Characterization and Valorization of COVID-19 Biological Samples through Data Linkage

Hôpital Erasme ULB

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INTRODUCTION

Generally, when collecting human body material (HBM), biobanks record minimal dataset (gender, age and major clinical diagnoses). Although highly desirable, association of biological samples with comprehensive medical dataset is not systematic. Collaboration between biobank managers and clinicians is warranted.

Automatic connection of biobank database to patient medical file represent a real opportunity in the valorization of human samples. However this link requires a robust IT infrastructure and can face several data privacy issues. Hence, creating a link between GDPR-compliant data registries and biobanks can solve both issues.

The Hôpital Erasme – Université Libre de Bruxelles used the opportunity yielded by the COVID-19 outbreak and the resulting academic research to link the data stored in an international patients registry with a collection of biological samples.

METHODS

BIOBANKING
The biobanks collected 4 different types of COVID-19 HBM:
- blood samples and derivatives
- respiratory tract samples
- fresh frozen tissue and formalin-fixed paraffin embedded tissue (Remmelink et al)
- DNA samples (Zhang et al.)

REGISTRY
With approval of the ethics committee, a registry "ULB-COVID-19" was set up, composed of 469 variables, gathering clinical, biological and lifestyle data from patients with COVID-19. The 469 variables were grouped into 22 different categories.
The "ULB-COVID-19" registry included :
- Demographics (e.g. sexe, age, ethnicity)
- Pre-admission Medications
- Comorbidities (e.g. asthma, diabetes)
- Infection respiratory disease pathogen testing (type of testing, results)
- Treatment
- Complication (e.g. liver dysfunction, pancreatitis)
- Outcome (e.g. discharged alive, death)
Information documented in the medical file of patients hospitalized with suspicion of COVID-19 were recorded daily in the registry during their hospitalization.

THE LINKAGE
Each biobank regularly sent its sample lists to the hospital's biobank coordinator, allowing samples and patient information to be centralized and linked.
New categories were added in the "ULB-COVID-19" registry, indicating for each patient :1) Sample availability; 2) Type(s) of sample(s) available, and 3) Name of the associated biobank

RESULTS

BIOBANKING
In total, approximatively 7400 HBM samples from a total of 986 COVID-19 patients were collected, processed and stored between March and June 2020.

REGISTRY
Data from 615 patients with suspicion of COVID-19 were entered into this registry.

THE LINKAGE
For 301 patients on the registry (50%) , the availability and localization in tissues, blood & derivatives, respiratory tract and DNA samples were added into the ULB-COVID-19 registry (Figure 1)
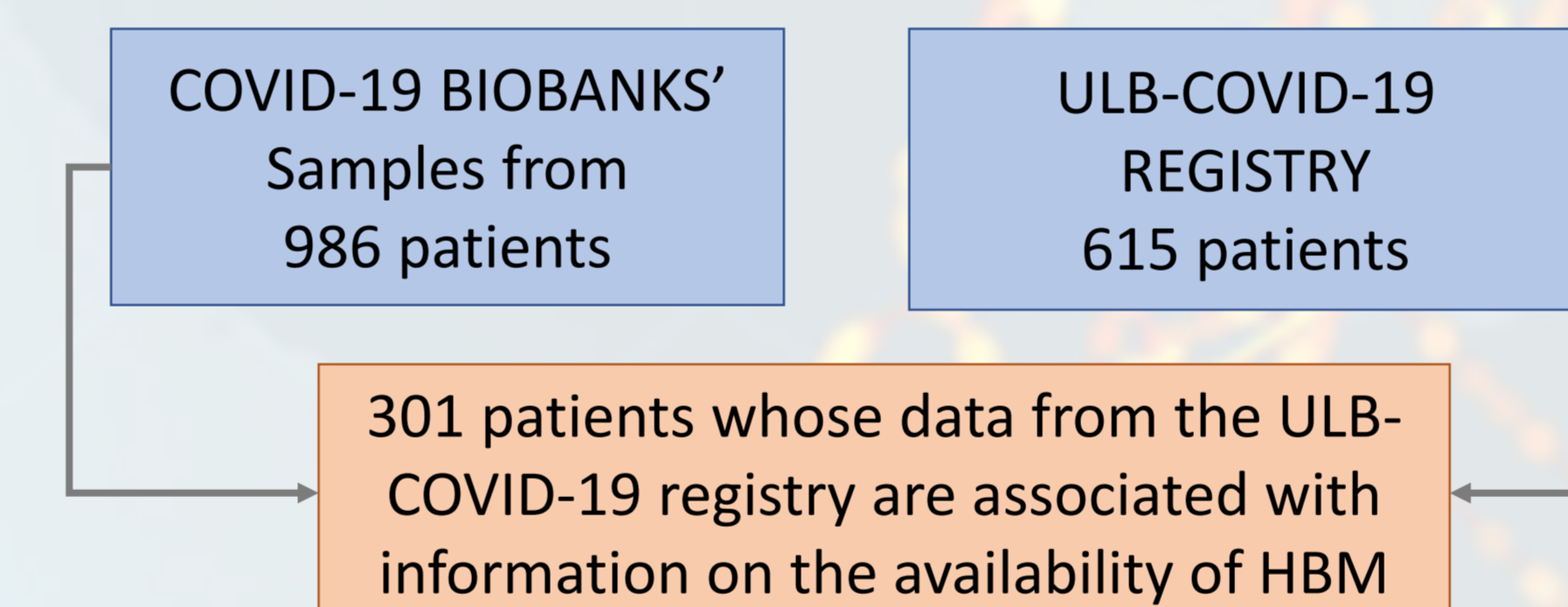
COVID-19 BIOBANKS' Samples from 986 patients

