

## Epigenome Studies of Natural & Herbal Medicinal Products: A New Frontier

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### Biographical Sketch

My current research integrates epigenomics, biomarkers, animal models and in vitro/in vivo prevention efficacy by natural products (NPs). I have published over 230 peer-reviewed papers on efficacy and mechanism studies using *in vitro* cell culture models and *in vivo* models including the Nude mice, Nrf2  $-/-$  mice for colon and skin, APC<sup>min/+</sup> mice for intestinal and TRAMP mice for prostate, regulation of phase II/III DME/transporters via Nrf2, and PK-PD in vivo studies and modeling-simulation of dietary natural products. In addition, using Nrf2 $-/-$  vs  $+/+$  mice coupled with Affymetrix 45 K microarray, I have reported the pharmacogenomic expression profiles of genes induced by sulforaphane (SFN), curcumin (CUR), epigallocatechin-3-gallate (EGCG), and soy isoflavone that required Nrf2 for induction; tissue differences in gene expression as well as the role of Nrf2 in SFN-induced anti-inflammatory effects. Most recently, my lab was the first to report the expression of Nrf2 was suppressed epigenetically by promoter methylation associated with methyl-CpG-binding protein 2 (MBD2) and histone modifications in the prostate tumor of TRAMP mice. I found that dietary NPs CUR, SFN, diindolylmethane (DIM), gTmT, Z-ligustilide and tanshinone IIA epigenetically modified expression of Neurog1 and Nrf2 via CpG methylation and or histone modifying proteins. Recently, my lab reported the requirement and epigenetics reprogramming of Nrf2 in suppression of tumor promoter TPA-induced mouse JB6 skin cell transformation by SFN. Using Next-generation Sequencing (NGS), we found the alterations of the epigenomics (CpG methylation; correlating with mRNA expression) during progression of AOM-DSS induced colon cancer and interestingly, these CpG epigenomics could be modified by dietary NPs also correlating with mRNA expression coupled with prevention of these cancers. In this lecture, I will discuss the latest integration of epigenetics/epigenomics using next-generation sequencing (NGS) or deep sequencing to examine the epigenome changes during development of colon cancer and prevention by natural products.

<https://www.ncbi.nlm.nih.gov/pubmed/?term=kong+an>

[DNA methylome and transcriptome alterations and cancer prevention by curcumin in colitis-accelerated colon cancer in mice.](#)

Guo Y, Wu R, Gaspar JM, Sargsyan D, Su ZY, Zhang C, Gao L, Cheng D, Li W, Wang C, Yin R, Fang M, Verzi MP, Hart RP, **Kong AN**.

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