Quorum sensing and biofilm formation in Streptococcal infections

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Members of the bacterial genus Streptococcus are responsible for causing a wide variety of infections in humans. Many Streptococci use quorum-sensing systems to regulate several physiological properties, including the ability to incorporate foreign DNA, tolerate acid, form biofilms, and become virulent. These quorum-sensing systems are primarily made of small soluble signal peptides that are detected by neighboring cells via a histidine kinase/response regulator pair.


Streptococcal infections

Members of the genus Streptococcus (i.e., streptococci) are ubiquitous parasites of humans. Some are part of the indigenous microflora that are involved in opportunistic infections such as dental caries and others are exogenous pathogens that cause infections ranging from mild respiratory or skin diseases to life-threatening conditions such as pneumonia, septic shock, and necrotizing fasciitis. Contemporary research has found that many species of streptococci and other Gram-positive bacteria have evolved similar peptide pheromone quorum-sensing systems that probably help them adapt to and survive host-imposed fluctuations in their local environment and coincidentally regulate the expression of virulence factors that promote their pathogenicity. This review focuses on streptococcal peptide signaling pathways that are population density-dependent and that impact on vital survival and virulence traits.

Biofilms

Biofilms are dense aggregates of surface-adherent microorganisms embedded in an exopolysaccharide matrix. The study of bacteria residing in biofilms as an interactive community rather than free-living planktonic cells has recently gained a great deal of attention. This has arisen, in part, because of the estimate by the Centers for Disease Control and Prevention that 65% of human bacterial infections involve biofilms. Many species of streptococci are known to form biofilms; however, the relationship between the pathogenic state and the biofilm mode of growth has been most clearly established with the oral streptococci, which are known to initiate dental caries when the bacteria are living in the biofilm environment of dental plaque.

Dental plaque

The human oral cavity is a complex ecosystem that supports an extremely diverse microflora consisting of about 500 species of microorganisms (1). Numerous physical and nutritional interactions between oral bacteria contribute to a complex biofilm community (Figure 1) (2). Streptococci, including Streptococcus mutans, are ubiquitous in the oral microbiota of humans. S. mutans is considered to be a principal etiological agent of dental caries, where it can cause dissolution of tooth enamel by acid end-products resulting from carbohydrate metabolism. The tooth surface is an indispensable natural habitat for S. mutans (3). S. mutans’ dental biofilm tropism most likely reflects its evolution of glucan synthesis and binding functions as well as its relative aciduricity. Its competitiveness for this ecological niche may also relate to cell density-dependent regulation of its acid tolerance response (ATR), natural genetic competence, and bacteriocin activity. Since S. mutans has evolved to depend on a biofilm lifestyle for survival and persistence in the oral cavity combined with its role as an opportunistic pathogen, it has become the best-studied example of a biofilm-forming, disease-causing Streptococcus (4). Biofilm-like populations of pathogenic streptococci may also reach higher densities in confined areas like heart valves, prosthetic devices, sinuses, tonsillar crypts, terminal respiratory passages, and in infectious skin lesions.
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**ComX gene** is regulated by ComE, the response regulator of the quorum-sensing system (10). The ComX sigma factor then initiates the transcription of competence-specific operons involved in DNA uptake and recombination by recognizing a **com-box** (also referred to as *cin-box*) consensus sequence (TACGAATA) in their promoter regions (9). *S. mutans* and *S. pyogenes* also have **comX** genes present in their genomes (9, 11), and inactivation of one copy of the **com** renders the cell transformation deficient (12). The presence of the conserved **com-box** consensus sequence in the promoter region of *S. mutans* late-competence genes such as **comFA**, **celA**, and **cglA** supports the hypothesis that transcriptional regulation of these genes is also mediated by the ComX sigma factor (13). There is much accumulating evidence that many genes not involved in competence are under the control of the CSP-ComX system. This includes the observations that many “other” *S. pneumoniae* genes contain the **com-box** sequence and are activated by CSP (14, 15). These genes likely encode products that aid in the cell’s adaptation to a high cell density, and it is likely that they (or their homologs in other streptococci) contribute to the biofilm phenotype.

**LuxS quorum sensing**

Recently, the luxS gene has been identified in streptococci (16, 17). The LuxS protein is required for the biosynthesis of the type 2 autoinducer, AI-2, which is involved in quorum sensing in a wide range of bacterial species. Mutation of luxS in *S. mutans* caused a defect in biofilm formation, while disruption of this gene in *S. pneumoniae* resulted in reduced virulence in mouse infections. It has been suggested that the AI-2 pathway is a very good target for chemotherapeutic control of bacterial virulence.

