



# Workshop #1 Harmonization of Clinical and Biological Data Session 3

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## Workshop General Goals and Structure

Goal: Discuss strategies and plan an international partnership to advance the harmonization of biological and clinical data in support of childhood cancer research

Session 1: Core data elements: patient, tumor, prognostic factors

Session 2: Treatment and outcome + standards mapping

**Session 3: Genetic/molecular data + challenges to harmonization** 

Session 4: Summary of discussions + pilot project





## Intro to session 3

- Pediatric tumors differ from tumors in adults in cellular origin, genetic complexity, driver mutations, and potential mutational processes, therapy decision and response to treatment
- Genomic sequencing, molecular profiling, and liquid biopsy characterization at the time of diagnosis
- Genetic/Molecular characterization helps survivors and medical providers select the best and most appropriate treatment





## Intro to session 3 (continued)

- Childhood Cancer Data Initiative, an NCI program that ensures data are shared by survivors, clinicians and researchers in the USA; similar projects in Europe
- Increased concerns about protection of personal health information
- NCI platforms with controlled access- dbGAP, Seven Bridges





## **Session-Specific Questions and issues for consideration**

• Identify genomic variables and data standards relevant for childhood cancer research

• Discuss solutions to challenges in harmonization of genetic and molecular data

• Plan activities to integrate data and standards for phenotypic and genetic/molecular data into a childhood cancer data resource/platform





## **Session 3 topics and Discussants**

• Dr. Arnaud Petit

Challenges in harmonization and sharing of pediatric AML data

• Dr. Frank Westermann

Combining genetic and molecular data with phenotypic data for childhood tumors





## Discussants

#### Arnaud PETIT

#### France

Armand Trousseau Hospital French Society for Childhood and Adolescent Cancer and Leukemia Pediatric Oncologist



Frank WESTERMANN Germany German Cancer Research Cancer (DFKZ) Head of the Department of Neuroblastoma Genomics



Newcap Event Center (Paris, France), November 7-8, 2023



## DOREMy

Base de **DO**nnées cliniques et biologiques harmonisées pour une **RE**cherche intégrée à la prise en charge des leucémies aiguës **MY**éloïdes pédiatriques

Harmonized Clinical and Biological Data Bases for an Integrated research dedicated to Pediatric Acute Myeloid leukemia

## Arnaud Petit, MD, PhD, Paris, France



DOREMy is supported by a grand from InCa (parpedia19-008)

CONECT-AML is supported by a grant from InCA, Fondation ARC, Ligue nationale contre le cancer (InCa-ARC-LIGUE 11905), and the following partners





















#### **Objectives of DOREMy**









#### Funding : 2019, Start of the project : September 2020

### **REGULATORY PROCESS**

Main blocking difficulty

- 1. Authorization by the CNIL
- Prerequisite for any further steps -
- 1<sup>st</sup> submission : summer 2021
- Withdrawal for inadequate security of health data
- Health data host 2.
- Completed mid-2023

## CASD C.

- 3. Next step
- 2nd submission to CNIL, Q4 2023

### **CLINICAL DATABASE**

- Data collection from previous trials 1. - Selection of clinical and biological data
- Data harmonization (clinical data) 2.
- According to PDCD INTERACT\* AML Dictionnary

Myechild01 LAME89/91 ELAM02 Post-ELAM02 registry

- Integration into a closed database 3.
- REDCAP, completed Q3 2023



- 4. Next steps
- Update survival data (link with LEA project)
- Prospective data : ALARM<sup>3+</sup> and Co-DoReMy registry

\*International Pediatric Acute Mveloid Leukemia Consortium

+ Granted by Imagine For Margo (FKC), Enfants Cancer Santé, AFER

## **GENOMICS DATABASE**

#### Data from CONECT-AML 1.

- Generated in 2021 and 2022
- n≈90 paired sample diag/CR
- WGS/RNAsea
- SNVs, Indels, SVs, CNVs, fusion

#### transripts

- 2. Integration ElioPortal
- Started mid-2023
- Still ongoing





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#### **TYPE 1 REQUEST**

Made by a P-DOREMy limited to the only data generated by the center or team

#### **TYPE 2 REQUEST**

Made by a P-DOREMy associating other P-DOREMy limited to the only data generated by all of these actors

#### **TYPE 3 REQUEST**

Nor type 1 or 2

#### Information to scientific committee

Need for approval by SC







### **BENEFITS**

Clear need for international cooperation to make progress on childhood myeloid leukemia

## STRENGTHS

IBFM AML SG : International cooperative group to discuss and promote collaborative projects Common standardized language for clinical data

## **KEY CHALLENGES**

- 1. Raise the good question to built the good database
- 2. Link the data to ensure it relates the same patient
- 3. Selection and harmonization for Omics data (Raw vs processed data ?)
- 4. Obtain regulatory authorizations for data reuse and data sharing
- 5. Terms and conditions of data sharing





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## **ITCC Data Integration Portal**

### Frank Westermann

David TW Jones, Patrick Kemmeren, Stefan M. Pfister







DEUTSCHES KREBSFORSCHUNGSZENTRUM IN DER HELMHOLTZ-GEMEINSCHAFT









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## The ITCC-data integration platform: Aims

- Real-time archiving of raw data in national EGA instances
- Harmonization of data dictionaries (molecular & clinical) as well as ICFs (e.g., also allowing data sharing with industry)
- Harmonization of omics pipeline and central collection of processed omics data for overarching analyses
- Data vizualization and sharing through <u>www.pedcanportal.eu</u> (internal and external) utilizing existing tools (R2, cbio, PedCan portal at St. Jude, etc.)
- Coordinating overaching analyses, similar to PCAWG (ICGC)
- Involving patient representatives as well as ethical and legal experts as key project partners



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### The ITCC-data integration platform: WP structure



David Jones (KiTZ) Patrick Kemmeren (PMC) Stefan Pfister (KiTZ) Frank Westermann (KiTZ)

+ fantastic global team!

10.5M € funding obtained from the Dietmar Hopp Foundation 1/2023





# Key decisions in the process of integrating and exchanging genetic/molecular and clinical/phenotypic data

- Establish a federated and harmonized bioinformatics pipeline
- => assessment of existing bioinformatic pipelines
- => develop a harmonized consensus pipeline
- => Establishing a validation procedure/quality management for the pipeline
- Complexities from data formats from multi omics layers
- => flag restricted/permissive data outputs,
- => define standard data formats (e.g., annotated variants in MAF, chromosome copy number as CBS segments)
- Establishing a data warehouse for secure access







## **Metadata harmonization – action items**

- Buid a Common Data Model (CDM)
- => Benchmarking of initiatives for clinical data harmonization (semantic interoperability)
- => Development of a CDM encompassing the relevant Common Data elements (CDE)
- => Prospective use of CDE
- Develop Secure Data Exchange
- => Design and implement pseudonymization processes
- => Design application programming interface (API) for data submission
- => Provide local node package
- => Operation and sustainabliity



## Looking forward to the discussion!







