Competitive Dominance within Biofilm Consortia Regulates the Relative Distribution of Pneumococcal Nasopharyngeal Density

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ABSTRACT Streptococcus pneumoniae is a main cause of child mortality worldwide, but strains also asymptomatically colonize the upper airways of most children and form biofilms. Recent studies have demonstrated that ~50% of colonized children carry at least two different serotypes (i.e., strains) in the nasopharynx; however, studies of how strains coexist are limited. In this work, we investigated the physiological, genetic, and ecological requirements for the relative distribution of densities, and spatial localization, of pneumococcal strains within biofilm consortia. Biofilm consortia were prepared with vaccine type strains (i.e., serotype 6B [S6B], S19F, or S23F) and strain TIGR4 (S4). Experiments first revealed that the relative densities of S6B and S23F were similar in biofilm consortia. The density of S19F strains, however, was reduced to ~10% in biofilm consortia, including either S6B, S23F, or TIGR4, in comparison to S19F monostrain biofilms. Reduction of S19F density within biofilm consortia was also observed in a simulated nasopharyngeal environment. Reduction of relative density was not related to growth rates, since the Malthusian parameter demonstrated similar rates of change of density for most strains. To investigate whether quorum sensing (QS) regulates relative densities in biofilm consortia, two different mutants were prepared: a TIGR4ΔluxS mutant and a TIGR4ΔcomC mutant. The density of S19F strains, however, was similarly reduced when consortia included TIGR4, TIGR4ΔluxS, or TIGR4ΔcomC. Moreover, production of a different competence-stimulating peptide (CSP), CSP1 or CSP2, was not a factor that affected dominance. Finally, a mathematical model, confocal experiments, and experiments using Transwell devices demonstrated physical contact-mediated control of pneumococcal density within biofilm consortia.

IMPORTANCE Streptococcus pneumoniae kills nearly half a million children every year, but it also produces nasopharyngeal biofilm consortia in a proportion of asymptomatic children, and these biofilms often contain two strains (i.e., serotypes). In our study, we investigated how strains coexist within pneumococcal consortia produced by vaccine serotypes S4, S6B, S19F, and S23F. Whereas S6B and S23F shared the biofilm consortium, our studies demonstrated reduction of the relative density of S19F strains, to ~10% of what it would otherwise be if alone, in consensual biofilms formed with S4, S6B, or S23F. This dominance was not related to increased fitness when competing for nutrients, nor was it regulated by quorum-sensing LuxS/AI-2 or Com systems. It was demonstrated, however, to be enhanced by physical contact rather than by a product(s) secreted into the supernatant, as would naturally occur in the semidry nasopharyngeal environment. Competitive in-
teractions within pneumococcal biofilm consortia regulate nasopharyngeal density, a risk factor for pneumococcal disease.

**KEYWORDS** Streptococcus pneumoniae, carriage, biofilm consortia, dominance, physical contact

*S. pneumoniae*, commonly known as pneumococcus, is a Gram-positive opportunistic pathogen that is the leading cause of bacterial pneumonia and acute otitis media (1, 2). Despite its propensity for causing severe diseases, pneumococcus is a common commensal that quiescently colonizes the upper respiratory tract, forming biofilms that adhere to the epithelium of the nasopharynx, ear epithelium, and lungs, rather than as planktonic cells that are associated with septicemia and meningitis (3–7). In the nasopharyngeal environment, replication slows and bacteria show reduced expression of virulence factors, such as the polysaccharide capsule; instead, they form a biofilm structure made of extracellular DNA, proteins, lipids, and polysaccharides that facilitates asymptomatic carriage. This ability to colonize the upper respiratory tract and persist via biofilms, without causing disease, makes carriage of pneumococcal strains common (4, 6, 7).

To date, over 90 pneumococcal serotypes have been described, and while widespread immunization with conjugate pneumococcal vaccines (PCVs) targeting 7, 10, or 13 serotypes has been effective at reducing mortality, carriage of targeted serotypes still occurs (1, 8). With the widespread use of new methodologies for pneumococcal serotyping, carriage of multiple *S. pneumoniae* strains (i.e., serotypes) was demonstrated to be as common as carriage of a single strain (9–12). For example, a high prevalence of multiple pneumococcal strain carriage was reported by Turner et al., who used both a sweep-latex agglutination method and microarray studies to demonstrate that 43% or 48.8%, respectively, of nasopharyngeal (NP) swabs from Thai children carried more than one pneumococcal serotype (9). A similar prevalence of multiple serotype carriage (~40%) was observed recently in Spain; serotypes were detected based on a combination of Quellung reactions, latex serotyping, and multiplex PCRs, and in another study serotypes carried by Peruvian children were identified by using serotype-specific quantitative PCRs (qPCRs) (10, 11). Therefore, simultaneous carriage of multiple serotypes is relatively common, meaning that these genetically distinct pneumococcal strains must compete not only with resident microflora and other opportunistic pathogens, such as *Haemophilus influenzae* and *Staphylococcus aureus*, but also with members of their own species (10–13).

