
ORAL MICROBIOME RECOVERY FOLLOWING ANTIMICROBIAL EXPOSURE: A SCOPING REVIEW OF MICROBIAL RESILIENCE AND RESTORATION OF HOMEOSTASIS

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ABSTRACT

The oral microbiome is a dynamic microbial ecosystem that can be disrupted by antimicrobial exposure, resulting in changes in microbial composition, diversity, and community structure. The capacity of the oral microbiome to withstand environmental disturbances and subsequently regain ecological stability represents an important characteristic of microbial resilience and is closely related to the maintenance of oral microbial homeostasis. This scoping review aimed to map the available evidence regarding oral microbiome responses following antimicrobial exposure, with particular emphasis on microbial resilience, recovery, and restoration of homeostasis. Literature was searched through PubMed, ScienceDirect, and Google Scholar using terms related to oral microbiome, antimicrobial exposure, microbial resilience, and microbial homeostasis. Relevant literature published within the predefined period was screened according to predetermined inclusion and exclusion criteria, followed by data extraction and descriptive evidence mapping. The findings indicate that antimicrobial exposure may substantially modify oral microbial composition, diversity, community structure, and ecological interactions. Evidence from the included studies suggests that oral microbial communities possess varying degrees of resilience following microbial disturbance, with recovery influenced by the type and intensity of antimicrobial exposure, characteristics of the microbial community, and host-related ecological factors. However, the extent and completeness of recovery toward the pre-exposure state vary across microbial communities and exposure conditions. These findings highlight the importance of understanding oral microbiome resilience and recovery as key processes in the

	<i>restoration and maintenance of oral microbial homeostasis and provide a basis for further longitudinal research on strategies to preserve microbial stability following antimicrobial disturbance.</i>
KEYWORDS	Antimicrobial Exposure; Microbial Resilience; Microbial Homeostasis; Oral Microbiome
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INTRODUCTION

The oral cavity harbors a highly diverse and dynamic microbial community that continuously interacts with the host and surrounding environment. The oral microbiome consists of numerous bacterial species and other microorganisms that occupy different ecological niches, including saliva, the tongue, dental surfaces, and gingival tissues. Under healthy conditions, interactions among microbial species and between the microbiota and the host contribute to the maintenance of ecological stability and oral health. These interactions involve microbial cooperation and competition, cross-feeding, antimicrobial production, saliva, and host immune mechanisms. Therefore, the oral microbiome should not be considered a static population but rather a dynamic ecosystem whose composition and function can change in response to environmental and host-related factors. The ability of this ecosystem to maintain or regain its stability following disturbances is an important characteristic of oral microbial resilience and plays a role in preventing dysbiosis (Rosier et al.).

Antimicrobial exposure represents one of the important disturbances that may influence oral microbial ecology. Antibiotics and other antimicrobial agents can modify microbial abundance, community composition, microbial interactions, and the selection of antimicrobial resistance determinants. The magnitude and nature of these effects may depend on several factors, including the type, concentration, duration, and route of antimicrobial exposure. Evidence from an ex vivo human oral biofilm model demonstrated that even low concentrations of ampicillin could significantly alter the taxonomic profile of the oral microbial community while increasing biofilm viability. Similarly, exposure to amoxicillin in individuals undergoing third molar extraction was associated with changes in the salivary microbiome that could persist during follow-up. These findings indicate that antimicrobial exposure does not necessarily result in a simple reduction in microbial abundance. Instead, antimicrobial agents, particularly at sublethal concentrations, may produce ecological changes within microbial communities and influence the relative abundance of specific bacterial groups (Menon et al.).

The concept of microbial resilience is particularly important for understanding how the oral microbiome responds to antimicrobial exposure and other environmental disturbances. Microbial resilience refers to the capacity of a microbial ecosystem to withstand a disturbance and maintain or regain its ecological functions and community structure. The oral microbiome has been described as remarkably resilient despite exposure to various environmental influences, including dietary factors, host conditions, systemic diseases, and drug treatments. Systemic antimicrobial administration may produce relatively limited changes in the oral bacterial community compared with some other body sites, whereas locally delivered antimicrobials may exert stronger effects. The biofilm lifestyle of oral microorganisms and the ecological characteristics of the oral cavity may contribute to this resilience. However, resilience should not be interpreted as an immediate

return of every microbial component to its original condition. Following amoxicillin exposure, for example, the overall microbiome may demonstrate resilience while several microbial taxa remain altered for a prolonged period (Wade;Menon et al.).

