

# Disease Manifestations and Pathogenic Mechanisms of Group A *Streptococcus*

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## SUMMARY

*Streptococcus pyogenes*, also known as group A *Streptococcus* (GAS), causes mild human infections such as pharyngitis and impetigo and serious infections such as necrotizing fasciitis and streptococcal toxic shock syndrome. Furthermore, repeated GAS infections may trigger autoimmune diseases, including acute poststreptococcal glomerulonephritis, acute rheumatic fever, and rheumatic heart disease. Combined, these diseases account for over half a million deaths per year globally. Genomic and molecular analyses have now characterized a large number of GAS virulence determinants, many of which exhibit overlap and redundancy in the processes of adhesion and colonization, innate immune resistance, and the capacity to facilitate tissue barrier degradation and spread within the human host. This improved understanding of the contribution of individual virulence determinants to the disease process has led to the formulation of models of GAS disease progression, which may lead to better treatment and intervention strategies. While GAS remains sensitive to all penicillins and cephalosporins, rising resistance to other antibiotics used in disease treatment is an increasing worldwide concern. Several GAS vaccine formulations that elicit protective immunity in animal models have shown promise in nonhuman primate and early-stage human trials. The development of a safe and efficacious commercial human vaccine for the prophylaxis of GAS disease remains a high priority.

## INTRODUCTION

In 1909, Meakins reported serotype-specific immunity stimulated by experimental vaccination of humans against streptococci. One 24-year-old male subject, presenting with endocarditis and a history of scarlatina and acute rheumatic fever, received 16 doses of vaccine over a 3-month period, prepared from streptococci isolated from the subject's own blood, yet died 7 days after the final dose (1). Over 100 years later, a safe and effective com-

mercial vaccine against *Streptococcus pyogenes* (group A *Streptococcus* [GAS]) is still not licensed for human use (2–4).

GAS causes a diverse range of human infections, both benign and serious, which include pharyngitis, impetigo, cellulitis, scarlet fever, puerperal sepsis, bacteremia, pneumonia, streptococcal toxic shock syndrome (STSS), necrotizing fasciitis, and endocarditis. In addition, GAS infection can trigger serious postinfectious immune-mediated disorders, including acute poststreptococcal glomerulonephritis (APSGN), acute rheumatic fever (ARF), and rheumatic heart disease (RHD) (5–9). Global disease burden figures reported by the World Health Organization (WHO) rank GAS as the ninth leading infectious cause of human mortality, with the majority of deaths being attributable to invasive infections and RHD, primarily in nonindustrialized countries (5, 10). Several studies had noted a reduction in GAS disease burden in industrialized countries in the mid-20th century (11–14). However, in the last 50 years, there have been widespread reports of significant outbreaks of ARF (15, 16), APSGN (17, 18), GAS invasive disease (14, 19–21), puerperal sepsis (22–24), and scarlet fever (25, 26).

Treatment regimens for GAS infections naturally center on the use of appropriate antibiotics. GAS remains exquisitely and universally sensitive to penicillin, while antibiotics such as cephalosporins, macrolides, and clindamycin are also used clinically (27–29). In some regions of the world, GAS resistance to antibiotics such as macrolides, clindamycin, and lincosamide has become an increasing concern (25–28, 30), and epidemiological vigilance is required to ensure that treatment matches the antibiotic sensitivity profile of circulating GAS strains. The human population is the only known natural reservoir for GAS, and thus, a safe and effective human vaccine holds the promise of reducing disease burden and blocking transmission and even has the potential to eradicate this important human pathogen. Hurdles for the development of

TABLE 1 Clinical symptoms and epidemiology of the major group A *Streptococcus* infections

Disease	Sign(s) and/or symptom(s)	Estimated global incidence <sup>a</sup>	Associated M type(s) <sup>b</sup>	Reference(s)
<b>Superficial</b>				
Pharyngitis	Sore throat, malaise, fever	>600 million/yr	1, 3, 5, 6, 12, 14, 17, 19, 24	6, 46, 58, 62, 63
Scarlet fever	Deep red rash, "strawberry tongue," exudative pharyngitis			61, 64–66
Impetigo	Skin pustules that mature into honey-colored scabs	111 million	33, 41, 42, 52, 53, 70	6, 69, 75
<b>Sequelae</b>				
Acute rheumatic fever	Polyarthritis, carditis, rapid and jerky movements, rash, subcutaneous nodules	>471,000/yr	1, 3, 5, 6, 11, 12, 14, 17, 18, 19, 24, 27, 29, 30, 32, 41	72, 73, 589–591
Rheumatic heart disease	Mitral and/or aortic regurgitation with possible stenosis over time	15.6 million–19.6 million		66
Acute poststreptococcal glomerulonephritis	Edema, hypertension, urinary sediment abnormalities, complement deficiency	>470,000/yr	1, 4, 12, 49, 55, 57, 60	66, 75, 591
<b>Invasive</b>				
Bacteremia	High fever, nausea, vomiting	660,000 cases and 160,000 deaths/yr (all invasive diseases)		592
Puerperal sepsis	Fever, chills, abdominal pain in a pregnant or early postpartum woman		28	593
Cellulitis	Acute, tender, erythematous, and swollen area of skin			594
Necrotizing fasciitis	Fever, exquisitely tender skin lesions, vomiting, diarrhea, toxemia, tissue destruction		1, 3, 28	285
Streptococcal toxic shock syndrome	High fever, rapid-onset hypotension, accelerated multisystem failure		1, 3	291

<sup>a</sup> Data from reference 5.

<sup>b</sup> Data from reference 60.

a safe human vaccine include significant genetic diversity and antigenic variability among GAS strains and, crucially, the prerequisite to ensure that any vaccine antigen does not trigger autoimmune sequelae such as ARF and APSGN (2–4, 31, 32).

Significant progress has been made in the understanding of the molecular mechanisms underlying GAS disease pathogenesis. Recently, this work has been accelerated by publications of numerous GAS genome sequences (33–41), which have greatly facilitated molecular investigations of virulence. A large number of GAS virulence determinants have been characterized, many of which exhibit functional redundancy in the processes of adhesion and colonization, resistance to innate immunity, and the capacity to spread within the human host. Based on such molecular data, disease models have been formulated for progression to severe disease outcomes such as invasive infection, STSS, ARF, and APSGN. Unraveling the contribution of GAS virulence factors to specific disease processes will provide an improved basis for targeted therapeutic intervention.

#### EPIDEMIOLOGY, DISEASE BURDEN, AND OUTBREAKS

GAS colonizes epithelial surfaces, primarily of the throat and skin, but also colonizes other surfaces such as the vagina and rectum, from where it can cause a remarkably wide array of superficial, invasive, and immune-mediated diseases. In 2005, the WHO reported a global estimate of 18.1 million cases of severe GAS disease, with 1.78 million new cases of severe disease and 517,000

deaths per year (5). In addition, there were >111 million prevalent cases of GAS pyoderma and >616 million incident cases of GAS pharyngitis per year (5). An overview of the GAS disease spectrum and global burden is given in Table 1.

