Biotechnological Approaches to Reversing Antibiotic-Induced Dysbiosis: Biochemical Pathways to Restored Microbiota Health

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Abstract. Antibiotic-induced dysbiosis disrupts the gut microbiota's biochemical symphony, impairing metabolic, immune, and signalling functions essential for health. This multidisciplinary review consolidates molecular, biochemical, and translational insights into biotechnological strategies for microbiota restoration. Topics include engineered probiotics, synthetic microbial consortia, phage-based therapeutics, and metabolic reconstruction of short-chain fatty acid and bile acid pathways. Computational modelling and multi-omics integration are examined as tools for pathway prediction and ecological resilience testing. Clinical and ethical perspectives highlight ongoing trials, biosafety frameworks, and equitable access in low-resource settings. Synthesising findings from systems biology and clinical translation, the review concludes that the next frontier of microbiome therapeutics lies in rationally engineered metabolic restoration—a convergence of biotechnology, computation, and ethics aimed at transforming post-antibiotic medicine into a programmable, functionally resilient ecosystem.

Keywords: antibiotic-induced dysbiosis; metabolic reconstruction; engineered probiotics; computational modelling; clinical microbiome therapeutics; systems biology.

INTRODUCTION

The Dutch scientist and entrepreneur, Antonie van Leeuwenhoek, was the first to observe and describe microorganisms in the 1670s, calling them"animalcule" (living animals) using a glass (simple lens) [1]. His discovery of the world of tiny, invisible living organisms marked the birth of microbiology. Microorganisms are ubiquitous; while some are beneficial members of the normal flora, others are opportunistic and/or parasitic in the environments they inhabit [2].

More recent research has shown that the human body harbours ~39 trillion diverse symbiotic microbes, collectively known as the human microbiota. The human gastrointestinal microbiota is a vast and dynamic ecosystem of microbes, including bacteria, viruses, fungi, archaea, and protozoa, that work harmoniously together to regulate the immune system, metabolise nutrients and facilitate the absorption of vitamins, maintain homeostasis, and, in general, affect overall health [3]. Along the gastrointestinal tract, microbial density varies: the colon harbours a more diverse and stable community of microorganisms. In contrast, the small intestine harbours fewer because of higher oxygen levels and faster transit [4]. The use of broad- or narrow-spectrum antibiotics in the treatment of bacterial infections is indispensable. However, exposure of the human gut to antibiotics can disrupt the diversity of the symbiotic microbial community, thereby truncating their beneficial functions [5]. This disruption, medically known as dysbiosis, is characterised by decreased microbial diversity and alterations in community structure, with profound physiological and therapeutic implications. Through horizontal gene transfer, antibiotics can facilitate the development of antibiotic resistance [6]. Disruptions in early life may have long-term effects on the immune system, metabolism, and cognition.

Current advances in microbiome science have led to a transition from conventional/empirical treatment approaches (probiotics, prebiotics, and faecal microbiota transplantation (FMT)) to more precise methods for reversing antibiotic-induced dysbiosis. These precise biotechnological approaches, whose results are consistent, include CRISPR-mediated editing (selectively targeting pathogens or ARGs), synthetic probiotics (engineered strains with specific metabolic/immunomodulatory functions), and engineered phage therapy (engineered bacteriophages to modulate the microbiota) [7]. In this review, we critically examine biotechnological and synthetic biology strategies to overcome conventional approaches for reversing antibiotic-induced dysbiosis.

RESULTS AND DISCUSSION

Molecular and Biochemical Underpinnings of Antibiotic-Induced Dysbiosis

The biological roles of the gut microbiota are significantly impaired by exposure to both narrow- and broad-spectrum antibiotics, leading to the disruption of enzymatic pathways regulated by the gut microbiota [8].