Monostrain pneumococcal biofilms and biofilms made by pneumococcus and other species, such as *H. influenzae* or *Moraxella catarrhalis*, have been extensively studied during the last few years (4, 5, 13–16). During early stages of formation of monostrain biofilms (i.e., within 8 h), the pneumococcus utilizes the quorum-sensing (QS) LuxS/AI-2 and Com systems as a proxy of population density to begin forming the biofilm structure (6, 17–19). Supporting the role of QS in the control of monostrain pneumococcal biofilms, Carrolo et al. (17) demonstrated that strains expressing competence-stimulating peptide 1 (CSP1), a quorum-sensing pheromone, produced denser biofilms than strains producing CSP2. When pneumococcal monostrain biofilms are formed in an enclosed system (i.e., in a polystyrene plate), quorum-sensing-regulated fratricidal factors, including some bacteriocins, accumulate in the microenvironment and cause irreversible death of biofilm cells that begins after ~12 h of incubation (18, 19). Biofilm lysis did not occur in a biofilm bioreactor with cultures of human pharyngeal cells (18) or in a plate biofilm model with immobilized pharyngeal cells where the culture medium was changed every 4 h (20, 21). With appropriate modifications, these biofilm models can be utilized to investigate chronic colonization or pneumococcal disease involving the upper organs (e.g., ear) or lower airways (e.g., lungs).

Despite compelling evidence of how monostrain pneumococcal biofilms are formed and how the biofilm structure is regulated, little is known about the coexistence and relative densities of pneumococcal strains within nasopharyngeal biofilm consortia. In
this work, we investigated the physiological, genetic, and ecological requirements for the relative distribution densities and spatial localizations of different pneumococcal serotypes during the formation of biofilm consortia. Mixtures of invasive strains recently isolated from pneumococcal disease cases and belonging to vaccine serotypes 6B (S6B), S19F, and S23F were utilized to produce biofilm consortia. The relative densities of individual strains forming biofilm consortia were investigated by serotype-specific qPCR and CFU counts. These studies demonstrated higher relative densities (i.e., dominance) of strains S6B, S23F, and TIGR4 in forming biofilm consortia with S19F strains. The relative densities were similar (i.e., tolerant) when S6B and S23F formed pneumococcal biofilms. The spatial arrangement of pneumococcal strains within biofilm consortia was investigated by using confocal microscopy imaging. Our data revealed that the QS systems LuxS/AI-2 and Com play no role in controlling dominance within a biofilm consortium. Moreover, a secreted molecule appeared not to be involved in the dominance of the relative densities, while spatial physical contact of pneumococcal strains within biofilm consortia was required for dominance.

RESULTS

Population dynamics of pneumococcal biofilm consortia produced by vaccine strains. S. pneumoniae persists in the human nasopharynx in a biofilm state, and highly sensitive methods to investigate pneumococcal colonization include quantitative PCR assays (11, 22–24). Therefore, we first evaluated by qPCR the density of monostrain pneumococcal biofilms produced by vaccine strains and compared the densities to those produced by a mixture of two strains of different serotypes. Pneumococcal strains chosen for these studies belonged to vaccine types (e.g., 6B, 19F, and 23F) (Table 1) and were recently isolated from invasive pneumococcal disease (IPD) cases in the United States. They had not been genetically modified since their isolation from patients. Experiments showed that vaccine-type strains inoculated alone formed robust biofilms (>8 × 10⁹ genome equivalents/ml) at 8 h postinoculation on both abiotic substrates (Fig. 1A) and human pharyngeal cells (Fig. 1B). These biofilms produced by S6B, S19F, and S23F were similar, i.e., not statistically significantly different, on either substrate (Fig. 1). Almost identical results were obtained when the densities of planktonic bacteria or of biofilms were obtained by culturing (see Fig. S1 in the supplemental material). When S6B was coinoculated in the same well with either S19F or S23F, the relative density was similar to that produced in wells inoculated only with S6B. Similarly, biofilms produced by a mixture of S19F and S23F were similar to those produced in wells inoculated with only S19F or S23F (Fig. 1). These results indicated that in vitro formation of pneumococcal biofilm consortia reaches a plateau, and they led us to hypothesize that strains may partition a biofilm consortium to coexist.

### Table 1

<table>
<thead>
<tr>
<th>Streptococcus pneumoniae strain</th>
<th>Serotype</th>
<th>Description</th>
<th>Source or reference</th>
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<td>D39</td>
<td>2</td>
<td>Avery’s virulent strain, isolated in 1916, CSP1</td>
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<tr>
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<td>Invasive isolate from blood of 30-yr-old male in Norway, CSP2</td>
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<td>This study</td>
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<td>TIGR4ΔcomC:erm(B), Ery’</td>
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<td>This study</td>
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<td>2</td>
<td>R6 derivative, Str’</td>
<td>D. Zanher</td>
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<tr>
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<td>Invasive isolate, utilized as qPCR control</td>
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<tr>
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<td>CDC</td>
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Abbreviations: Ery, erythromycin; Str, streptomycin; Pen, penicillin; Cl, clindamycin; Trm, trimethoprim; Tet, tetracycline.
Relative densities of pneumococcal strains within biofilm consortia: dominance and tolerance. To compare the relative density of each strain forming early biofilm consortia, we utilized serotype-specific quantitative reactions (11, 24). The density of each strain within a consortium was compared with biofilms formed by individual strains at 8 h postinoculation. As shown in Fig. 2A, the relative density of S6B was similar (P = 0.57) whether incubated alone or coincubated with S19F, whereas it significantly decreased when forming biofilm consortia with 23F. Similarly, biofilms made by S23F were significantly reduced when coincubated with S6B, in comparison to biofilms obtained in wells inoculated with S23F alone, but S23F density did not change when coincubated with S19F (Fig. 2B). In contrast, when inoculated alone, the density of S19F was significantly higher than that of S19F coincubated with S6B or S23F (P < 0.05 for both cases) (Fig. 2C).

