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Breast cancer risk in relation to plasma metabolites among Hispanic and African American women

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Abstract

The metabolic etiology of breast cancer has been explored in the past several years using metabolomics. However, most of these studies only included non-Hispanic White individuals. To fill this gap, we performed a two-step (discovery and validation) metabolomics profiling in plasma samples from 358 breast cancer patients and 138 healthy controls. All study subjects were either Hispanics or non-Hispanic African Americans. First, a panel of 14 identified metabolites significantly differed between breast cancer cases and healthy controls in both the discovery and validation sets. Most of these identified metabolites were lipids. In the pathway analysis, citrate cycle (TCA cycle), arginine and proline metabolism, and linoleic acid metabolism pathways were observed, and they significantly differed between breast cancer cases and healthy controls in both sets. From those 14 metabolites, we selected 9 non-correlated metabolites to generate a metabolic risk score. Increased metabolites risk score was associated with a 1.87 and 1.63-fold increased risk of breast cancer in the discovery and validation sets, respectively (Odds ratio (OR) =1.87, 95% Confidence interval (CI): 1.50, 2.32; OR=1.63, 95%CI: 1.36, 1.95). In summary, our study identified metabolic profiles and pathways that significantly differed between breast cancer cases and healthy controls in Hispanic or non-Hispanic African American women. The results from our study might provide new insights on the metabolic etiology of breast cancer.

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Conflict of interest

The authors declare that they have no conflict of interest.

Ethics approval

All procedures performed in this study were approved by the Institutional Review Board at M D Anderson Cancer Center and in accordance with the ethical standards of 1964 Helsinki declaration and its later amendments or comparable ethical standards.

Informed consent

Written informed consent was obtained from all participants.

Keywords

metabolomics; breast cancer; racial minority

Introduction

Breast cancer is the most common form of cancer and the second most common cause of cancer death in women worldwide. The expected number of new breast cancer cases is predicted to increase in the next two decades [1]. Especially, the cancer incidence among Hispanic and African American populations continues to grow, mainly estrogen receptor positive (ER+) breast cancer, despite the mortality rate decline in some populations [2]. Although racial disparities in breast cancer are well-established, the contributing factors largely remain to be determined. A better understanding of the differences in the biological characteristics of breast cancers among racial groups could provide important insights into observed racial differences.

The investigation of metabolites may help solve the mystery of breast cancer racial disparity. Metabolites are the end products of intercellular pathways and are sensitive to host and environmental stimuli, thus, metabolite profiles may reflect changes in phenotype and function and serve as indicators of the overall physiological alterations in chronic disease [3]. Some of those stimuli are racial specific, then the corresponding metabolic profiles may be racial specific too. Thus, studying racial difference in metabolic profiles may shed light on the racial difference in host and environmental exposure. Furthermore, evidence has shown that metabolic profiles are at least partially genetically determined [4].

In breast cancer, metabolomics profiling in circulation (e.g. serum and plasma) has been successfully applied in identifying cancer risk factors [5–7] as well as prognostic factors [8–10] and early detection biomarkers [11,12,7,13]. Unfortunately, racial minorities, including Hispanics and non-Hispanic African Americans are rarely included in those studies. Such omission leads to a missed opportunity to explore the role of metabolomics in racial disparity of breast cancer.

In the current study, we conducted a two-step (discovery and validation) metabolomics analysis in plasma samples from 358 breast cancer patients and 138 healthy controls. All study subjects were either Hispanics or non-Hispanic African Americans. Our goal was to identify metabolic profiles that could distinguish between breast cancer cases and controls.

Materials and Methods

Study population

Breast cancer patients were recruited from The University of Texas M. D. Anderson Cancer Center (Houston, TX) from patients with newly diagnosed (defined by the presence of malignant breast epithelial cells) and histologically confirmed (by microscopic analysis and molecular subtype) breast cancer. The blood samples were drawn prior to any cancer treatment. Specifically, the breast cancer patients included in the discovery set were selected from an existing breast cancer early detection study from 2003 to 2012 [14]. Written