Commensal, beneficial species such as Faecalibacterium and Bifidobacterium primarily ferment dietary fibre into short-chain fatty acids (SCFAs) in the human gut. Antibiotic therapy can disrupt critical microbial enzymatic systems involved in the synthesis of SCFAs (acetate, propionate, and butyrate), which are necessary for immune function by shaping immune cell phenotypes, reinforcing epithelial integrity, and mitigating inflammation [8, 9]. However, the depletion of these beneficial commensal taxa, such as Faecalibacterium, has been linked to antibiotic exposure, leading to a direct reduction in butyrate synthesis. SCFAs are useful for colonocyte function and anti-inflammatory signalling [8]. Biochemical pathways involving colonocyte energy metabolism, epithelial integrity, and anti-inflammatory signalling all depend on these fatty acids, as the gut microbiota facilitates the breakdown of complex carbohydrates into SCFAs. When these pathways are inhibited by antibiotics, bile acid metabolism is disturbed, intestinal permeability increases, and mucosal barriers are weakened [9]. One of the key roles of the gut microbiota is the conversion of primary bile acids into secondary bile acids that regulate lipid catabolism and host metabolic homeostasis. However, when this process is inhibited by antibiotic exposure, toxic bile intermediates accumulate, leading to metabolic dysregulation [10].

Beyond metabolic disruption, antibiotics also influence cell-cell communication systems, notably quorum sensing and biofilm dynamics. There are three major groups of QS systems in bacteria, these include;

1) Gram-negative bacteria that utilise N-acyl homoserine lactones as the signalling molecule.

2) Gram-negative bacteria utilise small, processed oligopeptides.

3) Gram-positive and Gram-negative bacteria, in which autoinducer-2 (AI-2) is produced [11].

The multicellular lifestyle of bacterial colonies is advantageous because biofilms, which form in response to stress and nutrient constraints, protect against adverse conditions [12]. QS uses autoinducing peptides (AIPs) to control every step of the biofilm [8]. Antibiotic pressure promotes biofilm formation and QS-driven resistance in Pseudomonas aeruginosa, while QS through the las, rhl, and quinolone systems regulates virulence factors such as elastase and pyocyanin [13].

Toll-like receptors (TLRs) mediate interpathway communication between the microbiota and the host. Still, this communication becomes severely compromised when commensal microbial ligands can no longer regulate cytokine balance and immunological tolerance through their interaction with TLR2, TLR4, and TLR9 [8]. In a situation where the interaction is distorted by dysbiosis, TLR signalling will shift towards pro-inflammatory states, marked by decreased regulatory T-cell (Treg) activity, increased TNF-α, and interleukin-6 (IL-6) [8], and, as such, depleting the host's innate immune sensing function. SCFAs are significantly vital because they promote regulatory T-cell (Treg) populations, reduce inflammation, and encourage epithelial homeostasis [14]. Treg induction and epithelial tight junction maintenance are compromised by decreased SCFA synthesis in the gut when it is exposed to antibiotics, due to reduced SCFA-producing bacteria. Thus, exacerbates mucosal inflammation and barrier leakage [15].

Dysbiosis's metabolomic profile reveals significant alterations in key metabolic processes. Antibiotic administration modifies gut microbiota composition, thus affecting Trp metabolism via the indole, kynurenine, and serotonin pathways. It lowers faecal Trp and IPA levels, increases kynurenine levels, inhibits TPH1 expression, and reduces 5-HT synthesis, disrupting microbial balance and promoting metabolic dysbiosis [16, 17]. This imbalance impairs immunological regulation, disrupts serotonin synthesis, and affects the gut–brain axis, linking antibiotic-induced dysbiosis to higher risks of neurodegenerative and psychological disorders [10, 16-18]. Altered secondary metabolites such as bile acids and indoles increase liver strain, while reduced butyrate and propionate contribute to metabolic syndrome.

Multi-omics systems, including metagenomics, metatranscriptomics, metabolomics, and metaproteomics, are being used to understand antibiotic-driven dysbiosis [19]. These tools provide the high-resolution profiling of resilience dynamics, functional pathways, and microbiota composition [20]. Researchers have linked the depletion of Faecalibacterium and reduced butyrate synthesis—both key markers of microbiota stability—to antibiotic use. Similarly, genome-scale metabolic models predict how various antibiotic regimens generate SCFAs. According to some group researchers, Lactobacillus-based interventions help restore microbial imbalance. Also, they noted that machine learning can identify critical shifts in microbial networks that signal the onset of dysbiosis [21].

