Correlation Of Lipid Metabolism Genes With Drug Resistance Markers

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ABSTRACT
One defining feature of cancer cells is metabolic pathway dysregulation, which prevents them from meeting their bioenergetic and biosynthetic demands. Lipid moieties are physiologically and clinically significant because they are a concentrated source of energy and a source of numerous precursors that fuel cancer's high growth rate Therefore, this review set out to compile and organize data about how samples are prepared for lipid analysis in relation to obesity research. The emergence of medication resistance is a major challenge in cancer treatment. In both the local and TCGA cohorts, research examining the relationship between drug resistance genes and lipid metabolism genes found that ABCC1 was positively associated with CERK and SPHK1.

KEYWORDS: Correlation, Lipid, Metabolism, Drug, and Resistance

INTRODUCTION

The position and quantity of double bonds in fatty acids are also associated with their dietary sources and fatty acid de novo synthesis. As an example, among the monoenoic fatty acyls found in both plant and animal tissues, the 18:1 (n-9) isomer is by far the most numerous. Bacterial lipids often include the 18:1 (n-7) fatty acyl isomer, which is a monoenoic fatty acyl group that is present in small amounts in the majority of plant and animal tissues. Carrot, parsley, and coriander seed oils, which are members of the umbellifers family, contain lipids mostly in the 18:1 (n-12) fatty acyl isomer.

Research into the causes of obesity and its treatments is important since the disease is still a major health concern in the contemporary world. From rigorous assessments of biochemical markers to in-depth psychological studies, a broad variety of research methodologies may be used according to the premise. Standard approaches, such as assessing fat content or body mass index (BMI) in human participants, are often used in research. We begin by looking at the biochemical markers that are most affected by obesity: lipid profile, fasting glucose, insulin, and so on.

Numerous systematic and retrospective reviews are based on the massive amounts of data collected on obesity, which permits their meta-analysis.

Research on bariatric procedures, which include alterations to the intestines or the stomach in order to achieve weight reduction, provides particularly useful information. Furthermore, cardiovascular problems have been linked to obesity in several research. metabolic syndrome, diabetes, and Lots of research is being on in the areas of nutrition, psychology, and neuroscience.

While researchers can use their imaginations and the tools at their disposal to study obesity in isolation, studies that examine obesity in relation to other diseases typically use a small number of parameters, like body mass index (BMI) and total fat content, because these variables are considered secondary to the study area. Furthermore, the most popular approach for making a diagnosis of obesity is the computation of body mass index (BMI). Using body mass index (BMI), the World Health Organization classified people as underweight (<18.5), normal weight (18.5-24.9), overweight (25-29.9), or obese (BMI > 30).

It is possible to assess body fat, total body water, and concurrent states of lipid changes in blood (dyslipidemias), hyperinsulinemia, etc., in athletes and bodybuilders, as body mass index (BMI) may not be a reliable measure of obesity for these populations. Standard plasma measurements and changes in particular lipid groups in serum should be studied because obesity is directly associated with lipid metabolism. It is sometimes necessary to adjust the sample preparation procedures used in lipidomic research on people who are overweight or obese because of the significantly increased lipid buildup and many changes in the lipid composition.

Therefore, this review set out to compile and organize data about how samples are prepared for lipid analysis in relation to obesity research. Our attention was divided between tried-and-true techniques and innovative approaches. Nonetheless, the majority of these techniques may also be used to individuals who are not overweight or who suffer from other types of dyslipidemia.

LITERATURE REVIEW

Ying. Et.al (2014) As components of cell membranes, participants in cell-signaling pathways, and secondary energy stores, lipids perform a wide variety of important functions in living systems. So, lipid abnormalities may have a role in illness progression. Therefore, clinical lipidomic, the in-depth study of lipids in clinical samples, is essential for advancing our knowledge of disease processes and progression and creating new therapeutic options. The lipidomics process is

detailed in this review, which starts with methods for preparing lipid samples. Additionally, we detail the evolution of mass spectrometry technology, which paved the way for other popular methods of lipid analysis.

