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Mobile Genetic Elements in Microbial Genetics: Mechanisms of Horizontal Gene Transfer and Their Role in the Evolution of Antimicrobial Resistance: A Mini Review

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ABSTRACT
Objective: *This mini-review discusses the major types of mobile genetic elements (MGEs), their molecular mechanisms of mobility, their role in horizontal gene transfer, and their contribution to the evolution and dissemination of antimicrobial resistance in microbial populations.* ***Method:*** *The review applies a structured narrative synthesis of the peer-reviewed articles, standard microbiology references, and international surveillance reports cited in the manuscript. Evidence was organized thematically around microbial genome organization, horizontal gene transfer, major MGE classes, genomic islands, antimicrobial resistance dissemination, and genomic approaches for MGE detection and surveillance.* ***Results:*** *The literature indicates that plasmids, transposons, insertion sequences, integrons, integrative and conjugative elements, bacteriophages, and genomic islands form interconnected genetic vehicles that accelerate the acquisition and spread of resistance, virulence, and adaptive traits. Whole-genome sequencing, metagenomics, comparative genomics, and bioinformatics increasingly enable high-resolution tracking of these elements, while CRISPR-Cas systems influence the interaction between microbes and mobile DNA.* ***Novelty:*** *This review integrates the molecular mechanisms, genomic architecture, antimicrobial-resistance consequences, and surveillance implications of MGEs within a single concise framework and highlights their relevance to clinical microbiology, environmental microbiology, and biotechnology.*

INTRODUCTION

Microbial genetics is a major branch of microbiology concerned with the organization, transmission, expression, and evolution of genetic material in microorganisms. Advances in molecular biology and genome sequencing have substantially expanded understanding of microbial genetic regulation and of the mechanisms that enable rapid adaptation to environmental and clinical pressures [1], [2].

A central feature of microbial evolution is the capacity to acquire genetic material from sources other than a direct parent. Horizontal gene transfer (HGT) allows genes to move between unrelated cells and even across species boundaries, complementing mutation and vertical inheritance and accelerating the spread of advantageous traits within microbial communities [3], [4].

Mobile genetic elements (MGEs), including plasmids, transposons, insertion sequences, integrons, integrative and conjugative elements (ICEs), bacteriophages, and genomic islands, are major vehicles of this process. Their mobility contributes to genome rearrangement, genetic diversity, virulence, metabolic adaptation, and especially the dissemination of antimicrobial resistance determinants [5], [6]. The global expansion of multidrug-resistant organisms has made MGE-mediated resistance a major concern for antimicrobial-resistance surveillance and control [7].

Whole-genome sequencing, metagenomics, comparative genomics, and bioinformatics now permit increasingly detailed characterization of MGE structure, diversity, and transmission. International surveillance emphasizes the need to integrate genomic and epidemiological information to track resistance across clinical and environmental settings [8]. CRISPR-Cas systems also shape the interaction between microbial genomes and invading mobile DNA and therefore add an important regulatory layer to MGE evolution [9]. Studies of the mobile gene pool further show that HGT provides a continuing source of genetic innovation across bacterial populations [10]. Accordingly, this mini-review provides an updated overview of MGEs in microbial genetics, focusing on their types, mechanisms of horizontal transfer, genomic consequences, role in antimicrobial resistance, analytical approaches, and future research priorities.

RESEARCH METHOD

This article was prepared as a mini-review using a structured narrative approach. The evidence base consisted of the peer-reviewed journal articles, academic microbiology texts, and international antimicrobial-resistance surveillance reports cited in the manuscript. Sources were selected for their direct relevance to microbial genetics, horizontal gene transfer, mobile genetic elements, genomic islands, antimicrobial resistance, and molecular or genomic approaches for detection and characterization. Foundational studies were retained when they describe mechanisms that remain central to the field, while more recent references were used to represent current genomic and surveillance perspectives.

The selected literature was synthesized thematically rather than statistically. Information was grouped into six analytical domains: microbial genetics and genome organization; mechanisms of horizontal gene transfer; major classes of mobile genetic elements; genomic islands; the contribution of MGEs to antimicrobial resistance; and the implications of genomic technologies for surveillance and microbial evolution. Because this is a narrative mini-review, no meta-analysis, pooled effect estimate, or formal risk-of-bias scoring was performed. The synthesis emphasizes conceptual agreement, mechanistic relationships, and clinically relevant implications supported by the cited literature [3], [5], [6], [8], [10].