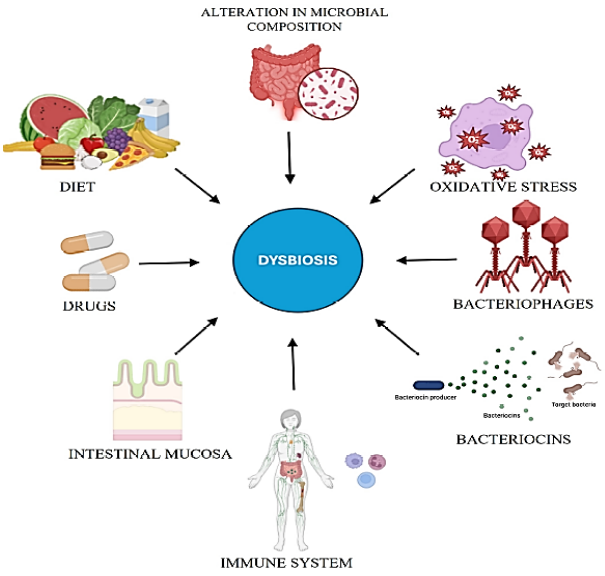

Figure 1 – Dysbiosis as a result of the interacting factors

Figure 1 highlights that dysbiosis results from multiple interacting factors, including diet, drugs, mucosal integrity, and immune function, with oxidative stress, bacteriophages, and bacteriocins further influencing microbial balance and sustaining disruption of gut homeostasis [8].

Biotechnological Intervention for Microbiota Restoration

1) Engineered Bacteria and Phage Therapy. The lack of tools to precisely modulate specific members of complex microbial communities is one of the most significant drawbacks of current meth-

ods for modulating the gut microbiota. To get around these limitations, several strategies have been proposed, including introducing ex vivo-designed bacteria into the gut or utilising engineered bacteriophages to modify the microbiome in situ [22] genetically.

The "ex vivo" approach uses bacteria engineered to release therapeutic molecules or sense biomarkers introduced into the microbiome. There are three main classes of engineered gut bacteria: drug factory probiotics, diagnostic gut bacteria, and smart probiotics [23]. Lactococcus lactis strains that secreted IL-10 decreased inflammation in a rat colitis model, whereas other strains secreted anti-TNF nanobodies, IL-27, and rmHO-1 [24]. Lactobacillus gasseri that secreted GLP-1 improved glucose control in diabetic rats. Diagnostic gut bacteria, such as E. coli Nissle 1917, identified liver metastasis, and thiosulphate was identified as a biomarker for colitis; smart probiotics that can deliver therapeutics to diseased tissue are still being developed [25]. Obstacles include maintaining microbial balance, achieving stable engraftment, and individual microbiome variability.

Phage therapy is a state-of-the-art approach to microbiota modification that is "in vivo." Some phages targeting Enterococcus faecalis reduced ethanol-induced liver damage. In contrast, others that target adherent-invasive E. coli protected mice from colitis and are undergoing clinical trials for Crohn's disease (NCT03808103) [26]. In situ microbiome editing is made possible by engineered phages, which circumvent the limitations of ex vivo techniques [25]. But issues such as controlling bacterial specificity, overcoming bacterial immunity, and ensuring biocontainment remain [25]. Solutions are provided by databases such as REBASE [25] and phage specificity engineering through host recognition domain modification. Although they require additional preclinical and clinical testing, synthetic bacteria and phage-based treatments generally show promise for regulating gut microbiota.

2) CRISPR Application Therapy. Microbiome engineering has been revolutionised with the advent of CRISPR-based technologies, providing unparalleled accuracy in regulating host-microbe interactions for the prevention and treatment of infectious diseases. Gene editing technologies, particularly CRISPR-Cas systems, have enabled precise modification of targeted microbial genes or strains, restoring dysbiotic microbial communities without harming the broader community [25]. Based on their structural and functional traits, the various CRISPR-Cas systems can be roughly divided into two classes. Class 2 systems depend on a single, multidomain effector protein, whereas Class 1 systems use multi-protein effector complexes. In CRISPR-based treatment, a single-guide RNA (sgRNA) directs the Cas protein to identify a complementary DNA sequence in the microbial genome and create a double-strand break. The target sequence is then modified or removed by the cell's repair machinery, resulting in precise genetic modifications. Researchers have used this biotechnological approach to integrate advantageous traits into commensal microorganisms, modify metabolic pathways, and selectively destroy harmful pathogens [25]. They have also used it to restore microbial balance, strengthen immunity against infections, and improve overall health outcomes [25]. Developed initially as bacterial immune defences, CRISPR-Cas systems store foreign DNA fragments as spacers to protect and enable sequence-specific recognition [27, 28]. Most commonly, Streptococcus pyogenes' Class 2 Type II CRISPR-Cas9 is employed [29]. However, delivery challenges, off-target effects, and gene transfer risks require stringent safety and regulatory measures [30].