Guofeng et.al (2022) Lipidomics has come a long way in the last 10 years, providing solid support for both the qualitative and quantitative data on lipid molecules extracted from consumable muscle meals and physiological animal tissues. Mass spectrometry (MS) and nuclear magnetic resonance (NMR) are the primary analytical platforms for lipidomics. MS-based methods, such as "shotgun lipidomics," UPLC-MS/MS, and MALDI-TOF-MS, have a high level of availability, sensitivity, and accuracy when it comes to identifying and quantifying basal lipid profiles from a complex biological perspective. The current methods have their limitations when it comes to analyzing lipid-species, such as fatty acids, triglycerides (TGs), and phospholipids (PLs).

Matej et.al (2023) An all-inclusive synopsis of recent methodological developments and developing trends in clinical research using lipidomics is the goal of this study. We evaluate new lipidomics approaches that are very sensitive and selective, and which may produce many molecular lipid species from little amounts of biological matrices. The research that was examined show that molecular lipid signatures may be used as sensitive diagnostic tools for illness prediction and monitoring, opening up new possibilities for precision medicine. The most recent developments in microstamping methods may also significantly advance clinical lipidomics. The study also highlights the need for more research on avoiding major mistakes in processing and reporting and harmonizing data across different lipidomics platforms.

Peter et.al (2021) The development and progression of inflammatory illnesses, cardiometabolic diseases, neurological disorders, and various cancers are all influenced by dysregulation of lipid metabolism. Thanks to new developments in lipidomic technology, researchers can now conduct in-depth lipidomic profiling on biological samples that are clinically relevant. This allows them to link the genesis and progression of diseases to specific lipid species and metabolic pathways. We may use the results to improve our understanding of the illness process and create risk assessment models to aid in diagnosis and treatment with the use of this data. At now, the majority of in-depth lipidomic profiling's clinical uses are confined to the analysis of clinical trial sample sets using techniques derived from research. We do, however, anticipate the creation of purpose-built clinical platforms that will aid healthcare practitioners in the evaluation, diagnosis, and monitoring of disease risks; these platforms will be engineered for continuous operation and clinical integration.

Asavari et.al (2023) Investigating lipidomic analysis in depth, this article delves into its uses and consequences in the realms of biology and phytochemistry. In order to decipher complex metabolic pathways and the processes that regulate them, the research involves a thorough analysis of lipid profiles in living systems. Extending into the phytochemical domain, the study delves into the various lipid compositions found in plant extracts and their possible medicinal applications. Novel insights into lipidomic differences are unveiled via improved analytical methods, leading to a fuller knowledge of cellular processes and the complicated interaction between botanical and biological lipidomics. The results given here add to what is already known and provide interesting new avenues for investigation into nutrition, medicine, and plant-based therapies in the future. Hey there! --Fatty acids: A wide variety of biomolecules fall into this category; they are insoluble in water but dissolve in nonpolar solvents. Energy storage.

RESEARCH METHODOLOGY

Patients with breast cancer who had surgical resection at the Department of Surgery Dept, SAMC & PGI, Indore, had their tumors and surrounding normal tissues removed Isolation of the lipids was accomplished by slightly altering the procedure described by Shaner et al. (2009). Bertin Technologies' Minely's Homogenizer (Montigny-le-Bretonneux, France) and Badelin Electronics' Using a Scanvac Centrifuge Vacuum Concentrator (Labogene, Denmark), the organic phase extract and single-phase extract were dried the estrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor 2 (Her2) were used as conventional pathology markers to describe breast tissue samples. In order to isolate lipids, RNA, and proteins, the tissue samples were kept at a temperature of -80ºC.

DATA ANALYSIS

The emergence of medication resistance is a major challenge in cancer treatment. We looked at the relationship between lipids and known drug resistance indicators to see whether they have a role in drug resistance. Both the drug resistance genes ABCC1 (***$p<0.0001$) (Figure 1 A) and ABCG2 (**$p=0.0033$) (Figure 1 B) showed a significant connection with CERK. Figure 1 C likewise shows a positive correlation between SPHK1 and ABCC1 (**$p=0.0016$). Figure 1 D shows that there was no correlation between the SPHK1 and ABCG2 levels.

