, print and hard copy comments and fax it, etc.

2. Order Panels – Could use more order panels

- 2.1 Looking for panels structures – when the panel is defined in terms of LOINC codes. Still hopeful we will get more panels from VA and/or from Canada.
- 2.2 Clem mentioned that we are encouraging donations from those who have mapped their local panels and children to LOINC codes.

3. Status report – LOINC – CPT (Stan Huff – IHC)

- 3.1 The general approach of this mapping started with asking for codes from those who have existing mappings. After reviewing and enhancing these mappings, about 2,000 of the most common lab tests mapped were mapped to CPT. These mappings were sent to AMA for review. Since the first batch was sent for review IHC has completed an additional 1,000 mappings. The next area of mapping will focus on radiology orderables, which is of high priority. A conference call/review with CMS is also needed. Stan clarified that these mappings will be released through the NLM, via Metathesaurus. These mapping could only be used if you have a valid CPT license.

4. Status report: Genomic tests in LOINC – draft effort being developed by Partners and IHC (Stan Huff)

- 4.1 Partners will be interfacing its Genetics lab to their Clinical Data repository (CDR) soon. Stan is working with the genetics lab at partners.
- 4.2 The general plan is to set up an interface b/w IHC and Partners using valid HL7 messages between these groups. This effort also will require the development of LOINC codes needed to represent the sequence info, etc. Chris Raines is the project manager from Partners. They are close to a go-live for sending messages.
- 4.3 This project involves work with a SIG within HL7. Amnan Chibaud is very active in creating a model. There is interest in developing a live implementation. The IHC – Partners group wants to create an implementation in v.2.x since that's what both of their institutions use. A quick review of suggest the possibility that some changes to the current LOINC conventions for genomics tests (e.g., amino acids), may be needed and we will need a standard approach for reporting genomic sequences based on differences between a standard reference sequence and the patient's sequence. This project will definitely require the creation of new LOINC codes.
- 4.4 Current genetics reports state whether the observed genomic difference are well know differences or a novel change, and speculate about whether the observations could account for the patents disease/findings, vs. being incidental variants. LOINC codes will also be required to obtain key clinical history elements to help in the interpretation of the results. (Things important to direct the testing: family history, age, symptoms).
- 4.5 Stan noted that the current narrative reports from the Partners genetics labs have been very informative. They include information about the (areas of gene examined, exons, differences, and correlates with the disease that might be seen in the person). The reports appear to be generated from a pathology system, which puts every line of the report as a separate OBX segment, which is 'ugly.' This format is a result of data coming from an existing system, but they are also keeping an XML document which has more discrete data elements.

- 4.6 Partners agreed to send their current set of proposed terms in the normal LOINC submission format for review, with notation indicating that they were related to this discussion.
 - 4.7 Steve Steindel (CDC) asked about seeing the sample – but de-identified reports and Stan agreed to distribute them.
- 5. Status report: Electronic Children’s Health Network (eCHN) – an Ontario RHIO (Gil Hill)**
- 5.1 eCHN is a voluntary network (20 members), of these 4 are pediatric hospitals, others are more general institutions with a pediatric care unit. This network will soon cover 90% of all pediatric care in the province and carries patient demographics, laboratory reports, op notes, etc in a central repository. The goal of the project is the aggregation of results in a long term clinical repository – not test ordering. The care of children who move among providers – is a special challenge. And this eCHN network is helpful for the intuitions caring for these children. Lab data in this network is coded with LOINC. Term mapping terms is done centrally. Clem McDonald and Steve Steindel echoed the value of centralized mapping and concentrating the expertise.
- 6. Status report: Ontario Laboratories Information System Project (OLIS) (Beverly Knight)**
- 6.1 OLIS
 - 6.1.1 OLIS is a Jurisdictional Lab Information System (JLIS) to facilitate electronic lab data exchange (laboratories, hospitals, providers). It will use LOINC coding, and HL7 version 2.x messaging. The project is currently working with early adopters, and hopefully will go live in the next few months. Beverly mentioned collaboration with eCHN group as well.
 - 6.2 Canada Health Infoway
 - 6.2.1 Canada Health Infoway is a group working on establishing nomenclature/messaging standards for the entire country, creating resources for each province, like the Ontario project, they are just beginning. The Pan-Canadian Laboratory Nomenclature Standards uses LOINC for order, result, SNOMED for result valuable. The group is using pieces of the LOINC name for creating a ‘display name’ – and encourages the creation of good display names within LOINC.
- 7. Status report: CDC/Federal Activities (Steve Steindel)**
- 7.1 CDC
 - 7.1.1 CDC – The current main project is BioSense (biosurveillance). It started rolling out last year (10 cities, 30 hospitals). They decided to code the data they receive from hospitals centrally. In each participating hospital, they install a server with code tables for conversion and secure messaging to CDC. Data is pseudo-anonymized when sent to CDC. The project is expanding to 350 hospitals by the end of the year.
 - 7.1.2 National Electronic Disease Surveillance System (NEDSS) – Routine public health system, rolled out to about 30-40 states.
 - 7.2 Other Federal Updates

