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Metabolomics and Cancer Research

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Metabolomics, which represents a growing field in systems biology, is the study of the concentrations and fluxes of small molecular metabolites (e.g. amino acids, organic acids, fatty acids and sugars) presented in biofluids, cells, tissue or organs of living systems. By comparative analysis of the concentration changes of these metabolites, researchers can identify biomarkers that change as the body fights disease, reacts to a drug or responds to environmental stress. The number of primary metabolites contained in the human body is thought to be roughly 2,500~6,000, excluding lipid molecules. Although this number is expected to change as the metabolite detection technologies become more sensitive and comprehensive, it is still much lower than the number of genes (>30,000), RNA transcripts (>100,000) or proteins (>1,000,000) that exist in the body. Unlike genes and proteins, most endogenous metabolites are identical across different cells, tissues and organs, and can be straightforward to track the metabolite level changes between different species. All these features make metabolic profiling a much more direct and simpler approach to collect useful information.

As a comprehensive tool, metabolomics is composed of different technologies from analytical measurements to data analysis. The common objective in metabolomics is the selection of a set of reliable, key metabolites that can be used to identify and follow changes in biological systems. NMR and MS provide quantitative and reproducible measurements of the metabolic profile, while statistical analyses are used to select important metabolites. As one of its most valuable application, metabolic profiling of populations could allow the development of 'molecular epidemiology' — the ability to identify the susceptibilities of specific groups to cancer, which might allow metabolites to be identified as risk identifiers (biomarkers), with implications for health screening programs, therapy monitory or prediction. By applying advanced metabolomics methods, one can evaluate the altered metabolite levels for disease development, which opens a window of opportunity for both patients and oncologists to improve treatment.

While the field of metabolomics-based cancer detection is growing rapidly and attracting increasing interest, the main problems in metabolomics-based cancer research include the lack of homogeneous standard protocols, insufficient exploitation of the data and data overfitting, incomplete metabolite identification in metabolomics fingerprints, and biochemical interpretation. Efforts have been made among laboratories to manage the standardization of metabolomics experiments from sample collection, through chemical analysis, to data processing.

Current work is also focused on defining "normal" concentrations as compared to concentrations characterizing disease states, and further understanding the biochemical relationships between metabolic pathways and network biology to develop new testable hypotheses about future disease risk.

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