informed consent was obtained from each study subject. A total of 134 cases were included in the discovery set. They were selected according to the availability of plasma samples and clinical characteristics at baseline, as well as race and ethnicity (Hispanics and non-Hispanic African Americans). Self-reported ethnic background was used to define the race and ethnicity. The validation set included 224 breast cancer patients selected from an ongoing breast cancer case control study that has been recruiting participants since 2012. The same selection criteria were used. In addition to the cases, each study also recruited control subjects. Controls for the discovery study were identified from healthy women who participated in breast cancer screening at MD Anderson Cancer Center and were found to be negative for the disease. Controls for the validation study were identified largely from female residents of Harris County using random digit dialing. In the current study, the discovery set had 57 Hispanic or non-Hispanic African American female controls selected from the existing breast cancer early detection study, and the validation set had 81 Hispanic or non-Hispanic African American female controls selected from the ongoing breast cancer case control study. The selection criteria included the availability of plasma samples and epidemiological characteristics at baseline, as well as race and ethnicity (Hispanics and non-Hispanic African Americans). The study protocol was approved by the Institutional Review Board at M D Anderson Cancer Center.

Metabolomics Analysis

Metabolomics profiling was conducted on plasma samples at Metabolon Inc (Durham, NC) using ultra high performance liquid chromatography/mass spectroscopy and gas chromatography/mass spectroscopy. The protocol was described previously [7]. Forty batches of case-control pairs and quality control (QC) replicate samples (N=16) were analyzed. Raw data was extracted, peak-identified and QC processed on the assay platform as previously described [15,16]. After excluding metabolites that had 30% missing values, 561 identified compounds remained for analysis. The missing values were treated as the result of low signal intensity. They were replaced by half of the minimum positive values detected in the data. Based on existing literature, metabolites were categorized as eight mutually exclusive chemical classes (amino acids, carbohydrates, cofactors and vitamins, energy metabolites, lipids, nucleotides, peptides and xenobiotics). The median and interquartile range of the coefficient of variation (CV) across the metabolites was 10% (4–20%), similar to previous reports analyzed by Metabolon [17].

Statistical Analysis

Any missing values were assumed to be below the limits of detection, and these values were imputed with the compound minimum (minimum value imputation). Basic statistical analysis of log-transformed data was conducted using MetaboAnalyst 3.0 (<http://www.metaboanalyst.ca/>). Non-parametric Wilcoxon rank tests comparing metabolites differences between cases and controls were used in metabolomics data analyses and performed independently for the discovery and validation sets. To control the multiple comparison, we set the false discovery rate (FDR) at 0.05 [18]. To assess the association with breast cancer risk, logistic regression analysis was used, adjusting for age, obesity status and race differences. The assumptions of logistic regression, including the independence of each observation, collinearity among the independent variables, and

linearity of independent variables and log odds, were assessed. Using significant metabolites in both discovery and validation sets, we applied partial least squares – discriminant analysis (PLS-DA) to assess the difference between the case and control groups. Metabolic pathway analysis was conducted to identify the enriched metabolite sets and significant metabolic pathways that could differentiate breast cancer cases and controls. The latest version of The Human Metabolome Database (HMDB) 3.0 was used in metabolic pathway analysis [19]. In addition, pathway topology analysis was used to estimate the impact of a certain metabolite or a group of metabolites in a certain metabolic pathway, and relative-betweenness centrality test was used to estimate the impact [20]. To further assess whether associations were independent, we evaluated the pairwise correlations between all metabolites significantly associated with breast cancer risk in both discovery and validation sets among the controls. Metabolites whose pairwise correlations greater than 0.5 were considered highly correlated and to have possible redundancy. The selection of 0.5 as the cutoff point is based on our previously published studies [21,22]. Using 9 non-redundant metabolites, we generated a metabolic risk score. For each metabolite, using the median level in the controls as the cutoff point, we stratified the study subjects into high and low level categories. Next, based on the relationship between metabolite levels and breast cancer risk, we scored the study subjects as either high or low breast cancer risk (0 or 1) and summed scores across 9 metabolites to generate a metabolic risk score (range: 0–9). Then, we generated a metabolic risk score based on the number of high level of those 9 metabolites. Logistic regression analysis was applied to assess the relationship between the metabolic risk score and breast cancer risk, adjusted for co-variables above. All analyses were performed with STATA software version 10.1 (STATA, College Station, TX).