#### Epidemiology of GAS Infections

Historically, GAS isolates were typed by using serotype-specific anti-serum raised against the M protein, an immunodominant surface antigen and key virulence determinant (6). GAS strains are now more commonly typed based on the sequence of the 5' variable region of the *emm* gene encoding the M protein, of which there are over 200 *emm* types (<http://www.cdc.gov/ncidod/biotech/strep/strepindex.htm>). Large-scale epidemiological studies have shown a remarkable difference in the distribution of *emm* types in geographically and socioeconomically distinct regions of the world (2–4, 31, 32, 42). In industrialized societies, a significant percentage of GAS isolates belong to a few *emm* types, most notably *emm* types 1, 3, 12, and 28, which account for approximately 40% of disease in these countries (4, 43–47). These types are also the types most commonly isolated from asymptomatic carriers (43). In contrast, these *emm* types are less commonly isolated from cases of human disease in Africa and are rarely isolated from indigenous populations in the Pacific region and the Indian subcontinent (4, 48–50).

While certain *emm* types are responsible for a significant percentage of infections in industrialized societies, large-scale epidemiological analyses have revealed significant temporal and geo-

graphic variability in the isolation rates of individual *emm* types and subtypes, with prevalent *emm* types in a particular year being replaced by other *emm* types in subsequent years (46, 51–54). Furthermore, substantial variability is observed even within individual *emm* types. For example, Hoe et al. observed extensive allelic variation in streptococcal inhibitor of complement-mediated lysis (SIC) alleles in a large collection of *emm* 1.0 isolates (55). Likewise, Beres et al. demonstrated that successive waves of M3 infections in Canada were attributed to different subclones that arose primarily by horizontal phage transfer (56). Together, these observations suggest that, rather than being isolated at constant rates, individual *emm* types and subtypes display features of epidemic behavior, constantly expanding and subsiding as a result of host immune selective pressure.

The isolation frequency for *emm* types from different GAS diseases generally parallels their rate of asymptomatic carriage in the same population (57). However, there are significant associations of some *emm* types with particular disease manifestations (Table 1). Examples include the association of *emm* types 1, 3, and 49 with invasive disease and *emm* types 2, 4, 6, 12, and 44/61 with superficial disease (46, 58, 59). Additionally, some *emm* types are associated with particular GAS disease manifestations such as ARF (e.g., *emm* types 1, 3, 5, 6, 11, 12, 14, 17, 18, 19, 24, 27, 29, 30, 32, and 41), APSGN (e.g., *emm* types 1, 4, 12, 49, 55, 57, and 60), and puerperal sepsis (*emm* type 28) (60).

### Burden of Superficial GAS Infections

The vast majority of GAS diseases are superficial infections of the throat and skin, resulting in pharyngitis and impetigo, respectively (6, 61).

**Pharyngitis.** GAS is the most common bacterial cause of pharyngitis, with over 600 million cases per year (5). The clinical symptoms of GAS pharyngitis include a sudden-onset fever accompanying a sore throat, which frequently manifests physically as inflammation of the pharynx and tonsils, often with patchy exudates and cervical lymph node adenopathy. Other common symptoms include malaise, fever, headache, nausea, abdominal pain, and vomiting (62, 63). Uncomplicated GAS pharyngitis is generally self-limiting. Pharyngitis is spread by person-to-person contact, presumably via nasal secretion or saliva droplets from carriers or infected individuals (63, 64). As such, the incidence of pharyngitis is highest in places of crowding, such as schools and military training facilities. Approximately 15% of schoolchildren and 4 to 10% of adults may suffer an episode of GAS pharyngitis each year in developed countries (5), whereas incidence rates in developing countries are 5 to 10 times higher (5).

**Scarlet fever.** Occasionally, GAS pharyngitis is accompanied by scarlet fever, which is thought to result from pharyngeal infection with a GAS strain that secretes bacteriophage-encoded streptococcal pyrogenic exotoxins, most notably SpeA (64–66). Also known as scarlatina, scarlet fever manifests as a deep red, finely papular, erythematous rash; “strawberry tongue”; and exudative pharyngitis (61). While scarlet fever was a significant cause of childhood morbidity and mortality in the 19th and early 20th centuries, global rates have steadily declined over the last 150 to 200 years such that it was considered a relatively rare disease until recently (67, 68). However, recent outbreaks of scarlet fever in Hong Kong and mainland China illustrate that scarlet fever remains a significant health problem (see below).

**Impetigo.** Impetigo is a contagious infection of the skin that

manifests as pustules that gradually enlarge and rupture, forming thick, honey-colored scabs (64, 69). The disease is spread through direct skin contact and most commonly affects children living in tropical and subtropical climates in areas with poor hygiene and crowded living conditions (69, 70). The annual global disease burden is estimated to be 111 million cases (5).

### Burden of Immune Sequelae

Prior GAS infection may result in a number of postinfectious sequelae, which include ARF/RHD, APSGN, and, debatably, pediatric autoimmune neuropsychiatric disorders.

**Acute rheumatic fever.** Acute rheumatic fever (ARF) is a systemic disorder that can follow untreated GAS pharyngeal infection (71). Diagnosis of ARF is based on updated Jones criteria and consists of fulfilling a certain number of major and minor disease criteria (72). The major manifestations are inflammation of the joints (arthritis) (60 to 80% of cases), inflammation of the heart (carditis) (30 to 45% of cases), and/or neurological symptoms (e.g., Sydenham chorea) (10% of cases). Less common manifestations of the skin include erythema marginatum (2% of cases) or, rarely, subcutaneous nodules (73). ARF is a major source of morbidity and mortality worldwide, particularly as it may result in long-term damage to the heart, termed RHD, with an estimated 15.6 million cases worldwide in 2005, including 282,000 new cases and 233,000 deaths each year (5). This disease burden includes over 2.4 million cases in patients aged 5 to 14 years, making RHD the most common cause of pediatric heart disease worldwide (73). ARF is a particularly serious problem in indigenous populations and developing nations, where the highest rates of disease are observed. In a 2005 study, the highest rates of ARF were found in sub-Saharan Africa (5.7 cases per 1,000), in the Pacific Islander and indigenous minority populations of Australia and New Zealand (3.5 cases per 1,000), and south central Asia (United Nations regional classification) (2.2 cases per 1,000) (5). Due to the high rates of impetigo and low rates of GAS pharyngitis in the indigenous Australian population, it has been proposed that ARF can also occur as a complication of impetigo, although this has not been confirmed (74).

