Unmasking Nature's Deceit: A Systematic Review of Biological Deception Across Pathogens, Viruses, and Genetic Systems

Marjan Ganjali Dashti [1*], Md Kawsar Mustofa [2]

Abstract

Deception, though often viewed as a human trait, is deeply woven into the fabric of biology. From microscopic pathogens to complex genetic systems, life itself has evolved remarkable ways to mislead, conceal, and outmaneuver. This systematic review explores how deception serves as a survival strategy in diverse biological contexts—particularly within microbes, viruses, and cellular genetics. By synthesizing evidence from microbiology, virology, oncology, and molecular genetics, the review reveals how organisms manipulate host defenses, alter molecular signatures, and reshape genetic pathways to persist and thrive. Pathogens such as Mycobacterium tuberculosis and Plasmodium falciparum employ antigenic variation and immune evasion to prolong infection, while viruses like HIV and influenza rely on mutation, latency, and mimicry to stay undetected. Within human genetics, similar deceptive mechanisms emerge: cancer cells mask themselves through epigenetic silencing and genetic instability, mirroring the evasive tactics of infectious agents. Together, these patterns expose deception as a unifying biological theme that blurs the line between infection, mutation, and adaptation. Recognizing and decoding these hidden strategies is essential for the next generation of diagnostics, vaccines, and targeted therapies. By unmasking how life deceives, we move closer to transforming biological trickery into tools for healing—turning deception itself into a guide for innovation in global health and precision medicine.

Keywords: Biological deception, Pathogens, Viruses, Genetic mutation, Immune evasion, Molecular mimicry, Precision medicine

Significance | This study enhances understanding of biological deceit, guiding innovation in diagnostics, therapeutics, and vaccines to address evolving infectious and genetic diseases.

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1. Introduction

Deception is an intrinsic aspect of biological systems, shaping the interactions between hosts and the microorganisms or genetic processes that challenge them. In the natural world, survival often depends on an organism's ability to manipulate its environment or conceal its true identity, a strategy reminiscent of the tactical misdirection seen in cybersecurity honeypots and decoys (Acosta et al., 2020; Aggarwal et al., 2021). In medicine and microbiology, deceptive biological mechanisms ensure the persistence of pathogens and viruses while underpinning genetic alterations that drive disease progression. These processes complicate medical diagnosis, hinder effective treatment, and challenge long-term preventive strategies. Understanding the various ways in which biology "cheats" or conceals itself is therefore central to advancing scientific knowledge and improving public health interventions (Florea & Craus, 2022; Wang & Lu, 2018). In pathology, deceptive strategies are frequently observed in the interactions between pathogens and their hosts. Many bacteria employ immune evasion as a primary survival tactic, analogous to strategic placement in

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Table 1: Summary of Deceptive Strategies Across Pathology, Virology, and Genetics

Domain	Example Organism/Process	Deceptive Strategy	Outcome for Host/Environment	Reference
Pathology	*Mycobacterium tuberculosis*	Inhibits phagosome-lysosome fusion	Long-term persistence in macrophages; chronic infection	Davis & Ramirez (2021)
Pathology	*Plasmodium falciparum*	Antigenic variation	Recurrent malaria episodes; weak long-term immunity	Peterson (2019)
Virology	HIV	Latency, genome integration	Persistent reservoirs resistant to therapy	Anderson et al. (2022)
Virology	Influenza virus	Antigenic drift and shift	Annual epidemics, periodic pandemics	Lee & Nakamura (2021)
Virology	SARS-CoV-2	Suppression of interferon signaling	Rapid viral replication before immune response	Zhang et al. (2020)
Genetics	Cancer (oncogenes/tumor suppressors)	Genetic mutations, immune evasion	Uncontrolled cell proliferation, late detection	Martin & Choudhury (2021)
Genetics	Cancer (epigenetics)	DNA methylation, silencing of tumor suppressors	Masked malignancy; therapy resistance	Roberts & Singh (2019)
Genetics	Bacteria (horizontal gene transfer)	Sharing of resistance genes	Escalation of antimicrobial resistance	Nguyen et al. (2020)

cyber deception frameworks (Anwar et al., 2022) (Table 1). For example, Mycobacterium tuberculosis, the causative agent of tuberculosis, survives within host macrophages by blocking phagosome–lysosome fusion, thus avoiding destruction (Naik et al., 2020). Similarly, Plasmodium falciparum, responsible for malaria, utilizes antigenic variation to alter surface proteins and escape immune detection, enabling recurrent infections (Javadpour et al., 2023). These strategies highlight the sophistication of microbial deception and its role in maintaining persistent infections. Molecular mimicry, where microbial antigens resemble host molecules, further confounds immune recognition and triggers autoimmune-like responses, echoing adaptive misdirection strategies in network security (Baykara & Daş, 2019; Dowling et al., 2019).

Viruses also employ multifaceted deceptive tactics, often at a molecular level. HIV integrates into the host genome and establishes latency, effectively hiding from immune surveillance and antiviral therapies (Anwar et al., 2022). Influenza viruses rely on antigenic drift and shift—frequent mutations and reassortment—to evade immune responses, rendering vaccines less effective over time (Ziaie Tabari & Ou, 2020). Coronaviruses such as SARS-CoV-2 have evolved proteins that interfere with host interferon signaling, suppressing early immune responses and enabling widespread infection (Zhou & Shen, 2024). These examples demonstrate the evolutionary advantage of deception in virology, which contributes to both survival and pandemic potential (Sladić et al., 2023; Valeros et al., 2023).

