



Hyphenated technique based metabolomics approach for the pathogenesis of respiratory diseases

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The hyphenated techniques such as LC/MS and GC/MS have been developed rapidly with systematic omics advent. However, their efficacy to clinics is still unclear. Among diverse omics approaches we performed metabolomics approach using LC/QTOFMS (liquid chromatography/quadrupole-time of flight mass spectrometry) and GC/MS (gas chromatography/mass spectrometry) combined with advanced statistical algorithm. Because endogenous metabolites identified from the patient samples directly showed pathological functions on respiratory diseases, mass spectrometry based metabolomics could evaluate clinical treatment effectively with the help of bioinformatics tools. We selected two major respiratory diseases of BALF (bronchoalveolar lavage fluid) and IPF (idiopathic pulmonary fibrosis) and analyzed using two representative metabolomics instruments, LC/QTOFMS and GC/MS. After sample preparation, data was collected from hyphenated techniques, both LC/QTOFMS and GC/MS. Then data was processed into regulated digital dataset format for the bioinformatics application. As a final step, postulated target was validation using molecular biology techniques. Hyphenated techniques and their applications in clinics will be helpful for the customized treatment and guide to right tract for functional metabolomics for the systematic omics era. This work was supported by the Bio-Synergy Research Project (NRF-2012M3A9C4048796) of the Ministry of Science, ICT and Future Planning through the National Research Foundation.

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