**Acute poststreptococcal glomerulonephritis.** APSGN is an immune complex-mediated disorder of the kidneys, resulting in symptoms such as edema, hypertension, urinary sediment abnormalities, and decreased levels of complement components in the serum (66, 75). Globally, there are over 470,000 annual cases, resulting in approximately 5,000 deaths worldwide (5). APSGN rates are highest in children in less developed countries, with incidence rates as high as 94.3/1,000 being reported in the Northern Territory of Australia (76). Unlike ARF, APSGN tends to occur in outbreaks associated with “nephritogenic” strains of GAS (e.g., *emm* types 1, 4, 12, 49, 55, 57, and 60) and contributing risk factors such as crowding, poor hygiene, and poverty (75–77). With proper supportive care, long-term renal damage as a result of APSGN is rare.

**Pediatric autoimmune neuropsychiatric disorders associated with streptococcal infections.** GAS infection has been hypothesized to be temporally associated with rare obsessive-compulsive disorders and Tourette’s syndrome in children, termed pediatric autoimmune neuropsychiatric disorders associated with streptococcal infections (PANDAS). However, the relationship of GAS to these behavioral disorders remains highly controversial, and recent studies have failed to provide a conclusive link of GAS infec-



tion to the exacerbation of disease symptoms (78, 79). As such, the pathogenesis of PANDAS remains unknown, but it has been hypothesized that GAS infection results in antineuronal antibodies (79).

### Burden of Invasive Disease

Less common than the superficial diseases and the immune sequelae described above, GAS has the capacity to breach epithelial barriers and cause a variety of invasive diseases, with high rates of morbidity and mortality. Approximately 8 to 23% of patients with GAS invasive disease die within 7 days of infection (7, 80, 81). The most common invasive diseases are bacteremia and cellulitis. GAS may also less commonly cause necrotizing fasciitis, septic arthritis, pneumonia, meningitis, abscess, osteomyelitis and other focal infections, endocarditis, and peritonitis. GAS invasive disease may be complicated by the development of STSS, which increases mortality rates; 23 to 81% of STSS patients die within 7 days postinfection (7, 80–82). There has been a notable global increase in the percentage of invasive GAS infections that are severe since the late 1980s (19, 20, 83, 84). A 2005 WHO study estimated that at least 663,000 cases of invasive GAS disease occur each year, resulting in 163,000 deaths (5). Similar rates of disease are observed in a number of developed countries (2 to 3 per 100,000), which corresponds to approximately 10,000 cases per year in the United States (7, 80, 81, 85, 86). As with other GAS diseases, the rates of invasive GAS disease are higher in less developed regions, with the highest rates being observed in indigenous populations in Australia (13.2 to 82.5 per 100,000 [87–89]), Africa (13.0 per 100,000 [90]), and the Pacific Islands (9.9 to 11.6 per 100,000 [91, 92]).

### Outbreaks of GAS Diseases

While GAS is traditionally considered a pathogen in which disease results as a consequence of asymptomatic carriage or recent acquisition from a close contact, it also has the capacity to cause outbreaks. Small-scale localized outbreaks of GAS pharyngitis have been described in the literature and appear to occur as a result of transmission of a GAS strain to susceptible individuals through either a common source or, particularly in crowded settings, person-to-person spread. Examples include outbreaks in military training centers as a result of crowding (93, 94), multiple outbreaks following consumption of contaminated foods (95–102), and hospital-acquired puerperal sepsis outbreaks (22–24).

Large-scale GAS outbreaks also occur as a result of the emergence of dominant clones, which may arise through the horizontal acquisition of DNA that encodes toxins or antibiotic resistance determinants (19, 26, 40, 103), or through more subtle genetic changes (104, 105). The increase in the percentage of severe invasive GAS disease since the 1980s has paralleled the emergence of the MIT1 clone. This clone has disseminated globally and accounts for a significant proportion of clinical isolates throughout the developed world. The MIT1 clone has acquired three regions of heterologous DNA: a 36-kb chromosomal region that encodes the toxins streptolysin O (SLO) and NAD-glycohydrolase and two bacteriophages that encode the DNase Sda1 and the superantigen SpeA (19, 20, 40, 103). Similarly, outbreaks of M3 GAS disease in Canada have been attributed to the rapid expansion of clonal GAS strains following multiple genetic changes, including the acquisition of prophages encoding phospholipase A2 and SpeA and the duplication of 4 amino acids in the N-terminal region of the M3

protein (105–107). An *emm* 59 GAS outbreak of invasive disease in North America beginning in 2004 has been reported (21, 108).

A large ongoing outbreak of scarlet fever in Hong Kong and mainland China is being monitored (109–111). Starting in 2011, there was an alarming increase in the number of scarlet fever cases, including >1,500 cases in Hong Kong (110) and over 6,000 cases in Beijing (111). The Chinese Ministry of Health reported a combined 110,000 cases of scarlet fever in mainland China in 2011 to 2012. The genome sequence of 2 GAS *emm* 12 strains from Hong Kong revealed the acquisition of a 64.9-kb integrative and conjugative element encoding tetracycline and macrolide resistance and a 46.4-kb prophage encoding the superantigens streptococcal superantigen (SSA) and SpeC and the DNase Spd1 (26). However, broader molecular analysis identified multiclonal outbreak isolates that were likely circulating in the population prior to 2011. Thus, the reason for the rapid increase in the number of scarlet fever cases in Hong Kong and Beijing may be related to either population immune status and/or other unknown environmental factors (26).

## GAS TRANSMISSION, ADHESION, AND TISSUE TROPISM

### Transmission of GAS

The nasopharyngeal mucosa and skin are the principal sites of GAS asymptomatic colonization. These sites are also the most common sources of infections such as pharyngitis and impetigo. These tissue sites represent the primary reservoirs responsible for the maintenance and transmission of GAS to a new host. The characterized ability of GAS to overcome the innate and acquired immune mechanisms present in saliva allows the bacterium to remain viable for long periods (112), permitting transmission from infected persons or asymptomatic carriers via respiratory droplets. Similarly, the ability of GAS to colonize and persist in skin tissue permits transmission through person-to-person skin contact. Therefore, family members or close contacts of primary cases are at greater risk than the general population for subsequent infection. While GAS is transmitted primarily from person to person, there have been numerous reports of disease outbreaks caused by food-borne GAS (95–102).

### Adherence of GAS

Lipoteichoic acid (LTA) and several proteins on the cell surface of GAS are important for the adherence of these bacteria to cultured human cells and to extracellular matrix (ECM) proteins (reviewed in reference 113). Initial bacterial attachment is hypothesized to be a two-stage process involving weak and/or long-range interactions followed by more specific, high-affinity binding (114). LTA, a membrane-bound amphiphilic polymer of glycerol phosphate containing glucose and D-alanine substitutes (115), may contribute to the initial adherence of GAS to host surfaces by establishing weak hydrophobic interactions between bacterial cells and host components (114). This weak interaction permits longer-distance first-attachment events to be mediated through long surface appendages such as pili, allowing the second stage of adherence to occur, involving multiple, higher-affinity binding events such as protein-protein or lectin-carbohydrate interactions.