**Quorum sensing in S. mutans biofilms**

Horizontal gene transfer through genetic transformation has been observed in many natural ecosystems, and recent studies suggest that growth of bacteria in biofilms may facilitate horizontal gene transfer among bacterial species via either transformation or conjugation (18, 19). Natural genetic transformation has been extensively studied in streptococci, but these studies relied exclusively on bacteria grown in fluid cultures, where they would become transiently competent after reaching a critical cell density. Since biofilms are more representative of bacterial growth in natural environments and *S. mutans* is an organism that relies on a biofilm lifestyle, we set forth to investigate the ability of this bacterium to transport and integrate exogenous DNA when living in its biofilm state. To facilitate assays for genetic transformation of biofilm-grown cells, we utilized a chemostat-based continuous flow biofilm system, which allows observation of physiological activities of a bacterial population under controlled growth conditions (20). Using this system, we have demonstrated that growth rates, culture pH, and biofilm age are several important factors that influence competence development of *S. mutans* growing in biofilms.

**Evidence for the existence of other CSP-modulated pathways**

It has been recently recognized that the quorum-sensing signal in *S. pneumoniae* initiates competence through the activity of a global transcription modulator, ComX, which acts as an alternate sigma factor during the development of genetic competence (9). Transcription of the **comX** gene is regulated by ComE, the response regulator of the quorum-sensing system (10). The ComX sigma factor then initiates the transcription of competence-specific operons involved in DNA uptake and recombination by recognizing a **com-box** (also referred to as **cin-box** consensus sequence (TACGAATA) in their promoter regions (9). *S. mutans* and *S. pyogenes* also have **comX** genes present in their genomes (9, 11), and inactivation of one copy of the **com** renders the cell transformation deficient (12). The presence of the conserved **com-box** consensus sequence in the promoter region of *S. mutans* late-competence genes such as **comFA**, **celA**, and **cglA** supports the hypothesis that transcriptional regulation of these genes is also mediated by the ComX sigma factor (13). There is much accumulating evidence that many genes not involved in competence are under the control of the CSP-ComX system. This includes the observations that many “other” *S. pneumoniae* genes contain the **com-box** sequence and are activated by CSP (14, 15). These genes likely encode products that aid in the cell’s adaptation to a high cell density, and it is likely that they (or their homologs in other streptococci) contribute to the biofilm phenotype.

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The most fascinating finding using this system was that *S. mutans* cells growing in biofilms were able to incorporate foreign DNA much more efficiently than their free-living counterparts. The transformation frequencies of biofilm-grown cells of *S. mutans* strains tested were about 10- to 600-fold higher than those of the planktonic cells (20). To our best knowledge, this is the first report to provide direct evidence that biofilm-grown bacteria can be efficiently induced to become genetically competent for transformation. In addition, *S. mutans* grown in a biofilm appeared to maintain a subpopulation of cells that were constantly competent for taking up DNA from the environment. This static state of competence is in contrast to that observed in fluid where most streptococci, including *S. mutans*, enter a transient physiological state that usually lasts for only 15–30 minutes during their growth cycle. The evidence from our study and another recent study that demonstrated genetic exchange in *S. pneumoniae* biofilms (21) clearly suggests that biofilm-growth mode in transformable streptococci appears to favor the induction and maintenance of genetic competence. It also appears that the biofilm environment provides conditions for optimal function of streptococcal cell-cell peptide signaling systems to activate genetic competence and facilitate genetic exchange.

**Quorum sensing in biofilm formation**

The discovery that the *S. mutans* quorum-sensing system functions optimally in growing biofilms led us to investigate other roles of this system in biofilm formation and biofilm physiology. Dental plaque is a complex biofilm community that harbors the most diverse resident microflora associated with humans. Bacteria in dental biofilms, including *S. mutans*, are frequently exposed to various stresses, such as extreme nutrient shortage or excess, low pH, high osmolarity, oxidation, and consumption of antimicrobial agents or antibiotics by the host. Formation of a biofilm is considered an important mechanism used by a bacterium for adaptation to this environment (22). Although adaptation to environmental stress by genetic transformation is believed to occur very infrequently, such a rare event can be highly significant if the transforming DNA, such as an antibiotic resistance gene or a virulence factor, provides a selective advantage to the recipient cells (23). In addition to providing the community with an abundant extracellular gene pool, the biofilm environment facilitates the bacteria with a localized neighborhood where cell-cell signaling mechanisms likely abound.