RESULT AND DISCUSSION

Results

The reviewed literature consistently identifies horizontal gene transfer and mobile genetic elements as major drivers of microbial genome plasticity. Across the sources, the most recurrent findings are that MGEs provide transferable platforms for accessory genes, that multiple MGE classes can be nested within the same genetic structure, and that these combinations facilitate rapid dissemination of antimicrobial-resistance and virulence determinants [3], [5], [6]. The thematic findings are presented below according to microbial genome organization, HGT mechanisms, MGE classes, genomic islands, and antimicrobial-resistance dissemination.

Microbial Genetics: An Overview

The Concept of Microbial Genetics

Microbial genetics is a basic branch of microbiology that deals with the genetic materials of microorganisms such as bacteria, archaea, microscopic fungi, some protists, and viruses. This field is concerned with the study of the organization, transfer and expression of genetic information, the changes that occur in it and its role in the adaptation of microorganisms to different environments [1]. The field has grown enormously since the discovery of DNA as the genetic material and the elucidation of the mechanisms of replication, transmission and expression. These advances have contributed to the understanding of several biological phenomena, such as the emergence of antibiotic resistance, acquisition of virulence factors, adaptation to harsh environmental conditions and genetic variation among microbial strains [2].

Microorganisms have a rapid reproduction rate and small genome sizes compared to higher organisms, making them ideal models for studying fundamental genetic processes [3], [10]. They also have a remarkable ability to take up genetic material from the environment or other microorganisms, which gives them high genetic plasticity and the ability to respond quickly to selective pressures, such as antibiotic exposure or environmental change [4]. In microbial genetics, genetic information is transferred vertically from parent cells to daughter cells and horizontally between different individuals or species without a direct parent-offspring relationship [3], [4]. Horizontal transfer is therefore a major force in rapid microbial evolution and contributes to the dissemination of antimicrobial-resistance genes, virulence factors, and diverse metabolic capabilities [3]. Mobile genetic elements are central to this process and function as carriers of gene transfer between microorganisms. They include plasmids, transposons, integrons, bacteriophages, and integrative and conjugative elements, which continuously reshape microbial genomes and enhance adaptation [5], [10]. With advances in whole-genome sequencing, metagenomics, and bioinformatics, it has become possible to track the movement of MGEs and investigate their dynamics within microbial communities with increasing precision [6], [10]. See Tables 1 and 2.

Table 1. Major Characteristics of Microbial Genetics

Feature	Description	Biological Significance
Genetic Material	DNA or RNA depending on the microorganism	Stores hereditary information
Genome Organization	Chromosomal and extrachromosomal DNA	Controls cellular functions
Vertical Gene Transfer	Transmission from parent to offspring	Maintains genetic continuity

Feature	Description	Biological Significance
Horizontal Gene Transfer	Exchange of genes between unrelated microorganisms	Enhances adaptation and evolution
Mutation	Permanent alteration in DNA sequence	Generates genetic diversity
Recombination	Rearrangement of genetic material	Produces novel genetic combinations
Mobile Genetic Elements	Plasmids, transposons, integrons, bacteriophages	Disseminate adaptive traits
Gene Regulation	Control of gene expression	Enables environmental adaptation

Table 2. Major Genetic Processes in Microorganisms

Genetic Process	Mechanism	Main Outcome
DNA Replication	Semi-conservative replication	Genome duplication
Mutation	Spontaneous or induced DNA changes	Genetic variation
Transformation	Uptake of naked DNA	Acquisition of new genes
Conjugation	Cell-to-cell DNA transfer	Spread of plasmids and resistance genes
Transduction	Phage-mediated DNA transfer	Gene exchange among bacteria
Recombination	Exchange of homologous DNA sequences	Genome diversification

Microbial Genome Organization

The genome serves as the complete repository of genetic information determining the structural and functional traits of microorganisms. Genome organization in microorganisms differs markedly from that of eukaryotes; most bacteria and archaea possess a single circular chromosome located within the nucleoid region, although some species may contain multiple chromosomes or linear chromosomes, in addition to extrachromosomal genetic elements such as plasmids and mobile genetic elements [1], [2]. The simplicity of genomic organization in microorganisms is a primary reason they serve as ideal models for studying genetic processes; their genomes are easily analyzed, mutations can be tracked, and gene transfer between different strains can be investigated. Furthermore, their small genome size—compared to higher organisms—facilitates rapid

DNA replication, which translates into faster cell division and adaptation to diverse environmental conditions [2].