The cell surface proteome of GAS includes numerous protein adhesins that permit bacterial interactions with multiple host components, which allow GAS to colonize diverse tissue sites in the human body (Table 2). GAS surface proteins are attached to

TABLE 2 Adhesins of *S. pyogenes*<sup>a</sup>

Protein group	Protein(s)	Cell surface linkage <sup>b</sup>	Substrate(s) and/or function(s)	M type distribution <sup>c</sup>	Reference(s)
Pili	Spy0130, Spy0128, Cpa	LPxTG	Pilus structural proteins; collagen binding, gp340 binding, bacterial aggregation, biofilm formation	FCT-specific M type	119, 126, 130
M and M-like proteins	M1, M3, M6, protein H	LPxTG	Fibronectin binding, fibrinogen binding	M-type specific	135, 141, 151
AgI/II family	AspA	LPxTG	gp340; bacterial aggregation	M2, M28	595, 596
Fibronectin binding	PrtF1/SfbI	LPxTG	Fibronectin binding	FCT-specific M type (FCT 1, 4, 5, 7, 8, 9)	126, 169, 597
	PrtF2/PFBP/FbaB	LPxTG	Fibronectin binding	FCT-specific M type (FCT 3, 4, 6, 7, 8)	126, 598–600
	SOF/SfbII	LPxTG	Fibronectin binding, fibrinogen binding	In 55% of GAS strains	168, 171
	SfbX	LPxTG	Fibronectin binding	In 55% of GAS strains	601
	Fbp54	Anchorless	Fibronectin binding, fibrinogen binding	In 100% of GAS strains	172, 566, 602
	FbaA	LPxTG	Fibronectin binding	M1, M2, M4, M9, M13, M22, M28, M44, M49, M60, M67, M75, M77, M79, M80, M82, M87, and M89	143
Collagen-like	Scl1, Scl2	LPxTG	Laminin binding and $\alpha 2\beta 1$ and $\alpha 11\beta 1$ integrin binding	In 100% of GAS strains	153, 159, 603, 604
Laminin binding	Lbp	LXXC/XXGC	Laminin binding	In 100% of GAS strains	155
	Shr	Anchorless	Laminin binding, fibronectin binding	In 100% of GAS strains	154, 605
Plg binding	GAPDH/Plr	Anchorless	Fibronectin binding, plasminogen binding	In 100% of GAS strains	606
	SEN	Anchorless	Plasminogen binding	In 100% of GAS strains	343

<sup>a</sup> Abbreviations: FCT, fibronectin binding, collagen binding, T antigen region.

<sup>b</sup> LPxTG, sortase A motif; LXXC/XXGC, lipoprotein consensus sequence.

<sup>c</sup> One or more M types can be associated with a specific FCT variant, but strains belonging to a specific M type carry the same FCT region (184).

the bacterial surface by three known mechanisms: covalently to the cell wall peptidoglycan anchored via a C-terminal LPxTG (where x is any amino acid) motif, which is recognized by sortase A (116–118); covalently bound to the cell membrane through N-terminal modifications with lipid (lipoproteins) (113, 118); and through noncovalent interactions with cell surface components (113).

**GAS pili.** Discovered in 2005, GAS pili, or fimbriae, appear as long, flexible rods protruding up to 3  $\mu$ m from the cell surface (119). GAS pili are heteropolymeric structures consisting of a pilus shaft made up of the major pilin protein subunit (Spy0128), which is assembled by a series of transpeptidase reactions catalyzed by a class B accessory sortase, SrtC (Spy0129) (120–122). Additionally, this class B sortase also mediates the attachment of the minor pilin proteins, including the adhesin Cpa (Spy0125), which attaches to the tip of the pilus, and the basal pilin Spy0130, which acts as a linker protein for attachment to the cell wall (122, 123). Sortase A is responsible for linking the pilus structure to the cell wall (124). The pilus biosynthesis and sortase genes are grouped together as a pathogenicity island located in the FCT region of the GAS genome, which encodes fibronectin binding proteins, collagen binding proteins, and T antigens (pilus subunit

genes) (125). Among GAS isolates, this region displays considerable genetic diversity, with nine different FCT variants identified (126, 127). Pili contribute to GAS pathogenesis through direct involvement in bacterial adhesion. Pili mediate the attachment of M1 GAS (strain SF370) to human tonsillar epithelium and to primary human keratinocytes (128). Additionally, pili contribute to microcolony formation on human cells and the formation of biofilm (129). GAS pili also bind the salivary scavenger receptor glycoprotein gp340 to promote bacterial cell aggregation in saliva. This aggregation reduces bacterial adhesion to pharyngeal cells and therefore may serve as a bacterial clearance mechanism (130).

**Role of M proteins in adherence.** The M protein is a major surface protein and virulence factor of GAS, which is anchored to the cell wall peptidoglycan through an LPxTG motif (117, 131). The M protein exists as a dimer consisting of two polypeptide chains complexed into an  $\alpha$ -helical coiled-coil configuration that extends beyond the GAS surface as hairlike projections (132). The M protein typically consists of four repeat regions (designated regions A to D) that vary in size and amino acid composition. The C terminus of the molecule (including the C and D repeat regions) is highly conserved among GAS strains. The surface-exposed N terminus of the M protein usually consists of a hypervariable re-

gion (encompassing the A repeat region) and a semivariable B repeat region (reviewed in reference 133). While the genetic variability of M proteins is used as an epidemiological tool, such variability also imparts a diverse range of physiological functions. Numerous studies have demonstrated that GAS strains utilize M proteins for adherence to and internalization into epithelial cells and keratinocytes (134–139). M proteins (M1, M3, and M6) may promote bacterial colonization by binding directly to components of the ECM, such as fibronectin (140, 141). Additionally, ECM proteins such as fibronectin, which also bind to the host cell surface integrin  $\alpha 5\beta 1$ , can act as bridging molecules between bacterial cells and host cells that express integrins on the cell surface. This interaction also promotes integrin-mediated internalization of GAS into host cells (135, 139, 142–144). Additionally, the M6 protein binds directly to ligands present on host cells, such as the keratinocyte membrane cofactor CD46 (145), and the M1 protein can bind to surface-expressed glycosaminoglycans, including dermatan sulfate, heparan sulfate, and heparin (146). Furthermore, the M1 protein promotes interbacterial aggregation to enhance bacterial adherence to and invasion of epithelial cells (147).

