**Metabolic Aberrations in Barth Syndrome**

Metabolomics Analysis: RTI RCMRC

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**Abstract:**

The overall objective of this pilot research project is to investigate metabolic mechanisms involved in disturbed intermediary metabolism in Barth Syndrome. Barth Syndrome (BTHS) is x-linked disorder characterized mainly by dilated cardiomyopathy, skeletal muscle weakness and neutropenia. BTHS is caused by defects in Tafazzin, an enzyme responsible for modifying the acyl chain moieties of cardiolipin, a critical phospholipid of the mitochondrial inner membrane. While a few comprehensive clinical studies of BTHS have been published detailing its cardiac and hematologic features, descriptions of its biochemical characteristics are limited.

In this pilot and feasibility study, NMR broad spectrum metabolomics analysis was performed using plasma from patients and age-matched controls to obtain a broader understanding of perturbed metabolic pathways and mechanisms involved in Barth Syndrome.

**Goals**

1) To characterize differences in the plasma metabolome in Barth Syndrome patients compared to age-matched controls.

2) To determine pathways perturbed by Barth Syndrome, other than that for which TAZ is included.

**Data Package Description**

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

Procedures: 1. Barth Syndrome Metabolomics Procedure.docx

Study Design Table: 2. Barth Syndrome Study Design Table.xlsx

Metadata: 3. Barth Syndrome METADATA.xlsx

Processed Data: 4. Barth Syndrome Normalized Binned Data.xlsx

Raw Data (folders): 5. Barth Syndrome Raw\_NMR\_Data

**Notes:**

Each of the bin integrals were normalized to the total integral of each of the NMR spectrum (for more details, see accompanying Procedures file, **1. Barth Syndrome Metabolomics Procedure.docx**

Descriptions of abbreviations for factors are available in the Variable Dictionary in the accompanying Study Design Table files, organized by sub-study i.e. **2. Barth Syndrome Study Design Table.xlsx.**

The normalized binned NMR data are available in the accompanying Processed Data file (i.e. **4. Barth Syndrome Normalized Binned Data.xlsx)**. Sample ID and factors can be found in the first 3 columns in the file no. 4. Other columns in the spreadsheet contain the normalized binned data.

If the 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.