The response and recovery of oral microbial communities following antimicrobial exposure are also influenced by interactions among microorganisms. Microbial interactions within oral communities can affect stress tolerance and susceptibility to environmental changes, including antibiotic exposure. Metabolic interactions such as cross-feeding may have context-dependent effects on microbial fitness and can, under certain conditions, increase susceptibility to antibiotics. These findings emphasize that the response of a microbial community cannot be fully understood by examining individual microorganisms independently. Instead, interactions among microorganisms and their ecological relationships contribute to the overall resilience of the community (Lewin et al.). Longitudinal evidence also demonstrates that recovery following disturbance can vary according to the type and severity of the disturbance. Oral microbial communities may recover following substantial clinical and treatment-related disturbances, although recovery is not necessarily uniform across all microbial taxa or ecological parameters (Laheij et al.).

Restoration of oral microbial homeostasis may be influenced by factors beyond antimicrobial exposure itself. Experimental gingivitis provides an example of a microbial and ecological disturbance followed by restoration of oral hygiene. Research investigating probiotics during the resolution phase of experimental gingivitis demonstrated differences in the composition of supragingival microbiota between probiotic and placebo groups. This finding supports the concept that modulation of microbial communities may influence the restoration of oral microbial homeostasis (Olsen et al.). In addition, changes following antimicrobial exposure may have implications beyond microbial diversity alone, as alterations in community structure can affect microbial functions, ecological interactions, and antimicrobial resistance. Consequently, recovery should be evaluated at multiple levels rather than only by determining whether the microbial community returns to its initial composition. A community may demonstrate resilience at the overall level while specific taxa, microbial functions, or resistance-associated characteristics remain altered (Brar et al.).

Despite increasing evidence regarding oral microbiome resilience and antimicrobial-associated microbial changes, the available evidence remains heterogeneous. Existing studies differ in the antimicrobial agents used, concentrations, exposure duration, experimental models, oral niches, microbial analysis methods, and follow-up periods. Some studies primarily investigate immediate microbial changes following antimicrobial exposure, whereas others examine longer-term recovery. Furthermore, evidence describing resistance to disturbance, recovery toward the pre-exposure state, and restoration of microbial homeostasis is distributed across experimental, clinical, and longitudinal studies. This heterogeneity makes it difficult to obtain a comprehensive understanding of how the oral microbiome responds to antimicrobial exposure and subsequently recovers. Therefore, systematic mapping of the available evidence is needed to identify patterns of microbial disruption, resilience, recovery over time, and restoration of oral microbial homeostasis. This scoping review aims to map the available evidence regarding oral microbiome recovery following antimicrobial exposure, with particular emphasis on microbial disruption, resilience, recovery, and the restoration of oral microbial homeostasis.

RESEARCH METHOD

Study Design and Research Question

This study employed a scoping review design to map the available evidence regarding oral microbiome recovery following antimicrobial exposure, with particular emphasis on microbial resilience and restoration of oral microbial homeostasis. The review was conducted based on the methodological framework of the Joanna Briggs Institute (JBI) for scoping reviews and reported according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses extension for Scoping Reviews (PRISMA-ScR) (Figure 1).

The research question was developed using the Population, Concept, and Context (PCC) framework. The population included human oral microbial communities and relevant experimental or ex vivo oral microbiome models. The concept focused on oral microbiome changes, microbial resilience, recovery, and restoration of microbial homeostasis following antimicrobial exposure. The context included oral microbial niches such as saliva, dental biofilms, supragingival and subgingival microbiota, and other relevant oral environments. The research question was: “What evidence is available regarding oral microbiome changes and recovery following antimicrobial exposure, and how do microbial resilience and restoration of microbial homeostasis vary across different exposure conditions?”

Inclusion Criteria

Studies were included if they met the following criteria: (1) original research articles published between 2016 and 2026; (2) articles published in international scientific journals; (3) articles available as free full text; (4) articles written in English; (5) studies investigating the oral microbiome, oral microbiota, or oral microbial communities; (6) studies involving antimicrobial exposure, including antibiotics or other antimicrobial agents that may cause microbial disturbance; and (7) studies reporting outcomes related to changes in microbial composition, diversity, community structure, microbial resilience, recovery, or restoration of microbial homeostasis.

