Asthma exhaled breath markers translation into actionable clinical tool for treatment monitoring

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Chronic lung inflammation is major challenge for healthcare professionals. Asthma and COPD are uncurable and represent a high burden on healthcare system. According to WHO, asthma is the most common chronic disease among children. It affected around 262 million people in 2019 and caused 455 000 deaths. Proper asthma management requires efficient monitoring tools in order to define and adjust treatment using personalized approaches [1].

Exhaled breath analysis holds strong promise for non-invasive monitoring, especially for chronic lung inflammation. The best example is the use of FeNO measurement to access asthma phenotype [2]. Building on this link between inflammation and breath composition, breathomics has demonstrated its capacity to reveal the inflammatory phenotype in asthma cohorts [2,3]. In the past five years, we have demonstrated the capabilities of exhaled breath analysis to identify eosinophilic and neutrophilic asthma in large cohort (> 500 patients). We have also worked on in vitro model development in order to identify metabolic pathways linked to our breath markers [4]. Indeed, most of documented metabolic pathway investigations stopped prior to reaching volatile organic molecules, which are usually found in breath, generating a gap in our understanding of the breath composition. However, exhaled breath is not the answer to all questions. In recent studies, we have also demonstrated the inefficiency of exhaled breath analysis to identify airflow decline in asthma [5] and to correlate with physical training induced patient improvements.

Following up on those investigations, our latest research focuses on the prediction of treatment response in the context of biologic therapy, with a focus on anti-IL5/IL5Rα. In a longitudinal multicentric design (80 patients), we have demonstrated the capabilities of transferring eosinophilic markers into treatment response prediction (AUC > 0.95). In addition, we have established a direct link with reactive aldehyde species in exhaled breath (AUC > 0.90). This study represents a major step forward regarding breath marker transferability across studies and research centers using different analytical workflows.

References

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