One Health Microbiology & Infection

OPEN ACCESS

eISSN:3054-5161

Opinion article

Biofilms in human and veterinary infections: a central link in One Health frameworks

Tiziano A. Schweizer[1]

[1]Department of Cranio-Maxillo-Facial and Oral Surgery, University Hospital Zurich, University of Zurich, Zurich, Switzerland

***Corresponding author**: Tiziano A. Schweizer, tiziano.schweizer@usz.ch

Article history: Received 1 July 2026; Accepted 27 July 2026; Available online 2 August 2026

Article information: Schweizer TA, 2026. *One Health Microbiol. Infect*. Vol. 2, No. 1: 101-109. https://doi.org/10.66585/ohmi.2026.2.0021

Abstract

Antimicrobial resistance (AMR) is widely recognized as a One Health (OH) challenge requiring coordinated action across the human, veterinary, and environmental sectors. However, current frameworks primarily focus on antimicrobial use, transmission pathways, and resistant organisms, while largely overlooking the ecological source from which resistance develops. Biofilms, the predominant lifestyle of many clinically relevant microorganisms, represent such a source. Their extracellular matrix and phenotypic heterogeneity contribute to antimicrobial tolerance, while their spatial arrangement facilitates horizontal gene transfer, making biofilms reservoirs for AMR evolution. Biofilm-associated infections are common in both human and veterinary medicine, including surgical site infections (SSIs), chronic wounds, periodontal disease, and device-related infections. Despite similarities in causative pathogens, infection biology, antimicrobial exposure, and clinical management, these infections are largely investigated independently. Opportunities to identify shared biological mechanisms and develop cross-sector preventive, diagnostic, and therapeutic strategies remain unexplored. This opinion article proposes to implement the OH biofilm framework, recognizing biofilms as shared ecological and evolutionary entities across human and veterinary medicine. SSIs and periodontitis are used as illustrative examples to demonstrate the similarities between the two sectors. Integrating biofilm biology into OH surveillance, research, prevention, diagnostics, and antimicrobial stewardship may provide a more mechanistic and effective framework for combating AMR.

Keywords: Antimicrobial resistance, Biofilms, Healthcare-associated infections, Human healthcare, Medical devices, One Health, Veterinary medicine

Introduction

Antimicrobial resistance (AMR) is widely recognized as one of the most prominent global health threats, requiring coordinated action across the human, animal, and environmental sectors under the umbrella of the One Health (OH) framework. Over the past decade, the OH framework has highlighted the relationship between these different sectors, with respect to antimicrobial use and AMR development. This has helped to significantly improve awareness of the interconnectedness of antimicrobial use in clinical medicine, veterinary practice, and agriculture. However, despite this substantial progress and changing of perspectives, current OH strategies to combat the spread of AMR remain too narrowly focused, centering on antimicrobial prescription and use patterns, isolation and characterization of resistant pathogens, and transmission routes within and between defined sectors [1, 2]. While this conceptual thinking has proven valuable, it implies that resistance is primarily an attributable property of individual microbial strains moving between hosts and sectors, thereby neglecting a fundamental biological reality of infections. Specifically, the fact that most clinically relevant microorganisms do not cause infections in a state of single planktonic cells, but rather in the form of aggregates or biofilms [3]. These aggregates represent highly organized and structured microbial ecosystems (Figure 1). They are surrounded by an extracellular matrix layer, which confers protection against host immune responses, antimicrobial therapy, and disinfectants [4, 5]. In addition, profound changes in gene and protein expression, among others, occurring within the biofilm aggregate community further promote physiological adaptations that enhance antimicrobial tolerance and facilitate the emergence of resistance towards antimicrobial treatment [6, 7].

In both human and veterinary medicine, biofilm-associated infections are not the exception, but rather the prominent form of chronic and recurrent infections [8]. Common examples in humans as well as animals include catheter-associated urinary tract infections, orthopedic infections with or without implant involvement, mastitis, periodontal disease, and chronic wound infections. Despite their prevalence, biofilms are frequently regarded as a complication rather than a potential reservoir for the development of AMR, or at least tolerance towards antimicrobials [9, 10]. This concept has recently been developed within the OH framework and termed One Biofilm by Jacques and Malouin [11]. In contrast to conventional OH approaches, which primarily emphasize resistant microorganisms and their transmission, the one biofilm concept proposes that biofilm formation might be a conserved feature of microorganisms and also pose the unique trait linking AMR development across all the OH sectors. Indeed, biofilm formation enables long-term survival of microorganisms under sustained antimicrobial or disinfectant pressure. Furthermore, the biofilm environment favors the emergence of tolerant or persistent phenotypes, which are less susceptible to

antimicrobials but may also not be detected by standard culture-based surveillance approaches as easily as planktonic bacteria [12]. This might lead to an underestimation of the true epidemiological significance of biofilm formation in the context of AMR and persistent, as well as recurrent infections.

