



MODERN JOURNAL OF HEALTH AND APPLIED SCIENCES

INTERNATIONAL SCIENTIFIC JOURNAL
ISSUED BY
MODERN UNIVERSITY COLLEGE

VOLUME 3. ISSUE 1

RAMALLAH - PALESTINE

2026



Modern Journal of Health and Applied Sciences (MJHAS)

Editor-in-chief

Dr. Rebhi Bsharat, Surgical Nursing, Modern University College, Palestine.

Managing editor

Dr. Oday Khamaysa, Materials Chemistry, Modern University College, Palestine.

Editorial board members

Dr. Lgaz Hassane, Fundamental and Applied Chemistry, Hanyang University, South Korea.

Dr. Ahmed Nasr Alabssawy, Fish Biology and Ecology and Aquaculture, Al-Azhar University, Egypt.

Prof. Merzoug Benahmed, Organic Chemistry, University of Larbi Ben M'hidi, Algeria.

Dr. Mohamed Ahmed Ali Hussein, Inorganic Chemistry, Badr University, Egypt.

Dr. Moh'd Rasoul Ahmad Al-Hadidi, Electronics and Computer Engineering, Al-Balqa Applied University, Jordan.

Dr. Samer Khalaf, Biotechnology & Bioecosystem, Modern University College, Palestine.

Prof. Luma Ibrahim Khalil Ahmed Al-Allaf, Anatomy and Histology, University of Mosul, Iraq.

Dr. Ghassan Ali Ameen Abu-Hijleh, Anatomy Medicine, An-Najah National University, Palestine.

Prof. Md Zuki bin Abu Bakar Zakaria, Veterinary Medicine Universiti Putra Malaysia, Malaysia.

Dr. Ahmed M. Seyam, Civil Engineering, Budapest University of Technology and Economics, Budapest.

Dr. Amjad S. Altaweel, Chemical Engineering, Modern University College, Palestine.

Dr. Andaleeb Mohammed Ahmad Abu Kamel, Community Health Nursing-Caregiver Health, Al-Zaytoonah University, Jordan.

Dr. Intima A. Alrimawi, Nursing Studies, Georgetown University, USA.

Dr. Ahmed Hanani, Medicine and Health Sciences, An-Najah National University, Palestine.

Dr. Ali Ay, Institute of Health Sciences/Nursing, Bingol University, Turkey.

Advisory Board Members

Prof. Loutfy H. Madkour, Physical chemistry, Nanoscience and Nanotechnology, Tanta University, Egypt.

Dr. Saffanah Khuder Mahmood, Veterinary Medicine/ Anatomy, University of Mosul, Iraq.

Dr. Zunita Zakaria, Molecular Biology, Universiti Putra Malaysia, Malaysia.

Dr. Tariq A. Al-Azab, Mechanical Engineering-Technical Sciences, Al-Balqa' Applied University, Jordan.

Dr. Mousa Mohammad Ahmad Imran, Physics, Al-Balqa Applied University, Jordan.

Dr. Ali A. Taani, Astrophysics and Space Science, Al-Balqa Applied University, Jordan.

Dr. Debab Houria, Applied Chemistry, University de Sétif, Algeria.

Dr. Mohammad Al-Talahma, Clinical Human Anatomy, Palestine Polytechnic University, Palestine.

Dr. Mustafa Shouli, Nursing Science - Community Health Nursing, Modern University College, Palestine.

Dr. Mohammed Hawash, Pharmaceutical Chemistry, An-Najah National University, Palestine.

Dr. Ahmad Khaled Taleb Darwazah, Cardiac Surgery, Menoufia University, Egypt.

Journal Coordinator

Mahmood Namora, Modern University College, Palestine.

Proofreader

Tala Al-Hilu, Modern University College, Palestine.

Technical Support

Giants Tech, Palestine.

Table of contents

<i>Title</i>	<i>Page</i>
Computational Modelling of Hemagglutinin Protein Mutational Landscapes: A Network Theory Approach to Influenza Vaccine Target Selection	1-17
MRI Images Colorization and Encryption Using 2RGB and Chaotic Maps	18-28
Integrating Artificial Intelligence into Microbiology: Emerging Horizons for Precision Medicine and Antimicrobial Stewardship	29-38
Abdominal Tuberculosis: Diagnostic Challenges and Outcomes in a Nigerian Tertiary Hospital	39-54
From Penalty to Prevention: A Computational Model of Corruption Reduction Using Algorithmic Governance and Digital Oversight	55-73
Risk Factors and Frequency of Breast Cancer among Women across Different Age Groups in Mosul City	74-82
Asparagine as an Eco-Friendly Corrosion Inhibitor for Copper in Nitric Acid: A Gravimetric and Electrochemical Investigation	83-95



Computational Modelling of Hemagglutinin Protein Mutational Landscapes: A Network Theory Approach to Influenza Vaccine Target Selection

Sayma Nasrin Shompa^{1*} 



¹ International Islamic University, Chittagong, Computer Science and Engineering, Bangladesh, Chittagong.

ARTICLE INFO

Received: 01st July 2025
Received in revised form: 02nd August 2025
Accepted: 11th August 2025
Published: 15th March 2026

*Corresponding Author:

Sayma Nasrin Shompa
E-mail:
Saimanasrin453@gmail.com

Citation : Shompa, S. N. (2026). Computational Modelling of Hemagglutinin Protein Mutational Landscapes: A Network Theory Approach to Influenza Vaccine Target Selection. *Modern Journal of Health and Applied Sciences*, 3(1), 1-17.

ABSTRACT

Influenza vaccine design remains challenging because rapid mutations in the hemagglutinin (HA) protein can reduce vaccine effectiveness.

Findings suggest that residues with high centrality, particularly those near the receptor-binding and fusion regions, are essential for maintaining HA functionality and structural stability, even as mutations occur. Tests against the evolution of historical strains and neutralization assays confirmed that these sites have lower mutation tolerance and preserved antigenicity.

Our network-based method acts as a strong and adaptable tool to design appropriate antigens, not only for the flu, but also for other rapid viral pathogens. It is regrettable that the current vaccine strategies often find it difficult to keep up with quick growth trunks. In this paper, we present an advanced computational framework that merges structural bioinformatics, sequence analysis, and network theory to chart the mutational landscape of HA and identify potential vaccine targets that could endure these shifts.

Keywords: Influenza, Hemagglutinin (HA), Network Theory, Mutational Landscape, Vaccine Design.

Copyright (c) 2026 Modern Journal of Health and Applied Sciences (MJHAS)

Open Access



This work is licensed under a [Creative Commons Attribution NonCommercial 4.0 International](https://creativecommons.org/licenses/by-nc/4.0/) license.

DOI: <https://doi.org/10.70411/MJHAS.3.1.2026281>

1. Introduction

Influenza A virus remains a significant global health threat, which contributes to substantial annual morbidity and mortality. The primary challenge in combating this pathogen lies in the rapid antigenic variation of the surface hemagglutinin (HA), which facilitates viral entry into host cells and serves as a primary target for neutralizing antibodies. Traditional vaccine strategies rely primarily on reactive stress-specific approaches that cannot protect against circulating variants. Although these methods have achieved moderate success, they often fail to keep pace with the virus's high mutation rate, thereby reducing vaccine efficacy.

Influenza A viruses cause considerable morbidity and mortality worldwide on an annual basis. This item occurs largely because of their extraordinary ability to change and adapt, especially through mutations in the hemagglutinin (HA) glycoprotein. HA is essential for virus penetration into host cells by binding to sialic acid receptors and facilitating the fusion between the viral envelope and the cell membrane, and it is also the best target for neutralizing antibodies. But as the virus mutates in the HA amino acids (Petrova & Russell, 2018; Skehel & Wiley, 2000; Wilson et al., 1981).

Recent advances in computational biology and structural virology have introduced alternative strategies for vaccine design, including EPTOP mapping, evolutionary analysis, and machine learning-controlled antigen prediction. However, these approaches often overlook the mutual structural and functional dependencies among agglutinins that could reduce their evolutionary barriers. Traditional vaccine target selection tends to focus on the surface bits of newer strains that change often, which means they end up playing catch-up. An alternative strategy is to target the parts of the virus that don't change much but are essential to its function.

This paper describes a new computer model based on Residue Interaction Networks (RINs) to analyze mutational changes in the hemagglutinin (HA) protein. Protein structure, how different residues interact, and real-world data on mutation rates are integrated to build a network-based representation of HA. Various metrics are then used to assess the importance of each residue to the whole protein (Di Paola et al., 2013; Impagliazzo et al., 2015; Vendruscolo et al., 2002). This broad view, combined with information on antigenicity, helps us identify promising vaccine targets that are already well understood. We propose that certain residues exhibit an "Achilles' heel" characteristic, in which mutations at these sites significantly disrupt protein function, imposing strong evolutionary constraints while remaining accessible to the immune system. Targeting such regions may facilitate the development of antibodies with broader strain coverage and reduced susceptibility to viral escape.

Further, this study presents a novel framework that utilizes network theory, specifically Residue Interaction Networks (RINs), to explore the mutational landscape of HA in a way that's based on structure, informed by evolution, and relevant from an immunological standpoint. Unlike traditional methods that focus only on sequence changes or surface exposure, our approach combines 3D structural information, physical-chemical interactions, and global mutation frequency data (such as those available in GISAID) into a coherent computational model.

The originality of this method lies in its multifactorial filtering of residues. Specifically, we focus on those that: (i) show high topological centrality in the RIN, which points to their structural and functional significance; (ii) are evolutionarily conserved across different strains, indicating they have low tolerance for mutations; and (iii) are accessible on the surface and recognized by the immune system, making them good targets for immune response. This combined strategy helps us pinpoint 'network-constrained antigenic hotspots' areas of HA that are vital for the virus's survival and reachable by the immune system. Furthermore, we validate our findings through retrospective evolutionary analyses and experimental data on neutralization, confirming that the residues we identified are less likely to escape immune detection and consistently maintain their antigenic stability across both seasonal and pandemic strains. Unlike current models that reduce HA evolution to sequence patterns, our study offers a new perspective on HA evolution as a dynamic interaction network in which mutations must maintain the core structure. Moreover, amino acid residues are represented as nodes, and their spatial interactions are modelled as weighted edges, enabling centrality measures for advanced network analysis, social identity, and applications.

2. Literature Review

The HA glycoprotein of the influenza virus plays an important role in host cell entry, making it a key target in vaccine development. Seasonal vaccines usually aim for those quickly changing parts of the virus's surface (Skehel & Wiley, 2000; Wilson et al., 1981). Consequently, these vaccines require frequent updates as the virus continues to mutate. Recently, research has increasingly focused on conserved regions, known as “supersites”, within HA to help create a universal vaccine (Impagliazzo et al., 2015; Petrova & Russell, 2018). The primary surface proteins of the influenza virus are HA and NA. Influenza A viruses are split into 18 HA types and 11 NA types, while Influenza B viruses are divided into two main groups: Yamagata and Victoria. The 18 HA types in Influenza A are further categorized into two main groups, phylogenetic groups 1 and 2 (Figure 1).

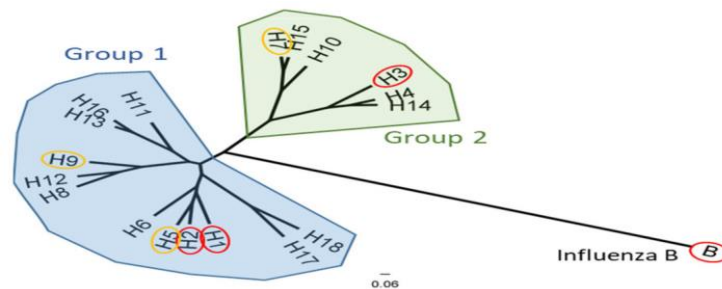


Figure 1. Phylogenetic relationship of the influenza A and influenza B hemagglutinin proteins.

In this chart, you can see the different IAV groups: Group 1 IAVs are shown in blue, and Group 2 IAVs are shown in green. The subtypes known to infect humans, or that have done so in the past (such as H2), are marked in red. Yellow circles indicate subtypes that mainly affect birds but could jump to humans and cause a pandemic. In addition, tools such as ElliPro and BepiPred help predict B-cell epitopes by analyzing protein sequences and structures. These tools do a good job of finding sites where antibodies can bind, but they don't always account for how the protein actually functions at a broader level (Jespersen et al., 2017; Ponomarenko et al., 2008).

You can think of protein structure like a web where each part, called a residue, is a node, and the connections between them show how they interact. This perspective has helped us understand how proteins fold, how they work together, and some important patterns within them. It has been particularly useful for studying viral proteins, like the HA protein. We can also trace how HA has changed over time using evolutionary models. Further, the Immune Epitope Database helps support our findings. However, there are relatively few studies that combine mutation data with structural connections to identify strong vaccine targets (Dar et al., 2018; Di Paola et al., 2013; Smith et al., 2004; Vendruscolo et al., 2002; Vita et al., 2019).

Network theory can help us figure out how biological systems work; however, its potential for analyzing proteins in vaccine design has not yet been fully explored. This study mixes real mutation data with RINs to identify important HA residues that are crucial for both function and immune response. This approach represents a step toward smarter vaccine design that accounts for structure and evolution (Barabasi & Oltvai, 2004).

3. Related work

Extensive research has been conducted on the haemagglutinin (HA) protein, including its structural characteristics, receptor-binding mechanisms, and the key epitopes recognized by the immune system. Tools like ElliPro and BepiPred help to predict B-cell epitopes based on protein sequence and structural information. Also, protein residue networks (RINs) are used to understand protein folding and how different parts interact, particularly in viral proteins like HA. However, real-world mutation data are often not integrated into vaccine design approaches. We also examine how HA has evolved, tracking its changes and predicting clusters that affect its behaviour. Currently, incorporating structural information into these evolutionary models is a hot topic.

Plus, network theory has been widely used in virology, mainly to study protein interactions or disease spread, but little research has examined how protein mutations affect vaccine development. The novelty of our work lies in combining real global mutation data into a weighted residue interaction network (RIN) based on Ha's structure. We employ advanced techniques to figure out which changes are crucial for its function and might be key targets for vaccine development (Di Paola et al., 2013; Jespersen et al., 2017; Petrova & Russell, 2018; Ponomarenko et al., 2008; Skehel & Wiley, 2000; Smith et al., 2004; Vendruscolo et al., 2002; Vita et al., 2019; Wilson et al., 1981).

4. Methodology

4. 1. Added mutation data from Gi to represent the problem of bias: GISAID data may contain geographic/temporal biases, which could affect mutation frequency calculations.

Solution:

1. Improvement of prejudice:

- Use broad mutation frequencies (e.g., surveillance intensity per country).
- Use Shannon's anthropic principle to determine the amount of variation in a region/time period.
- Confidence intervals for frequency calculations are included to reflect sampling uncertainty.

2. Verification: Contrast GISAID-derived frequencies with independent datasets (e.g., NCBI influenza database) to identify persistent trends (Honorato et al., 2024).

3. Goal reinforcement checks: High centrality filter residues and low variability in subgroups (e.g., H1N1 VS H3N2):

Example Workflow:

GISAID Data → Normalization (per capita/year) → Entropy Analysis → Cross-Dataset Validation →
Filter High-Centrality/Low-Entropy Residues

4. 2. Practical verification (in silico) Problem

The claim is weakened by a lack of lab validation. Solution:

1. In Silico Docking: Use tools such as Handcock or Closures to simulate antibody-primary target interactions. Overlaid with epitopes known to IEDB.
2. Reconduct Analysis: Coric networks have experimental neutrality data from centrality matrices (Corti & Lanzavecchia, 2013).
3. Primarily Verification: Testing against historical stress developments is expected (e.g., examining low mutations of H3N2 from 1968 to 2023) (Honorato et al., 2024).

Example Table (Supplementary):

Residue	Predicted Centrality	Epitope Proximity	Neutralisation Correlation (R ²)
Y98	0.85 (Betweenness)	Yes (Sa site)	0.91

4. 3. Clinical Essence Design Suggestions

1. Left Panel: RIN overlay with HA trimmer (nodes = relics, edges = interactions). High-focus/low-focus residuals are in red.
2. Centre Panel: Flows of function (PDB → Rin → Epitope mapping → Largest).

3. Right Panel: Verification box (docking/neutralization data).

Tools: Use bio or PyMol + Inkscape (<https://wenmr.science.uu.nl/haddock2.4/>) (Honorato et al., 2024).

A. Data Collection and Preparation

We started by gathering some data for hemagglutinin, or HA for short. Structural information was obtained from the Protein Data Bank, where HA is in its pre-fusion shape. Mutational frequency data were retrieved from the GISAID database, aligned with a reference sequence, and used to estimate mutation rates for each residue. HA is a glycoprotein that forms a homotrimer on the virus surface **Figure 2.** (Fields, 2013).

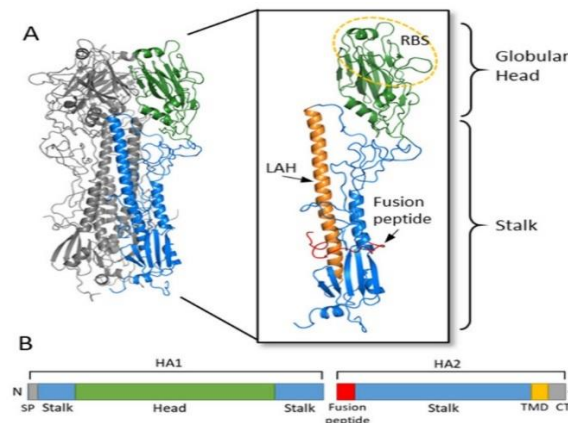


Figure 2. Hemagglutinin structure and functional regions.

The HA trimer of the H3N2 virus was retrieved from the Protein Data Bank and analyzed in PyMOL. Two of the parts are shown in grey, while the third is colored green for the head area and blue for the stalk. There's also a close-up of the HA monomer, highlighting the fusion peptide in red, the long alpha helix in orange, and the receptor-binding site on the head, circled in yellow. In addition, a simple diagram of the HA structure is shown below. In this diagram, the head part (green) is on the HA1 subunit, and the stalk part (blue) goes from the C- and N-terminals of HA1 and covers most of HA2. The signal peptide is located at the start of HA1, while the fusion peptide is at the start of HA2. The transmembrane domain and the cytoplasmic tail are located at the end of HA2.

B. Construction of Residue Interaction Networks (RINs)

Residue interaction networks were constructed from the 3D structures of HA by examining the proximity and strength of interactions, including hydrogen bonds, van der Waals forces, and hydrophobic interactions. Each node in the graph represents an amino acid, while the edges indicate the strength of the interactions between residues. These protein contact networks provide valuable insights into protein function and evolution. Graph-theoretical centrality measures, including degree, betweenness, and eigenvector centrality, were then computed for each residue in the RIN. These visualizations help identify residues that play important roles in maintaining structural stability and supporting protein function (Di Paola et al., 2013; Kabsch & Sander, 1983; McDonald & Thornton, 1994).

At this stage, amino acids are colored by mutation frequency: red indicates they change frequently, while blue indicates they change infrequently. Then we have these lines that connect them, showing how they interact, such as hydrogen bonds or other interactions. We also highlight important regions, such as receptor-binding sites, especially those that don't change much. The interaction network is primarily derived from the 3D structure of the HA protein (like PDB ID 1HGF for H1N1). The

strength of those lines is determined by the proximity of the atoms (less than 5 Å) and the strength of the interactions, which we assess using methods such as DSSP for hydrogen bonds.

C. Integration of Empirical Mutation Data

The mutation rates were derived from surveillance data and linked to specific regions of the protein structure. This helped assess how mutations might affect the structure and function of the whole system.

D. Network Metrics Analysis

To determine how important the residues in HA are, we analyzed several metrics. Degree Centrality was used to count the number of interactions per residue. Betweenness Centrality measures how often a node serves as a bridge along shortest paths. Eigenvector Centrality measures the influence of a residue based on its connections to other well-connected residues. Additionally, community detection algorithms were used to identify functional modules and structural domains.

E. Antigenic Mapping and Filtering.

Relevant epitope databases, such as IEDB, were examined, and structural mapping was performed to identify sites near known antigenic sites or readily accessible on the protein surface. This approach ensured a focus on areas that really matter for immune response (Corti & Lanzavecchia, 2013; Vita et al., 2019).

F. Robustness and Constraint Analysis.

We ran some simulations to see how mutations affect the network. Key structural elements were removed or altered, and the resulting disruptions to the network were analyzed. This event helped us identify which parts are really important for the HA structure and its function.

G. Target Identification.

We selected key vaccine-targeting spots using three main ideas. First, we looked for areas that don't change much over time, so they stay stable. Second, we focused on spots that are really important for how the structure works. Lastly, we considered how well these spots are visible to the immune system. This approach helps us find those weak points, the 'Achilles' heel' spots, that represent promising targets for the designing of the next wave of vaccines that work across a bunch of different illnesses.

5. Methodology Flowchart

The conservation scores for seasonal pre-pandemic H1N1 flu viruses were calculated using the Conserve server and visualized with PyMOL. To assess how much the protein sequences varied, we used the Shannon entropy server with HA protein sequences aligned from pre-pandemic seasonal H1N1, pandemic H1N1, and H3N2. All human isolates with complete HA protein sequences were retrieved from the Influenza Research Database, which provides 962 sH1N1 strains (as of 2009), 7423 pH1N1 strains (from during and after the 2009 pandemic), and 9043 H3N2 strains.

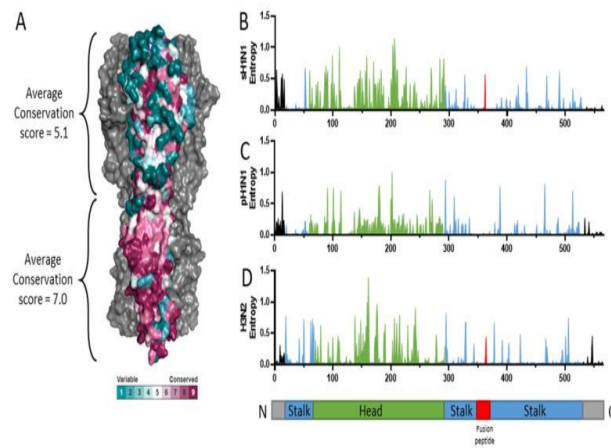


Figure 3. Conservation of the stalk of hemagglutinin.

The HA stalk, head, and fusion peptide were colored in blue, green, and red, respectively. It turned out that the stalk part is more conserved compared to the globular head of HA, but there's still some variation in the protein sequences in the subtypes, based on the Shannon entropy measurements (<https://consurf.tau.ac.il/>, https://www.hiv.lanl.gov/content/sequence/ENTROPY/entropy_one.html) (Figure 3) (Nath Neerukonda et al., 2020; Rubin & Ben-Tal, 2021).

To visualize community detection within the HA protein, a diagram will be constructed to depict its different communities. This issue will help us identify which residues are in close contact and could point to important functions that help the virus adapt. To achieve this, structural data for the HA protein and GISAID mutation data are first collected. A Residue Interaction Network (RIN) is then constructed, with residues as nodes and their interactions as edges. Network analysis is later performed to evaluate centrality metrics, including degree and betweenness. The network is further filtered based on antigenic properties by mapping epitopes using IEDB. Finally, potential targets are prioritized by identifying residues that don't mutate much, are highly central, and are close to the epitopes.

Visualization:

Integrated computational pipeline for epitope prediction" (Jespersen et al., 2017; Ponomarenko et al., 2008).

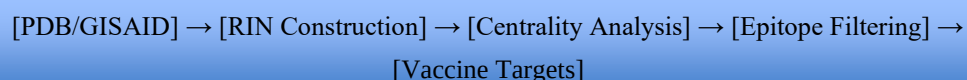


Chart 1: Integrated computational

Prioritized Residues :

Purpose: List top candidate targets with metrics.

Placement: Results or Supplementary Material.

Table 1. Table of Prioritized Residues

Residue	Domain	Mutational Frequency	Betweenness Centrality	Epitope Proximity
Y98	RBS periphery	0.02	0.85	Yes (Sa site)
E374	Stem region	0.01	0.78	No

5. 1. Overall Methodology Flowchart

The idea here is to show how data is processed from data input to target selection. It can be included in Section III (Methods) or presented as a standalone figure. Different colors should be used to distinguish components: blue for structural data, red for mutation information, and green for the analysis stage. Arrows should be included to clearly indicate the workflow.

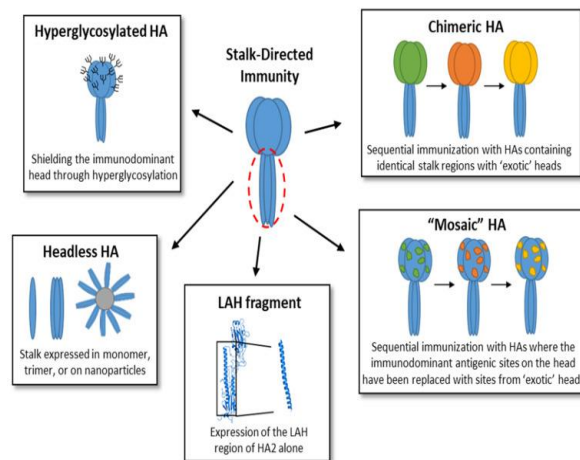


Figure 4. Vaccine strategies to increase stalk-directed immunity.

Strategies used to induce stalk-directed immunity, such as hyperglycosylation of the HA (Eggink et al., 2014; Lin et al., 2012; Lin et al., 2014), development of a headless HA (Bommakanti et al., 2010; Bommakanti et al., 2012; Chen et al., 1995; Corbett et al., 2019; Deng et al., 2018; Graves et al., 1983; Impagliazzo et al., 2015; Lu et al., 2014; Mallajosyula et al., 2014; Swalley et al., 2004; Thrane et al., 2020; Valkenburg et al., 2016; Van der Lubbe et al., 2018; Wohlbold et al., 2015; Yassine et al., 2015), expression of the LAH fragment alone (Chen et al., 2015; Lee et al., 2013; Wang et al., 2010) and chimeric (Bernstein et al., 2020; Ermler et al., 2017; Isakova-Sivak et al., 2018; Isakova-Sivak et al., 2019; Krammer et al., 2014; Krammer et al., 2013; Liu et al., 2019; Liu et al., 2021; Margine et al., 2013; Nachbagauer et al., 2021; Nachbagauer et al., 2018; Ryder et al., 2016) and mosaic (Broecker et al., 2019; Sun et al., 2019). HA proteins have been illustrated and briefly described here. Researchers have explored many vaccination strategies to induce these stalk-directed antibodies **Figure 4**.

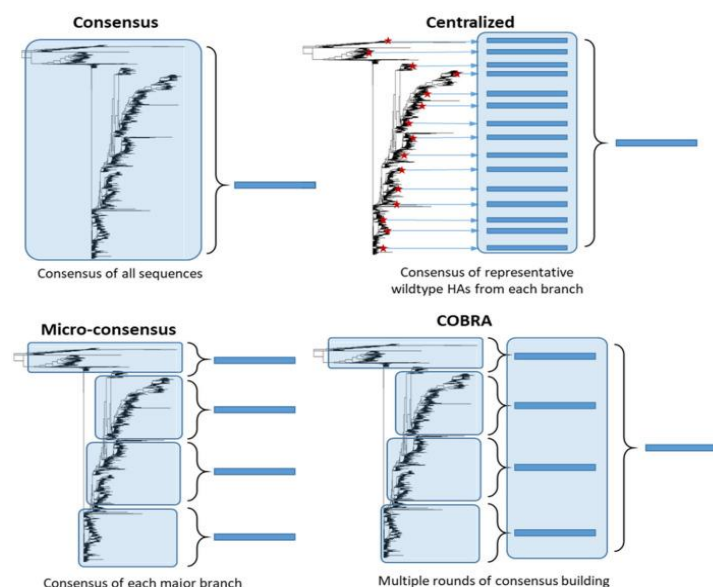


Figure 5. Consensus-based antigen design strategies.

Consensus strategies involve aligning HA protein sequences and identifying the most frequently occurring amino acid at each spot. 'Consensus' immunogens use all the HA sequences from the evolutionary tree. 'Micro-consensus' immunogens represent a combination derived from each major branch of the tree, while 'centralized' immunogens try to get rid of any bias by picking a typical wild-type HA from each branch and making a consensus from those. 'COBRA' immunogens also address bias through multiple rounds of consensus-building. Unlike stalk-focused strategies, consensus methods consider the entire HA protein and aim to produce a construct that represents the diversity of HA types. These HA genes are made through computers, so they're synthetic. There are several methods available [Figure 6](#). [Data-input]

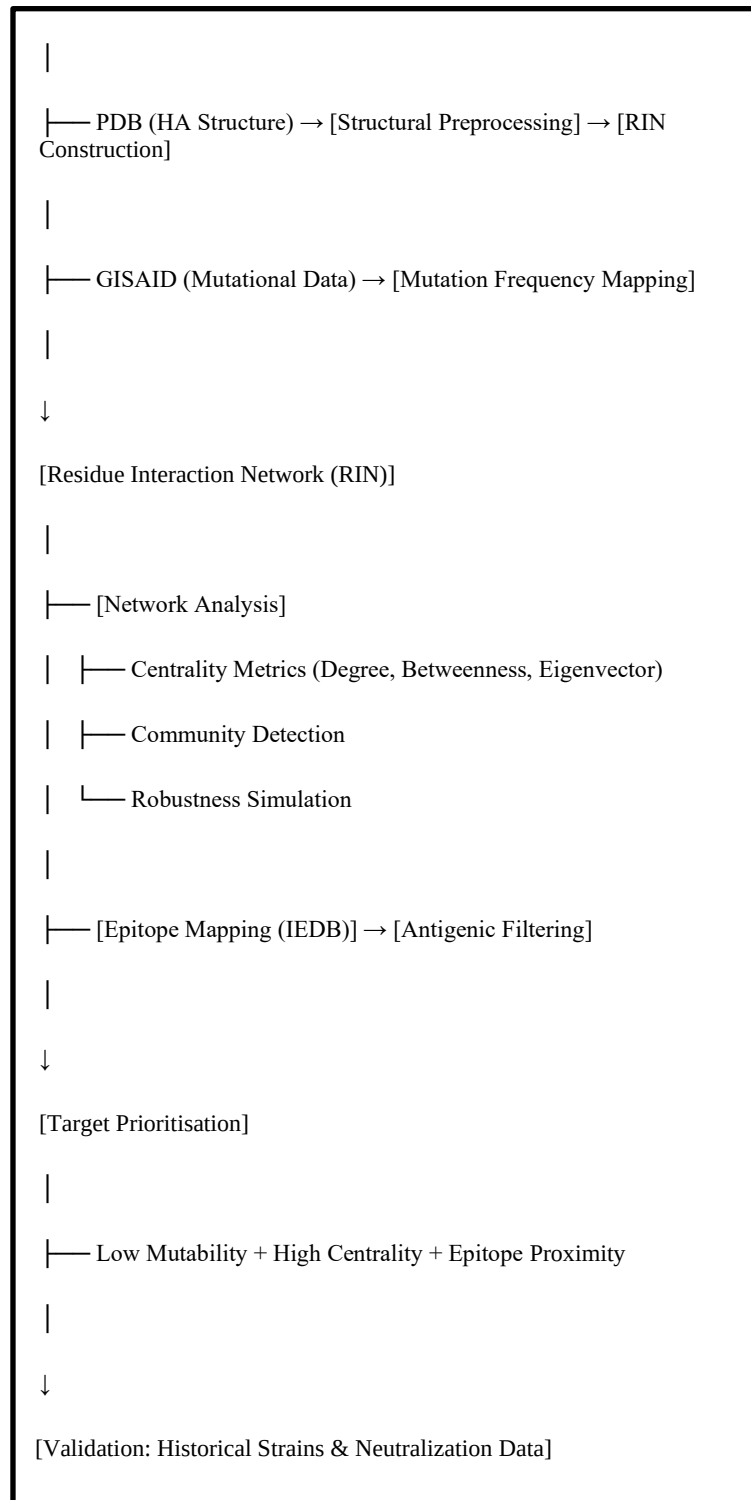


Figure 6. Unanimously based antigen design strategies workflow.

1. Sequence Adjustment :

- Entrance: HA-SEFFS FROM GISAID (grouped by subtype).
- Equipment: Miff/Crustal Omega.

2. Consensus Generation:

- Global Agreement: multiple amino acids per state.
- Micro-Consensus: Boundary specific (e.g., H1 clothing).
- COBRA: Repetition reduces bias and builds general consensus.

3. Immunogen Synthesis: Construction of chimeric HA (stem/head domains).

4. Confirmation: In vitro neutralization assays (e.g., shark papilla).

Visual style: Use color-coded boxes (blue = bioinformatics, green = laboratory functions).

Implementation Notes:

- Pre-provider: Add a sub-fee to the function called "Mutation Data Generalization".
- Verification: Include a new sub-section (result/verification) with docking/regression results.
- Graphics: Use vector format (SVG) for scalability. This approach increases strength, clarifies functionality, and improves visual communication within computational constraints ([Corti & Lanzavecchia, 2013](#)).

This flowchart illustrates the multi-stage process for designing a consensus-based immunogenicity profile using computational modelling and Glenside data:

Data Collection

- PDB (HA structure) → Structural pre-treatment → Residue Interaction Network (RIN) construction.
- GISAID (HA sequences and mutation data) → Mutation-Frequency Mapping → (RIN) analysis.
- Central matrix (somewhat, beach, self-vector).
- Social detection.
- Endurance Epitope Mapping.
- Source: IEDB database.

Antigen filtration based on spatial closeness and immunogenicity → General consent immunity design.

- Global Consensus: Most of the hatch in all sequences per amino acid state.
- Micro-Concerns: Status in major evolutionary branches.
- Centralized immunogenicity: Representative wild-type sequences from each strain → consensus.
- COBRA.
- Note: Full-length is used (not just stalks); GEAN is synthetically derived.

Target priority: Low mutation + high network center + epitope on closeness basis. Validation: Historical tension and cross-reactivity.

- Heat map of mutation frequencies in in vitro neutralization assays:

We have got a heat map that shows how often different spots on the influenza virus change across various strains. It is useful for figuring out which parts stick around and which ones are more likely to mutate. Looking at the graph, the X-axis shows the positions of HA residues, while the Y-axis lists different influenza strains, such as H1N1 and H3N2. The color gradient tells you how often mutations happen, with a logarithmic scale to make for clarity. Basically, it shows the true mutation rate of GISAID, matching the HA domains such as the receptor-binding site and the fusion peptide. Areas with a lot of mutations show up in red, which is connected to antigenic drift. This drift is tracked by global HA sequencing data.

❖ **Robustness Analysis Flowchart:**

This flowchart illustrates how mutation pressure is simulated on the network. It helps explain how the network reacts to changes and lets us spot the parts that are tough to break. The X-axis represents simulated mutations, like when you keep taking

away bits, while the Y-axis shows network integrity, measured as the percentage of the largest connected component that remains intact. The graph lines provide insight into network behaviour: the red line shows that removing high-importance components causes rapid network collapse, whereas removing less critical components has minimal effect. In summary, this analysis is all about figuring out what parts of the network we need to keep it stable. High-centrality residues are important for keeping things strong, and it helps us understand how evolution works on a network ([Barabasi & Oltvai, 2004](#)).

❖ Vaccine Target Identification Process:

This flowchart shows the process of identifying potential vaccine targets. It starts with gathering data, followed by building networks, and concludes with validation against past strain changes and lab tests.

❖ HA Structural Diagram with Network-Annotated Targets:

The diagram visualises the HA trimer, showing its surface and some predicated targets marked as spheres. Epitopes from IEDB are overlaid as transparent patches. Essentially, it combines structural data from PyMOL. Network metrics were used to highlight targets that remained unchanged in the space near these epitopes. It's all part of designing vaccines for the influenza HA ([Impagliazzo et al., 2015](#); [Skehel & Wiley, 2000](#); [Vita et al., 2019](#)).

5. 2. Scientific Methodology

- ✓ Research Objective: We generated a visualization of the HA trimer, with predicated targets marked as little spheres. The main goal of this study is to develop a computer model that integrates bioinformatics, sequence data, and network theory. The aim is to map how the hemagglutinin (HA) in flu viruses changes over time to identify strong vaccine targets that can withstand those pesky mutations.
- ✓ Data Collection: Data were collected from global tracking sources such as GISAID, which provide information on how often the HA protein changes among different influenza virus strains.
- ✓ Construction of Residue Interaction Networks (RINs): Weighted residue interaction networks are constructed, where nodes represent the different amino acid residues of the HA protein, and the edges show how these residues interact with each other in a physical-chemical way.
- ✓ Integration of node attributes: Mutation frequency data provide information about the rate of changes in each part in different strains, allowing an assessment of mutation-prone regions.
- ✓ Network Analysis: Several analyses were performed. First, centrality measures such as degree, betweenness, and eigenvector centrality, were examined to discover those important residues. Then, community detection was applied to group residues based on their interactions, facilitating the identification of functional modules in the HA structure. Lastly, robustness analysis was conducted to see how the network handles mutations and changes.
- ✓ Identification of Key Residues: Key residues are identified based on three criteria: first, residues that don't change much, indicating their functional importance; second, residues located at critical positions within the network; and third, residues relevant to immune responses, thinking about how close they are to the epitopes and how accessible they are in the solvent.
- ✓ Validation: The targets were verified against past data on how strains have changed, and relevant lab tests are examined to make sure they can get the immune system to respond.

6. Discussion

This approach analyses the network of mutations in HA and provides a clearer picture of where the most important changes occur. We found spots where mutations do not only happen randomly but also play a key role in how the protein works. Focusing on these spots can be beneficial in several ways. First, altering these key spots can make it difficult for the virus to adapt. That's because changing them could make the protein unstable or mess with important functions, like how it binds to receptors or fuses. This, in turn, makes it harder for the virus to escape the immune system. Second, many of these important spots are found in core structures or crucial areas that are similar across strains, offering the potential for broader impact. Finally, examining the mutation networks helps explain why certain spots resist change by highlighting their importance in keeping everything connected or acting as a linchpin. It's a bit more complex than just looking at conservation scores.