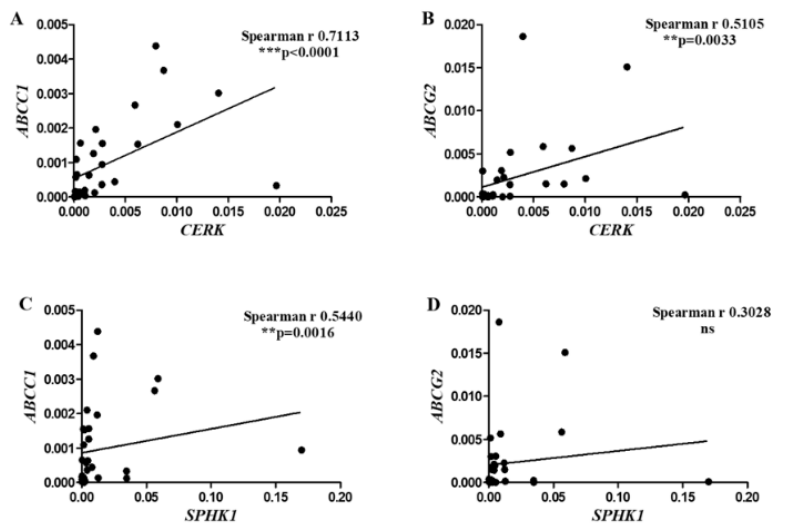

Figure 1 A local cohort study on the correlations between CERK and A. ABCC1, B. ABCG2, and SPHK1 and C. ABCC1, D. ABCG2.

The TCGA data collection provided further validation for the local cohort studies. Figure 2 A and Figure 2 C show that CERK and SPHK1 are positively correlated with the drug transporter ABCC1, respectively. But there was no correlation between ABCG2 and SPHK1 (Figure 2 D), and a negative correlation with CERK (Figure 2 B).

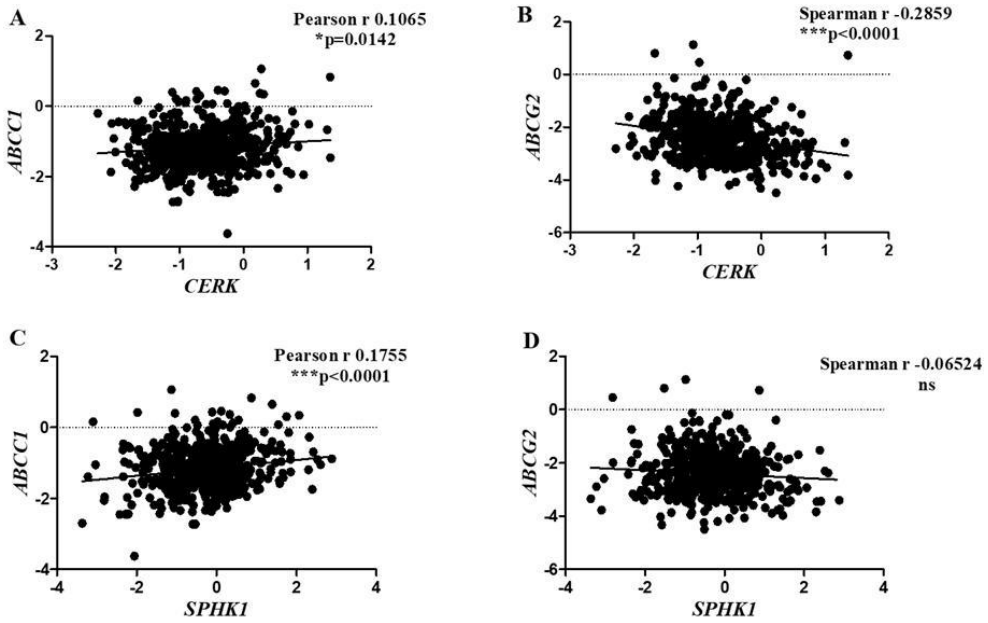

Figure 2 A. ABCC1, B. ABCG2, and C. ABCC1, D. ABCG2 are correlated with CERK and SPHK1, respectively, in the TCGA cohort.