Results

Characteristics of the study populations

The discovery set included 134 breast cancer patients and 57 healthy controls, and the validation set included 224 breast cancer patients and 81 healthy controls. Characteristics of case and control groups were described in Table 1. All study subjects are either Hispanic or non-Hispanic African American women. Specifically, 77 (57.46%) cases and 38 (66.67%) controls were Hispanics in the discovery set, and 133 (58.48%) cases and 24 (29.63%) controls were Hispanics in the validation set. In the discovery set, the mean ages were 51 and 51 for the cases and controls. And in the validation set, the mean ages were 51 and 58 for the cases and controls, subsequently. In the discovery set, 71 (52.99%) cases and 25 (43.96%) controls were obese. Similarly, in the validation set, 133 (59.64%) cases and 45 (55.56%) controls were obese.

Metabolites differed between breast cancer cases and controls

In the discovery set, we identified a total of 31 metabolites whose levels significantly differed between breast cancer cases and controls, after adjusting age, BMI category, race/ethnicity, and multiple comparison (Table 2). Among them, 9 were significantly higher in the cases than controls, and 22 were significantly lower in the cases than controls. The top three metabolites higher in the cases than controls were thioproline, inosine, and 3-hydroxyoctanoate. Higher levels of those three metabolites were associated with 3.90, 2.83,

and 1.69-fold increased odds of breast cancer. On the other hand, the top three metabolites lower in the cases than controls were cysteines-sulfate, sphingomyelin, and threonylphenylalanine. Higher levels of those three metabolites were associated with 76, 70, and 56% decreased odds of breast cancer. In the validation set, 14 of those 31 metabolites were confirmed. Among them, 7 were higher in the cases than controls, and 7 were lower in the cases than controls. In the validation set, the top 3 metabolites whose levels were most significantly increased in breast cancer cases than controls were linoleate (18:2n6) (OR=1.98, 95%CI: 1.46, 2.70), dihomolimonoleate (OR=1.82, 95%CI: 1.34, 2.47), and 10-nonadecenoate (19:1n9) (OR=1.76, 95%CI: 1.31, 2.36). On the other hand, the top 3 metabolites in the validation set whose levels were most significantly decreased in breast cancer cases than controls were bilirubin (OR=0.48, 95%CI: 0.34, 0.69), glucuronate (OR=0.56, 95%CI: 0.35, 0.90), and 1-(1-enyl-stearoyl)-2-dihomolimonolenoyl-GPE (OR=0.65, 95%CI: 0.46, 0.92). In terms of metabolic pathways, 10 metabolites were lipids (including 6 fatty acids), 1 amino acid, 1 xenobiotics, 1 cofactors and vitamins, and 1 carbohydrate. Using those 14 metabolites, we generated the 3-D plot to differentiate the breast cancer cases and controls. We found that the cases and controls were separated with three components. Component 1, 2 and 3 could account for 30, 16.2, and 14.4% of the difference between the cases and controls. We also investigated whether the significant metabolites differed between African American and Hispanic women among the controls. However, none of them differed.

Metabolic pathways differed between breast cancer cases and controls

Next, metabolic pathway analysis was conducted to identify the enriched metabolic pathways that differed between breast cancer cases and controls (Table 3). In the discovery set, we identified 12 metabolic pathways with P value less than 0.10. The top 3 most significant pathways were Glycerophospholipid metabolism ($P < 0.001$), Sphingolipid metabolism ($P < 0.001$), and Citrate cycle (TCA cycle) ($P < 0.001$). Using P values of 0.10 and 0.05 as the cutoff points, 6 and 3 of the 12 identified metabolic pathways in the discovery set were confirmed in the validation set. After further considered the impact factor (the significance of each individual metabolite in a relative metabolic pathway), the most significant and consistent metabolic pathways were Linoleic acid metabolism, Arginine and proline metabolism, and Citrate cycle (TCA cycle). Particularly, the significant metabolites involved in linoleic acid metabolism had the highest impact factor, 0.656 in both sets, suggesting the identified significant metabolites involved in linoleic acid metabolism pathway are significantly involved in breast cancer development.