Both clinical/human studies and relevant experimental or ex vivo studies were considered when they directly addressed the review question. Studies were considered particularly relevant when they included information regarding the microbial response during or after antimicrobial exposure and, where available, follow-up observations describing recovery or persistence of microbial alterations.

Exclusion Criteria

Studies were excluded if they met one or more of the following criteria: (1) published before 2016; (2) not available as free full text; (3) not written in English;

(4) not an original research article, including review articles, systematic reviews, meta-analyses, scoping reviews, editorials, commentaries, letters, conference abstracts, protocols, and opinion papers; (5) studies that did not investigate the oral microbiome or oral microbial communities; (6) studies focusing exclusively on the gut microbiome or other non-oral microbial ecosystems; and (7) studies that did not provide information relevant to antimicrobial exposure, microbial disturbance, microbial resilience, recovery, or oral microbial homeostasis.

Studies were also excluded when the relationship between the reported microbial findings and the research question could not be established from the available full-text information.

Information Sources and Search Strategy

Literature searches were conducted using three electronic databases or search platforms: PubMed, ScienceDirect, and Google Scholar. The search period was limited to publications from 2016 to 2026. The primary search strategy used the following keywords: “Oral Microbiome” AND “Antimicrobial Exposure” AND “Microbial Resilience” AND “Microbial Homeostasis.” Additional related terms were used when necessary to identify studies using alternative terminology, including oral microbiota, oral microbial community, antibiotic exposure, antimicrobial treatment, microbiome recovery, microbial recovery, resilience, dysbiosis, and homeostasis. The search was restricted to studies that met the predefined publication and accessibility criteria.

Study Selection

All records identified from PubMed, ScienceDirect, and Google Scholar were collected and compiled into a single reference pool. Duplicate records identified across the three sources were removed before screening. The remaining records were screened based on their titles and abstracts. Articles considered potentially relevant were retrieved and assessed through full-text screening.

During full-text assessment, each article was evaluated against the predefined inclusion and exclusion criteria. The assessment considered the publication year, article type, full-text availability, study population or model, oral microbial focus, antimicrobial exposure, and relevance to microbial resilience, recovery, or restoration of microbial homeostasis. Studies that did not fulfill the eligibility criteria were excluded, with the reason for exclusion recorded.

Data Charting

Data from the included studies were extracted using a structured data-charting form. The extracted information included author and publication year, study design, study population or experimental model, oral niche examined, antimicrobial agent, exposure concentration or regimen, duration of exposure, microbiome analysis method, microbial changes following exposure, follow-up period, evidence of microbial resilience, recovery pattern, and factors influencing recovery or restoration of microbial homeostasis.

Particular attention was given to whether studies reported resistance to disturbance, partial recovery, complete recovery, delayed recovery, or persistent microbial alteration following antimicrobial exposure.

Data Synthesis

The extracted evidence was synthesized descriptively and narratively. Because the included studies differed in their study designs, antimicrobial agents, exposure conditions, oral niches, microbiome analysis methods, and follow-up periods, no statistical meta-analysis was performed. The findings were organized into four major themes: (1) changes in the oral microbiome following antimicrobial exposure; (2) microbial resilience to antimicrobial disturbance; (3) patterns and duration of microbiome recovery; and (4) restoration or persistent alteration of oral microbial homeostasis. The evidence was subsequently compared across different antimicrobial exposures and study models to identify common patterns, differences, and research gaps.

RESULT AND DISCUSSION

Selection and Characteristics of Included Studies

The literature search identified studies addressing changes in the oral microbiome following antimicrobial exposure or other relevant microbial disturbances. Following the removal of duplicate records and screening according to the predefined inclusion and exclusion criteria, eligible original research studies were included in the final evidence synthesis. The selection process consisted of identification of relevant records, removal of duplicates, title and abstract screening, full-text assessment, and final inclusion. The included studies varied in study design, oral microbial niche, type of antimicrobial exposure or disturbance, microbiome analysis method, and duration of follow-up. This methodological heterogeneity allowed the present scoping review to map different aspects of oral microbiome disruption, microbial resilience, recovery, and restoration of microbial homeostasis.

