Project title: Center of Excellence for Cancer Research (2014 to 2017), National

Taiwan University Hospital

Program title: Colorectal Cancer Research Team

Analysis of the Factors Affecting the Incidence of Colorectal Cancer in Taiwan by Metabolomic Approach

Shu-Chen Wei¹, Ching-Hua Kuo², Yufeng J. Tseng ³, San-Yuan Wang⁴, Yin-Wen Shiue⁵ Deng-Chyang Wu⁶, Jau-Min Wong⁷

魏淑鉁,郭錦樺,曾宇鳳,王三源,薛茚文,吳登強,翁昭旼

¹National Taiwan University Hospital and College of Medicine, ²School of Pharmacy, College of Medicine, National Taiwan University, ³Graduate Institute of Biomedical Electronics and Bioinformatics, National Taiwan University, ⁴Master Program for Clinical Pharmacogenomics and Pharmacoproteomics, School of Pharmacy, Taipei Medical University, ⁵Department of Internal Medicine, Kaohsiung Medical University Hospital, ⁶Institute of Biomedical Engineering and School of Medicine, National Taiwan University

The incidence of colorectal cancer (CRC) increased in Taiwan recently. According to the cancer registration data from the Bareau of Health Promotion, Department of Health, R.O.C (Taiwan), the crude incidence (per 100,000 population) of CRC in Taiwan increased from 32.38 in 2000 to 60.62 in 2010. And interestingly, there is a difference between the South and North of Taiwan. For instance, the crude incidence (per 100,000 population) of CRC of Taipei was 48.42 while for Kaohsiung was 28.69 in 2000; and the crude incidence of CRC of Taipei was 80.47 and for Kaohsiung was 76.73 in 2010. Metabolomic is the "systematic study of the unique chemical fingerprints that specific cellular processes leave behind", the study of their small-molecule metabolite profiles. It is now coming of age as an important area of investigation which may help reveal answers to questions left unanswered or only partially understood from proteomic or genomic approaches. Metabolomics is one means to determine a biological endpoint, or metabolic fingerprint, which reflects the balance of all these forces on an individual's metabolism. In this study, we used the metabolomics analysis (LC-MS and GC-MS) to compare the metabolites phenotypes between CRC tissue diagnosed and collected in 2000 and 2010; and the phenotypes between CRC tissue from the North (NTUH) and South Part (KMUH) of Taiwan. Our results demonstrated that the fingerprinting of CRC as well as the adjacnet normal tissue were different between 2000 and 2010. Also, the metabolites phenotypes between North and South Taiwan CRC tissue were different. By using the metabolites analysis, we also establish the models for differentiating early and late CRC, as well as predicting models for survival. By using the possible candidate metabolites, it might be another way to improve the CRC screening and treatment stratification.