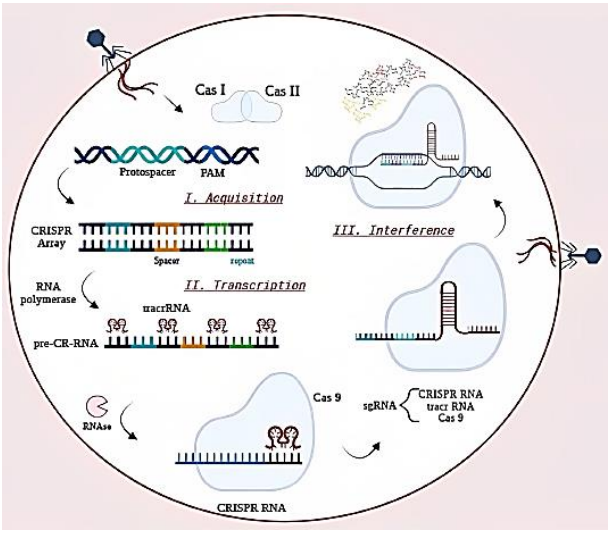

Figure 2 – The CRISPR/Cas bacterial immune system functions through spacer acquisition, crRNA formation, and viral DNA interference [10]

Metabolic Engineering and Biochemical Pathway Reconstruction

Antibiotics typically disrupt the metabolic processes that maintain the gut ecosystem in a bal-

anced, stable state. In this scenario, the value of recovery extends beyond repopulating taxa. It is an inherently occurring process that restores lost metabolic fluxes, maintaining host homeostasis. This section focuses on rebuilding damaged metabolic circuits and also describes common approaches. These techniques are crucial for removing any remaining xenobiotics and restoring enterohepatic bile acid signalling. Furthermore, they play a significant role in regulating small-molecule mediators that are essential for maintaining mucosal integrity, such as polyamines and redox couples. Here, it is necessary to highlight the modular and testable designs that impact both system-level validation and the synthesis of genetic pathway installation.

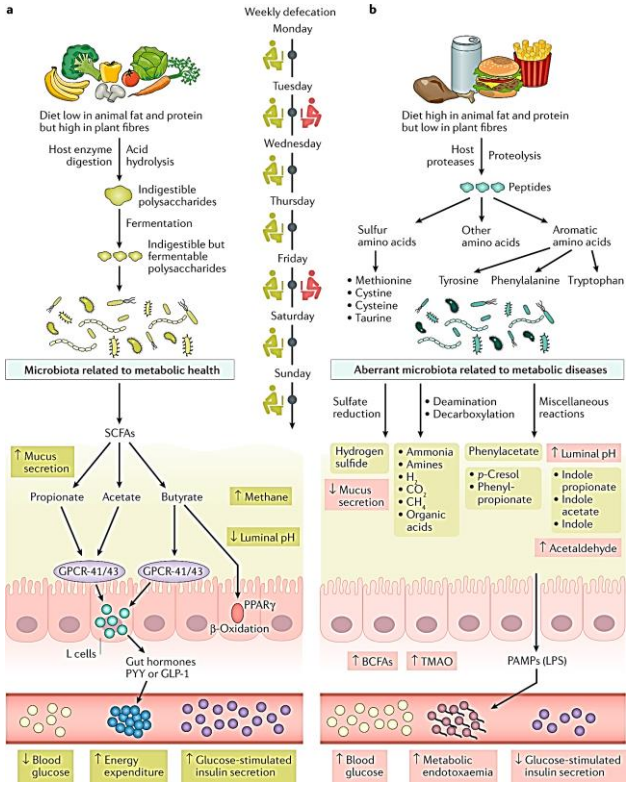

Figure 3 – The figure depicts the biochemical interactions between host metabolic systems and the gut microbiota, demonstrating that restored microbial pathways and dysbiosis contribute to disease [31]

Reconstituting short-chain fatty acid (SCFA) networks. Butyrate is an essential metabolite for SCFA reconstitution. This metabolite supports colonocytes and maintains hypoxia, both of which are necessary for the survival of obligate anaerobes. Additionally, butyrate plays a key role in modulating immunological tone. After antibiotic depletion, butyrogenesis is restored by two main processes:

1) Complete butyrate pathways, such as acetyl-CoA → butyryl-CoA → butyrate via butyryl-CoA: acetate CoA-transferase or butyrate kinase pathways, can be expressed by transplanting or engineering commensal chassis.