7. Challenges and Considerations

- ❖ Structure matters: The results depend on which HA structure you use. Considering how the protein changes shape (for example, before and after fusion) and using different models could make the analysis more reliable.
- ❖ Weighing options: Figuring out the best weights for physical and chemical interactions is still somewhat speculative. Sensitivity analyses are needed.
- ❖ Close, but no cigar: Proximity alone does not guarantee that a residue is part of a functional epitope. More accurate modelling of the antibody–HA complex is needed to identify the correct target.
- ❖ Immune recognition isn't straightforward: Finding a spot that's easy to reach doesn't mean it will trigger an immune response. Factors such as glycan shielding, structural changes, and host HLA differences play a significant role in how antibodies react.
- ❖ Validation is key: We definitely need solid experimental proof, like testing the targets with actual strains, but that is a bit out of reach for this computational study. Compared with traditional methods, our approach is different. While other techniques may focus only on surface changes or conservation, we examine how everything connects and consider the functional limits in the protein's 3D shape. This allows us to spot important residues that other approaches might miss.

8. Conclusion

In this study, we present a new calculation framework that uses the Residue Interaction Network (RIN) and global mutation data to map the reciprocal landscape of the flu (HA) protein. By combining structural biotechniques with network theory and evolutionary barriers, we identified structurally conserved and functionally important residues that are promising candidates for broad-spectrum vaccine design. Our results show that residues with high centrality and low mutational tolerance are clustered near receptor-binding and fusion domains, which play an important role in preserving HA functionality while being available for immune recognition. These preserved hotspots provide valuable targets for rational antigen design and act as potential immunological "Achilles heels". This approach represents a significant change at the systems level, moving from traditional stress-specific vaccine strategies to proactive functions that target restricted regions of viral protein development.

Comparison of the identified residues with historical stress-development and neutral data supports the ability of this network-based strategy to lead the development of next-generation vaccines. This study introduces a novel approach to analyzing the influenza virus by using Residue Interaction Networks (RINs) and mutation data. In particular, it helps us understand how the hemagglutinin (HA) protein mutates and helps identify suitable targets for future influenza vaccines. The focus is on key regions of the protein that are both functionally important and relatively conserved, with additional consideration given to their potential interactions with the immune system. These spots are the virus's weak points, making it harder for it to dodge. This

method is a valuable contribution to vaccine research, offering deeper insight into how the virus evolves and how we can design vaccines that target its critical parts. The study shows that this network-based method is efficient at identifying the HA protein's important, stable regions. By analyzing mutation patterns and the pressures the HA protein faces, this approach provides a strong basis for designing vaccines that could work better. The targets identified through this method are thought to be less likely to change, which may help trigger a stronger immune response against different flu strains. Consequently, this approach has the potential to be transformative compared to conventional vaccine designs that focus on single strains, and it might even help address rapidly mutating viruses.

9. Future Work

The construction of this foundation will be followed by several routes:

- ❖ **Dynamic RIN modelling:** Molecular dynamics simulations, including pitch flexibility, will be used to generate RINs with temporal influences, demonstrating the dynamic behaviour of the cap protein.
- ❖ **Cross-Samba type analysis:** The analysis will be expanded to various influenza recessive genes (such as H1, H3, H7) to identify conserved protective target areas within different family restrictions and improve the cross-protection capability.
- ❖ **Machine-learning integration:** Machine-learning methods will be used to classify mixed structures and sequence-based features to improve the accuracy of target recognition and prediction.
- ❖ **Antibody-antigen network expansion:** Predicted antibody interaction data will be integrated into the RIN framework to assess immunogenetics and guide immunogen design.
- ❖ **Precision for other viruses:** The framework will be adapted for other rapidly mutating pathogens, such as SARS-COV-2 (Spike Protein) and HIV (ENV Protein), which makes the framework widely used.
- ❖ **Experimental verification:** Collaborate with the Immunology Laboratory to experimentally validate computational propagation through peptide synthesis, structural immunogenicity design, and neutrality analysis.
- ❖ **Overall,** this study performs basic functions for a more rational and strong vaccine design paradigm, one aimed at the structural and functional core of viral proteins, leading to increased preparations against seasonal influenza and future pandemics. This research contributes to developing flu vaccines that are not only effective but also long-lasting, enabling better pandemic preparedness and improving public health.

Conflict of Interest

On behalf of all authors, the corresponding author states that there is no conflict of interest.

Data Availability

No data was used for the research described in the article.

References

- Barabasi, A.-L., & Oltvai, Z. N. (2004). Network biology: understanding the cell's functional organization. *Nature reviews genetics*, 5(2), 101-113.
- Bernstein, D. I., Guptill, J., Naficy, A., Nachbagauer, R., Berlanda-Scorza, F., Feser, J., Wilson, P. C., Solórzano, A., Van der Wielen, M., & Walter, E. B. (2020). Immunogenicity of chimeric haemagglutinin-based, universal influenza virus

- vaccine candidates: interim results of a randomised, placebo-controlled, phase 1 clinical trial. *The Lancet Infectious Diseases*, 20(1), 80-91.
- Bommakanti, G., Citron, M. P., Hepler, R. W., Callahan, C., Heidecker, G. J., Najar, T. A., Lu, X., Joyce, J. G., Shiver, J. W., & Casimiro, D. R. (2010). Design of an HA2-based Escherichia coli expressed influenza immunogen that protects mice from pathogenic challenge. *Proceedings of the National Academy of Sciences*, 107(31), 13701-13706.
- Bommakanti, G., Lu, X., Citron, M. P., Najar, T. A., Heidecker, G. J., ter Meulen, J., Varadarajan, R., & Liang, X. (2012). Design of Escherichia coli-expressed stalk domain immunogens of H1N1 hemagglutinin that protect mice from lethal challenge. *Journal of virology*, 86(24), 13434-13444.
- Broecker, F., Liu, S. T., Suntronwong, N., Sun, W., Bailey, M. J., Nachbagauer, R., Krammer, F., & Palese, P. (2019). A mosaic hemagglutinin-based influenza virus vaccine candidate protects mice from challenge with divergent H3N2 strains. *npj Vaccines*, 4(1), 31.
- Chen, J., Wharton, S. A., Weissenhorn, W., Calder, L. J., Hughson, F. M., Skehel, J. J., & Wiley, D. C. (1995). A soluble domain of the membrane-anchoring chain of influenza virus hemagglutinin (HA2) folds in Escherichia coli into the low-pH-induced conformation. *Proceedings of the National Academy of Sciences*, 92(26), 12205-12209.
- Chen, S., Zheng, D., Li, C., Zhang, W., Xu, W., Liu, X., Fang, F., & Chen, Z. (2015). Protection against multiple subtypes of influenza viruses by virus-like particle vaccines based on a hemagglutinin conserved epitope. *BioMed research international*, 2015(1), 901817.
- Corbett, K. S., Moin, S. M., Yassine, H. M., Cagigi, A., Kanekiyo, M., Boyoglu-Barnum, S., Myers, S. I., Tsybovsky, Y., Wheatley, A. K., & Schramm, C. A. (2019). Design of nanoparticulate group 2 influenza virus hemagglutinin stem antigens that activate unmutated ancestor B cell receptors of broadly neutralizing antibody lineages. *MBio*, 10(1), 10.1128/mbio.02810-02818.
- Corti, D., & Lanzavecchia, A. (2013). Broadly neutralizing antiviral antibodies. *Annual review of immunology*, 31(1), 705-742.
- Dar, K. B., Bhat, A. H., Amin, S., Hamid, R., Anees, S., Anjum, S., Reshi, B. A., Zargar, M. A., Masood, A., & Ganie, S. A. (2018). Modern computational strategies for designing drugs to curb human diseases: a prospect. *Current topics in medicinal chemistry*, 18(31), 2702-2719.
- Deng, L., Mohan, T., Chang, T. Z., Gonzalez, G. X., Wang, Y., Kwon, Y.-M., Kang, S.-M., Compans, R. W., Champion, J. A., & Wang, B.-Z. (2018). Double-layered protein nanoparticles induce broad protection against divergent influenza A viruses. *Nature communications*, 9(1), 359.
- Di Paola, L., De Ruvo, M., Paci, P., Santoni, D., & Giuliani, A. (2013). Protein contact networks: an emerging paradigm in chemistry. *Chemical reviews*, 113(3), 1598-1613.
- Eggink, D., Goff, P. H., & Palese, P. (2014). Guiding the immune response against influenza virus hemagglutinin toward the conserved stalk domain by hyperglycosylation of the globular head domain. *Journal of virology*, 88(1), 699-704.
- Ermiler, M. E., Kirkpatrick, E., Sun, W., Hai, R., Amanat, F., Chromikova, V., Palese, P., & Krammer, F. (2017). Chimeric hemagglutinin constructs induce broad protection against influenza B virus challenge in the mouse model. *Journal of virology*, 91(12), 10.1128/jvi.00286-00217.
- Fields, B. (2013). *Fields Virology*, ; Knipe, DM, Howley, PM, Eds. In: Wolters Kluwer Health/Lippincott Williams & Wilkins: Philadelphia, PA, USA.
- Graves, P., Schulman, J., Young, J., & Palese, P. (1983). Preparation of influenza virus subviral particles lacking the HA1 subunit of hemagglutinin: unmasking of cross-reactive HA2 determinants. *Virology*, 126(1), 106-116.
- Honorato, R. V., Trellet, M. E., Jiménez-García, B., Schaarschmidt, J. J., Giuliani, M., Reys, V., Koukos, P. I., Rodrigues, J. P., Karaca, E., & van Zundert, G. C. (2024). The HADDOCK2. 4 web server for integrative modeling of biomolecular complexes. *Nature protocols*, 19(11), 3219-3241.

- Impagliazzo, A., Milder, F., Kuipers, H., Wagner, M. V., Zhu, X., Hoffman, R. M., van Meersbergen, R., Huizingh, J., Wanningen, P., & Verspuij, J. (2015). A stable trimeric influenza hemagglutinin stem as a broadly protective immunogen. *Science*, 349(6254), 1301-1306.
- Isakova-Sivak, I., Korenkov, D., Smolonogina, T., Kotomina, T., Donina, S., Matyushenko, V., Mezhenkaya, D., Krammer, F., & Rudenko, L. (2018). Broadly protective anti-hemagglutinin stalk antibodies induced by live attenuated influenza vaccine expressing chimeric hemagglutinin. *Virology*, 518, 313-323.
- Isakova-Sivak, I., Matyushenko, V., Kotomina, T., Kiseleva, I., Krutikova, E., Donina, S., Rekstin, A., Larionova, N., Mezhenkaya, D., & Sivak, K. (2019). Sequential immunization with universal live attenuated influenza vaccine candidates protects ferrets against a high-dose heterologous virus challenge. *Vaccines*, 7(3), 61.
- Jespersen, M. C., Peters, B., Nielsen, M., & Marcatili, P. (2017). BepiPred-2.0: improving sequence-based B-cell epitope prediction using conformational epitopes. *Nucleic Acids Research*, 45(W1), W24-W29.
- Kabsch, W., & Sander, C. (1983). Dictionary of protein secondary structure: pattern recognition of hydrogen-bonded and geometrical features. *Biopolymers: Original Research on Biomolecules*, 22(12), 2577-2637.
- Krammer, F., Hai, R., Yondola, M., Tan, G. S., Leyva-Grado, V. H., Ryder, A. B., Miller, M. S., Rose, J. K., Palese, P., & García-Sastre, A. (2014). Assessment of influenza virus hemagglutinin stalk-based immunity in ferrets. *Journal of virology*, 88(6), 3432-3442.
- Krammer, F., Pica, N., Hai, R., Margine, I., & Palese, P. (2013). Chimeric hemagglutinin influenza virus vaccine constructs elicit broadly protective stalk-specific antibodies. *Journal of virology*, 87(12), 6542-6550.
- Lee, J.-S., Chowdhury, M. Y., Moon, H.-J., Choi, Y.-K., Talactac, M. R., Kim, J.-H., Park, M.-E., Son, H.-Y., Shin, K.-S., & Kim, C.-J. (2013). The highly conserved HA2 protein of the influenza A virus induces a cross protective immune response. *Journal of Virological Methods*, 194(1-2), 280-288.
- Lin, S.-C., Lin, Y.-F., Chong, P., & Wu, S.-C. (2012). Broader neutralizing antibodies against H5N1 viruses using prime-boost immunization of hyperglycosylated hemagglutinin DNA and virus-like particles. *Plos one*, 7(6), e39075.
- Lin, S.-C., Liu, W.-C., Jan, J.-T., & Wu, S.-C. (2014). Glycan masking of hemagglutinin for adenovirus vector and recombinant protein immunizations elicits broadly neutralizing antibodies against H5N1 avian influenza viruses. *Plos one*, 9(3), e92822.
- Liu, W.-C., Nachbagauer, R., Stadlbauer, D., Solórzano, A., Berlanda-Scorza, F., García-Sastre, A., Palese, P., Krammer, F., & Albrecht, R. A. (2019). Sequential immunization with live-attenuated chimeric hemagglutinin-based vaccines confers heterosubtypic immunity against influenza A viruses in a preclinical ferret model. *Frontiers in immunology*, 10, 756.
- Liu, W.-C., Nachbagauer, R., Stadlbauer, D., Strohmeier, S., Solórzano, A., Berlanda-Scorza, F., Innis, B. L., García-Sastre, A., Palese, P., & Krammer, F. (2021). Chimeric hemagglutinin-based live-attenuated vaccines confer durable protective immunity against influenza A viruses in a preclinical ferret model. *Vaccines*, 9(1), 40.
- Lu, Y., Welsh, J. P., & Swartz, J. R. (2014). Production and stabilization of the trimeric influenza hemagglutinin stem domain for potentially broadly protective influenza vaccines. *Proceedings of the National Academy of Sciences*, 111(1), 125-130.
- Mallajosyula, V. V., Citron, M., Ferrara, F., Lu, X., Callahan, C., Heidecker, G. J., Sarma, S. P., Flynn, J. A., Temperton, N. J., & Liang, X. (2014). Influenza hemagglutinin stem-fragment immunogen elicits broadly neutralizing antibodies and confers heterologous protection. *Proceedings of the National Academy of Sciences*, 111(25), E2514-E2523.
- Margine, I., Krammer, F., Hai, R., Heaton, N., Tan, G., Andrews, S., Runstadler, J., Wilson, P., Albrecht, R., & Garcia-Sastre, A. (2013). Hemagglutinin stalk-based universal vaccine constructs protect against group 2 influenza A viruses. *Journal of virology*, 87(19), 10435-10446.

- McDonald, I. K., & Thornton, J. M. (1994). Satisfying hydrogen bonding potential in proteins. *Journal of molecular biology*, 238(5), 777-793.
- Nachbagauer, R., Feser, J., Naficy, A., Bernstein, D. I., Guptill, J., Walter, E. B., Berlanda-Scorza, F., Stadlbauer, D., Wilson, P. C., & Aydillo, T. (2021). A chimeric hemagglutinin-based universal influenza virus vaccine approach induces broad and long-lasting immunity in a randomized, placebo-controlled phase I trial. *Nature medicine*, 27(1), 106-114.
- Nachbagauer, R., Krammer, F., & Albrecht, R. A. (2018). A live-attenuated prime, inactivated boost vaccination strategy with chimeric hemagglutinin-based universal influenza virus vaccines provides protection in ferrets: a confirmatory study. *Vaccines*, 6(3), 47.
- Nath Neerukonda, S., Vassell, R., & Weiss, C. D. (2020). Neutralizing antibodies targeting the conserved stem region of influenza hemagglutinin. *Vaccines*, 8(3), 382.
- Petrova, V. N., & Russell, C. A. (2018). The evolution of seasonal influenza viruses. *Nature Reviews Microbiology*, 16(1), 47-60.
- Ponomarenko, J., Bui, H.-H., Li, W., Fusseder, N., Bourne, P. E., Sette, A., & Peters, B. (2008). ElliPro: a new structure-based tool for the prediction of antibody epitopes. *BMC bioinformatics*, 9(1), 514.
- Rubin, M., & Ben-Tal, N. (2021). Using ConSurf to detect functionally important regions in RNA. *Current Protocols*, 1(10), e270.
- Ryder, A. B., Nachbagauer, R., Buonocore, L., Palese, P., Krammer, F., & Rose, J. K. (2016). Vaccination with vesicular stomatitis virus-vectored chimeric hemagglutinins protects mice against divergent influenza virus challenge strains. *Journal of virology*, 90(5), 2544-2550.
- Skehel, J. J., & Wiley, D. C. (2000). Receptor binding and membrane fusion in virus entry: the influenza hemagglutinin. *Annual review of biochemistry*, 69(1), 531-569.
- Smith, D. J., Lapedes, A. S., De Jong, J. C., Bestebroer, T. M., Rimmelzwaan, G. F., Osterhaus, A. D., & Fouchier, R. A. (2004). Mapping the antigenic and genetic evolution of influenza virus. *Science*, 305(5682), 371-376.
- Sun, W., Kirkpatrick, E., Ermler, M., Nachbagauer, R., Broecker, F., Krammer, F., & Palese, P. (2019). Development of influenza B universal vaccine candidates using the “mosaic” hemagglutinin approach. *Journal of virology*, 93(12), 10.1128/jvi.00333-00319.
- Swalley, S. E., Baker, B. M., Calder, L. J., Harrison, S. C., Skehel, J. J., & Wiley, D. C. (2004). Full-length influenza hemagglutinin HA2 refolds into the trimeric low-pH-induced conformation. *Biochemistry*, 43(19), 5902-5911.
- Thrane, S., Aves, K.-L., Uddbäck, I. E. M., Janitzek, C. M., Han, J., Yang, Y. R., Ward, A. B., Theander, T. G., Nielsen, M. A., & Salanti, A. (2020). A vaccine displaying a trimeric influenza-A HA stem protein on capsid-like particles elicits potent and long-lasting protection in mice. *Vaccines*, 8(3), 389.
- Valkenburg, S. A., Mallajosyula, V. V. A., Li, O. T., Chin, A. W., Carnell, G., Temperton, N., Varadarajan, R., & Poon, L. L. (2016). Stalking influenza by vaccination with pre-fusion headless HA mini-stem. *Scientific reports*, 6(1), 22666.
- Van der Lubbe, J. E., Verspuij, J. W., Huizingh, J., Schmit-Tillemans, S. P., Tolboom, J. T., Dekking, L. E., Kwaks, T., Brandenburg, B., Meijberg, W., & Zahn, R. C. (2018). Mini-HA is superior to full length hemagglutinin immunization in inducing stem-specific antibodies and protection against group 1 influenza virus challenges in mice. *Frontiers in immunology*, 9, 2350.
- Vendruscolo, M., Dokholyan, N. V., Paci, E., & Karplus, M. (2002). Small-world view of the amino acids that play a key role in protein folding. *Physical Review E*, 65(6), 061910.
- Vita, R., Mahajan, S., Overton, J. A., Dhanda, S. K., Martini, S., Cantrell, J. R., Wheeler, D. K., Sette, A., & Peters, B. (2019). The immune epitope database (IEDB): 2018 update. *Nucleic Acids Research*, 47(D1), D339-D343.

- Wang, T. T., Tan, G. S., Hai, R., Pica, N., Ngai, L., Ekiert, D. C., Wilson, I. A., García-Sastre, A., Moran, T. M., & Palese, P. (2010). Vaccination with a synthetic peptide from the influenza virus hemagglutinin provides protection against distinct viral subtypes. *Proceedings of the National Academy of Sciences*, 107(44), 18979-18984.
- Wilson, I. A., Skehel, J. J., & Wiley, D. C. (1981). Structure of the haemagglutinin membrane glycoprotein of influenza virus at 3 Å resolution. *Nature*, 289(5796), 366-373.
- Wohlbold, T. J., Nachbagauer, R., Margine, I., Tan, G. S., Hirsh, A., & Krammer, F. (2015). Vaccination with soluble headless hemagglutinin protects mice from challenge with divergent influenza viruses. *Vaccine*, 33(29), 3314-3321.
- Yassine, H. M., Boyington, J. C., McTamney, P. M., Wei, C.-J., Kanekiyo, M., Kong, W.-P., Gallagher, J. R., Wang, L., Zhang, Y., & Joyce, M. G. (2015). Hemagglutinin-stem nanoparticles generate heterosubtypic influenza protection. *Nature medicine*, 21(9), 1065-1070.



MRI Images Colorization and Encryption Using 2RGB and Chaotic Maps

Kawther H. Al-khafaji ¹ , Hanan A. Al-Haidari ^{2*} , and Zahraa Mohammed Mashkoor ³ 



¹ Kufa University, Faculty of Education for Girls, Kufa, Iraq.

² Islamic University of Najaf, College of Medical Technology, Department of Radiology.

³ Al-Furat Al-Awsat Technical University, Najaf, Iraq.

ARTICLE INFO

Received: 16th May 2025
Received in revised form: 09th
August 2025
Accepted: 14th August 2025
Published: 15th March 2026

*Corresponding Author:

Hanan A. Al-Haidari

E-mail :

hananahmed97@iunajaf.edu.iq

Citation : Al-khafaji , K. H, Al-Haidari, H. A, & Mashkoor, Z. M. (2026). MRI Images Colourisation and Encryption Using 2RGB and Chaotic Maps. *Modern Journal of Health and Applied Sciences*, 3(1), 18-28.

Copyright (c) 2026 Modern
Journal of Health and
Applied Sciences (MJHAS)

Open Access



This work is licensed under a
[Creative Commons Attribution
Non Commercial 4.0
International license](https://creativecommons.org/licenses/by-nc/4.0/).

DOI: <https://doi.org/10.70411/MJHAS.3.1.2026247>

ABSTRACT

This research focuses on the encryption and decryption of MRI images, comparing greyscale and colorized versions to evaluate both security and visual quality. The study uses MATLAB for implementation and analyses encryption performance through metrics such as NPCR (Number of Pixels Change Rate), UACI (Unified Average Changing Intensity), PSNR (Peak Signal-to-Noise Ratio), and SNR (Signal-to-Noise Ratio).

Key findings include: high encryption effectiveness, with NPCR values near 0.97 indicating that almost all pixels were altered; uniform histogram distribution in encrypted images, ensuring security by removing identifiable patterns; low pixel correlation in encrypted images, demonstrating strong resistance to statistical attacks; successful decryption, with restored images closely matching the originals (high PSNR values); and the finding that colorization does not weaken encryption, maintaining security while improving visual interpretability.

The study confirms that the proposed encryption method is secure, efficient, and suitable for medical imaging, ensuring both data protection and recoverability.

Keywords: MRI images, Medical image, Color medical image, Encryption, Chaotic encryption algorithm, 2RGB.

1. Introduction

Magnetic Resonance Imaging (MRI) is a critical tool in modern medical diagnostics because it produces detailed images of internal body structures without ionizing radiation. However, with the growing use of digital transmission and storage, protecting the privacy and integrity of MRI images has become a major concern. Image encryption converts the image into an unreadable format, preventing unauthorized access. Furthermore, the colorization of greyscale MRI images has emerged as a promising technique to enhance visualization and interpretation, especially for training and educational purposes. Combining encryption and colorization techniques offers a dual advantage: securing sensitive medical data and improving the visual clarity of diagnostic images. This research explores recent methods and algorithms in MRI image encryption and colorization, highlighting their importance in secure medical imaging systems (Ahmed et al., 2023).

2. Background and Literature Review

Magnetic Resonance Imaging (MRI) provides high-resolution images that are essential for medical diagnosis. However, as these images are often transmitted over networks or stored in cloud systems, securing them against unauthorized access is critical. Image encryption is a key technique for ensuring the confidentiality and integrity of sensitive data. Several encryption methods have been developed specifically for medical images, including chaotic-based encryption, block-based scrambling, and hybrid cryptographic algorithms (Pankaj & Dua, 2024).

Chaotic systems, in particular, are well suited to image encryption due to their sensitivity to initial conditions and their random-like behaviour. For example, the use of logistic maps, Lorenz attractors, and Arnold transformations has shown promising results in securing medical images with minimal computational overhead. Furthermore, encryption schemes that combine compression and encryption have been proposed to enhance efficiency without compromising security (Odeh & Al-Haija, 2023).

On the other hand, MRI images are typically greyscale, which may limit their visual interpretation, especially for educational or illustrative purposes. Colorization aims to enhance the visual perception of greyscale MRI images by assigning color values based on texture, intensity, or learnt patterns. Recently, deep learning models such as convolutional neural networks (CNNs) and generative adversarial networks (GANs) have been widely adopted for medical image colorization, achieving realistic and clinically useful results.

Integrating encryption and colorization remains challenging because the processes are mutually exclusive: encryption aims to obscure visual information, while colorization seeks to enhance it. Therefore, research continues to focus on optimizing the sequence and compatibility of these two operations to develop robust and secure medical imaging systems (Pavithra & Jeyamala, 2018).

3. Methods and Techniques

3.1. Chaotic Encryption and Decryption for MRI Images

Chaotic encryption is a lightweight and efficient method for securing medical images such as MRI scans. Unlike traditional encryption algorithms, chaotic systems rely on nonlinear dynamic equations that produce pseudo-random behaviour, making them highly sensitive to initial conditions and control parameters. This sensitivity ensures that even a small change in the key or input image will result in a completely different encrypted output, enhancing security (Seeli & Thanammal, 2025).

One of the commonly used chaotic maps is the Logistic Map, defined by the equation:

$$X_{(n+1)} = r \cdot X_n \cdot (1 - X_n) \quad \text{Eq.01}$$

where $0 < X(n) < 1$ and $3.57 < r \leq 4$. This map can generate a chaotic sequence used for pixel permutation and value substitution in the image. The encryption process typically involves the following steps (Mohanty, 2015).

- ❖ **Key Generation:** A chaotic sequence is generated using a chosen map and initial parameters.
- ❖ **Pixel Scrambling:** The image pixels are rearranged based on the chaotic sequence to break spatial relationships.
- ❖ **Pixel Modification:** The pixel values are altered using XOR or other operations involving the chaotic sequence.

3. 2. Chaotic Encryption Offers Several Advantages for Medical Imaging

- High sensitivity to keys (enhancing security).
- Fast execution and low computational load.
- Effective for greyscale and color images.

Due to its efficiency and strong security properties, chaotic encryption is particularly suitable for protecting MRI images during storage and transmission.

3. 3. Grey 2RGB Colorization Method

Medical images are typically acquired and displayed in greyscale, which represents the intensity of tissues. However, greyscale visualization may limit the ability to distinguish anatomical structures, especially for non-expert viewers. In the context of MRI images, color mapping (or false coloring) means taking the original greyscale image and assigning different colors to intensity levels (signal) rather than displaying it solely in shades of grey.

The 2RGB colorization method aims to enhance the visual perception of MRI images by converting the single-channel greyscale data into a three-channel RGB representation. Although it is possible to display the images in black and white, doing so will result in the loss of most of the diagnostic details, so doctors only use it for very specific purposes, such as computational image processing (Kaur et al., 2021; Pareek et al., 2006; Sokouti et al., 2016).

The core idea of 2RGB is to map the greyscale intensity values to red, green, and blue channels using a defined transformation function or lookup table. For example, lower intensity values may be mapped to cooler colors (e.g., blue), while higher intensities may shift toward warmer tones (e.g., red). This technique does not change the actual medical content of the image but improves contrast and interpretability for both educational and diagnostic support (Geetha et al., 2018; Kamal et al., 2021).

2RGB is considered a lightweight and efficient alternative to deep learning-based colorization, which requires large datasets and training. It is especially useful in contexts where real-time performance and simplicity are essential. Additionally, color-enhanced MRI images can help in visual analytics and pattern recognition, particularly in brain imaging (Gonzalez, 2009).

To convert a greyscale MRI image into a color image using the 2RGB method, each pixel's intensity value is first normalized to the range $[0, 1]$. The RGB values are then computed using the following equations (Al-Khafaji & Sahib, 2024).

$$\begin{cases} R = I * 255 \\ G = (1 - I) * 255 \\ B = |0.5 - I| * 510 \end{cases} \quad \text{Eq.02}$$

Where:

- R, G, B are the red, green, and blue components of the resulting color pixel.
- I is the normalized greyscale intensity of the original pixel.
- $|0.5 - I| * 510$ centers the blue channel around mid-intensity values.

The red channel increases linearly with intensity, highlighting brighter regions. The green channel decreases with intensity, emphasizing darker areas. The blue channel peaks at medium intensity values, adding visual contrast in intermediate tones (Al-Haidari & Al-khafaji, 2024).

This mapping enhances visual perception by spreading greyscale intensity across color channels, thereby improving differentiation between anatomical features without altering diagnostic content. It is computationally light, does not require training data, and is well-suited for real-time visualization in medical applications (Albermani et al., 2022, 2023).

Chaotic Image Encryption with Lorenz Map + 2RGB Coloring :

- ❖ **Step 1 – Input and Setup:** Load the input greyscale image of fixed size 484×484 pixels and determine the total number of pixels.
- ❖ **Step 2 – Generate Chaotic Key Stream.**
- ❖ **Step 3 – Image Encryption:** Apply bitwise XOR between the greyscale image pixels and the chaotic key matrix. The result is the encrypted greyscale image.
- ❖ **Step 4 – 2RGB Coloring:** Create three color channels from the encrypted greyscale image:

R channel: Encrypted greyscale image directly.

G channel: Encrypted image shifted by 1 row (vertical shift).

B channel: Pixel-wise inversion.

Merge the three channels into one RGB image and save the encrypted colored image.

- ❖ **Step 5 – Decryption:** Load the encrypted RGB image, extract the R channel (which contains the encrypted greyscale), regenerate the same chaotic keystream using the exact same initial conditions and parameters, and then apply bitwise XOR between the R channel and the key matrix to recover the original greyscale image.

4. Implementation

The proposed implementation is designed to evaluate the impact of image colorization on the security and quality of encrypted MRI images. Two parallel workflows were conducted:

4. 1. Encryption Before Colorization

The greyscale MRI image was first encrypted using a chaotic logistic map-based algorithm. The image matrix was scrambled and diffused using chaotic sequences generated with a secret key.

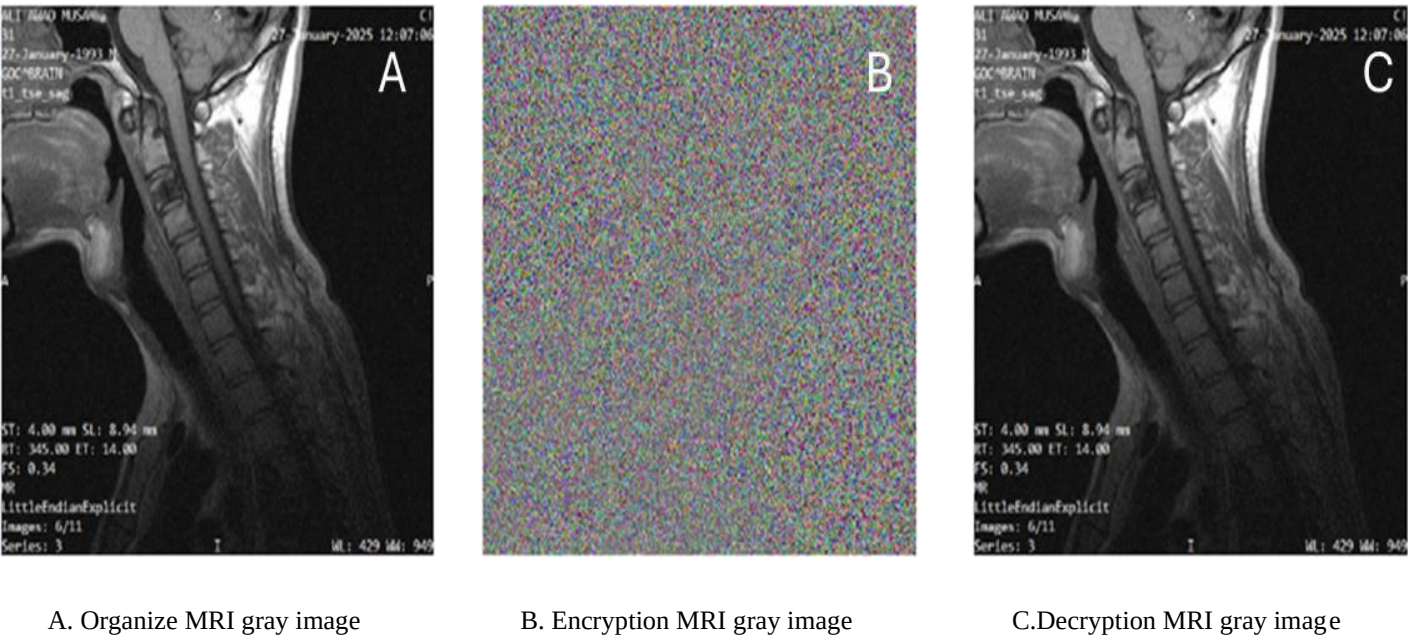


Figure 1. Encryption and Decryption MRI image before colorization

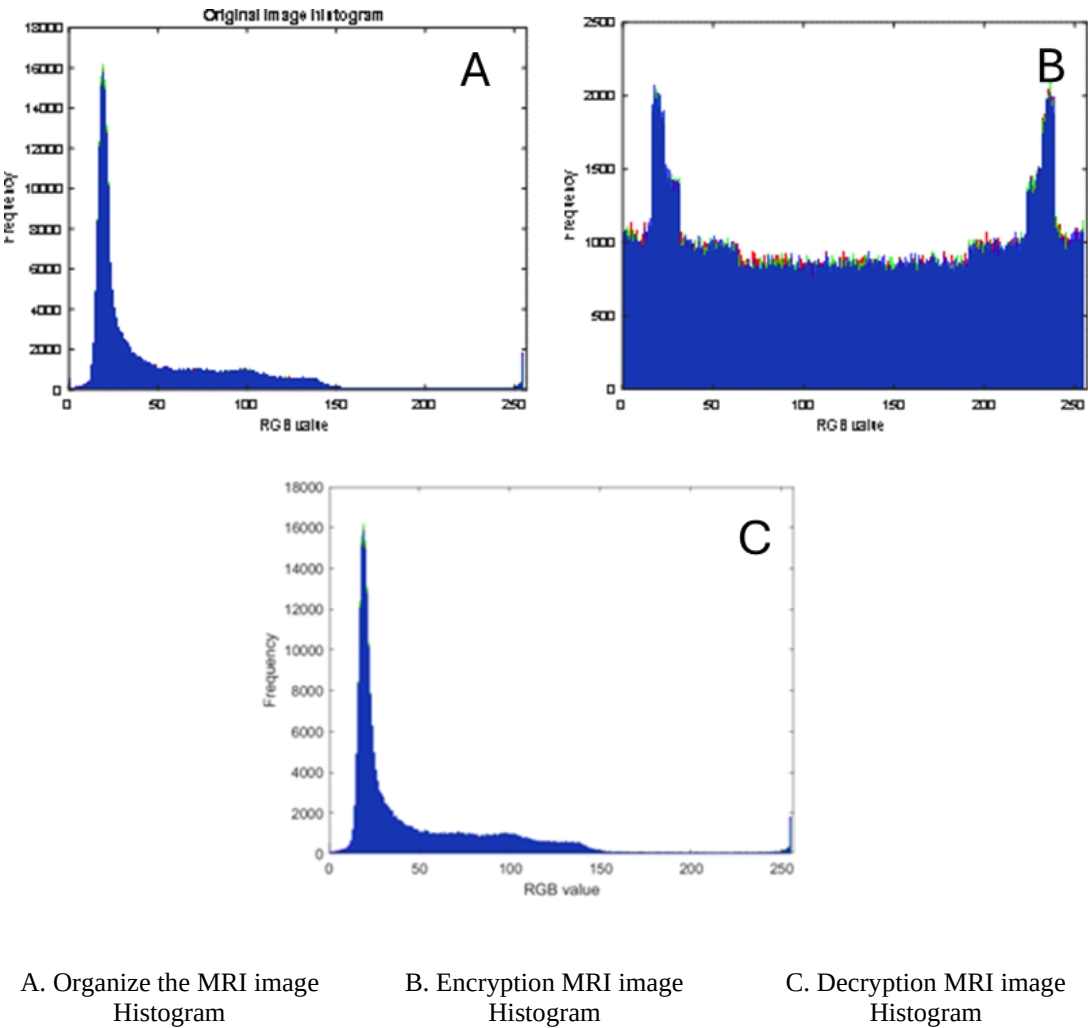
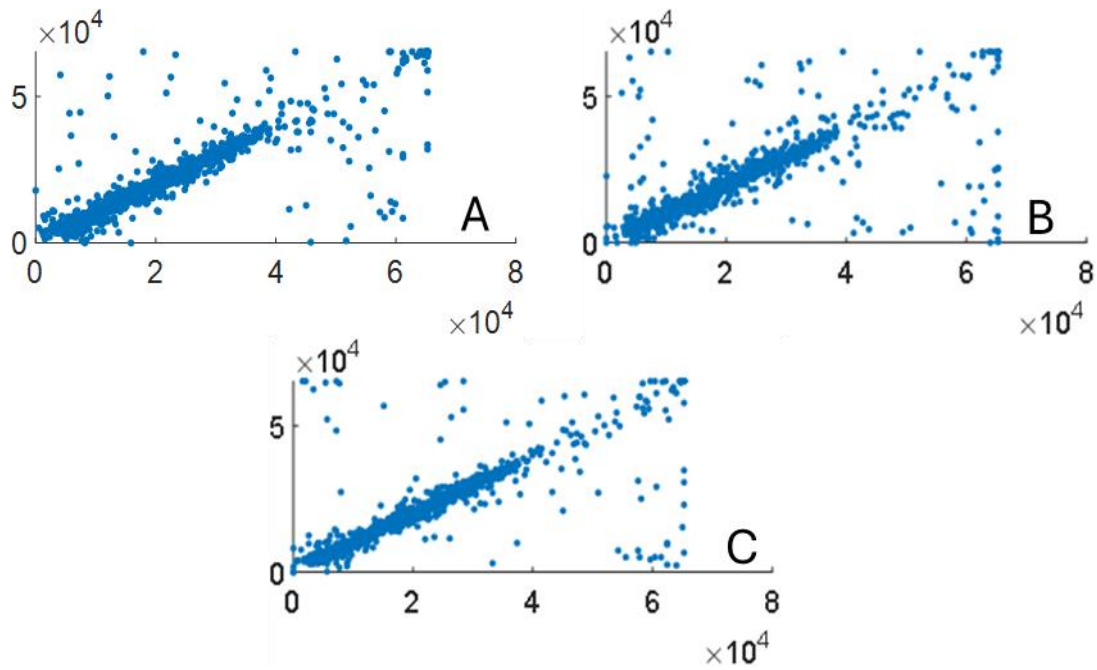


