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Interdisciplinary Approaches in Modern Biomedical Sciences: Applications in Infectious Diseases, Cancer, and Drug Discovery

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Keywords

Phytomedicine, Natural products, Computational drug discovery, Infectious disease, epidemiology.

Abstract

Modern biomedical sciences increasingly demand interdisciplinary approaches that integrate diverse fields to effectively address the multifaceted challenges posed by infectious diseases, cancer, and antimicrobial resistance. This comprehensive review explores the synergistic application of epidemiology, microbiology, phytomedicine, nanotechnology, and computational drug discovery in advancing disease prevention and therapeutic development. Epidemiological investigations of infectious diseases, encompassing intestinal parasitic infections, helminthiasis, oral candidiasis, Tinea capitis, urinary tract infections, dental caries, and viral infections including human papillomavirus and human immunodeficiency virus, provide critical baseline data essential for designing evidence-based public health interventions. Phytochemical investigations of medicinal plants, including *Boerhaavia diffusa, Euphorbia hirta, Achyranthes aspera, Ficus carica, Ipomoea obscura,* and *Terminalia chebula*, have revealed significant antioxidant, antibacterial, antifungal, anti-inflammatory, and anticancer properties, underscoring their therapeutic potential. Nanotechnology-based approaches, particularly biosynthesized silver nanoparticles and advanced nanomaterials, have demonstrated enhanced antimicrobial and anticancer efficacy. Computational drug discovery

methodologies, including molecular docking, in silico peptide design, virtual screening, and chemical repurposing, have accelerated identification of novel therapeutic candidates targeting cancer-associated proteins, antimicrobial resistance mechanisms, and vector-borne disease pathogens. Collectively, these interdisciplinary strategies represent a transformative paradigm, fostering innovative, accessible, and effective solutions for complex global health challenges.

1. Introduction

There is something almost inevitable about the way modern biomedical research has evolved. Problems that once seemed manageable within a single discipline kept revealing deeper layers, layers that required different tools, different perspectives, and sometimes entirely different scientific languages. Infectious diseases, for instance, are no longer just a microbiologist's concern. They intersect with immunology, genomics, environmental science, and increasingly with computational modeling [1, 2]. Cancer, similarly, has moved well beyond the surgical theater or the oncology ward and into the realm of molecular biology, bioinformatics, and even materials science [3, 4].

The idea of interdisciplinary biomedical research is not new, but its pace and depth have accelerated considerably over the last two decades. What changed was partly technological, the arrival of high-throughput sequencing, powerful computational tools, and advanced imaging systems made collaboration across disciplines not just possible but necessary [5, 6]. But it was also conceptual. Researchers began to realize that the most stubborn problems, antimicrobial resistance, metastatic cancer, neglected tropical diseases, simply could not be solved by one field working alone [7, 8].

This review tries to capture some of that convergence. It does not aim to be exhaustive, which would be nearly impossible given how broad the territory is. Instead, it focuses on three interrelated themes: the evolving landscape of infectious disease research, the growing role of natural compounds and computational approaches in cancer, and the emerging methodologies that are reshaping drug discovery [9, 10]. Along the way, it draws on work spanning clinical microbiology, ethnobotany, in silico modeling, nanotechnology, and public health epidemiology.

What becomes clear, reading across this literature, is that the most exciting advances are almost always happening at the borders between fields. A peptide derived from a medicinal plant becomes a lead compound against a mosquito vector. A computational docking study reveals a new use for an existing antibiotic. A biosynthesized nanoparticle turns out to have unexpected antifungal properties [11, 12, 13]. These are not accidents. They are the natural result of researchers who stopped asking only the questions their own discipline trained them to ask.

2. Infectious Diseases: From Clinical Observations to Molecular Insights

2.1 Parasitic and Fungal Infections in Vulnerable Populations

Intestinal parasitic infections have remained a persistent public health concern, particularly among school-age children in low- and middle-income settings. Studies tracking the incidence of protozoan infections in children have consistently highlighted the role of poor sanitation, overcrowding, and limited access to clean water as major contributing factors [14, 15]. Helminthic infections follow similar patterns, with prevalence rates in some regions reaching levels that significantly impair childhood development and educational outcomes [16, 17].Fungal infections add another layer to this burden. Tineacapitis, a dermatophytic infection of the scalp, remains surprisingly common among school children in tropical and subtropical regions [18]. Oral candidiasis, or oral thrush, has similarly been documented at notable prevalence rates, particularly in immunocompromised individuals

and children with limited access to antifungal treatment [19, 20](Table 1). The continued reliance on fluconazole as a primary antifungal agent raises questions about emerging resistance patterns, a concern that mirrors broader anxieties about antimicrobial resistance globally [21].