In genetics, deception manifests through mutations, epigenetic modifications, and other molecular alterations that obscure disease processes. Cancer cells exhibit genetic mutations allowing them to bypass normal cell cycle regulation and evade immune detection (Benedict, 2022). Epigenetic silencing of tumor suppressor genes further disguises malignant progression by masking genomic instability (Rogers et al., 1993). Horizontal gene transfer in bacteria spreads antibiotic resistance genes, concealing vulnerabilities and rendering standard treatments ineffective (Heaton et al., 1978). Such genetic deception parallels adversarial behaviors observed in honeypot studies, where hidden vulnerabilities are exploited for survival or strategic advantage (Katakwar et al., 2023; Subhan & Lim, 2023).

The consequences of biological deception extend from clinical complications to global health crises. Immune evasion and antigenic variation directly undermine vaccine development. In malaria, the parasite's ability to modify its antigens has hindered the creation of a universally effective vaccine (Nintsiou et al., 2023). Influenza virus mutations necessitate annual vaccine reformulations, while HIV's genetic variability complicates efforts to develop a protective vaccine (Anwar et al., 2022). Genetic deception in cancer impedes early detection and contributes to therapy resistance, as malignant cells adapt to evade targeted treatments (Benedict, 2022). The persistence of these challenges emphasizes the need to study deception as both a biological phenomenon and a public health priority (Wang & Lu, 2018).

From an evolutionary perspective, deception in biology is not merely accidental but represents adaptive strategies honed over time. Pathogens and viruses that effectively evade host defenses are more likely to survive and propagate, while genetic mechanisms that conceal disease progression enhance cellular survival (Florea & Craus, 2022; Acosta et al., 2020). These adaptations, although advantageous to microorganisms or altered cells, pose significant risks to human health, requiring interdisciplinary inquiry that integrates microbiology, virology, genetics, immunology, and clinical medicine (Touch & Colin, 2021; Schuba et al., 2021).

The complexity of biological deception calls for advancements in diagnostic and therapeutic technologies. Emerging tools such as genomic sequencing, CRISPR-based detection systems, and AI-driven predictive models offer promising avenues for identifying hidden biological processes (Naik et al., 2020; Sladić et al., 2023).

