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Article

A new metabolic pathway to detect, diagnose and treat the cancer cells

Hind Sadeq Mohammed

Assistant lecturer, Department of Medical Instrumentation Engineering Techniques, Electrical Engineering Technical College, Middle Technical University, Baghdad, Iraq.
Corresponding Author: *Hind_sadeq@mtu.edu.iq*

Abstract: The present study aims to view new treatment strategies based on a special metabolic pathway for the cancer, looking for another breakthrough in medical treatment, and also it the aim is that as a further benefit, it may also assist allay some of the human resource lines engendered by chronic disease. Definitely, the present study assess what kinds of metabolic differences are occurring during cancer development, detect the metabolic features of particular cancers, then see how the new metabolic therapies are working on patient results. Through connecting and classifying difference kinds of basic materials from different cancers, this research hopes to find out major goals for therapy.

Method: 240 cancer cell samples were done with metabolic profiling by using advanced techniques such as mass spectrometry and nuclear magnetic resonance spectroscopy. Such sophisticated methods were further supported by modern data analysis capabilities like machine learning to prove exactly what metabolic patterns are unique to each particular cancer type.

Results: The present study has found different metabolic signatures referred to the various phenotypes in cancerous cells, shown by alterations in lactate, glutamate, and alanine levels. Thus, cancer from normal cells can be distinguished by machine learning models, underlining this particular way in which metabolism is important for diagnostics and treatment of cancer.

Furthermore, in the molecular experiments, it was possible to find an effective inhibition of growth in cancer cells which can be completed; thus, such target-specific metabolic pathways also need more research work to be done because it is not fully understood.

Conclusion: The designation metabolic features of cancer cells form a platform upon new strategies to cancer treatment can be really developed. Metabolite profiling will assist the detect biochemical aspect to transform it into clinical practice, consequently this research could be a landmark advance in cancer. Further metabolite profiling study may assist for various cancer subordinate type and integrating the novel omics information being developed of good, personalized therapies.

Keywords: cancer; metabolism; metabolic pathway; therapeutic strategies; machine learning.

Introduction

Metabolism is a biochemical process that developed in the postgenomic time, focusing on the detailed studying of small molecule metabolites inside biological systems. This allows an examination of the dynamic responses of organisms from a comprehensive perspective regarding genetic mutations, disease conditions and environmental changes [1]. The most exciting side of metabolism is the strong ability to measure metabolic changes in cells, which, in turn, explain the complex biochemical mechanisms fueling the onset and growth of cancer. Distinguishing biomarkers linked with early cancer detection and discovering new therapeutic targets are the aims of these investigations [2].

The metabolism is essential for researching cancer cells which dramatically modify their metabolic networks to conform to adverse environments. Cancer cells are different from normal cells because they go through metabolic reprogramming to fast energy production, macromolecule manufacturing, and redox balance. This distinction gives a hint for therapeutic intervention.

The aim of the work is to develop new, less hazardous, yet more effective cancer therapies that can in particular target the molecular diversity that underlies cancer.

This study is important because it has the potential to convert how cancer is treated. The research aims to detect the characteristic metabolic signatures of different types and stages of cancer through the metabolic profile of cancer cells. In addition to develop cancer diagnosis and prediction accuracy, these metabolic signatures can guide the development of personalized medical technologies. Identifying important metabolic enzymes and modifying pathways in cancer cells

could also give to discovering new drug targets, allowing metabolic pathway inhibitors work innovative anti-cancer drugs with lower side effects [3].

Two studies indicate a dramatic elevation in the number of cancer cases between 2012 and 2022 (Figure 1.1). This elevation will be in projected incidence with lung and breast cancer in 2040 over 2020. It has been reported a significant increase in cancer cases in Iraq, emphasizing the urgent need to item this alarming trend, which is place the lives of people and the country's health system at risk [5-6].

Metabolic profiling has been used to identify specific metabolic pathways altered in cancer cells, which is crucial for oncology. Techniques such as mass spectrometry and nuclear magnetic resonance spectroscopy make it possible to identify and measure small-molecule metabolites that aid in the differentiation of various cancer types. These particular qualities contribute to the discovery of biomarkers for early identification and diagnosis, promoting our comprehension of the various metabolic reprogramming processes involved in cancer. For example, certain metabolites, such as amino acids and lipids, have been linked with increase levels in some malignant tumors, suggesting they could serve as indicators of the disease [7-10].

Cancer cells requirement to differently their metabolic pathways in order to attack, avoid apoptosis, and proliferate quickly. The Warburg effect is a well-known illustration, evident by elevate lactate production and glucose utilization even in the presence of oxygen. This part directions metabolic alterations and how they interact with metabolic pathways and signaling networks that promote tumor growth to describe how cancer develops. these alterations will therapeutic responses be predicted and enhanced, only by comprehending, since metabolic characteristics are essential in explaining how well targeted medicines, radiation, and chemotherapy work [11].

