Opinion

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A Cutting-Edge Omics Technique used recently in the Study of Herbal Medicine: Metabolomics

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Abstract

Omics approaches, such as (meta) genomics for DNAs, transcriptomics for RNAs, proteomics for proteins, metabolomics for small hydrophilic compounds, and lipidomics for tiny lipophilic molecules, all aim to assess the entire composition of a particular biochemical group. This therapy option has not yet been refined into a specific clinical application, despite numerous studies still being conducted on it. Recent advancements in medical research and our understanding of biological systems have been made possible by omics, a high-throughput method for comprehending the genome, transcriptome, proteome, and metabolome. Advanced omics methods have been used to research numerous cancer immunotherapies, including multi-omics, single-cell omics, and conventional omics.

Keywords: Genomics, Herbal medicine, Metabolimics.

Introduction

More and more experts concur that before carrying out extensive treatment trials, it is crucial to create a scientific basis for dosing and standardisation of biologically active chemicals. These initiatives may enhance researchers' capacity to weigh the advantages and disadvantages of taking part in extensive trials of herbal remedies. To improve long-term efforts to improve risk-benefit ratio estimation for trial participation, more stringent monitoring of adverse events and uniform reporting of research results for both safety and efficacy data are also necessary [1].

When evaluating the dangers and advantages of herbal medicine research, cultural issues may also play a role. For instance, a cultural familiarity with many traditional Chinese herbal remedies in China may encourage a familiarity bias, adopting a generalised cultural presumption of safety based on the past use of herbal remedies. The importance given to standardised adverse event reporting in China may differ culturally from other countries. Having a favourable risk-benefit ratio that meets agreed-upon norms is more challenging due to these cultural variations. Prior to carrying out extensive clinical trials testing the effectiveness of herbal medicines, it will be crucial to develop standards of evidence for the demonstration of safety in order for worldwide collaborative herbal medicine research to fulfil its goals [2].

The full complement of tiny molecules in a biological system or fluid is known as the metabolome, a term that Oliver and colleagues originally used in 1998 while doing groundbreaking research on yeast metabolism. In light of this, the study of the metabolome-the tiny molecules in a biological sample—represents the core of the field of metabolomics. In some circles, the term "metabolomics" is also used in place of "metabonomics" or "metabolic profiling," however this article uses the more popular phrase "metabolomics." Perhaps the oldest example of what we now refer to as metabolomics dates back to the 1970s and the use of gas chromatography-mass spectrometry for metabolite profiling of clinical urine samples. The evolution of prostate cancer, the onset of diabetes, or the prognosis of survival from sepsis are just a few examples of how metabolic profile can be utilised to provide information regarding the cause, diagnosis, or progression of a disease. It is crucial to have non-invasive ways to monitor the progression of prostate cancer; researchers discovered that one metabolite found in urine could be used to do so [3, 4]. Additional research revealed that experiments in which the sarcosine-related enzymes sarcosine synthesis and degradation were knocked out resulted in attenuated and increased cancer invasion, respectively. Similarly, it has been demonstrated that a panel of blood metabolites can be used to predict future diabetes and survival in sepsis patients.

Systems biology methods called OMICS, which integrate data from genomes, transcriptomics, proteomics, and metabolomics, are frequently used to fully reflect the molecular profiles in mechanistic studies of medicinal plants. The identification of major molecular targets and signalling interaction networks of medicinal plants with potential to treat gastrointestinal cancer is made easier by single- and multi-OMICS techniques. Although medicinal plants have seen some limited technological application, herbal medications have a significant role in contemporary medical and pharmaceutical care [5]. The omics methods, including genomes, transcriptomics, proteomics, and metabolomics, are at the forefront of high-throughput approaches. This book, a volume in the Exploring Medicinal Plants series, presents a thorough and in-depth overview of innovations in high-throughput methods for the study of medicinal plants.

Conclusion

Recent advancements in various omics technologies have given plant scientists an unheard-of potential to gain significant biological knowledge by integrating study of various omics datasets. Genomes, transcriptomes, proteomes, metabolomes, and other omics datasets produced from different MPs have been described, and associated bioinformatic databases and tools have been created. For examining MPs, integrated analysis of multi-omics datasets is incredibly thorough. Results from multi-omics datasets offer a theoretical foundation for stable biotransformation of desired secondary metabolites using synthetic biology, as well as a platform for developing MP species with high yield, good quality, and disease resistance through molecular breeding.

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