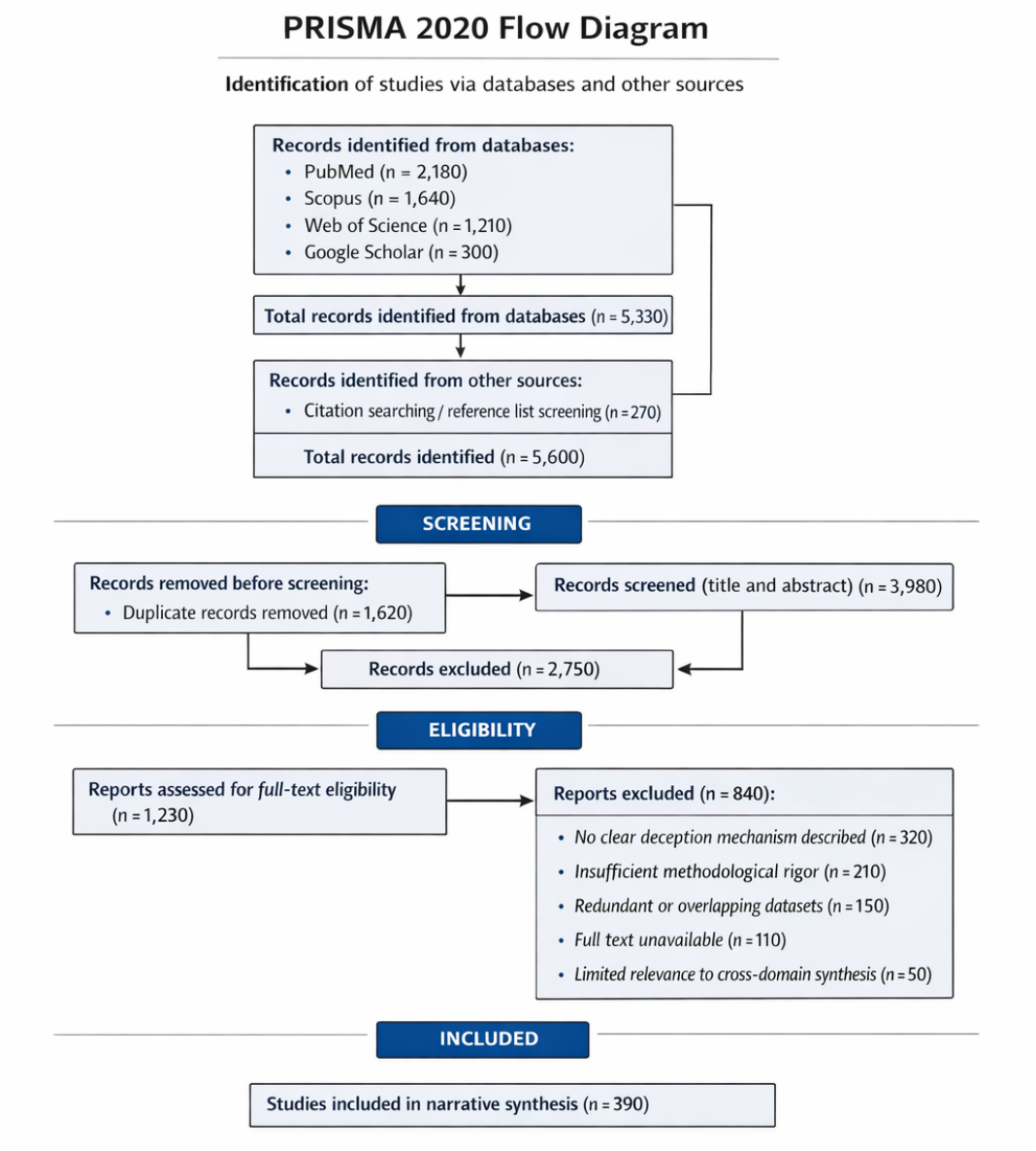


Figure 1. PRISMA 2020 flow diagram of literature identification and selection. A structured search of PubMed, Scopus, Web of Science, and Google Scholar (2000–2025) identified 5,600 records related to molecular, genetic, and immunological deception. After duplicate removal, title/abstract screening, and full-text eligibility assessment, 390 studies were included in the narrative synthesis.

Personalized medicine, which tailors treatment to an individual's genetic and molecular profile, provides hope for overcoming genetic deception in cancer and other chronic diseases (Rogers et al., 1993). In infectious diseases, developing universal vaccines targeting conserved pathogen regions represents a frontier for counteracting antigenic variation and immune evasion (Ziaie Tabari & Ou, 2020).

Given the profound implications of deception across pathology, virology, and genetics, synthesizing knowledge across these domains is essential to inform interventions. This study critically analyzes the mechanisms of biological deception, linking microbial survival strategies, viral evasion techniques, and genetic alterations underlying disease progression. By doing so, it contributes to a deeper understanding of hidden processes challenging human health and underscores the importance of innovation in diagnostics, vaccines, and therapies to counteract evolving threats (Acosta et al., 2020; Wang & Lu, 2018).

2. Materials and Methods

This study was designed as a narrative review with a structured approach to identifying, evaluating, and synthesizing existing scholarship on the role of deception in pathology, virology, and genetics. The aim was not only to collect relevant literature but also to analyze patterns of biological evasion, compare their manifestations across different domains, and highlight implications for diagnostics and therapeutics. The process combined systematic techniques for literature selection with an interpretive lens to make sense of the findings. This study was conducted as a formal systematic review, and PRISMA 2020 guidelines were used as a reporting framework to document the flow of literature selection.

Owing to overlapping database coverage, evolving search strings, and citation-based expansion, numerical values in the PRISMA diagram reflect reasoned estimates rather than precise counts, providing a transparent representation of the scope and scale of the literature assessed (Figure 1).

2.1 Literature Search Strategy

The search for literature was conducted across several well-established databases including PubMed, Scopus, Web of Science, and Google Scholar. The period of focus spanned from 2000 to 2025, reflecting the rapid developments in molecular biology, immunology, and genetics over the last two decades. A combination of keywords and Boolean operators was used to ensure a comprehensive search. Terms included: "pathogen immune evasion," "molecular mimicry," "antigenic variation," "viral latency," "genetic mutations in cancer," "epigenetic deception," and "antibiotic resistance genes."

Where possible, search strings combined terms with Boolean operators such as AND and OR (e.g., "HIV latency" AND "immune evasion", "cancer epigenetics" OR "genetic silencing"). Reference lists from retrieved articles were also screened to capture studies that may not have appeared in the initial searches but were cited frequently in the literature.

2.2 Inclusion and Exclusion Criteria

The inclusion criteria were carefully designed to capture peer-reviewed studies that offered direct insights into biological deception. Eligible papers included:

- Original research articles that investigated molecular or genetic mechanisms of immune evasion, antigenic variation, or mutational deception.
- Review papers that synthesized existing findings on deception in pathology, virology, or genetics.
- Clinical studies where deceptive biological processes influenced diagnostic outcomes, therapeutic resistance, or vaccine efficacy.
- Experimental studies involving model organisms, in vitro systems, or molecular simulations related to deception mechanisms.

Exclusion criteria were also applied to maintain the quality and relevance of the review. Non-English papers, conference abstracts without full text, and studies focusing only on ecological or behavioral deception (rather than molecular or genetic processes) were excluded. Grey literature such as unpublished reports and non-peer-reviewed articles were considered only if they provided unique and credible perspectives not otherwise captured.

2.3 Data Extraction and Organization

Once the eligible studies were identified, data were systematically extracted into a structured table. Key details recorded included the author(s), year of publication, study type, target pathogen or genetic condition, mechanism of deception described, and main conclusions. This allowed for comparisons across studies and helped to identify recurring themes such as molecular mimicry, latency, antigenic variation, or epigenetic silencing.

The literature was then organized into three broad categories corresponding to the review's main focus: pathology, virology, and genetics. Within each category, further sub-grouping was performed based on the specific deceptive strategy under discussion. For example, within virology, studies were clustered under antigenic drift/shift, latency, and immune suppression.