Metabolites risk score differed between breast cancer cases and controls

To further analyze the relationships among those 14 identified significant metabolites, we performed the pairwise correlation analysis among the controls (Figure 1). Using correlation coefficient (γ) of 0.5 as the cutoff point, 9 metabolites were found to have median to low correlation ($\gamma < 0.50$) with any of the other metabolites. This includes glucuronate, stearate (18:0), 3-hydroxyoctanoate, 1-palmitoyl-GPA (16:0), 1-(1-enyl-stearoyl)-2-dihomolimonolenoyl-GPE, sphingomyelin, bilirubin, urea, and 3-methylxanthine. Using those 9 metabolites, we generated a metabolic risk score. The method used to generate the risk score was detailed in previous Statistical Analysis section. Using the risk score as a continuous

variable, we found that increased risk score was 1.87-fold and 1.63-fold more likely observed in breast cancer cases than controls after adjusting for age, race, and BMI category in the discovery and validation sets, respectively (adjusted OR=1.87, 95% CI=1.50–2.32; adjusted OR=1.63, 95% CI=1.36–1.95) (Table 3). Next, we stratified the study subjects into 3 strata based the risk score among the control subjects: low (0 to 4), medium (5–6) and high (at least 7). When compared with study subjects with low risk scores, medium risk scores were more likely observed in the breast cancer cases than controls in both discovery and validation sets (adjusted OR=8.68, 95% CI=3.31–22.75; and adjusted OR=4.12, 95% CI=2.06–8.22). The odd was further elevated when we compared high to low risk score group. Those with high risk score were associated with 18.44-fold and 6.96-fold increased odds of breast cancer in the discovery and validation sets, respectively (adjusted OR=18.44, 95% CI=6.75–50.37; adjusted OR=6.96, 95% CI=3.27–14.81).

Discussion

In the current two-stage study of metabolomics profiling in plasma samples from 358 breast cancer patients and 138 healthy controls, we identified metabolic signatures and pathways significantly associated with breast cancer risk. Intriguingly, all seven metabolites, namely 3-hydroxyoctanoate 3-hydroxybutyrate (BHBA), stearate (18:0), 3-hydroxydecanoate, linoleate (18:2n6), 10-nonadecenoate (19:1n9), and dihomo-linoleate, whose levels were increased in breast cancer cases than controls, were lipids. The finding is consistent with our previous study in non-Hispanic Whites and African Americans that showed the levels of all 7 metabolites were higher in breast cancer cases than the controls [7]. The agreement between two studies suggested that lipids may play a key role in breast carcinogenesis.

Among the 7 lipids mentioned above, 6 were fatty acids, including 2 monohydroxy fatty acids, 2 long chain fatty acids, and two polyunsaturated fatty acids. Elevated levels of monohydroxy and long chain fatty acids may indicate altered fatty acid β -oxidation in patients with breast cancer [7]. Fatty acid β -oxidation has been reported to support functional mitochondria and is essential for the accelerated proliferation of cancer cells [23,24]. Interestingly, in a recent study, Wang et al reported that fatty Acid β -Oxidation plays a critical role in breast cancer stem cell self-renewal and chemoresistance [25]. Therefore, altered fatty acids β -oxidation may promote the aggressive tumorigenic phenotypes and breast carcinogenesis [26]. Similar observations were also seen in several other breast cancer case control analyses [27,28]. Furthermore, another significant metabolite, ketone body 3-hydroxybutyrate (BHBA), which is the end product of ketogenesis and downstream of fatty acid β -oxidation, was also found associated with breast cancer risk in our study. The higher BHBA level in the cases is another sign of altered fatty acid β -oxidation in breast cancer subjects. Consistent with our previous study [7], the essential fatty acids linoleate (18:2n6) and dihomo-linolenate (20:3n3 or n6) were significantly higher in the cases than controls. Linolenic acid has been suggested to promote the tumorigenic phenotype of breast cancer [29]. In a genome-wide association study, genetic variants in genes involved in the regulation of linolenic acid metabolism were associated with breast cancer risk [30].

Another finding of interest is that all 5 significant amino acids in the discovery set were associated with decreased risk of breast cancer. Although only urea remained statistically significant in the validation set, the impact on breast cancer risk is still evident. In fact, this observation is consistent with the notion that amino acids play important roles in carcinogenesis. For example, Maddocks and colleagues found that restriction of dietary Serine and Glycine could reduce tumor growth in xenograft and allograft models [31]. In circulation, amino acids have been reported to be reduced in patients of a variety of cancers [32–34]. The reduced levels of amino acids may reflect the increased amino acid demand by tumors and therefore amino acid malnutrition seen in tumors. In the current study, our observation on urea is consistent with a previous report that showed plasma urea level was significantly lower in breast cancer cases than healthy women [35]. However, the biological relevance of urea in breast carcinogenesis is still unclear.

