Asthma phenotyping using Breath-GC×GC-HRTOFMS

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Abstract

Asthma is one of the most prevalent chronic disorder worldwide, affecting 235 million people [1]. This represents a serious public health issue associated with high direct and indirect health costs, mainly due to diagnosis and treatment [2]. A European study has estimated the total cost of asthma to be 19.3 billion of euro per year [3]. Asthma is characterized by an inflammation of the airways, involving several different underlying mechanisms. The inflammation goes along with oxidative stress, which yield to the conversion of polyunsaturated fatty acids, from the membranes, into volatile compounds that are secreted by the lungs, which could be used for diagnostic purposes [4]. This study focuses on the analysis of volatile organic compounds (VOCs) from breath as a non-invasive diagnostic approach to differentiate between the inflammatory profiles. The characterization of the different inflammation phenotypes is of great importance to provide an adjusted treatment to each patient [5]. As an example, recent studies have shown that inhaled corticosteroids, considered as the pillar of asthma treatment, have a higher therapeutic effect on eosinophilic airway inflammation than on neutrophilic inflammation [6]. 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 ability of exhaled breath VOCs to distinguish between asthma inflammatory phenotypes. In this study, 50 patients covering a range of different asthma phenotypes were considered. The extraction of the volatile profile of their exhaled breath following dedicated data (pre-)processing and statistical treatments 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