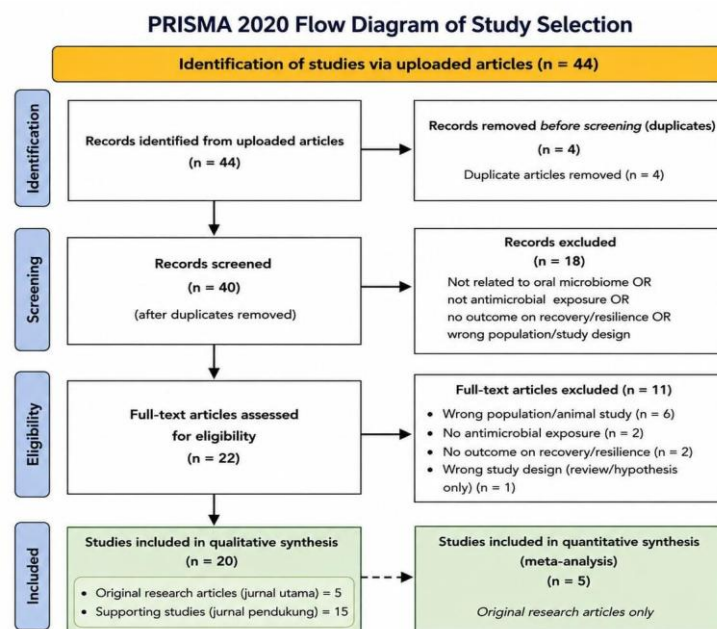


Figure 1. PRISMA 2020 Flow Diagram of the Literature Selection Process

Figure 1. The literature selection process was conducted based on the PRISMA 2020 framework. A total of 44 records were identified from the uploaded articles, of which 4 duplicate records were removed, leaving 40 records for screening. During the screening stage, 18 records were excluded because they were not related to the oral microbiome or antimicrobial exposure, did not assess recovery or resilience outcomes, or did not meet the required population or study design criteria. Subsequently, 22 full-text articles were assessed for eligibility. At this stage, 11 articles were excluded due to inappropriate population or animal study design ($n = 6$), absence of antimicrobial exposure ($n = 2$), absence of recovery or resilience outcomes ($n = 2$), and inappropriate study design ($n = 1$). The remaining studies were then considered for qualitative and quantitative synthesis according to the predefined eligibility criteria.

The characteristics of the included studies are presented in Table 1. The extracted information included study author and publication year, study design, population or experimental model, oral niche, antimicrobial exposure or disturbance, microbiome analysis method, follow-up period, and principal findings relevant to microbial resilience

and recovery. The included evidence comprised clinical longitudinal studies and experimental or ex vivo oral biofilm models, providing both clinical and mechanistic perspectives on the response of the oral microbiome to disturbance.

Table 1. Characteristics of the included original research studies

No	Study	Study Design	Oral Model	Antimicrobial or Disturbance	Main Finding	Relevance
1.	Menon et al. (2019)	Prospective Cohort	Salivary Microbiome	Amoxicillin	Changes in selected microbial groups with overall evidence of microbiome resilience during follow-up	
2.	Laheij et al. (2022)	Longitudinal clinical study	Oral Microbiome	Clinical/treatment-related disturbance	Evidence of oral microbiome resilience and recovery over time	
3.	Lewin et al. (2024)	Experimental model Main	Oral Microbial Community	Antibiotic/stress exposure	Microbial interactions influenced community stress tolerance and antibiotic response	Main
4.	Brar et al. (2024)	Ex vivo biofilm study	Human Oral Biofilm	Antibiotic/stress exposure	Antimicrobial exposure altered microbial community characteristics	Main
5.	Olsen et al. (2023)	Randomized controlled trial	Oral Microbiota	Experimental gingivitis	Oral microbial changes occurred during disturbance and resolution, demonstrating microbial resilience	Main

Table 1. Summarizes the characteristics of five included original research studies examining oral microbiome responses to antimicrobial or ecological disturbances. The studies used different designs, including prospective cohort, longitudinal clinical, experimental, ex vivo biofilm, and randomized controlled studies, with oral models involving salivary microbiome, oral microbial communities, human oral biofilm, and oral microbiota. The disturbances included amoxicillin exposure, antibiotic or stress exposure, clinical or treatment-related disturbances, and experimental gingivitis. Overall, the studies demonstrated that these disturbances could alter oral microbial communities, while the microbiome also showed varying degrees of resilience and recovery over time. Menon et al. (2019) reported changes in selected microbial groups following amoxicillin exposure, Laheij et al. (2022) demonstrated oral microbiome resilience and recovery following clinical or treatment-related disturbances, and Lewin et al. (2024) showed that microbial interactions influenced community stress tolerance and antibiotic responses. Brar et al. (2024) found that antimicrobial exposure altered microbial community characteristics in an ex vivo oral biofilm model, while Olsen et al. (2023) observed microbial changes during disturbance and resolution, supporting the presence of microbial resilience.