- 7.2.1 SNOMED – Recent meeting focused on re-organizing the organism – (up to large animals) hierarchy. Jim Case added that the meeting focused reconciling inconsistencies that exist in the current SNOMED organism hierarchy. They plan to make it a strict Linnean hierarchy, but with 2 new attributes (characteristics and common animal groups). CDC and others have wanted common animal groups that would be linked to the common Linnean hierarchy.
- 7.2.2 The output was a plan – not a new hierarchy – and efforts to fund this plan are underway.
- 7.2.3 Steve also provided brief updates on other various ONCHIT activities.

8. Proposal for quantitative vs. ordinals in hepatitis C and EBV testing (S/CO) reporting (Quest/Pam Banning, others).

8.1 Example report

Hepatitis C Antibody	Reactive *	(Nonreactive)
Signal to Cutoff	1.00 H	<1.00 Ratio

This patient's sample tests reactive with a low s/co ratio: ≥ 1.00 and < 8.00 . The CDC recommends supplemental testing such as RIBA or nucleic acid amplified testing (NAAT) for confirmation. (MMWR No. RR-3, 2003). If NAAT is chosen, please submit a new, frozen plasma or serum specimen.

Definition – This is a ratio calculated by dividing the optical density (OD) of the sample being tested by OD of the assay cut-off for that run.

Rationale – They realize that they lose information by reporting only the binary (positive/negative) answer. Depending upon the test – a high continuous value implies a very high probability that the patient is a true positive – enough so that confirmatory testing may not always be required (INCLUDE citation to reference).

- 8.2 Clem argued that the shift toward more yes/no reporting and away from reporting the quantitative observation on which the yes/no is based – as we see increasingly in toxicology and serology is a bad thing – they should always report the number – as well as their pos/negative conclusion.
- 8.3 Discussion: For 3-4 yrs CDC has recommended reporting (Hepatitis C Virus and EBV). Journal of Clinical Chemistry 49:479-486,2003;10.1373/49.3.479; <http://www.clinchem.org/cgi/content/abstract/49/3/479>.
- 8.4 CDC calls this the S/CO – (Signal /Cut off) ratio. Many thought that this is probably the same as a typical EIA result which is a number based on the ratio of optical density of obtained from the specimen over the control.
- 8.5 **Action: But the denominator has enough semantic specialization – it is the ratio of the labs internal cut off for positive for a specific run of samples – that we will proceed to define a specialized term with the S/CO in the name. Furthermore, that is how everyone will expect to see it named.**
- 8.6 Jim Case will further research the deeper question about how this differs from the standard EIA result for this test.

