Nutritional Genomics for the Determination of the Mechanism of Action of the Beneficial Effect of Bioactive Extracts in Tumor Progression
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[Introduction]: Much effort is dedicated to the development of herbal therapeutics in cancer. Extracts from common herbs possess bioactivities such as antioxidant or anti-inflammatory properties, and natural supplements with antioxidant activity have been reported to reduce the incidence or mortality of gastrointestinal tumors. However, different antioxidants display different effects and clinical trials are controversial, maybe due to the lack of knowledge of their specific mechanism of action.

[Methods]: Supercritical fluid extracted herbs with known antioxidant activity (HE) were used to analyze their effect on human colon cancer cells and determine its mechanism of action. Antiproliferative effect was analyzed by MTT assay in SW620 and HT-29 cells determining growth inhibition (GI50), citostacity (TGI50) and citotoxicity (LC50). Anchorage-independent growth assays were performed for cell transformation. Gene expression and ontology analysis after HE treatment were developed under different conditions according to the biological effects using Agilent G4112F Whole Human Genome Microarray and Ingenuity Pathways Analysis.

[Results]: HE exhibited dose-dependent viability suppression and inhibition of cell transformation. Gene expression analysis revealed that the most significant altered network was involved in cell death and protein degradation. Lipid and carbohydrate metabolism-related genes were also altered with a greater score than those related to oxidative stress or inflammatory response, suggesting a stronger effect of HE in tumors in which these networks are involved.

[Conclusions]: Phytochemical compounds display bioactivities pointing at them as promising supplements in nutritional-related diseases such as colon cancer. However, not all antioxidant phytochemicals are beneficial for all patients, and the analysis of the specific mechanism of action of each compound is necessary for including them in personalized treatments. Nutrigenomic analysis of phytochemical-induced modulation of gene expression is a powerful tool for understanding the biological effect of these products, and might result in an improvement of personalized therapies of cancer patients.