The observed proportion of each strain within consortial biofilms was analyzed next. The observed proportion was compared to the null proportion of 0.5, as the same amounts of each strain were coincubated together. When S6B and S19F were coincubated, the proportion of biofilms made by S6B (0.91) was significantly higher than that observed for S19F (0.09) (Fig. 2D). As expected, a significantly different proportion was observed when S19F and S23F were coincubated: 0.07 and 0.93, respectively. The proportions of biofilms made by S6B and S23F, however, were similar: 0.56 and 0.44, respectively. Overall similar proportions were obtained when early biofilm consortia were produced on human pharyngeal cells (data not shown). Together, these results demonstrated dominance of S6B, or of S23F, within pneumococcal biofilm consortia produced along with S19F. Data also indicated that relative densities of S6B and S23F within biofilm consortia were similar (i.e., strains shared the niche equally).

Rate of change of density of pneumococcal strains. To investigate if the increased relative densities of S6B, or of S23F, in consortial biofilms with S19F were related to an accelerated consumption of resources, the Malthusian parameter, which evaluates the rate of change in density per minute, was obtained. Growth curves (based on the optical density at 600 nm [OD_{600}]) first showed a delayed growth of S6B and S23F in comparison to S19F at 5 h postinoculation (Fig. 3A). Accordingly, the calculated Malthusian parameter (i.e., growth rate per minute) was significantly lower for S23F and S6B than for S19F (Fig. 3B), thus indicating that faster consumption of resources by dominant S6B and S23F strains did not account for the observed increased relative densities.
Spatial localization of S19F strains within pneumococcal biofilm consortia. Strains utilized in the above-described experiments were recently isolated from patients with pneumococcal disease, and therefore genetic information was not available. To gain insights into the potential mechanism controlling relative densities of biofilm consortia, we incubated S19F along with a reference genome sequenced strain, TIGR4 serotype 4 (vaccine type) \(^{25}\). These experiments showed that, in biofilm consortia including TIGR4 and S19F strain 5131, the relative density of S19F decreased to the same extent as that observed when S19F was coinoculated with S6B or S23F \(^{25}\) (Fig. 4A).

The density of a different S19F strain, 4924, in consortial biofilms with TIGR4 was tested with similar results \(^{25}\) (Fig. 4B). This TIGR4-induced reduction of density of S19F strains was specific, since the relative density of reference strain D39 (serotype 2) was similar in both culture types when incubated alone or in biofilm consortia with TIGR4 (data not shown).

To visualize the spatial localization of each strain within biofilm consortia, we stained their capsule by fluorescence, using serotype-specific anticapsule antibodies and confocal microscopy. Micrographs first revealed that attachment to the glass substratum varied between S19F strains. At 4 h postinoculation, strain S131 attached and formed
a net-like pattern (Fig. 4C), whereas 4924 formed biofilm aggregates (Fig. 4E). After 8 h of incubation, however, the aggregates formed by 4924 had apparently disaggregated, covering just 70% of the substrate (Fig. 4F). A similar biofilm phenotype was produced by strain 5131 8 h postincubation (Fig. 4B). As expected, as we and others have reported that decreased transcription of capsule genes when biofilms mature (26, 27), the pneumococcal capsule was clearly observed 4 h postinoculation but capsule staining decreased after 8 h of incubation. Selection of unencapsulated pneumococci binding to the substrate and then increasing in density after 8 h could also be a possibility. In the case of TIGR4 (Fig. 4O and P), the capsule aggregated in bacterial poles (Fig. 4Q, arrows) or was apparently lost (Fig. 4Q, asterisks). Due to this effect, to further confirm the presence of bacterial cells, the DNA was also stained. When TIGR4 was incubated with S19F strains, there was a dramatic reduction in S19F bacteria at both 4 h and 8 h postinoculation (Fig. 4, red bacteria [S19F] inoculated alone versus those inoculated with TIGR4). The density of TIGR4 bacteria in these consortia was not affected.

**Density of S19F decreases in nasopharyngeal biofilm consortia with TIGR4.** To investigate whether the relative density of S19F decreases in mature nasopharyngeal biofilm consortia with TIGR4, we incubated both strains in a bioreactor containing living cultures of human pharyngeal cells for 24 h. Mature biofilms already form after 24 h of incubation in a biofilm bioreactor (18). The density of S19F biofilms and numbers of S19F planktonic cells coming off the bioreactor chamber were significantly reduced when S19F was coincubated with TIGR4, in comparison with bioreactor chambers incubated only with S19F (Fig. 5A and B). Confocal experiments additionally demonstrated that pneumococcal strains were in close proximity when incubated together (Fig. 5C); physical contact was confirmed through optical sections of confocal micrographs (Fig. 5D, yellow circles).