Our study is first to report the association between plasma bilirubin and breast cancer risk. Endogenous antioxidant bilirubin has shown to inhibit cancer development [36]. Bilirubin was associated with reduced breast cancer risk in our study, which was consistent with its anti-carcinogenic property [37,38]. Serum bilirubin has been reported to associated with reduced lung cancer risk in two prospective studies [39,40] and reduced cancer mortality in a population-based set [41]. However, how bilirubin modulates breast carcinogenesis remains largely unknown.

In the pathway analysis, 3 metabolic pathways were significantly associated with higher risk of breast cancer risk in both sets, including Citrate cycle (TCA cycle), Arginine and proline metabolism, and Linoleic acid metabolism. Even though fumarate was the only significant metabolite directly involved in the TCA cycle, several other significant metabolites were involved in biological pathways relevant to the TCA cycle, including fatty acid β -oxidation, amino acid metabolism and ketone bodies [42]. Dysfunction of mitochondrial based metabolic pathways, including TCA cycle and oxidative phosphorylation, has been frequently observed in breast cancer [43–47,42]. Arginine and proline metabolism pathway plays an important role in cancer by impacting various regulatory targets, influencing apoptosis, autophagy, and regulating redox homeostasis [48]. In breast cancer, altered proline and arginine metabolism has also been linked to metastasis formation [49]. It's not a surprise that Linoleic acid metabolism was significantly associated with breast cancer risk. As mentioned above, the omega-3 polyunsaturated fatty acids linoleate (18:2n6) and dihomo-linolenate (20:3n3 or n6) have been reported to upregulate breast cancer growth, enhance tumor progression, and play an important role in breast tumorigenesis [50].

Recently, two breast cancer metabolomics studies have been published using samples from the Prostate, Lung, Colorectal and Ovarian (PLCO) cohort [5,6]. A few diet and BMI related metabolites were found associated with the risk of breast cancer. Although both studies identified lipids as the top significant metabolites, they were not overlapped. More than 90% of the study participants included in their studies were postmenopausal non-Hispanic Whites aged 55–74 years old. While our study only included Hispanics and non-Hispanic African Americans with mean age less than 55 years old. It is possible that the difference in population demographics may contribute to the difference in significant metabolites. As one example, 3-hydroxyoctanoate was one of the significant metabolites identified in our study.

While in their studies, 2-hydroxyoctanoate, which was fried food-associated, was found associated with estrogen receptor positive (ER+) breast cancer.

In summary, we identified a panel of plasma metabolites associated with breast cancer risk among African American and Hispanic women, which may provide new insights in breast tumorigenesis in different populations. The major limitations of this study are that the plasma samples were collected after diagnosis, and matched tissue samples were not available. However, validity of using plasma as the surrogate tissue has been reported [51]. Due to the nature of case control study, we cannot infer the causal relationship between metabolites and breast cancer risk. Other limitations may include the lack of dietary data and single metabolite measurement, etc. Thus, we need to be very cautious to interpret our results. Even though our study had biggest sample size among similar studies to compare the blood metabolic signatures between breast cancer cases and controls, validation of our results in larger and prospective populations in the future are warranted.

Finally, it seems that metabolite profiles didn't differ between African American and Hispanic women among the controls. However, the number of controls in two races (n=138 in total) are very too small, so it is very likely that we don't have enough power to detect the difference. In our previous metabolomics study in African American (n=24) and Caucasian (n=36) female controls, metabolite profiles were found significantly differed between them [7]. Clearly, whether metabolic profiles differ by the race/ethnicity and whether the potential difference may play a role in the association between plasma metabolites and breast cancer risk are still unclear. Future large multi-ethnic studies are needed.