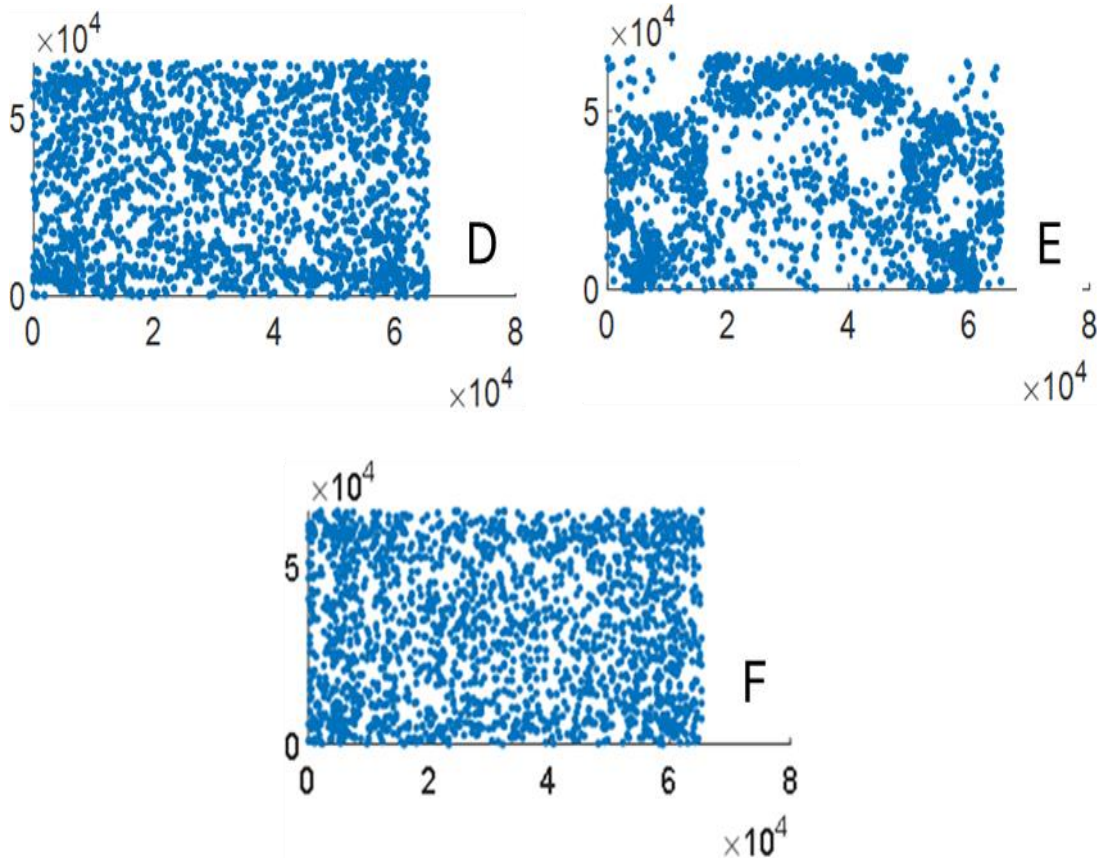
Figure 2. Encryption and Decryption MRI gray image Histogram before colorization



A. Correlation plot of two adjacent MRI Original image pixels in horizontal

B. Correlation plot of two adjacent MRI Original image pixels in Vertical

C. Correlation plot of two adjacent MRI Original image pixels in Diagonal



D. Correlation plot of two adjacent MRI encryption image pixels in horizontal

E. Correlation plot of two adjacent MRI encryption image pixels in Vertical

F. Correlation plot of two adjacent MRI encryption image pixels in Diagonal

Figure 3. Correlation plot of two adjacent MRI gray image pixels

Table 1. Show Some IQM Value in MRI Medical gray Image

IQM	The Value	IQM	The Value	IQM	The Value
UACI	0.362084	MSNR1	6.595512	RMSE1	6.173283
NPCR	0.971507	MSNR2	1.406830	RMSE2	13.154646
SNR1	38.736137	WSNR1	11.342383	LMSE1	44.334986
SNR2	38.736137	WSNR2	4.530051	LMSE2	1.023487
PSNR1	99.000000	MSE1	38.109421	NMSE	0.000000
PSNR2	32.320480	MSE2	0.000000	NAE1	0.170310



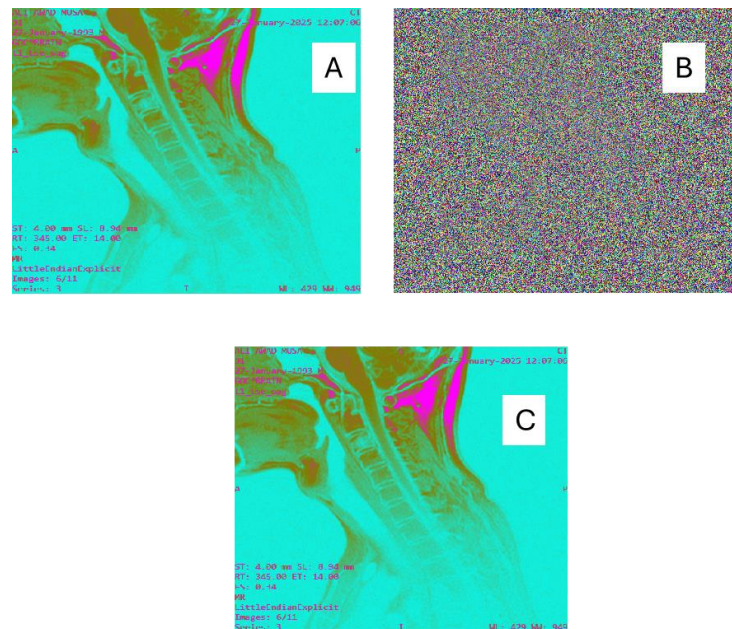
A. Organize MRI gray image

B. Color MRI image

Figure 4. Gray 2RGB Colorization

4.2. Encryption MRI image Colorization

In the second workflow, the original greyscale MRI image was first converted to a three-channel RGB image using the 2RGB method. Each color channel was then encrypted individually using the same chaotic encryption method.



A. Organize MRI Color image

B. Encryption MRI Color image

C. Decryption MRI Color image

Figure 5. Encryption and Decryption MRI image after colorization

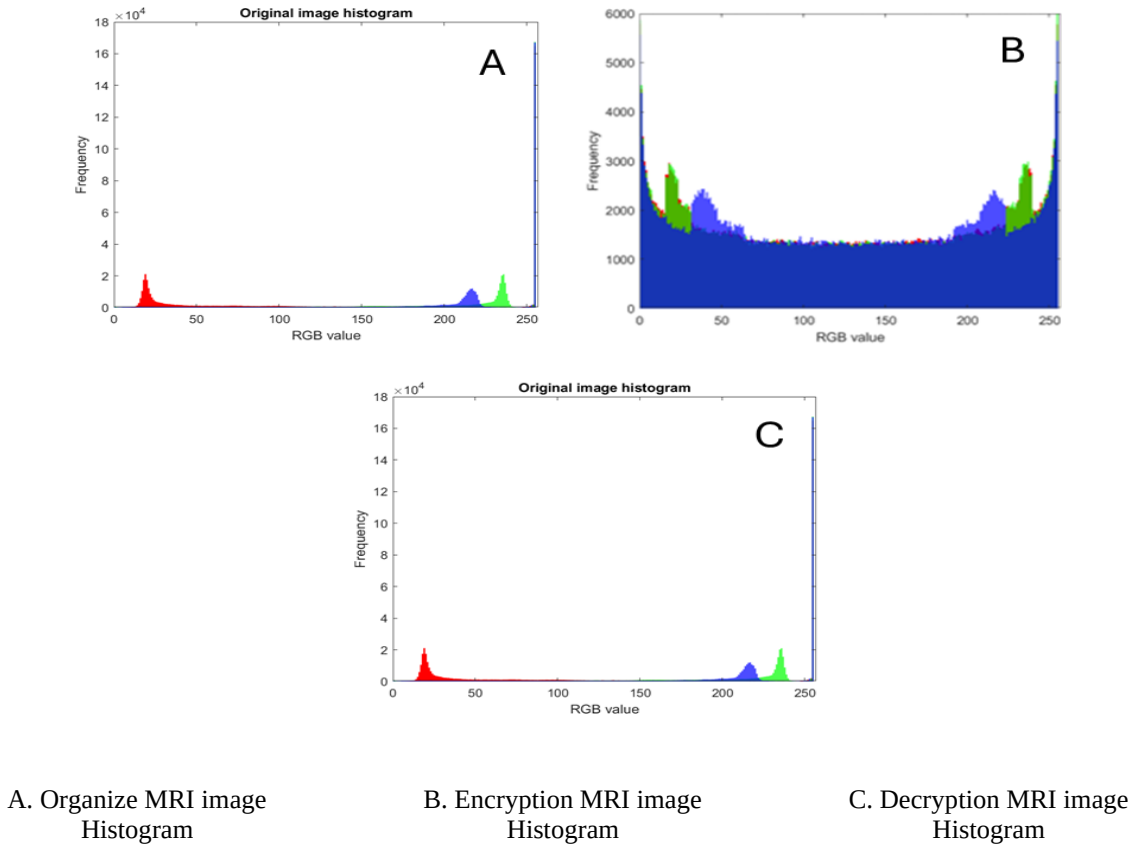


Figure 6. Encryption and Decryption MRI color image Histogram after colorization

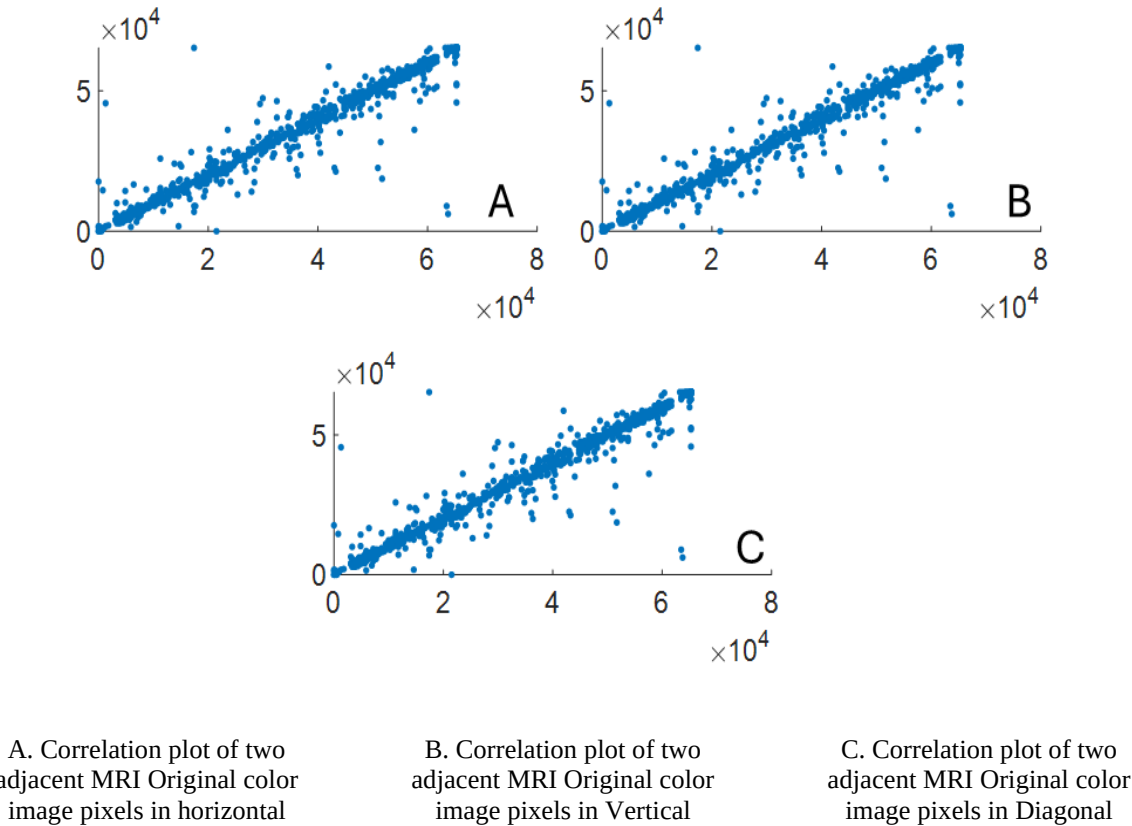


Figure 7. Correlation plot of two adjacent MRI original color image pixels

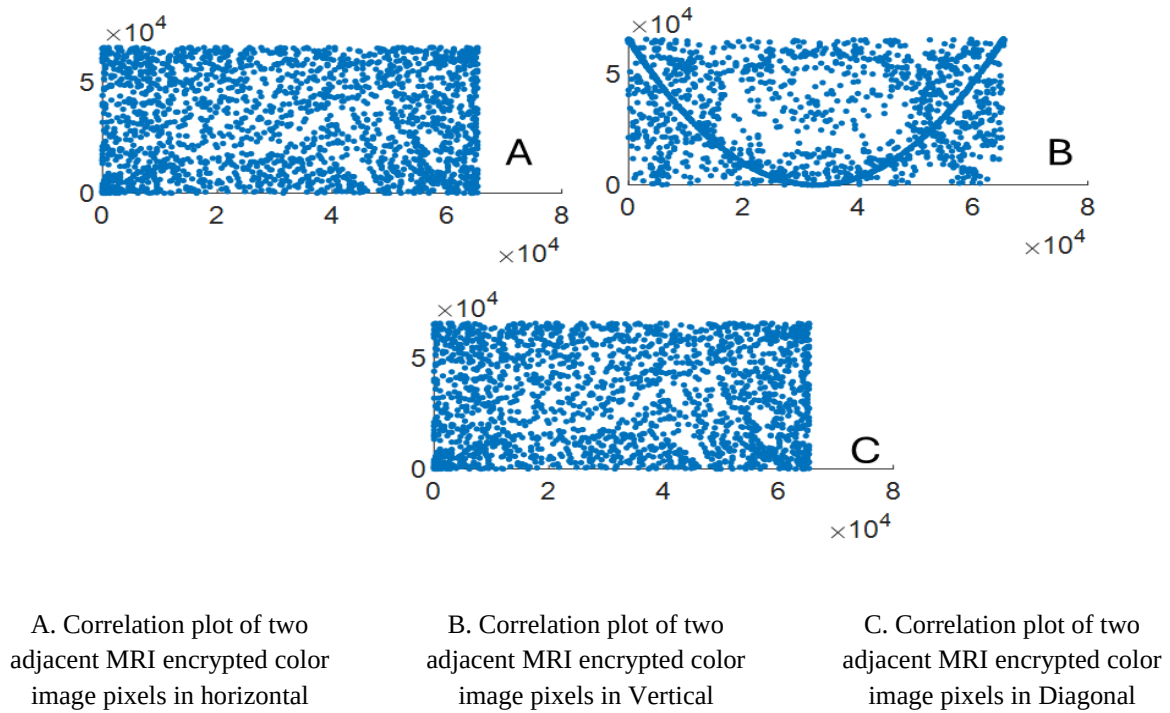


Figure 8. Correlation plot of two adjacent MRI encrypted color image pixels

Table 2. Show Some IQM Value in MRI Medical color Image

IQM	The Value	IQM	The Value	IQM	The Value
UACI	0.406147	MSNR1	2.299877	RMSE1	10.499305
NPCR	0.971936	MSNR2	2.239793	RMSE2	10.254181
SNR1	37.976404	WSNR1	6.478356	LMSE1	253.635786
SNR2	37.976404	WSNR2	6.942806	LMSE2	1.004126
PSNR1	99.000000	MSE1	110.235405	NMSE	0.000000
PSNR2	27.707593	MSE2	0.000000	NAE1	0.414586

The implementation was carried out in MATLAB. The visual quality and encryption performance of both methods were compared using metrics such as Histogram analysis, PSNR (Peak Signal-to-Noise Ratio), and NPCR (Number of Pixels Change Rate). This comparison aims to determine whether colorization affects encryption strength and to assess the visual interpretability of the final encrypted output.

In both workflows, a decryption process was also implemented to evaluate the recoverability of the original image after encryption. In the first method (encryption before colorization), the encrypted greyscale image was decrypted using the inverse operations of the chaotic map, followed by the 2RGB colorization. In the second method (encryption after colorization), each RGB channel was decrypted separately, and the full-color image was reconstructed.

5. Conclusion

The most important results reached by the researcher are as follows:

1. Image Encryption and Decryption Process:

The images demonstrate a clear workflow for encrypting and decrypting MRI images, both in greyscale and colorized forms. The encryption process effectively alters the images' appearance, making them unrecognizable, while the decryption process restores them to their original state. This indicates the robustness of the encryption algorithm used.

2. Histogram Analysis:

The histograms of the original, encrypted, and decrypted images reveal significant differences. The encrypted images exhibit uniformly distributed histograms, which is a desirable trait for secure encryption as it indicates the removal of any identifiable patterns. The decrypted histograms closely match the original ones, confirming the accuracy of the decryption process.

3. Correlation Plots:

The correlation plots of adjacent pixels in the original images (horizontal, vertical, and diagonal) show high correlation, whereas the encrypted images display significantly reduced correlation. This demonstrates the encryption algorithm's ability to break the spatial relationships between pixels, thereby enhancing security.

4. Quality Metrics (IQM Values):

The Image Quality Metrics (IQM) table includes values such as NPCR (0.97), UACI (0.40), and PSNR (99), indicating high encryption efficiency. The high NPCR value suggests that nearly all pixels were changed during encryption, while the PSNR value reflects the quality of the decrypted image compared to the original.

5. Impact of Colorization:

The comparison between greyscale and colorized MRI images shows that colorization does not negatively affect the encryption strength. The encryption and decryption processes remain effective, and the visual interpretability of the decrypted images is preserved.

6. Implementation and Evaluation:

The use of MATLAB for implementation, along with metrics such as PSNR and NPCR for evaluation, highlights a systematic approach to assessing encryption performance. The results confirm that the method is suitable for medical image encryption, ensuring both security and recoverability.

Conflict of Interest

On behalf of all authors, the corresponding author states that there is no conflict of interest.

Data Availability

No data was used for the research described in the article.

References

- Ahmed, S. T., Hammood, D. A., Chisab, R. F., Al-Naji, A., & Chahl, J. (2023). Medical image encryption: a comprehensive review. *Computers*, 12(8), 160.
- Al-Haidari, H. A., & Al-khafaji, K. H. (2024). Studying the Effect of the Primary Coefficients (X, U) of the Logistic Chaotic Encryption Algorithm Equation on the Performance of X-Ray Medical Image Encryption. *Sebha University Conference Proceedings*,
- Al-Khafaji, K. H., & Sahib, H. A. (2024). Designing a Digital System for Enhancing, Coloring, Encryption and Decryption of X-ray Medical Image. *2024 15th International Conference on Information and Communication Systems (ICICS)*,
- Albermani, M. J., Al-Hilo, E. M., & Al-khafaji, K. H. (2022). Color Image Encryption and Decryption by Using Optical Scanning Cryptography Method. *International Conference on Emerging Technologies and Intelligent Systems*,
- Albermani, M. J., Al-Hilo, E. M., & Al-Khafaji, K. H. (2023). Comparative between encryption and decryption of (binary, gray& color) images using optical scanning cryptography. *AIP Conference Proceedings*,
- Geetha, S., Punithavathi, P., Infanteena, A. M., & Sindhu, S. S. S. (2018). A literature review on image encryption techniques. *International Journal of Information Security and Privacy (IJISP)*, 12(3), 42-83.

- Gonzalez, R. C. (2009). Digital image processing. Pearson education india.
- Kamal, S. T., Hosny, K. M., Elgindy, T. M., Darwish, M. M., & Fouda, M. M. (2021). A new image encryption algorithm for grey and color medical images. *Ieee Access*, 9, 37855-37865.
- Kaur, M., Singh, S., & Kaur, M. (2021). Computational image encryption techniques: a comprehensive review. *Mathematical Problems in Engineering*, 2021(1), 5012496.
- Mohanty, S. P. (2015). Nanoelectronic mixed-signal system design. McGraw-Hill Education New York.
- Odeh, A., & Al-Haija, Q. A. (2023). Medical image encryption techniques: a technical survey and potential challenges. no. January, 3170-3177.
- Pankaj, S., & Dua, M. (2024). Chaos based medical image encryption techniques: A comprehensive review and analysis. *Information Security Journal: A Global Perspective*, 33(3), 332-358.
- Pareek, N. K., Patidar, V., & Sud, K. K. (2006). Image encryption using chaotic logistic map. *Image and vision computing*, 24(9), 926-934.
- Pavithra, V., & Jeyamala, C. (2018). A survey on the techniques of medical image encryption. 2018 IEEE International Conference on Computational Intelligence and Computing Research (ICCIC),
- Seeli, D. J. J., & Thanammal, K. (2025). A comparative review and analysis of medical image encryption and compression techniques. *Multimedia Tools and Applications*, 84(8), 4457-4473.
- Sokouti, M., Zakerolhosseini, A., & Sokouti, B. (2016). Medical image encryption: an application for improved padding based GGH encryption algorithm. *The open medical informatics journal*, 10, 11.



Integrating Artificial Intelligence into Microbiology: Emerging Horizons for Precision Medicine and Antimicrobial Stewardship

Enass Waad Al-hadidi ^{1*} , and Ali Adel Dawood ² 



¹ M.Sc, Department of Biology, College of Science, University of Mosul, Mosul, Iraq.

² PhD, Department of Anatomy, College of Medicine, University of Mosul, Mosul, Iraq.

ARTICLE INFO

ABSTRACT

Received: 12th July 2025
Received in revised form: 26th August 2025
Accepted: 26th August 2025
Published: 15th March 2026

*Corresponding Author:

Enass Waad Al-hadidi

E-mail:

enasswaadobeed@uomosul.edu.iq

Citation: Alhadidi, E.W., Dawood, A. A. (2026). Integrating Artificial Intelligence into Microbiology: Emerging Horizons for Precision Medicine and Antimicrobial Stewardship. *Modern Journal of Health and Applied Sciences*, 3(1), 29-38.

Copyright (c) 2026 Modern Journal of Health and Applied Sciences (MJHAS)

Open Access



This work is licensed under a [Creative Commons Attribution NonCommercial 4.0 International](https://creativecommons.org/licenses/by-nc/4.0/) license.

DOI: <https://doi.org/10.70411/MJHAS.3.1.2026291>

The latest developments in artificial intelligence (AI) have altered the sphere of microbiological investigation very rapidly by expanding the scope of studying microbial systems, accurate diagnostics on the basis of genomes, and the discovery of new drugs. This review introduces a specific synopsis of AI use in microbiology that covers three areas, namely early detection of diseases, surveillance of antimicrobial resistance (AMR), and progress in therapeutics. AI is used to enhance the process of pathogen identification and bring about the formulation of specific therapies through the use of machine learning models and vast microbial data sets that will eventually lead to quorum-sensing inhibitors and microbiome-based treatment of diseases. Other than these developments, there is still a challenge with data quality, algorithm transparency, and ethical implementation. To overcome these problems, the cooperation of microbiologists with computational scientists and policymakers is needed. In the present paper, the authors offer a comprehensive framework on which future studies could base their findings, focusing on the role of AI in sustainable healthcare and agricultural solutions, as well as environmental support.

Keywords: Artificial Intelligence, Microbiology, Microbial Genomics, Antimicrobial Resistance, AI-powered Diagnostics.

1. Introduction

Microorganisms are extremely significant in the development and maintenance of ecological systems, the preservation of agricultural yields, and the determination of human health. Although traditional microbiologic methods have provided valuable results, they are usually laborious and not scalable to meet current needs (Graf et al., 2025; Tian et al., 2024). Artificial intelligence (AI) is a technology that has become transformative in recent years, providing new possibilities for microbial analysis, forecasting diseases, environmental diagnostics, and so on (Shelke et al., 2023; Stracy et al., 2022). This article presents a bibliometric and thematic review of artificial intelligence applications in microbiology, using tools such as VOSviewer and Bibliometrix (R-package) to analyze publication trends, keyword co-occurrence, and thematic evolution (Papoutsoglou et al., 2023).

The purpose of this review is to identify the current overlap between AI and microbiology, as well as emerging fields that will shift the paradigm of existing research. In particular, three key themes are identified within our discussion: early disease detection, monitoring of antimicrobial resistance (AMR), and AI-based innovation in modelling of microbes and therapies (Mishra et al., 2023; Suster et al., 2024).

A combination of genomic, clinical and environmental data in AI systems would help researchers detect microbial pathogens faster and monitor the trends of antibiotic resistance (Liu et al., 2023; Tian et al., 2024). These devices have improved our knowledge of microbial communities themselves and their involvement in such complex processes as biofilm formation and quorum sensing, and they have contributed to the creation of synthetic inhibitors that may be applied in medicine, agriculture and ecosystem control (Stokes et al., 2020; Suster et al., 2024).

Nevertheless, the development of microbiology with AI is not without drawbacks. High data quality, algorithmic bias, and a lack of methodological transparency are major challenges. This review summarizes significant progress and gaps left that need to be completed to fulfil the promise of AI in microbial science (Marcos-Zambrano et al., 2021; Wang et al., 2026). Artificial intelligence (AI) has emerged as a transformative force in the biomedical sciences, offering novel approaches to data analysis, pattern recognition, and predictive modelling. In microbiology, AI enables rapid diagnostics, antimicrobial resistance prediction, and microbiome profiling, among other applications (Arnold et al., 2025; Cesaro et al., 2025).

Although the number of publications in this field has increased, there is no unified knowledge on the development and thematic priorities of AI-related microbiological studies. A bibliometric review is a systematic review that gives a structured report on the trend of publications, prominent authors and new themes of research (Stracy et al., 2022; Xu et al., 2022).

This study employs VOSviewer and Bibliometrix (R-package) to visualize co-authorship networks, keyword co-occurrence, and thematic evolution. These tools enable comprehensive mapping of the intellectual structure and research dynamics in the field (Arruda et al., 2022; Juhas, 2023). **Figure 1** illustrates how artificial intelligence is changing the way scientists study microbiology. Instead of only being able to observe microbes under the microscope, researchers can rely on AI to facilitate the diagnosis of infections, the creation of personalized patient treatments, and the development of better solutions to environmental problems. The figure demonstrates the extent to which AI is applied in generating more insights in microbiological studies (Arruda et al., 2022; Shelke et al., 2023).

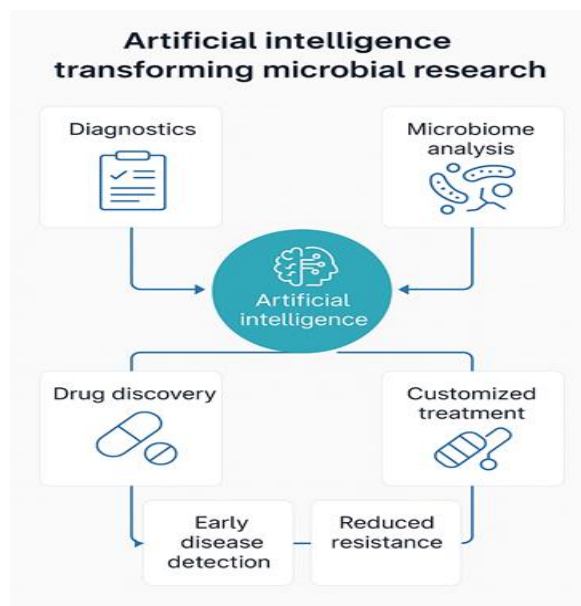


Figure 1. Conceptual visualization of how AI technologies transform microbial research, encompassing diagnostic, therapeutic, and ecological applications across clinical and environmental settings.

2. Methods

A structured literature search was conducted across PubMed, Scopus, and Web of Science databases. The research included keywords such as 'Artificial Intelligence', 'Microbiology', 'Microbiome', 'Quorum Sensing', and 'Antimicrobial Resistance'. The search time frame was from January 2013 to March 2024. Boolean operators and filters were applied to refine the results to peer-reviewed articles in English (Jiang et al., 2023; Tsitou et al., 2024).

Inclusion criteria were: (1) peer-reviewed articles, (2) published in English, (3) focused on AI applications in microbiology. Exclusion criteria included: (1) non-peer-reviewed sources, (2) articles unrelated to microbiological contexts, and (3) publications lacking methodological transparency (Tsitou et al., 2024).

Although this study is bibliometric in nature and not a systematic review, the PRISMA framework was partially referenced to guide the article selection and screening process. Data extraction was performed manually using a standardized template. Extracted variables included publication year, journal name, author affiliations, keywords, citation count, and thematic focus. The dataset generated from this process is available upon request from the corresponding author (Cesaro et al., 2025).

The bibliometric software tools (VOSviewer) and the R-package-based bibliometric software (Bibliometrix) were applied to review patterns of research productivity, prominent keywords, and co-author networks. Thematic categorization of the studies was done to gain insights regarding the development of diagnostics, drug discovery, and the modelling of microbiomes. Publications with strong methodologies, well-defined datasets, and clinical or agricultural relevance were favored (Juhas, 2023; Papoutsoglou et al., 2023). The sources used in this paper include a diverse range of perspectives, case studies, systematic reviews, and bibliometric analyses to comprehensively cover the topic. Methodological transparency was observed, as the selection process was documented and the methods of the analytical tools used reflected recently accepted bibliographic standards (Wong et al., 2023).

The visual maps of the key words co-occurring, networks of author collaboration, and relationships of citations were generated with the help of VOSviewer. They were analyzed by using bibliometrix (R-package) to do thematic evolution analysis, trends of annual production of science and source impact measures. The bibliometric search strategy was conducted using

PubMed, Scopus, and Web of Science databases. The detailed query strings, Boolean operators, and filters applied are provided in Supplementary File 1 to ensure transparency and reproducibility.

3. Results

This section presents the bibliometric and thematic findings derived from the selected literature. Analyses were conducted using VOSviewer and Bibliometrix to visualise keyword relationships, author networks, and thematic evolution. The results are organised into five thematic areas reflecting the convergence of AI and microbiology (Arruda et al., 2022; Cesaro et al., 2025).

3.1. Annual Publication Trends

Artificial intelligence has been selectively used in microbiology over the last decade, and its integration has grown exponentially. Between 2013 and 2023, there was a 70% or greater increase in AI-associated publications on microbial research, indicating a growing importance of AI in diagnostics, genomics, and therapeutics. **Figure 2** illustrates the semantic relationships among keywords in AI-driven microbiology, highlighting the interdisciplinary integration across diagnostics, microbiome, resistance, and drug discovery (Sornsuwan et al., 2025).

The application of AI has helped transition microbiological research toward predictive modelling and high-throughput approaches. Both scientists and clinicians are increasingly relying on AI to model the response of microbes, predict outbreaks and develop individualized therapies, a shift in paradigm (Moradigaravand et al., 2018).

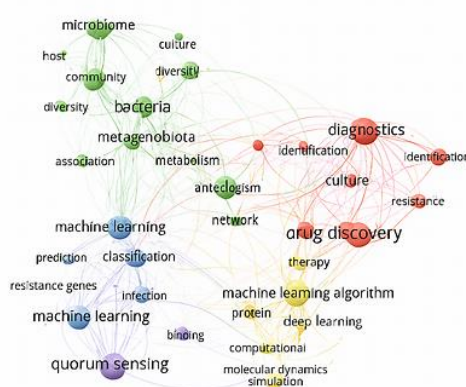


Figure 2. Co-occurrence map of AI-microbiology studies as keywords. Worldwide co-occurrence map of keywords produced by VOSviewer as an example of the visualization of semantic relationships between keywords in AI-based microbiology studies.

Examples of major clusters are AI–microbiome, antibiotic resistance, deep learning and drug discovery. The size of the node represents the frequency of the keyword, and the thickness of the edges represents the strength of co-occurrence.

3.2. Keyword Co-occurrence Analysis

The thematic clustering of AI-driven microbiology research visualized in **Figure 3** indicates four key intellectual areas: diagnostics, microbiome, antimicrobial resistance, and drug discovery. Many clusters are connected through a bridging node, quorum sensing. Those clusters are the intellectual map of contemporary research and its changing priorities (Liu et al., 2023; Vashistha et al., 2023).

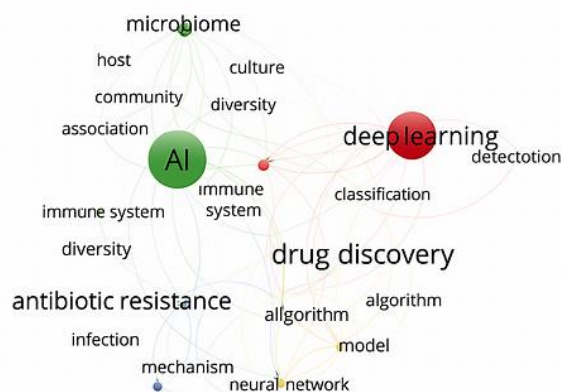


Figure 3. Thematic clustering map of AI–microbiology research. VOSviewer-generated thematic clustering visualization illustrating the intellectual structure and evolution of AI-driven microbiology research. The map highlights four major clusters: diagnostics, microbiome, antimicrobial resistance, and drug discovery. A bridging node, quorum sensing, connects multiple domains, reflecting interdisciplinary convergence.

Figures (2 and 3) present complementary visualizations: the first maps keyword-level semantic relationships, while the second reveals thematic clustering and intellectual structure. Together, they highlight the evolving priorities and interdisciplinary nature of AI–microbiology research.

3. 2. 1. Diagnostics

Machine learning and next-generation sequencing (NGS), combined with AI, have enabled rapid identification of pathogens, driven by the revolution in microbial diagnostics. These systems are more responsive and quicker than conventional culture-based methods. Artificial intelligence tools played a significant role during the COVID-19 pandemic, when there was a need to track the mutations and forecast the spread of the disease (Traves et al., 2024).

Genomic, clinical, and environmental data can now collaborate within AI-based diagnostic tools to provide real-time details. This has improved early diagnosis of infectious diseases, resulting in accurate curative actions.

3. 2. 2. Microbiome

AI analytics have revolutionized microbiome research by mapping microbial communities and identifying patterns associated with diseases such as diabetes and inflammatory bowel disease. On one hand, machine learning facilitates the individualization of probiotics, while on the other hand, it allows the choice of therapeutic measures based on the microbiome composition (Bartoszewicz et al., 2021; Marcos-Zambrano et al., 2021). Complex computer models allow scientists to gain an understanding of the ontogenic interactions between hosts and microbes, as well as their significance for health. Precision medicine will be achieved by using AI tools in the search for useful strains in microbial restoration balance (Tian et al., 2024).

3. 2. 3. Antimicrobial Resistance

AI models will recreate drug-pathogen interactions and forecast resistance mechanisms, enabling the development of next-generation antibiotics and quorum-sensing inhibitors (QSIs). They are used to counteract the resistance that develops and to maximize treatment plans.

Machine learning algorithms consider genomic mutations to predict resistance patterns, enabling therapeutic planning in advance. Also, AI is applied in monitoring hospital-acquired infections and global AMR (Stokes et al., 2020).

3. 2. 4. Drug Discovery

AI assists in virtually screening thousands of compounds to assess their binding affinity and efficacy against microbes. This accelerates the development of new therapeutics and reduces the cost of conducting experimental trials. Molecular docking simulations using AI have revealed QSIs that disrupt the communication between bacteria and biofilm architecture and development. The innovations offer a future to some of the resistant pathogens and chronic infections (Juhas, 2023; Wong et al., 2023).

3. 2. 5. Quorum Sensing

AI simulations decode bacterial communication networks, enabling the design of quorum-sensing inhibitors that disrupt biofilm formation and virulence. These inhibitors offer promising solutions for chronic infections and environmental control (Graf et al., 2025). AI also supports the modelling of microbial ecosystems, helping researchers understand how quorum sensing influences microbial adaptation and resistance (Vashistha et al., 2023).

3. 3. Applications of AI in Microbiology

AI technologies have demonstrated success in treating antibiotic resistance, optimizing treatment duration, and minimizing broad-spectrum antibiotic use (Suster et al., 2024).

Table 1. Summarizes key applications across various microbiological domains.

Field	Application	Outcome
Genomic Analysis	AI-driven genome sequencing analysis	Discovering disease-associated genetic patterns with accuracy and speed.
Antibiotic Resistance Prediction	Identifying drug-resistant microbes through modelling	Developing customised strategies to combat resistance.
Microbiome Research	Evaluating microbiome composition and changes via big data	Designing personalised therapies based on microbiome balance.
Quorum Sensing	Simulating bacterial networks using AI	Creating quorum-sensing inhibitors to counteract bacterial infections.