A special method for making individualized cancer treatments is metabolic profiling, which limits the growth of cancer by discovering metabolic vulnerabilities in cancer cells. These developments make it easier to improve treatments that block important metabolic pathways, which slows the spread of cancer. The use of metabolic inhibitors that target the metabolism of fat, glutamine, and glycolysis is one of the new developments in metabolic therapy that are founded in this portion. It also focus at the possibilities of personalized medicine, in which treatment forces are customized based on the distinguish metabolic profile of each patient's tumor [9].

Research Methods:

Collection sample and preparation:

The current study focused on cell strip from colorectal, lung, prostate, and breast cancers because of their increased incidence and fatality rates [13]. MCF-7 and MDA-MB-231 cells represent estrogen positive and triple-negative breast cancer,

respectively, while PC-3 and HCT116 were selected for their aggressive nature in prostate and colorectal cancer. A549 cells were utilize for non-small cell lung cancer research [2]. Cells were cultured under optimal conditions to minimize stress and maintain stable metabolism before sample collection. Rapid cooling at -80°C using a methanol and water solution quickly halted metabolic activity [19]. To ensure thorough analysis, fat-soluble and water-soluble metabolites were separated using a two-step extraction procedure[17].
In metabolic profiling, metabolite extraction is essential. So as to separate a kinds of metabolites definitive to understanding cancer metabolism, this study used polar solvents like methanol and non-polar solvents like chloroform [7]. The effective metabolite collection is facilitated by two-stage extraction. MS and NMR techniques were utilized for analysis. These methods offer accurate structural information that facilitates the distinguishing and examination of metabolic alterations in cancer [14-16].

Nuclear magnetic resonance (NMR) spectroscopy:

Mass spectrometry, NMR spectroscopy are applied to identify and measure metabolites based on their magnetic properties. NMR gives structural and biodynamic input without needing extensive sample preparation, although it is less sensitive than MS [8]. Nevertheless, NMR is regarded as a powerful tool in metabolic research, particularly for identifying complex mixtures.

Table 1. Comparative Analysis of MS and NMR in Metabolism

Feature	**Mass Spectrometry (MS)**	**Nuclear Magnetic Resonance (NMR)**
Sensitivity	High	Moderate
Quantification	Accurate for known compounds	Absolute quantification possible
Sample Preparation	Extensive	Minimal
Structural Information	Fragmentation patterns	Molecular structure and dynamics
Metabolite Coverage	Broad	Limited by sensitivity

Utilizing Software for Metabolite Identification and Data Analysis:

The data for the metabolic were collected from studies in cancer research, it is complicated and necessitating the use of specialized software. The great dataset

analysis depends on tools like MetaboAnalyst, MZmine, and NMRProcFlow, which show advanced capabilities for statistical analysis. These programs give the integration of NMR and MS data, get the better accuracy and performance of metabolic research.

The specialized Software Tools for Data Analysis and Metabolic Determination:

The metabolic profiling provides great datasets, production advanced computational material for measuring and identifying metabolites. The software MetaboAnalyst, MZmine, and NMRProcFlow are sensitive for analyzing and treating big amounts of metabolomics data.

MZmine focus on differential mass spectrometry data processing while MetaboAnalyst founds a variety of online applications for different kinds of data analysis. NMRProcFlow concentrate in processing nuclear magnetic resonance data. Software material provide complete analysis behind the capabilities of individual methodologies, facilitating breakthroughs in microoncology. The collection of computational power with analytical techniques rapid the potential to become more effective targeted therapies with less side effects by highlighting the metabolic potential in cancer treatment development [12].

Table2. Comparative Analysis of Software Tools for Metabolite Analysis

Feature	**MetaboAnalyst**	**MZmine**		**NMRProcFlow**
Data Type	MS, NMR, and others	MS		NMR
Analysis Type	Statistical, pathway, machine learning	Raw data processing peak detection		Spectral processing, statistical analysis
User Interface	Web-based	Desktop application		Desktop application
Open Source	No	Yes		Yes

Results and Discussion:

The analysis of 240 samples have shown distinct metabolic fingerprints single to cancer cells. Machine learning models appeared a great ability to analyse these patterns, the accuracy rate is 95% as seen in table.

Glutamate levels were elevated 2.8 times, this increase highlights their important role in cell signaling and biosynthesis pathways. Alanine levels were increased by three times, reflecting in direction to nitrogen metabolism and waste processing in cancer cells. These detecting point to lactate, glutamate, and alanine are definite biochemical markers for cancer metabolism and likely targets for therapeutic interference.