Using a Kaplan-Meier plot, researchers examined the correlation between ABCC1, ABCG2, CERK, SPHK1, MMP-2, MMP-9, and overall survival (OS) in breast cancer patients. According to the median expression, 526 breast cancer patients from the TCGA dataset were categorized as either having low expression or high expression. Overall survival was not correlated with expression of the aforementioned genes. Patients were categorized into several categories to have a better grasp of the correlation between genes and survival. There was a correlation between high CERK expression and poor overall survival in two groups: late-stage breast cancer patients (*p=0.040) and patients with lymph node metastases (*p=0.023) (Figure 3 K). Patients who tested negative for estrogen receptors had a worse chance of survival if their SPHK1 and ABCC1 genes were not overexpressed (*p=0.034; Figure 3 M and **p=0.006, Figure 3 M, respectively). The current study found that patients with breast cancer metastasis who had high tumoral expression of MMP-9 had a poor prognosis (*p=0.032) (Figure 3 I), whereas patients with nodal positive (*p=0.031) (Figure 3 G), late stage (*p=0.039) (Figure 3 K),

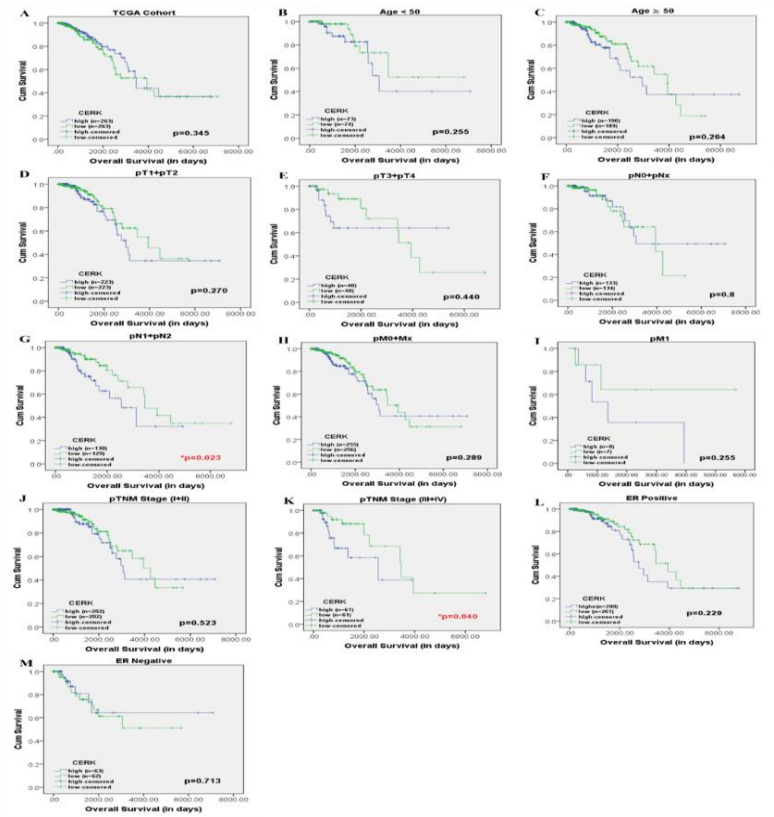

Figure 3 A. Using a Kaplan-Meier survival curve that is stratified by CERK expression, the overall survival in the TCGA cohort is shown.

From B to M General prognosis for breast cancer patients categorized by subtype: B. Age 50 and under C. Must be fifty years of age or older (D) The sum of pT1 and pT2 for example, pT3+pT4 in F, pN0+pNx the sum of pN1 and pN2 Hi. pM0+pMx First, pM1. John pTNM (I+II) I. pTNM (III+IV) Lymph Node Positive Examination of the ER was negative, M.