**The factor(s) allowing reduction of S19F relative density is not regulated by quorum-sensing systems LuxS/AI-2 and Com.** Given that the quorum-sensing systems LuxS/AI-2 and Com have been implicated in formation of monostrain pneumococcal biofilms with strain D39 and are key regulators of fratricide and competence (18, 26, 27), TIGR4ΔluxS and TIGR4ΔcomC mutant strains were prepared and evaluated for regulating the factor(s) that allows dominance of S19F biomass in biofilm consortia. Densities of monostrain biofilms were similar when 4924, 5131, mutant strain TIGR4ΔluxS, or mutant strain TIGR4ΔcomC were compared (P > 0.05 for all comparisons) (Fig. 6A).
When biofilm consortia were produced with either the TIGR4ΔluxS or TIGR4ΔcomC mutant strains, the relative density of S19F strains 4924 or 5131 decreased ~20% in comparison to the biomass produced by these strains when incubated alone (Fig. 6B and C). This reduction of S19F density was similar to that induced by the wild-type (wt) TIGR4 strain (data not shown). Therefore, the TIGR4 factor(s) that allows reduction of S19F density is not regulated by the QS systems LuxS/AI-2 and Com. Biofilms of the mutant strains TIGR4ΔluxS and TIGR4ΔcomC were not affected by the presence of S19F strains (P > 0.05 for all comparisons) (data not shown).

Confocal micrographs were also obtained. As expected, at 4 h postinoculation S19F 4924 formed aggregates (Fig. 6D). In wells incubated for 4 h with 4924 and mutant strain TIGR4ΔluxS or TIGR4ΔcomC, these aggregates were formed by a mixture of both strains (Fig. 6D, first row [red shows 4924 and green shows TIGR4 derivatives]). After 8 h of incubation, however, S19F aggregates had disappeared from wells incubated with either TIGR4 derivative QS mutant, reducing the population of 4924 bacteria. In contrast, S19F 4924 incubated alone formed robust biofilms. A similar reduction of 5131 biofilms attached to the substratum was observed when mutant strain TIGR4ΔluxS, or TIGR4ΔcomC was incubated with 5131, while the strain
growing alone was able to form robust biofilms at 8 h postinoculation (Fig. 6D). The biomass of mutant strain TIGR4ΔluxS or TIGR4ΔcomC, whether incubated alone or with S19F, did not change.

Physical contact is required for dominance within pneumococcal biofilm consortia. To investigate whether physical contact is required to dominate a biofilm consortium, we simulated physical interaction of an S4 strain and an S19F strain. (Parameters utilized to simulate the interactions are described in Materials and Methods.) The simulation showed that after 4 h of coincubation, the S4 strain limited the growth of the S19F strain by about 1 order of magnitude, 2.1 \times 10^7 versus 1.1 \times 10^6 log_{10} CFU/ml (Fig. 7A). Biofilm dominance was not related to an increased consumption of resources by the dominant S4 strain, since the hourly growth rates of individual strains were similar (Fig. 3). Moreover, at 4 h, when S19F inhibition was observed, we detected a \( \sim 90\% \) level of resources necessary to produce new cells (Fig. 7A). At 8 h postinoculation, the difference in densities of individual strains within a biofilm consortium made of S4 and S19F strains was about 2 orders of magnitude (Fig. 7A). Contact-dependent reduction of S19F density was verified by colony counts. To do this, we utilized S19F strain 4924, which is naturally resistant to erythromycin, and generated a TIGR4 strain encoding resistance to streptomycin, SPJV21. Figure 7B shows a statistically significant, \( \sim 2\)-log reduction of the S19F strain when incubated with TIGR4, whereas the density of TIGR4 was not affected by coincubation with the S19F strain (Fig. 7C).

To experimentally demonstrate whether reduction of the relative density of S19F required physical contact or whether it was mediated by a soluble factor(s), strain TIGR4 and S19F strain 4924, or S19F strain 5131, were inoculated into the same well but the strains were separated with a Transwell system device, i.e., TIGR4 was inoculated in the
top chamber and the S19F strain (either 4924 or 5131) was inoculated in the bottom. Experiments with the TIGR4Δ\textit{luxS} mutant were also included. The biomass of 5131 incubated with either TIGR4 strain (i.e., wt or the TIGR4Δ\textit{luxS} mutant) was similar or actually increased after 8 h of incubation in comparison to wells where strain 5131 was inoculated alone (Fig. 7D). Similar results were obtained with S19F strain 4924. These data demonstrated that physical contact is required to reduce the density of S19F strains in consortia with TIGR4. A similar density of TIGR4 was observed in incubation wells that also contained 5131, in comparison with wells where only TIGR4 was inoculated (data not shown). As expected, given that the TIGR4Δ\textit{luxS} mutant does not produce AI-2, in Transwell experiments where the TIGR4Δ\textit{luxS} mutant and 5131 were
inoculated together, the density of the TIGR4ΔluxS mutant increased, perhaps due to LuxS/AI-2 produced by S19F (Fig. 7E).