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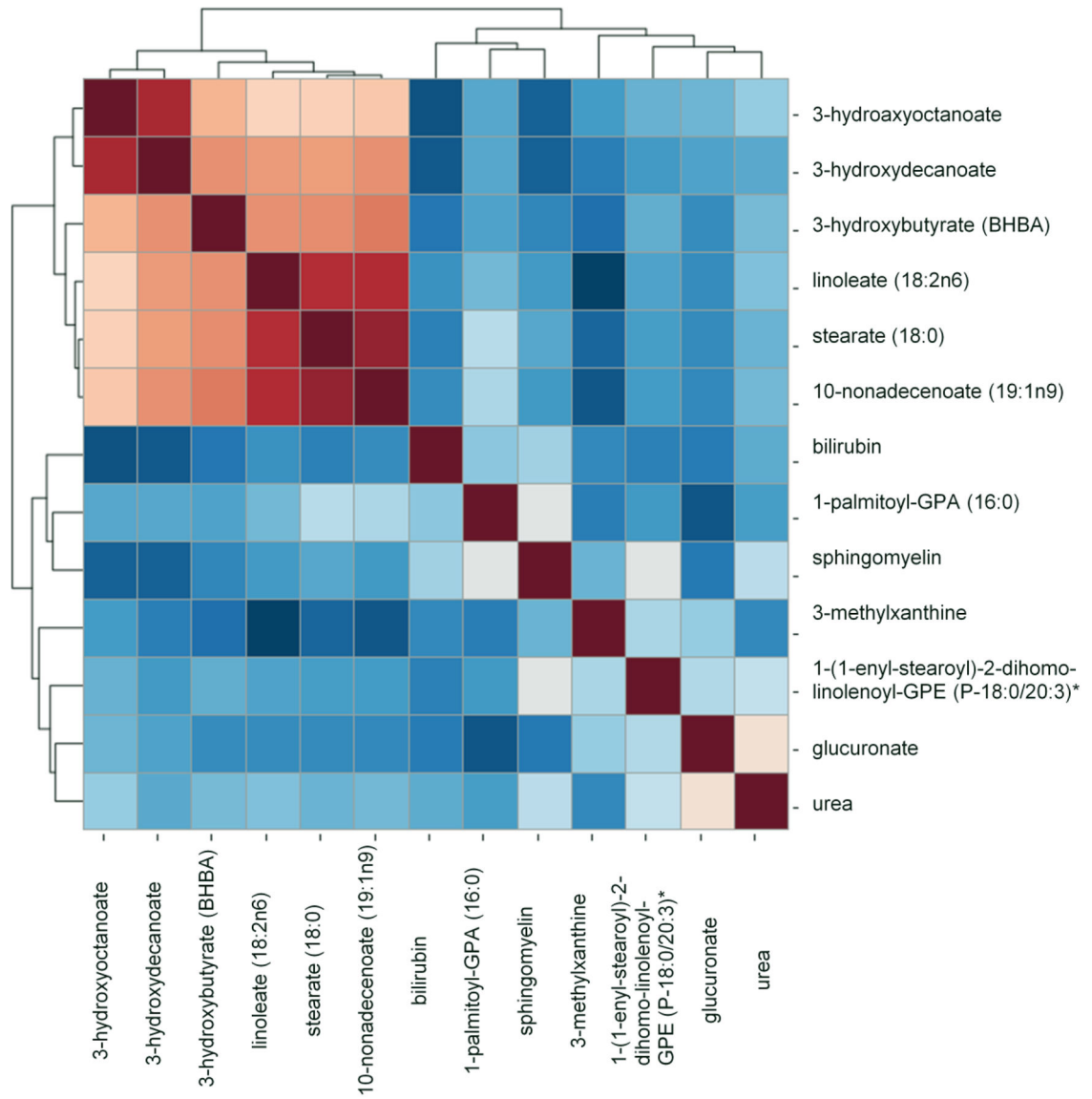


Figure 1. Pair-wise correlation analysis to assess the redundancy among significant metabolites.

Table 1

Selected demographic variables by case-control status by study

	Discovery			Validation		
	Case (N=134)	Control (N=57)	P-value*	Case (N=224)	Control (N=81)	P-value*
Age, mean(SD)	51.1(12.0)	51.1(6.7)	0.990	50.6(10.7)	58.4(14.8)	<0.001
BMI, mean(SD)	31.1(6.2)	30.4(7.0)	0.499	32.8(7.7)	33.4(8.3)	0.599
BMI category N(%)						
normal(<25)	18(13.43)	17(29.82)		28(12.11)	10(12.35)	
overweight(25–<30)	45(33.58)	15(26.32)		63(28.25)	26(32.10)	
obese(30+)	71(52.99)	25(43.86)	0.027	133(59.64)	45(55.56)	0.790
Race						
African Americans	57(42.54)	19(33.33)		93(41.52)	57(70.37)	
Hispanic	77(57.46)	38(66.67)	0.234	131(58.48)	24(29.63)	<0.001
Family history of breast cancer						
0	113(84.33)	50(87.72)		195(87.05)	70(86.42)	
1	21(15.67)	7(12.28)	0.544	29(12.95)	11(13.58)	0.885
ER						
positive	100(74.63)			157(70.09)		
negative	34(25.37)			67(29.92)		
PR						
positive	77(57.46)			134(59.82)		
negative	57(42.54)			90(40.18)		
HER2						
positive	30(22.38)			35(15.63)		
negative	104(77.61)			189(84.37)		
Stage						
I	44(32.83)			72(32.14)		
II	44(32.83)			90(40.18)		
III & IV	46(34.33)			62(27.68)		