2) Installing cross-feeding modules (synthetic lactate → butyrate converters) that transform lactate and acetate generated by antibiotics into butyrate. Previous studies show that engineered lactic acid bacteria or Eubacterium chassis carrying heterologous gene cassettes can restore butyrate fluxes; however, these studies do not capture the full range of benefits and exclude critical downstream effects on the epithelium. To guarantee that new routes do not create metabolic sinks that destabilise community networks, design must consider the thermodynamic coupling and stoichiometric balances required [32].

Restoring bile acid transformations and enterohepatic signalling. Notable producers of secondary bile acids include sulfatases, 7α-dehydroxylases, and microbial bile salt hydrolases (BSHs). These bile acids, primarily FXR and TGR5, function as host signalling ligands. Microbial taxa also serve as ecological selectors. Targeted metabolic engineering can do the following:

1) Restoring deconjugation capacity by reintroducing BSH activity into the molecular environment of commensals that have been proven to be handy.
2) Rebuild secondary pools of bile acids by sorting and assembling modular 7α-dehydroxylation operons into a molecularly safe chassis.

3) Finally, bile-modifying enzymes that function under bile-responsive promoters can be expressed through targeted bioengineering; this is because bile metabolites need to be combined with enterohepatic pools that have been thoroughly and quantitatively profiled, as they directly impact a variety of parameters, including host metabolism, immunological responses, and route rebuilding. This configuration prevents the overproduction of hepatotoxic species [33, 34].

Xenobiotic degradation: enzymatic sinks for residual antibiotics. It is also essential to consider subtherapeutic antibiotic residues, a class of metabolites in the lumen that might perpetuate dysbiosis and select for resistance. The operational use of this metabolite involves the adoption of xenobiotic-degrading enzymes, including amidases, hydrolases, and monooxygenases, that target class-specific antibiotic bonds; hence, their use-

fulness in the design of gut commensals. The installation of a biochemical sink, whose primary purpose is to lessen residual selection pressure, makes this procedure significant. Here, a variety of tactics are effective. One involves initiating surface- or periplasmic expression of degrading enzymes that prevent antibiotics from being absorbed by cells. Metabolic channelling, which converts breakdown products into harmless compounds that support native species, is another successful tactic. Fundamentally, degradative genes work best when engineered with genetic protections, such as kill-switch linkage, inducible promoters, and reduced horizontal transfer potential [35].

Polyamines, mucosal reinforcement, and redox homeostasis. In general, polyamines (spermidine, putrescine) facilitate wound healing, tight-junction function, and epithelium restitution following antimicrobial damage. Research shows that scientists can accelerate barrier recovery by engineering commensals to regulate polyamine flux. Their expression of decarboxylases, which alter host-accessible pools and aid in barrier healing, is an alternative. Additionally, redox equilibrium can be reestablished by a procedure known as parallel engineering. Since they can recreate the anaerobic niches crucial for obligate butyrate production, microbial NADH/NAD+ modulators and hydrogenase circuits are often used to this end. It should be noted, nonetheless, that these treatments need to be titrated, as excessive polyamine synthesis can have pro-proliferative effects. For this reason, adjustable expression systems in combination with metabolite-sensing feedback loops are essential [36].

Computational modelling and resilience testing. Before wet-lab implementation, in silico pathway fluxes and, consequently, cross-feeding and ecological effects can be predicted using biochemical mechanisms such as genome-scale metabolic models (GEMs), constraint-based reconstructions, and, most importantly, community flux balance analysis. Technologists can reduce the risk of starting competitive collapses by simulating designed pathways in multi-species community models and forecasting the effectiveness of additional reactions in restoring target metabolites. Therefore, a practical method for investigating colonisation and detecting the host response during an antibiotic-recovery procedure is provided by iterative cycles of modelling and bench validation, primarily using chemostat/bioreactor consortia and gnotobiotic animal testing [37].