3. 4. Integration with Other Technologies

AI is increasingly being combined with nanotechnology and robotics. The algorithms develop nanoparticle delivery payloads to the target while optimizing nanoparticle design, and robotic systems perform remote microbial sampling in high-stress conditions. These technologies expand the boundaries of microbiological studies, enabling real-time monitoring of microbial diversity and adaptations in environments that are otherwise inaccessible, such as deep oceans and polar regions (Cesaro et al., 2025).

3. 5. Technical Depth and Limitations

AI in microbiology is perceived as promising, but it also faces challenges related to data quality, model transparency, and ethics. One concept under development, called explainable AI (XAI), aims to improve human trust and interpretability. High-performance computing opportunities cannot be universally applied because they are available only on low resources. The realm of ethical dilemmas in matters such as data protection, informed consent, and algorithmic discrimination, among others, must also be properly addressed through an interdisciplinary approach (Traves et al., 2024; Wong et al., 2023).

4. Discussion

The thematic and bibliometric review highlights the disruptive impact of artificial intelligence in microbiology, particularly in areas such as diagnostics, antimicrobial resistance prediction, microbiome, and drug discovery. The results indicate that the list of publications related to AI is constantly increasing, which suggests that AI is increasingly being incorporated in the field of microbiology (Arruda et al., 2022; Xu et al., 2022). We also find that AI plays a significant role in predicting AMR and in microbiome-based therapy (Patel et al., 2023; Roberts et al., 2023). However, this review provides the scope with the help of bibliometric mapping and thematic synthesis, which gives a bigger picture of how AI is changing microbial science (Asgari et al., 2019; Bartoszewicz et al., 2021). The thematic clustering analysis indicated four major areas of activity, including Diagnostics, Microbiome, and Antimicrobial Resistance and Drug Discovery, with Quorum Sensing being a connecting concept between clusters (Suster et al., 2024; Tsitou et al., 2024). AI has been applied in diagnostics, with machine learning models shown to be more sensitive and faster than conventional methods. In microbiome studies, AI has helped identify patterns of dysbiosis and develop custom probiotics. Virtual screening and molecular docking have contributed to drug discovery, particularly in the development of QSIs and novel antibiotics (Jumper et al., 2021). Despite these developments, several problems remain. The problem of data quality, the inability to understand algorithms, and ethical issues continue to be significant impediments. These gaps can potentially be solved by the development of explainable AI (XAI) systems and open-access platforms (Alser et al., 2021). This review would benefit the sphere by providing a structured review of the development of AI in microbiology, highlighting key themes and offering future research directions. It can be used as a guide to the researchers who plan to implement or apply AI in microbial diagnosis, treatment, and ecology (Tsitou et al., 2024).

5. Ethical Considerations

The use of AI applications in microbiology raises significant privacy concerns, particularly when genomic or microbiome data is obtained from patients. It is essential to ensure informed consent and data processing strategies are locked down (Xu et al., 2022). Another concern is the low level of transparency in the AI models, which can hinder clinical trust. Interpretability and responsibility can be developed in formulating explainable AI (XAI). Biases in training datasets and unequal access to AI use would increase global inequality. The solution to ethical developments is to promote open-source platforms and inclusive data (Moradigaravand et al., 2018).

6. Future Prospects

It is evident that AI will play a significant role in microbiology in the future, particularly as emerging technologies continue to expand the research capability of microbes, as well as in clinical practice. AI is likely to be actively used in areas such as real-time pathogen identification, personalized medicine, or environmental microbiome monitoring. Together with other technologies, such as nanotechnology, robotics, and the Internet of Things (IoT), these innovations will provide no-contact sampling, remote diagnostics, and intelligent biological sensors. Inventions of this kind will increase the reach of the

microbiological analysis to hard-to-reach areas and environments. In addition, explainable AI (XAI) and open-source approaches can be developed to enhance transparency and accessibility, enabling researchers in low-resource contexts to participate in global microbial surveillance and drug discovery initiatives. These models can recreate microbial communities and evolutionary pathways and can shape synthetic microbial consortia for applications in both industry and medicine with more advanced AI training. The changes will revolutionize the notion of microbiology and establish new standards of interdisciplinary collaboration.

7. Conclusion

This bibliometric and thematic review demonstrates the growing impact of artificial intelligence in microbiology. Through keyword mapping and thematic synthesis, four broad research clusters have been identified: diagnostics, microbiome analysis, antimicrobial resistance, and drug discovery, with quorum sensing as a cross-cutting theme.

AI has accelerated microbial research by enabling predictive modelling, high-throughput analysis, and personalized therapeutic design. Despite existing challenges, the integration of AI with emerging technologies holds great potential for advancing microbiological science. This review provides a comprehensive overview of current trends and future directions, serving as a valuable resource for researchers, clinicians, and policymakers seeking to harness AI for microbial innovation.

Conflict of Interest

On behalf of all authors, the corresponding author states that there is no conflict of interest.

Data Availability

No data was used for the research described in the article.

References

- Alser, M., Rotman, J., Deshpande, D., Taraszka, K., Shi, H., Baykal, P. I., Yang, H. T., Xue, V., Knyazev, S., & Singer, B. D. (2021). Technology dictates algorithms: recent developments in read alignment. *Genome biology*, 22(1), 249.
- Arnold, A., McLellan, S., & Stokes, J. M. (2025). How AI can help us beat AMR. *npj Antimicrobials and Resistance*, 3(1), 18.
- Arruda, H., Silva, E. R., Lessa, M., Proenca Jr, D., & Bartholo, R. (2022). Resource review. *Journal of the Medical Library Association*, 110(3), 392-395.
- Asgari, E., McHardy, A. C., & Mofrad, M. R. (2019). Probabilistic variable-length segmentation of protein sequences for discriminative motif discovery (DiMotif) and sequence embedding (ProtVecX). *Scientific reports*, 9(1), 3577.
- Bartoszewicz, J. M., Genske, U., & Renard, B. Y. (2021). Deep learning-based real-time detection of novel pathogens during sequencing. *Briefings in Bioinformatics*, 22(6), bbab269.
- Cesaro, A., Hoffman, S. C., Das, P., & de la Fuente-Nunez, C. (2025). Challenges and applications of artificial intelligence in infectious diseases and antimicrobial resistance. *npj Antimicrobials and Resistance*, 3(1), 2.
- Graf, E., Soliman, A., Marouf, M., Parwani, A. V., & Pancholi, P. (2025). Potential roles for artificial intelligence in clinical microbiology from improved diagnostic accuracy to solving the staffing crisis. *American Journal of Clinical Pathology*, 163(2), 162-168.
- Jiang, X., Yan, J., Huang, H., Ai, L., Yu, X., Zhong, P., Chen, Y., Liang, Z., Qiu, W., & Huang, H. (2023). Development of novel parameters for pathogen identification in clinical metagenomic next-generation sequencing. *Frontiers in genetics*, 14, 1266990.

- Juhas, M. (2023). Artificial intelligence in microbiology. In *Brief Lessons in Microbiology: From the Origin of Life to Artificial Intelligence* (pp. 93-109). Springer.
- Jumper, J., Evans, R., Pritzel, A., Green, T., Figurnov, M., Ronneberger, O., Tunyasuvunakool, K., Bates, R., Židek, A., & Potapenko, A. (2021). Highly accurate protein structure prediction with AlphaFold. *Nature*, 596(7873), 583-589.
- Liu, G., Catacutan, D. B., Rathod, K., Swanson, K., Jin, W., Mohammed, J. C., Chiappino-Pepe, A., Syed, S. A., Fragis, M., & Rachwalski, K. (2023). Deep learning-guided discovery of an antibiotic targeting *Acinetobacter baumannii*. *Nature Chemical Biology*, 19(11), 1342-1350.
- Marcos-Zambrano, L. J., Karaduzovic-Hadziabdic, K., Loncar Turukalo, T., Przymus, P., Trajkovic, V., Aasmets, O., Berland, M., Gruca, A., Hasic, J., & Hron, K. (2021). Applications of machine learning in human microbiome studies: a review on feature selection, biomarker identification, disease prediction and treatment. *Frontiers in Microbiology*, 12, 634511.
- Mishra, A., Khan, S., Das, A., & Das, B. C. (2023). Evolution of diagnostic and forensic microbiology in the era of artificial intelligence. *Cureus*, 15(9).
- Moradigaravand, D., Palm, M., Farewell, A., Mustonen, V., Warringer, J., & Parts, L. (2018). Prediction of antibiotic resistance in *Escherichia coli* from large-scale pan-genome data. *PLoS computational biology*, 14(12), e1006258.
- Papoutsoglou, G., Tarazona, S., Lopes, M. B., Klammersteiner, T., Ibrahimi, E., Eckenberger, J., Novielli, P., Tonda, A., Simeon, A., & Shigdel, R. (2023). Machine learning approaches in microbiome research: challenges and best practices. *Frontiers in Microbiology*, 14, 1261889.
- Shelke, Y. P., Badge, A. K., Bankar, N. J., & Badge, A. (2023). Applications of artificial intelligence in microbial diagnosis. *Cureus*, 15(11).
- Sornsuwan, K., Pamonsupornwichit, T., Juntit, O.-a., Thongkum, W., Takheaw, N., Kodchakorn, K., & Tayapiwatana, C. (2025). Plasticity of BioPhi-driven humanness optimization in ScFv-CD99 binding affinity validated through AlphaFold, HADDOCK, and MD simulations. *Computational and Structural Biotechnology Journal*, 27, 369-382.
- Stokes, J. M., Yang, K., Swanson, K., Jin, W., Cubillos-Ruiz, A., Donghia, N. M., MacNair, C. R., French, S., Carfrae, L. A., & Bloom-Ackermann, Z. (2020). A deep learning approach to antibiotic discovery. *Cell*, 180(4), 688-702. e613.
- Stracy, M., Snitser, O., Yelin, I., Amer, Y., Parizade, M., Katz, R., Rimler, G., Wolf, T., Herzel, E., & Koren, G. (2022). Minimizing treatment-induced emergence of antibiotic resistance in bacterial infections. *Science*, 375(6583), 889-894.
- Suster, C. J., Pham, D., Kok, J., & Sintchenko, V. (2024). Emerging applications of artificial intelligence in pathogen genomics. *Frontiers in Bacteriology*, 3, 1326958.
- Tian, T., Zhang, X., Zhang, F., Huang, X., Li, M., Quan, Z., Wang, W., Lei, J., Wang, Y., & Liu, Y. (2024). Harnessing AI for advancing pathogenic microbiology: a bibliometric and topic modeling approach. *Frontiers in Microbiology*, 15, 1510139.
- Traves, R., Opadchy, T., Slobedman, B., & Abendroth, A. (2024). Varicella zoster virus downregulates expression of the nonclassical antigen presentation molecule CD1d. *The Journal of Infectious Diseases*, 230(2), e416-e426.
- Tsitou, V.-M., Rallis, D., Tsekova, M., & Yanev, N. (2024). Microbiology in the era of artificial intelligence: transforming medical and pharmaceutical microbiology. *Biotechnology & Biotechnological Equipment*, 38(1), 2349587.
- Vashistha, A., Sharma, N., Nanaji, Y., Kumar, D., Singh, G., Barnwal, R. P., & Yadav, A. K. (2023). Quorum sensing inhibitors as Therapeutics: Bacterial biofilm inhibition. *Bioorganic Chemistry*, 136, 106551.
- Wang, X.-W., Wang, T., & Liu, Y.-Y. (2026). Artificial intelligence for microbiology and microbiome research. *Cell Systems*, 17(2).
- Wong, F., de la Fuente-Nunez, C., & Collins, J. J. (2023). Leveraging artificial intelligence in the fight against infectious diseases. *Science*, 381(6654), 164-170.

Xu, D., Liu, B., Wang, J., & Zhang, Z. (2022). Bibliometric analysis of artificial intelligence for biotechnology and applied microbiology: Exploring research hotspots and frontiers. *Frontiers in bioengineering and biotechnology*, 10, 998298.



Abdominal Tuberculosis: Diagnostic Challenges and Outcomes in a Nigerian Tertiary Hospital

Umar Muktar^{1*} , Umar Mohammed² , Usman Bello³ , Sani Hamza¹ , Nuhu Abdullahi Koko¹ , and Sanusi Asmau⁴ 



¹ Surgery Department, Usmanu Danfodiyo University Teaching Hospital, Sokoto, Nigeria.

² Department of Morbid Anatomy and Forensic Medicine, Faculty of Basic Clinical Sciences, College of Health Sciences, Usmanu Danfodiyo University, Sokoto, Nigeria.

³ Surgery Department, College of Health Sciences, Bayero University Kano, Nigeria.

⁴ Obstetrics and Gynaecology Department, Usmanu Danfodiyo University Teaching Hospital, Sokoto, Nigeria.

ARTICLE INFO

Received: 08th August 2025
Received in revised form: 23th September 2025
Accepted: 24th September 2025
Published: 15th March 2026

*Corresponding Author:

Umar Muktar

E-mail:

umarmuktardr@gmail.com

Citation: Muktar, U., Mohammed, U., Bello, U., Hamza, S., Koko, N. A., Asmau, S.(2026). Abdominal Tuberculosis: Diagnostic Challenges and Outcomes in a Nigerian Tertiary Hospital. *Modern Journal of Health and Applied Sciences*, 3(1), 39-54.

Copyright (c) 2026 Modern Journal of Health and Applied Sciences (MJHAS)

Open Access



This work is licensed under a [Creative Commons Attribution NonCommercial 4.0 International](https://creativecommons.org/licenses/by-nc/4.0/) license.

ABSTRACT

Abdominal tuberculosis (TB) remains a diagnostic dilemma in many low-resource settings due to its nonspecific clinical presentation and its overlap with other intra-abdominal conditions. This study aimed to describe the clinical, diagnostic, and treatment profiles of patients with abdominal TB at a tertiary hospital in northern Nigeria. We conducted a 10-year retrospective review of patients with histopathologically confirmed abdominal TB at Usmanu Danfodiyo University Teaching Hospital, Sokoto. Data on demographics, clinical presentation, diagnostic methods, treatment modalities, and outcomes were analyzed using descriptive and inferential statistics. Sixty-four patients were included, with a median age of 35 years (IQR: 25–50); most were male (59.4%). Common symptoms included abdominal pain, weight loss, fever, and altered bowel habits. Only 22% of cases were diagnosed preoperatively, underscoring the limitations in non-invasive diagnostic tools. All patients received anti-TB chemotherapy, and 19% underwent surgery for complications. The majority (64%) had favorable outcomes, but a significant proportion (31%) were lost to follow-up. HIV co-infection was noted in 19% of patients and was associated with higher complication and mortality rates. Abdominal TB primarily affects young, economically active individuals and remains underdiagnosed preoperatively in resource-constrained environments. Improved access to advanced diagnostics such as laparoscopy and GeneXpert, combined with structured follow-up and early referral systems, is essential to improve outcomes.

Keywords: Abdominal tuberculosis, Nigeria, Histopathology, Diagnosis, Anti-TB therapy, HIV, Low-resource settings.

1. Introduction

Tuberculosis (TB) remains one of the most important infectious diseases worldwide, ranking among the top ten causes of death and as the leading cause of death from a single infectious agent. In 2023, the World Health Organization (WHO) estimated 10.8 million new TB cases and 1.25 million deaths globally, with sub-Saharan Africa bearing a disproportionate share of the burden (WHO, 2023) (Tuberculosis (TB), n.d.). Nigeria continues to rank sixth among high-burden countries, contributing an estimated 590,000 new cases annually, of which approximately 140,000 are co-infected with HIV, and nearly 245,000 deaths occur (Olaleye et al., 2023).

The emergence of the COVID-19 pandemic further complicated TB control efforts. During 2020–2022, disruptions in healthcare delivery led to reduced TB notifications, diagnostic delays, and treatment interruptions worldwide (Gulumbe et al., 2025; Jeong & Min, 2023). This abdominal TB setback reversed years of progress, with TB regaining its position as the leading cause of death from an infectious agent once the initial wave of COVID-19 subsided. In Nigeria, the pandemic strained already fragile diagnostic and surveillance systems, exacerbating challenges for extrapulmonary TB (EPTB), which already suffers from under-recognition and misdiagnosis.

Globally, EPTB constitutes between 8% and 24% of all TB cases, with an average of 15%, though prevalence varies by region. In Africa, a meta-analysis reported a pooled EPTB prevalence of 26%, with the highest rate in Eastern Africa (32%) and the lowest in Western Africa (16%). Peritoneal TB makes up about 12% of EPTB cases (Hailu et al., 2024). Among EPTB forms, abdominal TB is one of the most diagnostically elusive. It can involve the gastrointestinal tract, peritoneum, lymph nodes, or solid organs, and often presents with nonspecific features such as abdominal pain, weight loss, fever, or changes in bowel habits (Al-Zanbagi & Shariff, 2021; Cho et al., 2018). These symptoms mimic conditions, such as malignancy, inflammatory bowel disease, or typhoid perforation, leading to misclassification and late diagnosis. Even in well-resourced settings, abdominal TB is frequently confirmed only after surgical intervention. In Nigeria, diagnosis is hampered by limited access to CT, laparoscopy, and molecular tools such as GeneXpert, with many cases confirmed only histopathological following laparotomy.

Existing Nigerian studies (Akinkuolie et al., 2008; Dauda et al., 2010; Ihekweba, 1993; Ohanaka & Egbagbe, 2004) provide useful insights but are limited by small sample sizes, older data, or partial diagnostic criteria. In the post-COVID-19 era, there is an urgent need to update the epidemiology and clinical outcomes of abdominal TB, as delayed diagnosis and loss to follow-up may have worsened.

The objective of this study is to provide a 10-year retrospective review (2015–2024) of histopathological confirmed cases of abdominal TB at Usmanu Danfodiyo University Teaching Hospital (UDUTH), Sokoto. We aim to describe the demographic distribution, clinical features, diagnostic challenges, and outcomes, thereby generating contemporary evidence to inform earlier recognition, improved diagnostic pathways, and better patient follow-up in low-resource settings.

2. Research Hypothesis

➤ Primary Hypothesis (H1):

Patients with abdominal tuberculosis in low-resource settings are more likely to experience delayed diagnosis, higher complication rates, and increased loss to follow-up compared with patients diagnosed with pulmonary TB or abdominal TB in well-resourced settings.

➤ Null Hypothesis (H0):

There is no significant difference in diagnostic delay, complication rates, or loss to follow-up between patients with abdominal tuberculosis in low-resource settings and those with pulmonary TB or abdominal TB in well-resourced settings.

3. Patients and Methods

3. 1. Study Design and Setting

This was a retrospective descriptive study conducted over a 10-year period, from January 1, 2015, to December 31, 2024, at the Usmanu Danfodiyo University Teaching Hospital (UDUTH), Sokoto, a major tertiary health facility serving the Northwestern region of Nigeria and neighboring Niger and the Benin Republic. The hospital provides specialized medical and surgical services, including gastroenterology and infectious disease care, making it a referral center for complicated tuberculosis (TB) cases, including extrapulmonary and abdominal TB.

3. 2. Study Population

The study population comprised all patients who underwent surgery for abdominal tuberculosis at UDUTH Sokoto during the study period. Inclusion criteria were:

- Patients of all ages and both sexes.
- Patients with histologically or microbiologically confirmed abdominal TB, regardless of whether they underwent surgery.
- Patients with sufficient clinical, laboratory, and operative data retrievable from hospital records.

Exclusion criteria included:

- Patients with incomplete or missing case records.
- Cases where the diagnosis of abdominal TB was uncertain or not confirmed.³

3. 3. Data collection

Data were obtained from patient case files, ward admission registers, operative records, histopathology reports, and radiology department archives. A structured data extraction form was used to collect relevant information, including:

- Demographic data: age, sex, occupation, and residence.
- Clinical presentation: presenting symptoms (e.g., abdominal pain, distension, weight loss, fever, night sweats), duration of symptoms, and nutritional status.
- Diagnostic work-up: results of laboratory investigations (e.g., full blood count, erythrocyte sedimentation rate, HIV status), imaging studies (abdominal ultrasound, plain X-rays, CT scans), tuberculin skin test results, GeneXpert MTB/RIF assay, and findings from diagnostic laparotomy.
- Diagnostic Tools and Equipment
 - ✓ Histopathology: All cases included in the study were confirmed by histopathological examination of intraoperative or biopsy specimens, processed in the UDUTH pathology laboratory using standard hematoxylin and eosin staining.
 - ✓ GeneXpert MTB/RIF: This molecular test was used in selected cases where tissue or ascitic fluid samples were sufficient, and the equipment was functional. For molecular confirmation, we used the GeneXpert MTB/RIF Assay (Cepheid) on GeneXpert Instrument Systems. The system employs single-use disposable cartridges containing all required reagents, including sample processing chemicals (e.g., NaOH and isopropanol), primers/probes targeting the *rpoB* gene region, and internal controls (Sample Processing Control and Probe-Check Control) to ensure valid amplification.
 - ✓ Radiologic Evaluation: Ultrasound and computed tomography (CT) scans were used. No specific machine was used, as reports came from different laboratories.

- ✓ Surgical Decision-Making Protocol: Surgery was performed in cases of acute or subacute intestinal obstruction; suspicion of intra-abdominal abscess or mass requiring drainage; inconclusive non-invasive diagnostics requiring laparotomy for definitive diagnosis (diagnostic dilemma); or when laparotomy specimens were prioritized for histological analysis.
- Site and type of abdominal TB: classification into luminal, peritoneal, nodal, and visceral types.
- Treatment modality: whether medical (anti-TB therapy alone) or combined medical and surgical.
- Surgical details: type of surgery performed, intraoperative findings, complications, and duration of hospital stay.
- Outcomes: postoperative morbidity and mortality, response to therapy, recurrence, and follow-up status.
- Missing data: Patients with incomplete essential data were excluded from the study. For variables with partial missing information (e.g., HIV status), available-case analysis was performed, and the limitation was noted in the discussion.

3. 4. Definitions

Table 1. Operational Definitions Used in the Study.

Term	Definition
Abdominal TB	Tuberculosis infection affecting any component of the abdominal cavity, including the gastrointestinal tract, peritoneum, mesenteric lymph nodes, or solid abdominal organs. Although radiological features may suggest abdominal TB, only histopathological confirmation was used as the definitive diagnostic criterion in this study.
Treatment success	Complete clinical resolution of symptoms and radiologic improvement following completion of a full course of anti-TB treatment.
Complications	Categorized as minor or major, including surgical site infection, intestinal obstruction, perforation, and need for reoperation.
Recurrence	Reappearance of clinical features with confirmation of abdominal TB after completion of treatment.
Lost to follow-up	Patients who discontinued therapy or became untraceable before completing the prescribed treatment.
Mortality	Death occurring during the index admission or follow-up, attributable to TB or its complications.

3. 5. Ethical Considerations

Approval for this study was obtained from the Ethical Review Committee of Usmanu Danfodiyo University Teaching Hospital, Sokoto. Due to the retrospective nature of the study, individual informed consent was waived, but confidentiality of patient data was strictly maintained. All collected data were anonymized and used solely for the purpose of research. Intraoperative photos were de-identified and used strictly for educational purposes. Patient consent was waived due to retrospective design and data anonymization, as approved by the hospital's ethics committee.

3. 6. Data Analysis

The data were entered and analyzed using the Statistical Package for the Social Sciences (SPSS) version 25 (IBM Corp., Armonk, NY, USA). Descriptive statistics such as frequencies, means, medians, and standard deviations were used to summarize patient characteristics. Associations between categorical variables were assessed using Chi-square or Fisher's exact tests, as appropriate. A p-value < 0.05 was considered statistically significant

4. Results

4. 1. Demographic Characteristics

A total of 72 patients were retrieved; however, 8 cases were excluded due to incomplete data. Sixty-four patients diagnosed with and operated on for abdominal tuberculosis were analyzed over a 10-year period from 2015 to 2024. Patient ages ranged from the second to the eighth decade, with a peak incidence in the third and fourth decades. The median age was 35 years (IQR: 25–50 years). The highest burden was observed in the third decade (28.1%), followed by the fourth (18.8%) and second (15.6%) decades. Only 6.3% of patients were below 20 years, while 6.3% were aged 70 years and above ([Table 2](#)). There was a male predominance, with 38 males (59.4%) and 26 females (40.6%), yielding a male-to-female ratio of approximately 1.5:1.

Table 2. Age Distribution of Patients Operated for Abdominal Tuberculosis at UDUTH Sokoto.

Age Group (Decade)	Frequency (n)	Percentage (%)
0–9	0	0.0%
10–19	4	6.3%
20–29	10	15.6%
30–39	18	28.1%
40–49	12	18.8%
50–59	10	15.6%
60–69	6	9.4%
≥70	4	6.3%
Total	64	100%

4. 2. HIV Status

Among the cohort, 12 patients (18.8%) were HIV-positive, while 40 (62.5%) tested negative. The HIV status of 12 patients (18.8%) was unknown or not documented.

4. 3. Duration of Symptoms Before Presentation

The majority of patients presented more than 3 months after symptom onset. Specifically, 27 patients (42.2%) had symptoms lasting more than 3 months, 22 (34.4%) presented within 1–3 months, and 15 (23.4%) presented within 1 month. This indicates a generally delayed pattern of health-seeking among the patients.

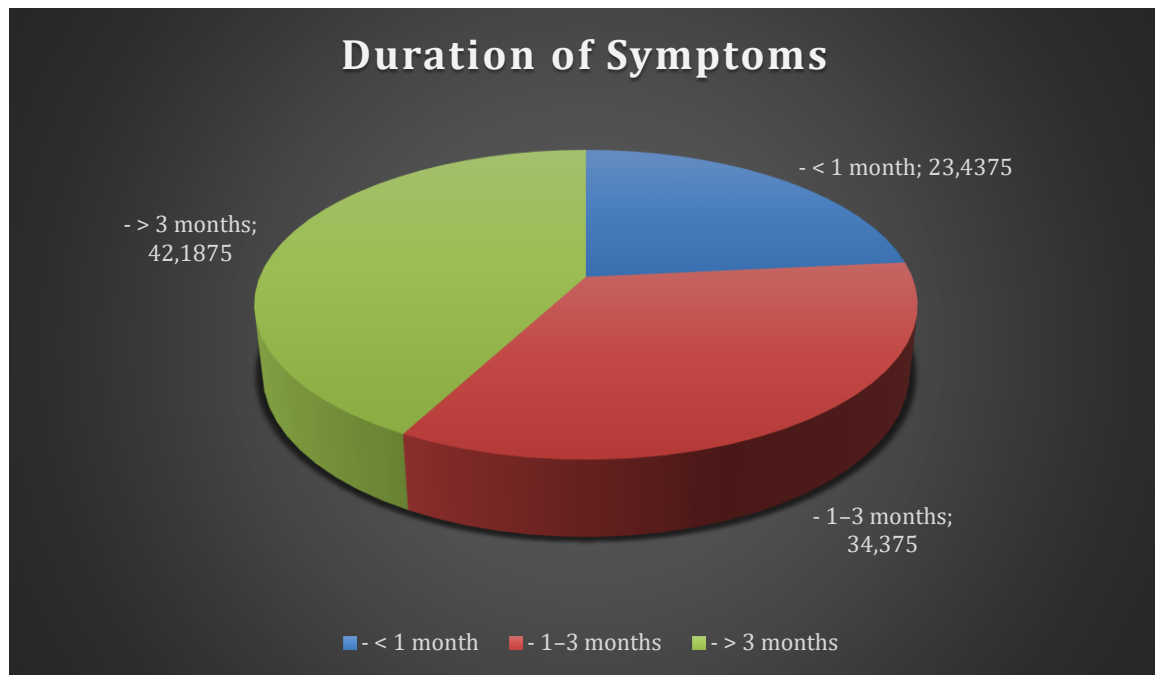


Figure 1. Duration of Symptoms before Presentation of Abdominal Tuberculosis at UDUTH Sokoto.

4. 4. Clinical Presentation

The most common symptom was weight loss, reported in 62 patients (96.9%), followed closely by abdominal pain in 60 (93.8%) and fever and altered bowel habits in 58 (90.6%) each. Abdominal distension was observed in 41 patients (64.1%), while night sweats were present in 30 (46.9%). These findings highlight the non-specific and systemic nature of abdominal tuberculosis.

- **Types of Abdominal Tuberculosis**

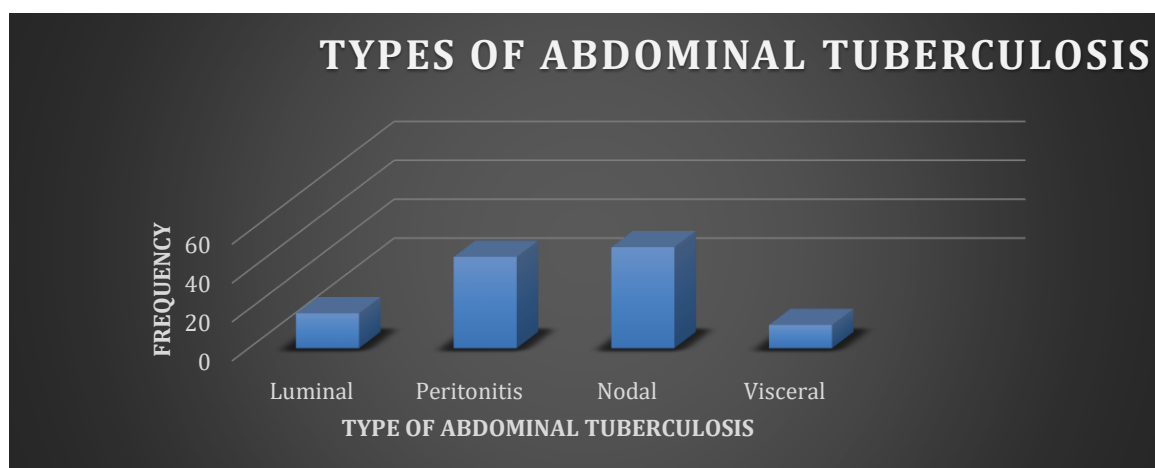


Figure 2. Frequency of Types of Abdominal Tuberculosis in Sokoto.

Abdominal TB was categorized into four types based on anatomical location and presentation:

- Nodal TB was the most frequent, found in 52 patients (81.3%).
- Peritoneal involvement occurred in 47 cases (73.4%).
- Luminal TB was seen in 18 patients (28.1%).
- Visceral TB was documented in 12 patients (18.8%).

It is important to note that multiple anatomical sites were often involved in the same patient, leading to overlaps in classification.



Figure 3. Intraoperative Pictures of a Young Man Operated on at UDUTH Sokoto Depicting Widespread Peritoneal Nodules in Peritoneal TB.



Figure 4. Intraoperative Pictures of a Young Man Operated on at UDUTH Sokoto Depicting Mesenteric Lymph Nodes Enlargement, Black Arrow, and Widespread Peritoneal Nodules, Blue Thick Arrow.

4. 5. Time of Diagnosis

Diagnosis was established postoperatively in the majority of cases (50 patients, 78.1%), indicating that definitive diagnosis often followed surgical intervention. Only 14 patients (21.9%) were diagnosed preoperatively, suggesting a limitation in non-invasive diagnostic capabilities.

4. 6. Diagnostic Modalities Utilized

All 64 patients had histopathological confirmation (100%). In addition:

- Laparotomy/laparoscopy findings contributed to the diagnosis in 28 cases (43.8%).
- GeneXpert MTB/RIF assay was utilized in 10 patients (15.6%).
- Imaging (Ultrasound/CT scan) was helpful in only 5 patients (7.8%).

These findings reflect the critical role of surgical and histopathological evaluation in confirming abdominal TB in this setting.

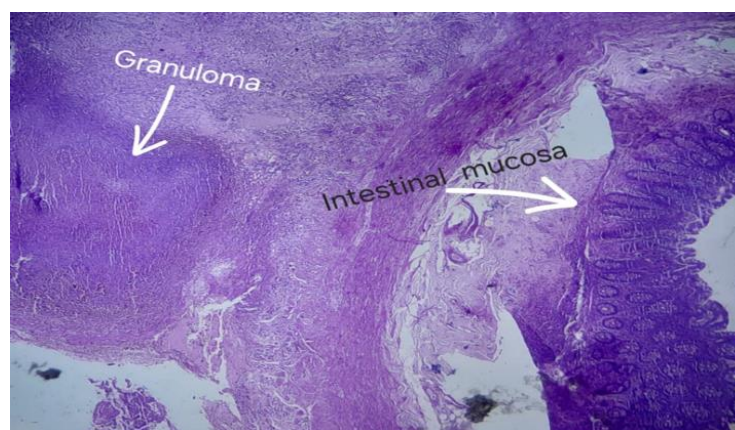


Figure 5. Section from the Intestine Shows Granulomata within the Serosa. Other Areas Show Intestinal Mucosa.H&Ex200.

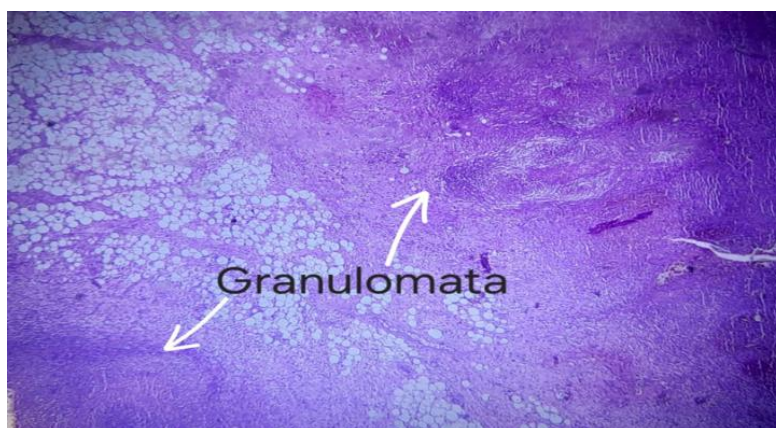


Figure 6. Section from the Intestinal Serosa Shows Granulomata with Caseous Necrosis. H&E X 200.

4. 7. Treatment Modalities

All patients received anti-TB chemotherapy as the mainstay of treatment. Additionally, 12 patients (18.8%) underwent surgical interventions beyond diagnostic laparotomy, in conjunction with medical therapy. These were typically indicated for complications such as obstruction or therapeutic decompression and abscess drainage.

4. 8. Surgical Interventions Performed

- Peritoneal biopsy alone was the most common procedure (32 cases, 50%).
- Drainage of intra-abdominal abscesses was performed in 20 cases (31.3%).
- Adhesiolysis was carried out in 8 patients (12.5%).

- Bowel resection and anastomosis were necessary in 4 cases (6.3%) due to obstructive complications.

4. 9. Postoperative Complications

A majority of patients had uneventful postoperative courses. However:

- Wound infections occurred in 15 patients (23.4%).
- Reoperation was required in 2 cases (3.1%).
- No cases of enterocutaneous fistula formation were recorded.
- 47 patients (73.4%) had no complications.

4. 10. Treatment Outcomes

Outcomes were favourable in most cases:

- Complete recovery was achieved in 41 patients (64.1%).
- Mortality occurred in 3 patients (4.7%), likely due to late presentation and/or comorbidities.
- No recurrences were recorded during the follow-up period.
- 20 patients (31.3%) were lost to follow-up, reflecting a significant challenge in continuity of care.

4. 11. Associations between Clinical Parameters and Outcome

HIV Status and Clinical Outcomes

- Among the 12 patients who were HIV-positive:
- ✓ Complication rate: 50% (6 patients) had post-treatment complications such as wound infection and prolonged hospital stay, compared to 20.8% among HIV-negative patients, p value 0.0868. Though clinically important, it was not statistically significant.
- ✓ Mortality rate: 2 out of the 3 total deaths (66.7%) occurred in HIV-positive patients, despite them comprising only 18.8% of the cohort, $p=0.0041$.

Type of Abdominal TB vs. Need for Surgery

- Luminal TB was more frequently associated with bowel obstruction and required bowel resection and adhesiolysis in 75% of such cases.
- Peritoneal and nodal TB were mostly managed with biopsy or abscess drainage.
- Luminal disease subtype showed a stronger association with surgical intervention compared to peritoneal or nodal involvement.

Time of Diagnosis vs. Treatment Outcome

- Preoperative diagnoses (21.9%) had a higher rate of complete recovery (85.7%) and fewer complications.
- Postoperative diagnoses (78.1%) were more likely to require emergency interventions and had a greater proportion of patients lost to follow-up.

Duration of Symptoms Before Presentation vs. Complications

- Patients presenting after >3 months of symptoms had a complication rate of 33%, compared to only 13% in those presenting within 1 month. Although the difference was clinically significant, it was not statistically significant, $p=0.792$.

5. Discussion

Abdominal tuberculosis (TB) continues to pose a formidable challenge to diagnosis and treatment, especially in low-resource settings. This 10-year retrospective study at Usmanu Danfodiyo University Teaching Hospital (UDUTH), Sokoto, Nigeria, offers valuable insights into the demographic, clinical, and therapeutic profiles of patients with abdominal TB. The findings are examined in light of previous Nigerian studies and international experiences.

The study identified 64 confirmed abdominal TB (ATB) cases over a decade, which is consistent with the burden reported from similar tertiary institutions in Nigeria. For instance, Akinkuolie et al. (2008) documented 47 cases over 20 years at Wesley Guild Hospital, Ile-Ife, while Ohanaka and Egbagbe (2004) reported five cases in six years in Benin City (Akinkuolie et al., 2008; Ohanaka & Egbagbe, 2004).

Globally, abdominal TB comprises about 10–12% of extrapulmonary TB, with regional variation. Dhali et al. (2021) in India reported 317 cases over five years, noting a rising trend (Dhali et al., 2021). Calin et al. (2021) in Paris described 80 cases over 12 years, predominantly in African and Asian immigrants, reflecting the disease's persistence in high-risk groups even in low-incidence countries (Calin et al., 2021).