* Student T test was used to calculate the P value for continuous variables; and Chi square was used to calculate the P value for categorical variables.

Table 2.

Serum metabolites associated with breast cancer risk

Metabolites	Pathways	Sub-Pathways	Discovery		Validation	
			OR(95%CI)*	P-value	OR(95%CI)*	P-value
thioprine	Xenobiotics	Chemical	3.90 (2.34,6.51)	<0.001	1.42 (0.95, 2.13)	0.087
inosine	Nucleotide	Purine Metabolism, (Hypo)Xanthine/Inosine	3.83 (2.49, 5.90)	<0.001	0.73 (0.55, 0.96)	0.025
3-hydroxyoctanoate	Lipid	Fatty Acid, Monohydroxy	1.69 (1.16, 2.45)	0.006	1.62 (1.20, 2.18)	0.002
3-hydroxybutyrate (BHBA)	Lipid	Ketone Bodies	1.67 (1.18,2.35)	0.004	1.62 (1.17, 2.23)	0.004
stearate (18:0)	Lipid	Long Chain Fatty Acid	1.52 (1.10, 2.09)	0.011	1.66 (1.24, 2.22)	<0.001
3-hydroxydecanoate	Lipid	Fatty Acid, Monohydroxy	1.48 (1.04, 2.10)	0.028	1.67 (1.22, 2.27)	0.001
linoleate (18:2n6)	Lipid	Polyunsaturated Fatty Acid (n3 and n6)	1.42 (1.04, 1.95)	0.028	1.98 (1.46, 2.70)	<0.001
10-nonadecenoate (19:1n9)	Lipid	Long Chain Fatty Acid	1.38 (1.01,1.89)	0.049	1.76 (1.31, 2.36)	<0.001
dihomo-linoleate	Lipid	Polyunsaturated Fatty Acid (n3 and n6)	1.35 (1.01, 1.86)	0.044	1.82 (1.34, 2.47)	<0.001
fumarate	Energy	TCA Cycle	0.69 (0.50, 0.95)	0.025	0.73 (0.54, 1.00)	0.052
3-methylxanthine	Xenobiotics	Xanthine Metabolism	0.67 (0.48, 0.94)	0.021	0.68 (0.51, 0.90)	0.008
bilirubin	Cofactors and Vitamins	Hemoglobin and Porphyrin Metabolism	0.66 (0.47, 0.94)	0.019	0.48 (0.34, 0.69)	<0.001
1-palmitoyl-GPA (16:0)	Lipid	Lysophospholipid	0.65 (0.46, 0.92)	0.014	0.74 (0.55, 0.99)	0.049
isobutyryl-carnitine	Amino Acid	Leucine, Isoleucine and Valine Metabolism	0.64 (0.45, 0.90)	0.011	0.84 (0.62, 1.13)	0.246
1-palmitoyl-2-linoleoyl-GPC	Lipid	Phosphatidylcholine (PC)	0.63 (0.42, 0.94)	0.025	1.01 (0.74, 1.39)	0.951
N-acetyl-leucine	Amino Acid	Leucine, Isoleucine and Valine Metabolism	0.62 (0.42, 0.91)	0.015	0.86 (0.64, 1.15)	0.308
1-(1-enyl-oleoyl)-2-docosahexaenoyl-GPE	Lipid	Plasmalogen	0.60 (0.40, 0.90)	0.014	0.71 (0.50, 1.03)	0.070
glucuronate	Carbohydrate	Aminosugar Metabolism	0.59 (0.43, 0.83)	0.002	0.56 (0.35, 0.90)	0.016
uridine	Nucleotide	Pyrimidine Metabolism, Uracil containing	0.58 (0.41, 0.82)	0.002	1.47 (1.11, 1.95)	0.007
3-hydroxy-3-methylglutarate	Lipid	Mevalonate Metabolism	0.58 (0.40, 0.83)	0.003	0.78(0.56, 1.07)	0.118
N-acetylvaline	Amino Acid	Leucine, Isoleucine and Valine Metabolism	0.57 (0.39, 0.83)	0.003	0.88 (0.66, 1.18)	0.409
1-(1-enyl-stearoyl)-2-dihomo-linolenoyl-GPE	Lipid	Plasmalogen	0.55 (0.38, 0.80)	0.002	0.65 (0.46, 0.92)	0.014
urea	Amino Acid	Urea cycle; Arginine and Proline Metabolism	0.54 (0.37, 0.79)	0.002	0.74 (0.55, 0.99)	0.040
retinol (Vitamin A)	Cofactors and Vitamins	Vitamin A Metabolism	0.54 (0.37, 0.78)	0.001	0.78 (0.59, 1.04)	0.089
trans-4-hydroxyproline	Amino Acid	Urea cycle; Arginine and Proline Metabolism	0.51 (0.36, 0.74)	<0.001	0.79 (0.60, 1.04)	0.097
perfluorooctanesulfonic acid (PFOS)	Xenobiotics	Chemical	0.47 (0.31, 0.71)	<0.001	0.99 (0.69, 1.42)	0.949
1-linoleoyl-GPA(18:2)	Lipid	Lysophospholipid	0.46 (0.32, 0.68)	<0.001	0.81 (0.61, 1.07)	0.144