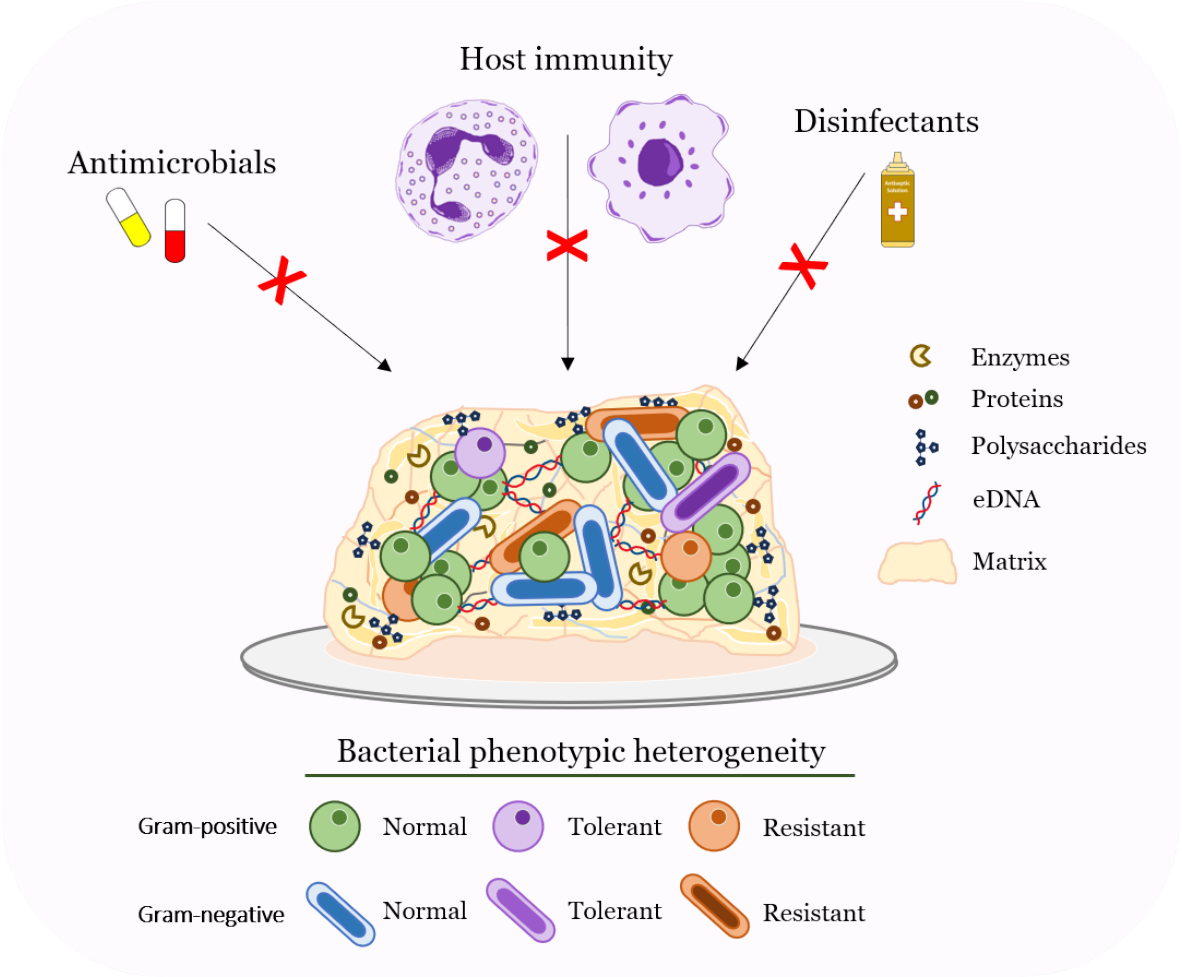

Figure 1: Conceptual model depicting polymicrobial biofilm aggregate formation as a protective strategy of bacteria against antimicrobials, host immune response, and disinfectants. Protection is governed by direct physical properties of the biofilm matrix itself, but also by diverse phenotypic heterogeneity which arises within the biofilm, such as the emergence of tolerant (persistent) and resistant bacteria.

Although the similarities between human and veterinary biofilm-associated infections are increasingly evident, these conditions are rarely investigated in a comparative manner to identify shared biological mechanisms, or regarded as equivalent models for the development of preventive and therapeutic strategies. Both sectors rely on similar technologies, such as indwelling medical devices, orthopedic or dental implants, intensive care interventions, and invasive diagnostic procedures. All of which can create an ideal environment for biofilm formation and AMR development. The OH framework has led to the successful integration of antimicrobial stewardship in humans and animals as well as zoonotic disease surveillance across sectors. However, the notion that biofilm formation is a common trait across the human and veterinary sectors and that it might be among the main drivers of AMR development has mostly been neglected. Hence, the OH framework and the goal of curbing AMR development would benefit greatly from interdisciplinary collaborations and initiatives that bring human and veterinary medicine closer together. Closer integration of human and veterinary biofilm research therefore offers a unique opportunity to identify shared mechanisms of biofilm formation, persistence, and resistance development. Such interdisciplinary collaboration could generate broadly applicable preventive, diagnostic, and therapeutic strategies and provide a critical missing component in current OH approaches to combating AMR.

Surgical site infections associated with implants

Across both human and veterinary medicine, the most clinically significant biofilm-associated infections are closely linked to the increasing use of indwelling medical devices and implanted materials. In human healthcare, well-recognized examples include catheter-associated urinary tract infections [13], central line-associated

bloodstream infections [14], ventilator-associated pneumonia [15], and surgical site infections (SSIs) associated with prosthetic joints (peri-prosthetic joint infection [16]), fixation devices for fractures (fracture fixation-related infection [17]), cardiovascular (e.g., pacemaker endocarditis [18] or vascular graft infections [19]), and dental implants (peri-implantitis [20]). These infections are difficult to treat due to biofilm formation in the vicinity of foreign body material, often necessitating surgical intervention for successful disease management. Importantly, similar clinical scenarios are increasingly encountered in veterinary medicine, particularly in companion animals, such as dogs and cats, and in horses [21, 22]. These animals are more frequently undergoing procedures involving fracture fixation with plates and screws, orthopedic joint replacement implants [23], urinary catheters [24], central venous catheters [25], and intensive care support [26]. All of these are scenarios that can provide favorable conditions for infections associated with biofilm formation [27]. Importantly, in both human and veterinary medicine, it is postulated that the vast majority of SSIs are caused by bacteria colonizing the patient's skin or mucosal surfaces, or from the surgical team [27, 28, 29]. Furthermore, these infections in animals share remarkable similarities in both their clinical presentation and microbial etiology. While the Gram-positive, non-motile, coccoid bacterium *Staphylococcus aureus* (*S. aureus*) is a leading cause of SSIs in humans, the closely related *Staphylococcus pseudintermedius* (*S. pseudintermedius*) is the primary cause of SSIs in companion animals, especially dogs and cats [30, 31, 32]. Both can colonize their respective host and active colonization status is a risk factor for infection. Of note, while cases documenting infections of *S. pseudintermedius* in humans exist (although they are rare), *S. aureus* infections in companion animals are reported more frequently [33]. These observations underscore the importance of bidirectional transmission between humans and companion animals, but instead of the usual, expected direction from animals to humans, it matters in the opposite direction, from humans to animals, as well.

Beyond the similar patterns underlying colonization, the two pathogens also share common traits in terms of biofilm formation (Figure 2). Surface-associated adhesins, including fibronectin-binding proteins (FnBPA and FnBPB), clumping factors (ClfA and ClfB), and the collagen adhesin (Cna), facilitate initial attachment and biofilm formation in *S. aureus* [34, 35], while homologous surface proteins such as the staphylococcal proteins SpsD, SpsL, and SpSO mediate adhesion in *S. pseudintermedius* [36, 37, 38]. Regarding biofilm matrix formation, both organisms produce extracellular matrix components, including the polysaccharide intercellular adhesin (PIA), synthesized by the icaADBC operon; extracellular DNA (eDNA); and surface-associated proteins such as Bap and SasG or their homologues, which facilitate intercellular adhesion and biofilm matrix stability [39, 40, 41]. Both pathobionts also produce coagulase (Coa), which promotes fibrin deposition within the biofilm matrix [42, 43].

Additional virulence factors are also highly conserved between the two species, such as α-hemolysin (Hla) and β-hemolysin (Hlb) [44, 45, 46]. Regarding bicomponent leukocidins, *S. aureus* is well known to produce a wide array of them (PVL, LukAB, LukED, HlgAB, HlgCB, LukMF', LukPQ) [47], while for *S. pseudintermedius*, a PVL homologue, termed Luk-I (consisting of LukS-I and LukF-I), has been described [38, 39], which similarly targets host leukocytes. Both organisms also produce extracellular proteases and lipases that facilitate tissue invasion, nutrient acquisition, and biofilm remodeling. Immune evasion is further mediated by protein A (SpA) in *S. aureus* and the protein A homologue SpsQ in *S. pseudintermedius* [48]. The emergence of methicillin-resistant lineages, namely methicillin-resistant *S. aureus* and methicillin-resistant *S. pseudintermedius*, largely associated with acquisition of the *mecA* gene, delivers further evidence for shared evolutionary traits between human and veterinary medicine [49, 50].