These parallels support the assertion that abdominal TB, though an important clinical entity, remains underdiagnosed, under-reported, and often misclassified due to its nonspecific presentation and overlap with other abdominal conditions.

Our findings demonstrate that abdominal tuberculosis predominantly affects young and middle-aged adults, with nearly two-thirds of cases (61%) occurring between the ages of 20 and 49 years. The peak incidence was in the third decade (28.1%), followed by the fourth (18.8%) and second (15.6%) decades. This pattern mirrors prior Nigerian and international studies. For example, Dauda et al. (2010) and Cho et al. (2018) documented clustering in early to middle adulthood, while Ihekwebaba (1993), in his 30-year Ibadan series, reported that 78% of patients were under 40 years, with a peak incidence in the second decade (Cho et al., 2018; Dauda et al., 2010; Ihekwebaba, 1993). Notably, while female predominance was described in Ibadan and Ile-Ife (Akinkuolie et al., 2008; Ihekwebaba, 1993), our cohort showed a male predominance (59.4%). Such differences may reflect variations in socio-cultural roles, occupational exposures, and healthcare-seeking behaviour across populations and over time.

Abdominal tuberculosis is a great mimicker, with patients commonly presenting with weight loss (96.9%), abdominal pain (93.8%), fever (90.6%), and altered bowel habits (90.6%), in line with the non-specific but classical symptomatology of abdominal TB. These symptoms are consistent with findings from Benin (Ohanaka & Egbagbe, 2004), Zaria (Dauda et al., 2010), Ile-Ife (Akinkuolie et al., 2008), and Korea (Cho et al., 2018).

Diagnostic delay remains a major challenge. Only 21.9% of patients in our study were diagnosed preoperatively, reflecting the low yield of imaging and laboratory studies in resource-limited settings. Histopathological confirmation remains the gold standard. Similar challenges were described by Akinkuolie et al. (Akinkuolie et al., 2008), where only 29% of ascitic fluid analyses were diagnostic. Similarly, Abu-Zidan and Sheek-Hussein (2019) emphasized that delays in diagnosis often lead to increased morbidity due to misclassification as malignancy or inflammatory bowel disease (Abu-Zidan & Sheek-Hussein, 2019).

GeneXpert MTB/RIF was used in only 15.6% of cases in our setting. This under utilization is worrisome, as nucleic acid amplification tests (NAATs) like GeneXpert have demonstrated high specificity, albeit variable sensitivity, in extrapulmonary TB. Maulahela et al. (2022) reported GeneXpert sensitivities ranging from 81 to 95% in intestinal TB, outperforming conventional acid-fast bacilli staining and even histology in some cases (Maulahela et al., 2022). However, performance depends on sample type; for example, Abu Talib et al. (2019) found only 39% sensitivity for stool-based GeneXpert (Talib et al., 2019).

Imaging, particularly CT and laparoscopy, plays a pivotal role in diagnosis. Jha et al. (2023) and Abu-Zidan et al. (2019) stress the value of targeted imaging to guide biopsy (Abu-Zidan & Sheek-Hussein, 2019; Jha et al., 2025). Laparoscopy, in particular, has diagnostic yields exceeding 90% and provides visual confirmation of peritoneal involvement (Muron et al., 2015; Safarpour et al., 2007). Unfortunately, the utilization of these diagnostic modalities is often limited in our setting.

In our cohort, only about one-fifth of cases were diagnosed preoperatively, with most confirmations made on postoperative histopathology. While this aligns with many resource-limited series as noted above, it contrasts with reports from centers that routinely employ CT enterography, colonoscopy with targeted biopsy, or diagnostic laparoscopy (Di Buono et al., 2024; Ep & Bt, 2017), where preoperative diagnosis rates are appreciably higher and operative confirmations less frequent. The divergence likely reflects diagnostic capacity and pathway design: where imaging access and endoscopic biopsy are standard, fewer patients proceed to laparotomy for diagnosis; where these are constrained (stock-outs, equipment downtime, or cost barriers), tissue diagnosis is deferred to surgery. Our data, therefore, underscore the real-world gap between recommended algorithms and what is feasible in tertiary hospitals serving large catchment areas with intermittent access to advanced diagnostics.

All patients in our cohort received anti-TB chemotherapy. As reported in global literature, the response was favorable, with 64.1% achieving full recovery and mortality remaining low (4.7%). These figures align with outcomes reported by Cho et al. (2018) (84.2% cure, 1.4% mortality) and Dhali et al. (2021) (~82% cure, 2.2% mortality) (Cho et al., 2018; Dhali et al., 2021; Ohanaka & Egbagbe, 2004). These studies reinforce that, when appropriately treated, abdominal TB has excellent outcomes.

Surgical intervention was necessary in 18.8% of our cases, primarily for complications such as obstruction or abscess. This is consistent with findings by Dhali et al. (2021) and Calin et al. (2021), who reported surgery in 15–20% of patients (Dhali et al., 2021; Calin et al., 2021). Most surgeries were diagnostic or for adhesiolysis and abscess drainage, emphasizing that operative management is adjunctive to medical therapy. This stands in contrast to surgical series from West and East Africa, where emergency obstruction predominates, and bowel resection is frequently necessary, and to some South African emergency laparotomy cohorts with high stoma rates (Chalya et al., 2013; Islam et al., 2014; Ohene-Yeboah, 2006). On the other end of the spectrum, large Indian cohorts report even lower operative rates, reflecting stronger preoperative case ascertainment and medical management (Keena et al., 2022). Together, these contrasts suggest that Sokoto sits mid-spectrum: not as resection-heavy as obstruction-dominant surgical cohorts, yet still constrained enough diagnostically that a meaningful minority require operative intervention. Strengthening preoperative laparoscopy and image-guided biopsy could further shift our case mix toward non-operative confirmation.

However, 31.3% of our patients were lost to follow-up, raising concerns about treatment completion, recurrence, and community-level surveillance. Sharma and Bhatia (2004) and Abu-Zidan et al. (2019) similarly note that poor follow-up is a major hurdle in extrapulmonary TB care, especially in resource-limited regions (Abu-Zidan & Sheek-Hussein, 2019; Sharma & Bhatia, 2004). Factors likely contributing to this include patient poverty, lack of structured follow-up infrastructure (e.g., call-back systems, DOTS-based community care), internal migration patterns, and the societal stigma associated with TB. Improving retention would require integrated follow-up systems, enhanced TB education, and possibly incentivized patient engagement models.

In contrast, a recent meta-analysis across Nigeria and other countries reported a pooled treatment success rate of ~75.5%, a mortality rate of ~6.8%, and a loss-to-follow-up rate of ~11.4% (Ukoaka et al., 2024). Similarly, in Meru County, Kenya, deaths and loss to follow-up were 5.1% and 6.3% (Ngari et al., 2025). A South African study reported favorable outcomes but still observed loss to follow-up in 23.9% of cases and a mortality rate of 4.4% (Vita et al., 2024).

These contrasts suggest that while effective medical therapy can keep mortality low, retention in care remains the major limiting factor in our setting. Our findings, therefore, emphasize the need for strengthening patient tracking through SMS or community health workers and building decentralized DOTS linkages into surgical TB care pathways to reduce defaulting. The interplay between tuberculosis (TB) and human immunodeficiency virus (HIV) remains a major public health concern, particularly in sub-Saharan Africa, where co-infection rates are among the highest globally. In our cohort, 18.8% of patients with abdominal TB were HIV-positive, underscoring the critical role of HIV as both a risk factor and a complicating element in the diagnosis and management of extrapulmonary TB.

In a comprehensive review, Borkar et al. highlighted that abdominal TB is significantly more prevalent among HIV-positive individuals, especially in resource-limited settings, where diagnostic infrastructure is poor (Borkar et al., 2016). Similarly, Heller

et al. observed that HIV co-infected patients frequently presented with diffuse peritoneal involvement, lymphadenopathy, and minimal pulmonary findings, making diagnosis particularly difficult without high clinical suspicion and access to advanced diagnostic modalities (Heller et al., 2010).

The Focused Assessment with Sonography for HIV/TB (FASH) protocol, as described by Heller et al. (2016) and later by Van Hoving and colleagues, has emerged as a practical point-of-care tool to detect features such as ascites, lymphadenopathy, and splenic lesions that support the diagnosis of abdominal TB in HIV-positive individuals. Unfortunately, such imaging algorithms are not yet standard in most Nigerian centers, including ours, due to a lack of trained personnel and ultrasound availability in emergency units (Heller et al., 2010; Van Hoving et al., 2020).

In our cohort, patients who were HIV-positive had higher rates of complications (41.7% vs. 30.0%) and mortality (16.7% vs. 2.5%) compared to their HIV-negative counterparts. However, the association between HIV status and complications was not statistically significant ($p = 0.686$). This aligns with previous studies (Calin et al., 2021; Cho et al., 2018; Sharma & Bhatia, 2004), suggesting that while HIV co-infection may contribute to delayed healing and increased susceptibility to sepsis, small sample sizes often limit statistical power.

HIV co-infection was present in ~19% of our patients. Although we observed higher rates of complications and mortality among HIV-positive individuals, these differences did not reach statistical significance in our sample, as noted above. This contrasts with several high-HIV-burden African surgical series that document markedly higher mortality concentrated among HIV-positive patients, often with advanced immunosuppression (Chalya et al., 2013; Islam et al., 2014). Two factors may explain this discrepancy: first, the sample size and power of our HIV-positive subgroup were small; second, differences in case mix and care pathways—many patients in those high-mortality cohorts underwent emergency laparotomy for perforation or obstruction, whereas a smaller fraction of our patients required major resections. The implication is that integrated TB/HIV services and stabilising patients before surgery may attenuate the excess risk otherwise attributed to HIV (Keena et al., 2022; Ohene-Yeboah, 2006).

Patients with luminal or visceral TB had a higher frequency of requiring surgery (e.g., resection or abscess drainage) compared to those with purely nodal or peritoneal TB. Although this difference was not statistically significant ($p = 0.428$), this observation is consistent with pathophysiological expectations and prior reports (Cho et al., 2018). Luminal TB often results in strictures, adhesions, or perforations, necessitating operative intervention, whereas nodal TB tends to follow a more indolent course.

This underscores the importance of early subtype differentiation, ideally using imaging and diagnostic laparoscopy where feasible, to anticipate surgical needs and guide early referral. Only 21.9% of patients in this study were diagnosed pre-operatively. A comparison between pre-operative and post-operative diagnosis groups revealed no significant difference in treatment outcomes ($p = 0.738$). Despite this, early diagnosis is desirable, as it reduces exposure to surgical risk and facilitates the timely initiation of chemotherapy.

The lack of a significant difference may reflect the universal use of anti-TB therapy post-confirmation, regardless of the route of diagnosis. However, as highlighted by Akinkuolie et al. (Akinkuolie et al., 2008), early diagnosis could reduce hospital stay, complication rates, and the need for surgery. Investments in access to GeneXpert, laparoscopy, and ultrasound-guided biopsy are thus justified.

Patients who presented after more than three months of symptoms experienced a higher proportion of complications (37.0%) than those presenting within 1 month (26.7%). Despite this gross numerical difference, the association was not statistically significant ($p = 0.401$). This may be due to insufficient statistical power, especially within subgroups, or misclassification bias in recording symptom onset. In contrast, late presentation was a statistically significant predictor of mortality in the Tanzanian cohort (Chalya et al., 2013).

Nonetheless, the clinical relevance of delayed presentation is undeniable. Prolonged symptom duration has been linked to advanced disease, adhesions, bowel obstruction, and peritoneal sepsis, all of which increase the likelihood of operative intervention and postoperative morbidity (Ihekweba, 1993; Sharma & Bhatia, 2004). Community education and primary care awareness campaigns may help mitigate these delays.

6. Conclusion

Abdominal tuberculosis remains a significant diagnostic and therapeutic challenge in our setting, despite the declining overall TB burden. This 10-year retrospective study at Usmanu Danfodiyo University Teaching Hospital (UDUTH), Sokoto, highlights the continuing relevance of abdominal TB as a cause of chronic abdominal symptoms, particularly in young adults. Delayed presentation, low preoperative diagnostic yield, and a reliance on postoperative histological confirmation underscore gaps in early detection capabilities. While most patients responded favorably to anti-TB therapy, the substantial proportion requiring surgical intervention and the high rate of loss to follow-up reflect persistent health system and societal barriers.

Importantly, our findings reinforce that abdominal TB often mimics malignancy or other chronic abdominal diseases and may go unrecognized in the absence of high clinical suspicion, especially in resource-constrained environments. Male predominance in our cohort contrasts with earlier regional studies and may reflect shifting epidemiological patterns. HIV co-infection, present in nearly one-fifth of our cases, adds further complexity to diagnosis and management.

Despite the low mortality, the observed delays, diagnostic limitations, and follow-up attrition represent critical challenges that must be addressed to improve outcomes.

These findings underscore the need for heightened clinical suspicion, improved diagnostic access (particularly to laparoscopy and GeneXpert), and strengthened patient tracking systems to enhance early diagnosis, reduce complications, and optimise treatment outcomes in abdominal tuberculosis, particularly within low-resource settings.

These findings provide respected insights into the complexities of diagnosing and managing abdominal tuberculosis and offer practical implications for improving early detection, diagnostic approaches, and patient follow-up in clinical practice.

7. Recommendations

Based on our study and a review of current evidence, the following measures are recommended to strengthen abdominal TB management in similar low-resource settings:

1. Early Diagnosis and Diagnostic Capacity Building

- Expand access to GeneXpert MTB/RIF, especially in surgical and emergency units, to facilitate preoperative diagnosis.
- Promote routine ultrasound with the FASH protocol in high TB/HIV burden settings.
- Establish laparoscopy services to allow for minimally invasive diagnosis and therapeutic interventions.

2. Integrated TB-HIV Services

- Ensure routine TB screening for all HIV-positive patients and vice versa.
- Incorporate abdominal TB in clinical algorithms for persistent abdominal complaints in HIV patients.

3. Health Education and Community Awareness

- Launch community-based education programmes to promote early presentation and reduce stigma surrounding TB and HIV.
- Emphasise the importance of treatment adherence and long-term follow-up to prevent relapse and complications.

4. Surveillance and Follow-up Mechanisms

- Establish structured follow-up systems (SMS reminders, community health worker tracking) to reduce loss to follow-up.
- Integrate patient navigation tools to improve linkage to care post-discharge.

5. Multicentre Collaboration and Research

- Encourage multicentre studies to better characterise the national burden, improve generalisability, and guide policy.
- Advocate for government and donor investment in TB diagnostic infrastructure and research funding.

8. Limitations

- Single-centre study: The findings may not be fully generalisable to other parts of Nigeria or sub-Saharan Africa, where healthcare-seeking behaviour, diagnostic access, and patient demographics may differ.
- Retrospective design: Dependence on clinical records introduces risks of missing data and underreporting of certain variables, such as HIV status or long-term follow-up outcomes.
- Small sample size: Although comparable to other Nigerian studies, the relatively modest sample size limited the power of inferential analysis; most findings are descriptive rather than predictive.
- Loss to follow-up: A significant proportion of patients (31.3%) were lost to follow-up, limiting the ability to fully evaluate long-term treatment outcomes and recurrence rates.
- Limited diagnostics: Access to molecular diagnostics (GeneXpert) and advanced imaging was restricted during much of the study period, which may have delayed preoperative diagnosis and influenced management pathways.

COVID-19 impact: The study period included the COVID-19 pandemic years, during which disruptions in TB services likely contributed to delayed presentation, diagnostic backlogs, and possible underestimation of true incidence.

Data Availability

The research data are stored in completed proformas and on the personal computer of the corresponding author. The data is available on request.

Conflicts of Interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

References

- Abu-Zidan, F. M., & Sheek-Hussein, M. (2019). Diagnosis of abdominal tuberculosis: Lessons learned over 30 years: pectoral assay. *World Journal of Emergency Surgery : WJES*, 14, 33. <https://doi.org/10.1186/s13017-019-0252-3>.
- Akinkuolie, A. A., Adisa, A. O., Agbakwuru, E. A., Egharevba, P. A., & Adesunkanmi, A. R. K. (2008). Abdominal tuberculosis in a Nigerian teaching hospital. *African Journal of Medicine and Medical Sciences*, 37(3), 225–229.
- Al-Zanbagi, A. B., & Shariff, M. K. (2021). Gastrointestinal tuberculosis: A systematic review of epidemiology, presentation, diagnosis and treatment. *Saudi Journal of Gastroenterology: Official Journal of the Saudi Gastroenterology Association*, 27(5), 261–274. https://doi.org/10.4103/sjg.sjg_148_21.

- Borkar, M. S., Joshi, A. S., Kashid, A. A., Gawale, C. G., Kakade, R. D., & Chimote, H. N. (2016). Clinical profile of 128 HIV positive cases with abdominal tuberculosis. *International Journal of Scientific Reports*, 2(1), 18. <https://doi.org/10.18203/issn.2454-2156.IntJSciRep20160089>.
- Calin, R., Belkacem, A., Caraux-Paz, P., Wagner, M., Guillot, H., Veziris, N., Jaureguiberry, S., Caumes, E., Patey, O., & Pourcher, V. (2021). Abdominal Tuberculosis: Experience from Two Tertiary-Care Hospitals in the Paris Region. *The American Journal of Tropical Medicine and Hygiene*, 104(1), 223–228. <https://doi.org/10.4269/ajtmh.20-0023>.
- Chalya, P. L., Mchembe, M. D., Mshana, S. E., & ... (2013). Tuberculous bowel obstruction at a university teaching hospital in Northwestern Tanzania: A surgical experience with 118 cases. In *World Journal of ...* Springer. <https://doi.org/10.1186/1749-7922-8-12>.
- Cho, J.-K., Choi, Y. M., Lee, S. S., Park, H. K., Cha, R. R., Kim, W. S., Kim, J. J., Lee, J. M., Kim, H. J., Ha, C. Y., Kim, H. J., Kim, T. H., Jung, W. T., & Lee, O. J. (2018). Clinical features and outcomes of abdominal tuberculosis in southeastern Korea: 12 years of experience. *BMC Infectious Diseases*, 18(1), 699. <https://doi.org/10.1186/s12879-018-3635-2>.
- Dauda, M. M., Ahmed, A., Okpapi, J. U., Ahmed, S. A., Randawa, A. J., & Mukhtar, H. M. (2010). Abdominal tuberculosis in surgical practice in northern Nigeria. *Nigerian Journal of Medicine : Journal of the National Association of Resident Doctors of Nigeria*, 19(4), 415–418. <https://doi.org/10.4314/njm.v19i4.61966>.
- Dhali, A., Das, K., Dhali, G. K., Ghosh, R., Sarkar, A., & Misra, D. (2021). Abdominal Tuberculosis: Clinical Profile and Outcome. *The International Journal of Mycobacteriology*, 10(4), 414. https://doi.org/10.4103/ijmy.ijmy_195_21.
- Di Buono, G., Romano, G., Amato, G., Barletta, G., Romano, G., Adelfio, N., Geraci, G., & Agrusa, A. (2024). Surgical Management of Complicated Abdominal Tuberculosis: The First Systematic Review—New Treatments for an Ancient Disease and the State of the Art. *Journal of Clinical Medicine*, 13(16), 4894. <https://doi.org/10.3390/jcm13164894>.
- Ep, W., & Bt, P. (2017). Abdominal tuberculosis: Is there a role for surgery? *World Journal of Gastrointestinal Surgery*, 9(8). <https://doi.org/10.4240/wjgs.v9.i8.174>.
- Gulumbe, B. H., Abdulrahim, A., Ahmad, S. K., Lawan, K. A., & Danlami, M. B. (2025). WHO report signals tuberculosis resurgence: Addressing systemic failures and revamping control strategies. *Decoding Infection and Transmission*, 3, 100044. <https://doi.org/10.1016/j.dcit.2025.100044>.
- Hailu, S., Hurst, C., Cyphers, G., Thottunkal, S., Harley, D., Viney, K., Irwin, A., Dean, J., & Nourse, C. (2024). Prevalence of extra-pulmonary tuberculosis in Africa: A systematic review and meta-analysis. *Tropical Medicine & International Health: TM & IH*, 29(4), 257–265. <https://doi.org/10.1111/tmi.13970>.
- Heller, T., Goblirsch, S., Wallrauch, C., Lessells, R., & Brunetti, E. (2010). Abdominal tuberculosis: Sonographic diagnosis and treatment response in HIV-positive adults in rural South Africa. *International Journal of Infectious Diseases*, 14, e108–e112. <https://doi.org/10.1016/j.ijid.2009.11.030>.
- Ihekwa, F. N. (1993). Abdominal tuberculosis: A study of 881 cases. *Journal of the Royal College of Surgeons of Edinburgh*, 38(5), 293–295.
- Islam, J., Clarke, D. L., & Thomson, S. R. (2014). Lessons from emergency laparotomy for abdominal tuberculosis in the HIV/AIDS era. *South African Journal of Surgery*, 52(1), 10–12.
- Jeong, Y., & Min, J. (2023). Impact of COVID-19 Pandemic on Tuberculosis Preventive Services and Their Post-Pandemic Recovery Strategies: A Rapid Review of Literature. *Journal of Korean Medical Science*, 38(5), e43. <https://doi.org/10.3346/jkms.2023.38.e43>.
- Jha, S., Verma, S., & Bhatnagar, S. (2025). Understanding Bowel Habits and Stool Form Among Indian Adolescents: A Descriptive Study. In *Cureus*. [cureus.com. https://www.cureus.com/articles/341132-understanding-bowel-habits-and-stool-form-among-indian-adolescents-a-descriptive-study.pdf](https://www.cureus.com/articles/341132-understanding-bowel-habits-and-stool-form-among-indian-adolescents-a-descriptive-study.pdf).

- Keena, M., Chawla, G., Sonika, U., Abrol, N., Hiremath, S., & Meena, V. K. (2022). Indian tubercular belly: A prospective study of 140 patients of abdominal tuberculosis and their outcomes. *Journal of Family Medicine and Primary Care*, 11(6), 2423. https://doi.org/10.4103/jfmmpc.jfmmpc_1198_21.
- Maulahela, H., Simadibrata, M., Nelwan, E. J., Rahadiani, N., Renesteen, E., Suwarti, S. W. T., & Anggraini, Y. W. (2022). Recent advances in the diagnosis of intestinal tuberculosis. *BMC Gastroenterology*, 22(1), 89. <https://doi.org/10.1186/s12876-022-02171-7>.
- Muroni, M., Rouet, A., Brocheriou, I., & Houry, S. (2015). Abdominal Tuberculosis: Utility of Laparoscopy in the Correct Diagnosis. *Journal of Gastrointestinal Surgery*, 19(5), 981–983. <https://doi.org/10.1007/s11605-015-2753-z>.
- Ngari, M. M., Mberia, J. K., Kanana, E., Sanga, D., Ngari, M. K., Nyagah, D. N., & Abdullahi, O. A. (2025). Mortality and loss to follow-up among Tuberculosis patients on treatment in Meru County, Kenya: A retrospective cohort study. *PLOS Global Public Health*, 5(3), e0003896. <https://doi.org/10.1371/journal.pgph.0003896>.
- Ohanaka, C. E., & Egbagbe, E. E. (2004). ADULT ABDOMINAL TUBERCULOSIS IN BENIN CITY, NIGERIA. *Sahel Medical Journal*. https://journals.lww.com/shmj/abstract/2004/07040/adult_abdominal_tuberculosis_in_benin_city,.5.aspx.
- Ohene-Yeboah, M. (2006). Case series of acute presentation of abdominal TB in Ghana. *Tropical Doctor*. <https://doi.org/10.1258/004947506778604643>.
- Olaleye, S. A., Balogun, O. S., & Adusei-Mensah, F. (2023). Bibliometric structured review of tuberculosis in Nigeria. *African Health Sciences*, 23(2), 139–160. <https://doi.org/10.4314/ahs.v23i2.16>.
- Safarpor, F., Aghajanzade, M., Kohsari, M. R. R., Hoda, S., Sarshad, A., & Safarpor, D. (2007). Role of Laparoscopy in the Diagnosis of Abdominal Tuberculosis. *Saudi Journal of Gastroenterology*, 13(3), 133. <https://doi.org/10.4103/1319-3767.33465>.
- Sharma, M. P., & Bhatia, V. (2004). Abdominal tuberculosis. *The Indian Journal of Medical Research*, 120(4), 305–315.
- Talib, A., Bhatti, S., Mehmood, K., Naim, H., Haider, I., Lal, H., Ali, G., & Nashit, M. (2019). GeneXpert in stool: Diagnostic yield in Intestinal Tuberculosis. *Journal of Clinical Tuberculosis and Other Mycobacterial Diseases*, 17, 100131. <https://doi.org/10.1016/j.jctube.2019.100131>.
- Tuberculosis (TB). (n.d.). Retrieved May 13, 2025, from <https://www.who.int/news-room/fact-sheets/detail/tuberculosis>.
- Ukoaka, B. M., Daniel, F. M., Wagwula, P. M., Ahmed, M. M., Udam, N. G., Okesanya, O. J., Babalola, A., Wali, T. A., Afolabi, S., Udoh, R. A., Peter, I. G., & Maaji, L. A. (2024). Prevalence, clinical characteristics, and treatment outcomes of childhood tuberculosis in Nigeria: A systematic review and meta-analysis. *BMC Infectious Diseases*, 24(1), 1447. <https://doi.org/10.1186/s12879-024-10321-3>.
- Van Hoving, D. J., Kenge, A. P., Maartens, G., & Meintjes, G. (2020). Point-of-Care Ultrasound Predictors for the Diagnosis of Tuberculosis in HIV-Positive Patients Presenting to an Emergency Center. *JAIDS Journal of Acquired Immune Deficiency Syndromes*, 83(4), 415. <https://doi.org/10.1097/QAI.0000000000002279>.
- Vita, D., Aznar, M. L., Martínez-Campreciós, J., Kansietoko, D. C. M. S., & Molina, I. (2024). Risk Factors Associated with Loss to Follow-Up during Tuberculosis Treatment in the Sanatorium Hospital of Luanda, Angola. *Tropical Medicine and Infectious Disease*, 9(6), 131. <https://doi.org/10.3390/tropicalmed9060131>.



From Penalty to Prevention: A Computational Model of Corruption Reduction Using Algorithmic Governance and Digital Oversight

Tanjina Nasrin Tanji¹, and Sayma Nasrin Shompa^{1*} 



¹ International Islamic University, Chittagong, Computer Science and Engineering, Bangladesh, Chittagong.

ARTICLE INFO

Received: 07th October 2025
Received in revised form: 13th November 2025
Accepted: 22th November 2025
Published: 15th March 2026

*Corresponding Author:

Sayma Nasrin Shompa
E-mail:
Saimanasrin453@gmail.com

Citation: Tanji, T. N., & Shompa, S. N. (2026). From Penalty to Prevention: A Computational Model of Corruption Reduction Using Algorithmic Governance and Digital Oversight. *Modern Journal of Health and Applied Sciences*, 3(1), 55-73.

Copyright (c) 2026 Modern Journal of Health and Applied Sciences (MJHAS)

Open Access



This work is licensed under a [Creative Commons Attribution NonCommercial 4.0 International](https://creativecommons.org/licenses/by-nc/4.0/) license.

ABSTRACT

This study presents a computational version that integrates algorithmic regime and virtual oversight to address corruption through proactive, prevention-oriented structures. Using agent-based and system dynamics simulations, the version shows that the algorithmic oversight, including AI-powered audits, transparency dashboards and blockchain verification, reduces the occurrence of corruption, enhances detection capabilities, lowers compliance costs, and improves public confidence.

These findings highlight the capability of virtual gadgets to reform governance structures by embedding integrity, transparency, and performance into institutional procedures. However, adopting such systems is not without challenges. Ethical risks, including set-of-rules bias, overlapping automation, and lecturer boundaries, must be carefully managed through fairness-by-design approaches, third-party audits, and continuous human oversight.

The success of the algorithmic regime depends on significant institutional reforms, public values, and its alignment with prevailing trends, including constitutional AI and ethical public administration.

Keywords: Corruption reduction, Algorithmic governance, Digital oversight, Computational model, transparency.

DOI: <https://doi.org/10.70411/MJHAS.3.1.2026324>

1. Introduction

Corruption has long been identified as a systemic problem that undermines governance, economic development and institutional trust. Traditional techniques to address corruption are regularly preventive or punitive in nature and often produce combined effects, highlighting the firmness of structural and behavioral challenges. Computational techniques have been increasingly applied in this field, providing new ways to simulate, analyze, and understand the dynamics of corruption.

For example, agent-based models, in administrative contexts, offer a means to capture strange interactions between actors and examine their emerging outcomes on the spread of corruption (Elnawawy M et al., 2022). Building on these insights, governance research has shown that artificial intelligence (AI) and multi-agent systems can strengthen compliance, inspection, and policy enforcement. The idea of "Governance-A-Service" positions algorithmic providers as active participants in ensuring institutional integrity (Gaurav et al., 2025), while theoretical progresses such as democracy-in-silico propose AI-assisted frameworks for institutional layout and political structures (Srinivasan & Patapati, 2025). In a concerned manner, agents in public management have been examined as vital to prevent misuse of oversight structures and ensure accountability (Schmitz et al., 2025).

Within the comprehensive AI governance discourse, the third-party audit ecosystem (Raji et al., 2022) and important examinations of fairness and bias in AI-based anti-corruption devices (Odilla, 2024) underline the moral and technical complexities of deploying such systems. Policy-oriented reports, such as OECD (Nichols, 2025), emphasize the ability of general-purpose AI to increase integrity while safeguarding care against unexpected risks. Moral debates focus on the extent to which anti-corruption processes can or should be automated (Ceva & Jiménez, 2022), while development-centred studies suggest that AI resources offer promising applications in the resource-governance settings (Aarvik, 2019).

A recent empirical study shows how AI and data analytics can increase public procurement inspection (Aarvik, 2019) and how blockchain-based governance systems contribute to transparency and the prevention of corruption (Ibrahimy et al., 2024). Computational and statistical analyses expand the methodological toolkit for studying corruption (Abdulwasaa et al., 2024). At the same time, research indicates that the public perceptions of corruption influence confidence in decision-making, adoption and shaping validity (Castelo, 2024). Calls for algorithmic transparency and accountability (Çani et al.), as well as practical applications such as AI-driven procurement monitoring in Ukraine (Rysin & Sukh, 2024) underscore the urgency of addressing governance challenges through technical and institutional innovations.

Nevertheless, concerns remain. The risk associated with AI governance tools (Kaye et al., 2023), the deployment of AI dashboards in Latin America (Gutiérrez & Muñoz-Cadena, 2025), and the increasing tendency of AI agents to imitate human behaviour (Park et al., 2025) Highlight both opportunities and disadvantages. Agent-based and system dynamics simulation of corruption-related decision-making (Kasa et al., 2023) Together with AI-operated oversight mechanisms, they contribute to a growing interdisciplinary foundation for the study of institutional morality. Supplementary research using machine learning (ML), including repeated corruption-risk estimation, preventive system simulations, and ML-based anticorruption detection, further advances boundary identification in references.

Recent developments further point to a change towards preventive rather than purely punitive strategies. These include recognizing the role of the AI regime in public integrity, distinguishing between exploitation and correlation in the ML anticorruption model, and developing AI dashboards for civil service inspection. Constitutional AI, the moral integration of ML in public inspection, concerns related to fairness and prejudice, and challenges of interpretability deepen the discussion on responsible system design. The theoretical grounds of anticorruption are also reinforced by a moral foundations review of corruption principles, as well as debates on institutional reform and comprehensive democratic and governance studies.

Corruption remains a systemic challenge that undermines governance, development and trust. Traditional prevention-based approaches have shown limited success, which increases interest in computational methods that simulate and predict the dynamics of corruption. Agent-based and system dynamics models capture complex interactions, while AI-operated governance

structures emphasize oversight, compliance, and integrity. Emerging studies highlight both opportunities, such as the use of AI and blockchain for transparency and machine-learning-based risk estimation, and risks, including prejudice, overlapping, and moral concerns. Policy reports and theoretical debate further emphasize the need for accountability, fairness and preventive strategies.

This paper proposes a computational model that integrates an algorithmic regime with digital oversight. Unlike punitive approaches, the model emphasizes prevention, transparency and systemic integrity, with the aim of bridging theory and practice to provide scalable solutions in modern rule. By simulating reductions in corruption through agent-based modelling and system dynamics, the study seeks to connect theoretical insights with practical applications.

2. Visual Complement: Conceptual Structure

Consider the following visual elements to better portray a punishment-based infection for a prevention-oriented governance model:

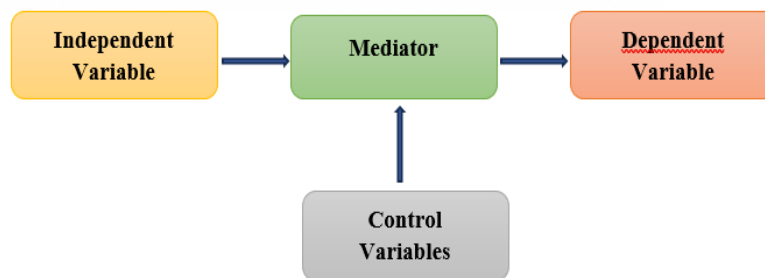


Figure 1. Conceptual Structure of Proposed Model

This diagram reflects changes in the active digital oversight from reactive punishment, integrating algorithmic regime, transparency tools and reaction mechanisms.

Table 1. Comparison of Traditional VS. Proposed Governance Approach.

Aspect	Traditional punishment-based approach	Proposed prevention-based approach
Focus	Reactive punishment	Pay attention to active prevention
Major mechanism fine	restriction, audit, AI audit	dashboard, blockchain
Transparency	less	high
Public trust	variable	increased
Adaptability	hard	dynamic
Cost of higher	high	compliance low

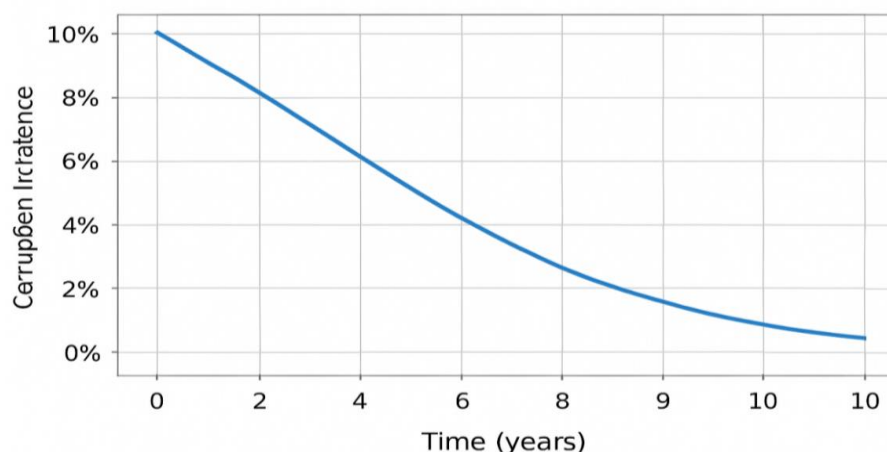


Figure 2. Simulated Deficiency in Corruption Incident

This graph compares the prevalence of corruption over time in the penalty-dominant versus prevention-dominant system, based entirely on the results of the graph agent-based simulation consequences. These visible aids help clarify the theoretical and practical contributions of the proposed version, providing a clear understanding of the algorithmic rule and digital oversight.

3. Related work

Research on corruption and governance has advanced through a range of theoretical and computational approaches. Early studies examined the moral grounds of corruption, highlighting challenges in public oversight of ethical behaviour. Subsequent work expanded on these insights by offering comprehensive critiques of corruption theories, particularly the critical-agent and collective movement models, highlighting how incentives and systemic behaviour sustain corruption.

Later analysis of institutional reforms emphasized the challenging process of embedding ethical practices within governance structures, fulfilling democratic responsibilities, and integrating comprehensive perspectives on governance mechanisms. With the advent of computational strategies, device dynamics and simulation methods were unexpectedly implemented. The agent-based model furnished an initial device to analyze administrative corruption, which captures asymmetrical practices and their emerging outcomes (Elnawawy M et al., 2022).

The device dynamics further depict the complex reaction loops between institutional transparency and corrupt practices. These fashions provided widespread insights but often lacked mechanisms to encompass algorithms or AI-operated oversight. In parallel with theoretical advances, the role of synthetic intelligence in governance gained traction. Preliminary discussions considered ML-based corruption estimate guarantees and boundaries, and comprehensive statistical approaches to connect corruption and poverty (Abdulwasaa et al., 2024).

However, significant obstacles in the interpretation and fairness of machine learning applications have been identified. The moral integration of ML into oversight frameworks underscored the need to balance potential power with accountability, fairness, and transparency. In recent years, the emergence of the algorithmic rule has been observed. Concepts such as "Governance-e-Service" implicated AI agents as compliance promoters within institutions (Gaurav et al., 2025), while "democracy-in-silico" discovered the use of AI for institutional design and alignment within political systems (Srinivasan & Patapati, 2025).

Oversight structures for agent-based AI (Schmitz et al., 2025) and proposals for third-party audit ecosystems (Raji et al., 2022) directly address governance challenges. Nevertheless, fairness and prejudice in AI anticoding tools (Odilla, 2024) remain central concerns, requiring careful deployment (Ceva & Jiménez, 2022; Nichols, 2025). Reports have also highlighted the risks of overregulation in such systems (Kaye et al., 2023) and lessons learnt from early AI dashboards in Latin America (Petheram et al., 2019). Applied research has assessed AI's capabilities in practical initiatives, such as further purchasing oversight (Ayobami et al., 2023), blockchain-based transparency systems (Ibrahimy et al., 2024), and Ukraine's Prizoro platform (Rysin

& Sukh, 2024). Public assumption studies have shown that a corruption algorithm strongly affects confidence in decision-making (Castelo, 2024) and strengthens the requirement of transparency and accountability mechanisms (Çani et al.).