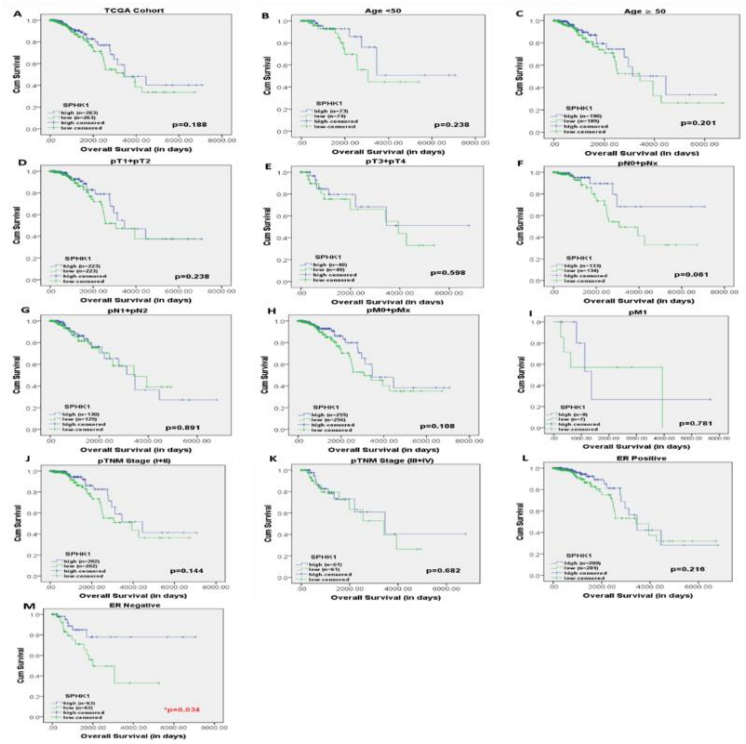

Figure 4 A. Survival curves based on Kaplan-Meier analysis of the TCGA cohort, with SPHK1 expression serving as a stratification variable.

From B to M General prognosis for breast cancer patients categorized by subtype: B. Age 50 and under C. Must be fifty years of age or older (D) The sum of pT1 and pT2 for example, pT3+pT4 in F, pN0+pNx the sum of pN1 and pN2 Hi. pM0+pMx First, pM1. John pTNM (I+II) I. pTNM (III+IV) Lymph Node Positive Examination of the ER was negative, M.

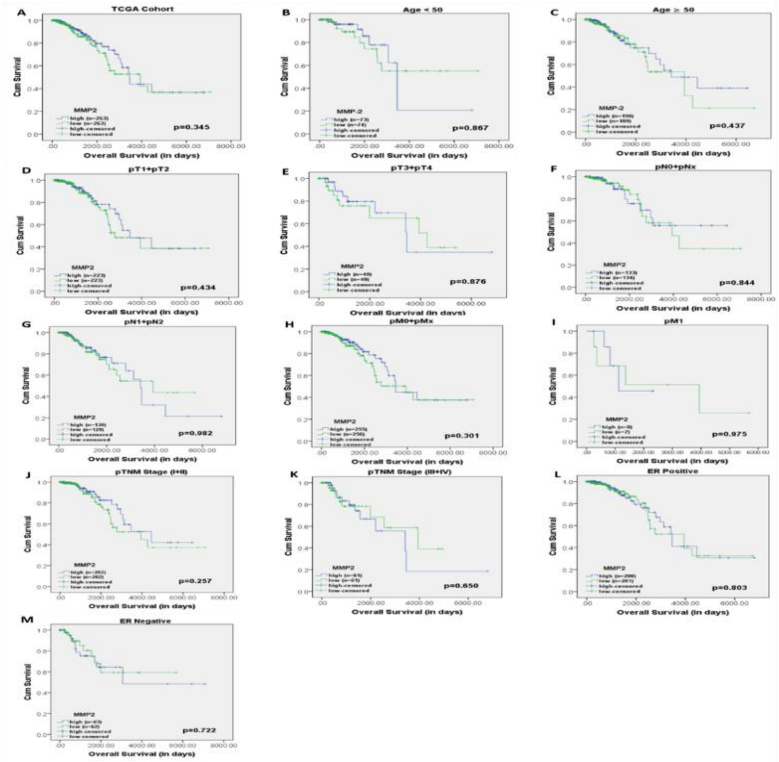

Figure 5 A. Using Kaplan-Meier survival curves, we can see how the TCGA cohort was divided up according to the presence or absence of MMP-2.

From B to M General prognosis for breast cancer patients categorized by subtype: B. Age 50 and under C. Must be fifty years of age or older (D) The sum of pT1 and pT2 for example, pT3+pT4 in F, pN0+pNx the sum of pN1 and pN2 Hi. pM0+pMx First, pM1. John pTNM (I+II) I. pTNM (III+IV) Lymph Node Positive Examination of the ER was negative, M.

