**Fetal metabolomic signature of exposure to iAs during pregnancy**

Metabolomic Analysis: RTI RCMRC

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IRB Number: 10-1583 (UNC Chapel Hill)

**Abstract:** Original sample collection was performed under the Biomarkers of Exposure to ARsenic (BEAR) study funded by National Institute of Environmental Health Sciences (ES010126, ES005948, ES019315 and ES07018), Rebecca Fry, PI). The BEAR study has been established to assess the health effects associated with prenatal arsenic exposure during neonatal and early life. The study area is in Gómez Palacio, Durango, Mexico where women are exposed to levels of inorganic arsenic (iAs) in drinking water up to 236.0 μg As/L.

This metabolomics pilot study was aimed to identify a fetal metabolomic signature of exposure to iAs during pregnancy. Fetal cord blood serum was collected immediately after delivery from a saline cleaned umbilical cord using an anticoagulant-free vacutainer tube, after clot formation the tube was centrifuged at 1200 rpm and the serum was collected and stored at -70°C. A subset of 50 cord blood serum samples were selected from the larger BEAR cohort to represent a wide range of iAs exposure as determined by iAs in drinking water (DW-iAs). The exposure during pregnancy was confirmed using total urinary As (U-tAs). A total of 50 cord blood serum samples were used in the metabolomics analysis. The samples included 25 newborns with lower maternal iAs exposure levels (DW < 25μg As/L, mean U-tAs=16 μg/L) and 25 newborns with higher maternal iAs exposure levels (DW> 25μg As/L, mean U-tAs =107 μg/L).

The data required for the metabolomics analysis can be found in the accompanying files:

Procedures: 1. Fetal Metabolomics of iAs exposure Procedure.docx

Study Design Table: 2. Fetal Metabolomics of iAs exposure Study Design table.xlsx

Metadata: 3. Fetal Metabolomics of iAs exposure Metadata and Analytical Metadata.xlsm

Processed Data: 4a. Fetal Metabolomics of iAs exposure Phenotypic and Normalized Binned Data.xlsx

4b. Fetal Metabolomics of iAs exposure Phenotypic and Normalized Concentration Data.xlsx

Raw Data: 5. Fetal Metabolomics of iAs exposure Raw NMR Data.xlsx

**Notes:**

Each of the bin integrals were normalized to the total integral of each of the NMR spectrum (for more details, see accompanying file no. **1. Fetal Metabolomics of iAs exposure Metabolomics Procedure.docx**)

Descriptions of abbreviations for factors are available in the Variable Dictionary in the accompanying file no. **2. Fetal Metabolomics of iAs exposure Study Design table.xlsx**.

The phenotypic and normalized binned NMR data are available in the accompanying file **4a (Fetal Metabolomics of iAs exposure Phenotypic and Normalized Binned Data.xlsx)**. Sample ID and factors can be found in the first 2 columns in file 4a. Other columns in the spreadsheet contain the normalized binned data.

The phenotypic and normalized relative concentration data (M, profiled using Chenomx Software) are available in the accompanying file **4b (Fetal Metabolomics of iAs exposure Phenotypic and Normalized Concentration Data.xlsx)**. Sample ID and factors can be found in the first 2 columns in file 4b. Other columns in the spreadsheet contain the normalized relatiave metabolite concentrations.

If your statistical program does not allow variable names to begin with a number then add a prefix to the column names, for example, bin\_8.98 instead of 8.98.

Sample ID serves as the unique identifier of the individual samples and is used as the NMR folder name in the raw NMR data file.