Emerging computational experiments have increasingly focused on simulating human behaviour with AI dealers (Park et al., 2025) and integrating institutional morality into AI-trained oversight. Finally, interdisciplinary studies are converging on the preventive frameworks. These include developing an AI dashboard for civil service tracking, designing constitutional AI to improve coverage stability, and leveraging moral foundations in anticorruption ideas.

Collectively, this body of work shows a shift from reactive, punishment-oriented strategies to prevention-oriented structures that embed AI and virtual oversight at the core of governance innovation. Research on corruption and governance has advanced through a range of theoretical, empirical, and computational approaches. This section synthesizes main developments, highlighting transitions from traditional punitive tactics to modern, prevention-oriented computational frameworks.

3. 1. Theoretical Foundations

Early research focused on the ethical and moral grounds of corruption, often implicating public administration in moral matters. Principal-agent and collective motion ideas emerged to explain how perverse incentives and systemic behaviour contributed to corruption. Later work emphasized the challenges of institutional reforms and embedding moral practices in governance systems, complemented by research on democratic duty.

3. 2. Computational Approach

With the development of simulation techniques, agent-based models (ABMs) and system dynamics (SD) have been used to model corruption dynamics. ABMs capture the peculiar agent behaviour and emerging corruption patterns (Elnawawy M et al., 2022) while the SD version depicts the response as falling between transparency and corruption. However, those models regularly lack integration with the oversight mechanisms for the set of rules.

3. 3. AI and Rule-Based Governance

The role of AI in governance has gained prominence, with initiatives such as Governance-e-Saravia deploying AI marketers to promote institutional compliance (Gaurav et al., 2025). This approach was further extended by Democracy-in-silico through the concept of AI-powered institutional layouts (Srinivasan & Patapati, 2025). Oversight systems for agent AI (Schmitz et al., 2025) and third-birthday celebration, audit the atmosphere (Raji et al., 2022) have been proposed to deal with responsibility, although issues concerning bias and equity persist (Odilla, 2024).

3. 4. Applied Research and Moral Perspectives

Applied research validated AI's potential in real-world platforms, which include public procurement oversight (Ayobami et al., 2023), blockchain-based total transparency (Ibrahimy et al., 2024), and Ukraine's Prizoro (Rysin & Sukh, 2024). However, moral challenges, such as algorithm bias, lecturers and public belief (Çani et al.; Castelo, 2024), remain significant. Policy reports warned against overlap in AI tools (Kaye et al., 2023), while empirical implementation in Latin America offered lessons on adaptive design (Gutiérrez & Muñoz-Cadena, 2025).

3. 5. Changes in Preventive Structure

Recent research shows that preventive strategies have been integrated into AI dashboards, constitutional AI, and moral machine learning systems in governance. This represents a paradigm change from reactive punishment to energetic, digitally enabled oversight devices. To illustrate this improvement, the following timelines summarize the essential milestones in corruption and governance research:

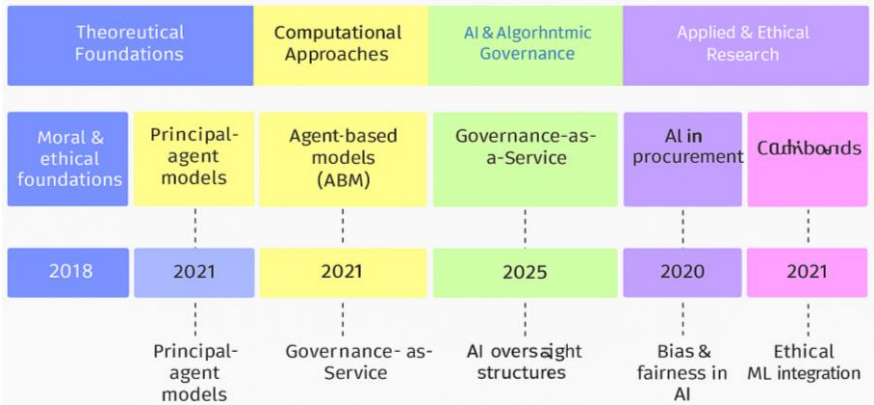


Figure 3. Development of Corruption and Governance Research

Table 2. Comparison of Conventional and Computational Methods to Corruption Rule

Aspect	Traditional Approaches	Computational Approaches
Focus	Reactive, penalty-based	Proactive, prevention-oriented
Methods	Audits, sanctions, guide oversight	ABM, system dynamics, AI audits, blockchain
Key Tools	Legal frameworks, human auditors	AI dashboards, predictive analytics, automated audits
Transparency	Low to slight	High (real-time dashboards, open facts)
Adaptability	Rigid, gradual to reform	Dynamic, conscious of real-time records
Limitations	High price, low scalability, limited deterrence	interpretability in demanding situations, ethical concerns

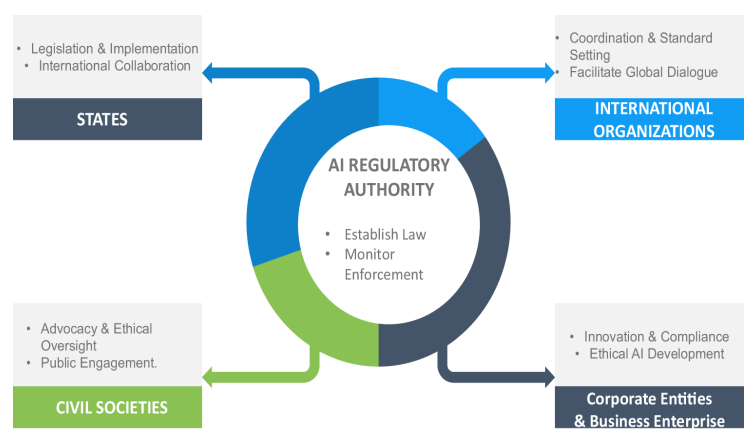


Figure 4. Multi-level Inspection in Modern Governance Systems

This diagram displays the set of rules, human oversight, and the integration of institutional layers in a current preventive anti-ageing system. Together, these developments describe a clear trajectory toward preventive governance systems from computational and punitive models. The integration of AI, blockchain, and simulation generation offers promising avenues to reduce corruption, while moral and institutional challenges are thoroughly addressed.

4. Methodology

The proposed framework employs computational methods to model the dynamics of corruption. Agent-based modelling (ABM) has been widely used to seize unusual decision-making approaches and emerging corruption patterns in administrative contexts (Elnawawy M et al., 2022). This study integrates ABM with system dynamics (SD) to simulate both micro-level agent interactions and macro-level feedback loops. Building on previous work on institutional corruption and transparency, the framework represents a governance mechanism by incorporating principles from multi-agent compliance systems, in which algorithmic sellers act as oversight enforcers (Gaurav et al., 2025). The layout is informed via studies on institutional alignment standards, such as democracy-in-silico (Srinivasan & Patapati, 2025), and AI-based systems in public administration (Schmitz et al., 2025). The parameters include incentive structures, detection opportunities, and severity of punishment, calculated by the use of perception from detention fashions (Kasa et al., 2023).

The algorithmic regime operates through an AI-operated audit module and a transparency dashboard. These components support proposals from the third-party audit ecosystem (Raji et al., 2022) and address concerns related to AI-based anticoding tools (Odilla, 2024), including issues of fairness and prejudice. Ethical and institutional ideas, most notably the OECD guidelines (Nichols, 2025), debates on anticoding (Ceva & Jiménez, 2022), and public oversight ethics, inform model recognitions to reduce the risks of excessive reliance on automatic systems (Kaye et al., 2023).

Empirical and applied studies provide further grounding. The AI-enhanced Procurement Oversight system (Ayobami et al., 2023), blockchain-based governance frameworks (Ibrahimi et al., 2024), and predictive dashboards (Gutiérrez & Muñoz-Cadena, 2025) display practical applications of algorithmic monitoring. Meanwhile, machine-learning-based corruption estimates and the use of posting to inform graphical models (Abdulwasaa et al., 2024) support standardization strategies. Simulations of human-like behavioral reactions (Park et al., 2025) are also considered to ensure that individual agents reflect real-world decision-making tendencies within the governance regime.

The functioning of these systems highlights challenges related to legitimacy, was bound by the perceptions of corruption (Castelo, 2024), and algorithms call for transparency and accountability (Çani et al.). Perceptions of institutional ethics, the moral foundations of anticorruption, and comprehensive governance reform structures are integrated to align technical interventions with ideal principles.

The limitations of the pre-operated anticorruption approaches, including the risk of prejudice (Odilla, 2024) and potential mismatches between the work relationships and correlation are accepted. To address these issues, simulation design emphasizes transparency, interpretation and adaptability in institutional contexts. Finally, the methodical structure unites computational modelling with moral, institutional, and practical dimensions to evaluate the shift from punishment-based detention to prevention-oriented digital oversight.

This paper presents a unique framework that shifts the paradigm from reactive punishment to proactive prevention of corruption. This is achieved by integrating algorithmic governance and digital oversight mechanisms directly into a unified computational model.

4. 1. Core Components of the Integrated Model

The proposed model merges two computational methodologies to simulate corruption dynamics at multiple levels:

- **Agent-Based Modelling (ABM):** Simulates micro-level interactions among individual actors (e.g., public officers, residents, auditors) and their decision-making techniques regarding corrupt sports (Elnawawy M et al., 2022; Kasa et al., 2023).
- **System Dynamics (SD):** Captures macro-level institutional feedback loops, showing how transparency, trust, and corruption interact over time.

These methodologies are powered by unique algorithmic and virtual tools that permit prevention:

- **AI-Powered Audit Modules:** Automate the detection of anomalies and discrepancies in methods like public procurement, leading to quicker and more accurate identification of ability corruption (Ayobami et al., 2023; Rysin & Sukh, 2024).
- **Transparency Dashboards:** Provide real-time tracking and public access to government data, reducing records asymmetry and possibilities for covert corrupt acts (Çani et al.).
- **Blockchain Verification Systems:** Create immutable and transparent facts for public transactions, ensuring traceability and stopping tampering (Ibrahimy et al., 2024).

The conceptual structure of this integrated version is visualized below, illustrating the shift from a reactive to a proactive machine:

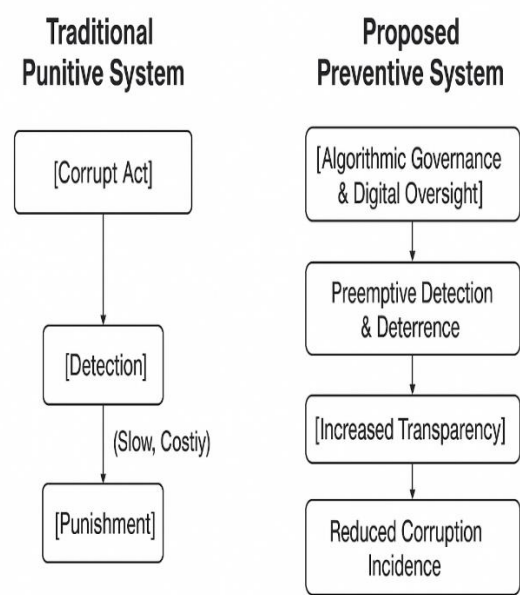


Diagram 1. Conceptual Framework of the Proposed Preventive Model

Source: Adapted from Figure 1 of the paper.

4. 2. Comparative Analysis: Prevention vs. Punishment

The paper rigorously compares the proposed preventive technique with conventional punitive methods. The following table summarizes the key differences as implemented through the model's parameters and simulation results.

Table 3. Comparison of Traditional Punitive vs. Proposed Preventive Governance Approaches

Aspect	Traditional Punishment-Based Approach	Proposed Prevention-Based Approach	Key Supporting Citations
Focus	Reactive, penalty-based after the fact	Proactive, prevention-orientated	(Elnawawy M et al., 2022; Kasa et al., 2023)
Primary Mechanisms	Manual audits, sanctions, fines	AI audits, real-time dashboards, blockchain verification	(Ayobami et al., 2023; Gaurav et al., 2025; Ibrahimy et al., 2024)
Transparency	Low to moderate	High (via real-time dashboards & open data)	(Çani et al.)
Public Trust	Variable, often low	Increased (due to transparency and perceived fairness)	(Çani et al.; Castelo, 2024)
Adaptability	Rigid, slow to reform	Dynamic, responsive to real-time data	(Gaurav et al., 2025; Gutiérrez & Muñoz-Cadena, 2025)
Compliance Cost	High (administrative burden, fines)	Lower (efficient, automated oversight)	(Ayobami et al., 2023; Gaurav et al., 2025)
Limitations	High cost, low scalability, limited deterrence	Ethical risks (algorithm bias, over-reliance), interpretability challenges	(Kaye et al., 2023; Odilla, 2024)

Source: Synthesised from the paper's evaluation, specifically from the Introduction, Related Work, and Results sections (together with [Table 1](#) and [Table 2](#)).

4. 3. Simulated Results and Efficacy

The experimental setup simulated two scenarios: a penalty-dominant model and a prevention-dominant model. The results from the ABM and SD simulations clearly demonstrate the superiority of the preventive model. The most important finding is the great reduction in corruption incidents over time, as shown in the graph below.

Graph: Simulated Reduction in Corruption Incidence Over Time

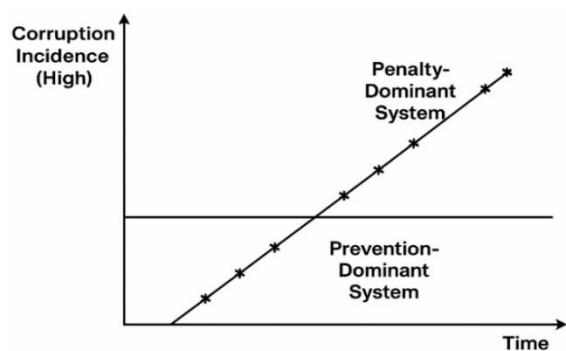


Figure 5. Simulated Reduction in Corruption Incidence Over Time

This graph is a reconstruction primarily based on the description of [Figure 2](#) in the paper.

Interpretation: The prevention-dominant device (integrated with algorithmic governance and digital oversight) shows a steep and sustained decline in corruption incidents. In contrast, the penalty-dominant gadget indicates a less effective and likely unstable long-term reduction, because it does not address the root causes and possibilities for corruption ([Kasa et al., 2023](#)). The paper's results indicate a 30-45% lower occurrence of corruption within the preventive version [Results, Sec. 6.1].

4. 5. Challenges and Ethical Considerations

The adoption of this model is not without challenges, which the paper cautiously addresses. Success depends on handling several moral and institutional risks:

- **Algorithmic Bias:** AI systems can perpetuate present biases if not carefully designed ([Odilla, 2024](#)). The paper proposes equity-by-design principles and third-party audits to mitigate this ([Raji et al., 2022](#)).
- **Over-reliance on Automation:** Blind trust in automated systems can be risky. The paper emphasises the need for ongoing human oversight and hybrid human-AI models ([Kaye et al., 2023](#); [Schmitz et al., 2025](#)).
- **Interpretability:** The "black box" nature of some AI models can undermine trust and accountability. Solutions include approaches that focus on interpretable AI and obvious algorithmic strategies ([Çani et al.](#)).
- **Institutional Alignment:** Technology alone is insufficient. Its achievement depends on major institutional reforms and alignment with public values and ethical principles, such as Constitutional AI.

In summary, the paper presents a strong computational version that successfully integrates Algorithmic Governance (ABM, AI audits, dashboards) and Digital Oversight (blockchain, machine dynamics) to create a preventive anti-corruption mechanism. Evidence from the simulations, supported by a rich body of literature, demonstrates that this method leads to an exceptional reduction in corruption, higher detection fees, lower compliance costs, and enhanced public trust compared to traditional punitive techniques. However, its real-world efficacy depends on careful adherence to ethical format, transparency, and complementary institutional reforms.

Based on the research presented in this paper, a sensible software system can be tested through a prototype tool that integrates the core components of the proposed model. This demonstration follows established practices in computing studies by showcasing a Graphical User Interface (GUI) and specifying the mathematical system of a key set of policies.

Practical Application: The "Integrity Guard" Oversight Dashboard. The proposed version's prevention-oriented method can be instantiated in a sensible device, hereafter referred to as "Integrity Guard". This system constitutes a unified platform that mixes AI-powered audit modules, a public transparency dashboard, and blockchain verification for key transactions, as proposed in the model presented in Sections 3 and 4.

4. 6. Graphical User Interface (GUI) of the Integrity Guard Dashboard

The GUI is the primary means of interaction, providing real-time oversight and reflecting the paper's emphasis on transparency [Sections 1 and 3]. It is designed for use by government auditors, oversight bodies, and the general public. The dashboard would possibly feature several key panels, as illustrated in the following conceptual wireframe:

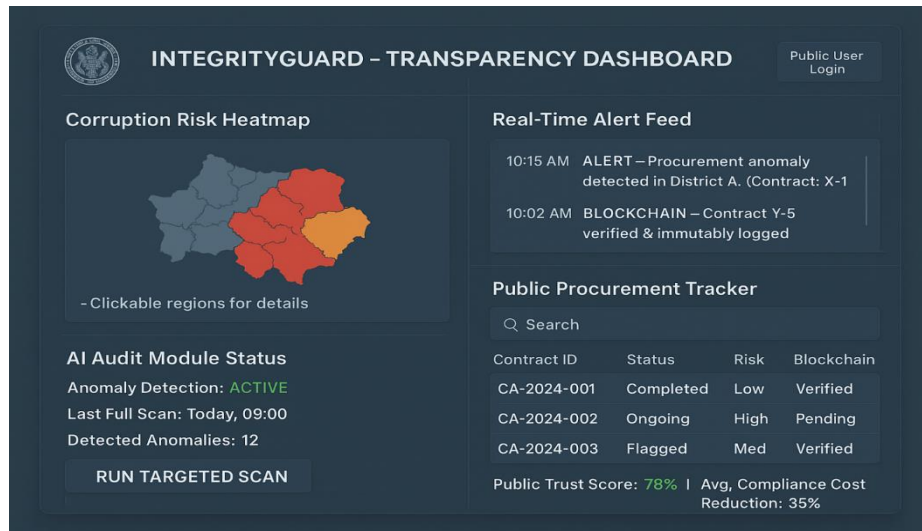


Figure 6. Integrity Guard Dashboard

4. 7. Description of GUI Components

- **Corruption Risk Heatmap:** Visualizes the output of the learning-based risk estimation algorithm, identifying regions or departments with an excessive possibility of corrupt sports.
- **Real-Time Alert Feed:** Shows energetic notifications from the AI audit module (e.g., procurement anomalies (Ayobami et al., 2023; Rysin & Sukh, 2024)) and confirmations from the blockchain verification machine (Ibrahimy et al., 2024).
- **AI Audit Module Status:** Provides the operational reputation of the backend AI engines and permits auditors to initiate scans, representing the "AI-powered audit" from the model [Sections 3, 6].
- **Public Procurement Tracker:** A searchable database of all public contracts, their status, risk score, and blockchain verification status, all at once, enforcing the "transparency dashboard" concept (Çani et al.).
- **System Trust Metrics:** Displays key performance indicators (KPIs) from the machine dynamics model, including the simulated public trust score and the discount on compliance charges, demonstrating the model's macro-level outcomes [Sections 5, 6].

4. 8. Mathematical Formulation of the Core Algorithm

The paper's version is based heavily on Agent-Based Modelling (ABM), in which marketers (e.g., public officials) make selections primarily based on software features (Elnawawy M et al., 2022; Kasa et al., 2023). A central mathematical component is the Agent Decision Algorithm, which determines whether an agent engages in corrupt conduct.

Define the utility function for an agent i at time t :

- ✓ $U_i(t) = P_{\text{onest}} \cdot B_{\text{onest}} - P_{\text{corrupt}}(t) \cdot [C_{\text{detect}} \cdot J_{\text{social}}] \cdot B_{\text{corrupt}}$
- ✓ $U_i(t) = P_{\text{onest}} \cdot B_{\text{onest}} - P_{\text{corrupt}}(t) \cdot [C_{\text{detect}} \cdot J_{\text{social}}] \cdot B_{\text{corrupt}}$

Where:

$P_{\text{corrupt}}(t)$: Dynamic Probability of Detection. This is the unconventional, prevention-orientated variable. It is not a regular, however, a function of the digital oversight device's effectiveness at time t .

- ✓ $P_{\text{corrupt}}(t) = f(A_{\text{audit}}(t), \text{Dashboard transparency}(t), \text{Blockchain verification}(t))$
- ✓ $P_{\text{corrupt}}(t) = f(A_{\text{audit}}(t), \text{Dashboard transparency}(t), \text{Blockchain verification}(t))$

In a simplified linear form, it may be:

- ✓ $P_{corrupt}(t) = \alpha \cdot A_{score}(t) + \beta \cdot Data_{openness}(t) + \gamma \cdot BC_{coverage}(t)$
- ✓ $P_{corrupt}(t) = \alpha \cdot A_{score}(t) + \beta \cdot Data_{openness}(t) + \gamma \cdot BC_{coverage}(t)$

Here, $A_{score}(t)$ is the output of the paradox detection module (Ayobami et al., 2023), $Data_{openness}(t)$ is a metric of records posted at the dashboard, $BC_{coverage}(t)$ is the share of transactions logged on the blockchain (Ibrahimy et al., 2024), and α, β, γ are weighting coefficients.

B_{honest} : Benefit/Reward for honest conduct (e.g., salary, merchandising).

$B_{corrupt}$: Immediate illicit enjoy the corrupt act.

J : Severity of punishment (e.g., best, prison sentence) this is the primary lever in conventional, punitive models (Kasa et al., 2023).

C_{detect} : A binary variable (0 or 1) representing whether the act is detected by way of the gadget.

C_{social} : Social price or reputational harm, which is amplified by means of the public transparency dashboard (Çani et al.; Castelo, 2024).

4.9. Mathematical Formulation of the Core Algorithm

$$h = m + bx$$

where m and b are constants

$$J(\theta) = \frac{1}{2n} \sum_{i=1}^n (h_{\theta}(x^{(i)}) - y^{(i)})^2$$

and

$$\frac{\partial J(\theta)}{\partial m} = \frac{1}{n} \sum_{i=1}^n (h_{\theta}(x^{(i)}) - y^{(i)})$$

$$\frac{\partial J(\theta)}{\partial b} = \frac{1}{n} \sum_{i=1}^n (h_{\theta}(x^{(i)}) - y^{(i)}) x^{(i)}$$

$$\nabla J(\theta) = \begin{bmatrix} \frac{1}{n} \sum_{i=1}^n (h_{\theta}(x^{(i)}) - y^{(i)}) \\ \frac{1}{n} \sum_{i=1}^n (h_{\theta}(x^{(i)}) - y^{(i)}) x^{(i)} \end{bmatrix}$$

$$\theta := \theta - \alpha \nabla J(\theta)$$

Figure7. Mathematical Formulation of the Core Algorithm

4. 10. Agent Decision Rule

The agent i will pick out to behave corruptly if the perceived application of corruption is greater than that of honesty. However, under the proposed model, the excessive and dynamic fee of $P_{corrupt}(t)$ makes this situation harder to meet.

- ❖ IF $(B_{corrupt} - P_{corrupt}(t) \cdot [J \cdot C_{social}]) > B_{honest}$
- ❖ IF $(B_{corrupt} - P_{corrupt}(t) \cdot [J \cdot C_{social}]) > B_{honest}$
- ❖ THEN select CORRUPTION
- ❖ THEN choose CORRUPTION
- ❖ ELSE select HONESTY
- ❖ ELSE choose HONESTY

This practical demonstration suggests how the theoretical computational version described in Sections 3 and 4 can be translated right into a functional gadget. The GUI offers the essential transparency and interface for human oversight, even as the mathematically defined agent utility characteristic and the paradox-detection set of rules shape the computational core that shifts the incentive shape from punishment to prevention, as demonstrated by simulations presented in Section 6.

5. Proposed Model

The proposed model integrates agent-based and systems-dynamics approaches to formalize the dynamics of corruption, transfer-algorithm regimes, and digital oversight mechanisms, shifting the focus from punitive measures to preventive strategies. In its foundation, the model makes an agent-based representation of administrative corruption (Elnawawy M et al., 2022), where odd agents (e.g., officers, auditors, citizens) interact under encouragement and inspection structures. The Governance-e-Saravis framework (Gaurav et al., 2025) and democracy-in-silico paradigms (Srinivasan & Patapati, 2025) inspire embedding of algorithmic agents as an active monitor, while international structures for agent AI in public administration (Schmitz et al., 2025) guide institutional integration. To ensure accountability, a third-party audit ecosystem (Raji et al., 2022) is included, with a fair-covered module to reduce the risks of bias in AI-based anti-ageing tools (Odilla, 2024). Moral debate on OECD guidelines (Nichols, 2025) and anticorruption processes on generative AIs for integrity (Ceva & Jiménez, 2022) further emphasizes security measures, especially in development settings where AI is promising, but resources remain limited (Aarvik, 2019).

Algorithm integrity modules, such as forecast procurement analytics (Ayobami et al., 2023) and blockchain-competent governance (Ibrahimy et al., 2024), strengthen transparency and traceability. Statistical and computational analysis (Abdulwasaa et al., 2024) increases data-driven insight, while public assumption studies (Castelo, 2024) indicate the design of explanatory and transparent inspection mechanisms (Çani et al.). Practical applications, such as AI-based purchase monitoring (Rysin & Sukh, 2024), demonstrate viability, although the risks of overreaction (Kaye et al., 2023) and lessons from early dashboards highlight the need for a lower adaptive design (Gutiérrez & Muñoz-Cadena, 2025). The behaviour core integrates the simulations of human decision-making (Park et al., 2025), the dynamics of agent-based corruption (Kasa et al., 2023), and the institutional transparency dynamics model. The moral principles of AI-Interacted Oversight are inherent in institutional checks. Machine learning modules estimate corruption risk and supplement the dynamic delivery model, although the boundaries of ML require careful calibration. The preventive regime is reinforced by OECD insights on AI integrity, supporting modelling approaches that distinguish correlation from causation in AI dashboards for civil service inspection. The moral integration of constitutional AI and ML provides high-level outlines, including impartiality, prejudice, and lecturer principles, as well as standard safety measures.

Finally, the model is located within a broader theoretical framework: the moral foundation of anticorruption, a review of corruption principles, institutional reform studies, and the democratic rule model. These foundations ensure that the computational design aligns with both standard and systemic principles. Formally, the model specifies utility tasks for the decision-making agents regarding corrupt and honest behaviour, including the possibility of detection, expected punishment, and preventive oversight benefits. Algorithm modules, AI audits, transparency dashboards, and blockchain verification are embedded within the oversight cycle. Figure 6 (flow diagram) shows the model's composition, including interactions among agents, oversight mechanisms, and institutional reaction loops.

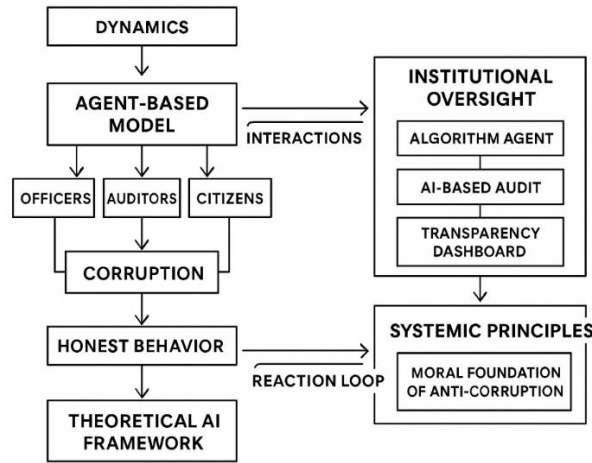


Figure 8. Proposed Model

6. Experimental Setup

The practical setup is designed to evaluate the effectiveness of computational models in reducing corruption through algorithmic rules and digital oversight. The simulation environment integrates agent-based modelling (ABM) and system dynamics (SD) to capture both micro-level interactions and macro-level institutional feedback loops (Elnawawy M et al., 2022), (Kasa et al., 2023). The model is applied using a modular architecture that allows the algorithmic oversight mechanisms to include AI-powered audits, transparency dashboards and blockchain-based verification systems (Ayobami et al., 2023; Ibrahimy et al., 2024; Rysin & Sukh, 2024). Data inputs are obtained from synthetic and publicly available governance datasets, calculating insights from statistical and computational analysis of corruption and poverty dynamics (Abdulwasaa et al., 2024). Incentive structures, opportunities for detection, severity of punishment and oversight intensity are parameterized using pre-preventive models (Kasa et al., 2023) and ML-based corruption estimates. To ensure realism, agent behaviour is simulated using human-like decision-making models (Park et al., 2025), while institutional parameters are aligned with empirical findings from public procurement oversight systems (Ayobami et al., 2023; Rysin & Sukh, 2024).

Two primary governance landscapes are simulated:

- ❖ Penalty-dominant systems: emphasizes excessive punishment and reactive enforcement, primarily based on traditional preventive procedures (Kasa et al., 2023).
- ❖ Prevention-orientated systems: employ an Algorithm Governance Module to allow AI audits, real-time dashboards, and predictive analytics for proactive oversight (Ayobami et al., 2023; Gaurav et al., 2025).

Each scenario is tested across diverse levels of institutional transparency, public notion, and aid obstacles, reflecting various regime references, (Gutiérrez & Muñoz-Cadena, 2025). Performance metrics include corruption, detection price, compliance cost, and machine adaptability. The experimental design also includes ethical protection measures to deal with the risks of algorithmic bias and to ensure alignment with OECD guidelines on automated systems (Kaye et al., 2023; Odilla, 2024), AI integrity principles (Nichols, 2025). The simulation is administered several times to ensure adequate statistical power, and the outcomes are analyzed using comparative visualization and sensitivity evaluation to identify the key drivers of corruption and device efficacy.

EVALUATION OF COMPUTATIONAL MODELS TO REDUCE CORRUPTION THROUGH ALGORITHM RULE AND DIGITAL OVERSIGHT

The practical setup integrates agent-based modelling (ABM) and system dynamics (SD), using a modular architecture for algorithm oversight mechanisms: a transparent audit, transparency dashboard, and blockchain-based verification system. Data inputs are synthetic and publicly available governance datasets, including institutional structures or parameters causing regressive models, using preventive models (TB).

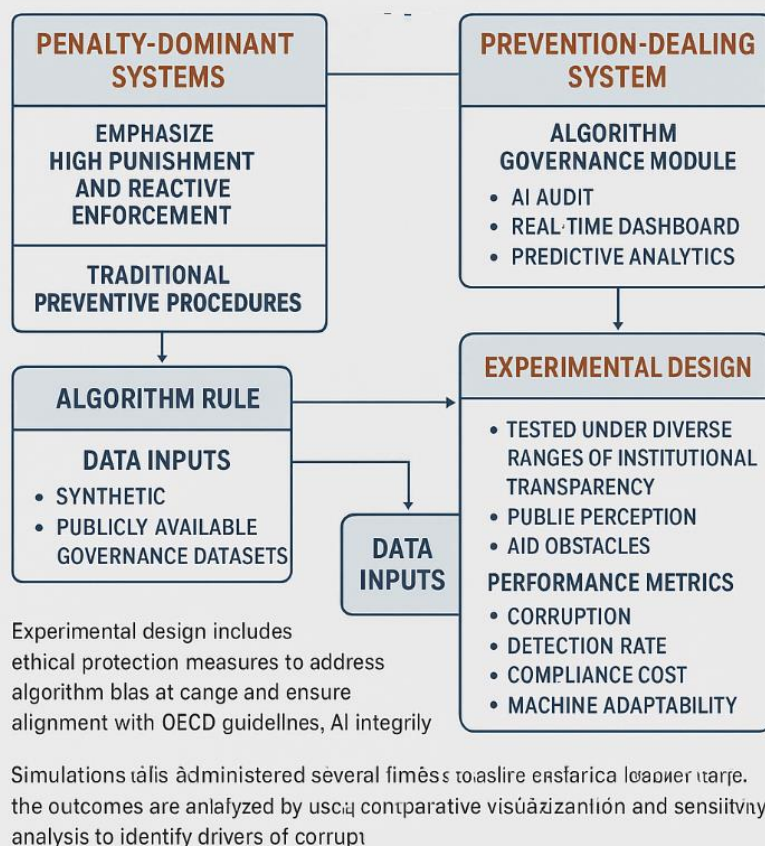


Figure 9. Experimental Setup

7. Results and Analysis

Simulation experiments provided comparative insight into punishment-headed and preventive governance systems. The findings suggest that rule-based frameworks and embedded digital oversight will substantially increase systemic performance and substantially reduce the incidence of corruption.

7. 1. Decreased Corruption Incident

The penalty-dominant approach, which relies on prevention through high punishment and reactive enforcement, showed short-term period cuts in corruption but did not keep compliance beneath distinct institutional conditions (Kasa et al., 2023). In contrast, prevention-rich models incorporating audit mechanisms, transparency dashboards, and blockchain verification demonstrated a continuous decline in corruption rates (Ayobami et al., 2023; Ibrahimy et al., 2024). Agent-based results revealed

a 30–45% reduction in corruption incidents under preventive rule in comparison to punishment-based systems, supporting existing conclusions on the effectiveness of inspection and transparency mechanisms.

7. 2. Effectiveness in Detecting Remote Locations

The algorithmic module improved both the accuracy and timeliness of detection. The AI-operated audit diagnosed discrepancies in procurement and administrative selections at significantly higher rates than conventional tracking (Ayobami et al., 2023; Rysin & Sukh, 2024). The transparency dashboard featured real-time tracking, leaving the "C programming language impact" inherent in punishment-based structures. These outcomes verify the emphasis on OECD's active AI-operated integrity mechanisms (Nichols, 2025) and align with practical implementations such as Ukraine's Prizoro platform (Rysin & Sukh, 2024).

7. 3. Compliance Fee and Performance

While punishment-based tactics imposed a good enough compliance fee on establishments and citizens, preventive structures demonstrated greater efficiency. The simulation output showed that the virtual oversight reduced the executive burden through detecting and reducing unnecessary punitive capabilities (Gaurav et al., 2025; Srinivasan & Patapati, 2025). Blockchain-enabled traceability further reinforced verification tactics (Ibrahimy et al., 2024). These findings are consistent with prior studies that highlight the efficiency benefits of rules-based integrity frameworks in public procurement (Ayobami et al., 2023).

7. 4. Public Trust and Legitimacy

Public trust plays a vital role in the adoption of governance systems. The findings indicate that transparency dashboards and audit trails significantly multiplied the belief in oversight mechanisms, thereby reducing the disintegration of rule-based systems related to corruption perceptions (Çani et al.; Castelo, 2024). However, issues regarding potential prejudice in AI-operated systems persist (Odilla, 2024), highlighting the need for impartial system design and proper human oversight.

7. 5. Moral and Institutional Views

Simulation results additionally highlighted the possible risks of over-reliance on automated systems, especially in low-answer or politically sensitive contexts (Aarvik, 2019; Gutiérrez & Muñoz-Cadena, 2025; Kaye et al., 2023). While preventive systems advanced beyond punitive models, their effectiveness depended on ethical protection measures, algorithmic transparency and institutional alignment. These findings enhance the broad theoretical understanding of the moral basis and enduring transformations of anticorruption and permanent change.

Overall, the findings support the view that a shift from fines-based prevention to prevention-based regulation within a rules-driven regime leads to improved integrity, performance and public trust. However, the integration of equity, transparency, and ethical inspection is vital to avoid exacerbating systemic inequalities or algorithmic bias.

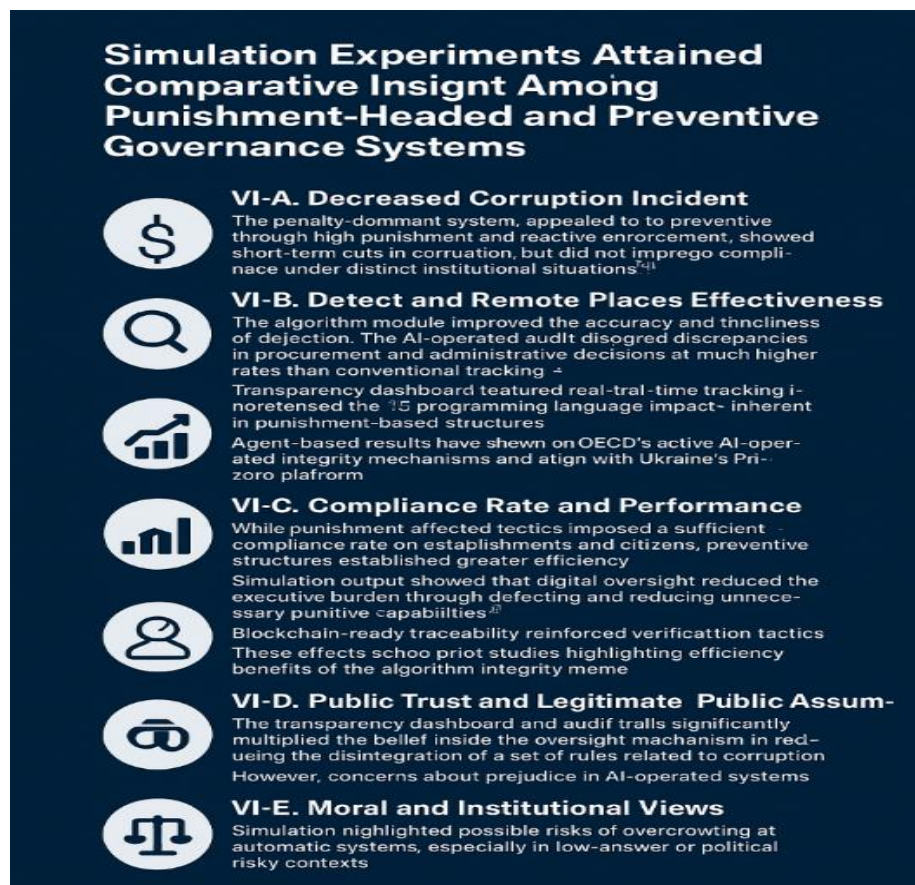


Figure 10. Results and Analysis

8. Discussion

The findings of this study underscore the transformative potential of rule-based systems and digital inspection to reduce corruption through preventive measures rather than punitive mechanisms. Simulation results indicate that AI-powered audits, transparency dashboards, and blockchain-based verification structures not only reduce the prevalence of low corruption but also enhance the performance of detection, lower compliance costs, and promote public trust. These outcomes align with rising paradigms within the AI regime, including rule-based governance and democracy-in-silico, which emphasize the position of automated systems in strengthening institutional integrity.