Table 1: Prevalence of Common Infectious Diseases Among School Children in Tropical Regions

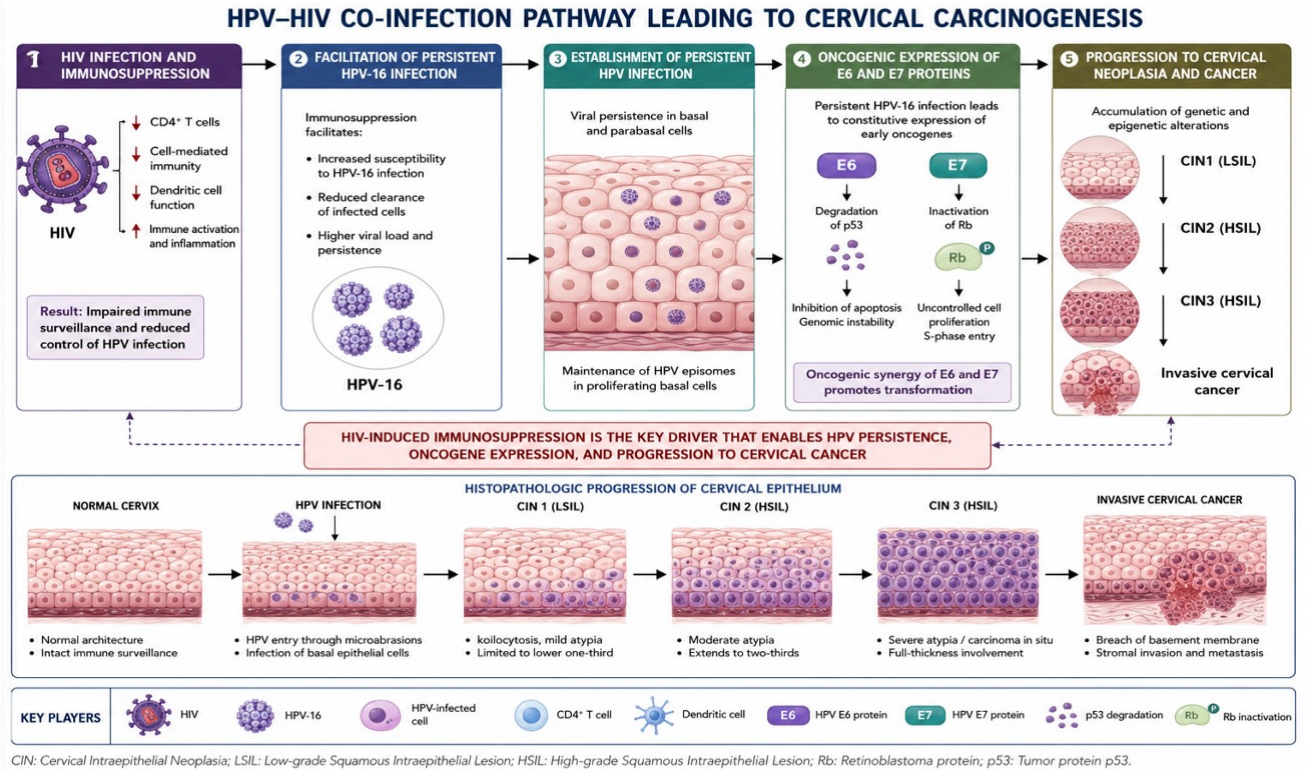
Disease	Causative Agent	Prevalence Range (%)	High-Risk Group	Key Risk Factors
Intestinal Protozoa	*Entamoeba*, *Giardia* spp.	15–45	School children	Poor sanitation, contaminated water
Helminthic Infections	*Ascaris*, *Trichuris* spp.	20–60	Rural school children	Soil exposure, open defecation
TineaCapitis	Dermatophytes	5–30	Urban/rural children	Overcrowding, shared items
Oral Thrush	*Candida albicans*	8–25	Immunocompromised	HIV, antibiotic overuse
Urinary Tract Infections	*E. coli*, *Klebsiella* spp.	10–35	All age groups	Poor hygiene, catheterization

Urinary tract infections (UTIs) represent another clinically significant burden, particularly in settings where diagnostic resources are limited. Bacterial isolates from UTI cases in South Asian populations have shown worrying patterns of antibiotic resistance, complicating standard treatment protocols [22, 23]. These findings underscore why clinical microbiology cannot operate in isolation; they demand engagement with pharmacology, public health policy, and sometimes even environmental science [24].

