Encoding Microbiology Test using LOINC® Terminology: Challenges from Identification Systems

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INTRODUCTION

Patient care is based upon broad information sharing, both between diverse devices and information systems. Ensuring fluid communication and data integration among various devices and multiple healthcare information systems has become a huge interoperability challenge to build consistent Electronic Medical Records. Adoption of controlled standard terminology such as Logical Observation Identifiers Names and Codes (LOINC®) for identifying medical laboratory observations, brings the opportunity of addressing that important issue.

OBJECTIVE

The objective of this study was to determine the most suitable LOINC® code matches for the bioMérieux systems dedicated to identification of micro-organisms: API®/ID32, RAPIDEC® strips and the VITEK® MS system.

METHODS

The VITEK® MS system and 28 identification API®/ID32, RAPIDEC® strips were included in the present study.
Since LOINC® codes are comprised of six attributes:
i) Component/analysis (name), ii) Kind of Property (what is measured), iii) Time aspect (time of execution), iv) System (biological sample), v) Type of scale (quantitative or nominal response), vi) Type of method (analytical methodology), all identification systems listed above were described using this structure by selecting individual descriptors listed within the LOINC® user guide. The RELMA® software and database (V6.10) was used to search and retrieve the relevant corresponding LOINC® codes.

RESULTS

LOINC® codes were found for 2/28 (7.1%) of the API®/ID32 and RAPIDEC® strips with a complete match for all 6 attributes for Anaerobes testing strips (Table1).

Table 1: Examples of cases for perfect, partial and no match codes

STRIP	LOINC® attributes and Codes						Result
	Component (what we want to analyze)	Property (what we want to measure)	Time (moment of time vs integrated over time)	System (the biological specimen used)	Scale (specify the scale of the measure)	Method (method used)	
API® 20 A rapid ID 32 A	Bacteria identified	Prid	Pt	Isolate	Nom	Anaerobic culture	Perfect LOINC® code 20878-5
API 20 E™ API® 10 S ID 32 E Rapid ID 32 E ID 32 GN API® 50 CHE	Gram negative bacilli identified	Prid	Pt	Isolate	Nom	Aerobic, facultatively anaerobic culture	Partial No LOINC® code
API® Staph ID 32 STAPH	Gram positive cocci positive catalase identified	Prid	Pt	Isolate	Nom	Aerobic, facultatively anaerobic culture	
API® Coryne	Gram positive bacilli coryneform identified	Prid	Pt	Isolate	Nom	Aerobic Culture	
API® Campy	*Campylobacter* sp identified	Prid	Pt	Isolate	Nom	Aerobic Culture	
API® NH	*Neisseria* sp identified	Prid	Pt	Isolate	Nom	Aerobic specific Culture	
API® 20 Strep Rapid ID 32 STREP	Gram positive cocci negative catalase identified	Prid	Pt	Isolate	Nom	Aerobic, facultatively anaerobic culture	
API® Candida API® 20 C AUX ID 32 C	Yeast identified	Prid	Pt	Isolate	Nom	Culture	
RAPIDEC® ur	Urinary Germs identified	Prid	Pt	Isolate	Nom	Aerobic, facultatively anaerobic culture	
API® Listeria RAPIDEC® Lmono	*Listeria* sp identified	Prid	Pt	Isolate	Nom	Aerobic, facultatively anaerobic culture	
api® ZYM	Enzymatic activity identified	Prid	Pt	Isolate	Nom	Culture	No match No LOINC® code

In red: Examples of suitable changes to the existing code
Prid: Presence or Identity Pt: Point in time Nom: Nominal

For 25/28 (89.3%) of the strips a LOINC® code was found with an incomplete match of the attributes (less than or equal to 5 attributes). For 1/28 (3.6%), enzymatic activity identification strip, no match was found at all.
A LOINC® code for VITEK® MS (76346-6) was found with a full match for all of the attributes.

CONCLUSIONS

This study represents the first attempt to adhere to a unique identifier terminology standard for a defined set of commercially available microbiology tests.

The current LOINC® codes cannot be implemented *stricto sensus* for the identification products. Some code additions are required to provide a better accuracy for the description of the Component attribute (to adjust the scope to targeted bacterial classification), System (isolate) and Type of Method (micro-organism respiration process). Through a joint collaboration with the LOINC® Institute, detailed analysis will allow to perfectly define the necessary codes.

When pathogen identification is performed in different locations by different providers, the patient records may end-up as being scattered across several health systems, causing an increased potential for documentation errors. Leveraging standardized terms and concepts, as data is transmitted, preserves the relevance of the content and creates a way for clinicians to co-analyze or synthesize data from all collaborating systems. With the intent to accelerate patient diagnosis leading to better informed treatment decisions.