

# **Metabonomics Approach to Understanding the Traditional Chinese Medicine**

## **Abstract**

Traditional Chinese medicine (TCM) assumes synergy to be taking place in a combination herbal formula and it has become an intrinsic part of its philosophy. The treatment of common multi-factorial, system-wide diseases using multi-component therapeutic agents such as TCMs can be regarded as a "system to system" approach. It is difficult to evaluate the systemic pharmacological effect of these multi-component agents in the context of single-target based pharmacological models. We conceive that the drug intervention is to alter or reverse the pathological process via multiple biochemical mechanisms in order to restore a homeostasis of the perturbed physiology, and the characteristic biochemical alterations in this "system to system" approach will result in a unique, time-dependent metabolite expression pattern, and can therefore be measured using a metabonomics approach. We demonstrate with the hydrocortisone induced model and the 1, 2-dimethyl hydrazine (DMH)-induced precancerous colon model in Wistar rats that the systemic and dynamic response to multi-component drug intervention can be delineated by an endogenous urinary metabolite profiling technique, which revealed that multiple metabolic pathways are altered between the healthy control group and the model group. Another example is Chinese ginseng, an ancient medicinal herb with a worldwide reputation for maintaining good health, has been extensively used in many prescriptions as a tonic to increase resistance to fatigue and stress. However, most of its claimed effects can not be readily evaluated in modern pharmacological models. The ginseng extracts typically contain more than 50 known compounds, mainly, ginsenosides. We demonstrated that ginseng extracts were able to attenuate alterations in several metabolic pathways in response to acute cold stress and chronic unpredictable mild stress, using a combined chemical profiling and metabolic profiling approach. The results indicate that comprehensive molecular descriptions of a pathophysiological state and the response to drug intervention can be achieved, so that the global biochemical changes contributing to a disease or drug response can be taken into account, leading to a systems-level understanding of the drug efficacy, toxicity and mechanisms of action.