The Bacterial Chromosome

The bacterial chromosome serves as the primary source of genetic information, containing most genes essential for life, including those responsible for DNA replication, cell division, metabolism, cell wall synthesis, and protein production. Typically composed of a circular, double-stranded DNA molecule, the chromosome contains millions of base pairs and several thousand genes. Although bacteria lack a nuclear membrane, the chromosome is organized within a nucleoid region by specialized proteins that compact and structure the DNA inside the cell [1], [2].

Extrachromosomal DNA

In addition to the main chromosome, many microorganisms possess independent genetic elements known as extrachromosomal DNA; plasmids are the best-known examples. Plasmids are usually small, circular DNA molecules capable of replicating independently of the chromosome. They often carry genes that confer adaptive advantages, such as resistance to antibiotics or heavy metals, toxin production, or specialized metabolic functions [4], [10].

Essential and Accessory Genes

Genes within a microbial genome can be categorized into two main types. Essential genes are required for cell survival and include genes involved in DNA replication, protein production, and fundamental metabolic processes. Accessory genes are not essential under normal conditions but can confer important adaptive advantages, including antimicrobial resistance, tolerance to environmental stress, toxin production, and host colonization [1], [4].

Genome Plasticity

Microbial genomes are characterized by a high degree of genome plasticity—the ability to acquire, lose, or rearrange genetic material in response to environmental pressures. This plasticity is achieved through several mechanisms [2], [4], [10]:

a. Genetic mutations.
b. Genetic recombination.
c. Horizontal gene transfer.
d. The activity of mobile genetic elements.

Genome plasticity is a key factor driving the rapid evolution of bacteria and the emergence of drug-resistant strains; it also plays a role in the acquisition of virulence factors and the ability to colonize new environments. See Tables 3 and 4.

Table 3. Components of the Microbial Genome

Component	Structure	Function	Examples
Chromosome	Circular or linear DNA	Essential genetic information	*Escherichia coli*, *Borrelia burgdorferi*

Component	Structure	Function	Examples
Plasmid	Circular extrachromosomal DNA	Antibiotic resistance, virulence, metabolism	R plasmids, Col plasmids
Integrative Elements	Chromosomal integrated DNA	Horizontal gene transfer	ICEs
Prophage	Integrated bacteriophage DNA	Virulence and gene transfer	Lambda prophage
Genomic Islands	Large chromosomal DNA segments	Pathogenicity and adaptation	Pathogenicity islands

Table 4. Essential Genes vs. Accessory Genes

Feature	Essential Genes	Accessory Genes
Importance	Required for survival	Enhance adaptation
Conservation	Highly conserved	Variable
Location	Chromosome	Chromosome or plasmids
Transferability	Rare	Frequently transferred
Examples	DNA replication genes, ribosomal proteins	Antibiotic resistance genes, toxin genes

Horizontal Gene Transfer (HGT)

Horizontal gene transfer (HGT) is one of the most significant mechanisms contributing to microbial evolution because it enables the transfer of genetic material between microorganisms that do not share a direct parent-offspring relationship, unlike vertical gene transfer from a parent cell to daughter cells during division [3], [4]. This concept has transformed understanding of microbial evolution by showing that adaptation depends not only on mutation and natural selection but also on gene exchange between different lineages [3]. HGT plays a fundamental role in the acquisition of traits such as antimicrobial resistance, toxin production, utilization of new nutrient sources, and tolerance to environmental stress, thereby increasing the capacity of microorganisms to adapt to changing environments [4].

Mechanisms of Horizontal Gene Transfer

Horizontal gene transfer in bacteria relies on three main mechanisms: transformation, conjugation, and transduction. While these mechanisms differ in the way DNA is transferred, they all contribute to increasing genetic diversity and the spread of acquired traits.

Transformation

Genetic transformation is a process in which a bacterial cell takes up free DNA from the surrounding environment and integrates it into its own genome, provided the DNA is compatible. Bacteria capable of performing this process are referred to as "competent bacteria"—examples include *Streptococcus pneumoniae* and *Bacillus subtilis* [4]. This mechanism serves as an effective means of acquiring new genes without requiring direct cell-to-cell contact. It was also among the first phenomena to demonstrate that DNA is the genetic material, as evidenced by Griffith's experiment in 1928 and the subsequent experiment by Avery, MacLeod, and McCarty in 1944 [11].