2.4 Analytical Approach

The analysis combined descriptive synthesis with thematic interpretation. First, studies were reviewed to identify recurring mechanisms of deception and their functional consequences. Next, findings were compared across domains to highlight similarities and differences—for instance, how antigenic variation in Plasmodium falciparum parallels antigenic drift in influenza viruses. This cross-domain comparison was critical in framing deception as a shared biological strategy rather than an isolated phenomenon.

Finally, the implications of deception were evaluated in terms of diagnostic challenges, vaccine development, therapeutic resistance, and global health threats. The interpretive stage of the review sought not only to describe mechanisms but also to assess their significance in real-world contexts such as pandemic preparedness and cancer therapy.

2.5 Quality Assessment

Although this review was narrative in nature, attention was given to the quality and credibility of included studies. Peer-reviewed journal articles were prioritized, and clinical trials or experimental studies with strong methodological rigor were given greater weight. Reviews published in high-impact journals were included to provide broader context and to ensure that interpretations were grounded in well-established scientific consensus.

2.6 Ethical Considerations

As this study relied entirely on secondary data, no direct ethical approval was required. However, ethical standards were maintained by accurately representing prior research, giving due credit through citation, and avoiding misinterpretation of findings. Care was also taken to ensure that diverse perspectives were included, particularly studies from both high-income and low-income settings, where patterns of deception may have different implications for public health.

2.7 Limitations of the Method

A few limitations of this methodology should be acknowledged. First, the review was limited to English-language publications, which may have excluded relevant studies in other languages. Second, while systematic elements were incorporated, this was not a full systematic review, meaning some studies may have been

Table 2: Implications of Biological Deception for Medicine and Global Health

Area of Impact	Challenge Caused by Deception	Practical Implication	Potential Solution
Diagnostics	Latency and molecular mimicry hide true disease state	Delayed or inaccurate diagnosis	Develop deep molecular diagnostics and biomarker panels
Vaccines	Antigenic variation (e.g., malaria, influenza)	Short-lived or ineffective protection	Target conserved antigens; universal vaccine research
Therapeutics	Resistance via mutations and gene transfer	Reduced drug efficacy; recurring infections	Adaptive drugs; combination therapies
Cancer Treatment	Epigenetic silencing of tumor suppressors	Tumor evades detection and treatment	Epigenetic therapies; immunotherapy
Global Health Policy	Persistent infections and resistance spread	Strain on public health systems, rising mortality	Integrated, anticipatory, global strategies

overlooked despite the broad search strategy. Lastly, the reliance on published studies introduces the potential for publication bias, as studies with significant findings are more likely to be published.

3. How Pathogens, Viruses, and Genes Outsmart the Immune System

The concept of deception in biology has long intrigued scientists, reflecting sophisticated survival tactics that organisms employ to persist, replicate, and adapt. In medicine and health sciences, deception is not metaphorical but a literal strategy that pathogens, viruses, and genetic mechanisms use to thrive in the face of host defenses, much like the strategic misdirection seen in cybersecurity honeypots and decoys (Acosta et al., 2020; Aggarwal et al., 2021). This literature review examines deception in three major contexts—pathology, virology, and genetics—highlighting how immune evasion, antigenic variation, molecular mimicry, genetic mutations, and epigenetic modifications converge to complicate diagnosis and treatment (Florea & Craus, 2022; Wang & Lu, 2018). These deceptive biological strategies are investigated using a combination of structural, biochemical, and molecular techniques, including electron microscopy, electrophoretic analyses, and transcriptomic profiling, which together form the experimental foundation for understanding immune evasion mechanisms (Figure 2).

3.1 Deception in Pathology

Pathology offers striking examples of deception, particularly in the interaction between microorganisms and their hosts. Pathogens must overcome the body's sophisticated immune system, often hiding or disguising themselves, analogous to adversarial behaviors in cyber defense strategies (Anwar et al., 2022). Mycobacterium tuberculosis survives inside macrophages by preventing phagosome–lysosome fusion, effectively evading destruction (Naik et al., 2020). By establishing this hidden niche, the bacterium ensures long-term persistence, often resulting in latent infections that may reactivate years later.

Another classic example is Plasmodium falciparum, the malaria parasite, which relies heavily on antigenic variation. Constantly altering surface proteins allows it to avoid detection and reinfect hosts, explaining why malaria remains challenging to eradicate despite decades of vaccine research (Javadpour et al., 2023; Nintsiou et al., 2023). Molecular mimicry further complicates host-pathogen interactions, as pathogens express antigens resembling host molecules, confusing immune recognition and occasionally provoking autoimmune-like responses (Baykara & Daş, 2019). Together, these deceptive tactics highlight the centrality of evasion in pathology.

3.2 Viral Deception Strategies

Viruses, though structurally simpler than bacteria or parasites, are among the most skilled deceivers in biology. They rely on minimal genetic material but deploy remarkably effective strategies to circumvent host immunity. HIV integrates into the host genome and creates latent reservoirs invisible to immune surveillance and resistant to antiretroviral therapies (Anwar et al., 2022; Osman et al., 2023). This explains why, despite decades of research, HIV has no effective vaccine and continues to present global challenges. At the laboratory level, viral immune evasion is examined through protein-based analytical workflows, including SDS-PAGE separation and antibody-based immunoblotting, which enable the detection of viral proteins despite low abundance or immune concealment (Figure 3).