Changes in the Oral Microbiome Following Antimicrobial Exposure

The included evidence indicates that antimicrobial exposure can produce measurable changes in the oral microbial community, although the magnitude and persistence of these changes vary between studies. These changes may involve microbial abundance, relative

composition, community structure, biofilm characteristics, and ecological interactions between microorganisms. The findings indicate that antimicrobial exposure should therefore be considered an ecological disturbance rather than simply a process of microbial elimination. Changes in particular microbial populations may occur while the overall community retains a degree of ecological stability.

The prospective study by Menon et al. demonstrated that amoxicillin exposure was associated with changes in selected microbial groups during follow-up, while the overall salivary microbiome demonstrated evidence of resilience. This finding suggests that antimicrobial exposure may selectively influence susceptible microbial populations without necessarily causing complete disruption of the entire microbial community. The persistence of community-level stability despite taxonomic changes provides an important indication that oral microbiome resilience may operate at different ecological levels.

Experimental evidence from oral biofilm models provides additional support for the ecological effects of antimicrobial exposure. Studies examining amoxicillin and ampicillin demonstrated changes in oral biofilm characteristics and microbial composition following antimicrobial treatment. These findings suggest that the response of the oral microbiome depends not only on the antimicrobial agent but also on exposure conditions, microbial susceptibility, biofilm organization, and interactions between microbial species. Antimicrobial pressure may therefore result in selective ecological changes, with susceptible microorganisms decreasing while relatively tolerant organisms become more prominent within the community.

Microbial Resilience Following Antimicrobial Disturbance

The reviewed evidence demonstrates that the oral microbiome possesses a capacity for resilience following microbial disturbance. Microbial resilience refers to the ability of a microbial community to tolerate disturbance and maintain or regain its ecological characteristics following environmental stress. The observed resilience does not indicate that no microbial changes occur. Instead, it suggests that the community can absorb a degree of disturbance while retaining sufficient ecological organization to recover toward a more stable state.

Longitudinal clinical evidence indicates that oral microbial communities can recover following substantial clinical and treatment-related disturbances. However, recovery does not necessarily occur uniformly across all microbial taxa. Some organisms may return toward their previous abundance relatively rapidly, whereas others may remain altered for a longer period. This variation indicates that resilience is a dynamic property and that individual microorganisms may have different responses to the same disturbance. The experimental evidence further indicates that microbial interactions contribute to resilience. Interactions between oral microorganisms, including metabolic cooperation, competition, and cross-feeding, can modify the response of individual organisms to antimicrobial or environmental stress. Consequently, resilience should not be interpreted solely as a property of individual bacterial species. Rather, it represents an emergent characteristic of the microbial community and its ecological interactions.

Microbiome Recovery Following Disturbance

The findings indicate that recovery of the oral microbiome occurs as a dynamic process over time rather than as an immediate return to the pre-exposure condition. Longitudinal studies provide evidence that microbial communities can demonstrate recovery following antimicrobial or ecological disturbance, although the extent and speed of recovery differ among microbial populations and ecological characteristics. Measurements performed immediately after exposure may reflect the acute disturbance phase, whereas later observations may demonstrate partial or substantial recovery.

The study by Menon et al. provides evidence that the salivary microbiome can retain

ecological stability following amoxicillin exposure despite changes in individual microbial groups. This finding suggests that recovery may occur at the community level even when some taxonomic alterations remain detectable. Similarly, longitudinal observations following clinical disturbance indicate that oral microbial communities can demonstrate recovery over extended periods, supporting the concept that the oral microbiome is capable of restoring ecological stability after substantial perturbation.

The evidence therefore suggests that microbiome recovery should not be interpreted simply as a binary outcome of recovered or not recovered. Instead, recovery may involve gradual restoration of community structure, persistence of selected taxonomic changes, or establishment of a microbial configuration that is functionally stable but not identical to the original baseline state. This distinction is important when interpreting longitudinal oral microbiome studies.

