Submitter Name: Reza Ghanbari
Submitted email: reza_ghanbari@unc.edu
PI Name: Susan Sumner
PI email: susan_sumner@unc.edu

An Untargeted NMR-based Metabolomics Analysis to Investigate the Urinary Metabolites in Opium Users

Reza Ghanbari[1, 2], Wimal Pathmasiri[1], Susan McRitchie[1], Delisha Stewart[1], Arash Etemadi[3], Christian Abnet[3], Jonathan Pollock[4], Reza Malekzadeh[2], Susan Sumner[1]

[1]Nutrition Research Institute, University of North Carolina at Chapel Hill; [2]Digestive Diseases Research Institute, Tehran University of Medical Sciences; [3]Division of Cancer Epidemiology and Genetics, National Cancer Institute; [4]Genetics, Epigenetics, and Developmental Neuroscience Branch, National Institute on Drug Abuse

Illicit use of opiate is a major public health threat across the world, causing numerous potential adverse health outcomes. Opium and their derivatives can modulate the gene expression through epigenetic and possibly RNA modifications, ultimately change the intracellular signaling cascades and long-lasting changes in the metabolome.

Metabolomics is a powerful technique that has been used in clinical and laboratory medicine for the discovery of potential diagnostic, prognostic and therapeutic biomarkers. The result of this study could lead to identification of significant altered metabolites and can improve our knowledge of underling etiology and molecular pathways behind the opium addiction.

In this study we used 1H-NMR-based metabolomics technology to analyze the urine metabolite profiling of 535 individuals from Golestan Cohort Study (GCS). The GCS is conducted in northeast of Iran in which more than 50,000 volunteers were analyzed for opium use. More than 8,000 of participants reported opium use either smoked or orally consumed. The metabolomics profiles of samples from 285 current daily and 158 non-daily opiate users have be compared with profiles obtained for 92 non user controls.

After sample preparation, data was collected using a Bruker Avance III 700 MHz NMR Spectrometer. TopSpin and ACD Spectrus Processor softwares were used to data processing and NMR binning. Metabolites were identified by using Chenomx NMR Suite 8.3 Professional software. NMR metabolomics revealed several metabolites including hydroxyisovalerate, alanine, choline, citrate, creatinine, glucose, lactate, malonate, methylhydantoin, phenylalanine, phosphocholine, sucrose, tyrosine, acetylsalicylate and inositol that contribute to the differentiation of the case and control groups.