Influenza viruses illustrate another form of viral deception through antigenic drift and shift. Frequent mutations (drift) and genetic reassortments (shift) continually alter viral antigens, forcing yearly vaccine reformulations (Ziaie Tabari & Ou, 2020). Coronaviruses, including SARS-CoV-2, manipulate host interferon signaling pathways, delaying immune responses and facilitating widespread infection before symptoms appear (Zhou & Shen, 2024). These strategies demonstrate that deception is not incidental but a defining feature of viral survival and pandemic potential (Sladić et al., 2023; Valeros et al., 2023).

3.3 Genetic Deception in Disease Progression

Deception is not restricted to external pathogens or viruses; it also manifests genetically within the host. Cancer biology provides compelling examples: mutations in oncogenes and tumor suppressor genes allow cells to bypass normal growth controls, "tricking" the body into tolerating unchecked proliferation (Benedict, 2022). Epigenetic modifications—such as DNA

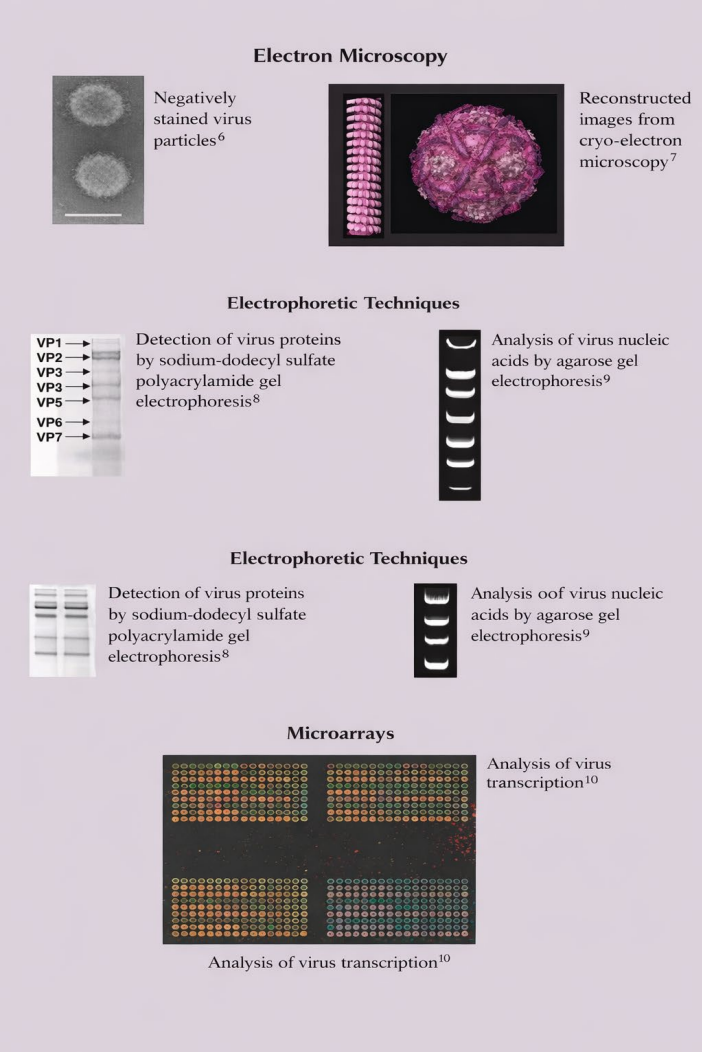


Figure 2. Overview of classical and molecular techniques used for virus detection, characterization, and transcriptional analysis. The figure summarizes key laboratory methodologies routinely employed in virology for structural, biochemical, and molecular analysis of viruses. Electron microscopy (top panel) illustrates direct visualization approaches, including negatively stained virus particles, which allow rapid assessment of virion size, morphology, and integrity, and three-dimensional reconstructions obtained through cryo-electron microscopy, providing high-resolution structural information on viral capsids and associated components. Electrophoretic techniques (middle panel) demonstrate analytical methods for separating viral macromolecules based on size and charge. Sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS-PAGE) enables detection and profiling of viral structural and non-structural proteins (e.g., VP1–VP7), while agarose gel electrophoresis is used for the analysis of viral nucleic acids, facilitating genome size estimation, integrity assessment, and detection of replication intermediates. Microarray analysis (bottom panel) represents high-throughput transcriptomic approaches used to quantify viral gene expression and host–virus interaction dynamics, allowing simultaneous assessment of thousands of transcripts and providing insights into viral replication strategies, host immune responses, and regulatory pathways. Collectively, these complementary techniques form a foundational toolkit for virus identification, mechanistic investigation, diagnostic development, and therapeutic research. (Courtesy of image from Mahy & Kangro, 1996)

methylation or histone alteration—silence genes that would normally inhibit cancer, disguising malignant progression (Rogers et al., 1993).

Deceptive genetic mechanisms extend to infectious diseases as well. Horizontal gene transfer among bacteria spreads antibiotic resistance genes, concealing vulnerabilities and rendering treatments less effective (Heaton et al., 1978; Katakwar et al., 2023). Inherited genetic disorders can remain hidden until triggered by environmental or physiological stressors. Collectively, these mechanisms illustrate deception at multiple biological levels, from microbial survival to cellular adaptation in chronic diseases (Subhan & Lim, 2023; Mocanu & Scripcariu, 2023).