Periodontal infections

Periodontitis is among the most prevalent types of infections in both human and veterinary medicine [51, 52]. Its development is consistently associated with the establishment of complex, multispecies biofilms that cause inflammation of the gingiva and the underlying jaw bone, irrespective of the host species [53]. In humans, periodontitis is associated with a dysbiotic shift in the oral microbiome that favors anaerobic and proteolytic bacteria capable of inducing inflammation and tissue destruction [54]. Species such as *Porphyromonas gingivalis* (*P. gingivalis*), *Tannerella forsythia*, *Treponema denticola*, *Fusobacterium nucleatum*, *Prevotella intermedia*, and *Aggregatibacter actinomycetemcomitans* have long been recognized as major contributors to periodontal inflammation [55]. The formation of polymicrobial biofilms with complex microbial networks promotes persistence, immune evasion, and progressive destruction of periodontal tissues.

Periodontitis in companion animals is characterized by the accumulation of structured biofilms containing predominantly anaerobic bacterial populations [52]. Especially in dogs, it is highly prevalent and affects up to 80% of dogs over three years of age [56]. Several bacterial taxa commonly associated with veterinary periodontal disease belong to the same genera that are implicated in human periodontitis, including *Porphyromonas* spp., *Bacteroides* spp., *Prevotella* spp., *Actinomyces* spp., and *Tannerella* spp. [57]. Among these organisms,

Porphyromonas gulae (*P. gulae*) has received considerable attention because of its high prevalence and close phylogenetic relationship to the human counterpart, *P. gingivalis* [58].

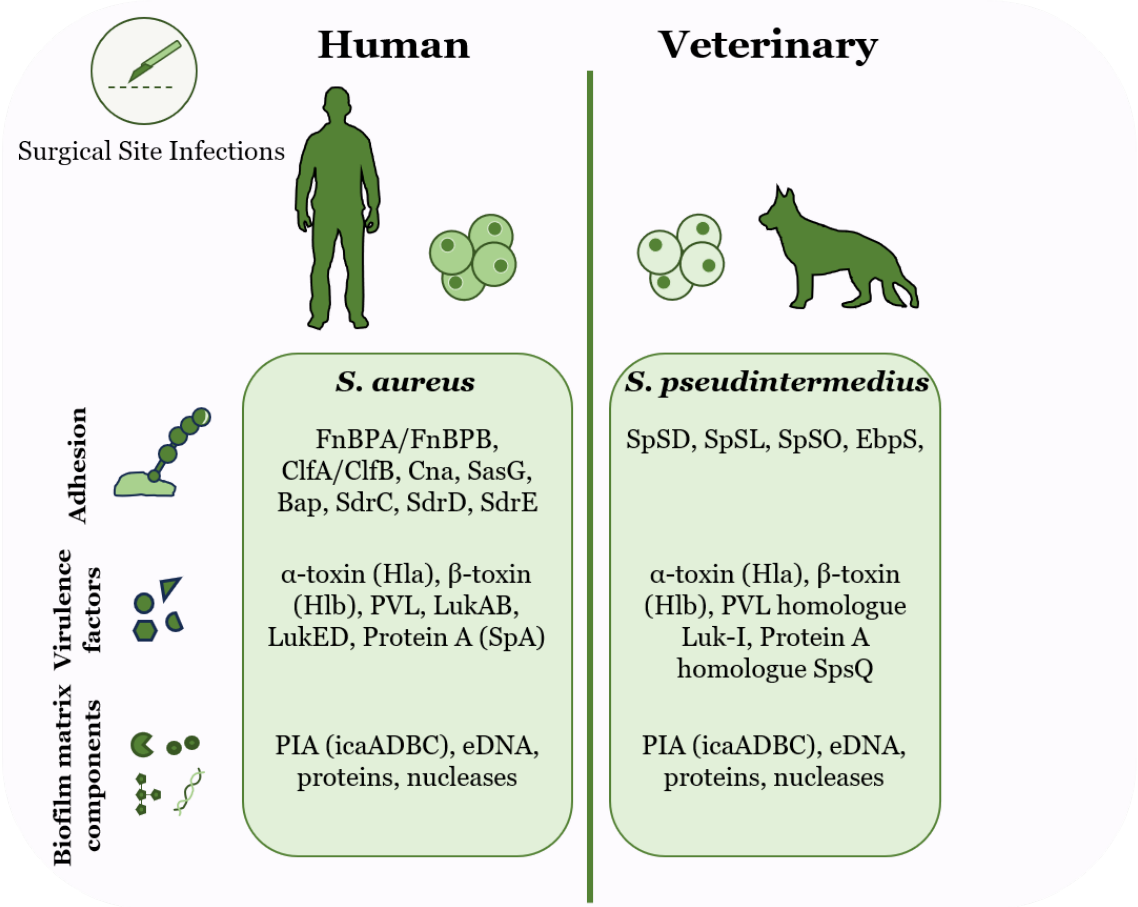

Figure 2: Comparison of virulence traits and mechanisms of *S. aureus* and *S. pseudintermedius*, involved in human and veterinary SSIs, respectively. Note: No direct evidence for the presence and functionality of all the listed proteins in *S. pseudintermedius* exists. Instead, some of them are inferred from gene presence analysis.

A shared virulence trait of the Gram-negative, non-motile, anaerobic bacteria is the expression of fimbrial structures that mediate adhesion to host tissues, extracellular matrix proteins, and neighboring microorganisms (Figure 3). In *P. gingivalis*, the major fimbria is FimA, encoded by the *fim* gene cluster, consisting of *fimA*, *fimB*, *fimC*, *fimD*, and *fimE*, and the minor fimbria is Mfa1, encoded by the *mfa* cluster, consisting of *mfa1*, *mfa2*, *mfa3*, *mfa4*, and *mfa5* [59]. In *P. gulae*, homologous fimbrial genes, especially various *fimA* genotypes (type A, type B and type C), have been described as well as homologues of the mfa operon (*mfa1* and *mfa2*) [60, 61, 62], suggesting similar mechanisms of adhesion and biofilm development between the human and veterinary isolates. In addition, both produce gingipains, a family of cysteine proteases. In *P. gingivalis*, the arginine-specific proteases RgpA and RgpB and the lysine-specific protease Kgp are major virulence factors involved in the degradation of host proteins, acquisition of nutrients, tissue invasion, and modulation of immune responses [63]. Proteolytic activity resembling the gingipain system of *P. gingivalis*, including Kgp-like and Rgp-like enzymes, has been described in *P. gulae*, although these virulence determinants remain less extensively characterized [64, 65].

The persistence of infection and inflammation in both *P. gingivalis* and *P. gulae* is further supported by biofilm formation and the production of extracellular biofilm matrix components. In *P. gingivalis*, biofilm architecture is stabilized by proteins, eDNA, polysaccharides, lipids, and outer membrane vesicles (OMVs) [66]. OMVs represent particularly important virulence factors. In *P. gingivalis*, OMVs contain numerous bioactive molecules, including gingipains, lipopolysaccharides (LPS), adhesins, and hemin-binding proteins, which facilitate nutrient acquisition, tissue invasion, and modulation of host immune responses [67]. Although considerably less studied than *P. gingivalis*, available evidence suggests that *P. gulae* produces extracellular matrix components, including eDNA, proteins, and OMV-like structures, that contribute to biofilm development and persistence [68].