9. Proposal for Newborn screening – Gil Hill ([Handout H](#))

- 9.1 The group accepted Gills proposal with the addition of one more higher level of test names as described on the American Genetics Association and we will add Screen to the method name to clarify that the test is intended for screening of the disease in question.
- 9.2 **Action: Accept Gills proposal with the additions described above. Create a panel that includes at least three levels.**
 - 9.2.1 Newborn screening panel (the top).
 - 9.2.2 A lumpier test term to accommodate the larger categories (because we see reports with tests at that level too).
 - Endocrine Disorders
 - Hemoglobin disorders
 - Genetic disorders
 - Galactosemias
 - Fatty Acid Oxidation Disorders
 - Organic Acidemias
 - Amino Acidemias
 - 9.2.3 If possible, link the actual confirmatory tests as a fourth level to the third level (level that Gil gives in his template report).
 - 9.2.4 Add the text explaining the notation for fatty carotene and fatty acid lengths that Gil provided to the LOINC user guide (also add something that specifies what “OH” means in this nomenclature).
- 9.3 Kate Johnson (3M) says they have submitted these before, and were asked them to submit again so we can compare to Gil’s proposal. *Pediatrix* (<http://www.pediatrix.com>) – has some of the details for these terms on their website.

10. Proposal from Stan Huff regarding collections ([Handout I](#))

- 10.1 **Action: accept Stan’s proposal with modification as follows:**
 - 10.1.1 **Use Doc rather than Collection in Stan’s proposal.**
 - 10.1.2 **Use panel as the scale for items that have formal definitions of the structure of the panel (though they are collections also in Stan’s sense. The rationale I Distinguish panels as scale – as a badge of perfection – to avoid sliding back – simply a well defined set of discrete content.**
 - 10.1.3 **Review terms with Nars and Nom – Nars would all be made Doc. Many corresponding nom’s would be deprecated – will have to look at these terms case by case.**
 - 10.1.4 **Include the rules about this in the users guide.**
- 10.2 **This proposal also aims to make LOINC codes for collections of different types uniform between Clinical and Lab LOINC. After group discussion, ‘DOC’ (Document) was preferred scale, using it in the general sense of the word.**
- 10.3 **Action Item: Stan to fix handout and we will include in the LOINC User’s Guide.**

11. Proposals from Pam Banning (3M):

- 11.1 Change System from SER to SER/PLAS for serology tests

- 11.1.1 Can we systematically change the specimen in all antibody test from SER to SER/PLAS in the class Micro and Serology? For example, Specialty Labs and ARUP accept plasma for Thyroid Peroxidase Ab, but Mayo and LabCorp do not. Recognize that some labs may be designed to run a given test off of plasma and others serology. Is there any reason to believe that some antibodies can't be found in plasma as well as in serum?
- 11.1.2 After discussion, group consensus was to make this change only for tests we know for certain are done on both serum and plasma, but to keep the subject open for discussion.
- 11.2 Culture name changes (Covered in a separate larger proposal).
- 11.3 Distinguishing rapid organism identification methods from routine
 - 11.3.1 Rationale: Every lab does it. Important for ordering.
 - 11.3.2 Examples:
 - Rapid strep (based on smear)
 - Rapid cryptosporidium /giardia combo tests on stool. (? Important to make any distinction in the kind of method).
 - The ColorPAC Giardia/Cryptosporidium (Becton Dickinson) (12 minutes)
 - The ImmunoCard STAT! Cryptosporidium/Giardia rapid assay (Meridian Bioscience, Inc.) X IVD Inc.
 - Cryptosporidium/Giardia Direct Fluorescent Antigen Assay – Simultaneously detects Cryptosporidium cysts and Giardia cysts in a fecal sample.
 - 11.3.3 Proposal distinguishes “rapid” “POC” tests from the slower kinds e.g.
 - 11.3.4 Jim Case, Stan Huff, and others expressed concern about using the term ‘rapid,’ since it is a relative measure of time. Stan suggested making a distinction on the basis of methodology, perhaps by including some aspect of timing in the method.
 - 11.3.5 So will come up with something like rapid (<30 min) for method. Some one will have to propose the time cut offs that would separate the routine from the rapid by test type.
 - 11.3.6 Michael Montgomery (Kaiser) asked about discussing POC tests, and Clem spoke in favor of re-opening this discussion at the next meeting.
- 11.4 Line Immunoassay
 - 11.4.1 Should we make a distinction between LIA from immune blot? Articles suggest that IB false positives from interfering antibodies are reduced in LIA studies. (Or include it as a specific sub type that would be classified as IB).