**Other GAS proteins that bind ECM components.** Binding to ECM components is a common strategy used by numerous pathogens for host colonization. Cell surface adhesins that recognize ECM components have been termed MSCRAMMs (microbial surface components recognizing adhesive matrix molecules) (148), which interact directly with ECM components such as fibronectin, collagen, and laminin. In GAS, 11 fibronectin binding proteins have been characterized, with the majority of these proteins being anchored to the cell wall through an LPxTG motif (Table 2).

Fibronectin binding proteins can be divided into two types: those that contain fibronectin binding repeats (PrtF1/SfbI, FbaA, PrtF2/FbaB/PFBP [*S. pyogenes* fibronectin-binding protein], SfbII/SOF [serum opacity factor], SfbX, and Fbp54) and those with no repeats (M proteins, protein H, glyceraldehyde-3-phosphate dehydrogenase [GAPDH]/Plr, Shr, and Scl1) (reviewed in reference 149). Fibronectin binding repeat sequences are generally located toward the C-terminal end of the protein and can vary in length and number (149). Each fibronectin binding repeat can potentially bind one fibronectin dimer via a specific protein-protein interaction called a “tandem  $\beta$ -zipper,” whereby a repeat sequence forms additional antiparallel  $\beta$ -strands on sequential  $\beta$ -sheet motifs located at the N terminus of fibronectin (150).

Other multifunctional surface adhesins possess the ability to bind to fibronectin despite lacking fibronectin binding repeat domains. These adhesins include M proteins (serotypes M1, M3, and M6) (135, 141), protein H (151), GAPDH (152), the hemoprotein binding protein Shr, and the collagen-like protein Scl1, which can bind both fibronectin and laminin (153, 154). Additionally, GAS strains possess a laminin binding lipoprotein, Lbp, which plays a role in epithelial cell adherence (155).

**Epithelial cell adherence and internalization.** Many of the cell surface adhesins expressed by GAS are also involved in internalization into epithelial cells. Bacteria may utilize ECM proteins bound to MSCRAMMs as bridging molecules to bind to integrins present on the surface of host cells. This interaction activates cellular signaling pathways that lead to the rearrangement of cytoskeletal actin in host cells and the uptake of invading bacteria. The most well-characterized example of this signaling mechanism involves MSCRAMM-bound fibronectin and its subsequent inter-

action with integrin  $\alpha 5\beta 1$  (139, 144). When fibronectin binds to MSCRAMMs, it undergoes a conformational change which exposes an RGD motif allowing it to interact with the  $\alpha 5\beta 1$  integrin (149) and results in integrin clustering and the formation of focal complexes on the host cell surface (156), followed by internalization into the endocytic pathway via a “zipper-like” mechanism (156–158). Focal adhesion kinase (FAK); integrin-linked kinase (ILK); Rac; CDC42; and the Src kinases Src, Yes, and Fyn have also been shown to be involved in  $\alpha 5\beta 1$ -mediated GAS internalization (144, 156). Similarly, the collagen-like protein Scl1 can also mediate epithelial cell adherence and internalization by directly binding to integrins  $\alpha 2\beta 1$  and  $\alpha 11\beta 1$  through their collagen-like domains (159, 160). Once internalized, some GAS strains are susceptible to autophagy following escape from endosomes into the cytoplasm (161, 162). However, expression of the secreted cysteine protease SpeB results in proteolytic clearance of autophagy components from the bacterial surface, allowing intracellular proliferation (161).

**Role for human plasminogen in adherence and internalization.** Plasminogen bound to the cell surface of GAS can also act as a bridging molecule for bacterial interactions with host cells. Plasminogen bound to the GAS cell surface can interact with keratinocytes via the cell-exposed integrins  $\alpha 1\beta 1$  and  $\alpha 5\beta 1$  (137). This interaction promotes integrin-mediated binding and internalization of GAS in a process which is similar to that of bacterial bound-fibronectin-mediated pathways.

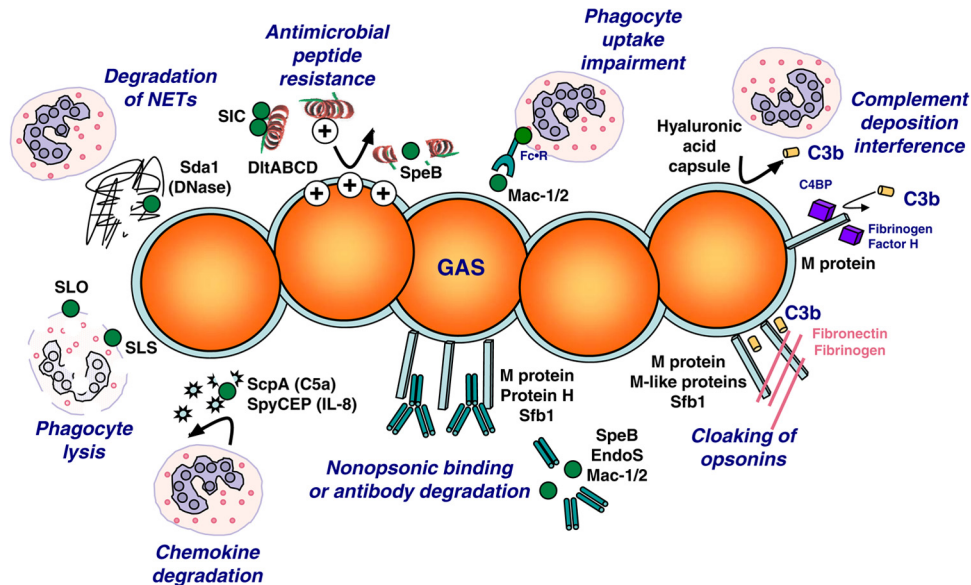
### GAS Tissue Tropism

Since GAS bacteria possess a large repertoire of adhesins, there is the possibility of a high degree of functional redundancy. However, the majority of adhesins are not present in all GAS serotypes. Of the adhesins listed in Table 2, only Fbp54, GAPDH, streptococcal surface enolase (SEN), and Lbp genes are present in all GAS strains examined. Additionally, the expression of GAS adhesins is highly regulated in response to environmental factors (163). Therefore, the production of functionally similar adhesins by GAS could be regarded as an adaptation mechanism that allows bacteria to successfully colonize the different tissue environments encountered during the infection process.

Numerous epidemiological studies support the existence of throat-tropic and skin-tropic GAS strains; i.e., certain *emm* types have a strong tendency to cause throat infection but not superficial skin infection, while other *emm* types are often recovered from cases of impetigo but rarely from cases of pharyngitis (164). The chromosomal arrangement of *emm* and *emm*-like genes is a genetic marker for tissue site preference, and these arrangements, referred to as *emm* patterns, consist of five major groups, patterns A to E (165). *emm* pattern A to C isolates are considered throat specialists, whereas *emm* pattern D strains are skin specialists. Furthermore, *emm* pattern E isolates are considered generalists and can be found at both tissue sites (166). Risk factors for skin infection include crowding, poor living conditions, and high rates of scabies infection, which may explain the relative prevalence of *emm* pattern D strains in indigenous populations, while crowding in places such as schools is the major risk factor for pharyngeal infection with GAS strains belonging to *emm* patterns A to C (42).