ULB-COVID-19 REGISTRY 615 patients

301 patients whose data from the ULB-COVID-19 registry are associated with information on the availability of HBM

Figure 1– The linkage

DISTRIBUTION OF THE PATIENTS BY TYPES OF HBM
Figure 2 compares the number of patients per type of COVID-19 associated HBM and by whether or not the corresponding patient data is in the ULB-COVID-19 registry. We observed that 28% and 34% of patients with available blood & derivatives samples and respiratory tract samples, respectively, have information to the registry. However 97% and 82% of the patients who have DNA and tissue samples in biobanks, respectively, have data in the registry. This difference is likely explained by the large number of standard of care residual blood and respiratory samples.
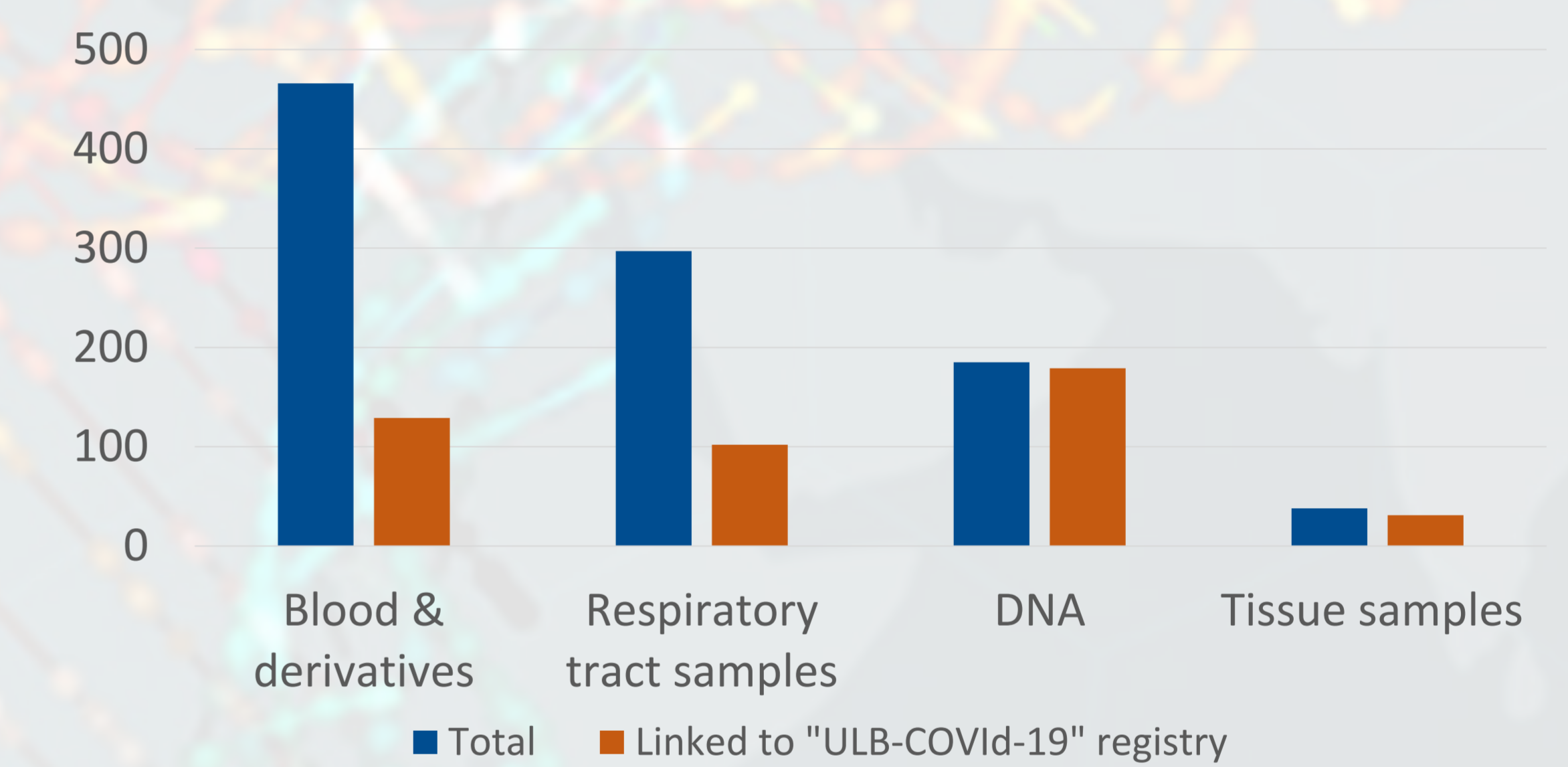

■ Total ■ Linked to "ULB-COVId-19" registry

Figure 2– Number of COVID-19 patients with biobanked biological samples by type of samples

CONCLUSIONS

Fifty percent of patients data captured in the ULB-COVID-19 registry are linked to biobank samples. As soon as they get published, the results of analysis performed on COVID-19 HBM will be added to existing entries in the ULB-COVID-19 registry.
In order to find ways of curing and preventing COVID-19, the scientific community needs to have access to patient's data associated with corresponding available HBM (Spjuth et al). This is the first time that such a transversal tool has been developed in our hospital. We hope that it will permit the development of numerous project leading to a better understanding of the COVID-19.

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