ONC Sync for Genes: review and update

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Sync for Genes Presentation for Data Standards Symposium and Hackathon (DaSSH3)

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ONC Mission and Priorities

**FEDERAL HEALTH IT MISSION**

Improve health and well-being of individuals and communities using technology and health information that is accessible when and where it matters most.

**ONC PRIORITIES**

Make health information more accessible, decrease documentation burden, and support EHR usability under 21st Century Cures and MACRA.
Sync for Genes Background

• **Launched:** 2017
• **MISSION:** Standardize sharing of genomic information between laboratories, providers, patients, and researchers

  • **Phase 1: Standardizing Genomic Data**
    » Updated HL7® FHIR® clinical genomic specification
  
  • **Phase 2: Integrating Genomic Data**
    » Demonstrated connectivity and exchange of data
  
  • **Phase 3: Laboratory Genomic Data**
    » Interoperability of genomic data from laboratories
  
  • **Phase 4: Sharing Genomic Data with Individuals**
    » Interoperability of genomic data between organizations and at least one data receiver, including patients or caregivers (if appropriate)
Sync for Genes Phase 1

Purpose:
• Standardize genomic data through test use cases using HL7 FHIR

Outcomes:
• Contributed to the development of the HL7 Clinical Genomics Implementation Guidance as part of FHIR Release 3.0
Sync for Genes Phase 1 Pilot Sites

- **Counsyl and Intermountain Healthcare**: Family Health History Genetics

- **Food & Drug Administration**: Sequencing Quality and Regulatory Genomics

- **Foundation Medicine and Vanderbilt**: Somatic/Tumor Next Generation Sequencing

- **Illumina**: Next Generation Sequencing Solutions

- **National Marrow Donor Program**: Patient and Donor Matching
Sync for Genes Phase 2

Purpose:
• Continue to support testing and refinement of standards for genomic standards integration

Outcomes:
• Tested FHIR® resources against various use cases
• Demonstrated exchange genomic diagnostic reports (GDR) using FHIR®
• Identified nationwide integration of genomic data into health IT challenges
Sync for Genes Phase 2 Pilot Sites

- **Lehigh Valley Health Network**: Pharmacogenomics
- **National Marrow Donor Program**: Patient and Donor Matching
- **Utah Department of Health**: Newborn Screening
- **Weill Cornell Medicine**: Cancer Genomic Decision Support
Sync for Genes Phase 3

Purpose:
• Standardize genomic data generated by laboratories

Outcomes:
• Sharing of clinical genetic reports that can be integrated and consumed into EHRs
• New, specialized human leukocyte antigen (HLA) reporting Implementation Guide using FHIR shorthand
Sync for Genes Phase 3 Pilot Sites

• Baylor College of Medicine Human Genome Sequencing Center: Integrating genetic variation testing information directly into EHR systems

• National Marrow Donor Program (NMDP): Exchanging genomic data requirements for human leukocyte antigen (HLA) use cases with HLA typing laboratories
2.1 eMERGE FHIR Specification Development

- Data Element Identification
  - Identify all data elements using existing reports

- FHIR Mapping & Gap Analysis
  - Map data elements and structures to FHIR CG GR IG
  - Identify structural & semantic mismatches

- eMERGE FHIR Specification
  - Resolve and harmonize eMERGE FHIR Specification with CG Genomics Reporting IG
  - Design eMERGE FHIR Specification with custom profiles & extensions

- XX Coverage of report content in CG IG

2.2 Use Case Pilot Projects Development

- Pilot Project Scoping
  - Identify pilot sites and objectives

- Report Data Selection
  - Select sample reports

Pilot FHIR Server(s)

- 2.2.2 BCM-HGSC Generation of Sample Reports
  - Generate & validate sample reports using FHIR specification

Lab

- 2.2.3 Northwestern University Pharmacogenomics
  - Ingest sample reports using FHIR specification

Clinical Site(s)

- 2.2.4 Johns Hopkins University Clinical Phenotypes

XX Review generated reports

XX Review of data exchange

XX Content & format validity ranking

Figure X: Methods used for the specification development and validation. The two columns represent work streams - the leftmost dedicated to the specification development, and the right on use cases. The dashed boxes describe the validation done for each part of the methods. The solid arrows represent the direction of sequential steps in the respective processes.
eMERGE Results FHIR Specification

Warning
This document is a work in progress and is not ready for production use.

Introduction
This is the eMERGE Phase III specification detailing the design for generating structured genetic test lab results using HL7 FHIR Genomics Reporting Implementation Guidelines.