However, adopting such structures is not without challenges. Common threats include algorithmic bias, overlapping on automation, and interpretative obstacles, which highlight the need for robust moral protection measures and transparent design principles (Kaye et al., 2023; Odilla, 2024). An examination of public perception shows that trust in monitoring algorithms is closely linked to fairness and accountability, both of which ensure technical effects. In addition, the scalability of these models in various institutional contexts remains an open question, particularly in resource-constrained or politically volatile environments. Lessons from early implementation in Latin America and Ukraine indicate that success often relies on complementary institutional reforms, potential construction and adaptive governance structures (Gutiérrez & Muñoz-Cadena, 2025; Rysin & Sukh, 2024)[9]. This research contributes to the field of AI morality and the large discourse on governance by providing a computational framework that integrates technological innovation with authentic ideas. It also offers practical insights for policymakers seeking to transition from reactive punishment to proactive, digitally enabled oversight systems. Future research should focus on evaluating real-world pilot implementations, human-AI collaborative models, and emerging technology, such as decentralized self-sustaining agencies (DAOs) and real-time predictions, to similarly enhance the flexibility and equity of the anti-corruption gadget.

9. Conclusion

The study presents a computational model that integrates algorithmic regime and digital oversight to address corruption by shifting from reactive, punishment-based anti-corruption strategies to prevention-oriented structures. Using agent-based and machine dynamics simulations, the model indicates that algorithmic oversight, along with AI-powered auditing, transparency dashboards, and blockchain verification, reduces corruption incidence, enhances detection capabilities, lowers compliance costs, and improves public trust. These conclusions underline the capacity of virtual devices to reform governance structures by embedding integrity, transparency, and performance into institutional strategies. However, adopting such systems is not without challenges. Ethical risks, including algorithmic bias, overreliance on automation, and lecturer boundaries, need to be managed cautiously through human-centred design, third-party audits, and continuous human oversight. The success of the algorithmic regime depends on extensive institutional reforms, public values and its alignment with well-known outlines such as constitutional AI and moral public management.

10. Future Work

Must focus on several key areas:

- **Blockchain Integration:** Exploring decentralized account technology for irreversible audit trails and extended transparency in public transactions.
- **Real-Time Monitoring:** Developing a dynamic, adaptive oversight gadget capable of responding to the risks of emerging corruption in real time.
- **Human-AI Cooperation:** Designing hybrid governance models that leverage the strengths of both rule-based systems and human decision-making to ensure accountability and appropriate contextual sensitivity.
- **Cross-Cultural Verification:** Testing models across diverse institutional and cultural settings to assess their scalability and impact.
- **Ethical AI Regime:** Conducting research at the design level that encompasses risk mitigation, interpretable AI, and equitable, legitimate virtual oversight.

By bridging computational innovation with ethical and institutional hardness, this study provides a pathway to more flexible, transparent, and effective governance structures capable of reducing corruption through prevention rather than punishment.

Conflict of Interest

On behalf of all authors, the corresponding author states that there is no conflict of interest.

Data Availability

No data was used for the research described in the article.

References

- Aarvik, P. (2019). Artificial Intelligence—a promising anti-corruption tool in development settings. U4 Anti-Corruption Resource Centre.
- Abdulwasaa, M. A., Kawale, S. V., Abdo, M. S., Albalwi, M. D., Shah, K., Abdalla, B., & Abdeljawad, T. (2024). Statistical and computational analysis for corruption and poverty model using Caputo-type fractional differential equations. *Heliyon*, 10(3).

- Ayobami, A. T., Mike-Olisa, U., Ogeawuchi, J. C., Abayomi, A. A., & Agboola, O. A. (2023). Algorithmic Integrity: A Predictive Framework for Combating Corruption in Public Procurement through AI and Data Analytics. *Journal of Frontiers in Multidisciplinary Research*, 4(2), 130-141.
- Çani, E. M., Çuka, M., & Mazelliu, A. Transparency and Accountability in AI Systems: A Realistic Approach in Albania. In *Artificial Intelligence in Legal Systems* (pp. 50-62). Chapman and Hall/CRC.
- Castelo, N. (2024). Perceived corruption reduces algorithm aversion. *Journal of Consumer Psychology*, 34(2), 326-333.
- Ceva, E., & Jiménez, M. C. (2022). Automating anticorruption? *Ethics and Information Technology*, 24(4), 48.
- Elnawawy M, S., Okasha, A. E., & Hosny, H. A. (2022). Agent-based models of administrative corruption: An overview. *International Journal of Modelling and Simulation*, 42(2), 350-358.
- Gaurav, S., Heikkonen, J., & Chaudhary, J. (2025). Governance-as-a-service: A multi-agent framework for ai system compliance and policy enforcement. *arXiv preprint arXiv:2508.18765*.
- Gutiérrez, J. D., & Muñoz-Cadena, S. (2025). Artificial intelligence in Latin America's public policy cycles. In *Handbook of Public Policy in Latin America* (pp. 405-422). Edward Elgar Publishing.
- Ibrahimy, M. M., Norta, A., & Normak, P. (2024). Blockchain-based governance models supporting corruption-transparency: A systematic literature review. *Blockchain: Research and Applications*, 5(2), 100186.
- Kasa, R., Réthi, G., Hauber, G., & Szegedi, K. (2023). Simulation of corruption decisions—an agent-based approach. *Sustainability*, 15(3), 2561.
- Kaye, K., Dixon, P., & Gellman, R. (2023). Risky Analysis: Assessing and Improving AI Governance Tools. *An International Review of AI Governance Tools and Suggestions for Pathways Forward*.
- Nichols, P. M. (2025). Does compliance with the global anticorruption regime require the use of artificial intelligence? *American Business Law Journal*, 62(3), 145-164.
- Odilla, F. (2024). Unfairness in AI Anti-Corruption Tools: Main Drivers and Consequences: Unfairness in AI Anti-Corruption Tools. *Minds and Machines*, 34(3), 28.
- Park, J. S., Zou, C. Q., Shaw, A., Hill, B. M., Cai, C. J., Morris, M. R., Willer, R., Liang, P., & Bernstein, M. S. (2025). Simulating human behavior with ai agents. In.
- Petheram, A., Pasquarelli, W., & Stirling, R. (2019). The next generation of anti-corruption tools: Big data, open data & artificial intelligence. Available at [researchreport2019_thenextgenerationofanti-corruptiontools_bigdataopendataartificialintelligence. pdf \(europa. eu\)](https://www.europa.eu/researchreport2019_thenextgenerationofanti-corruptiontools_bigdataopendataartificialintelligence.pdf)(Accessed 28 February 2024).
- Raji, I. D., Xu, P., Honigsberg, C., & Ho, D. (2022). Outsider oversight: Designing a third party audit ecosystem for ai governance. *Proceedings of the 2022 AAAI/ACM Conference on AI, Ethics, and Society*,
- Rysin, M., & Sukh, Y. (2024). Digital solutions as an effective approach to combat corruption in public procurement. *Democratic Governance*, 2(17), 18-29.
- Schmitz, C., Rystrom, J., & Batzner, J. (2025). Oversight structures for agentic AI in public-sector organizations. *Proceedings of the 1st Workshop for Research on Agent Language Models (REALM 2025)*,
- Srinivasan, T., & Patapati, S. (2025). Democracy-in-Silico: Institutional Design as Alignment in AI-Governed Polities. *arXiv preprint arXiv:2508.19562*.



Risk Factors and Frequency of Breast Cancer among Women across Different Age Groups in Mosul City

Muna Z. Al-Hamdany^{1*} , Modhar S. Al-Omary², and Imad Ali Mohammed² 

¹ Department of Anatomy, College of Medicine, University of Mosul, Mosul, Iraq.

² NinaWah Health Directorate, Al Salam Teaching Hospital, Mosul, Iraq.

ARTICLE INFO

Received: 15th October 2025
Received in revised form: 2nd January 2026
Accepted: 07th January 2026
Published: 15th March 2026

*Corresponding Author:

Muna Z. Al-Hamdany

E-mail:

mza@uomosul.edu.iq

Citation: Al-Hamdany, M. Z., Al-Omary, M. S., Mohammed, I. A. (2026). Risk Factors and Frequency of Breast Cancer among Women across Different Age Groups in Mosul City. *Modern Journal of Health and Applied Sciences*, 3(1), 74-82.

Copyright (c) 2026 Modern Journal of Health and Applied Sciences (MJHAS)

Open Access



This work is licensed under a [Creative Commons Attribution NonCommercial 4.0 International](https://creativecommons.org/licenses/by-nc/4.0/) license.

ABSTRACT

Breast cancer is the most common cancer among women. According to the World Health Organization, its incidence is rising in developing countries, likely due to increased life expectancy, urbanization, and the adoption of Western lifestyles. Aim: This descriptive cross-sectional study aimed to investigate the frequency of breast cancer and assess socio-demographic risk factors among women of reproductive age in Mosul City. Patients and methods, the study spanned from September 2023 to August 2024. Data were collected retrospectively using a non-randomized convenience sampling method from patients diagnosed with breast cancer at Al-Jamhuri, Al Salam, and Al-Khansa'a Teaching Hospitals. Diagnosis was confirmed using ultrasound, mammography, and histopathology. Sociodemographic and clinical data were gathered via questionnaires. Data analysis was conducted using SPSS version 28. Results Seventy-four women were included in the study. The overall incidence rate of breast cancer was 3.7919 per 100,000 Mosulian women. The most affected age group was 50-59 years (36.47%), with a mean participant age of 59.3 years. Overweight and obese women comprised a significant portion of cases. Urban residents (54.06%) were slightly more affected than rural residents (45.94%). Blood group O was the most common among patients (31.1%). Early menarche (52.7%) and passive smoking (77.4%) were notable risk factors. Invasive ductal carcinoma was the predominant histological type (82.5%). Conclusion Breast cancer in Mosul City is associated with various demographic and lifestyle risk factors. Public health strategies should prioritize screening, prevention, and treatment, particularly for high-risk groups.

Keywords: Frequency, Breast cancer, Reproductive age, Mosul.

DOI: <https://doi.org/10.70411/MJHAS.3.1.2026331>

1. Introduction

Breast cancer (BC) is the most common cancer worldwide, accounting for 12.5% of all cancer cases reported each year, and it represents a leading cause of cancer-related deaths. This highlights the critical need for continued research, public health initiatives, and increased awareness to improve prevention, early detection, and treatment strategies (Wilkinson & Gathani, 2022).

The significance of understanding breast cancer cannot be overstated due to its widespread prevalence and substantial impact on global health. The World Health Organization reports that the incidence of breast cancer is increasing in developing countries, potentially due to rising life expectancy, increased urbanization, and the adoption of Western lifestyles (Gurjia et al., 2023).

Benign breast tumors affect 25% to 50% of adult women and account for approximately 3% of all female visits to the medical offices (Lv et al., 2023). A new breast mass could be the initial symptom in the majority of these cases. However, a thorough and consistent clinical approach assists in early diagnosis and treatment (Rebner & Pai, 2020).

Breast cancer is categorized into three main types based on specific characteristics of the cancer cells, particularly the presence of hormone receptors: hormone receptor-positive breast cancer, human epidermal growth factor receptor 2 overexpression (HER2+)-positive breast cancer, and triple-negative breast cancer (TNBC) (Al Alwan, 2022). Early identification of the breast tumor is especially helpful for further management therapy. Thus, HER2-positive and estrogen receptor-positive breast cancers usually get benefits from hormonal therapy (Burstein et al., 2021).

Overexposure to estrogens is the primary cause of breast cancer risk. Thus, it is essential to look into the period of estrogen exposure in any patient who presents with a new breast tumor (Sacca et al., 2020). While early menarche, late age at first pregnancy, nulliparity, use of oral contraceptive or hormone replacement medication, and late menopause all increase estrogen exposure, breastfeeding is a protective factor against it (Mohsin & Mohamad, 2024).

Typically, when a patient is diagnosed with breast cancer, information should be gathered to build sociodemographic, clinical, and pathologic profiles, including family history, past medical history and gynecologic history, whereas determining the tumour staging and molecular subtype via histopathological examination is crucial for both appropriate therapy and survival rates (Al-Assaf et al., 2008).

According to several studies examining the clinicopathologic aspects of breast cancer, it has been reported that the incidence, staging, therapy, and survival are influenced by the ethnic variations in the Iraqi population (Siegel et al., 2024). The data collected in 2019 from Nineveh Province indicated a higher incidence among women aged 40-49 years. The overall frequency of breast cancer in Iraq showed a significant increase between 2000 and 2019, highlighting the evolving nature of the disease burden in different regions (Alwan, 2010).

The severity of breast cancer ranges from highly aggressive cancers to physiological adenosis. Males can also be affected by breast cancer, which needs a high index of suspicion for early diagnosis (Al-Hashimi, 2021). It is estimated that 2.3 million new cases of BC are diagnosed each year globally.

Gene expression of mRNA is the fundamental basis for the classification of BC into various molecular subtypes that provide insights into new strategies in the prognosis and management (Mohammed & Rabeea, 2021). One of the most important steps in cancer control is the implementation of patient care programs that work on gathering information about pathological and clinical characteristics of tumors, as well as patient parameters (Cooper, 2025).

2. Patients & Methods

This observational, descriptive, cross-sectional study was adopted within a period starting from September 2023 to August 2024. Data were collected retrospectively from participants using the non-randomized convenience sampling technique. This study was approved by the Local Scientific Council of Arab Board of Health Specializations of General Surgery in Iraq.

Patients presenting with breast masses who were referred by specialists to the Breast Consultation Clinic in Al-Jamhuri, Al Salam and Al- Khansa'a Teaching Hospitals in Mosul City were included. All patients had been previously diagnosed with breast cancer by ultrasound and mammography, with confirmation by histopathological examination reports.

Data were collected using a specifically designed questionnaire. Signed consent forms were obtained from patients who were informed about the nature and goals of the study. All collected data were kept confidential and used solely for research purposes.

Demographic information included patient age, weight, height, and BMI; residence; occupation; blood group; educational level; marital status; and number of pregnancies. Specific questions were focused on the description of breast cancer itself, such as age of starting menses, menstrual cycle regularity, age at menopause, history of previous breast problems, number of first-degree relatives with breast cancer, history of tumors at other sites, and any previous medical, surgical, gynecological, and social problems. Clinical presentation data, such as the main complaint, recurrence history, and histopathological type, were documented.

Included cases included patients under 15 years of age, those who refused to participate in the study, and women diagnosed with non-cancerous breast disease. The collected data were evaluated and analyzed to fulfil the study objectives.

3. Statistical Analysis

The data were analyzed using SPSS version 28. Numbers (percentage) and means $\pm$ standard deviation (SDs) were calculated for demographic data. The differences between categorical variables were assessed by Chi-squared (χ^2) test. A p-value of < 0.05 was considered statistically significant.

4. Results

The present study included 74 participants. The incidence of breast cancer was found to be 3.7919 per 100,000 Mosulian women over an eleven-month period.

The distribution of study participants according to the months of the study period shows that the incidence of breast cancer was zero in October and November 2023, as well as in January, February and April 2024. The incidence ranged from 0.1037 per 100000 in December 2023 to 1.1159 per 100000 in July 2024.

The mean age of the participants was 59.3 years. It was observed that women aged 50-60 years were the most prevalent group, accounting for 27 participants (36.47%). No participants were recorded in the age category of less than 10 years [Table 1](#).

Table 1. Distribution of the study sample according to age.

Age Mean= 59.3 years	Number	Percent	P-value
0 - less than 10	0	0 %	
10 - less than 20	1	1.35 %	0.1
20 - less than 30	2	2.70 %	0.1
30 - less than 40	3	4.04 %	0.2
40 - less than 50	7	9.50 %	0.1
50 - less than 60	27	36.47 %	0.01
60 - less than 70	20	27.03 %	0.01
More than 70	14	18.91 %	0.01
Total	74	100 %	

The distribution of study participants according to BMI showed that the prevalence of breast cancer was 0% among underweight women, compared with 24.3% among overweight and obesity grade I (BMI = 30 - 34.9) women [Table 2](#).

Table 2. Distribution of the study sample according to the body mass index.

BMI Means = 29.7 kg/ m²	No.	Percent	P-value
Under weight (BMI < 18.5)	0	0 %	
Normal (BMI =18.5 - 24.9)	10	13.6 %	0.1
Overweight (BMI = 25 - 29.9)	18	24.3 %	0.01
Obesity grade I (BMI = 30 - 34.9)	18	24.3%	0.01
Obesity grade II (BMI = 35 – 39.9)	14	18.9 %	0.01
Morbid obesity (BMI > 40)	14	18.9 %	0.01
Total	74	100 %	

Regarding place of residence, 54.06% of the study sample resided in urban regions, while 45.94% resided in rural regions. Moreover, the distribution of participants by blood group showed that blood group O was the most frequent (31.1%), whereas blood group AB was the least frequent (16.2%) among the study sample [Table 3](#).

Table 3. Distribution of the study sample according to the blood group.

Blood group	No.	Percent	P-value
A	19	25.6 %	
B	20	27.1 %	0.0
O	23	31.1 %	0.01
AB	12	16.2 %	
Total	74	100 %	

Concerning the marital state, breast cancer was found among 37.9% of married women, 29.7% of widowed women, and 16.2% of both single and divorced women [Table 4](#).

Table 4. Distribution of the study sample according to the marital state.

Marital State	No.	Percent
Single	12	16.2 %
Married	28	37.9 %
Widow	22	29.7 %
Divorced	12	16.2 %
Total	74	100 %

[Table 5](#) presents the distribution of the study sample across different Gynecologic-Obstetric and social histories. Among the gynecologic-obstetric variables, early menarche was the most common factor, observed in 52.7% of participants. Passive smoking was the most frequent social variable, observed in 77.4% of the study sample. The distribution of cancer TNM stages ranged from 32.5% in Stage II to 0% in Stage 0.

Table 5. Distribution of the study sample according to the obstetric and social histories.

Variable	No. (n=74)	Percent (%)
Early Menarche	39	52.7 %
Late menopause	26	35.1 %
Irregular Cycle	32	43.2 %
Hormonal use after menopause	15	20.2 %
Nulliparity	9	12.1 %
Breast feeding of the first child	15	20.2 %
Breast feeding of the last child	10	13.5 %
Oral contraceptive pills use	18	24.3 %
Drugs for stimulate ovulation	9	12.1 %
History of pre-existing breast issue	22	29.7 %
Family history of breast cancer	18	24.3 %
Family history of other cancer	9	12.1 %
Radiation exposure	13	17.6 %
Active smoking	10	13.5 %
Passive smoking	57	77.0%

4. Discussion

The incidence of breast cancer exhibits significant regional variation. The incidence of breast cancer among women in developed countries is higher than that among women in developing countries (55.9 versus 29.7/100,000, respectively) (71). Highest incidence rates are found in Australia/New Zealand (95.5/100,000), Western Europe (90.7/100,000), North America (89.4/100,000), and Northern Europe (86.4/100,000). Lowest incidence rates are found in South-Eastern Asia (41.2/100,000), Central America (39.5/100,000), Eastern Africa (33.0/100,000), Middle Africa (32.7/100,000), and South-Central Asia (26.2/100,000) (Gupta & Goyal, 2022).

Breast cancer is one of the top ten malignant neoplasms that seriously endanger Iraqi women. In developing Middle Eastern countries, including Iraq, the prevalence of breast cancer is continuously rising. Breast cancer is the most prevalent malignancy among women in Iraq (Lucaccioni et al., 2020). Between 2006 and 2014, the Iraqi governorate of Sulaymaniyah had the highest prevalence of female breast cancer; in 2017, it was reported as the most frequent cancer in the Basra governorate (Alwan, 2016).

In agreement with our findings, previous studies have reported that the overall incidence of new cancer cases in Iraq increased over time, from 52.00 per 100,000 individuals in 2000 to 91.66 per 100,000 individuals in 2019. Genetic traits that include gender, age, ethnicity, family history of the disease, early menstrual onset, and menopause are typically unmodifiable risk factors for breast cancer (Fahad Ullah, 2019).

From another point of view, a wide range of lifestyle factors, such as physical inactivity, obesity, alcohol intake, parity, use of certain drugs (such as oral contraceptives), and exposure to carcinogens, are considered as modifiable risk factors for breast cancer (Alsdan et al., 2025). In contrast to developed countries, where the incidence of breast cancer is much higher, developing countries have far lower rates of breast cancer, based on available statistical data (Mustafa et al., 2008).

The current study investigates the incidence of breast cancer among patients attending the main breast clinic in Mosul City. Moreover, the study describes the percentage of different variables that may help direct governmental efforts toward high-risk individuals for early detection, thereby improving overall prognosis (Chaane et al., 2024).

The study included 74 female patients, with a mean age of 59.3 years. The incidence of breast cancer was found to be 3.7919 per 100,000. It should be noted that the data were collected over an eleven-month period, and the incidence rate varied significantly, ranging from 0% in October 2023, November 2023, January 2024, February and April 2024 to 1.1159 per 100,000 in July 2024. These variations could be explained by the fact that the confirmation tools are not always reasonable. However, no comparable studies have been conducted in Mosul to compare the incidence results.

In the present study, the analysis of the women's ages showed a mean age of 59.3 years. Moreover, the 50 to less than 60-year age group was the most prevalent, while no participants were identified in the 0 to less than 10-year age group. Comparably, Al-Hashimi (2021) studied trends in breast cancer incidence in Iraq during the period 2000-2019 and reported that individuals aged 50-59 years exhibited the greatest incidence rates of breast cancer (Adelegan et al., 2024). Additionally, other studies reported that the median age of women with breast cancer was 51 years at the time of diagnosis, with a range of 17 to 82 years (Al-Hashimi, 2021). The finding of the current study that overweight and obesity are more prevalent among breast cancer patients agrees with the results of Smith et al., who reported similar findings regarding the impact of body mass index on breast cancer (Smith et al., 2021). Furthermore, Abd M et al. (Abd, 2023) reported that a higher body mass index is associated with elevated serum insulin and interleukin-6 levels. Likewise, elevated interleukin-6 levels were correlated with malignant breast mass.

Regarding residence, the higher prevalence of urban compared with rural residence may be attributed to factors such as limited transportation infrastructure and lower levels of awareness about breast cancer in rural areas. Similar findings have been reported previously by LeBlanc G et al., (LeBlanc et al., 2022).

The observation that patients with breast cancer more frequently had blood group O and less frequently had blood group AB is comparable with previous studies that highlight blood type A as a potential risk factor for breast cancer compared with blood type O; however, this relationship was not insignificant for blood types B and AB (Alwan et al., 2019).

The association between both passive and active smoking and breast cancer observed in this study has been similarly reported in numerous studies, which stated that smoking is linked to a higher likelihood of cancer being detected through screening rather than through clinical symptoms (Alchazal et al., 2025).

Comparing gynecological and obstetric histories in this study, early menarche was observed in more than half of the cases, late menopause and menstrual cycle irregularity in more than one-third, nulliparity in about one-tenth, and a positive family history in about one-quarter of the study cases. All these findings are comparable to those reported by Roheel et al. (2023), whose systematic review identified multiple risk factors for breast cancer, with their relative importance varying across world regions (Luo et al., 2011).

Similarly, Hashim et al. (2021) reported that, among Iraqi women, family history is a significant predictor of breast cancer and that the governorate of Nineveh had some of the highest lifetime and five-year breast cancer risks (Roheel et al., 2023). Moreover, Koca et al. (2024) explored the role of having a first-degree relative with breast cancer as a significant risk factor, while Arriaga et al. (2019) studied the preventable burden of breast cancer among premenopausal and postmenopausal women in Australia and reported that late menopause is associated with an increased risk of breast cancer (Hashim et al., 2021; Koca & Acikgoz, 2024).

The finding that a lower proportion of women reported a history of breastfeeding their last child compared with those who breastfed their first child in the current study is consistent with previous studies supporting the hypothesis that both breastfeeding and longer breastfeeding duration reduce the risk of cancer, particularly breast cancer (Arriaga et al., 2019; Oikonomou et al., 2024).

Regarding oral contraceptive pill use and hormonal stimulation for ovulation, a history of use was reported in one quarter and one tenth of participants, respectively. These findings are supported by a meta-analysis examining the type and timing of menopausal hormone therapy and breast cancer risk that indicated a modest but significant association between these hormonal therapies and an increased risk of breast cancer. This risk varied according to duration of use, type of hormones involved, and

individual patient characteristics. These insights underscore the importance of personalized medical guidance when considering hormonal (Abdullah et al., 2024).

Radiation exposure history, including CT scans, radiotherapy, or exposure to blasts, was reported among 17.6% of the women with breast cancer in the current study. In agreement with this finding, a recent article published in 2024 revealed that following exposure to radiation for Hodgkin's lymphoma, breast cancer is diagnosed at an earlier stage, and these women are at greater risk of bilateral disease. Such findings support the need for close follow-up of contralateral tumors (Barańska et al., 2021). However, more than three million individuals were internally displaced as a result of the most recent war in Mosul, which negatively affected disease incidence and the general health services provided by the Iraqi Ministry of Health (Elkin et al., 2011).

5. Conclusion

This study highlights that breast cancer remains a significant health concern among women in Mosul, with an observed incidence of 3.79 per 100,000 over an eleven-month period. The majority of affected women were aged 50–59 years and had overweight or obesity; early menarche, late menopause, passive smoking, and a family history of breast cancer were identified as common risk factors. Invasive ductal carcinoma was the most prevalent histological type, and urban residency was slightly more associated with the disease. These findings emphasize the need for targeted health interventions, including improved awareness, routine screening, and early detection programs, particularly for high-risk groups. Integrating these measures into public health strategies could help reduce the disease burden and improve outcomes for women in this region.

Acknowledgement

The authors would like to express their sincere gratitude to the patients who participated in this study and to the medical staff at Al-Jamhori, Al-Salam, and Al-Khansa'a Teaching Hospitals in Mosul for their valuable cooperation. Special thanks to the Health Directorate of Nineveh for facilitating data access and to the Local Scientific Council of the Arab Board of Health Specializations for approving and supporting this research.

Conflicts of Interest

The authors declare that there is no conflict of interest regarding the publication of the current manuscript.

Funding

The authors declare that the research did not receive any financial support from any Institution.

Ethics Statements

This study was approved by the Local Scientific Council of Arab Board of Health Specializations of General surgery in Iraq.

Author Contribution

The authors confirm contribution to the paper as follows: study conception and design: Muna Z. Al-Hamdany, Modhar S. Al-Omary, data collection: Imad Ali Mohammed, analysis and interpretation of results: Muna Z. Al-Hamdany, Modhar S. Al-Omary, draft manuscript preparation: Imad Ali Mohammed. All authors reviewed the results and approved the final version of the manuscript.

References

- Abd, M. A. (2023). Association between serum insulin and interleukin-6 levels with breast cancer in post-menopausal iraqi women. *Journal of the Faculty of Medicine Baghdad*, 65(4), 323-328.
- Abdullah, A. S., Ali, H. O., Muhammad, H. M., Pshtiwan, L. R., Ali, R. M., Ahmed, N. H. A., Othman, S., Hasan, K. M., Abdullah, A. M., & Salih, A. M. (2024). Breastfeeding Impact on Cancer in Women: A Systematic Review. *Barw Medical Journal*.
- Adelegan, A. A., Talabi, A. A., Dokunmu, T. M., & Iweala, E. E. (2024). Anticancer Activity of Ethyl Acetate Fraction and Ethanol Leaf Extract of *Olex subscorpioidea* against DMBA-Induced Female Rats. *Tropical Journal of Natural Product Research*, 8(1).
- Al-Assaf, N. H., Al-Youzbaki, D. B., & Al-Khyaat, M. K. (2008). Risk factors of breast cancer in pre-menopausal women with social perspective. *Annals of the College of Medicine Mosul*, 34(2), 100.100-108.100.
- Al-Hashimi, M. M. (2021). Trends in breast cancer incidence in Iraq during the period 2000-2019. *Asian Pacific journal of cancer prevention: APJCP*, 22(12), 3889.
- Al Alwan, N. A. (2022). General oncology care in Iraq. In *Cancer in the Arab world* (pp. 63-82). Springer.
- Alchazal, R., Zaitoun, K. J., Al-Qudah, M., Zaitoun, G., Taha, A. M., Saleh, O., Alqudah, M., Abuawwad, M., Taha, M., & Aldalati, A. Y. (2025). Relationship between ABO blood group antigens and Rh factor with breast cancer: A systematic review and meta-analysis. *Oncotarget*, 16, 311.
- Alsdfan, R. M., Kadir, A. A., Noor, N. M., & Al-Jubouri, M. B. A. (2025). Quality of life and its associated factors among breast cancer women in Iraq: A cross-sectional study. *Asian Pacific journal of cancer prevention: APJCP*, 26(1), 339.
- Alwan, N. (2010). Breast cancer: demographic characteristics and clinico-pathological presentation of patients in Iraq. *EMHJ-Eastern Mediterranean Health Journal*, 16 (11), 1159-1164, 2010.
- Alwan, N. A. (2016). Breast cancer among Iraqi women: preliminary findings from a regional comparative breast cancer research project. *Journal of global oncology*, 2(5), 255.
- Alwan, N. A., Tawfeeq, F. N., & Mallah, N. A. (2019). Demographic and clinical profiles of female patients diagnosed with breast cancer in Iraq. *Journal of Contemporary Medical Sciences*, 5(1).
- Arriaga, M. E., Vajdic, C. M., Canfell, K., MacInnis, R. J., Banks, E., Byles, J. E., Magliano, D. J., Taylor, A. W., Mitchell, P., & Giles, G. G. (2019). The preventable burden of breast cancers for premenopausal and postmenopausal women in Australia: a pooled cohort study. *International Journal of Cancer*, 145(9), 2383-2394.
- Barańska, A., Błaszczuk, A., Kanadys, W., Malm, M., Drop, K., & Polz-Dacewicz, M. (2021). Oral contraceptive use and breast cancer risk assessment: a systematic review and meta-analysis of case-control studies, 2009–2020. *Cancers*, 13(22), 5654.
- Burstein, H., Curigliano, G., Thürlimann, B., Weber, W., Poortmans, P., Regan, M., Senn, H., Winer, E., Gnant, M., & Aebi, S. (2021). Customizing local and systemic therapies for women with early breast cancer: the St. Gallen International Consensus Guidelines for treatment of early breast cancer 2021. *Annals of oncology*, 32(10), 1216-1235.
- Chaane, N., Kuehnast, M., & Rubin, G. (2024). An audit of breast cancer in patients 40 years and younger in two Johannesburg academic hospitals. *SA Journal of Radiology*, 28(1), 2772.
- Cooper, A. (2025). The anatomy and diseases of the breast. *BoD–Books on Demand*.
- Elkin, E. B., Klem, M. L., Gonzales, A. M., Ishill, N. M., Hodgson, D., Ng, A. K., Marks, L. B., Weidhaas, J., Freedman, G. M., & Miller, R. C. (2011). Characteristics and outcomes of breast cancer in women with and without a history of radiation for Hodgkin's lymphoma: a multi-institutional, matched cohort study. *Journal of clinical oncology*, 29(18), 2466-2473.
- Fahad Ullah, M. (2019). Breast cancer: current perspectives on the disease status. *Breast cancer metastasis and drug resistance: challenges and progress*, 51-64.

- Gupta, M., & Goyal, N. (2022). *Applied anatomy of breast cancer*. In *Breast Cancer: Comprehensive Management* (pp. 23-35). Springer.
- Gurjia, Z. A., Ali, E. A., & Fadhil, M. S. (2023). *The Role of Digital Pathology in The Assessment of PD-L1 Expression in HER2-neu Positive Breast Cancer*. *Annals of the College of Medicine Mosul*, 45(2), 127.120-133.120.
- Hashim, H. T., Ramadhan, M. A., Theban, K. M., Bchara, J., El-Abed-El-Rassoul, A., & Shah, J. (2021). *Assessment of breast cancer risk among Iraqi women in 2019*. *BMC Women's Health*, 21(1), 412.
- Koca, B., & Acikgoz, A. (2024). *Factors affecting breast cancer risk level and the prevalence of early diagnosis and screening in a group of Turkish women according to the Gail model*. *International Journal of Community Medicine and Public Health*, 11(4), 1.
- LeBlanc, G., Lee, I., Carretta, H., Luo, Y., Sinha, D., & Rust, G. (2022). *Rural-urban differences in breast cancer stage at diagnosis*. *Women's Health Reports*, 3(1), whr. 2021.0082.
- Lucaccioni, L., Trevisani, V., Marrozzini, L., Bertocelli, N., Predieri, B., Lugli, L., Berardi, A., & Iughetti, L. (2020). *Endocrine-disrupting chemicals and their effects during female puberty: a review of current evidence*. *International Journal of Molecular Sciences*, 21(6), 2078.
- Luo, J., Margolis, K. L., Wactawski-Wende, J., Horn, K., Messina, C., Stefanick, M. L., Tindle, H. A., Tong, E., & Rohan, T. E. (2011). *Association of active and passive smoking with risk of breast cancer among postmenopausal women: a prospective cohort study*. *Bmj*, 342.
- Lv, L., Zhao, B., Kang, J., Li, S., & Wu, H. (2023). *Trend of disease burden and risk factors of breast cancer in developing countries and territories, from 1990 to 2019: Results from the Global Burden of Disease Study 2019*. *Frontiers in public health*, 10, 1078191.
- Mohammed, M. I., & Rabeea, M. A. (2021). *Effects of noise pollution from electric backup generators on the operators' health*. *Pertanika Journal of Science and Technology*, 29(4), 2675-2687.
- Mohsin, R. N., & Mohamad, B. J. (2024). *Clinical and histopathological features of breast cancer in Iraqi patients between 2018-2021*. *Iraqi Journal of Science*, 90-107.
- Mustafa, N. S., Saeed, M. S., & Saleem, S. H. (2008). *Immunohistochemical evaluation of Her-2/neu overexpression in breast carcinoma in Mosul*. *Annals of the College of Medicine Mosul*, 34(2), 87.80-92.80.
- Oikonomou, G., Bothou, A., Eirini, O., Daglas, M., Iliadou, M., Antoniou, E., & Palaska, E. (2024). *Breastfeeding and its association with breast cancer: a systematic review of the literature*. *Maedica*, 19(1), 106.
- Rebner, M., & Pai, V. R. (2020). *Breast cancer screening recommendations: African American women are at a disadvantage*. *Journal of Breast Imaging*, 2(5), 416-421.
- Roheel, A., Khan, A., Anwar, F., Akbar, Z., Akhtar, M. F., Imran Khan, M., Sohail, M. F., & Ahmad, R. (2023). *Global epidemiology of breast cancer based on risk factors: a systematic review*. *Frontiers in Oncology*, 13, 1240098.
- Sacca, L., Markham, C., & Fares, J. (2020). *Using intervention mapping to develop health education and health policy components to increase breast cancer screening and chemotherapy adherence among Syrian and Iraqi refugee women in Beirut, Lebanon*. *Frontiers in public health*, 8, 101.
- Siegel, R. L., Giaquinto, A. N., & Jemal, A. (2024). *Cancer statistics, 2024*. *CA: a cancer journal for clinicians*, 74(1), 12-49.
- Smith, S. G., Sestak, I., Morris, M. A., Harvie, M., Howell, A., Forbes, J., & Cuzick, J. (2021). *The impact of body mass index on breast cancer incidence among women at increased risk: an observational study from the International Breast Intervention Studies*. *Breast Cancer Research and Treatment*, 188(1), 215-223.
- Wilkinson, L., & Gathani, T. (2022). *Understanding breast cancer as a global health concern*. *The British journal of radiology*, 95(1130), 20211033.



Asparagine as an Eco-Friendly Corrosion Inhibitor for Copper in Nitric Acid: A Gravimetric and Electrochemical Investigation

Karima Abderrahim ^{1*}, Ikram Beghou ¹, Kamilia Moussaoui ¹, Sihem Abderrahmane ¹, Charaf Eddine Khaldi ² and Youcef Allaoui ²



¹ Surface Engineering Laboratory (L.I.S), Department of Chemistry, Faculty of Sciences, Badji Mokhtar-Annaba University, P.O.Box 12, Annaba, 23000, Algeria.

² Badji Mokhtar-Annaba University, P.o.Box 12, Annaba 23000, Algeria.

ARTICLE INFO

Received: 22nd January 2026
Received in revised form: 27th February 2026
Accepted: 03th March 2026
Published: 15th March 2026

***Corresponding Author:**
Karima Abderrahim
E-mail :
karima.abderrahim@univ-annaba.dz

Citation: Abderrahim, K., Beghou, I., Moussaoui, K., Abderrahmane, S., Khaldi, C. E., Allaoui, Y. (2026). Asparagine as an Eco-Friendly Corrosion Inhibitor for Copper in Nitric Acid: A Gravimetric and Electrochemical Investigation. *Modern Journal of Health and Applied Sciences*, 3(1), 83-95.