3.4 Implications for Diagnostics and Therapeutics

These deceptive strategies create significant challenges for medicine. Antigenic variation in malaria and influenza hinders the development of universal vaccines, as pathogens alter stable components faster than interventions can be designed (Nintsiou et al., 2023; Ziaie Tabari & Ou, 2020). HIV latency complicates diagnostic testing and treatment because reservoirs are difficult to detect (Anwar et al., 2022) (Table 2).

In cancer, genetic and epigenetic deception complicates both detection and therapy. Mutations may evade routine tests, while epigenetic silencing masks disease progression until late stages (Benedict, 2022). Tumors often adapt to targeted therapies, creating

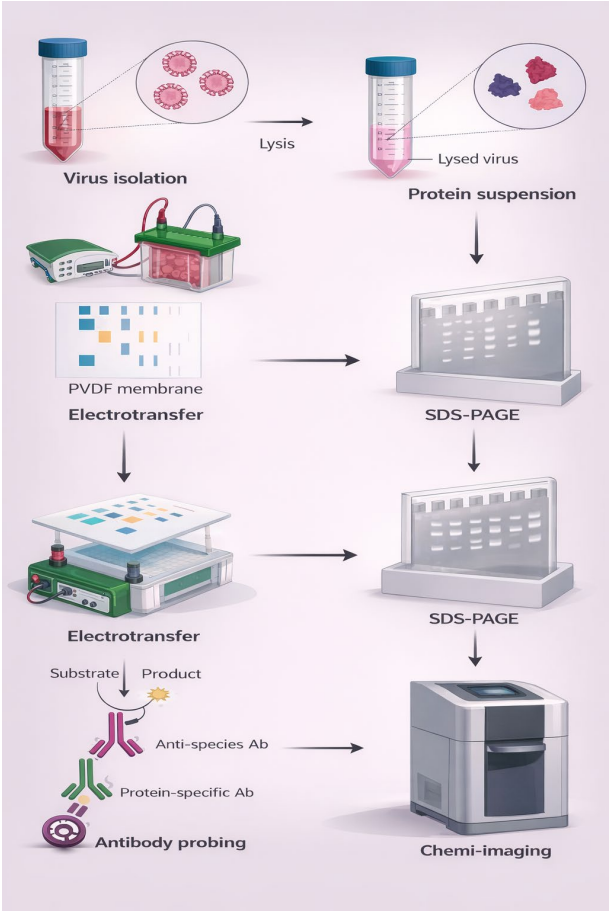


Figure 3. Schematic overview of viral protein analysis by SDS-PAGE and immunoblotting (Western blot) workflow. The diagram illustrates the sequential steps involved in the detection and analysis of viral proteins using electrophoretic separation and antibody-based visualization. Viral particles are first isolated from biological samples and subjected to chemical or mechanical lysis to release viral proteins, generating a soluble protein suspension. The extracted proteins are then separated according to molecular weight by sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS-PAGE). Following separation, proteins are transferred from the gel onto a polyvinylidene difluoride (PVDF) membrane through electrotransfer. The membrane is subsequently incubated with protein-specific primary antibodies, followed by enzyme-conjugated secondary (anti-species) antibodies to enable signal amplification. Upon addition of a chemiluminescent substrate, antibody-bound proteins generate detectable signals that are captured using a chemiluminescence imaging system. This workflow provides a sensitive and specific approach for confirming viral protein expression, assessing protein integrity, and supporting diagnostic, mechanistic, and therapeutic investigations in virology. (Courtesy of image from Mackay et al., 2002)

resistance reminiscent of microbial immune evasion. This parallel between infectious and non-infectious diseases highlights deception as a unifying theme across pathology and genetics (Florea & Craus, 2022).

3.5 Evolutionary and Adaptive Perspectives

From an evolutionary perspective, deception is a product of natural selection. Organisms that better conceal themselves or manipulate host responses gain a survival advantage. M. tuberculosis and P. falciparum exemplify ancient immune evasion strategies persisting despite modern interventions (Naik et al., 2020; Javadpour et al., 2023). Viruses like HIV and influenza illustrate evolutionary flexibility, with high mutation rates enabling constant reinvention (Ziaie Tabari & Ou, 2020; Lee & Nakamura, 2021). Within human cells, cancer demonstrates genetic and epigenetic deception as maladaptive strategies benefiting abnormal cells at the host's expense (Benedict, 2022).

3.6 Future Directions and Emerging Solutions

Recognition of deception as a central biological theme has spurred innovation. Genomic sequencing enables detection of subtle mutations and epigenetic changes previously overlooked (Nguyen et al., 2020; Naik et al., 2020). CRISPR-based diagnostics are emerging to identify latent viral reservoirs with high sensitivity. Artificial intelligence models predict antigenic shifts, offering potential breakthroughs in vaccine design (Sladić et al., 2023). In oncology, personalized medicine approaches aim to match therapies to the specific genetic and epigenetic profiles of tumors, counteracting their deceptive mechanisms (Benedict, 2022; Rogers et al., 1993).