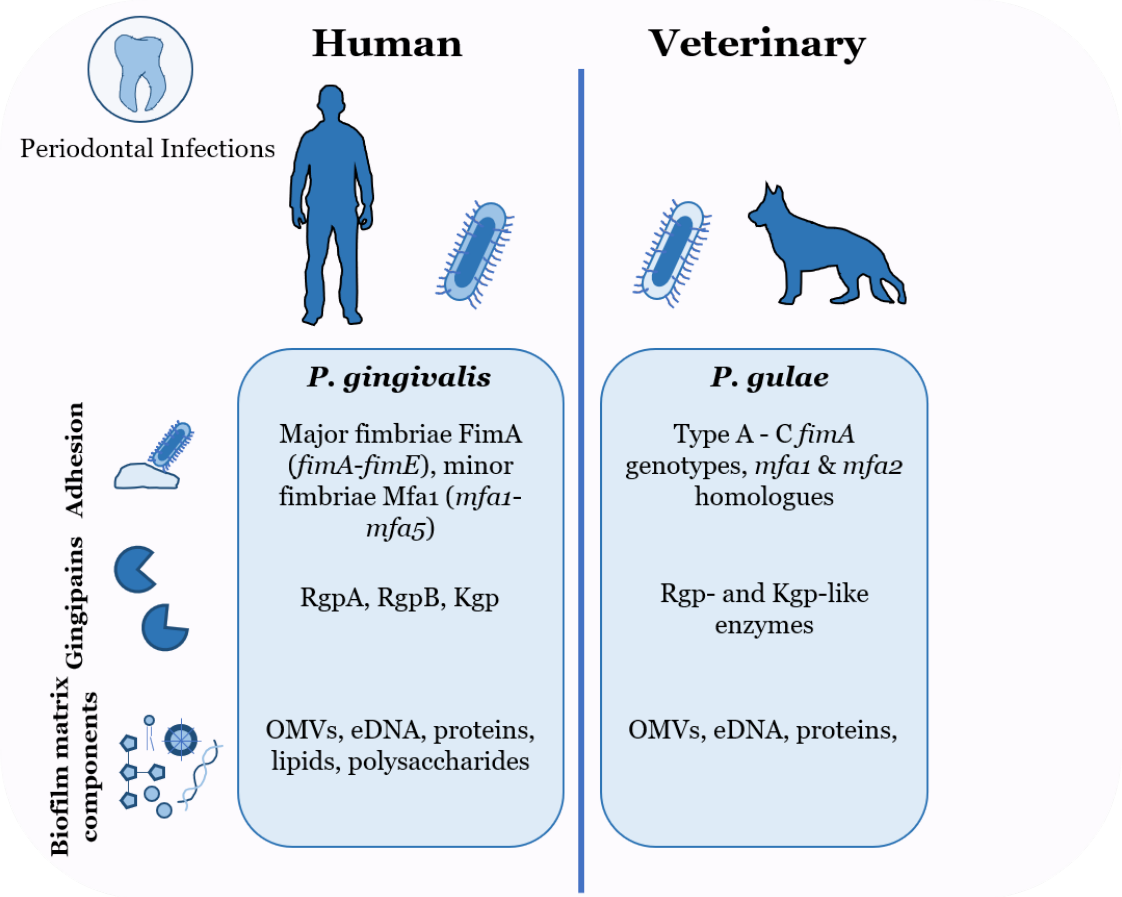

Figure 3: Comparison of virulence traits and mechanisms of *P. gingivalis* and *P. gulae*, involved in human and veterinary periodontitis, respectively. Note: Evidence for *P. gulae* stems from various sources, such as genomic, proteomic, experimental (functional), and biochemical analyses.

Both species possess additional strategies to evade or manipulate host immunity. The atypical LPS of *P. gingivalis* differentially activates Toll-like receptors (TLRs), particularly TLR2 and TLR4, leading to altered inflammatory signaling [69, 70, 71]. In addition, gingipains degrade complement components such as C3 and C5, impair neutrophil function, and dysregulate cytokine production [72]. Regarding *P. gulae*, surface-associated LPS may likewise influence innate immune signaling by modulating cytokine responses. Experimental studies in canine periodontal disease models have reported increased expression of pro-inflammatory mediators, including interleukin-1β, interleukin-6, and tumor necrosis factor-α, in association with *P. gulae* colonization and biofilm formation [73, 74, 75]. Although less extensively described than in *P. gingivalis,* these findings highlight additional shared characteristics between the two Gram-negative bacteria across human and veterinary medicine.

Biofilms as reservoirs for AMR development

Biofilms employ multiple complementary mechanisms that collectively reduce the efficacy of antimicrobial agents. The extracellular polymeric matrix acts as both a physical and chemical barrier that impedes antibiotic penetration [76]. Within the biofilm architecture, gradients of oxygen, nutrients, and waste products generate physiologically distinct subpopulations of bacteria, many of which adopt slow-growing or metabolically altered states [77]. Because most antibiotics target actively dividing cells, this reduced metabolic activity significantly enhances tolerance. In addition, biofilm-associated bacteria frequently upregulate stress response pathways, including the upregulation of drug efflux pumps, which further enhance survival under antimicrobial pressure [78]. Collectively, these features result in a phenotype of antimicrobial tolerance rather than classical resistance, enabling bacterial communities to withstand treatment without necessarily acquiring specific resistance-conferring mutations, thereby promoting persistent infection, clinical relapse, and chronic colonization. Importantly, prolonged survival under antimicrobial pressure favors the emergence of genetic AMR through spontaneous mutation [79]. Once AMR has emerged, horizontal gene transfer promotes its dissemination throughout the biofilm community [80]. The close spatial proximity of microbial cells within the biofilm, combined with the accumulation of eDNA and OMVs, facilitates the transfer of plasmids, integrons, transposons, and other mobile genetic elements [81].

Importantly, biofilm-associated AMR evolution is not restricted to single-species communities but also occurs within polymicrobial biofilms, where resistance determinants can be exchanged between commensal and pathogenic bacteria, thereby contributing to the expansion of the microbial resistome [82].

Discussion: towards implementation of the One Biofilm framework

Despite growing recognition of AMR as an OH priority, current frameworks conceptualize AMR through the transmission of pathogens, resistance genes, and antimicrobial compounds across the human, animal, and environmental sectors. While valuable, this perspective remains incomplete because it underrepresents an ecological and structural foundation from which AMR emerges, evolves, and persists: biofilms. Biofilms are not mere consequences of infection dynamics but represent the predominant lifestyle of many clinically relevant microorganisms and a central mechanism underlying persistence, tolerance, and horizontal gene transfer, all of which contribute to AMR development. This necessitates a conceptual shift toward implementing the One Biofilm framework [11]. In the One Biofilm framework, AMR is reframed not solely as the spread of resistant organisms, but as an emergent property of interconnected biofilm ecosystems spanning human and veterinary healthcare systems. Within this framework, hospitals, veterinary clinics, and associated infrastructures are functionally analogous nodes within a broader network of biofilm habitats shaped by shared selective pressures, including antimicrobial exposure, disinfectant use, invasive medical devices, surgical interventions, and immunocompromised hosts. Similar biofilm-driven ecological and evolutionary processes operate across both sectors, supporting a "study one for two" principle, where insights from one system are likely transferable to the other. Across both human and veterinary medicine, biofilms underlie many of the most clinically significant infections, including SSIs, chronic wounds, and periodontal disease. While the biofilm matrix acts as a physical and chemical barrier, biofilm formation further promotes drug tolerance and resistance development through close spatial organization, enhanced horizontal gene transfer, and prolonged microbial persistence, which can result in persistent and recurring infections linked to AMR.