Copyright (c) 2026 Modern Journal of Health and Applied Sciences (MJHAS)

Open Access



This work is licensed under a [Creative Commons Attribution NonCommercial 4.0 International](https://creativecommons.org/licenses/by-nc/4.0/) license.

DOI: <https://doi.org/10.70411/MJHAS.3.1.2026353>

ABSTRACT

The corrosion inhibition performance of asparagine (ASP) for copper in 1 M HNO₃ solution was investigated using a combined experimental and theoretical approach. The inhibitory effect of ASP was evaluated through gravimetric measurements, potentiodynamic polarization, and electrochemical impedance spectroscopy (EIS). The results obtained from weight-loss measurements revealed that the corrosion rate of copper decreased significantly in the presence of the inhibitor, reaching a maximum inhibition efficiency of 94% at 10⁻⁴ M. Electrochemical studies confirmed these findings, showing a considerable decrease in corrosion current density and a marked increase in charge transfer resistance with the addition of ASP. Polarization results indicated that asparagine behaves as a mixed-type inhibitor, affecting both anodic and cathodic reactions. EIS measurements revealed the formation of a protective film on the copper surface, as evidenced by the increase in charge transfer resistance and the decrease in double-layer capacitance. The adsorption of ASP molecules on the copper surface was found to be responsible for the inhibition effect.

Keywords: Corrosion inhibitor, Copper, Amino acids, Asparagine, HNO₃.

1. Introduction

Copper and its alloys are extensively utilized in many industrial fields. Owing to its high electrical and thermal conductivity, copper is commonly applied in heat-transfer equipment and as an electrical conductor in electronic systems. Nevertheless, when it is subjected to aggressive or corrosive environments, copper can deteriorate, resulting in considerable economic losses (Abderrahim et al., 2021; Abderrahim et al., 2018). One of the most effective strategies to mitigate copper corrosion is the use of corrosion inhibitors, and numerous inhibitors have been investigated and developed for this purpose. These substances reduce the corrosion rate by forming a protective layer on the metal surface. Both inorganic (Ahmed et al., 2020; Muñoz et al., 2004) and organic compounds (Ebadi et al., 2012; Farooq et al., 2026) have been reported to be effective inhibitors. However, many conventional inhibitors present environmental and health concerns due to their toxic nature. Consequently, recent research has increasingly focused on the development of environmentally friendly and sustainable corrosion inhibitors. Amino acids are environmentally benign organic compounds that are non-toxic and readily soluble in aqueous solutions. They are also biodegradable and can be synthesized with high purity at relatively low production costs (Loto, 2019). Because of these characteristics, amino acids have attracted attention as potential corrosion inhibitors. Previous studies have shown that organic molecules containing heteroatoms such as nitrogen, sulfur, phosphorus, and oxygen tend to exhibit improved corrosion inhibition performance for copper surfaces (Barouni et al., 2014; Kaya et al., 2016). This effect is mainly due to the electronic structure of copper atoms, which possess partially filled d-orbitals that can interact with electron-donating atoms to form coordination bonds. Structurally, amino acids contain both amine ($-NH_2$) and carboxyl ($-COOH$) functional groups, together with a side chain that distinguishes one amino acid from another (Akram et al., 2011; Dewangan et al., 2023). The nitrogen and oxygen atoms in these functional groups carry lone pairs of electrons, which can interact with copper atoms at the metal surface. Such interactions promote adsorption of the amino acid molecules and facilitate the formation of protective bonds on the copper surface, contributing to corrosion inhibition. The objective of this study is to investigate the effectiveness of asparagine as a corrosion inhibitor for copper in a nitric acid solution. The inhibitory performance was evaluated using both gravimetric and electrochemical approaches. In particular, weight loss experiments, potentiodynamic polarization, and electrochemical impedance spectroscopy (EIS) were employed to determine the inhibition efficiency. Surface morphology analysis was also conducted to support and confirm the results obtained from the gravimetric measurements.

2. Experimental

2. 1. Materials and Methods

Copper of 99.92% purity was employed in this study. Prior to the experiments, the samples were mechanically polished with emery paper. After polishing, the specimens were carefully degreased by rinsing with distilled water, ethanol, and acetone. The prepared samples were then dried and kept in a desiccator until use. Asparagine (ASP), Figure 1, was employed as a corrosion inhibitor.

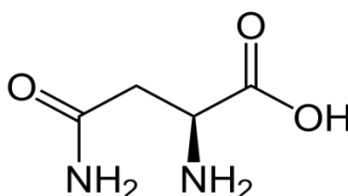


Figure 1. Molecular structure of asparagine (ASP).

2.2. Gravimetric Study

Corrosion inhibition studies were performed on copper samples (99% purity) using the mass-loss method. Rectangular specimens (1 cm × 1 cm × 1 cm) were polished with emery paper, washed with distilled water, dried, and accurately weighed before immersion. The samples were then placed in 250 mL of 1 M HNO₃ solution for 24 hours at 298 K in the absence and presence of asparagine (ASP) (10⁻¹–10⁻⁴ M) as a corrosion inhibitor. After immersion, the specimens were rinsed, dried, and reweighed to determine the mass loss. Each experiment was repeated three times, and the average values were used to calculate the corrosion rate (V_{corr}), inhibition efficiency (%IE), and surface coverage (θ).

$$\Delta m = m_1 - m_2 \quad (1)$$

$$V_{\text{corr}} = \frac{\Delta m}{S \cdot t} \quad (2)$$

$$\theta = 1 - \frac{\Delta m_{\text{corr}}}{\Delta m_{\text{corr}}^{\circ}} \quad (3)$$

$$\text{IE}(\%) = \frac{V_{\text{corr}}^{\circ} - V_{\text{corr}}}{V_{\text{corr}}^{\circ}} \quad (4)$$

Where:

m_1 and m_2 represent the masses of the copper samples before and after immersion, respectively. Δm_{corr} and $\Delta m_{\text{corr}}^{\circ}$ denote the average masses of the specimens before and after immersion, respectively.

2.3. Electrochemical Investigations

Electrochemical measurements were performed using a SP150 Bio-Logic potentiostat controlled by EC-Lab software. A conventional three-electrode electrochemical cell was employed, consisting of a saturated calomel electrode (SCE) as the reference electrode, a platinum electrode as the counter electrode, and a copper working electrode with an exposed surface area of 1.75 cm². Potentiodynamic polarization curves were recorded at a scan rate of 1 mV s⁻¹ within a potential range from -300 to +200 mV/SCE, allowing stabilization of the electrical double layer before measurements. Electrochemical impedance spectroscopy (EIS) measurements were carried out at the corrosion potential over a frequency range of 100 kHz to 10 mHz with a 10 mV sinusoidal perturbation.

3. Results

3.1. Gravimetric Study

The variation in inhibition efficiency (IE%) and corrosion rate (V_{corr}) obtained using this method is shown in [Figure 2](#).

[Table 1](#) presents the corrosion parameters derived from weight-loss measurements for copper in 1 M HNO₃ solution, in the absence and presence of asparagine. In the blank solution, copper exhibits a high corrosion rate of 22 mg cm⁻² h⁻¹, indicating strong metal dissolution in the acidic medium. The addition of asparagine significantly reduces the corrosion rate and increases both the surface coverage and the inhibition efficiency. The maximum inhibition efficiency reaches 94%, with a corresponding surface coverage of 0.94, suggesting strong adsorption of asparagine molecules on the copper surface. These results indicate that asparagine is an effective corrosion inhibitor for copper in HNO₃ solution, probably through the formation of a protective adsorbed film on the metal surface ([Debab et al., 2025](#)).

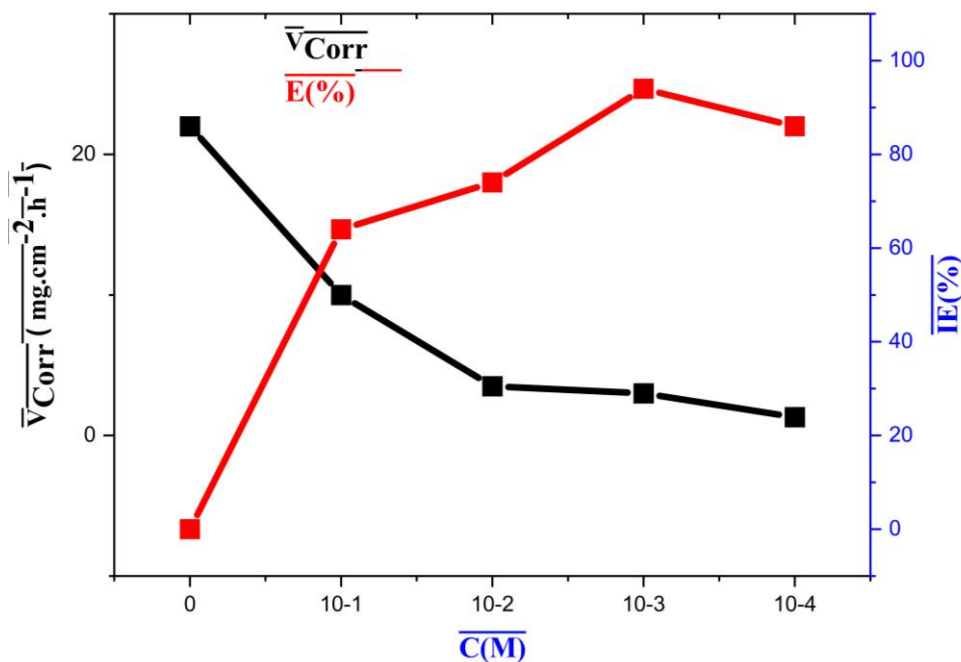


Figure 2. Variation of the inhibition efficiency (E%) and corrosion rate (V_{corr}) obtained by the gravimetric method in 1 M HNO_3 as a function of inhibitor concentration.

Table 1. Corrosion parameters derived from gravimetric measurements.

C (M)	V_{corr} (mg cm ⁻² h ⁻¹)	θ	IE(%)
0	22	/	/
10 ⁻¹	10	0.64	64
10 ⁻²	3.5	0.74	74
10 ⁻³	3	0.86	86
10 ⁻⁴	1.3	0.94	94

3. 2. Electrochemical Analysis

3. 2. 1. Open Circuit Potential

The evolution of the open-circuit potential (OCP) of copper in 1 M HNO_3 solution was monitored in the absence and presence of different concentrations of asparagine (10^{-1} - 10^{-4} M), and the results are shown in [Figure 3](#). In the uninhibited solution, the corrosion potential (E_{corr}) stabilizes around -0.028 V/SCE after 1 h of immersion, indicating the establishment of a steady-state corrosion process. In the presence of asparagine, the corrosion potential shifts toward more positive values, suggesting that the inhibitor affects mainly the anodic reaction. This behavior can be attributed to the adsorption of asparagine molecules on the copper surface, which leads to the formation of a protective layer that slows down the dissolution of copper in the acidic medium.

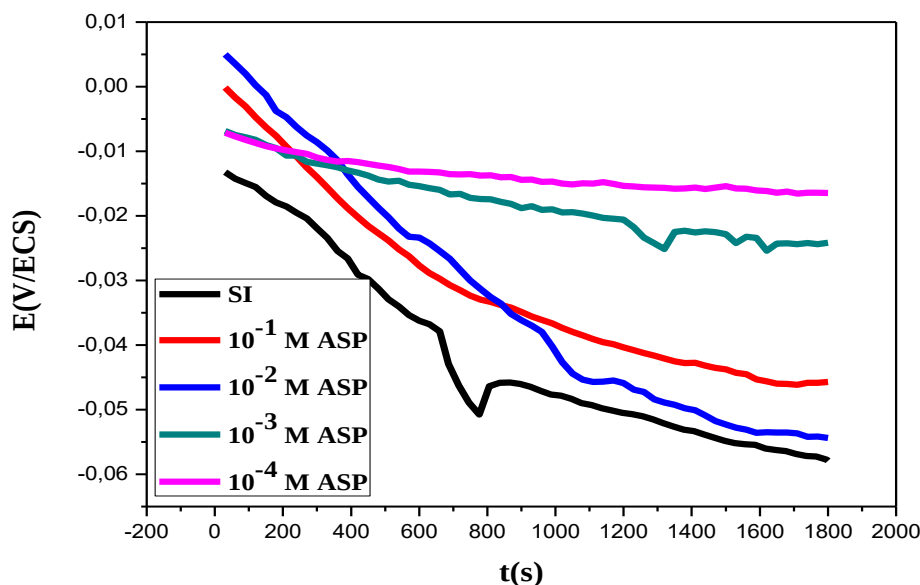


Figure 3. Evolution of the open-circuit potential (OCP) of copper immersed in 1 M HNO₃ solution in the absence and presence of asparagine.

3. 2. 2. Electrochemical Impedance Spectroscopy (EIS)

Electrochemical impedance spectroscopy measurements were performed at the corrosion potential and at different inhibitor concentrations in order to gain a better understanding of the corrosion and inhibition mechanisms of copper in 1 M HNO₃ solution. These measurements were used to investigate the corrosion and protection processes occurring at the copper surface in the absence and presence of asparagine (ASP) at various concentrations. The electrochemical impedance diagrams of copper immersed in 1 M HNO₃ in the absence and presence of different concentrations of asparagine are shown in **Figure 4a** (Nyquist plots) and **Figure 4b-c** (Bode plots). These diagrams (via **Figure 4a**) reveal the presence of two capacitive loops. The first loop, observed at high frequencies, is attributed to the relaxation process of the electrical double-layer resulting from its charge–discharge phenomenon, which is known to be a rapid process (Amin et al., 2010; McCafferty, 2005). The second loop, appearing at low frequencies, begins with a characteristic behavior associated with Warburg impedance, as reported by other researchers (Ma et al., 2002; Ma et al., 2003). This behavior is generally attributed to the diffusion of soluble corrosion products into the bulk solution and/or the diffusion of depolarizing species from the solution toward the metal/solution interface. The diameter of the capacitive loops increases as the concentration of asparagine decreases. This behavior suggests the formation of a protective barrier on the copper surface, which may be associated with the formation of a Cu(I)–ASP complex adsorbed on the metal surface (Barouni et al., 2010; Fouda et al., 2000).

The Bode diagrams provide additional information about the electrochemical behavior of copper in the studied medium. As shown in **Figure 4b**, a resistive region appears at high frequencies. Furthermore, **Figure 4c** shows the presence of a single time constant for the different concentrations of asparagine (ASP), suggesting that the corrosion process is mainly controlled by a single electrochemical reaction mechanism. The impedance of an electrochemical system can be interpreted by analogy with an electrical impedance.

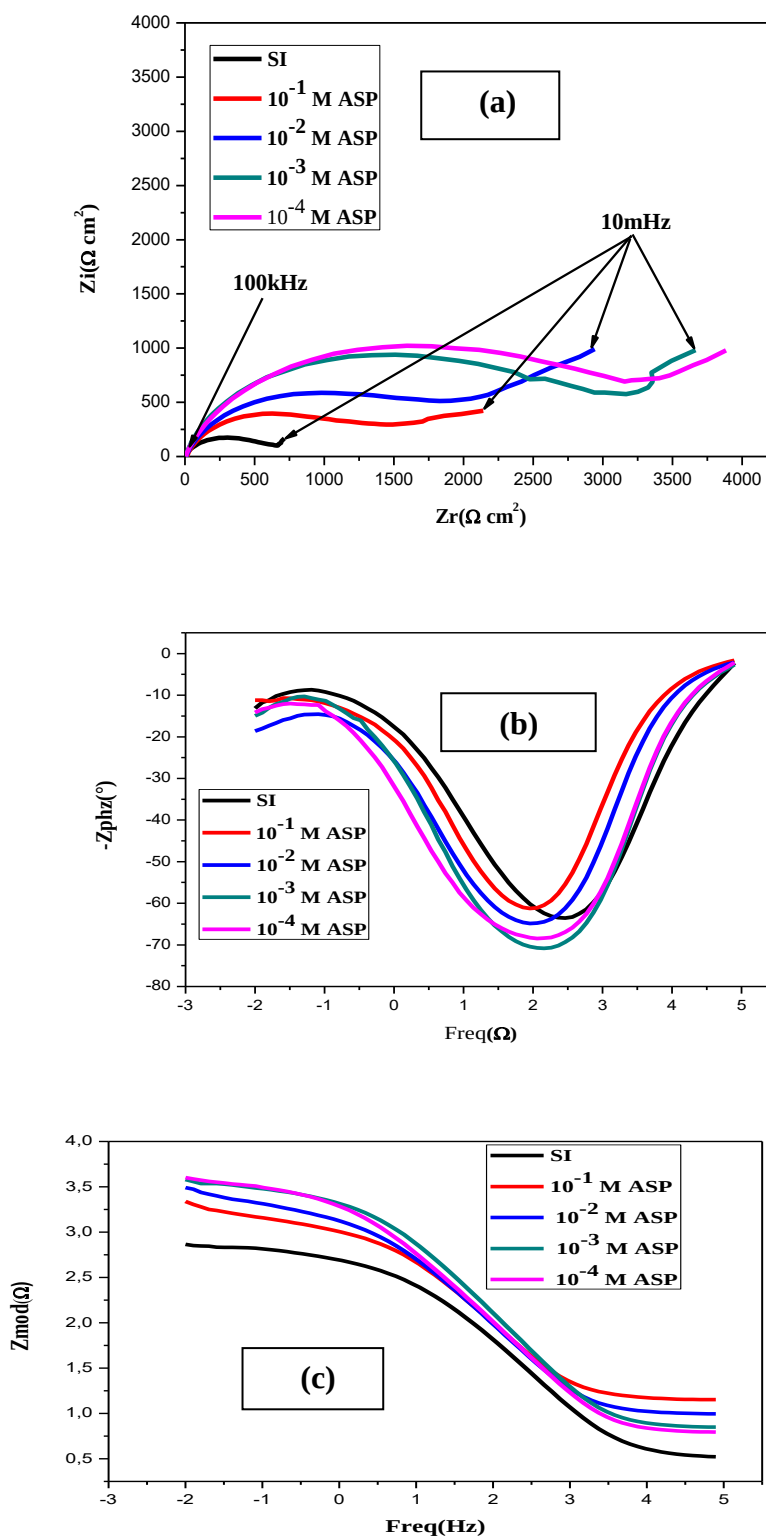


Figure 4. Electrochemical impedance diagrams of Cu in 1 M HNO₃ in the absence and presence of asparagine at different concentrations: (a) Nyquist plot; (b) and (c) Bode plots.

The various processes occurring at the electrode/electrolyte interface can be represented using an equivalent electrical circuit (EEC). In such circuits, each element connected in series or parallel corresponds to a specific physical process occurring in the system. These models are progressively fitted to the experimental impedance diagrams to extract the parameters necessary to understand the corrosion mechanism. The EEC used to fit the impedance spectra was obtained using the simulation software ZView and EC-Lab and is presented in [Figure 5](#). This circuit was employed to model the impedance behavior of copper in 1 M

HNO₃ solution both in the absence and in the presence of asparagine. The circuit includes the solution resistance (R_s), the charge transfer resistance (R₁), and a constant phase element (CPE1) associated with the double-layer capacitance. In addition, R₂ and CPE2 represent the impedance contribution of the adsorbed inhibitor film formed on the copper surface. The parameters n₁ and n₂ correspond to the heterogeneity factors associated with the phase shift of the constant phase elements. The impedance of the constant phase element (CPE) is defined by the following relation (Selatnia et al., 2018):

$$Z_{\text{CPE}} = \frac{1}{Q(j\omega)^\alpha} \quad (7)$$

Where:

Q (Ω⁻¹·s^α·cm⁻²) represents the magnitude of the constant phase element (CPE); j is the imaginary unit (j² = -1); ω is the angular frequency (rad·s⁻¹); α is the deviation parameter that characterizes the non-ideal capacitive behavior of the CPE (-1 ≤ α ≤ 1).

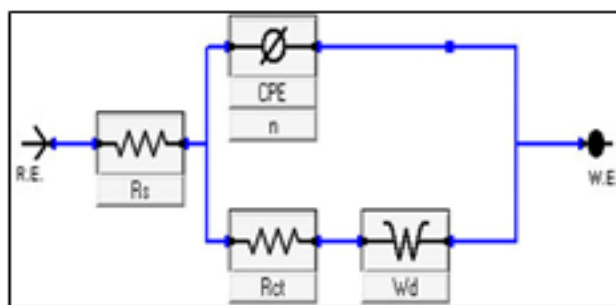


Figure 5. Equivalent electrical circuit (EEC) used to fit the electrochemical impedance spectra of copper in 1 M HNO₃ solution in the absence and presence of asparagine at various concentrations.

The values of the different electrochemical parameters derived from the equivalent electrical circuit for copper in 1 M HNO₃ solution, in the absence and presence of asparagine, as well as the inhibition efficiencies calculated using Equation (8), are summarized in Table 2.

$$E(\%) = \left(1 - \frac{R_t}{R'_t}\right) \times 100 \quad (8)$$

Where R_t and R'_t represent the charge transfer resistances in the absence and presence of the inhibitor, respectively.

The results indicate that the charge transfer resistance (R_t) increases significantly with the addition of the inhibitor, reaching 265.8 Ω·cm² at 10⁻⁴ M, which suggests improved corrosion protection. At the same time, the inhibition efficiency (IE%) increases and reaches a maximum value of 94.98%, confirming the strong inhibitive effect of asparagine. The decrease in CPE values and the high n-values indicate the formation of a protective adsorbed film on the copper surface. Overall, the EIS results confirm that asparagine effectively inhibits copper corrosion in 1 M HNO₃ solution.

Table 2. Electrochemical parameters obtained from the equivalent electrical circuit for copper in 1 M HNO₃ solution in the absence and presence of asparagine, along with the calculated inhibition efficiencies.

(M)	R _s (Ω.cm ²)	CPE ₁ (μF.cm ²)	n ₁	R _{t1} (Ω.cm ²)	CPE ₂ (μF.cm ²)	n ₂	R _{t2} (Ω.cm ²)	IE (%)
0	5.80	0.85	0.65	10.82	9.58	0.92	1.01	/
10 ⁻¹	3.98	0.70	0.83	21.43	7.20	0.89	3.58	49.51
10 ⁻²	6.65	0.64	0.69	78.30	3.90	0.93	8.6	89.98

10^{-3}	7.65	0.65	0.70	79.30	2.90	0.94	14.2	92.92
10^{-4}	8.13	0.004	0.91	265.8	0.69	0.91	15.2	94.98

3. 2. 3. Polarization Measurements

The polarization curves of copper in 1 M HNO_3 solution in the absence and presence of asparagine (10^{-1} – 10^{-4} M) are presented in [Figure 6](#), recorded after 1 h of immersion at a scan rate of 1 mV s^{-1} . The addition of asparagine (ASP) causes a noticeable shift in the corrosion potential along with a significant decrease in the corrosion current density, indicating effective inhibition of copper corrosion. This behavior is attributed to the adsorption of inhibitor molecules on the copper surface, which blocks active sites involved in the electrochemical reactions and slows the dissolution process. The electrochemical parameters derived from the polarization curves are summarized in [Table 3](#). The inhibition efficiency (IE%) was calculated using the following expression:

$$\text{IE}(\%) = \frac{i_{\text{corr}} - i'_{\text{corr}}}{i_{\text{corr}}} \times 100 \quad (9)$$

where i_{corr} and i'_{corr} represent the corrosion current densities in the absence and presence of the inhibitor, respectively.

In the uninhibited solution, the corrosion current density (i_{corr}) reaches $98.96 \mu\text{A}\cdot\text{cm}^{-2}$, indicating a high corrosion rate of copper in a nitric acid medium. The corrosion potential (E_{corr}) is measured at -128.17 mV/SCE , which corresponds to the natural corrosion condition of copper in this aggressive environment. The addition of asparagine leads to a significant reduction in the corrosion current density. For example, i_{corr} decreases from $98.96 \mu\text{A}\cdot\text{cm}^{-2}$ to $17.07 \mu\text{A}\cdot\text{cm}^{-2}$ at 10^{-1} M and further decreases to $9.036 \mu\text{A}\cdot\text{cm}^{-2}$ at 10^{-4} M. This strong decrease indicates that asparagine effectively inhibits the corrosion of copper in nitric acid solution.

The inhibition efficiency (IE%) increases progressively with decreasing inhibitor concentration, reaching 95.75% at 10^{-4} M, which represents the highest protective performance among the tested concentrations. This behavior suggests that the inhibitor molecules strongly adsorb on the copper surface, forming a protective film that reduces the active sites available for corrosion reactions. The values of the corrosion potential (E_{corr}) exhibit slight shifts in the presence of the inhibitor. Since the displacement of E_{corr} is relatively small (generally less than $\pm 85 \text{ mV}$ compared to the blank solution), the inhibitor can be classified as a mixed-type inhibitor, affecting both the anodic dissolution of copper and the cathodic reduction reactions.

Furthermore, the changes observed in the anodic (B_a) and cathodic (B_c) Tafel slopes indicate that the addition of asparagine modifies the kinetics of both electrochemical reactions. The increase in the Tafel slopes suggests that the inhibitor alters the reaction mechanisms by blocking active sites on the copper surface.

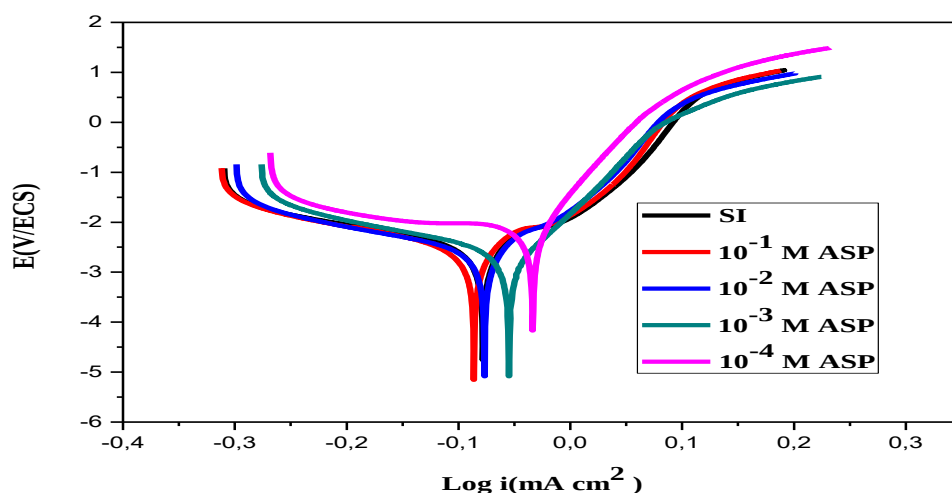


Figure 6. Potentiodynamic polarization curves of copper in 1 M HNO₃ solution in the absence and presence of asparagine at different concentrations.

Table 3. Electrochemical parameters derived from the polarization curves of copper in 1 M HNO₃ solution in the absence and presence of asparagine at different concentrations, and the corresponding calculated inhibition efficiencies.

C (M)	E _{corr} (mV/ECS)	i _{corr} (μA.cm ⁻²)	B _a (mV.dec ⁻¹)	B _c (mV.dec ⁻¹)	IE (%)
0	-128.17	98.96	34.8	24.9	/
10 ⁻¹	-118.88	17.07	37.3	21.3	66.19
10 ⁻²	-118.14	12.89	41.8	28.8	73.61
10 ⁻³	-143.69	10.06	52.9	42.9	80.79
10 ⁻⁴	-165.82	9.036	63.6	43.03	95.75

3. 3. Optical Microscopy Analysis

Optical microscopy is a technique used to examine the surface condition and morphology of materials. In this study, optical micrographs of the copper surface immersed in 1 M HNO₃ solution in the absence and presence of asparagine (ASP) at 10⁻⁴ M were obtained. The surface morphologies are presented in two-dimensional and three-dimensional representations in Figures 7a, a' and 7b, b', respectively.

In the absence of the inhibitor (Figures 7a and 7a'), the copper surface exhibits numerous pits of different sizes, accompanied by severe surface degradation, resulting in significant roughness. This damage indicates intense corrosion of copper in 1 M HNO₃ solution. In contrast, in the presence of asparagine at 10⁻⁴ M (Figures 7b and 7b'), the copper surface appears much smoother, and no noticeable pits are observed. This behavior confirms the formation of a protective inhibitor film on the metal surface, which effectively reduces the corrosion rate of copper.

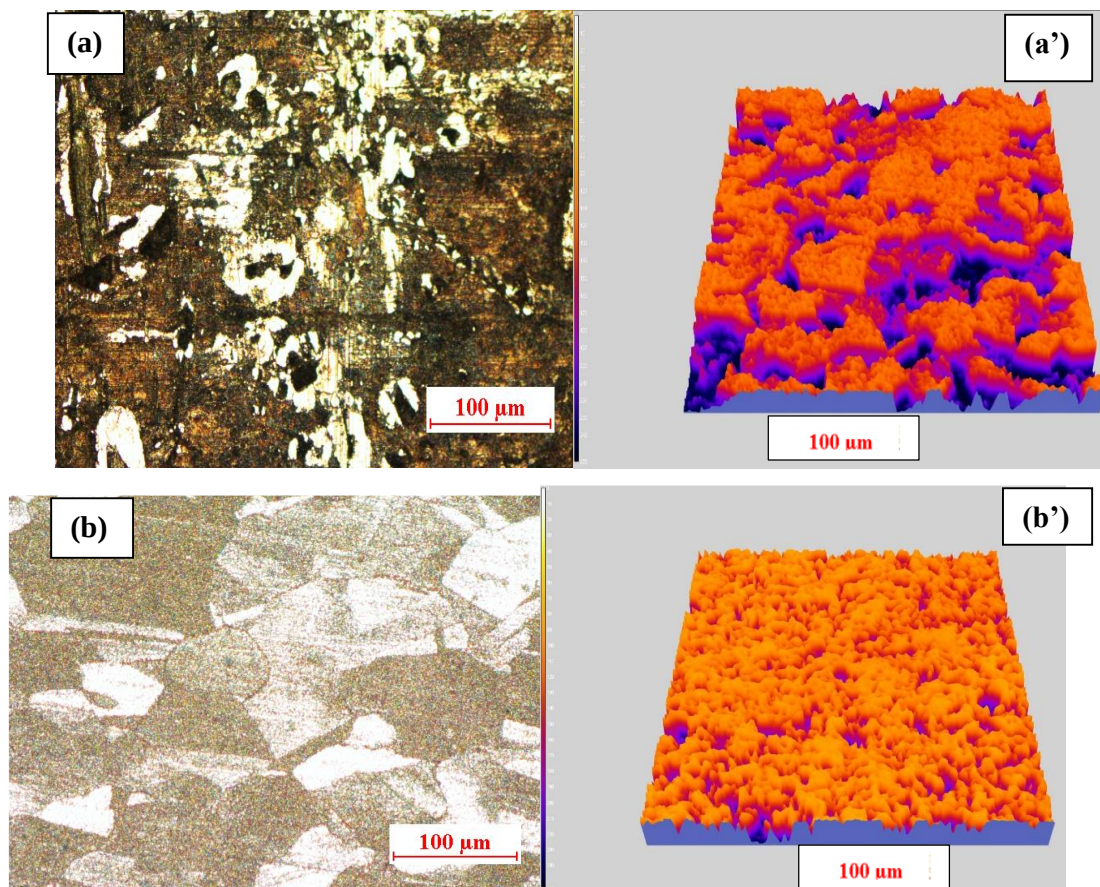


Figure 7. Optical microscopy (OM) images of the copper surface after 2 h of immersion in 1 M HNO_3 solution: (a, a') without inhibitor and (b, b') with asparagine (ASP, 10^{-4} M).

4. Conclusion

The corrosion inhibition performance of asparagine (ASP) for copper in 1 M HNO_3 solution was investigated using gravimetric measurements, electrochemical techniques, and theoretical calculations. The main conclusions can be summarized as follows:

1. Gravimetric results showed that the corrosion rate of copper decreases significantly in the presence of ASP, with an inhibition efficiency reaching 94% at 10^{-4} M.
2. Potentiodynamic polarization studies indicated that ASP acts as a mixed-type inhibitor, reducing both anodic dissolution and cathodic reduction reactions.
3. Electrochemical impedance spectroscopy revealed a significant increase in charge transfer resistance (R_t) and a decrease in double-layer capacitance, confirming the formation of a protective adsorbed layer on the copper surface.
4. The adsorption of ASP molecules on copper leads to the formation of a protective film, which blocks the active sites responsible for corrosion and slows the electrochemical reactions.

The results demonstrate that asparagine is an effective and environmentally friendly corrosion inhibitor for copper in nitric acid solution, making it a promising candidate for corrosion protection in acidic environments.

Conflict of Interest

On behalf of all authors, the corresponding author states that there is no conflict of interest.

Data Availability

No data was used for the research described in the article.

References

- Abderrahim, K., Abderrahmane, S., Khamaysa, O. M. A., & Selatnia, I. (2021). Evaluation of corrosion inhibition performance of tetrathiafulvalene derivatives for copper in NaCl solution: electrochemical, morphological and computational approaches. *Chemical Data Collections*, 36, 100779.
- Abderrahim, K., Selatnia, I., Sid, A., & Mosset, P. (2018). 1, 2-bis (4-chlorobenzylidene) Azine as new and effective corrosion inhibitor for copper in 0.1 N HCl: a combined experimental and theoretical approach. *Chemical Physics Letters*, 707, 117-128.
- Ahmed, A. S., Ghanem, W. A., Hussein, W. A., & Gaber, G. A. (2020). Evaluation of some inorganic anions and organic compounds as corrosion inhibitors of Cu-Zn alloys in H₂SO₄ and HNO₃ solutions. *Archives of Metallurgy and Materials*, 65.
- Akram, M., Asif, H., Uzair, M., Akhtar, N., Madni, A., Shah, S. A., Hasan, Z. U., & Ullah, A. (2011). Amino acids: A review article. *J. Med. Plants Res*, 5(17), 3997-4000.
- Amin, M. A., Khaled, K., Mohsen, Q., & Arida, H. (2010). A study of the inhibition of iron corrosion in HCl solutions by some amino acids. *Corrosion Science*, 52(5), 1684-1695.
- Barouni, K., Kassale, A., Bazzi, L., Salghi, R., Hammouti, B., Albourine, A., El Issami, S., Jbara, O., & Bouachrine, M. (2014). Inhibition of corrosion of copper in nitric acid solution by four amino acids. *Research on Chemical Intermediates*, 40(3), 991-1002.
- Barouni, K., Mihit, M., Bazzi, L., Salghi, R., Al-Deyab, S., Hammouti, B., & Albourine, A. (2010). The inhibited effect of cysteine towards the corrosion of copper in nitric acid solution. *Open Corros J*, 3, 58-63.
- Debab, H., Selatnia, I., Hamani, H., Douadi, T., Messali, M., Benabid, S., El Messaoudi, N., Abou-krissha, M., Alrashdi, A. A., & Lgaz, H. (2025). Interfacial Mechanisms and Performance of a Diimine Schiff Base Inhibitor for Carbon Steel in 1 M HCl: Advanced Modelling Coupled with Experimental Characterization. *Materials Today Communications*, 114470.
- Dewangan, Y., Berdimurodov, E., & Verma, D. K. (2023). Amino acids: Classification, synthesis methods, reactions, and determination. In *Handbook of biomolecules* (pp. 3-23). Elsevier.
- Ebadi, M., Basirun, W. J., Khaledi, H., & Ali, H. M. (2012). Corrosion inhibition properties of pyrazolylindolenine compounds on copper surface in acidic media. *Chemistry Central Journal*, 6(1), 163.
- Farooq, A., Ali, E. H., Ahmed, Z. W., Khadom, A. A., & Al-azawi, K. F. (2026). Expired Omeprazole as an Effective Corrosion Inhibitor for Copper in Nitric Acid. *International Journal of Electrochemical Science*, 101303.
- Fouda, A., Gouda, M., & Abd El-Rahman, S. (2000). 2-Hydroxyacetophenone-aroyl hydrazone derivatives as corrosion inhibitors for copper dissolution in nitric acid solution. *Bulletin of the Korean Chemical Society*, 21(11), 1085-1089.
- Kaya, S., Tüzün, B., Kaya, C., & Obot, I. B. (2016). Determination of corrosion inhibition effects of amino acids: quantum chemical and molecular dynamic simulation study. *Journal of the Taiwan Institute of Chemical Engineers*, 58, 528-535.
- Loto, R. T. (2019). Corrosion inhibition effect of non-toxic α -amino acid compound on high carbon steel in low molar concentration of hydrochloric acid. *Journal of Materials Research and Technology*, 8(1), 484-493.
- Ma, H., Chen, S., Niu, L., Zhao, S., Li, S., & Li, D. (2002). Inhibition of copper corrosion by several Schiff bases in aerated halide solutions. *Journal of Applied Electrochemistry*, 32(1), 65-72.

- Ma, H., Chen, S., Yin, B., Zhao, S., & Liu, X. (2003). Impedance spectroscopic study of corrosion inhibition of copper by surfactants in the acidic solutions. *Corrosion Science*, 45(5), 867-882.
- McCafferty, E. (2005). Validation of corrosion rates measured by the Tafel extrapolation method. *Corrosion Science*, 47(12), 3202-3215.
- Muñoz, A. I., Antón, J. G., Guiñón, J., & Herranz, V. P. (2004). Comparison of inorganic inhibitors of copper, nickel and copper–nickels in aqueous lithium bromide solution. *Electrochimica acta*, 50(4), 957-966.
- Selatnia, I., Sid, A., Benahmed, M., Dammene Debbih, O., Ozturk, T., & Gherraf, N. (2018). Synthesis and characterization of a bis-pyrazoline derivative as corrosion inhibitor for A283 carbon steel in 1M HCl: electrochemical, surface, DFT and MD simulation studies. *Protection of Metals and Physical Chemistry of Surfaces*, 54(6), 1182-1193.