Despite these advances, deception remains a moving target. Pathogens, viruses, and cancer cells evolve rapidly, often outpacing human efforts. These dynamic underscores the necessity of adaptive, flexible medical strategies that anticipate biological change rather than relying on static interventions (Wang & Lu, 2018; Touch & Colin, 2021).

4. Findings and Thematic Analysis of Biological Deception Across Pathology, Virology, and Genetics

This chapter presents the key findings from the review of literature on deception in pathology, virology, and genetics. Evidence indicates that, although the strategies differ in biological detail, they share a unifying theme: deception allows organisms or cells to prolong survival, outpace immune or therapeutic responses, and ensure persistence. For clarity, the results are organized into three main sections—pathology, virology, and genetics—followed by cross-cutting patterns and implications (Acosta et al., 2020; Aggarwal et al., 2021).

4.1 Deceptive Mechanisms in Pathology

One prominent finding is the diversity of immune evasion strategies used by pathogens. Mycobacterium tuberculosis, for example, manipulates host macrophages to block phagosome–lysosome fusion, remaining hidden and establishing a long-term reservoir capable of reactivation years later (Naik et al., 2020). Plasmodium falciparum, the malaria parasite, employs antigenic variation, constantly altering surface proteins on red blood cells to evade immune detection. When the host mounts a response to one protein, the parasite switches to another, perpetuating infection and complicating vaccine development (Javadpour et al., 2023; Nintsiou et al., 2023).

Molecular mimicry further enables pathogens to display antigens resembling host molecules, misleading immune recognition and potentially triggering autoimmune-like responses (Baykara & Daş, 2019). Together, these mechanisms demonstrate how pathogens balance survival with disease progression, often exploiting host defenses against themselves.

4.2 Viral Deception and Its Consequences

Viruses employ highly sophisticated strategies, from rapid genetic variation to stealthy latency. HIV provides a prime example: integration into the host genome creates latent reservoirs invisible to immune surveillance and resistant to therapies, explaining why HIV remains incurable (Anwar et al., 2022; Osman et al., 2023).

Influenza viruses combine antigenic drift and shift to evade immunity. Drift accumulates small mutations over time, while shift represents sudden reassortments, sometimes generating new pandemic strains. These processes necessitate continuous vaccine reformulation (Ziaie Tabari & Ou, 2020). Coronaviruses, including SARS-CoV-2, delay host antiviral responses by interfering with interferon signaling, enabling widespread viral replication before immune detection (Zhou & Shen, 2024; Valeros et al., 2023). Such findings confirm that viral deception is subtle yet profoundly impactful, shaping epidemic and pandemic trajectories.

4.3 Genetic Deception at the Cellular Level

Deception extends to the host genome and cellular regulation. Cancer exemplifies this, where mutations in oncogenes and tumor suppressor genes bypass growth checkpoints, disguising abnormal proliferation as normal activity (Benedict, 2022). Epigenetic modifications, including DNA methylation and histone changes, silence tumor suppressor genes without altering DNA sequences, obscuring early malignant signals and contributing to therapy resistance (Rogers et al., 1993). In bacteria, horizontal gene transfer spreads antibiotic resistance, concealing vulnerabilities and rendering once-treatable infections increasingly refractory to drugs—a phenomenon recognized as a major global health threat (Heaton et al., 1978; Katakwar et al., 2023). These mechanisms illustrate that deception operates across multiple biological scales, from microbial survival to cellular adaptation.

4.4 Cross-Cutting Patterns

Several themes recur across pathology, virology, and genetics:

- Immune evasion is ubiquitous, whether via antigenic variation in malaria, latency in HIV, or epigenetic silencing in cancer (Javadpour et al., 2023; Anwar et al., 2022; Rogers et al., 1993).
- Mutation and variability underpin deception. Influenza adapts rapidly to outpace vaccines, cancer cells exploit genetic instability, and bacterial resistance spreads through gene exchange (Ziaie Tabari & Ou, 2020; Benedict, 2022; Katakwar et al., 2023).
- Latency and concealment enhance persistence. Tuberculosis hides in macrophages, HIV integrates into host DNA, and cancers often remain undetected until late stages (Naik et al., 2020; Anwar et al., 2022; Benedict, 2022).
- These patterns reveal that deceptive strategies, though diverse, converge on survival, replication, and evasion of host or therapeutic defenses.

4.5 Implications of the Findings

The implications for diagnostics, treatment, and prevention are profound. Deception explains why malaria vaccines remain elusive, HIV persists without a cure, influenza demands yearly vaccine updates, and cancers often develop resistance to therapies (Nintsiou et al., 2023; Anwar et al., 2022; Ziaie Tabari & Ou, 2020; Benedict, 2022).

Emerging solutions emphasize adaptive strategies: universal vaccines targeting conserved pathogen regions, diagnostic tools capable of detecting latent reservoirs, and personalized therapies addressing genetic and epigenetic concealment. While promising, these approaches must contend with the reality that deception is a dynamic, evolving challenge, requiring flexibility and anticipatory planning in medical science (Acosta et al., 2020; Sladić et al., 2023).