A key limitation of current OH AMR strategies is that surveillance primarily targets planktonic isolates, thereby underestimating the contribution of biofilm-associated bacteria, which often display distinct phenotypic tolerance and genotypic resistance profiles. This extended framework therefore advocates incorporating biofilm-focused sampling from high-risk reservoirs such as indwelling medical devices, surgical sites, chronic wounds, and oral biofilms, in both human and veterinary settings. This would provide a more accurate representation of the resistome circulating within healthcare ecosystems and its potential connection to biofilm formation. Effective implementation also requires harmonized, cross-sectoral biofilm research. Standardized methodologies for assessing biofilm formation, antimicrobial tolerance and AMR development are needed to enable meaningful comparisons between human and veterinary studies. This also facilitates identification of shared mechanisms of persistence and AMR evolution. Such harmonization would strengthen the evidence base for interventions and support translational applications across host and bacterial species.

A coordinated OH response must also extend beyond the conventional antimicrobial stewardship program to include targeted anti-biofilm strategies. These can include surface modification of medical devices, quorum sensing interference, enzymatic matrix degradation, bacteriophage therapy, and localized antimicrobial delivery systems. In addition, prevention strategies aimed at reducing the colonizing pathobiont reservoir, either in patients themselves or the hospital staff, should also be prioritized. The same applies to novel diagnostic approaches aimed at identifying biofilm-associated infections more accurately. Crucially, healthcare environments themselves, such as water and ventilation systems [83, 84], should be recognized as active ecosystems harboring biofilms with the potential to spread AMR within the clinical setting. This could shift infection control from solely interrupting transmission to actively modifying ecological conditions that support biofilm establishment and persistence.

Importantly, the herein presented viewpoint is merely intended to provide a conceptual perspective rather than a review or quantitative synthesis of the available evidence. The two chosen examples, SSIs and periodontitis, were selected to illustrate the similarities between human and veterinary biofilm-associated infections and should not be interpreted as encompassing the full diversity of biofilm-associated infections across sectors. Although the representative pathogens *S. aureus*, *S. pseudintermedius*, *P. gingivalis,* and *P. gulae* share conserved virulence mechanisms and traits, including biofilm formation and similarities in the composition of the biofilm matrix, species-specific differences undoubtedly exist and should not be neglected.

In conclusion, integrating biofilm biology into OH thinking through the One Biofilm framework might provide an additional perspective to more fully address the global challenge posed by AMR. Without recognizing biofilms as central ecological and evolutionary entities, current strategies risk targeting only the visible fraction of resistance while leaving intact the underlying systems that sustain it, hidden in plain sight. The One Biofilm

framework, applied to the human and veterinary medical sectors, therefore provides a first step toward the necessary expansion of the AMR paradigm, offering a unified, mechanism-based approach to understanding and mitigating AMR across human and veterinary medicine. The proposed extension of the One Biofilm framework is not intended to imply that biofilm-associated infections are identical across sectors, but rather that they are comparable to justify integrated investigation. Future studies should systematically evaluate the extent to which biofilm biology, antimicrobial tolerance, and resistance evolution are conserved across human and veterinary settings, and determine whether biofilm-targeted prevention, diagnostic, and therapeutic strategies can be translated between sectors.

Declarations and supplementary information

Acknowledgments: Not applicable.

Author contributions: Not applicable.

Funding source: This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Conflict of interest statement: The author declares no conflict of interest.

Ethics statement: Not applicable.

Data availability: Not applicable.

Supplementary materials: Not applicable.

Declaration regarding the use of generative AI and AI-assisted technologies in the writing process: ChatGPT was used to structure the topics in this opinion article as well as for grammar and spell check.

Publisher's note: The claims, opinions, and data presented in this manuscript are solely those of the authors and do not necessarily reflect the views of Infinity IPC, its editors, or reviewers. Infinity IPC and the editors disclaim any responsibility for damages, injuries, or other consequences that may arise from the use of the information contained in this article.