2.2 Viral Infections and Co-morbidities

Human papillomavirus (HPV) infection occupies a particularly important space in the intersection of infectious disease and oncology. The well-established link between high-risk HPV types, especially HPV-16, and cervical cancer has made screening and early detection a global priority [25, 26] (Figure 1). Studies examining HPV prevalence among HIV-positive women have consistently found elevated rates of co-infection, a finding that has significant implications for cervical cancer screening protocols in HIV-endemic regions [27, 28].

Figure 1: Schematic representation of the HPV-HIV co-infection pathway leading to cervical carcinogenesis. The diagram illustrates how immunosuppression caused by HIV facilitates persistent HPV-16 infection, impairs viral clearance, promotes oncogenic E6/E7 protein expression, and ultimately contributes to cervical intraepithelial neoplasia and invasive cervical cancer.



CIN: Cervical Intraepithelial Neoplasia; LSIL: Low-grade Squamous Intraepithelial Lesion; HSIL: High-grade Squamous Intraepithelial Lesion; Rb: Retinoblastoma protein; p53: Tumor protein p53.

The relationship between HIV immunosuppression and HPV persistence is biologically well understood. As CD4+ T-cell counts decline, the immune system loses its capacity to suppress HPV replication effectively, allowing oncogenic strains to persist and potentially progress to malignancy [29, 30]. This dynamic has made integrated screening programs, those that address both HIV and HPV simultaneously, a priority in sub-Saharan Africa and other high-burden regions [31, 32].

Trypanosomiasis offers yet another window into the complexity of infectious disease management. Human African trypanosomiasis (HAT), caused by *Trypanosomabruceirhodesiense*, presents with neurological complications in its second stage, including seizures, which significantly complicate clinical management [33]. The neurological burden of stage-2 HAT has been documented in Zambian populations, where seizure prevalence adds to an already challenging treatment landscape [34].

2.3 Bacterial Infections and Antimicrobial Resistance

Bacterial infections, particularly those caused by resistant organisms, represent one of the most urgent challenges in contemporary medicine. *Pseudomonas aeruginosa*, for instance, has demonstrated remarkable adaptability in developing resistance to fluoroquinolone antibiotics, a group that was once considered highly reliable for Gram-negative infections [35, 36]. Understanding the resistance mechanisms of such organisms requires a genuinely interdisciplinary approach, one that combines clinical microbiology, molecular genetics, and pharmacodynamics [37].

Dental caries and oral microbial diseases, though sometimes overlooked in the broader infectious disease conversation, carry their own significant burden. Microbial characterization studies from dental caries cases have revealed complex

polymicrobial communities that resist simple antibiotic solutions [38, 39]. Oral infections in individuals with mental, physical, or social disabilities present additional layers of complexity, requiring care approaches that extend well beyond conventional antimicrobial therapy [40].

3. Cancer Biology and Natural Compound Therapeutics

3.1 Medicinal Plants and Anticancer Activity

The pharmacological potential of medicinal plants has attracted renewed scientific interest, not as a nostalgic return to traditional medicine but as a systematic investigation of bioactive compounds that evolution has already optimized over millennia [41, 42]. *Boerhaaviadiffusa*, a plant with deep roots in traditional medicine systems across Asia and Africa, has demonstrated measurable anticancer activity in in vitro studies [43, 44]. Its cytotoxic properties against human cancer cell lines have opened conversations about how its bioactive constituents might be developed into more targeted therapeutic agents [45].