Restoration of Oral Microbial Homeostasis

Restoration of oral microbial homeostasis represents a broader ecological outcome than the recovery of microbial abundance alone. Homeostasis involves the maintenance of balanced interactions between microorganisms and their host environment. The reviewed studies indicate that microbial composition, interspecies interactions, biofilm organization, host factors, and environmental conditions all contribute to the maintenance and restoration of oral microbial stability.

The experimental evidence demonstrates that interactions between microbial species can influence their tolerance to environmental and antimicrobial stress. Such interactions may modify microbial fitness and determine which organisms persist during and after disturbance. Therefore, restoration of homeostasis depends not only on the presence or absence of individual microorganisms but also on the restoration of ecological relationships within the microbial community.

Evidence from experimental gingivitis further demonstrates that the oral microbiome undergoes dynamic changes during both disturbance and resolution. Following the restoration of oral hygiene, microbial communities undergo restructuring as the oral environment returns toward a healthier state. This finding supports the interpretation that restoration of oral microbial homeostasis involves an active ecological transition rather than simply the disappearance of disease-associated microorganisms.

Factors Influencing Microbial Resilience and Recovery

The evidence mapped in this review indicates that microbial resilience and recovery are influenced by several characteristics of the disturbance and the surrounding ecological environment. The type, intensity, and duration of antimicrobial exposure may influence the magnitude of microbial disruption, while the initial composition and structure of the oral microbial community may determine its capacity to withstand and recover from disturbance. Microbial interactions within biofilms may also influence antimicrobial susceptibility and the persistence of specific organisms.

The host environment represents another important determinant of recovery. Saliva, nutrient availability, host immune responses, oral hygiene, and the physical structure of dental biofilms contribute to the ecological conditions experienced by oral microorganisms. These factors may provide buffering mechanisms that support microbial resilience or, under unfavorable conditions, may contribute to prolonged ecological disruption.

Time is also an essential factor in evaluating recovery. A substantial microbial alteration immediately following antimicrobial exposure does not necessarily indicate permanent dysbiosis. Conversely, apparent recovery at an early follow-up point does not necessarily demonstrate complete restoration of the original microbial state. Longitudinal

assessment is therefore required to distinguish transient disturbance from persistent ecological alteration.

Comparison of Findings Across Studies

Although the included studies differed in study design, microbial niche, antimicrobial exposure, analytical methods, and follow-up duration, several consistent patterns emerged. Antimicrobial exposure was generally associated with measurable changes in microbial composition or community structure, while the oral microbiome frequently demonstrated some degree of resilience. Recovery was variable across microbial taxa and over time, and microbial interactions appeared to influence the response to environmental and antimicrobial stress. These findings collectively indicate that oral microbiome recovery is a complex ecological process.

Table 2. Summary of major findings across the included evidence

Aspect	Findings identified across studies
Microbial disturbance	Antimicrobial exposure can alter oral microbial composition and community structure
Microbial resilience	Oral microbial communities can retain or regain ecological stability following disturbance
Recovery	Recovery varies among microbial taxa and according to follow-up duration
Microbial interactions	Interspecies interactions can modify antimicrobial response and stress tolerance
Homeostasis	Restoration involves microbial composition as well as ecological interactions and environmental conditions
Persistent alterations	Some microbial changes may remain after the major disturbance has ended

Table 2. Summarizes the major findings identified across the included evidence regarding oral microbiome responses to antimicrobial and ecological disturbances. The findings indicate that antimicrobial exposure can alter oral microbial composition and community structure, while oral microbial communities may retain or regain ecological stability through microbial resilience. Recovery was found to vary among microbial taxa and according to the duration of follow-up, suggesting that restoration may occur at different rates across the community. Microbial interactions also play an important role by modifying antimicrobial responses and tolerance to environmental stress. Furthermore, restoration of oral microbial homeostasis involves not only changes in microbial composition but also ecological interactions and environmental conditions. Despite evidence of resilience and recovery, some microbial alterations may persist even after the major disturbance has ended, indicating that recovery does not always represent a complete return to the initial microbial state.

Figure 2. Illustrates the overall response and recovery process of the oral microbiome following antimicrobial exposure. Under normal conditions, the oral microbiome maintains a state of homeostasis through balanced microbial communities. Antimicrobial exposure can disrupt this balance, leading to changes in microbial composition and community structure. Following the disturbance, the oral microbiome may exhibit microbial resilience, allowing the community to retain or gradually regain ecological stability. This process is followed by microbiome recovery, although the extent and rate of recovery may differ among microbial taxa and according to the duration of follow-up. Recovery may subsequently contribute to the restoration of oral microbial homeostasis. The final stage highlights the implications and remaining research gaps, particularly regarding the persistence of microbial alterations and the factors influencing complete recovery following antimicrobial exposure.