References

1. James R, Hardefeldt LY, Ierano C, Charani E, Dowson L, Elkins S, et al. Antimicrobial stewardship from a One Health perspective. Nat Rev Microbiol. 2026;24(2):146-162. https://doi.org/10.1038/s41579-025-01233-3
2. Velazquez-Meza ME, Galarde-López M, Carrillo-Quiróz B, Alpuche-Aranda CM. Antimicrobial resistance: One Health approach. Vet World. 2022;15(3):743-749. https://doi.org/10.14202/vetworld.2022.743-749
3. Domouchtsidou A, Ioannou P, Lianou A, Tsante KA, Tsakri D, Bonova E, et al. Biofilms in clinical infection: Pathophysiology, diagnosis, and the evolving therapeutic landscape. J Clin Microbiol. 2026;64(3):e01042-25. https://doi.org/10.1128/jcm.01042-25
4. Ragupathi H, Pushparaj MM, Gopi SM, Govindarajan DK, Kandaswamy K. Biofilm matrix: A multifaceted layer of biomolecules and a defensive barrier against antimicrobials. Arch Microbiol. 2024;206(11):432. https://doi.org/10.1007/s00203-024-04157-3
5. Hendricks AL, More KR, Devaraj A, Buzzo JR, Robledo-Avila FH, Partida-Sanchez S, et al. Bacterial biofilm-derived H-NS protein acts as a defense against neutrophil extracellular traps (NETs). npj Biofilms Microbiomes. 2025;11(1):58. https://doi.org/10.1038/s41522-025-00691-0
6. Banas JA, Miller JD, Fuschino ME, Hazlett KR, Toyofuku W, Porter KA, et al. Evidence that accumulation of mutants in a biofilm reflects natural selection rather than stress-induced adaptive mutation. Appl Environ Microbiol. 2007;73(1):357-361. https://doi.org/10.1128/AEM.02014-06
7. Usui M, Yoshii Y, Thiriet-Rupert S, Ghigo J-M, Beloin C. Intermittent antibiotic treatment of bacterial biofilms favors the rapid evolution of resistance. Commun Biol. 2023;6(1):275. https://doi.org/10.1038/s42003-023-04601-y
8. Grari O, Ezrari S, El Yandouzi I, Benaissa E, Ben Lahlou Y, Lahmer M, et al. A comprehensive review on biofilm-associated infections: Mechanisms, diagnostic challenges, and innovative therapeutic strategies. Microbe. 2025;8:100436. https://doi.org/10.1016/j.microb.2025.100436
9. Liu HY, Prentice EL, Webber MA. Mechanisms of antimicrobial resistance in biofilms. npj Antimicrob Resist. 2024;2(1):27. https://doi.org/10.1038/s44259-024-00046-3
10. Yaki LM. Bacterial biofilms and antimicrobial resistance: A global threat. Discov Bact. 2026;3(1):15. https://doi.org/10.1007/s44351-025-00035-5
11. Jacques M, Malouin F. One Health-One Biofilm. Vet Res. 2022;53(1):51. https://doi.org/10.1186/s13567-022-01067-4
12. Kim J-S, Chowdhury N, Yamasaki R, Wood TK. Viable but non-culturable and persistence describe the same bacterial stress state. Environ Microbiol. 2018;20(6):2038-2048. https://doi.org/10.1111/1462-2920.14075
13. Werneburg GT. Catheter-associated urinary tract infections: Current challenges and future prospects. Res Rep Urol. 2022;14:109-133. https://doi.org/10.2147/RRU.S273663
14. Yu Y, Li X, Ouyang B, Fang W, Hu B, Liu F, et al. Practice guideline on the prevention and treatment of central line-associated bloodstream infection: Part 1-diagnosis and prevention. J Intensive Med. 2026;6(2):83-92. https://doi.org/10.1016/j.jointm.2025.10.008
15. Díez-Madroñero CC, Moreno BR, Urrutia-Royo B, Muñoz IG, Iribarren ME, Álvarez CP, et al. Nosocomial and ventilator-associated pneumonia. Open Respir Arch. 2025;7(4):100488. https://doi.org/10.1016/j.opresp.2025.100488
16. Patel R. Periprosthetic joint infection. N Engl J Med. 2023;388(3):251-262. https://doi.org/10.1056/nejmra2203477
17. Moriarty TF, Metsemakers WJ, Morgenstern M, Hofstee MI, Vallejo Diaz A, Cassat JE, et al. Fracture-related infection. Nat Rev Dis Primers. 2022;8(1):67. https://doi.org/10.1038/s41572-022-00396-0
18. De Silva K, Fife A, Murgatroyd F, Gall N. Pacemaker endocarditis: An important clinical entity. BMJ Case Rep. 2009;2009. https://doi.org/10.1136/bcr.02.2009.1608
19. Hasse B, Husmann L, Zinkernagel A, Weber R, Lachat M, Mayer D. Vascular graft infections. Swiss Med Wkly. 2013;143:w13754. https://doi.org/10.4414/smw.2013.13754
20. Rokaya D, Srimaneepong V, Wisitrasameewon W, Humagain M, Thunyakitpisal P. Peri-implantitis update: Risk indicators, diagnosis, and treatment. Eur J Dent. 2020;14(4):672-682. https://doi.org/10.1055/s-0040-1715779
21. Faccin M, Wiener DJ, Rech RR, Santoro D, Rodrigues Hoffmann A. Common superficial and deep cutaneous bacterial infections in domestic animals: A review. Vet Pathol. 2023;60(6):796-811. https://doi.org/10.1177/03009858231176558
22. Wei AY, Thompson MF, Worthing KA, Venturini C, Brookes VJ, Norris JM. Frequency and antimicrobial susceptibility profiles of bacterial species isolated from canine and feline urine samples in Sydney, Australia, 2012-2021. Vet Microbiol. 2025;306:110541. https://doi.org/10.1016/j.vetmic.2025.110541
23. Thomas C, Amsellem P, Nascene D, Huang YH. Orthopedic applications of 3D printing in canine veterinary medicine. Front Vet