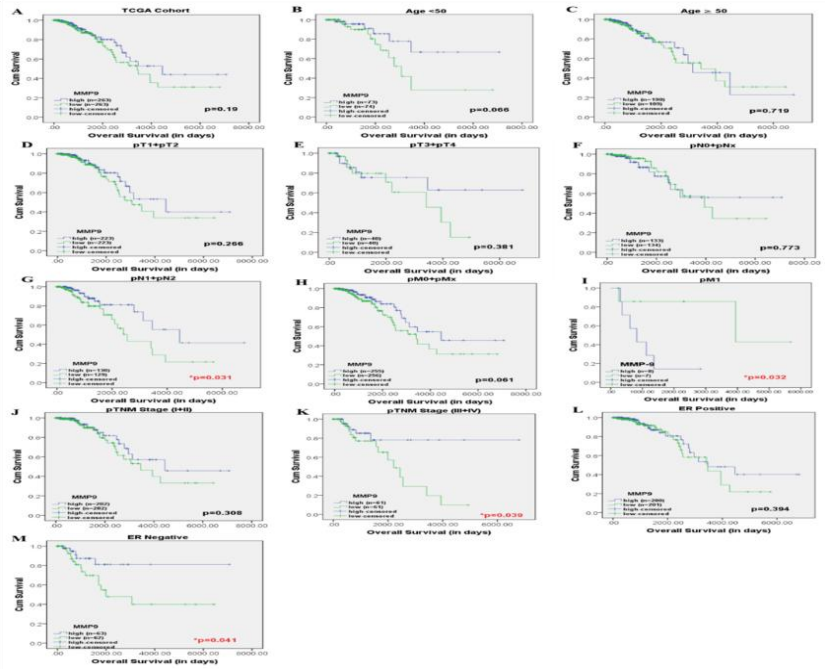

Figure 6 A. Survival curves based on Kaplan-Meier analysis of the TCGA cohort, with groups defined by MMP-9 expression levels.

From B to M General prognosis for breast cancer patients categorized by subtype: B. Age 50 and under C. Must be fifty years of age or older (D) The sum of pT1 and pT2 for example, pT3+pT4 in F, pN0+pNx the sum of pN1 and pN2 Hi. pM0+pMx First, pM1. John pTNM (I+II) I. pTNM (III+IV) Lymph Node Positive Examination of the ER was negative, M.

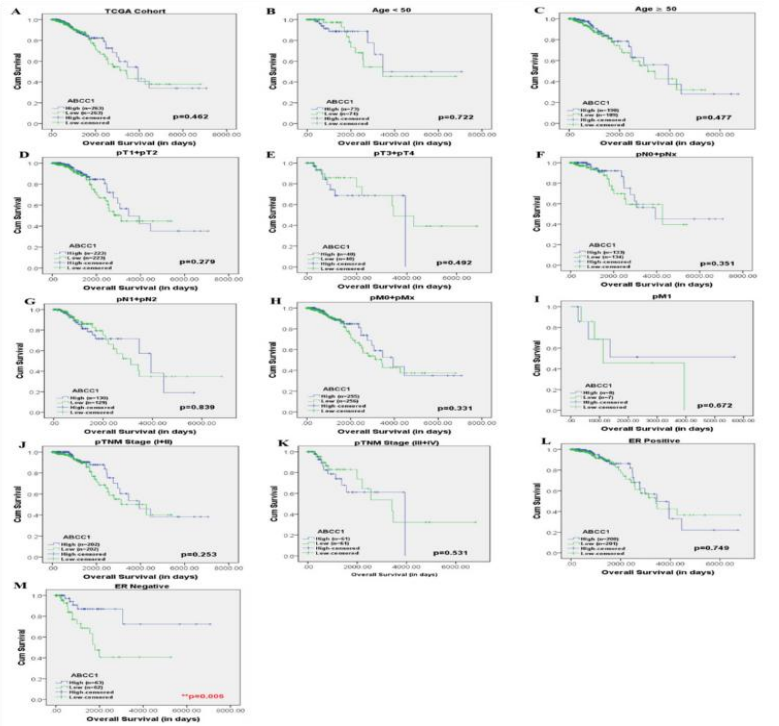

Figure 7 A. Overall survival in the TCGA cohort stratified by ABCC1 expression is shown by Kaplan Meier survival curves.