< antigens are stuck on a nitrocellulose strip>

P100 Comparison of Two Confirmatory Assays for HSV on Samples from a High-Risk Cohort Previously Unresolvable by Subtype-Specific HSV EIA kits

L. MALLOCH, Y. COTE, G. FORTIER, B. CALDER-KENT, T. WONG, S. SHIELDS, AND J. E. KIM*, Bureau of HIV/AIDS, STD and

TB, Health Canada, Ottawa, ON, Biochem Immunosystems, Montreal, QC Conclusion: The HSV western blot is the current ;gold standard; for HSV confirmatory testing. LIA had a high sensitivity of 100% (22/22), but a low specificity of 25% (2/8) with a positive predictive value of 79% and a negative predictive value of 100%. The LIA was unable to conclusively assign a subtype in 3.6% of samples testing as HSV positive. While the LIA may offer advantages because of its standardization, it has a high false positivity rate when compared against the western blot assay.

11.4.2 Other references from Pam Banning:

<http://jcm.asm.org/cgi/content/abstract/37/5/1324>

<http://www.microgenbioproducts.com/virology%20.htm>

From Pam: I'd like to hear from the pathologists if they'd consider LIA and IB unique enough to not both be described as IB.

Journal of Clinical Microbiology, May 1999, p. 1324-1328, Vol. 37, No. 5 Sabino, Zrein, et al "Evaluation of the INNO-LIA HTLV I/II Assay for Confirmation of Human T-Cell Leukemia Virus-Reactive Sera in Blood Bank Donations".... "In conclusion, the new serological confirmatory assay for HTLV (INNO-LIA HTLV I/II Ab) resolved the results for the majority of the indeterminate and positive-untypable samples frequently observed by WB assays."

Journal of Clinical Microbiology, March 2002, p. 973-978, Vol. 40, No. 3 Hagedorn, Kraminer-Hagedorn, et al on "Evaluation of INNO-LIA Syphilis Assay as a Confirmatory Test for Syphilis"
"The T. pallidum Western immunoblot assay is also used as an alternative confirmatory test to improve sensitivity and specificity, but indeterminate and false-positive reactivity patterns have been reported "

Some thought this was a variation on Immune blot – and we might be better off broadening the definition rather than defining a new method. The literature is not clear about whether this approach has consistent advantages over standard immune blot

Action: Do not add this distinction now.

Follow with Specialty lab for their view.

Jim Case mentioned that they could use another code in the OBX –17 field to distinguish the method.

- 11.5 Possible duplicates in LOINC. These will have to be dealt with off line. (Kathy and Pam).
- 11.6 Use of GEN vs. GENV specimen and cellular elements not consistent use, esp. for wet prep.

GEN was intended to be Genital (generic) and GENV – Genital Vaginal – more specific.

We should be specific and consistent (**see suggested changes below**).

Agree that we should expand to include all of the terms reported – but need some help defining them.

Create a panel for wet mount

WT VAG GL PLEO GVR NO CURRENT LOINC

Notations:

PLEO= pleomorphic
GVR = gram variable rod.

WT VAG GL YEAST
14370-1 YEAST:ACNC:PT:GENV:ORD:WET PREPARATION

WT VAG GL TRICHOMONAS
14367-7 TRICHOMONAS AGINALIS:ACNC: PT:GENV: ORD:WET PREP

WT MT VAG CLUE CELLS
20502-1 CLUE CELLS:PRID:PT:GENV:NOM:WET PREP
The property and scale wrong (this test is not defining the kind of clue cells)

WT MT VAG WBC
12226-7 LEUKOCYTES:ACNC:PT:GEN:ORD:WET PREP
New term or change system to GenV. Is this quantified at all?