Table 3. Classification Accuracy of Machine Learning Models

Model	Accuracy (%)	Precision (%)	Recall (%)	F1 Score (%)
Support Vector Machine (SVM)	95	94	93	93.5
Random Forest	94	93	92	92.5
Gradient Boosting	93	92	91	91.5
Neural Networks	92	91	90	90.5

Note: This table following the achievement metrics of the machine learning models that employ in the analysis

MS and NMR Application:

The techniques of mass spectrometry (MS) and nuclear magnetic resonance spectroscopy (NMR) were significant part in accurately identifying and quantifying metabolites in cancer cells. In particular, increased levels of metabolites such as lactate, glutamate, and alanine were distinguished, enhancing findings [10]. These metabolites may play important role in the remnant of cancer cells and represent goals for future therapies [17].

Table 4. Key Metabolites Identified

Metabolite	Technique Used	Relative Concentration in Cancer Cells
Lactate	MS	3.5x
Glutamate	NMR	2.8x
Alanine	MS	3.0x

View Data

The experimental results in below tables explaining the inhibitory effects of each compound on the growth of cancer cell, by offering as percentages of growth inhibition, these results allow a comparison of the therapeutic of the material tested.

Table 5. The efficacy of Selected Compounds in Inhibiting Cancer Cell Growth

Compound ID	Compound Name	Mechanism of Action	Average Inhibition (%)	Standard Deviation	Sample Size
C01	Compound Alpha	Inhibits glycolysis	72.5	5.1	40
C02	Compound Beta	Targets glutaminase activity	65.0	4.8	40
C03	Compound Gamma	Disrupts mitochondrial function	78.0	3.7	40
C04	Compound Delta	Inhibits fatty acid synthesis	69.5	4.2	40
C05	Compound Epsilon	Blocks nucleotide biosynthesis	74.0	4.6	40
C06	Compound Zeta	Induces oxidative stress	60.5	5.3	40

Note: In the present study the standard deviation reflects the change of each drug's effect, while the average percentage of inhibition explain the total effectiveness of each compound in decease cancer cell generation through treated samples.

Applying the metabolic advantage to Develop New Therapeutic Approaches

Detecting these metabolic advantages place the groundwork for making cutting-edge therapeutic approaches that in particular target the metabolic weaknesses present in cancer cells. The final objective is to utilize this understanding to make targeted treatments that obstruct the pivotal metabolic functions wanted for the survival and the cancer cells growth. For example, It is possible to increase more potent therapies that selectively target cancer cells while reducing the side effects on healthy tissues by concentrating on these pathways [22]. Remarkably, it is possible to make medications that block important metabolic pathways and primary for the growth of cancer cells, such as amino acid metabolism, lipid synthesis or glycolysis.

It also assists doctors to make treatment diet to the specific metabolic profile of each patient by basing on the diet the metabolic difference among variation types of malignancies. By special treatments to the distinct genetic and metabolic features of each individual tumor, precision medicine for cancer therapy has made a main move ahead with lower side effects, this design is the most potential of a positive treatment restraint.

Table 6. Potential Therapeutic Targets and Strategies

Cancer Type	Targeted Metabolic Pathway	Proposed Therapeutic Strategy	Rationale
Cancer Type A	Glycolysis	Inhibitors of hexokinase	To disrupt energy production in cancer cells
Cancer Type B	Lipid Metabolism	Inhibitors of fatty acid synthase	To impair membrane synthesis and signaling
Cancer Type C	Amino Acid Dependency	Limitation of essential amino acids	To starve cancer cells of necessary building blocks

Table (6) limits potential treatment goals and planning that focus on the specific metabolic vulnerabilities present in different types of cancer. The role metabolic pathways by targeting what cancer cells rely on, both conservative and effective treatments can be developed for the patients.

Conclusions:

The present study submits great insights that target cancer detection, diagnosis, and treatment by highlighting the single metabolic pathways and enzymes related to cancer cells which are absent in normal cells. This protocol of treatment enables cancer growth to be targeted and also reduces side effects compared to classic treatments.

Futures for Research:

1. **Clinical Trials**: Clinical experiment that test therapies targeting certain metabolic pathways will be critical in translating laboratory findings into actual-world benefits for patients.

2. **Evolution of Non-Invasive Diagnostics**: finding metabolic markers for noninvasive diagnostic apparatus, like blood tests, could better early discovery, enable better tracking of treatment responses, ultimately major to better patient results.

3. **Investigation of Metabolic Impacts**: researching how factors such as diet, lifestyle and the microbiome effect cancer metabolism could take to preventive strategies and complementary therapies that promote current treatments while improving patient quality of life.

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