Sci. 2025;12:1582720. https://doi.org/10.3389/fvets.2025.1582720

24. Aponrat P, Detkalaya O, Phlongtong N, Eksatit N, Kananub S, Kaewmongkol S, et al. Hospital-acquired catheter-associated urinary tract infections in critical care unit dogs with high rates of multidrug-resistant organisms. Open Vet J. 2025;15(1):339-347. https://doi.org/10.5455/OVJ.2025.v15.i1.32
25. Bach A, Just A, Berthold H, Ehmke H, Kirchheim H, Borneff-Lipp M, et al. Catheter-related infections in long-term catheterized dogs. Observations on pathogenesis, diagnostic methods, and antibiotic lock technique. Zentralbl Bakteriol. 1998;288(4):541-552. https://doi.org/10.1016/S0934-8840(98)80074-1
26. Ruple-Czerniak A, Aceto HW, Bender JB, Paradis MR, Shaw SP, Van Metre DC, et al. Using syndromic surveillance to estimate baseline rates for healthcare-associated infections in critical care units of small animal referral hospitals. J Vet Intern Med. 2013;27(6):1392-1399. https://doi.org/10.1111/jvim.12190
27. Nelson LL. Surgical site infections in small animal surgery. Vet Clin North Am Small Anim Pract. 2011;41(5):1041-1056, viii. https://doi.org/10.1016/j.cvsm.2011.05.010
28. Guarch-Pérez C, Riool M, de Boer L, Kloen P, Zaat SAJ. Bacterial reservoir in deeper skin is a potential source for surgical site and biomaterial-associated infections. J Hosp Infect. 2023;140:62-71. https://doi.org/10.1016/j.jhin.2023.07.014
29. Cheung GYC, Otto M. Virulence Mechanisms of staphylococcal animal pathogens. Int J Mol Sci. 2023;24(19):14587. https://doi.org/10.3390/ijms241914587
30. Lynch SA, Helbig KJ. The complex diseases of *Staphylococcus pseudintermedius* in canines: Where to next? Vet Sci. 2021;8(1):11. https://doi.org/10.3390/vetsci8010011
31. Khaled AAE-R, Abouelhag HA. Bridging the infected defect: Modern strategies for canine fracture-related osteomyelitis. Ricos Biol. 2026;4(4):10-14. https://doi.org/10.33687/ricosbiol.04.04.114
32. Bibby HL, Brown KL. Identification of *Staphylococcus pseudintermedius* isolates from wound cultures by matrix-assisted laser desorption ionization-time of flight mass spectrometry improves accuracy of susceptibility reporting at an increase in cost. J Clin Microbiol. 2021;59(11):e00973-21. https://doi.org/10.1128/jcm.00973-21
33. Costa SS, Ribeiro R, Serrano M, Oliveira K, Ferreira C, Leal M, et al. *Staphylococcus aureus* causing skin and soft tissue infections in companion animals: Antimicrobial resistance profiles and clonal lineages. Antibiotics. 2022;11(5):599. https://doi.org/10.3390/antibiotics11050599
34. Bannoehr J, Brown JK, Shaw DJ, Fitzgerald RJ, van den Broek AH, Thoday KL. *Staphylococcus pseudintermedius* surface proteins SpsD and SpsO mediate adherence to ex vivo canine corneocytes. Vet Dermatol. 2012;23(2):119-124, e26. https://doi.org/10.1111/j.1365-3164.2011.01021.x
35. Viela F, Mathelié-Guinlet M, Pietrocola G, Speziale P, Dufrêne YF. The molecular complex between Staphylococcal adhesin SpsD and fibronectin sustains mechanical forces in the nanonewton range. mBio. 2020;11(4):e00371-20. https://doi.org/10.1128/mbio.00371-20
36. Geoghegan JA, Smith EJ, Speziale P, Foster TJ. *Staphylococcus pseudintermedius* expresses surface proteins that closely resemble those from *Staphylococcus aureus*. Vet Microbiol. 2009;138(3-4):345-352. https://doi.org/10.1016/j.vetmic.2009.03.030
37. Paul NC, Latronico F, Moodley A, Nielsen SS, Damborg P, Guardabassi L. In vitro adherence of *Staphylococcus pseudintermedius* to canine corneocytes is influenced by colonization status of corneocyte donors. Vet Res. 2013;44(1):52. https://doi.org/10.1186/1297-9716-44-52
38. Branford I, Butaye P, Khine NO, Chapwanya A, Toka FN. The dynamic interplay between *Staphylococcus pseudintermedius* and canine immunity: Mechanisms of pathogenesis, evasion, and vaccination perspectives. Front Cell Infect Microbiol. 2026;16:1812880. https://doi.org/10.3389/fcimb.2026.1812880
39. Teixeira IM, de Moraes Assumpção Y, Paletta ACC, Antunes M, da Silva IT, Jaeger LH, et al. Investigation on biofilm composition and virulence traits of *S. pseudintermedius* isolated from infected and colonized dogs. Braz J Microbiol. 2024;55(3):2923-2936. https://doi.org/10.1007/s42770-024-01405-y
40. Wang Z, Guo L, Li J, Cui L, Dong J, Meng X, et al. Antibiotic resistance, biofilm formation, and virulence factors of isolates of *Staphylococcus pseudintermedius* from healthy dogs and dogs with keratitis. Front Vet Sci. 2022;9:903633. https://doi.org/10.3389/fvets.2022.903633
41. Idrees M, Sawant S, Karodia N, Rahman A. *Staphylococcus aureus* Biofilm: Morphology, genetics, pathogenesis and treatment strategies. Int J Environ Res Public Health. 2021;18(14):7602. https://doi.org/10.3390/ijerph18147602
42. Devriese LA, Vancanneyt M, Baele M, Vaneechoutte M, De Graef E, Snauwaert C, et al. *Staphylococcus pseudintermedius* sp. nov., a coagulase-positive species from animals. Int J Syst Evol Microbiol. 2005;55(Pt 4):1569-1573. https://doi.org/10.1099/ijs.0.63413-0
43. McAdow M, Missiakas DM, Schneewind O. *Staphylococcus aureus* secretes coagulase and von Willebrand factor binding protein to modify the coagulation cascade and establish host infections. J Innate Immun. 2012;4(2):141-148. https://doi.org/10.1159/000333447
44. Kmieciak W, Szewczyk EM, Ciszewski M. Searching for Beta-haemolysin hlb gene in *Staphylococcus pseudintermedius* with species-specific primers. Curr Microbiol. 2016;73(1):148-152. https://doi.org/10.1007/s00284-016-1038-4
45. Carroll KC, Burnham CD, Westblade LF. From canines to humans: Clinical importance of *Staphylococcus pseudintermedius*. PLoS Pathog. 2021;17(12):e1009961. https://doi.org/10.1371/journal.ppat.1009961
46. Vandenesch F, Lina G, Henry T. *Staphylococcus aureus* hemolysins, bi-component leukocidins, and cytolytic peptides: A redundant arsenal of membrane-damaging virulence factors? Front Cell Infect Microbiol. 2012;2:12. https://doi.org/10.3389/fcimb.2012.00012
47. Yoong P, Torres VJ. The effects of *Staphylococcus aureus* leukotoxins on the host: Cell lysis and beyond. Curr Opin Microbiol. 2013;16(1):63-69. https://doi.org/10.1016/j.mib.2013.01.012
48. Balachandran M, Bemis DA, Kania SA. Expression and function of protein A in *Staphylococcus pseudintermedius*. Virulence. 2018;9(1):390-401. https://doi.org/10.1080/21505594.2017.1403710
49. Nocera FP, De Martino L. Methicillin-resistant *Staphylococcus pseudintermedius*: Epidemiological changes, antibiotic resistance, and alternative therapeutic strategies. Vet Res Commun. 2024;48(6):3505-3515. https://doi.org/10.1007/s11259-024-10508-8
50. Abebe AA, Birhanu AG. Methicillin-resistant *Staphylococcus aureus*: Molecular mechanisms underlying drug resistance development and novel strategies to combat. Infect Drug Resist. 2023;16:7641-7662. https://doi.org/10.2147/IDR.S428103
51. Hashim NT, Babiker R, Padmanabhan V, Ahmed AT, Chaitanya NCSK, Mohammed R, et al. The global burden of periodontal disease: A narrative review on unveiling socioeconomic and health challenges. Int J Environ Res Public Health. 2025;22(4):624. https://doi.org/10.3390/ijerph22040624
52. Hendy E, Behery AE, Gomaa M, Abd El Raouf M, Ezzeldein SA. Overview of periodontal disease in Dogs and Cats. J Vet Dent. 2026;43(4):332-341. https://doi.org/10.1177/08987564261424349
53. Łasica A, Golec P, Laskus A, Zalewska M, Gędaj M, Popowska M. Periodontitis: Etiology, conventional treatments, and emerging bacteriophage and predatory bacteria therapies. Front Microbiol. 2024;15:1469414. https://doi.org/10.3389/fmicb.2024.1469414