Contents
- Introduction
- How to read this Guide
- FHIR Genomics Reporting IG

https://emerge-fhir-spec.readthedocs.io/en/latest/
Issues & Resolutions

#13 Pathogenicity phenotype cardinality change

#14 InhDisPath value (CC) made extensible

#15 Genomics Report category cardinality changed to 0,*

#16 Citing specific assessed medication implications

#17 Report Sign-Out v Report Sent Date

#18 RecommendedAction Task with Multiple Reasons

#19 Add Age to US-Core Patient Profile

#20 Clinical v Research Flag

#21 Why is the Report code fixed to LOINC:81247-9?

#22 RecommendedAction "code" should be extensible

#23 Inclusion of Disclaimers

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This section includes a review of the issues that required resolution. These issues and topics range in effort and complexity which are qualified as major or minor.

The section below pertains to the work performed by the BCM and Broad Institute teams to create the eMERGE FHIR Specification based on the Genomics Reporting IG (STU1) during 2019. It should be noted that with the Clinical Genomics WG continuing to work on upgraded versions of the IG (i.e. STU2, ...), there will be changes and variations between the STU1 version discussed here compared to any subsequent versions released or currently in development by the Clinical Genomics WG.

During the course of implementing the eMERGE Results using the Genomics Reporting IG (STU1) a number of issues were uncovered, discussed and resolved. Noteworthy issues are summarized below along with their outcome. Also included is extended documentation related to the collaboration and tracking of these items with the associated HL7 FHIR Working Groups.
ONC Sync for Genes: NMDP/CIBMTR

- **Phase 1**
  - Development of HLA Genotyping report using FHIR
  - Conversion of HML to FHIR
  - FHIR STU3

- **Phase 2**
  - Complete HML2FHIR tool
  - Pilot with Transplant Center partner (Moffit)
  - FHIR R4, prior to publication of HL7 Genomics Reporting IG STU1

- **Phase 3**
  - Development of HLA Reporting FHIR IG
    - Derived from & informed by Genomics Reporting IG STU1
  - Direct FHIR submission by HLA typing lab
    - Versiti - [https://www.versiti.org/](https://www.versiti.org/)
HLA Reporting IG

- 1st draft found at http://fhir.b12x.org/ig/hla-reporting
  - temporary home, in the future will be http://fhir.nmdp.org
- derived from HL7 Genomics Reporting IG
  - technical issues with slicing
  - Clinical Genomics WG is working on fixing issues
- FHIR Shorthand (FSH) & Sushi to develop
What's in the IG?

- Profiles
  - HLA Summary Report
  - HLA Genotype Observation
  - HLA Allele Observation
  - HLA Molecular Sequence

- Value Sets / Code Systems
  - HLA Gene Name Value Set
  - HLA HGNC GeneID CodeSystem
  - Genotype List String Code CodeSystem

- Extension
  - HLA Genotype Summary

- Examples!
HLA lab data → FHIR

- Versiti is currently using two HLA analysis software products
  - three possible paths to success

- Vendor 1
  - Develop direct FHIR export
  - We shared our HLA Reporting IG with them

- Vendor 2
  - Developing HML export module, use public HML2FHIR service
  - NMDP to develop vendor XML to FHIR translator
    - XML Schema (XSD) and examples to work from
1. Lab determines histocompatibility profile for donor

2. Results converted from native format to HL7 FHIR

3. Results stored in donor registry, ready to search for match to a patient
TARR2FHIR

- https://github.com/nmdp-bioinformatics/tarr2fhir
- Converts GenDx NGSEngine® XML (TARR) to FHIR transaction Bundle that conforms to the HLA Reporting Implementation Guide
- Input – single TARR XML file for a single locus, or a zip file containing multiple TARR XML files for a single subject.
- Output -  FHIR transaction Bundle containing
  - A single HLA Summary (profile based on GenomicsReport) for a single subject
  - HLA Genotype (profile based on Genotype Observation), one per HLA gene
  - HLA Allele (profile based on Haplotype Observation), one per allele
  - HLA MolecularSequence (profile based on MolecularSequence), one per sequence reported
  - A single Provenance resource (to describe how the resources were created based on what input file and what software)
  - A single Device resource (to describe TARR2FHIR conversion software & version)
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Sync for Genes Phase 4

Purpose:
• Testing and updating health IT infrastructure to enable interoperable sharing of genomic data and supporting information using FHIR APIs to support patients

Outcomes:
• Feedback on the FHIR IG
• Blueprint for future work
Sync for Genes Phase 4 Pilot Sites

• TBA!

• If you are interested in participating as a pilot site, please contact Tracy Okubo or Bob Freimuth
  • Tracy.Okubo@hhs.gov
  • Freimuth.Robert@mayo.edu
Discussion

• Core vs. custom IGs: finding the 80/20 balance
  • eMERGE, HLA, mCODE, phenopackets

• Collaboration and engagement
  • ONC, NLM, NHGRI

• CG WG effort
  • Standard development (new)
  • Fixes, clarifications, examples (existing)
  • Consultation to support adoption