**DISCUSSION**

In this work, we recreated the dynamics of competitive interactions within pneumococcal nasopharyngeal biofilm consortia and demonstrated a dominance of the relative density of S19F strains compared to all other strains tested, i.e., S6B, S23F, and TIGR4. Dominance and tolerance have been observed in recent epidemiological studies where the specific bacterial density of pneumococcal serotypes was obtained (explained in detail below) (11, 28). In this study, dominance against S19F strains within consortia required physical contact, since in experiments conducted in Transwell devices, the TIGR4 strain was not able to decrease the biomass of S19F strains. Dominance of pneumococcal cocolonization through a mechanism requiring physical contact recapitulates that it may naturally occur in the human nasopharynx, where pneumococcal strains cocolonize a nonaqueous microenvironment. Strain dominance was recently described in a mouse model of pneumococcal cocolonization (with use of serotype-specific qPCRs to evaluate serotype density) (29). Pneumococcal colonization...
has also been inhibited in vitro by incubating pneumococcal strains with probiotic bacteria (30, 31).

Vaccine serotypes 6B, 19F, and 23F evaluated in this study are the most common serotypes isolated in IPD in countries where the pneumococcal vaccine is not available (i.e., India and China); together, they cause ~30% of IPD cases (32). Unlike strains belonging to serotype 1 or 5, which are highly prevalent in IPD cases but display low prevalence in carriage studies, serotype 6B, 19F, and 23F strains are also the most prevalent serotypes carried in the nasopharynx of children (6, 32, 33). While strains were able to form biofilms on both abiotic and biotic surfaces (i.e., human pharyngeal cells), only S6B and S23F dominated biofilm consortia when S19F colonized the same niche.

Recent studies have investigated nasopharyngeal colonization by multiple pneumococcal serotypes, showing that up to 50% of children are cocolonized by 2 or more strains (i.e., serotypes) (11, 34, 35). In Malawian children, for example, more than 75% of cocolonization events included a vaccine type (35), whereas our study using single-plex qPCR demonstrated a vaccine type in 80% of cocolonized, nonvaccinated Peruvian children (11). The study from our laboratory also quantified the specific bacterial load of pneumococcal serotypes in the cocolonized children and demonstrated dominance of a pneumococcal strain in ~85% of cocolonization events (11). A semi-quantitative microarray approach resulted in similar evidence (11, 34). We define strain dominance, in children cocolonized by two or more strains, as those cocolonization events where the bacterial load (i.e., biomass) of a specific strain accounts for at least 60% of the total pneumococcal load. Therefore, based on new recent epidemiological evidence and this study’s findings, dominance appears to be the most common event during nasopharyngeal cocolonization by multiple pneumococcal strains.

Experiments comparing biofilm biomass formed by single strains versus the biomass of biofilm consortia suggest that dominance and tolerance within biofilm consortia are limited by the substrate. For example, whether S6B and S23F strains were inoculated separately or together, the total biomass was very similar (i.e., did not double in size). The in vivo situation in the human nasopharynx and oropharynx may be similar, although the host immune response should play an additional role in limiting the biomass of certain types. Experiments we have described here also demonstrated that when two strains cohabit a biofilm consortium produced on abiotic surfaces, the biomass of both strains will be proportionally similar (~50%). S19F strains, however, were dominated by all strains tested, whether grown on abiotic substrates or on human pharyngeal cells. Dominance of S6B, and S23F, against 19F correlates with the findings of an epidemiological study with Spanish children that demonstrated that S6B strains were more likely to cocolonize children with strains from other serotypes (10), and recent unpublished studies from our lab have shown that serogroup 6 strains and 23F are the most prevalent strains in cocolonized, nonvaccinated Peruvian children.

The specific mechanism(s) for dominance, or tolerance (if any), that is common to all pneumococci is under investigation by our laboratory and others. A candidate for modulating densities of pneumococcal types had been the blp locus, which encodes a bacteriocin system that produces a potent bacteriocin, BlpC, but it has been recently demonstrated that BlpC plays a minor role in cocolonization (36, 37). A secreted factor might not be involved in dominance of S19F strains by the S4 strain TiGR4, as demonstrated in experiments using Transwell systems, although our experimental design did not allow us to test for a factor(s) that could be only released when in close proximity. The factor(s) appears not to be regulated by the quorum-sensing LuxS/AI-2 and Com systems, since individual mutants prepared in the TiGR4 background were still able to reduce the population of S19F strains in biofilm consortia with S4 mutants. The possibility exists that a minimum amount of a QS molecule produced by the coincubated wt strain may complement the mutant strain. In the case of the TiGR4ΔuxS mutant, the absence of LuxS/AI-2 in TiGR4 could be supplied by that produced by S19F strains. This may be the same case for the absence of production of CSP (i.e., encoded by the comC gene) in the TiGR4ΔcomC mutant when incubated along with S19F S5131,
since both produced CSP2 but not in biofilm consortia with 4924, as this strain produced a different variant (i.e., CSP1).

It is likely that strains that dominate biofilm consortia induce cell lysis of the dominated strain, and therefore a source of DNA for recombination might be available. A study by Marks et al. (20) demonstrated higher frequencies of recombination in pneumococcal biofilms produced on human pharyngeal cells than on their planktonic counterparts. However, neither the recombination direction (i.e., when strains were incubated together) nor specific bacterial densities were obtained to allow us to determine whether, in mixtures of two different pneumococcal strains, the strain acquiring DNA from the other one dominates the biofilm consortium (20). We hypothesize that the strains which dominate biofilm consortia have an advantage, not just for colonization but also for acquiring DNA from other pneumococci. Studies in our laboratory are currently focused on investigating this hypothesis.