Conjugation

Conjugation is the most efficient mechanism of horizontal gene transfer; it occurs through direct contact between two bacterial cells via a sex pilus. During this process, a plasmid—or a portion of the chromosome—is transferred from the donor cell to the recipient cell [4].

Transduction

Transduction occurs when bacteriophages transfer genetic material from one bacterial cell to another during their life cycle. It occurs as generalized transduction, in which different regions of the bacterial genome may be transferred, or specialized transduction, in which genes located near a phage integration site are preferentially transferred [4], [5].

Table 5. Major Mechanisms of Horizontal Gene Transfer

Mechanism	DNA Source	Cell Contact Required	Main Vehicle	Examples
Transformation	Free environmental DNA	No	Naked DNA	*Streptococcus pneumoniae*
Conjugation	Donor bacterium	Yes	Conjugative plasmids	F plasmid, R plasmids
Transduction	Donor bacterium	No	Bacteriophages	Lambda phage, P22 phage

Mobile Genetic Elements (MGEs)

Mobile genetic elements (MGEs) are among the most significant components of the microbial genome and play a pivotal role in the evolution of microorganisms. These genetic units possess the ability to move within the genome itself or transfer between different microorganisms, thereby contributing to the reorganization of genetic material and driving rapid genetic changes that cannot be explained by mutations alone. These elements have revolutionized the traditional ideas about genome stability, and the microbial genome is now considered as a dynamic system, in constant process of gene acquisition, loss and rearrangement [4], [5]. Mobile genetic elements are a heterogeneous group of genetic structures including plasmids, transposons, insertion sequences, integrons, integrative and conjugative elements (ICEs) and bacteriophages. While they differ in their structures and mechanisms of transfer, they all have the ability to transfer genetic information between cells, increasing genetic diversity and speeding up adaptation to environmental and pharmacological pressures [6]. The importance of these elements lies not only in the transfer of antimicrobial resistance genes but also in the transmission of genes responsible for the production of toxins, biofilm formation, metabolism of organic compounds and in adaptation to harsh environments. Therefore, MGEs are considered as significant contributors to the evolution of bacteria and the emergence of multidrug-resistant pathogenic strains, and they are a subject of research in microbiology, molecular genetics and public health [12]. Significant advancements in whole-genome sequencing and metagenomics technologies have revealed the widespread prevalence of mobile genetic elements within microbial communities; these studies have shown that many clinically important genes are located on such elements rather than on the bacterial chromosome, a finding that explains the rapid dissemination of various adaptive traits across different species [10].

Table 6. Major Types of Mobile Genetic Elements

Mobile Genetic Element	Structure	Mobility Mechanism	Major Function
Plasmids	Circular dsDNA	Conjugation	Antibiotic resistance, virulence
Insertion Sequences	Small DNA segments	Transposition	Gene disruption
Transposons	DNA segments carrying accessory genes	Transposition	Dissemination of resistance genes
Integrons	Gene cassette capture system	Associated with transposons/plasmids	Gene acquisition
ICEs	Chromosomal integrated DNA	Excision and conjugation	Horizontal gene transfer
Bacteriophages	Viral DNA	Transduction	Gene transfer and virulence

Genomic Islands

Genomic islands (GIs) are large DNA regions within bacterial chromosomes that are believed to have been acquired through horizontal gene transfer [4], [5]. These regions often show molecular features that differ from the rest of the genome, including atypical GC content and codon usage, and they commonly contain mobility-associated genes such as integrases and transposases, supporting an exogenous origin [13], [14]. Genomic islands are important contributors to bacterial evolution because they can rapidly confer virulence, antibiotic resistance, environmental adaptation, or new metabolic capabilities. Unlike point mutations, which usually affect individual loci, genomic islands can transfer coordinated sets of functional genes in a single acquisition event and therefore produce substantial phenotypic change [13], [14]. Their general characteristics are summarized in Table 7, and their major functional classes are shown in Table 8.

