Use of exhaled volatile organic compounds to discriminate asthma phenotypes

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Abstract

Breath analyses for medical applications have gained widespread interest since the last decades [1]. This method is among the least invasive methods available for clinical diagnosis and disease state monitoring. Several studies have shown a correlation between the concentration patterns of exhaled volatile organic compounds (VOCs) and the occurrence of specific diseases [1,2]. This study focuses on the analysis of breath VOCs as non-invasive diagnostic tool for asthma phenotyping. Asthma has a complex pathophysiology characterized by many different inflammatory profiles of the airways. The inflammation goes along with oxidative stress, which yield the conversion of polyunsaturated fatty acids, from the membranes, into volatile compounds that are secreted by the lungs [4]. Currently, 334 million people of all ages are affected worldwide and recent trends indicates that there may be an additional 100 million more asthmatics by 2025. In Europe, the total health costs, comprising hospital care and medication, associated with asthma have been estimated to 19.3 billion euros [5]. However, it has been demonstrated that numerous patients do not respond to commonly used treatment, such as inhaled corticosteroids [6]. Therefore, there is an increasing need to characterize potential biomarkers to identify patients who are more likely to respond to a targeted therapy. Thermal desorption (TD) coupled with comprehensive two-dimensional gas chromatography – high resolution time-of-flight mass spectrometry (GC×GC-HRTOFMS) analysis was used to investigate the potential of exhaled breath VOCs to distinguish between asthma phenotypes. The use of high resolution and high accuracy enhances proper analyte identification when potential biomarkers are highlighted from cohorts' studies, improving confidence in the analysis of such complex samples. In this study, 50 patients covering a range of different asthma phenotypes were considered. The extraction of the volatile profile of exhaled breath following dedicated data processing and statistical treatment permitted the discrimination according to their respective phenotypes. The present study supports the hypothesis that exhaled air analysis allows deeper understanding of asthma phenotypes, and is going to lead to further development in clinical diagnosis.

References

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