7WT MT VAG RBC
NO CURRENT LOINC
Will create new one – would it be quantified at all?

7WT MT VAG BACTERIA
12178-0 BACTERIA:ACNC:PT:GEN:ORD:WET PREP
Create new term or change System name – is this every quantified?

7WT MT VAG YEAST
14370-1 YEAST:ACNC:PT:GENV:ORD:WET PREP

7WT MT VAG TRICHOMONAS
14367-7 TRICHOMONAS VAGINALIS:ACNC:PT:GENV:ORD:WET PREP

7WT MT VAG EPITHELIAL
12211-9 EPITHELIAL CELLS:ACNC:PT:GEN:ORD:WET PREP
Create new term or change system name to GenV

7WT MT VAG MYCELIA
14319-8 MICROSCOPIC OBSERVATION:PRID:PT:GENV:NOM:WET
PREP

Clarification is needed as to whether this is done on males.

- 11.7 Question about rRNA and DNA probes (see separate agenda item)
 - 11.7.1 Non amplified probes are used to detect Group A Strep, GC, and Chlamydia, Blastomyces, Coccidioides, Histoplasma, Campylobacter spp., enterococci, Group A and Group B strep, H. influenzae, Listeria monocytogenes, mycobacteria, GC, Staph. aureus and Strep pneumoniae from culture (GenProbe).
 - 11.7.2 **“Observations from the front”**
 - 11.7.2.1 In mapping for clients, we see a high number of databases set up with generic fields for micro reporting. Terms like SLIDE, PRELIM, FINAL is used interchangeably for different stain readings, any type of culture preliminary or final report. This makes it practically impossible to map/CM: Agree that some of these are a mess and make it very difficult to file such results in an appropriate slot that corresponds to the same cultures from another lab. . But, it is quite feasible to have terms such as Preliminary organism or smear results – as general terms that work as “panels” under these terms.
 - 11.7.2.2 More obvious education is apparently needed for groups just starting the creation of their HL7 interface messages. We get feedback from clients that & ampersands cause problems in the messages, and they are trying to transmit the formal LOINC analyte field, rather than just the LOINC code. Perhaps a ‘helpful tips’ section on the LOINC website, might include this and other useful hindsight items we’ve encountered over the years?
 - 11.7.2.3 Signal to cut off ratio – **see separate agenda item** (Hepatitis C Virus and EBV). Journal of Clinical Chemistry 49: 479-486, 2003; 10.1373/49.3.479; <http://www.clinchem.org/cgi/content/abstract/49/3/479>.

12. Methods in the User Guide. ([Handout J](#) for review)

13. Plans for blood bank work. (Anil Patel may be able to contribute some terminology here. Pam Banning also has some work done) – definitely needs more work. We see many styles of reporting.

- 13.1 Effort could be divided into at least 3-4 areas
 - 13.1.1 Serologic testing of patient for compatibility (can be considered much like any other lab test – but it varies too).
 - 13.1.1.1 We have seen following patterns:
 - Q = Blood type; A = type A
 - Q = Type A blood type; A = 1:128
 - Q = Blood type; A = Type A = 1:128
 - 13.1.2 Preparation and dispensing of blood products – probably the most complicated and variable.
 - 13.1.2.1 Our Current blood bank vendor:
 - Battery = Name of blood product, e.g., irradiated RBCs
 - Test 1 = Blood type
 - Test 2 = DAT
 - Test 3 = etc.
 - Test 4 = product number
 - 13.1.2.2 Previously would have
 - Battery = blood product unit
 - Test 1 = kind of unit
 - Test 2 = status e.g. types, available. Transfused
 - Test 3 = Volume of unit
 - Test 4 = ID of unit
 - 13.1.3 Apheresis panel
 - 13.1.4 Transfusion reaction panel
- 13.2 Canada Infoway participants indicated that there are about 70 or so codes that they will need. Clem requested that they be submitted as a panel.

