



Upper and lower respiratory tract microbiomes analysis in infants with severe asthma

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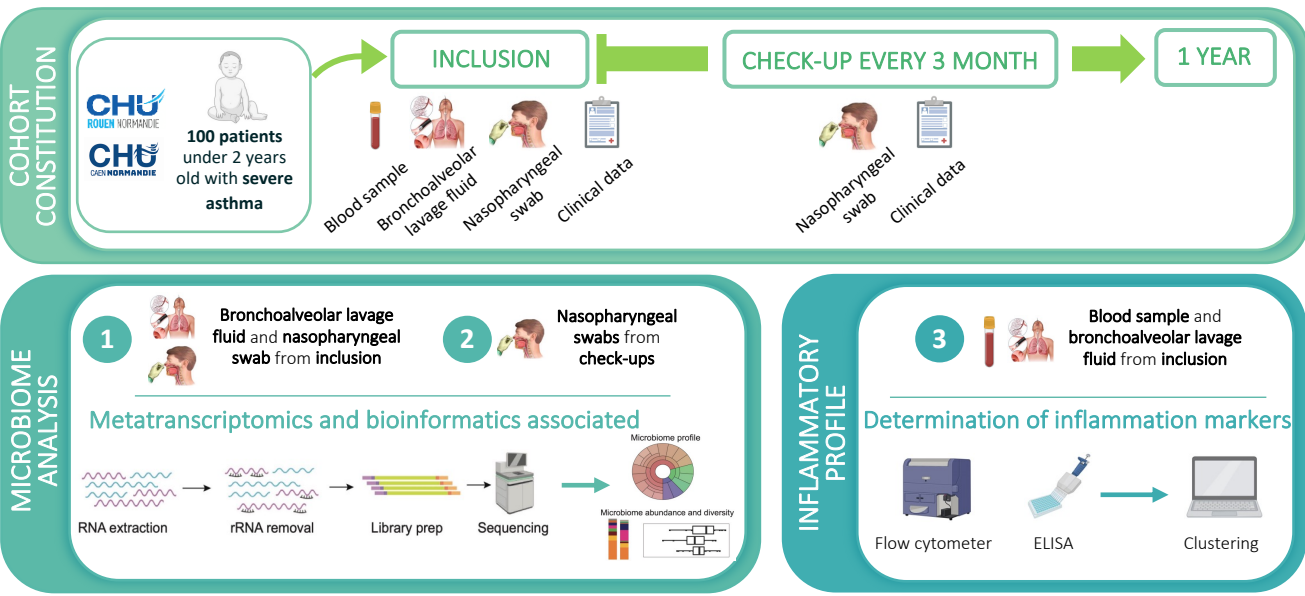
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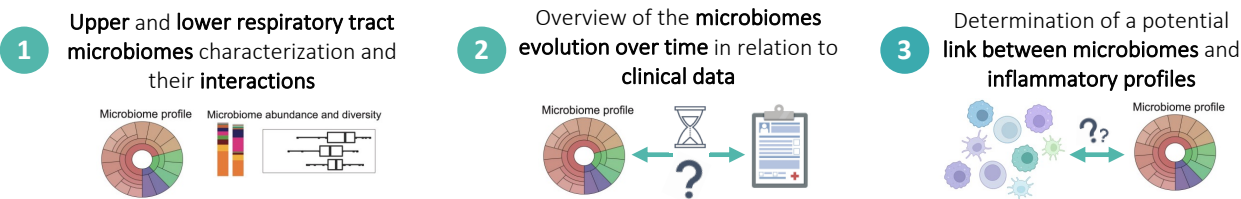
ABSTRACT

The **human respiratory tract** is colonized by microorganisms which constitute the **respiratory microbiota**. This microbiota is involved in the protection of the host against microbial infections. Its dynamics is regulated by mechanisms such as respiratory air flows, contributing to the inhalation of microorganisms, which is balanced by the host's immune system. An imbalance of these microbial communities, called **dysbiosis**, seems to be involved in the occurrence of respiratory pathologies such as **asthma**. This pathology affects about **25% of infants** and its pathophysiology suggests a **microbiota damage**, associated with an **inflammation**. Major aims of this project are to characterize the global composition of the **respiratory microbiome** of infants with severe asthma, to follow its evolution over time and to determine the **inflammatory profile** of these patients. The cohort will include **100 patients** from University Hospitals of **Rouen** and **Caen**. Nasopharyngeal and bronchoalveolar samples from these patients will be sequenced by **metatranscriptomic approach** and will allow to describe the respiratory microbiome composition. Inflammatory markers will also be analyzed through **flow cytometry** and **ELISA** to identify links between **inflammation profiles** involved in severe asthma and microbiome composition.

METHODS



OUTCOMES



CONCLUSIONS

This original project will allow to assess the **dynamics** of the **airway microbiome**, to determine the nature of potential **dysbiosis** promoting **severe asthma** in **infants**, potentially correlated with **inflammatory markers** involved in its pathogenesis. Leading to the **better management** of **patients** and to the discovery of **new therapeutic targets** as long-term aims.