Metabolites	Pathways	Sub-Pathways	Discovery		Validation	
			OR(95%CI) *	P-value	OR(95%CI) *	P-value
beta-citrylglutamate	Amino Acid	Glutamate Metabolism	0.45 (0.29, 0.69)	<0.001	1.70 (1.23, 2.36)	0.001
threonylphenylalanine	Peptide	Dipeptide	0.44 (0.29, 0.67)	<.001	1.64 (1.24, 2.17)	<0.001
sphingomyelin	Lipid	Sphingolipid Metabolism	0.30 (0.19, 0.48)	<0.001	0.68 (0.51, 0.90)	0.008
cysteine s-sulfate	Amino Acid	Methionine, Cysteine, SAM and Taurine Metabolism	0.24 (0.14, 0.40)	<0.001	3.25 (2.14, 4.95)	<0.001

* Logistic regression was used to calculate the ORs and P value with FDR<0.05 was used. Age, obesity status and race were adjusted.

Table 3.

Metabolic pathways associated with breast cancer risk

Metabolic pathway	Discovery		Validation	
	P value	Impact factor	P value	Impact factor
Glycerophospholipid metabolism	2.17E-05	0.314	0.071	0.205
Sphingolipid metabolism	2.12E-04	0.283	Not observed	
Citrate cycle (TCA cycle)	9.65E-04	0.236	0.012	0.090
Butanoate metabolism	0.013	0.108	0.076	0.040
D-Arginine and D-ornithine metabolism	0.014	0.500	Not observed	
Alanine, aspartate and glutamate metabolism	0.017	0.003	0.119	0.003
Ascorbate and aldarate metabolism	0.019	0.049	0.310	0.033
Arginine and proline metabolism	0.031	0.096	0.011	0.120
Pyruvate metabolism	0.037	0.320	Not observed	
Linoleic acid metabolism	0.046	0.656	0.005	0.656
Nicotinate and nicotinamide metabolism	0.081	0.017	0.095	0.038
Caffeine metabolism	0.084	0.045	0.413	0.015

Table 4.

Metabolite risk score associated with breast cancer risk

	Discovery		Validation	
Continuous variable	1.87 (1.50–2.32)	<0.001	1.63 (1.36–1.95)	<0.001
Categorical variable				
Low (0–4)	Reference		Reference	
Medium (5–6)	8.68 (3.31–22.75)	<0.001	4.12 (2.06–8.22)	<0.001
High (7–8)	18.44 (6.75–50.37)	<0.001	6.96 (3.27–14.81)	<0.001

* Logistic regression was used to calculate the ORs and P value. Age, obesity status and race were adjusted.

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