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Immune cell type or signaling-specific effects of four candidate phytomedicines for cancerous and inflammatory diseases

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In our recent studies, we showed that many phytochemicals or their derivatives can confer diverse pharmacological activities in preventing tumor metastasis (See References). These phytochemical activities regulate the immune system or non-malignant cells in a tissue microenvironment under various *in vivo* conditions. And these activities cannot be effectively addressed by the conventionally used cell culture systems *in vitro*. Our current strategy is to initiate our study through a combination of omics approaches and specified *in vivo* tumor model systems. Specifically, we first make predictions for candidate specific pharmacological activities according to the "omics screening" profile of differential responsive genes, proteins or involved metabolites. Then we make a list of hypothesis in priority sequence. Finally, we detect/evaluate the candidate mechanistic signaling cells/molecules for suppression of well-defined tumor metastasis activity. With this strategy, we have been successful in evaluating several pharmacological effects of nature plant phytochemicals or their derivatives on immune cell systems or the surrounding nonmalignant cells in defined tumor microenvironment. The omics approaches we used to predict and reveal the specific pharmacological activity of phytochemicals or medicinal herbal extracts/fractions, including genomics, transcriptomics, proteomics, metabolomics and the next generation sequencing (NGS) systems. The systematic analysis of the observed data is to "contemplate" the cellular or physiological responses, according to the various pattern changes detected in different response elements. Technically, in our task on pathway and net-working analyses, the overall or big trend/pattern of the different responsive elements or/and their signaling systems is the key for predicting specific pharmacological mechanisms, instead of the "super" inducer or suppressor single gene activities. For instance, the "expression pattern or trend", rather than the "fold change", of specific microRNA species is a much more important factor for predicting their suppressive effect on target genes. As a result, the understanding and background knowledge of specific targets or signaling networking pathways of specific disease targets are quite important and need to be carefully reviewed "first" before "searching the omics data" in a totally randomized way. With this approach, whether the expression trend of their downstream genes can fit the proposed hypothesis is also considered as a key factor.

Biography

Ning-Sung Yang is a Distinguished Professor and Distinguished Research Fellow of Academia Sinica and the associated universities in Taipei, Taiwan. He has helped the development of gene gun technology and pioneered its application to mammalian transgene experimental systems and gene therapy approaches. After thirty years of a research career in USA, Dr. Yang established the Agricultural Biotechnology Research Center in Academia Sinica, Taipei. He was elected in 2006 as a member of the American Association for the Advancement of Science (AAAS, USA). He has published more than 160 research papers, and obtained 14 USA patents.

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