Recent studies using genetic dissection of biofilm development have revealed that the formation of biofilms involves multiple, convergent signaling pathways and a genetic program for the transition from planktonic growth state to the biofilm mode of growth (24). In Gram negative bacteria such as *Pseudomonas aeruginosa*, cell-cell signaling through quorum sensing has been found to play an important role in biofilm differentiation (25). The first evidence to suggest that quorum-sensing systems might influence the structure of Gram positive biofilms came from a recent study of *S. gordonii* where a biofilm-defective mutant was found to have a transposon insertion in the *comD* gene encoding the histidine kinase sensor protein of the TCSTS required for genetic competence (26). This implied that biofilm formation by *S. gordonii* involved cell-cell communication through quorum sensing. To test if the...
S. mutans ComCDE quorum-sensing system was involved in biofilm formation, we examined the ability of S. mutans mutants defective in various components of the system to form biofilms. We found that inactivation of any one of the genes encoding the components of the quorum-sensing signaling system results in the formation of an abnormal biofilm (Figure 3) (12). Particularly, the comC mutant (unable to produce or secrete the signal peptide) formed a biofilm that lacked the wild-type architecture, whereas the comD and comE mutants defective in sensing and responding to the signal peptide formed biofilms with a reduced biomass. The architectural change in the comC mutant biofilms may be associated with a defect in cell separation with mutations in this gene resulting in the formation of large aggregates or “weblike” biofilms that were easily removed from the surface. The observation that the mutants unable to produce or secrete the CSP formed biofilms that differed from those formed by the mutant defective in the comD or comE genes suggested that S. mutans has multiple CSP receptors. Although we have clearly demonstrated that the ComCDE quorum-sensing system is directly connected to the ability of S. mutans to form biofilms, the molecular and biochemical mechanisms involved in expression of the “wild-type biofilm phenotype” remain to be investigated.

**CSP modulation of the ATR**

The pH levels in dental biofilms are highly variable and frequently shift from above pH 7.0 in the resting pH state to as low as pH 3.0 during the ingestion of dietary carbohydrates by the host. Thus, pH exerts a significant ecological pressure on S. mutans, and its ability to tolerate and grow in low pH environments is crucial to its survival and eventual dominance in dental plaque, leading to caries (27). Considerable evidence has shown that S. mutans has evolved a number of sophisticated mechanisms to survive these pH changes including induction of an ATR in which exposure of S. mutans cells to a mild or moderately acidic pH (5.0–6.0) results in enhanced survival of a significant proportion of the cell population in a lower pH of 3.0–3.5 (28). This ATR involves a number of de novo proteins that appear to be important for adaptation to an acidic environment (29). Although many of the molecular mechanisms of the ATR in S. mutans remain unclear, this “signal pH” that results in synthesis of protective proteins appears to be important for induction of the ATR.

It is widely accepted that bacteria living in biofilms are more resistant to mechanical, physical, and chemical stresses. Since S. mutans normally resides in high cell density biofilms, the ability to withstand acid in this physiological state is likely an important adaptive response. We therefore addressed the question of whether acid adaptation involved cell density–dependent events or cell-cell signaling in biofilms. Changes in external pH can significantly influence many physiological parameters, such as energy coupling, ion transport, proton movement, and export of metabolic products, thereby triggering numerous secondary signals. During growth at pH 5.0, *Escherichia coli* can signal stress tolerance to other unadapted cells by secreting a proteinlike molecule, termed extracellular induction component (EIC) (30). Although the signal molecule remains unidentified, induction of stress (including acid) adaptation in *E. coli* presumably involves cell-cell communication. Since S. mutans normally encounters acid while living in dense biofilm communities, we proposed that quorum sensing at high cell densities of S. mutans might facilitate its survival against low pH challenges. Testing this hypothesis has led us to find that the ATR interfaces with the density-dependent signaling pathway that also initiates genetic competence. We have demonstrated that mutants defective in the comC, D, or E genes have a diminished log-phase ATR and the neutralized culture filtrates prepared from acid-adapted wild-type cells also induce a partial log-phase ATR in cells that have never encountered the signal pH (31). S. mutans grown at high cell density established adaptation to the signal pH more rapidly than cells grown at low density. Similarly, S. mutans cells grown in a high cell-density biofilm were more resistant to the killing pH than planktonic-phase cells. In fact, S. mutans cells grown in biofilms not only survived better than the planktonic cells but also were capable of growth at the lower pH following a glucose pulse. Based on the evidence obtained from this work, we propose that S. mutans, upon exposure to low pH in a growing culture, releases extracellular signal molecules, one of which is the CSP, to enhance induction of acid adaptation in the population. It is likely that optimal induction of acid adaptation in a population of S. mutans requires a coordinated activity through mechanisms involving both low pH induction and cell density–dependent intercellular signals.
Biofilms likely provide bacterial cells with a unique environment to fully express their adaptive survival mechanisms. Because of three-dimensional structures, high cell density, and diffusion barriers, bacterial cells at different locations within a biofilm may not sense the same degree of extracellular stress simultaneously. The cells that first sense a pH stress may rapidly process the information and pass their “secondary signal” to the other members of the population through cell-cell signaling systems to initiate a coordinated protective response against potentially lethal forces, like acid. Unlike some planktonic cells that need to reach a critical concentration of signal molecules and cell density, biofilms can allow signal molecules to accumulate rapidly in the local environment to initiate coordinated activities far more quickly (25). In addition, physiological states of bacterial cells living in a biofilm, in terms of growth rate, growth phase, or metabolic activities, are heterogeneous; this allows the cells to respond to stress in different ways. Apparently, biofilm populations have several advantages over their free-living counterparts since the cells have more time, a sufficient concentration of signal molecules, and high population density to adapt to stress relative to planktonic cells. The high cell density biofilms may provide a unique environment for induction of acid adaptation via quorum sensing in S. mutans. It is likely that the S. mutans quorum-sensing signaling pathway is significant for the ATR to intersect with the regulatory networks initiating genetic competence as well as a switch to the “biofilm phenotype.”