From B to M General prognosis for breast cancer patients categorized by subtype: B. Age 50 and under C. Must be fifty years of age or older (D) The sum of pT1 and pT2 for example, pT3+pT4 in F, pN0+pNx the sum of pN1 and pN2 Hi. pM0+pMx First, pM1. John pTNM (I+II) I. pTNM (III+IV) Lymph Node Positive Examination of the ER was negative, M.

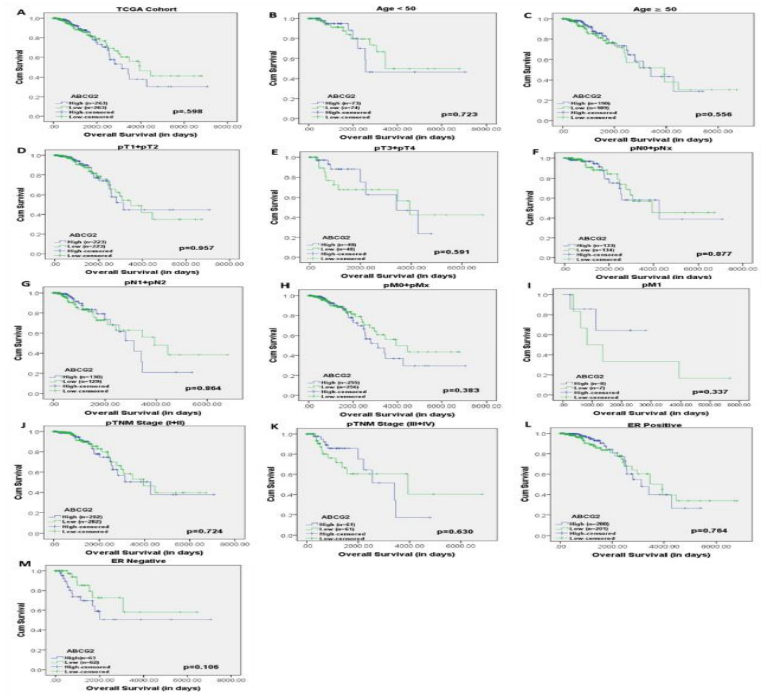

Figure 8 A. Using a Kaplan-Meier survival curve that is stratified by ABCG2 expression, the overall survival in the TCGA cohort is shown.

From B to M General prognosis for breast cancer patients categorized by subtype: B. Age 50 and under C. Must be fifty years of age or older (D) The sum of pT1 and pT2 for example, pT3+pT4 in F, pN0+pNx the sum of pN1 and pN2 Hi. pM0+pMx First, pM1. John pTNM (I+II) I. pTNM (III+IV) Lymph Node Positive Examination of the ER was negative, M.

CONCLUSION

In both the local and TCGA cohorts, research examining the relationship between drug resistance genes and lipid metabolism genes found that ABCC1 was positively associated with CERK and SPHK1. Clinical value as breast tumor biomarkers is further enhanced by the associations of lipid metabolism genes with treatment resistance genes ABCC1 and ABCG2, as well as recognized metastasis indicators MMP-2 and MMP-9.the breast tissues were dissected and then fixed in 10% neutral buffered formalin Using a Scanvac Centrifuge Vacuum Concentrator (Labogene, Denmark), the organic phase extract and single-phase extract were dried.