Euphorbia hirta represents another promising candidate. Phytochemical profiling using GC-MS and FT-IR analysis has revealed a rich metabolite composition, and cytotoxic evaluation against SiHa cervical cancer cells has yielded encouraging results [46](Table 2). What makes such studies particularly valuable is their methodological rigor. Moving beyond simple bioassays to incorporate spectroscopic profiling gives a much clearer picture of which compounds are responsible for observed biological activity [47, 48]

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Table 2: Summary of Medicinal Plants Investigated for Anticancer Activity

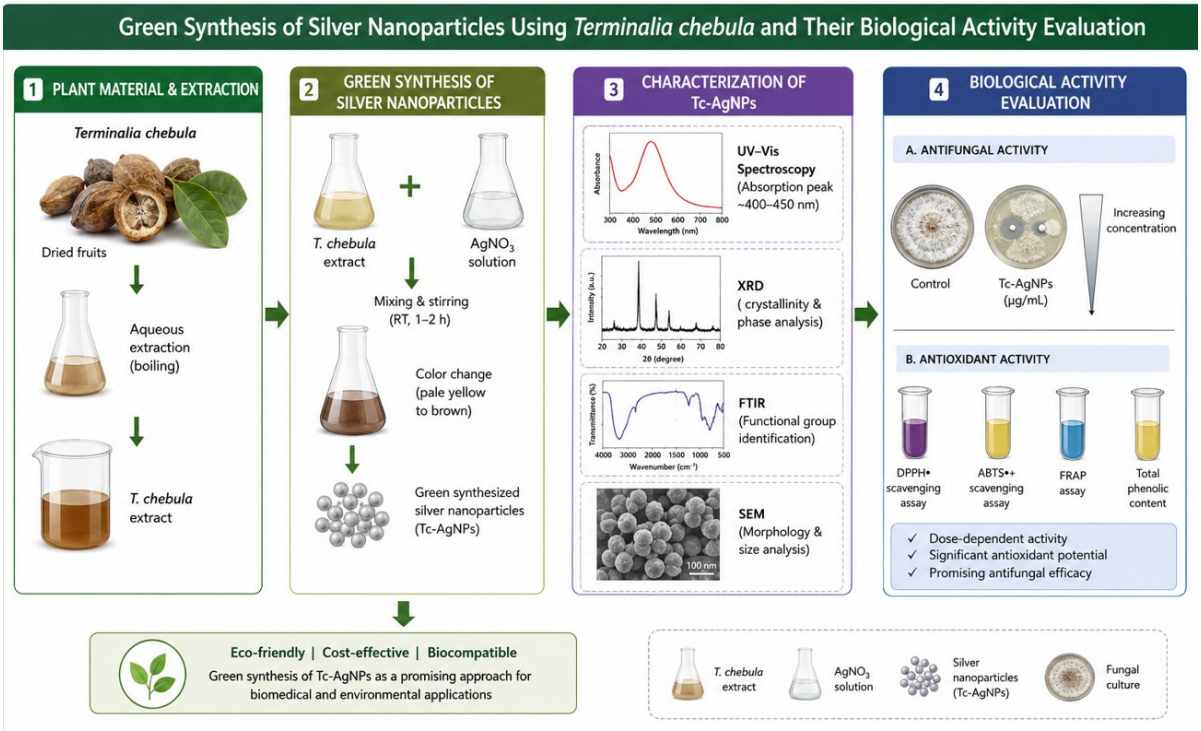
Plant Species	Extract/Compound	Cancer Cell Line Tested	Key Activity	Method Used
Boerhaavia diffusa	Methanol extract	HeLa, MCF-7	Cytotoxic, apoptotic	MTT assay
Euphorbia hirta	Methanol extract	SiHa	Cytotoxic, antioxidant	GC-MS, FT-IR, MTT
Ficus carica	Methanol extract	MCF-7	Anticancer	MTT, phytochemical screening
Achyranthes aspera	Methanol extract	SiHa	Antioxidant, anticancer	DPPH, MTT assay
Ipomoea obscura	Crude extract	Multiple lines	Anti-inflammatory, antioxidant	DPPH, ABTS, disk diffusion
Terminalia chebula	Silver nanoparticles	Fungal pathogens	Antifungal, antioxidant	Biosynthesis, disk diffusion

Ficus carica and *Achyranthes aspera* have similarly been evaluated for anticancer and antioxidant properties, with results suggesting genuine cytotoxic potential against breast and cervical cancer cell lines [49, 50]. *Ipomoea obscura* has added antioxidant, anti-inflammatory, and antibacterial dimensions to this growing portfolio of plant-based bioactive compounds [51]. The breadth of this research is notable, but so is its consistency: plant extracts prepared under rigorous conditions repeatedly demonstrate measurable biological activity that warrants deeper mechanistic investigation [52, 53].