The ComC signal peptide may activate more than one signal transduction pathway

Our previous study revealed that an S. mutans comC mutant unable to produce CSP formed a biofilm that differed from that formed by the mutant defective in the comD or comE genes suggested that there might be a second receptor that also responded to the CSP but activated a different pathway in order to invoke the phenotype (12, 20). Based on the available information, we have proposed a “two-receptor” cell-cell signaling model to illustrate how the quorum-sensing system in S. mutans functions to regulate genetic competence, biofilm formation, and the ATR (12). The principle of this model is that the signal peptide (CSP) encoded by comC can simultaneously interact with two cognate receptors, one encoded by comD and another encoded by an unknown gene. These receptors likely transfer the input signal through two different pathways. Although the genes encoding the components involved in the second transduction pathway remain unknown, the work in our lab has recently characterized another TCSTS, named HK/RR11, which is also demonstrated to involve biofilm formation and acid resistance in S. mutans (32).

One of the defects observed in HK/RR11 mutant biofilms was the development of a sponglike architecture composed of cells in very long chains, a feature that we previously observed with the biofilm formed by the comC mutant unable to produce CSP. Since there is no putative substrate, signal or function assigned for the HK/RR11 transduction system, we suspected that the TCSTS encoded by bk/rr11 may activate a second pathway to respond to the CSP. To test this hypothesis, we added CSP to the HK/RR11 mutant cultures to assess the effect on chain formation by the bk11 and rr11 mutant biofilm cells. The results revealed that addition of CSP to the mutant cultures had no observable impact on the length of cell chains comprising the mutant biofilms. This result was consistent with HK11 acting as a CSP receptor but provided no direct evidence to conclusively assign a role to HK11 as a CSP receptor. A study for characterizing the relationship between the comC-encoded signal peptide and the HK/RR11 signal transduction pathway is now underway.

Evaluation of CSP analogs to act as inhibitors of biofilm formation

Analogs of quorum-sensing peptides can competitively inhibit the activity of the peptide-mediated phenotype. It has been demonstrated that analogous signal peptides from Staphylococcus epidermidis can inhibit the agr signaling system of S. aureus, thereby modulating S. aureus virulence (33). Since peptide signaling–sensing systems are very similar among Gram positive bacteria (including the S. mutans CSP system) analogs of the S. mutans CSP may be able to interfere with the quorum-sensing process, leading to inhibition of induction of the “biofilm phenotype.”

Mucosal pathogens

Quorum sensing among mucosal pathogens may not require high cell density. In contrast to the very dense dental plaques colonized by S. mutans and several other oral streptococci, pathogenic streptococci that infect mucosal tissues colonize environments where bacterial microcolonies are usually less dense due to bathing effects of secretions and desquamation of epithelium. Yet, several of these streptococcal and other Gram positive species have evolved peptide pheromone signaling pathways that have autoregulating functions analogous to the quorum-sensing systems that we described above for S. mutans. The finding that initiation of genetic competence in S. pneumoniae is sensitive to relatively low levels of CSP at about 10^7 bacteria/ml (34) suggests that pathogenic streptococci of mucosal surfaces may respond to gradients of cell densities that occur frequently during natural infections, raising the question of whether quorum sensing affects pathways by which pathogenic streptococci grow to predominance over normally protective indigenous species. It has been recently established that mutants of S. pneumoniae defective in the quorum-sensing competence induction pathway have diminished virulence in a murine model relative to the parent strain (35). Differential fluorescence induction also showed that several Com genes were induced during infection in mice (36). Clearly, the role of quorum sensing during infection by S. pneumoniae warrants further examination.
Bacteriocins