54. Berezow AB, Darveau RP. Microbial shift and periodontitis. Periodontol 2000. 2011;55(1):36-47. https://doi.org/10.1111/j.1600-0757.2010.00350.x
55. Belibasakis GN, Belstrøm D, Eick S, Gursoy UK, Johansson A, Könönen E. Periodontal microbiology and microbial etiology of periodontal diseases: Historical concepts and contemporary perspectives. Periodontol 2000. 2023;00:1-17. https://doi.org/10.1111/prd.12473
56. Cunha E, Tavares L, Oliveira M. Revisiting periodontal disease in dogs: How to manage this new old problem? Antibiotics. 2022;11(12):1729. https://doi.org/10.3390/antibiotics11121729
57. Šakarnytė L, Mockeliūnas R, Šiugždinienė R, Merkevičienė L, Virgailis M, Dailidavičienė J, et al. Microbial composition of extracted dental alveoli in dogs with advanced periodontitis. Microorganisms. 2024;12(7):1455. https://doi.org/10.3390/microorganisms12071455
58. Bai Y, Song P, Shen Z, Shi H, Jiang Z, Lin J, et al. *Porphyromonas gulae* infection in canines, pet owners and veterinarians in China: An epidemiological study and risk factor analysis. One Health Adv. 2023;1(1):9. https://doi.org/10.1186/s44280-023-00007-x
59. Enersen M, Nakano K, Amano A. *Porphyromonas gingivalis* fimbriae. J Oral Microbiol. 2013;5:20265. https://doi.org/10.3402/jom.v5i0.20265
60. Yoshida S, Inaba H, Nomura R, Nakano K, Matsumoto-Nakano M. Role of fimbriae variations in *Porphyromonas gulae* biofilm formation. J Oral Biosci. 2024;66(4):28-33. https://doi.org/10.1016/j.job.2024.08.003
61. Oishi Y, Watanabe K, Kumada H, Ishikawa E, Hamada N. Purification and characterization of a novel secondary fimbrial protein from *Porphyromonas gulae*. J Oral Microbiol. 2012;4:19076. https://doi.org/10.3402/jom.v4i0.19076
62. Fujiwara-Takahashi K, Watanabe T, Shimogishi M, Shibasaki M, Umeda M, Izumi Y, et al. Phylogenetic diversity in fim and mfa gene clusters between *Porphyromonas gingivalis* and *Porphyromonas gulae*, as a potential cause of host specificity. J Oral Microbiol. 2020;12(1):1775333. https://doi.org/10.1080/20002297.2020.1775333
63. Li N, Collyer CA. Gingipains from *Porphyromonas gingivalis* - Complex domain structures confer diverse functions. Eur J Microbiol Immunol (Bp). 2011;1(1):41-58. https://doi.org/10.1556/EuJMI.1.2011.1.7
64. Pedrosa ME, Martin V, Fernandes MH, Gomes PS. Gingipain inhibitors as an innovative therapy for periodontal and associated systemic diseases: A systematic review. Clin Oral Investig. 2025;29(9):418. https://doi.org/10.1007/s00784-025-06472-5
65. Morales-Olavarría M, Nuñez-Belmar J, González D, Vicencio E, Rivas-Pardo JA, Cortez C, et al. Phylogenomic analysis of the *Porphyromonas gingivalis-Porphyromonas gulae* duo: Approaches to the origin of periodontitis. Front Microbiol. 2023;14:1226166. https://doi.org/10.3389/fmicb.2023.1226166
66. Gerits E, Verstraeten N, Michiels J. New approaches to combat *Porphyromonas gingivalis* biofilms. J Oral Microbiol. 2017;9(1):1300366. https://doi.org/10.1080/20002297.2017.1300366
67. Okamura H, Hirota K, Yoshida K, Weng Y, He Y, Shiotsu N, et al. Outer membrane vesicles of *Porphyromonas gingivalis*: Novel communication tool and strategy. Jpn Dent Sci Rev. 2021;57:138-146. https://doi.org/10.1016/j.jdsr.2021.07.003
68. Lambertz J, Buhl EM, Apel C, Preisinger C, Conrads G. *Porphyromonas gingivalis* bundled fimbriae interact with outer membrane vesicles, commensals and fibroblasts. Int J Mol Sci. 2026;27(1):383. https://doi.org/10.3390/ijms27010383
69. Wang PL, Ohura K. *Porphyromonas gingivalis* lipopolysaccharide signaling in gingival fibroblasts-CD14 and Toll-like receptors. Crit Rev Oral Biol Med. 2002;13(2):132-142. https://doi.org/10.1177/154411130201300204
70. Nativel B, Couret D, Giraud P, Meilhac O, d'Hellencourt CL, Viranaïcken W, et al. *Porphyromonas gingivalis* lipopolysaccharides act exclusively through TLR4 with a resilience between mouse and human. Sci Rep. 2017;7:15789. https://doi.org/10.1038/s41598-017-16190-y
71. Zhang D, Chen L, Li S, Gu Z, Yan J. Lipopolysaccharide (LPS) of *Porphyromonas gingivalis* induces IL-1β, TNF-α and IL-6 production by THP-1 cells in a way different from that of *Escherichia coli* LPS. Innate Immun. 2008;14(2):99-107. https://doi.org/10.1177/1753425907088244
72. Wingrove JA, DiScipio RG, Chen Z, Potempa J, Travis J, Hugli TE. Activation of complement components C3 and C5 by a cysteine proteinase (gingipain-1) from *Porphyromonas (Bacteroides) gingivalis*. J Biol Chem. 1992;267(26):18902-18907. https://doi.org/10.1016/S0021-9258(19)37046-2
73. Inaba H, Yoshida S, Nomura R, Kato Y, Asai F, Nakano K, et al. *Porphyromonas gulae* lipopolysaccharide elicits inflammatory responses through toll-like receptor 2 and 4 in human gingivalis epithelial cells. Cell Microbiol. 2020;22(12):e13254. https://doi.org/10.1111/cmi.13254
74. Nomura R, Inaba H, Yasuda H, Shirai M, Kato Y, Murakami M, et al. Inhibition of *Porphyromonas gulae* and periodontal disease in dogs by a combination of clindamycin and interferon alpha. Sci Rep. 2020;10(1):3113. https://doi.org/10.1038/s41598-020-59730-9
75. Fukuyama T, Shirahata S, Miura T, Odajima K, Kobayashi T, Kawata R, et al. Cetylpyridinium chloride and platinum nanoparticles effects in dogs with *Porphyromonas gulae*-infected periodontal disease. Vet Res Commun. 2026;50(1):26. https://doi.org/10.1007/s11259-025-10945-z
76. Flemming H-C, Wingender J. The biofilm matrix. Nat Rev Microbiol. 2010;8(9):623-633. https://doi.org/10.1038/nrmicro2415
77. Conlon BP, Rowe SE, Lewis K. Persister cells in biofilm associated infections. Adv Exp Med Biol. 2015;831:1-9. https://doi.org/10.1007/978-3-319-09782-4_1
78. Alav I, Sutton JM, Rahman KM. Role of bacterial efflux pumps in biofilm formation. J Antimicrob Chemother. 2018;73(8):2003-2020. https://doi.org/10.1093/jac/dky042
79. Santi I, Manfredi P, Maffei E, Egli A, Jenal U. Evolution of antibiotic tolerance shapes resistance development in chronic *Pseudomonas aeruginosa* infections. mBio. 2021;12(1):e03482-20. https://doi.org/10.1128/mbio.03482-20
80. Michaelis C, Grohmann E. Horizontal gene transfer of antibiotic resistance genes in biofilms. Antibiotics. 2023;12(2):328. https://doi.org/10.3390/antibiotics12020328
81. France MT, Cornea A, Kehlet-Delgado H, Forney LJ. Spatial structure facilitates the accumulation and persistence of antibiotic-resistant mutants in biofilms. Evol Appl. 2019;12(3):498-507. https://doi.org/10.1111/eva.12728
82. Manoharan-Basil SS, González N, Laumen JGE, Kenyon C. Horizontal gene transfer of fluoroquinolone resistance-conferring genes from commensal *Neisseria* to *Neisseria gonorrhoeae*: A global phylogenetic analysis of 20,047 isolates. Front Microbiol. 2022;13:793612. https://doi.org/10.3389/fmicb.2022.793612
83. Nahum Y, Muhvich J, Morones-Ramirez JR, Casillas-Vega NG, Zaman MH. Biofilms as potential reservoirs of antimicrobial resistance in vulnerable settings. Front Public Health. 2025;13:1568463. https://doi.org/10.3389/fpubh.2025.1568463
84. Flores-Vargas G, Bergsveinson J, Lawrence JR, Korber DR. Environmental biofilms as reservoirs for antimicrobial resistance. Front Microbiol. 2021;12:766242. https://doi.org/10.3389/fmicb.2021.766242