

Administration (2). It has been shown to increase the production of short-chain fatty acids, principally butyrate and propionate, and has been shown to decrease the generation and absorption of ammonia. Evidence also indicates human consumption of larch arabinogalactan has a significant effect on enhancing beneficial gut microflora, specifically increasing anaerobes such as Bifidobacteria and Lactobacillus (3). *In vitro* studies have indicated larch arabinogalactan can stimulate natural killer (NK) cell cytotoxicity, enhance other functional aspects of the immune system and inhibit the metastasis of tumor cells to

the liver (4), larch arabinogalactan has several interesting properties which appear to make it an interesting adjunctive supplement to consider in cancer protocols.

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SYSTEMATIC ANALYSIS OF TRADITIONAL CHINESE MEDICINES (TCM)

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Traditional Chinese medicine (TCM) has over 3000 years of history and played important role in the peoples' health and social development in Chinese history. In the past 50 years, Chinese scientists have made great effort to modernize TCM to make it a evidence-based medicine from the experience-based origin. In the past decade or so, we made a great endeavour to perform chemical, metabolic and biological analyses for the complex system of TCM aiming at elaborating scientific and feasible quality standards of these herbal medicines. A series chemical methods have been developed for the comprehensive analysis of the multicomponent TCM system including multiple marker quantification of single herbs or herbal combinations. Metabolic analysis for herbs also plays an important role for clarifying the active components of TCM complex systems. Metabolic fingerprint profiling method was developed for *Salvia miltiorrhiza* and other typical Chinese herbs.

Advances in high-throughput “omics” technologies to measure changes of genes, proteins, and other biomolecular components in complex biological systems have dramatically revolutionized research of traditional medicine. In the past 6 years, proteomics technologies such as 2-DE and nano-LC-MS/MS were used in our lab to study mechanisms of Chinese herbal medicines including *Salvia miltiorrhiza*, *Ganoderma lucidum*, *Panax notoginseng*. For study of *Salvia miltiorrhiza*, possible direct protein targets of salvianolic acid B, the main active component of *Salvia miltiorrhiza*, were predicted using a ligand-protein inverse docking algorithm. The possible signal network of salvianolic acid B from its direct protein target and its signal-related proteins was established based on protein-protein interaction databases and then certified. Results of proteomic study provide useful information for understanding the mechanism of TCM.

VARIATION OF SECONDARY METABOLITE PROFILES OF SALINISPORA SPECIES WITH THEIR GEOGRAPHICAL ORIGIN

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The genus *Salinispora* is an obligate marine actinomycete that produces a broad spectrum of secondary metabolites such as anticancer and antibiotic compounds. Taxonomic studies have formally identified two species *S. tropica* and *S. arenicola* (1). Jensen and co-workers (2) have found that *Salinispora* produces

secondary metabolites that are species-specific. In this study we investigated whether the secondary metabolite profile varies with the geographical location. Six *S. arenicola* isolates were derived from two sites (Cairns and Townsville) of Great Barrier Reef (GBR), on the east coast of Australia. Three biological replicates of each of