Design considerations and safety. To achieve optimal outcomes, biochemical reconstruction must not compromise efficacy or biosafety. The risk of horizontal gene transfer is reduced in operational settings by implementing practices such as non-replicating enzyme-delivery vectors, strict genetic containment (auxotrophy, kill switches), inducible control, and reduced mobile elements. Lastly, for tailored therapeutics aimed at restoring function following antibiotic harm, integrated metabolomic readouts should be used as the primary endpoints.

Table 1 – The new biotechnological strategies intended to repair antibiotic-induced dysbiosis involving metabolic recovery, microbial reconfiguration, and ecosystem resilience [33-36]

Biotechnological Approach	Mechanism of Action	Representative Studies / Findings	Therapeutic Implications
Synthetic Probiotics	Engineered bacterial strains designed to sense, secrete, or neutralise metabolites in disrupted microbiota environments.	Lactococcus lactis engineered to deliver IL-10 and reduce inflammation in dysbiotic mice [38]	Enables targeted immunomodulation and restores homeostatic gut function.
Microbiome Transplantation	Reintroduction of balanced microbial consortia through faecal or synthetic microbiota transplantation.	FMT restored microbial richness and metabolic diversity post-antibiotic treatment [39]	Accelerates microbiota recovery and reduces the risk of recurrent infections, such as C. difficile.
Phage Therapy	Utilisation of bacteriophages to selectively target pathogenic bacteria without harming beneficial strains.	Phage cocktails effectively reduced antibiotic-resistant Enterococcus faecalis in dysbiotic gut models [40]	Provides precision biocontrol and complements antibiotic alternatives.
Metabolic Engineering of Gut Commensals	Reprogramming gut bacteria to overproduce or consume specific metabolites essential for	Engineered Bacteroides thetaiotaomicron restored butyrate metabolism in	Supports restoration of key metabolic pathways and promotes colonisation

Biotechnological Approach	Mechanism of Action	Representative Studies / Findings	Therapeutic Implications
	ecosystem stability.	antibiotic-treated hosts [41]	resistance.
Prebiotic Nanocarriers	Nanostructured prebiotics that deliver substrates and protect probiotics during colon passage.	Nanocarrier-encapsulated inulin enhanced probiotic survival and short-chain fatty acid recovery [42]	Combines nanotechnology with nutrition for enhanced microbial resilience.
CRISPR-Based Modulation	Researchers use CRISPR-Cas systems to edit, silence, or enhance microbial genes that influence dysbiosis dynamics.	CRISPR-driven deletion of virulence genes in Escherichia coli reduced dysbiotic colonisation [43]	Enables high-precision gene-specific repair of microbiome disruptions.

Translational and Clinical Perspectives

The understanding, development, and therapeutic acceptance of biotechnological therapies for dysbiosis reception are currently at a turning point. The link between restorative treatment and conceptual biotechnology lies in the shift from laboratory concepts and design frameworks to clinical adoption and execution. In recent years, these interventions—which include phage-based systems, microbial consortia, and tailored probiotics—have advanced from preclinical proof-of-concept to controlled clinical evaluation. Ensuring translation with strong efficacy, safety, and regulatory alignment across a range of patient situations is one of the procedure's most urgent issues.

Clinical evaluation of engineered probiotics and synthetic consortia. As of the time of this study, phase I and II clinical studies for first-generation probiotics that can express metabolic enzymes and anti-inflammatory compounds have begun, primarily for gastrointestinal and certain metabolic illnesses. Genetically edited commensals as living medicines have precedence, thanks to the development of Lactococcus lactis, a bacterium engineered to release IL-10 and precisely target mucosal immunomodulation against inflammatory bowel disease [44]. Furthermore, numerous studies have demonstrated sustainable colonisation and reduced recurrence of Clostridioides difficile infection in synthetic microbiota consortia, the spore-forming groups such as SER-109 and VE303. This outcome confirms that modular ecosystem reassembly is a valuable therapeutic approach [45]. The integration of metabolic processes is necessary for subsequent translation. While maintaining ecological stability and host compatibility, this often entails restoring butyrate (or, less frequently, bile acid) to the consortia of interest.