REFERENCES

1. Sandhir, Rajat. (2014). Metabolic Pathways: Lipid Metabolism. 10.1016/B978-0-12-384730-0.00200-7.
2. Li, Chengliang & Öztürk Kerimoğlu, Burcu & He, Lichao & Zhang, Min & Pan, Jiajing & Liu, Yuanyi & Zhang, Yan & Huang, Shanfeng & Wu, Yue & Jin, Guofeng. (2022). Advanced Lipidomics in the Modern Meat Industry: Quality Traceability, Processing Requirement, and Health Concerns. Frontiers in Nutrition. 9. 925846. 10.3389/fnut.2022.925846.
3. Salihovic, Samira & Lamichane, Santosh & Hyotylainen, Tuulia & Oresic, Matej. (2023). Recent advances towards mass spectrometry-based clinical lipidomics. Current opinion in chemical biology. 76. 102370. 10.1016/j.cbpa.2023.102370.
4. Meikle, Thomas & Huynh, Kevin & Giles, Corey & Meikle, Peter. (2021). Clinical Lipidomics: Realizing the potential of lipid profiling. Journal of Lipid Research. 62. 100127. 10.1016/j.jlr.2021.100127.
5. Lokhande, Darshan & Jadhav, Sandip & Sable, Vijaysinh & Jatla, Arya & Chavan, Asavari. (2023). STUDY AND EVALUATION OF LIPIDOMIC ANALYSIS ON BIOLOGICAL AND PHYTOCHEMICAL ASPECTS. INTERNATIONAL JOURNAL OF RESEARCH AND ANALYTICAL REVIEWS. 10. 30-38. 10.1729/Journal.37238.
6. Xu, Jiesi & Huang, Xun. (2020). Lipid Metabolism at Membrane Contacts: Dynamics and Functions Beyond Lipid Homeostasis. Frontiers in Cell and Developmental Biology. 8. 10.3389/fcell.2020.615856.
7. Sandhir, Rajat. (2014). Metabolic Pathways: Lipid Metabolism. 10.1016/B978-0-12-384730-0.00200-7.
8. Guo, Yongjie & Shen, Kailin & Ge, Shuqing & Zheng, Qi & Gao, Jingchao & He, Xiaopo. (2025). Exploring the potential causal relationship between fatty acid metabolism ratios and major salivary gland carcinomas: A two-sample Mendelian randomization study. Medicine. 104. e41802. 10.1097/MD.0000000000041802.
9. Khan, Fahad & Elsori, Deena & Verma, Meenakshi & Pandey, Shivam & Rab, Safia & Siddiqui, Samra & Alabdallah, Nadiyah M & Saeed, Mohd & Pandey, Pratibha. (2024). Unraveling the intricate relationship between lipid metabolism and oncogenic signaling pathways. Frontiers in cell and developmental biology. 12. 1399065. 10.3389/fcell.2024.1399065.
10. Tkachenko, Oksana & Polishchuk, Iryna & Gorchakova, Nadiya & Zaychenko, Hanna. (2020). Metabolic syndrome and lipid metabolism disorders: Molecular and biochemical aspects. Acta Facultatis Medicae Naissensis. 37. 5-22. 10.5937/afmnai2001005T.
11. Maurotti, Samantha & Geirola, Nadia & Frosina, Miriam & Mirarchi, Angela & Scionti, Francesca & Mare, Rosario & Montalcini, Tiziana & Pujia, Arturo & Tirinato, Luca. (2024). Exploring the impact of lipid droplets on the evolution and progress of hepatocarcinoma. Frontiers in cell and developmental biology. 12. 1404006. 10.3389/fcell.2024.1404006.
12. Yang, Yueyi & Wei, Jieya & Li, Jiachi & Cui, Yujia & Zhou, Xuedong & Xie, Jing. (2021). Lipid metabolism in cartilage and its diseases: a concise review of the research progress. Acta biochimica et biophysica Sinica. 53. 10.1093/abbs/gmab021.
13. Wu, Xinyue. (2024). Lipid metabolism and insulin sensitivity. Theoretical and Natural Science. 46. 23-29. 10.54254/2753-8818/46/20240400.
14. dos Santos, Diandra & Souza, Josiany & Pimenta, Tatiana & Martins, Bárbara & Junior, Roberto & Butzene, Solenny & Tessarolo, Nayara & Lyra, Paulo & Victor Silva, Ian & Rangel, Leticia. (2023). The impact of lipid metabolism on breast cancer: a review about its role in tumorigenesis and immune escape. Cell Communication and Signaling. 21. 10.1186/s12964-023-01178-1.
15. Ahmad, Yusra & Seo, Dong & Jang, Younghoon. (2024). Metabolic Effects of Ketogenic Diets: Exploring Whole-Body Metabolism in Connection with Adipose Tissue and Other Metabolic Organs. International Journal of Molecular Sciences. 25. 7076. 10.3390/ijms25137076.