Attempts have been made to identify the specific adaptations responsible for niche specialization, and several GAS genes that display strong linkage disequilibrium with the *emm* pattern groupings have been identified (127, 167). Most of the linked





**FIG 1** The arsenal of virulence factors expressed by GAS to thwart the host innate immune response. The secreted proteases SpyCEP/ScpC and ScpA degrade the chemokines IL-8 and C5a, respectively, hindering phagocyte recruitment to the site of infection. Surface-associated M protein binds Fc domains of Ig and the complement-regulatory proteins C4BP and factor H to interfere with complement deposition. Mac-1/2 degrades Ig and binds phagocyte Fc receptors to block phagocytosis. Antimicrobial peptide resistance is mediated by hyaluronic acid capsule, D-alanylation of surface lipoteichoic acid by DltABC, and degradation by the cysteine protease SpeB. Ig and antimicrobial peptides are degraded by SpeB to facilitate the establishment of GAS infection *in vivo*. Secreted Sda1 DNase activity degrades NETs to promote neutrophil survival. The cytolysins SLS and SLO mediate lysis and apoptosis of neutrophils and macrophages.

genes currently identified are clustered within two genomic regions: the *emm* region itself and the FCT region (125). Genes with a differential presence or absence among tissue-tropic strains include *cpa* (encoding a type I collagen binding protein) (168), *prtF1* (encoding the fibronectin binding protein PrtF1) (169), *sof* (encoding serum opacity factor, which contains a fibronectin binding domain) (170, 171), and *prtF2* (encoding the fibronectin binding protein PrtF2) (172). Loci that form discrete phylogenetic lineages, which can then be associated with tissue-specific *emm* patterns, include the transcriptional regulators *mga* (a global regulator of numerous virulence factors) (173), *rofA* and *nra* (mutually exclusive transcriptional regulators of the genes in the FCT region) (167), and *ska* (encoding the plasminogen-activating protein streptokinase) (174, 175). While it is conceivable that tissue site preferences for infection in the throat or skin might be explained by the expression and/or regulation of tissue-specific colonization factors such as adhesins, the exact mechanisms responsible for tissue tropism are yet to be fully elucidated.

### RESISTANCE TO HOST IMMUNE DEFENSE SYSTEMS

As a human-adapted pathogen, GAS is protected by a multitude of surface-bound and secreted virulence factors that subvert host innate immune defenses. These factors include enhanced resistance to phagocytosis, complement deposition, antibody opsonization, antimicrobial peptides (AMPs), and neutrophil killing mechanisms (Fig. 1).

#### Resistance to Opsonophagocytosis

In order to facilitate local invasion and systemic spread, GAS must resist opsonophagocytic killing by neutrophils, which represent the main host clearance mechanism for extracellular pathogens. GAS strains possess an extensive repertoire of virulence factors

that play a crucial role in resistance to opsonophagocytosis, including complement inhibitors (M protein, hyaluronic acid capsule, and SIC), leukocidal toxins (SLO and streptolysin S [SLS]), immunoglobulin (Ig) binding proteins (PrtF1/SfbI, FbaA, and Sib), and Ig-degrading enzymes (IdeS, endo- $\beta$ -N-acetylglucosaminidase of streptococci [EndoS], and SpeB).

**Inhibitors of complement deposition and activation.** The M protein is expressed on the surface of all GAS isolates and plays a critical role in GAS resistance to opsonophagocytic clearance (176). Complement-inhibitory proteins, including C4b binding protein (C4BP) (177–179), factor H (180), and factor H-like protein 1 (FHL-1) (181), are bound by the M protein to thwart complement deposition and efficient opsonophagocytosis. Factor H binding accelerates the decay of the C3b opsonin deposited on the bacterial surface and limits the activation of the alternative complement pathway, thereby allowing GAS to persist in infected tissues (180). M-protein- and Mrp-mediated (182) fibrinogen binding confers resistance to phagocytosis by preventing complement C3 convertase deposition on the bacterial surface (183–185). Similarly, M-protein-mediated plasminogen binding prevents deposition of the opsonin C3b, preventing phagocytic uptake of GAS by neutrophils (186). Furthermore, the M protein impairs phagosome maturation by inhibiting the fusion of azurophilic granules within the phagosome (187).

Strains of most GAS serotypes are encased within a capsule composed of hyaluronic acid, a surface shield that further promotes resistance to opsonophagocytosis (188, 189). Capsule expression is upregulated in human blood (190, 191), and hyperencapsulated (mucoid) strains are frequently isolated from patients with GAS invasive disease (192). Encoded by the highly conserved *hasABC* synthase operon (193, 194), the capsule is a high-molec-



ular-mass polymer of glucuronic  $\beta$ -1,3-*N*-acetylglucosamine (195) and is structurally identical to the hyaluronic acid expressed on human cell surfaces and connective tissue, allowing GAS to subvert the host immune response through molecular mimicry (6). The membrane-associated hyaluronate synthase, encoded by the first gene in the operon, *hasA*, is essential for hyaluronic acid biosynthesis (196, 197) and forms the linear hyaluronic acid polymer by the alternate addition of glucuronic acid and  $\beta$ -1,3-linked *N*-acetylglucosamine residues (196, 198). In serotype M1T1 GAS strains, the second gene in the operon, *hasB*, is nonessential due to the presence of HasB2, a secondary UDP-glucose 6-dehydrogenase encoded by *hasB2* that is located outside *hasABC* (199). The third gene in the operon, *hasC*, is not essential for GAS capsule biosynthesis (196, 197).

The GAS capsule blocks antibody access to surface epitopes (200), inhibits complement deposition (188), promotes resistance to opsonophagocytosis (188, 189), enhances survival within neutrophil extracellular traps (NETs) (201), and is necessary for full virulence in mouse (202–205) and nonhuman primate (206) models of invasive GAS infection. Nonencapsulated GAS mutants are susceptible to phagocytic clearance *in vitro* and have dramatically reduced virulence in murine models of invasive GAS disease (202, 205). GAS *emm* 4 and *emm* 22 strains lack the *hasABC* operon, are nonencapsulated (207), and express a hyaluronic acid-degrading enzyme, hyaluronate lyase (HylA) (208). Despite the lack of capsule, *emm* 4 GAS strains proliferate in whole human blood *ex vivo* (207).