Table 7. General Characteristics of Genomic Islands

Characteristic	Description
Size	10–200 kb
GC content	Different from host genome
Integration site	Frequently adjacent to tRNA genes
Mobility genes	Integrase, transposase
Flanking repeats	Often present
Biological role	Adaptation and evolution

Table 8. Major Classes of Genomic Islands

Genomic Island Type	Main Function	Representative Examples
Pathogenicity Islands	Virulence	SPI-1, SPI-2 (*Salmonella*)
Resistance Islands	Antibiotic resistance	AbaR (*Acinetobacter baumannii*)
Metabolic Islands	Catabolic pathways	Toluene degradation islands
Symbiosis Islands	Plant interaction	*Mesorhizobium* symbiosis island

Biological Significance of Genomic Islands

Genomic islands play a fundamental role in microbial evolution by enabling the rapid acquisition of traits that can affect the following biological functions [13], [15]:

a. Increased virulence.

b. Enhanced antibiotic resistance.
c. Adaptation to diverse environments.
d. Diversification of metabolic capabilities.
e. Improved colonization and symbiotic abilities.
f. They also serve as clear indicators of horizontal gene transfer, making them valuable in evolutionary studies and genomic comparisons.

Role of Mobile Genetic Elements in Antimicrobial Resistance

Antimicrobial resistance (AMR) is one of the most serious global health challenges of the twenty-first century, contributing to increased morbidity and mortality, prolonged hospital stays, and rising healthcare costs [6], [7]. Although chromosomal mutations contribute to resistance, horizontal gene transfer is a major mechanism driving the rapid spread of resistance determinants among bacteria and across species [6]. Mobile genetic elements act as vehicles for transferring resistance genes among chromosomes, plasmids, and bacterial hosts, thereby promoting multidrug-resistant (MDR), extensively drug-resistant (XDR), and, in some cases, pandrug-resistant (PDR) phenotypes [6]. The interplay among plasmids, transposons, integrons, integrative and conjugative elements, bacteriophages, and genomic islands has accelerated the evolution and dissemination of resistance [6], [7].

Contribution of Different MGEs to AMR Dissemination

Mobile genetic elements contribute to the spread of antimicrobial resistance through several complementary mechanisms [6], [7], as summarized in Table 9.

a. Plasmids: Rapidly transfer resistance genes via conjugation and often carry multiple resistance genes simultaneously.
b. Transposons: Transfer genes between plasmids and chromosomes, facilitating genome rearrangement.
c. Insertion Sequences: Activate resistance genes or assist in the formation of composite transposons.
d. ICEs: Transfer large clusters of genes via conjugation, followed by integration into the chromosome.
e. Bacteriophages: May transfer certain resistance and virulence genes via phage-mediated transfer.
f. Genomic Islands: Contain clusters of resistance or virulence genes acquired through horizontal gene transfer.
g. Integrons: Assemble resistance gene cassettes and ensure their expression, though they rely on other elements for mobility.

Table 9. Contribution of Major Mobile Genetic Elements to Antimicrobial Resistance

Mobile Genetic Element	Mechanism	Major Resistance Genes	Clinical Importance
Plasmids	Conjugation	blaNDM, blaKPC, mcr-1	Very High
Transposons	Transposition	tet(M), blaTEM	High
IS Elements	Gene activation/rearrangement	ISAba1-associated blaOXA	High
ICEs	Conjugation	tet(M), erm(B)	High
Bacteriophages	Transduction	Selected resistance genes	Moderate
Genomic Islands	Horizontal acquisition	Multiple resistance determinants	High
Integrons	Gene cassette capture	aadA, dfrA, blaVIM	Very High

Emergence of Multidrug-Resistant Bacteria

The interaction between different mobile genetic elements can lead to the accumulation of multiple resistance determinants within a single bacterial host; for example, one plasmid may simultaneously carry transposons and integrons containing several resistance genes [6], [7]. Consequently, resistance to several antimicrobial classes can emerge through a single acquisition event. This pattern is particularly important in high-priority pathogens [6], [7], such as:

a. *Escherichia coli*
b. *Klebsiella pneumoniae*
c. *Acinetobacter baumannii*
d. *Pseudomonas aeruginosa*
e. *Enterococcus faecium*

Table 10. Major Clinically Important MDR Bacteria and Associated MGEs

Bacterial Species	Common MGEs	Frequently Detected Resistance Genes
Escherichia coli	Plasmids, Integrons	blaCTX-M, mcr-1
Klebsiella pneumoniae	Plasmids, Transposons	blaKPC, blaNDM
Acinetobacter baumannii	Genomic islands, IS elements	blaOXA-23, blaOXA-58

Bacterial Species	Common MGEs	Frequently Detected Resistance Genes
Pseudomonas aeruginosa	Integrons	blaVIM, blaIMP
Enterococcus faecium	ICEs	vanA, tet(M)

The rapid spread of mobile genetic elements has transformed antimicrobial resistance into a problem extending beyond hospitals. Resistance-associated MGEs are detected in wastewater, soil, agricultural environments, and food chains, creating opportunities for gene exchange between environmental and pathogenic bacteria [6], [7]. Consequently, modern surveillance increasingly relies on whole-genome sequencing and metagenomic analysis to identify MGEs and monitor their dissemination at local and global scales [6], [8], [10].