A very recent article from our laboratory demonstrated killing of Staphylococcus aureus biofilms and planktonic cells by TIGR4 and other pneumococci (38). The unknown factor required physical contact and completely eradicated preformed biofilms made by the S. aureus reference strain and methicillin-resistant S. aureus strain USA300-0114; whether the factor(s) that allows TIGR4 to limit the biomass of S19F strains is similar to that eradicating S. aureus strains needs to be investigated. The need for physical contact might correlate with the in vivo situation of the upper airways, where pneumococcal strains have a limited liquid environment in which to secrete products and must instead release and acquire these products when in close physical proximity to each other.

MATERIALS AND METHODS

Strains and bacterial culture media. S. pneumoniae strains utilized in this study are listed in Table 1. Strains were routinely cultured on blood agar plates (BAP) or grown in Todd-Hewitt broth containing 0.5% (wt/vol) yeast extract (THY). When indicated, ampicillin (1 μg/ml), streptomycin (100 μg/ml), or erythromycin (0.5 μg/ml) was added to the culture medium. Antibiotics were purchased from Sigma.

Preparation of TIGR4 derivative strains. SPJV16 and SPJV20, with a deletion within the luxS or comC gene, respectively, were prepared essentially as described for a previous study in our laboratory (18). Mutation was confirmed by PCR (i.e., different PCR product sizes compared to wt products, due to deletion within the target gene and insertion of the erm(B) gene) and by sequencing (data not shown). SPJV21 was prepared by transforming SPJV16 with DNA from R6Am9, which confers resistance to streptomycin, and plated onto BAP with the antibiotic. Transformation was done by standard methods (26, 39) (Table 1).

Cell cultures. Human pharyngeal Detroit 562 cells (ATCC CCL-138) were cultured in Eagle’s minimum essential medium (EMEM; Lonza, Walkersville, MD) supplemented with non-heat-inactivated 10% fetal bovine serum (FBS; Atlanta Biologicals), 1% nonessential amino acids (Sigma), 1% glutamine (Sigma), penicillin (100 U/ml), and streptomycin (100 μg/ml), and the pH was buffered with HEPES (10 mM; Gibco). Cells were harvested with 0.25% trypsin (Gibco), resuspended in the cell culture medium, and incubated at 37°C in a 5% CO2 humidified atmosphere.

Preparation of inocula. S. pneumoniae strains were streaked on BAP and incubated overnight at 37°C in a 5% CO2 atmosphere. Bacterial suspensions (OD600 of 0.05) were made in THY and further grown until they reached an OD600 of ~0.2; a 10% (vol/vol) final solution of glycerol was added to this culture, which was then stored at −80°C until used. Some aliquots were removed from the freezer and then diluted and plated to obtain the CFU per milliliter data for inoculants.

Production of early biofilm consortia on abiotic surfaces. Pneumococcal early biofilm consortia were generated by thawing inocula on ice, and then ~7 × 10^6 CFU/ml of each strain was inoculated into a CellBIND surface 24-well polystyrene plate (Corning) containing THY. Biofilm consortia and biofilm controls were incubated for 8 h in 5% CO2, and after extensive phosphate-buffered saline (PBS) washes, biofilms were sonicated for 15 s in a Bransonic ultrasonic water bath (Branson, Danbury, CT), followed by extensive pipetting to remove all attached bacteria. Biofilms were then retrieved by dilution and plating or frozen at −80°C for DNA extraction.

Production of early biofilm consortia on immobilized human pharyngeal cells. The biofilm model using immobilized pharyngeal cells was developed by Marks et al. (21) and has been utilized in pneumococcal biofilm research by different laboratories (18, 21, 40). Detroit 562 cells were grown until confluent (~5 days) on either 8-well glass slides (Lab-Tek), tissue culture treated 6-well polystyrene plates, or CellBIND surface 24-well polystyrene plates (Corning). Once confluent, cells were immobilized by fixation with 2% paraformaldehyde (PFA; Sigma) for 15 min at room temperature. After extensive washes with sterile PBS, immobilized pharyngeal cells were supplemented with cell culture medium without antibiotics and then inoculated with an aliquot containing ~7 × 10^6 CFU/ml of each strain. After 8 h of incubation, biofilms were harvested and counted.

Transwell experiments to physically separate biofilms. A Transwell support (Corning) was installed in each well of a 6-well plate, creating a bottom and a top compartment within the same well. The Transwell system has a permeable membrane (pore size, ~0.4 μm) that allows the exchange of small
molecules between compartments. The bottom compartment was inoculated with an S19F strain, whereas strain TIGR4 or the TIGR4ΔluxS mutant strain was inoculated directly into the Transwell device. The total volume was brought to 4 ml by addition of THY, and plates were incubated for 8 h at 37°C in a 5% CO2 atmosphere. Biofilms were then washed twice with PBS and fixed with a 4% paraformaldehyde solution.

**Quantification of biofilm biomass by quantitative PCR.** Primers, probes, and the concentrations utilized are listed in Table 2. Total pneumococcal DNA was extracted from 200 μl of the harvested biofilm samples with the QiAamp DNA minikit according to the manufacturer’s instructions. Final elution was done with 100 μl of elution buffer. DNA preps were quantified using a nanodrop spectrophotometer and stored at −80°C until used.