3.2 Nanoparticles in Cancer and Antimicrobial Research

The biosynthesis of silver nanoparticles using plant extracts has emerged as a particularly active area of research, sitting neatly at the intersection of green chemistry, nanotechnology, and biomedical science [54, 55]. Silver nanoparticles derived from *Terminaliachebula* extracts, for example, have shown notable antifungal and antioxidant activity, suggesting potential applications in both infectious disease management and oxidative stress-related conditions [56](Figure 2). The use of plant-mediated synthesis, rather than chemical methods, has environmental advantages that align well with broader sustainability goals [57, 58].

Figure 2: Workflow for green synthesis of silver nanoparticles from *Terminalia chebula* and their biological activity evaluation. Steps include plant extraction, nanoparticle synthesis, characterization (UV-Vis, XRD, FTIR, SEM), and biological testing for antifungal and antioxidant activities.



Nanomaterials more broadly have found applications in environmental pollution monitoring and remediation, another area where interdisciplinary thinking has proven essential [59]. The intersection of nanotechnology with environmental science and public health has generated new frameworks for understanding how pollutants interact with biological systems at the nanoscale [60, 61]. These insights, in turn, feed back into biomedical applications, where understanding nanoparticle behavior in biological environments is critical for safe and effective therapeutic use [62].Oleic acid production from mango kernel waste using probiotic bacteria represents a related but distinct strand of this research [63]. The valorization of agricultural waste through microbial biotechnology produces bioactive fatty acids with known anti-inflammatory and antimicrobial properties, again demonstrating how disciplinary convergence generates solutions that single-field approaches would likely miss [64, 65].

4. Computational Approaches in Drug Discovery

4.1 In Silico Methods and Molecular Docking

Computational drug discovery has matured considerably over the past two decades, moving from a supplementary tool to a genuinely central methodology in the early stages of drug development [66, 67]. Molecular docking, in particular, has proven invaluable for screening large numbers of compounds against target proteins without the time and cost of traditional wet-lab screening [68]. The ability to model protein-ligand interactions at atomic resolution has transformed how researchers think about lead compound identification [69, 70].Peptide-based drug discovery has benefited enormously from these advances. Novel peptides derived from *Boerhaaviadiffusa* have been computationally evaluated against cervical cancer targets, specifically Transmembrane Protein 50A (TMEM50A), using 3D peptide-protein docking protocols [71, 72](Table 3). The results of such studies do not replace experimental validation, but they provide a rational, cost-effective starting point that significantly narrows the experimental search space [73].

Table 3: Summary of In Silico Studies on Peptide and Drug Interactions with Target Proteins

Compound/Peptide	Target Protein	Organism/Disease	Docking Score	Key Finding
Novel peptide (*B. diffusa*)	TMEM50A	Cervical cancer	High affinity	Potential anticancer lead
Novel peptide	OBP1/AChE	*Anopheles gambiae*	Favorable binding	Antimalarial vector control
Novel peptide	Unknown target	*Aedesaegypti*	Favorable binding	Dengue vector control
Novel peptide	Unknown target	*Culexquinquefasciatus*	Favorable binding	Filariasis vector control
Novel peptide (*B. diffusa*)	β-Lactamase TEM	*Klebsiellapneumonia*	High affinity	Antibacterial lead
Tramadol HCl	MepA	*Staphylococcus aureus*	Inhibitory binding	Drug repurposing potential
Linezolid/Ciprofloxacin	Mutant ESR1	Breast cancer	Favorable binding	Antibiotic repurposing