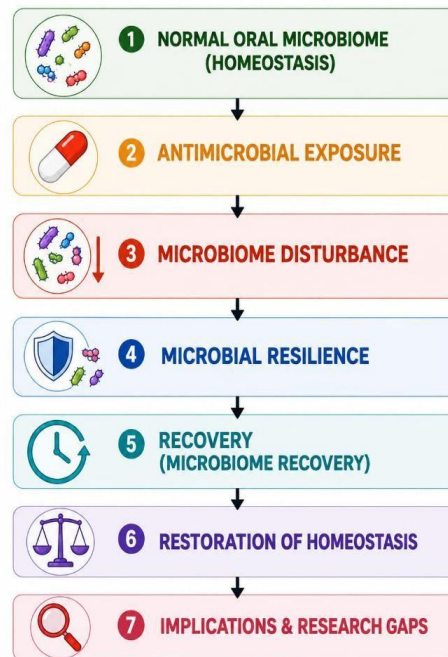


Figure 2. Oral Microbiome Response and Recovery Following Antimicrobial Exposure

Research Gaps

Despite the growing evidence regarding oral microbiome resilience, several gaps remain in the current literature. The included studies differ substantially in antimicrobial agents, exposure concentrations, treatment duration, oral niches, microbiome analysis methods, and follow-up periods. This methodological heterogeneity limits direct comparison between studies and makes it difficult to establish a universal recovery trajectory following antimicrobial exposure.

Another important gap is the limited number of studies that simultaneously evaluate the microbiome before exposure, during the disturbance phase, and throughout an adequately long recovery period. Many studies focus primarily on microbial changes following exposure, while fewer studies investigate whether those changes are temporary, persistent, or associated with the establishment of an alternative microbial state.

The available evidence also remains predominantly focused on taxonomic composition. Changes in microbial function, metabolic interactions, and antimicrobial resistance determinants may follow trajectories that differ from taxonomic recovery. Future research should therefore integrate longitudinal microbiome profiling with functional and ecological analyses to determine whether apparent microbial recovery represents true restoration of the pre-exposure state or the establishment of a different but stable microbial configuration.

Overall Discussion

The evidence indicates that the oral microbiome possesses a measurable capacity for resilience following antimicrobial and ecological disturbance. Antimicrobial exposure can modify microbial composition and community structure, but these changes do not necessarily result in permanent disruption of the oral microbial ecosystem. The ability of the community to recover appears to depend on the characteristics of the disturbance, the baseline microbial community, microbial interactions, host-related ecological conditions, and the duration of follow-up.

The findings further demonstrate that microbial resilience and complete restoration of

homeostasis should not be considered synonymous. A microbial community may regain overall ecological stability while selected taxa, microbial functions, or microbial interactions remain altered. Oral microbiome recovery should therefore be understood as a dynamic and multidimensional process involving microbial composition, community structure, ecological interactions, and host–microbe relationships. This perspective provides a more comprehensive framework for understanding the consequences of antimicrobial exposure and the mechanisms underlying restoration of oral microbial homeostasis.

CONCLUSION

The oral microbiome demonstrates a measurable capacity for resilience following antimicrobial and ecological disturbances. Antimicrobial exposure can alter microbial composition, diversity, community structure, and microbial interactions; however, these changes do not necessarily result in permanent disruption of the oral microbial ecosystem. The reviewed evidence indicates that recovery occurs dynamically over time and may vary according to the type, intensity, and duration of antimicrobial exposure, the characteristics of the initial microbial community, host-related ecological factors, and microbial interactions. Recovery should therefore not be interpreted solely as a return to the exact pre-exposure microbial composition, as some microbial taxa or ecological features may remain altered despite the restoration of overall community stability. Overall, oral microbiome resilience and recovery are important processes in maintaining and restoring oral microbial homeostasis. Further longitudinal and mechanistic studies are needed to clarify the trajectories of microbiome recovery, the persistence of antimicrobial-associated alterations, and strategies to support the restoration of a stable and health-associated oral microbial ecosystem.

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