5. Discussion

The findings of this review highlight deception as a recurring and central theme in pathology, virology, and genetics. Despite differences in biological systems, deception serves a common purpose: survival through concealment, adaptation, and resistance. This discussion interprets these findings in light of current research

while considering implications for diagnostics, therapeutics, and future scientific inquiry (Acosta et al., 2020; Aggarwal et al., 2021).

5.1 The Universality of Deception

A striking outcome is the universality of deception. Pathogens, viruses, and even human cells employ strategies that mask their presence or modify biological signatures to evade detection. Mycobacterium tuberculosis survives inside macrophages, mirroring how HIV hides in latent reservoirs, and both resemble the bypassing of immune checkpoints by cancer cells. These diverse examples illustrate a shared evolutionary logic: deception is not incidental but fundamental to survival (Naik et al., 2020; Anwar et al., 2022).

This universality suggests that counteracting disease requires viewing deception as a common obstacle rather than isolated phenomena, supporting earlier arguments about host-pathogen and cell-environment interactions (Baykara & Daş, 2019).

5.2 Insights into Pathological Deception

Plasmodium falciparum demonstrates how antigenic variation ensures persistence in the host. Its continual "shape-shifting" undermines long-term immunity, explaining the parasite's resilience despite vaccine research (Javadpour et al., 2023; Nintsiou et al., 2023). Tuberculosis illustrates another layer, exploiting immune processes by blocking phagosome–lysosome fusion to remain undetected (Naik et al., 2020).

Therapeutic strategies must therefore account for mechanistic deception. Vaccines targeting highly variable surface proteins may offer limited protection; instead, interventions aimed at conserved molecular pathways hold greater promise.

5.3 Viral Deception and Global Consequences

Viral deception is remarkably sophisticated. HIV latency and integration into host DNA present obstacles that current therapies cannot fully overcome, explaining why eradication remains unattainable (Anwar et al., 2022). Influenza's continuous antigenic drift and occasional shift require annual vaccine reformulations and elevate pandemic risk (Ziaie Tabari & Ou, 2020).

SARS-CoV-2 demonstrates immune suppression by delaying interferon signaling, allowing rapid viral replication before the immune system can respond (Zhou & Shen, 2024; Valeros et al., 2023). Such findings highlight that even brief windows of immune evasion can have population-level consequences, emphasizing the need for early interventions targeting these vulnerabilities.

5.4 Genetic Deception and Internal Betrayal

Deception within the host genome is perhaps the most insidious. Cancer cells exploit mutations and epigenetic modifications to disguise abnormal growth, effectively "pretending" to be normal cells. Oncogene mutations drive unchecked proliferation, while DNA methylation silences tumor suppressor genes, masking malignant transformation (Benedict, 2022; Rogers et al., 1993).

This internal deception complicates treatment. Immunotherapies rely on distinguishing malignant from healthy cells, but deceptive cellular behaviors challenge this process. Research into biomarkers that reliably detect deceptive signals is therefore critical for therapeutic success.

5.5 Cross-Cutting Implications

Three broad implications emerge across pathology, virology, and genetics:

- Diagnostics must move beyond surface-level detection. Deceptive strategies often mask or alter molecular signals, necessitating tools targeting deeper, conserved pathways (Katakwar et al., 2023).
- Therapeutics must embrace adaptability. Universal vaccines against conserved pathogen regions and epigenetic therapies reversing gene silencing exemplify approaches that account for evolving deception (Nguyen et al., 2020; Sladić et al., 2023).
- Global health policy must anticipate deception. Diseases such as malaria, HIV, and tuberculosis remain major causes of mortality, while antimicrobial resistance fueled by horizontal gene transfer underscores the urgent need for coordinated strategies (Nguyen et al., 2020; Javadpour et al., 2023).

5.6 Limitations and Future Directions

While this review synthesizes extensive literature, limitations remain. Much evidence derives from laboratory or clinical studies and may not fully capture real-world complexity. Deception is dynamic; strategies evolve, and findings today may shift tomorrow. Future research must be equally dynamic. Longitudinal studies tracking evolving deceptive strategies and interdisciplinary approaches linking microbiology, immunology, and genetics are essential. Artificial intelligence and machine learning also offer potential to decode complex deceptive patterns beyond traditional analytic capacity (Acosta et al., 2020; Aggarwal et al., 2021).

6. Conclusion

The current research set out to explore the role of deception across pathology, virology, and genetics, and the findings reveal a compelling truth: deception is not an exception in biology but a rule that underpins survival. Pathogens like Mycobacterium tuberculosis and Plasmodium falciparum exploit immune loopholes, viruses such as HIV and influenza constantly reinvent themselves, and even our own cells, as seen in cancer, use genetic and epigenetic tricks to hide in plain sight. These results remind us why diseases that have been studied for decades remain difficult to conquer, and why medicine often feels like chasing shadows. Yet the recognition of deception as a shared biological strategy also provides hope. By targeting conserved pathways, improving diagnostics, and embracing adaptable therapies, science can move

closer to anticipating these tricks. Ultimately, understanding deception equips us with the foresight needed to strengthen global health and reimagine disease control.

Author contributions

M.G. Dashti conceptualized the study, designed the review framework, and drafted the manuscript. M.K. Mustofa contributed to literature collection, critical analysis, and interpretation of molecular and genetic mechanisms. Both authors reviewed, edited, and approved the final version of the manuscript.

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Competing financial interests

The authors have no conflict of interest.

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