14. Request for more specific methods especially HPLC for some chemistry tests
(Assistance Publique – Paris Hospitals).

1|3-METHYLHISTIDINE|SCNC|PT|UR|QN|HPLC
5|ARGININE|SCNC|PT|PLAS|QN|HPLC
12|CITRULLINE|SCNC|PT|SER/PLAS|QN|HPLC
34|HOMOCYSTEINE|SCNC|PT|SER/PLAS|QN|HPLC
50|PHENYLALANINE|SCNC|PT|SER/PLAS|QN|HPLC

23|EPINEPHRINE|SCNC|24H|UR|QN|HPLC
21|EPINEPHRINE|SCNC|PT|UR|QN|HPLC
22|EPINEPHRINE|SRAT|24H|UR|QN|HPLC
44|NOREPINEPHRINE|SRAT|24H|UR|QN|HPLC
45|NOREPINEPHRINE|SCNC|PT|SER/PLAS|QN|HPLC
43|NOREPINEPHRINE|SCNC|24H|UR|QN|HPLC
42|NOREPINEPHRINE|SCNC|PT|UR|QN|HPLC

40|METANEPHRINE|SCNC|24H|UR|QN|HPLC
38|METANEPHRINE|SRAT|24H|UR|QN|HPLC
39|METANEPHRINE|SCNC|PT|UR|QN|HPLC
41|METANEPHRINE/CREATININE|SCRTO|24H|UR|QN|HPLC
48|NORMETANEPHRINE|SCNC|PT|UR|QN|HPLC
47|NORMETANEPHRINE|SCNC|24H|UR|QN|HPLC
46|NORMETANEPHRINE|SRAT|24H|UR|QN|HPLC
49|NORMETANEPHRINE/CREATININE|SCRTO|24H|UR|QN|HPLC

66|VANILLYLMANDELATE|SCNC|PT|UR|QN|HPLC
65|VANILLYLMANDELATE|SRAT|24H|UR|QN|HPLC
67|VANILLYLMANDELATE|SCNC|24H|UR|QN|HPLC
37|HOMOVANILLATE|SRAT|24H|UR|QN|HPLC
36|HOMOVANILLATE|SCNC|24H|UR|QN|HPLC
35|HOMOVANILLATE|SCNC|PT|UR|QN|HPLC
20|DOPAMINE/CREATININE|SCRTO|24H|UR|QN|HPLC

59|RETINOL|SCNC|PT|SER|PLAS|QN|HPLC
3|ALPHA TOCOPHEROL|SCNC|PT|SER|QN|HPLC

This request included a number of specific HPLC tests. Gil Hill previously reviewed the submission and some of the terms have already been created.

There was general discussion of when to include the method versus using methodless terms. Also, is there a list of what the methodless test is, or includes.

The consensus was that adding method specific terms isn't necessary when there isn't a significant difference between methods.

15. Further revisions of micro test names

- 15.1 Use BACTERIA rather than MICROORGANISM when that is the primary intent of the culture or smear. Granted we may grow out Candida and a few other fungi, but Microorganism screws up the hierarchy– because it includes viruses, and parasites. We have fungal cultures when that is the primary interest.

Action: accepted

- 15.2 Revise the component names for organism cultures and smears and direct observations (motivated by work on the hierarchy).

15.2.1 For cultures, instead of saying

- <bug> identified or just <bug>
 - say <bug> cultured <bug> isolated.
 - For smears and direct observation say <bug> seen.

15.2.2 This solve a continued complaint about “identified” for cultures across the board. It also will help separate out and balance the hierarchy:

Bug Ag
Bug DNA
Bug rRNA

Bug AB
Bug AB.IGG
Bug AB.IGM
Bug AB.IGA
Bug cultures (or isolated)
Bug seen (for smears and direct identification)

Discussion: Jim Case – what is the Symantec difference between these?
People get caught up on names. Several suggestions for just using <bug> with the method to identify. Group – people don't like 'IDENTIFIED'.