**Sequencing of the comC gene from clinical pneumococcal isolates.** Downstream and upstream sequences spanning the comC gene were amplified by PCR using primers JVS71L and JVS72R, and the amplified PCR product (~455 bp) was sequenced at Eurofins (Atlanta, GA). Sequences were analyzed with Lasergene software version 10.1.1 (DNASTAR) (3).

**Calculation of the Malthusian parameter.** Five (TIGR4), S6B (8655), S19F (5131), and S23F (8064) strains were cultured in THY at 37°C in a 5% CO2 atmosphere until they reached the early log phase, and then bacteria were diluted to approximately 10^5 CFU/ml. An aliquot (300 μl) of each strain was added into seven different wells of a Bioscreen C plate (Lab Systems, Helsinki, Finland), and the plate was incubated at 37°C in a Bioscreen C reader. OD_600 values were recorded by a Bioscreen C plate reader every 5 min. A growth curve graphic was prepared using the R language and environment for statistical computing and graphics (http://www.gnu.org/). The Malthusian parameter, the rate of change in density, was finally calculated using the GrowthRates software (version 2.1) (41).

**Antibiotic susceptibility testing.** Antibiotic resistance of invasive strains was investigated in order to count, using BAP with the appropriate antibiotic, individual strains when forming biofilm consortia. The Kirby-Bauer disc-diffusion method was used according to the Clinical and Laboratory Standards Institute (CLSI) guidelines (42). The following antibiotic discs (Becton-Dickinson, East Rutherford, NJ) were used: oxacillin (1 μg), erythromycin (15 μg), clindamycin (2 μg), chloramphenicol (30 μg), trimethoprim-sulfamethoxazole (1.25/23.75 μg), and tetracycline (30 μg). Isolates were regarded as susceptible, intermediate, or resistant by using the breakpoints set described by CLSI (42). Quality control was done with S. pneumoniae reference strain ATCC 49619.

**Quantification of biofilm biomass by quantitative PCR.** Primers, probes, and the concentrations utilized are listed in Table 2. Total pneumococcal DNA was extracted from 200 μl of the harvested biofilm samples with the QiAamp DNA minikit according to the manufacturer’s instructions. Final elution was done with 100 μl of elution buffer. DNA preps were quantified using a nanodrop spectrophotometer and stored at −80°C until used.

**Visualization of pneumococcal biofilms.** Biofilms inoculated into 8-well glass slides (Lab-Tek) were incubated for 8 h at 37°C in a 5% CO2 atmosphere. Biofilms were then washed twice with PBS and fixed with a 4% paraformaldehyde solution.

### Table 2 qPCR primers and probes utilized in this study

<table>
<thead>
<tr>
<th>Target</th>
<th>Primer or probe sequence (5’−3’)</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pan-pneumococcus <strong>lytA</strong></td>
<td>F, ACGCAATCTAGCAGATGAAGCA R, TCGTGCGTTTTAATTCGACCT FAM-GCCGAAAACGGTCTGACAGGGAG</td>
<td>43</td>
</tr>
<tr>
<td>Serotype 4</td>
<td>F, TGGGATGACATTTTCTACGGACTA R, CCGTCGCTGATGCTTATCA FAM-TCTATTTGAGATTAGGTTGGA</td>
<td>47</td>
</tr>
<tr>
<td>Serogroup 6</td>
<td>F, AGATTGTCGACTAGATGATGGAGGTT R, ACGATTCTGCTCCTTCGATAACAG FAM-TGTTCCTGCGCTCAGGCAACTTG</td>
<td>47</td>
</tr>
<tr>
<td>Serotype 19F</td>
<td>F, GGTCAATGGGAGATACGACAGAA R, TCCTCTACGTGCCAAACCAATT FAM-ACCTGAAAGGATAGCTGCTGGAACGTTG</td>
<td>47</td>
</tr>
<tr>
<td>Serotype 23F</td>
<td>F, TGGTATTTTGGGATCTGTCAT R, AGAGCTCCGGTTGTTTCGATAA FAM-CTTCTCCGGCATCAAACGTAAAG</td>
<td>47</td>
</tr>
<tr>
<td><strong>comC</strong> gene (JVS71L/JVS72R)</td>
<td>F, CTTTTACAAATAAATGGTAACGTG R, AATGCTTCTACCCAGCTGACCTAT</td>
<td>This study</td>
</tr>
</tbody>
</table>