Personalised microbiome therapeutics. In conventional practice today, precision-guided therapies tailored to a patient's microbiological deficiencies can be implemented using two significant clinical achievements in modern medicine: metagenomic and metabolomic analysis. Additionally, advances that enable the construction of patient-specific microbial metabolic networks can now be mapped using AI-driven models; this, in turn, helps predict the maximum functional restoration from modified strains or metabolic modules, feats not possible in the past [45]. Based on available research tools and prospects, this personalisation has shown great potential to shift the approach from empirical supplements to data-driven design, thereby enabling precision medicine. The implication and core impact are that researchers can now take unique microbiome signatures into account when choosing engineering outputs, such as synthetic pathways or xenobiotic-degrading enzymes. Most significantly, it is now possible to analyse patient data using safe, compatible platforms, which will be crucial for reducing privacy threats and guaranteeing reproducibility across health systems.

Regulatory and biosafety considerations. To address privacy and safety concerns, a few adjustments must be made to keep ethical concerns negligible; this pertains particularly to horizontal gene transfer and other procedures crucial to advancing the research, such as off-target colonisation and its long-term ecological effects. To address these concerns, the FDA and EMA proposed a regulatory framework recommending the adoption of multi-tier containment strategies, including auxotrophic dependence on gut metabolites, built-in kill switches, and chromosomal integration of therapeutic genes in place of plasmids [46]. Additionally, other clinical adherence recommendations have been discussed in this direction, too. One of which is strict metabolite kinetics monitoring, including patient immunological reactions, and attending doctors keeping a close eye for unexpected systemic absorption, which could happen in a few cases, a vigilance necessary for safety validation. On the other

hand, phage-based treatments have continually posed peculiar challenges, such as the need to prevent lysogenic conversion and the lack of consistent pharmacokinetics across intestinal niches [47].

Socio-economic and ethical dimensions. One major translational challenge is equitable access to underserved regions, particularly in Africa and other low-income nations. Cold-chain stability and great manufacturing precision are requirements for standard engineered microbiome therapeutics. Therefore, in health systems with limited resources, the main obstacle to adoption is affordability. On the other hand, because of their scalability and acceptance as viable processes, biotechnologists are also investigating low-cost alternatives such as dry-spore encapsulation and modular bioreactor manufacturing [48]. The bioengineering of human microbial ecosystems raises ethical questions regarding biological identity, particularly when metabolic pathways are artificially inserted. Transparency in gene circuit design and post-therapy microbiome monitoring would be essential to preserving trust in the procedure and ensuring long-term biosafety, thereby establishing an ethically sensitive research and clinical setting appropriate for the development of the technology.

The therapeutic potential of biotechnological methods lies in guiding nature's recovery rather than substituting for its diversity. Hence, three parallel pillars are crucial for well-rounded, ethically sound research and treatment practices. They are rigorous clinical testing and validation, ethically sensitive bioengineering, and equitable distribution. All three practices are necessary for translational success in modern-day. Furthermore, engineered ecosystems with keen research interest could revolutionise how medicine conceptualises and explores cellular metabolites and also how the whole microbial symphony supports human health as science advances from the laboratory to clinical application.

CONCLUSIONS

Without a doubt, one of the most revolutionary iatrogenic interventions in human physiology has been the discovery of antibiotic-induced dysbiosis. However, sufficient acknowledgement is due to biotechnological advancements such as metabolic engineering, precise phage therapy, and synthetic microbiota design. With the adoption of research processes in this field, there are now plausible routes to treatment and recovery. The most significant advantage of these techniques is that they allow for the reconstruction of the microbiome with biochemical precision rather than conjecture. Functional restoration over compositional repair is a paradigm to watch for in the future. Rebuilding the metabolic and enzymatic structures that support host-microbe symbiosis would be feasible with such an advancement.

With a focus on bioethical governance, future research must also incorporate multi-omics analytics and computational modelling into each design phase. Additionally, components such as a scalable chassis and verified safety circuits will be necessary for clinical translation. Frameworks for global access that go beyond high-income healthcare settings will also help ensure fair access in settings with limited resources. Therefore, the problem ahead is not just technological; it also has a significant impact on ecology, since products must be designed to restore complexity without sacrificing control by avoiding oversimplification.

In the near future, as biotechnology and personalised medicine merge, research goals would shift to reprogramme resilience within the microbiota rather than merely treat dysbiosis. A new class of living therapies may turn the gut's cellular environment from an antibiotic's casualty and side effects into a programmable ally for long-term human health, thanks to systems biology and ethical forethought.

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