Discussion

Taken together, the evidence indicates that mobile genetic elements should not be viewed as isolated units. Plasmids can carry transposons and integrons, transposons can relocate resistance determinants between replicons, and ICEs can integrate into chromosomes before excision and conjugative transfer. This modular architecture creates highly efficient networks for gene capture, recombination, and dissemination, helping explain why clinically important resistance traits can move rapidly between strains and species [5], [6], [12].

The most immediate clinical consequence of this genetic connectivity is antimicrobial resistance. Resistance determinants located on MGEs can be co-selected and transferred together, allowing a single acquisition event to produce resistance to several antimicrobial classes. This mechanism helps link local antibiotic selection to broader dissemination across healthcare, community, animal, food, wastewater, and environmental compartments. Consequently, genomic surveillance should not only identify resistance genes but also determine the mobile platforms on which those genes are carried [6], [7], [8], [10].

Genomic islands represent a larger-scale form of horizontally acquired adaptation. Their atypical sequence composition, association with mobility genes, and frequent localization near integration hotspots support their role as acquired genomic modules [13], [14]. Pathogenicity, resistance, metabolic, and symbiosis islands illustrate how horizontal acquisition can alter several phenotypic functions at once, thereby influencing ecological fitness, virulence, host association, and antimicrobial response [15], [16].

The relationship between MGEs and host defence is also dynamic. CRISPR-Cas systems can restrict the entry or persistence of foreign genetic material, while mobile elements can evolve counter-defence mechanisms that permit continued transfer. This interaction creates an evolutionary balance between genome protection and genetic innovation and helps explain why MGE prevalence differs among microbial lineages and ecological niches [9].

From a methodological perspective, whole-genome sequencing, long-read sequencing, metagenomics, comparative genomics, and specialized bioinformatics are increasingly important because phenotypic resistance testing alone cannot identify the genetic vehicle responsible for dissemination. Combining genomic characterization with epidemiological metadata can improve outbreak reconstruction, source attribution, and early recognition of emerging resistance platforms [6], [8], [10], [14]. The principal limitation of the present mini-review is its narrative design: the included literature is heterogeneous in organism, setting, and analytical method, and the review does not provide a formal meta-analysis or systematic risk-of-bias assessment. These limitations should be addressed by future systematic reviews and harmonized genomic surveillance studies.

CONCLUSION

Fundamental Finding: Mobile genetic elements are major forces in microbial genome evolution because they enable rapid acquisition, rearrangement, and horizontal dissemination of genes that influence antimicrobial resistance, virulence, metabolism, stress responses, and ecological adaptation. Plasmids, transposons, insertion sequences, integrons, ICEs, bacteriophages, and genomic islands collectively form interconnected genetic networks that can move multiple adaptive determinants within and between microbial populations. **Implication:** Understanding the structure and transmission of MGEs is essential for antimicrobial-resistance control, molecular diagnostics, epidemiological surveillance, environmental monitoring, and microbial biotechnology. Integrating whole-genome sequencing, metagenomics, long-read sequencing, and bioinformatics with routine surveillance can improve the detection of emerging resistance platforms and clarify their routes of dissemination. **Limitation:** This article is a narrative mini-review based on selected literature and surveillance sources; it does not include a systematic search protocol, quantitative meta-analysis, or formal risk-of-bias assessment, and the cited studies vary in microbial species, setting, and analytical approach. **Future Research:** Future work should prioritize longitudinal and One Health genomic surveillance, standardized annotation of MGEs, long-read resolution of plasmid and integron structures, experimental measurement of transfer dynamics, and investigation of CRISPR-Cas and other host-defence systems that regulate mobile DNA. These approaches may support more precise strategies to limit the emergence and global dissemination of antimicrobial resistance.

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