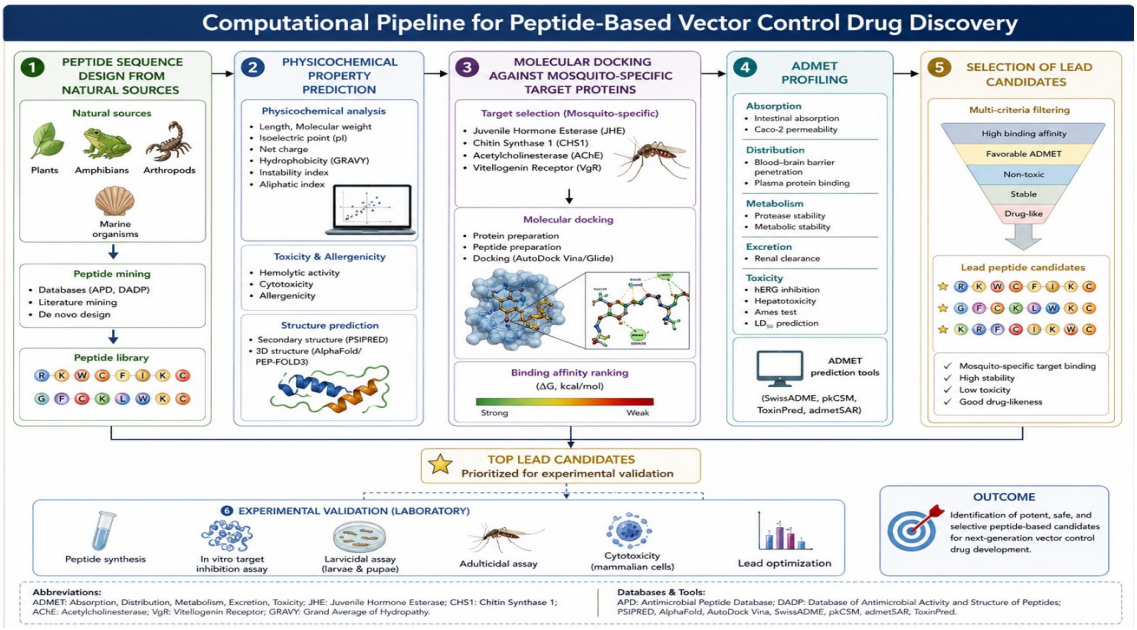
The concept of drug repurposing has gained significant traction within the computational community. Linezolid and ciprofloxacin, both established antibiotics, have been computationally evaluated against mutant ESR1 protein in breast cancer, yielding binding interactions that suggest potential oncological applications [74, 75]. This is a particularly exciting area because repurposed drugs already have known safety profiles, which substantially reduces the time and cost of bringing a new therapeutic application to clinical practice [76, 77].

4.2 Vector-Targeted Peptide Discovery

Mosquito-borne diseases remain among the deadliest infectious diseases globally, and the development of novel vector control strategies is urgently needed [78, 79]. Computational approaches have been applied to the discovery of peptide-based medicines against *Anopheles gambiae*, *Aedes aegypti*, and *Culex quinquefasciatus*, the primary vectors of malaria, dengue, and lymphatic filariasis respectively [80, 81, 82]. In silico screening of peptides derived

from natural sources against mosquito-specific target proteins represents a genuinely novel approach to vector control, one that sidesteps many of the toxicity concerns associated with conventional insecticides [83](Figure 3).

Figure 3: Computational pipeline for peptide-based vector control drug discovery. The workflow includes peptide sequence design from natural sources, physicochemical property prediction, molecular docking against mosquito-specific target proteins, ADMET profiling, and selection of lead candidates for experimental validation.



The use of chemical repurposing strategies extends to antimicrobial targets as well. Tramadol hydrochloride, primarily known as an analgesic, has been evaluated computationally against MepA, the multidrug export protein of *Staphylococcus aureus* [84, 85]. The finding that an anti-inflammatory medication might interfere with bacterial drug efflux is exactly the kind of unexpected discovery that in silico approaches make possible, discoveries that no traditional antibiotic screening program would have uncovered [86]. Novel peptides derived from *Boerhaavia diffusa* have also been evaluated against β-lactamase TEM of *Klebsiella pneumoniae*, one of the most clinically significant resistance mechanisms in Gram-negative bacteria [87, 88]. The ability of plant-derived peptides to potentially inhibit resistance enzymes opens a genuinely exciting therapeutic avenue, particularly given the global crisis of β-lactam antibiotic resistance [89, 90].

5. Emerging Themes and Future Directions

5.1 Orthostatic Hypotension, Aging, and Systemic Health

Interdisciplinary biomedical research does not always follow the most obvious paths. The intersection of aging physiology, cardiovascular function, and mental health, for instance, has produced important insights into how orthostatic hypotension affects quality of life in elderly populations [91, 92]. Cross-sectional studies examining the impact of aging on orthostatic hypotension and mental health outcomes have highlighted the need for integrated geriatric care

models that address both physiological and psychological dimensions simultaneously [93].These findings connect, perhaps unexpectedly, to broader themes in this review. The same interdisciplinary thinking that drives computational drug discovery and plant-based cancer research is equally essential in clinical geriatrics, where no single organ system or specialty can capture the full picture of a patient's health [94, 95].

