**Characterizing commonalities and differences between the breast and prostate cancer metabotypes in African-American cohorts**

Metabolomics Analysis: NIH Eastern Regional Comprehensive Metabolomics Resource Core (RTI RCMRC)

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**Abstract:**

Many attempts have been made to identify critical events responsible for the development and progression of breast cancer (BCa). In spite of this, the mechanisms underlying notably tumor invasion and BCa dissemination remain largely unclear. The pathological features of BCa follow a sequential progression from the transformation of a normal cell to benign proliferation, hyperplasia, atypical ductal hyperplasia (ADH), ductal carcinoma in-situ (DCIS) to invasive ductal carcinoma (IDC) and metastatic diseases. It has been reported that the disease phenotype is distinguishable in ADH and progresses along distinct pathways for each subtype. The genetic signature for disease heterogeneity across subtypes is greater than the heterogeneity of progression from DCIS to IDC within a subtype, suggesting that the disease subtypes have distinct progression pathways. Even so, genetics does not fully explain etiology nor progression. Additionally, a large population based study reported an increased risk of male BCa after prostate cancer (PCa).The two cancers share similarities with a wide heterogeneity of both phenotype and biology. A unique feature of PCa and BCa is that at least in the initial stages, they are hormone-dependent and have remarkable underlying biological similarities. Our recent study and others showed an increased level of common metabolites in BCa and PCa. Thus, understanding the metabolic profiles of breast and prostate cancer would pave the way for new biomarkers to improve diagnosis and treatment strategies. Thus, we aimed to 1) understand mechanisms related to the onset and progression of BCa, 2) identify precursors and targets for prevention and therapy for each stage, grade and subtype which may contribute to the disparate impact of BCa in African American women, and 3) Identify common and different BCa metabolite markers versus PCa markers.

**Sample Description:**

Samples were provided from an African American cohort of patients at the Howard University Cancer Center. A total of 48 breast tissue samples from women who had either undergone mammoplasty or BCa-associated surgery were shipped to the RTI RCMRC with corresponding de-identified tumor registry metadata. Samples were from women who ranged in age from 21-78 years old. Plasma samples from African American subjects were also provided from different women (compared to tissue samples), ranging in age from 25-82 years, for 18 women with no BCa or family history (controls) and 15 women with different stages of BCa (cases). Additional plasma samples were provided from men, ranging in age from 42-88 years, for 15 men with no PCa or family history (controls) and 18 men with PCa (cases).

Data obtained for the **tissue** NMR metabolomics analysis can be found in the accompanying files:

Procedures: 1. Breast Cancer Metabotype Tissue NMR Procedures.docx

Study Design Tables: 2. Breast Cancer Metabotype Tissue NMR Study Design Table.xls

Metadata: 3. Breast Cancer Metabotype Tissue METADATA.xlsm

Processed Data: 4. Breast Cancer Metabotype Tissue NMR Normalized Binned Data.xlsx

Raw Data: 5. Breast Cancer Metabotype Tissue NMR Raw Data.zip

**Notes:**

Full sample preparation and analysis procedures are available in the accompanying document entitled **1. Breast Cancer Metabotype Tissue NMR Procedures**.

Descriptions of abbreviations for factors are available in the Variable Dictionary in the accompanying file no. **2. Breast Cancer Metabotype Tissue NMR Study Design Table.xls**.

The phenotypic and normalized data are available in the accompanying files: **4. Breast Cancer Metabotype Tissue NMR Normalized Binned Data.xlsx** for normalized binned NMR data. Sample ID and factors can be found in the first 5 columns and other columns in the spreadsheet contain sample metadata and 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.

The Sample ID serves as the unique identifier (Graphical ID) of the individual samples and the Datafile name is used as the NMR folder name in the raw NMR data file **5. Breast Cancer Metabotype Tissue NMR Raw Data.zip**.