Streptococcal inhibitor of complement-mediated lysis (SIC) is a secreted 31-kDa virulence factor uniquely expressed by serotype M1 and M57 GAS strains (209) that binds and inhibits the complement C5b67 complex to prevent formation of the membrane attack complex (209, 210), which is generally ineffective against the thick and highly cross-linked Gram-positive bacterial cell wall. SIC also contributes to epithelial cell adherence (211) and mucosal colonization (212) and binds innate immune factors, including secretory leukocyte protease inhibitor, lysozyme, human  $\alpha$ -defensin-1, and human cathelicidin antimicrobial peptide LL-37 (213–215). The *sic* gene is highly polymorphic, suggesting that it is under strong immune selective pressure to avoid host neutralizing antibodies (55). Variants of SIC, termed CRS (closely related to SIC) and DRS (distantly related to SIC), also bind complement proteins C6 and C7 (216, 217).

The fibronectin binding protein FbaA is encoded in the genome of strains of GAS serotypes 1, 2, 4, 22, 28, and 49 and is positively transcribed by Mga (143). FbaA binds the human complement-regulatory proteins factor H and FHL-1, preventing the deposition of C3b on the GAS cell surface, and promotes survival in whole human blood (218).

**Leukocidins.** To avoid host defense mechanisms, GAS bacteria express extracellular toxins to directly attack immune cells or induce harmful by-products. SLO is a 69-kDa cholesterol-dependent and oxygen-labile cytolysin that contributes to beta-hemolysis under the surface of blood agar medium (219). SLO oligomerizes to form large pores ( $\sim$ 25 to 30 nm) in host cell membranes (220). SLO promotes resistance to phagocytic killing by disrupting the integrity of host cell membranes (220), inducing rapid caspase-dependent apoptosis in neutrophils, macrophages (221), and epithelial cells (222). SLO expression facilitates GAS escape from the endosome after host cell invasion (223) and reduces host tumor necrosis factor alpha (TNF- $\alpha$ ) and interleu-

kin-1 $\beta$  (IL-1 $\beta$ ) inflammatory cytokine responses, promoting virulence in mouse models of GAS invasive disease (221). Nicotinamide dehydrogenase (NAD-glycohydrolase) is coexpressed with SLO and transported into the cytoplasm of target cells through SLO-induced pores to deplete intracellular energy stores and augment host cell injury (224). In addition to protecting GAS from phagocytic killing, SLO contributes to tissue damage at the site of infection (221, 222). SLO has also been shown to facilitate penetration of stratified squamous cell mucosa by superantigens (225), enhancing the level of SLO-associated tissue damage during infection. Furthermore, for serotype M1 GAS strains, SLO has been shown to induce platelet-neutrophil aggregation (226), contributing to vascular occlusion and tissue damage in invasive disease. The central importance of SLO in GAS disease pathogenesis is supported by findings that SLO mutants are attenuated for virulence in subcutaneous, intravenous, and intraperitoneal mouse models of invasive GAS disease (221, 227, 228).

SLS is a potent membrane-active beta-hemolysin secreted by virtually all GAS isolates during stationary-phase growth, with structural similarities to the bacteriocin family of microbial toxins (229). SLS is encoded by a conserved nine-gene operon, comprised of the genes *sagA* to *sagI* (SLS-associated gene), which is responsible for the characteristic zone of beta-hemolysis surrounding GAS colonies on the surface of blood agar medium (229, 230). SLS is an oxygen-stable cytolytic toxin that enhances GAS resistance to phagocytosis by forming hydrophilic pores in neutrophil cell membranes (231). SLS contributes to GAS virulence and pathogenesis by lysing a broad spectrum of host cells, including lymphocytes, erythrocytes, platelets, and several other cells (232). The impairment of local inflammatory cells by SLS may promote the dissemination of GAS throughout the host (233). *In vitro* studies suggest that SLS may contribute to pathogenesis by direct cytotoxicity, inflammatory activation, and inhibition of neutrophil phagocytosis (234). Furthermore, the synergistic interaction between SLS, SpeB, and neutrophil-derived proteases has been shown to produce cellular injury *in vitro* (234). In a mouse model of streptococcal necrotizing soft tissue infection, wild-type GAS strains displayed enhanced virulence compared to SLS-deficient mutants, as measured by bacterial proliferation, neutrophilic inflammation, vascular injury, and tissue necrosis (230). These data suggest that SLS contributes to the rapid tissue necrosis that is characteristic of invasive GAS soft tissue infection. The expression of both SLO and SLS enhanced GAS virulence in a mouse model of bacterial sepsis (235).

**Ig binding proteins.** Invading microorganisms are bound with immunoglobulin to facilitate killing by phagocytosis, complement fixation, or both. IgA is found predominantly in mucosal secretions and is most effective at restricting bacterial adhesion. IgG is located in the bloodstream and injured tissues, facilitating bacterium-phagocyte contact via the Fc receptors on phagocytes. GAS isolates are commonly associated with the expression of surface-associated Ig binding proteins that bind the Fc region of human IgA or IgG (236). The GAS Ig binding M proteins, M-related proteins (Mrp), and M-like proteins (Mlp or Enn) are classified into the M protein family (237). M and Mlp typically bind the Fc region of IgA, while Mrp binds the Fc region of IgG, preventing complement activation on the GAS cell surface (238, 239).

The fibronectin binding repeats of PrtF1/SfbI bind the Fc region of human IgG in a nonimmune fashion, which prevents

phagocytosis by macrophages and antibody-dependent cell-mediated toxicity (240, 241). The secreted immunoglobulin binding protein from GAS, SibA, is a conserved 45-kDa protein that is encoded in the genomes of most GAS strains. SibA binds the Fc and Fab regions of IgG, IgA, and IgM antibodies (236). While SibA lacks sequence homology with M or M-related proteins, it has an N-terminal alpha-helical secondary structure, which is implicated in M protein Ig binding (236).

**Ig-degrading enzymes.** The IgG-degrading enzyme of *S. pyogenes* (IdeS), also known as Mac-1, Sib35, and MspA, inhibits phagocytosis, neutrophil activation, and the release of reactive oxygen species by binding Fc receptor CD16 (FcγRIIIB) on the surface of neutrophils (242, 243). IdeS exhibits cysteine protease activity and contributes to opsonophagocytosis resistance in whole human blood by cleaving the lower Fc region of surface-bound human IgG (244). However, isogenic mutant studies found that IdeS is not essential for phagocyte resistance or mouse virulence in serotype MIT1 GAS strains (245). Mac-2, a related IgG endopeptidase, binds Fcγ receptors and prevents the recognition of IgG bound to GAS by host phagocytes (246).