Consensus: just use <bug> and use method where sufficiently complete.
Instead of MICROORGANISM IDENTIFIED use BACTERIA.

Action: Rejected – Use just bug as the name-drop identified – find another way to organize the hierarchy.

15.3 Clarify rRNA vs. DNA for DNA probes.

15.3.1 Bacteria contain only one copy of the DNA, so detection of DNA by unamplified probe is not possible. A single bacterium contains >10K of rRNA sequence, which can be detected by unamplified probe. Unamplified probes always target rRNA. The probe is made from DNA. We get submissions that seem to be targeting DNA and have misnamed many terms. Most PCR probes target DNA, but some also target rRNA.

15.3.2 Wonder about changing method name to DNA probe – to clarify this situation (other issues is it always DNA?)

15.3.4 Jim Case inquired about whether there are any non-DNA probes, and the group consensus was that there were not. We have already changed the Chlamydia and Neisseria terms to rRNA. There are about 10 other bacteria that we have probe as method and DNA in the component.

Action: Will move toward changing <bacteria> DNA to <bacteria > rRNA when the method is pure probe. (without amplification). Will consider changing “probe” to “DNA probe” because that would clarify to mappers that yes they are using a DNA probe but they are detecting rRNA (10,000 copies per organism where as any DNA strip has only 1 copy per organism).

Jim Case will verify that these other bacteria probes are indeed probing for rRNA and that the probes are never done on RNA help identify some of these other ones.

16. Proposals/questions from Jim Case

16.1 BIOPLEX ([Handout K](#))

16.1.1 Tests that identify multiple signals (? DNA sequences, Amino acid sequences) and use them to identify bacterial species. Can identify many at a time.

- 16.1.2 The sequences are not yet standardized.
- 16.1.3 What can we do?
- 16.1.4 If the signatures correspond to a particular DNA/RNA or AA sequence report that as data linked to the results?
- 16.1.5 Any examples of how this is reported now, manually.

The issue involves identifying the result for each individual signature in a result message. The process is PCR followed by Luminex. A problem is that the signatures that are created are relatively unique. Need to be able to individually result the signatures, when we don't have a good way to uniquely identify the sequences. Some sequences are publicly available and others are not; you can't know how to equivalence across sources. We must assume they are not the same.

Steve Steindel noted that there are similar things with LRM labs. The general feeling was that the scientists wanted all the results that are available. Decision was that we would message only the result...kept the details internal.

Jim Case concluded that at this point, we'll probably keep these things internal.

- 16.2 Use of Impression ([Handout L](#))
 - 16.2.1 Clem McDonald noted that these seem to be ordinal, but Jim Case noted that some of the cases are not strictly ordinal.
 - 16.2.2 Clem noted that the specific answer list affords some type of branding.
 - 16.2.3 **Action: Jim Case to follow-up.**

17. Beverly Knight's requests

- 17.1 Needs terms with method = CULTURE for systems that currently have only anaerobic or aerobic for the method. – We need a micro semi-methodless term (or culture).
 - 17.1.1 **Action:**
 - **Clem McDonald said that we'll do it.**
 - **Beverly will submit term requests.**
- 17.2 Propertyless terms for protein C and few others.
 - 17.2.1 On the order side, there is a need for a generic kind of property.
 - 17.2.2 **Action:**
 - **Beverly will submit requests for further discussion.**
- 17.3 Decimal fraction and d-dimer issues from Gil Hill. Gil says that we are happy to park the issue for now.
 - Gill has found a hematologist who may help work on this.
- 17.4 Formal committee membership for a Canadian representative.
 - 17.4.1 Gil Hill is already a member.
 - 17.4.2 **Action:**
 - **Canada Infoway will put forward a name and CV.**
 - **Canada Agreed, with the requirements that they have knowledge about the lab and come to the meetings.**

18. Pan-Canadian Group method change request:

- 18.1 Suggestion to change AGAR DIFFUSION to DISK DIFFUSION.
- 18.2 **Action: There was no opposition, so change will be made.**