5.2 Integration Across Disciplines: Where the Field is Heading

Looking across the body of research reviewed here, a few clear directions emerge(Table 4). First, the integration of computational and experimental methods is becoming standard practice rather than a novelty [96, 97]. Second, natural products research is gaining methodological sophistication, moving beyond simple bioassay-based studies toward mechanistic understanding at the molecular level [98]. Third, the boundaries between infectious disease research, oncology, and pharmacology are continuing to blur in productive ways [99, 100].

Table 4: Emerging Interdisciplinary Research Areas and Their Biomedical Applications

Research Area	Disciplines Involved	Key Applications	Current Challenges
Computational drug discovery	Bioinformatics, pharmacology, chemistry	Lead identification, repurposing	Validation gap, computing costs
Green nanotechnology	Chemistry, microbiology, environmental science	Drug delivery, antimicrobials	Toxicity profiling, scalability
Plant-based cancer therapeutics	Ethnobotany, oncology, biochemistry	Anticancer leads, antioxidants	Mechanism elucidation, clinical trials
Vector control peptides	Entomology, computational biology, parasitology	Malaria, dengue, filariasis control	In vivo validation, delivery
Antimicrobial resistance	Microbiology, genomics, public health	Resistance surveillance, new targets	Global coordination, diagnostics
Aging and systemic health	Geriatrics, cardiology, psychiatry	Integrated care models	Multimorbidity management

6. Conclusion

Modern biomedical sciences have undergone a remarkable transformation, driven by the convergence of multiple scientific disciplines that collectively address the growing complexity of human diseases. This review has comprehensively examined the interdisciplinary applications spanning infectious disease epidemiology, cancer biology, phytomedicine, nanotechnology, and computational drug discovery, highlighting their individual contributions and collective synergies in advancing human health. Epidemiological investigations have provided foundational insights into the prevalence, distribution, and risk factors associated with diverse infectious diseases, including intestinal parasitic infections, helminthiasis, oral candidiasis, tineacapitis, urinary tract infections, dental caries, and viral infections such as human papillomavirus and human immunodeficiency virus. These epidemiological data are indispensable for designing targeted public health interventions, informing clinical practice, and developing evidence-based prevention strategies. The documented associations between viral infections, particularly human papillomavirus type 16, and cervical cancer underscore the critical importance of integrating epidemiological surveillance with cancer prevention programs.

Phytomedicine continues to represent a rich and largely untapped reservoir of bioactive compounds with demonstrated therapeutic potential. Medicinal plants *including Boerhaavia diffusa, Euphorbia hirta, Achyranthes aspera, Ficus carica, Ipomoea obscura,* and *Terminalia chebula* have exhibited remarkable pharmacological activities encompassing antioxidant, antibacterial, antifungal, anti-inflammatory, and anticancer properties. These findings validate traditional ethnopharmacological knowledge and provide a compelling scientific basis for developing plant-derived therapeutics as alternatives or complements to synthetic pharmaceuticals. The cytotoxic activities demonstrated against cancer cell lines, including SiHa cervical cancer cells and MCF-7 breast cancer cells, further reinforce the anticancer potential of these medicinal plants.

Nanotechnology has significantly enhanced the therapeutic landscape by enabling biosynthesis of silver nanoparticles and development of advanced nanomaterials with superior antimicrobial, antifungal, and anticancer properties. The green synthesis approach utilizing plant extracts offers environmentally sustainable, cost-effective alternatives to conventional chemical synthesis methods, aligning with global sustainability goals. Computational drug discovery has emerged as a transformative paradigm, revolutionizing the identification and development of novel therapeutic candidates. Molecular docking, in silico peptide design, virtual screening, and chemical repurposing strategies have accelerated the drug discovery pipeline, significantly reducing time, cost, and ethical concerns associated with traditional experimental approaches.

The successful identification of novel peptides targeting cancer-associated proteins, antimicrobial resistance mechanisms, and vector-borne disease pathogens demonstrates the immense power of computational methodologies in modern drug discovery. Collectively, the interdisciplinary integration of these complementary approaches represents the future of biomedical research, fostering innovative, accessible, and effective therapeutic solutions for complex multifactorial diseases affecting global populations. Continued investment in collaborative, multidisciplinary research frameworks will undoubtedly accelerate the translation of scientific discoveries into meaningful clinical applications, ultimately improving patient outcomes and global public health.

Conflict of interest

The author disclose no conflicts of interest.

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