Bacteriocins are antimicrobial peptides that are generated by some bacteria and target others that are sensitive. The signaling networks that regulate bacteriocin production and transport as well as immunity to bacteriocins involve peptide pheromone sensing pathways that are very similar to those involved in genetic competence (8). Operons encoding bacteriocin peptide precursors, cognate peptide processing transporters, and two-component regulatory sensors and response regulators are known to be under the control of cell density. For example, the virulence-related blp and com regulons of \textit{S. pneumoniae} have many analogous features including highly similar signal peptides and peptide secretion systems (15). Moreover, activation of the competence and bacteriocin peptide pheromone response regulators may, in turn, activate downstream pathways that intersect in a common regulatory gene. One such example is the previously mentioned \textit{comX}, a transcriptional regulator of so-called “late” competence genes (9). The genome of \textit{M1 S. pyogenes} strain SF370 contains \textit{comX} and a complete bacteriocin \textit{salA1} locus; yet, it lacks the genes \textit{comABC} that encode the CSP and its secretion apparatus (11). This implies that \textit{S. pyogenes} \textit{comX} (and downstream pathways) may be activated in response to environmental signals other than CSPs. \textit{S. pyogenes} is a pathogen with a host range limited to humans and a unique set of virulence properties not shared by other streptococci. It is possible that it has evolved a sophisticated bacteriocin peptide regulatory system to help its population competitively emerge on mucosal surfaces, yet protect its genome from contamination with foreign DNA by deleting (or never evolving) genes for the cell density–dependent CSP. Recently, Jenkinson’s lab reported that the sensory and immunity pathways for the pheromone antibiotics \textit{SalA1} of \textit{S. pyogenes} and \textit{SalA} of the indigenous oral species \textit{Streptococcus salivarius} are conserved, closely related, and cross-sensitive (37). Such novel findings suggest that determinants of population dynamics on bathed mucosal surfaces probably encompass subtle combinations of complex environmental sensing systems that are not limited to cell density, bacteriocin production, and competence stimulation. It is also possible that \textit{S. pyogenes} utilizes a bacteriocin-like hemolysin as a quorum-sensing molecule. Recently, \textit{Enterococcus faecalis} was shown to regulate gene expression by such a mechanism involving its cytolysin, a molecule with both antimicrobial and hemolytic activity (38). \textit{S. pyogenes} has a hemolysin that is genetically very similar to quorum-sensing autoinduction operons found in streptococci (39).

Fluctuations in total bacterial burden and population density also determine the pathogenicity of bacterial microcolonies and biofilms. For example, the ability to suppress competing streptococci through bacteriocin activity may be considered a virulence property if it allows the pathogenic species to emerge sufficiently to damage the host. Evidence is growing that cell density–dependent gene regulation also affects the expression of many other virulence-related proteins of pathogenic streptococci. For example, virulence factor expression and regulation are, in part, determined by growth phase and activation of two-component regulatory sensors of environmental signals, which are characteristics of quorum sensing in Gram positive bacteria (38). Thus, the extracellular concentration of autoregulating peptides appears to serve as one of several environmental conditions that regulate virulence genes through signal transduction pathways that are initiated via two-component regulatory systems. In \textit{S. pyogenes}, in addition to \textit{sagA}, there appear to be several coordinated regulatory loci such as \textit{mga}, \textit{crfRS}, \textit{fasBCA}, and \textit{rgg} that affect the expression of genes for its numerous and diverse virulence factors.

Such a pattern of global regulation is reminiscent of the induction of virulence genes via quorum-sensing pathways in biofilms of \textit{Pseudomonas aeruginosa}. Therefore, it is likely that the genomes of streptococci have evolved density-dependent regulons to control expression of downstream genes that affect bacterial survival in response to changing environmental conditions on mucosal and tooth surfaces, and the selective survival of the pathogenic streptococcal species leads to clinical infection. Although the key molecules of the quorum-sensing pathways of pathogenic streptococci such as \textit{S. pneumoniae}, \textit{S. pyogenes}, and \textit{S. mutans} are distinct from those first reported for Gram negative bacteria, they seem to serve an analogous function, to modulate physiologic homeostasis and adaptation to environmental conditions in response to fluctuations in population density. The use of this information to exploit these pathways to control streptococcal infections is now being implemented and in the near future we may see a more selective and targeted approach to controlling persistent biofilm-dwelling bacteria.

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