<sup>qPCR was conducted using primer and probe concentrations of 100 nM each for **lytA** qPCR and 200 nM each for serotype-specific qPCR. Forward (F) and reverse (R) primer sequences are shown for each target, followed by the specific probe sequence. All probes were labeled at the 5’ end with 6-carboxyfluorescein (FAM) and also with black hole quencher 1 dye at the 3’ end.</sup>
with 2% PFA for 15 min at room temperature. Once PFA was removed, biofilms were washed with PBS and blocked with 2% bovine serum albumin (BSA) for 1 h at 37°C. These biofilms were then incubated with serotype-specific polyclonal antibodies (∼40 μg/ml; Statens Serum Institute, Denmark) for 1 h at room temperature. Antibodies had been previously labeled with Alexa 488 (anti-S4) or Alexa 555 (anti-S19) following the manufacturer’s recommendations (Molecular Probes). Stained preparations were finally washed two times with PBS and mounted with ProLong Diamond antifade mountant with 4’,6-diamidino-2-phenylindole (DAPI; Molecular Probes). Biofilms produced on human pharyngeal cells were fixed with 2% PFA and washed three times with PBS. Nucleic acids were stained with TO-PRO-3 (1 μM), a carboxy cyanine monomer nucleic acid stain (Molecular Probes), for 15 min; S4 and S19F strains were stained as mentioned above. Confocal images were obtained using an Olympus FV1000 confocal microscope and analyzed with Image) version 1.49k (National Institutes of Health, USA) or the Imaris software (Bitplane, South Windsor, CT).

Production of biofilm consortia in a bioreactor with cultures of human pharyngeal cells. *S. pneumoniae* strains were inoculated as indicated above into a biofilm bioreactor, which simulated human airways. The bioreactor includes a continuous flow of nutrients to feed both the cell cultures and pneumococci but also to wash off toxic products, thus avoiding pneumococcus-induced cell cytotoxicity (18). Briefly, human pharyngeal cells were grown on Snapwells (Corning) with a polyester membrane (0.4 μm) supported by a detachable ring. Once confluent (4 to 5 days), cells were inoculated with bacteria and immediately placed in sterile vertical diffusion chambers. The apical side (inner chamber) was perfused with sterile minimal essential medium with no antibiotics, using a Master Flex L/S precision pump system (Cole-Parmer, Vernon, IL). To avoid the accumulation of toxic substances but allow biofilm formation, a low flow rate (0.20 ml/min) was applied. Bioreactor chambers containing biofilm consortia on human pharyngeal cells were incubated for 24 h at 37°C under a sterile environment. At the end of the incubation period, chambers of the bioreactor were opened and biofilm bacteria were harvested as described above. Planktonic specimens were also collected from the outflow of the bioreactor. DNA from biofilms or planktonic cells was purified as described and was used as a template in qPCRs targeting serotype-specific sequences (22, 44).

Final genome equivalents (CFU) per milliliter data were obtained as described above.

**Model for contact-mediated killing.** To run the contact-mediated killing model, we considered two populations with densities of $N_1$ and $N_2$ cells per milliliter, respectively. These populations grew at a rate proportional to the concentration of a limiting resource, $R$ (in micrograms per milliliter), and parameter $k$ (also in micrograms per milliliter), the Monod constant, which is the concentration of the resource when the population is growing at half its maximum rate, $v_1$ and $v_2$ (per cell per hour) for populations 1 and 2, respectively. As described by Levin and Udekwu (45), resources are consumed at a rate proportional to the growth rate and a conversion efficiency parameter, $e$ (in micrograms), which is the amount of resource necessary to produce a new cell. There are lags $L_1$ and $L_2$ (in hours) for populations 1 and 2, respectively. We assumed population 2 kills population 1 at a rate proportional to the product of their densities and kill rate constant. The killing commences when the time $t$ exceeds that of the lag for population 2 and is proportional to the concentration of the limiting resource. When the concentration of the limiting resource reaches a lower threshold, $R_{\text{MIN}}$ (in micrograms per milliliter), autolysis sets in and populations 1 and 2 die off at rates of $d_1$ and $d_2$ (per cell per hour).

With these definitions and assumptions, the rates of change in the concentration of the limiting resource are given by the following equations.

\[
\begin{align*}
\frac{dN_1}{dt} & = y_1 v_1 \phi(R) N_1 - L_1 d_1 N_1 \\
\frac{dN_2}{dt} & = y_2 v_2 \phi(R) N_2 - L_2 d_2 N_2
\end{align*}
\]

where

\[
\phi(R) = \frac{R}{(R + K)}
\]

\[
y_1 = 0 \text{ when } t < L_1 \text{ and } y_1 = 1 \text{ when } t \geq L_1
\]

\[
y_2 = 0 \text{ when } t < L_2 \text{ and } y_2 = 1 \text{ when } t \geq L_2
\]

\[
x = 1 \text{ when } R > R_{\text{MIN}} \text{ and } x = 0 \text{ when } R \leq R_{\text{MIN}}
\]

To solve these equations numerically (to simulate the dynamics), we used the Berkeley Madonna program.

**Statistical analysis.** The means of two pneumococcal densities were analyzed by a two-sample independent t test. For each t test, equality of variance was tested and, based on the result, equal or unequal variance was assumed for the corresponding t test. The means of more than two independent pneumococcal densities were analyzed by analysis of variance (ANOVA). Among samples that had two serotypes, proportions of a given serotype were compared using the Z test. The null hypothesis used was a proportion of 0.5, because equal amounts of each sample were added for the experiment. Two-tailed $P$ values of <0.05 were considered statistically significant. Statistical analyses were performed using OpenEpi (Open Source Epidemiologic Statistics for Public Health [http://www.openepi.com/Menu/OE _Menu.htm]) and the software SigmaPlot version 12.0 (Systat Software, Inc.).
SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at https://doi.org/10.1128/AEM.00953-17.

SUPPLEMENTAL FILE 1, PDF file, 0.2 MB.

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REFERENCES


