New Methods and Technology in Drugs Metabolism and Pharmacokinetics (Part-II)

Drug metabolism plays an important role in determining the pharmacological and toxicological properties of most drugs. The identification of drug metabolites can clearly reveal the changes of components after administration. And the metabolomics provides great assistance in the study of drug mechanisms. As a complex system, traditional Chinese medicine (TCM) is characterized by multi-component and multi-target function, which also bring difficulties in the exploration of its mechanism of action. The metabolites identification and metabolomics based on mass spectrometry can elucidate the pharmacodynamic material basis and mechanism of action of TCM, which are powerful tools to explore the application prospects of TCM and meet the needs of clinical demand.

We are delighted to introduce this special issue titled “New methods and technology in drugs metabolism and pharmacokinetics”. The present part consists of one review article and two research articles. In the review, Yang [1] reviewed metabolites and metabolomics of Polygonum multiflorum (PM). This review tentatively identified more than 100 metabolites, among which some toxic compounds are deemed as potential toxic markers of PM, facilitating further understanding of the potential hepatotoxic components of PM. In the first research, Dong [2] developed a rapid strategy for the detection and identification of metabolites of vitexin in rat urine, plasma and faeces based on UHPLC-Q-Exactive Orbitrap mass spectrometry. A total of 49 metabolites are fully or partially characterized, and these metabolites are presumed to be generated through glucuronidation, sulfation, deglucosylation, dehydrogenation, methylation, hydrogenation, hydroxylation, ring cleavage as well as their composite reactions. In the second research, Xiang [3] characterized the catalpol metabolites in rat urine, plasma and faeces using UHPLC-Q-Exactive mass spectrometry. A total of 29 catalpol metabolites are identified, and the presumed metabolism pathway are summarized as a process that catalpol aglycone occurred firstly due to deglycosylation reaction, followed by a series of reactions such as hydroxylation, dihydroxylation, hydrogenation, dehydrogenation, oxidation of methylene to ketone, glucuronidation, glycine conjugation and cysteine conjugation.

Moreover, we many thank the reviewers for their time, expertise, and comments to help improve the quality of the manuscripts. We believe that this special issue will be helpful for the drugs metabolism and pharmacokinetics of TCM.

REFERENCES


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