Encoded by the *ndoS* gene in serotype M1 GAS strains, the endo-β-N-acetylglucosaminidase of streptococci (EndoS) is a secreted endoglycosidase that hydrolyzes the chitobiose core of the asparagine-linked glycan on the heavy chain of native human IgG (247), impairing recognition by Fc receptors, complement activation, and phagocytosis (248). The heterologous expression of EndoS in strains of non-M1 serotypes enhances virulence in a mouse model of invasive GAS infection (249). EndoS<sub>2</sub>, encoded by *ndoS2*, is a unique and conserved endoglycosidase of serotype M49 GAS with 37% identity to the EndoS protein. EndoS<sub>2</sub> hydrolyzes biantennary and sialylated glycans on α1-acid glycoprotein (AGP) and all N-linked glycans on the heavy chain of IgG to impair immune effector functions (250).

Streptococcal pyrogenic exotoxin B (SpeB) is a broad-spectrum cysteine protease secreted by most GAS isolates (251) from late logarithmic to stationary phase (252). Encoded by the ubiquitous and conserved *speB* gene, SpeB is produced as an inactive 40-kDa zymogen and undergoes sequential N-terminal autocatalytic activation to the active 28-kDa protease (253). SpeB expression impedes the initial host immune response and is required for the establishment of localized skin infections (254), proliferation in human saliva (112), and full virulence in a humanized plasminogen mouse model of GAS infection (255). SpeB degrades IgG, IgA, IgM, IgD, and IgE (247).

### Resistance to Antimicrobial Peptides

Antimicrobial peptides (AMPs) are small cationic molecules produced by host cells, often exhibiting potent bactericidal activity. GAS resistance to AMPs is mediated through degradation (SpeB and plasmin), electrostatic repulsion (DltA), or binding/inactivation (SIC).

**Degradation or inactivation of AMPs.** SpeB cleaves and inactivates human cathelicidin LL-37 (256), a small cationic antimicrobial peptide of the innate immune system produced by skin keratinocytes, mucosal epithelial cells, and neutrophils with bactericidal activity and electrostatic affinity for negatively charged bacterial surfaces (257). The acquisition of plasmin protease activity on the GAS cell surface plays a key role in GAS pathogenesis (258). GAS surface-bound plasmin activity was recently demonstrated to promote degradation of human cathelicidin LL-37

(259). SIC also binds and inhibits antimicrobial peptide LL-37 (213–215).

**Electrostatic repulsion of AMPs.** The D-alanine–D-alanyl carrier protein ligase, DltA, is required for D-alanylation of lipoteichoic acid (LTA) (260), a surface-bound amphiphilic polyglycerolphosphate polymer important for GAS epithelial cell adherence (261, 262). The D-alanine esterification of LTA, coordinated by the *dltABCD* operon (263), increases the net positive surface charge, improving GAS resistance to LL-37, acidic pH, lysozyme, and neutrophil-mediated killing (264). Targeted mutagenesis of *dltA* reduces expression levels of the M protein and SIC, rendering the bacteria more susceptible to C3b complement deposition and killing in whole human blood (265).

### Impairment of Neutrophil Killing Mechanisms

**Degradation of neutrophil attractants.** The proteolytic degradation of chemotactic substances such as IL-8 and C5a by *S. pyogenes* cell envelope protease (SpyCEP) and ScpA, respectively, impairs neutrophil recruitment, impeding phagocytosis at the site of infection and promoting GAS survival *in vivo*.

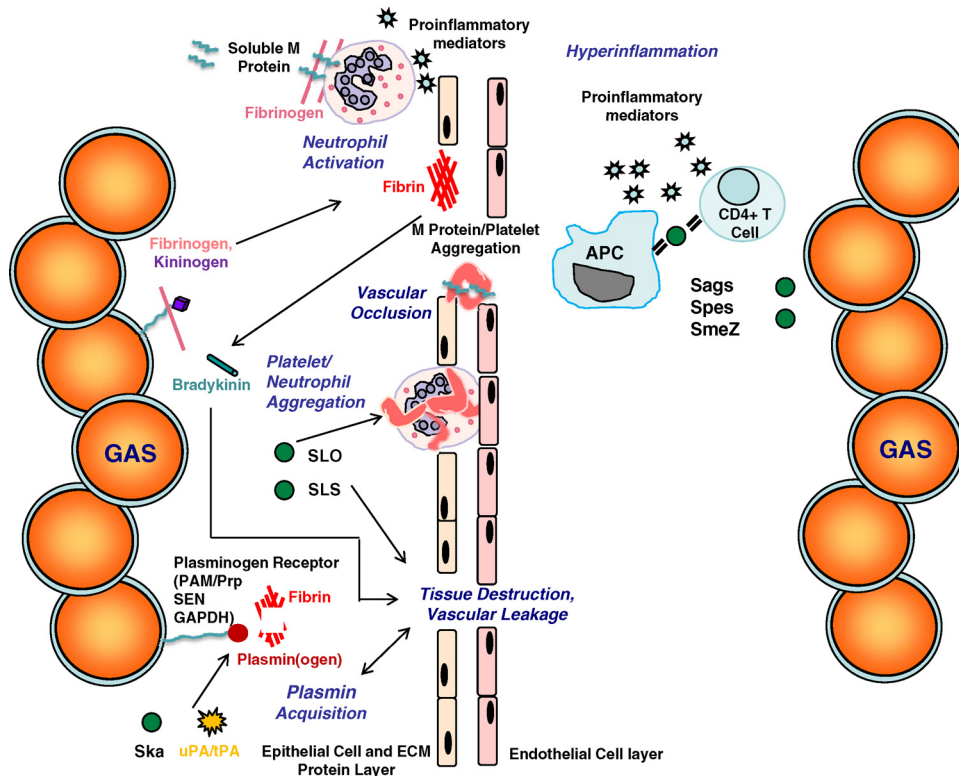
SpyCEP, also known as ScpC, is a cell wall-associated peptidase that perturbs neutrophil recruitment to the infection site by cleaving and inactivating the potent CXC chemokine IL-8 (266). SpyCEP activity increases GAS resistance to neutrophil-mediated killing (267) and enhances virulence in a murine model of systemic infection (268).

The streptococcal C5a peptidase, also known as SCPA, is a highly conserved and immunogenic 125-kDa proteolytic enzyme located on the cell surface of all GAS strains that prevents phagocytic activity at the site of GAS infection (269–271). The gene encoding C5a peptidase, *scpA*, is ubiquitous among clinical GAS isolates and is located within the *mga* regulon (269). C5a peptidase is a subtilisin-like serine protease that interferes with the host immune system by specifically cleaving the polymorphonuclear leukocyte (PMN) binding site of anaphylotoxin C5a (272), a potent 11-kDa chemotactic peptide component of the complement system involved in neutrophil recruitment and stimulation (273). This cleavage inactivates the chemoattractant activity of C5a and impairs the recruitment of phagocytes to the site of GAS infection (269, 271).

The GAS surface protein GAPDH/Plr/SDH binds human C5a to facilitate its degradation by SCPA, subsequently inhibiting neutrophil chemotaxis and H<sub>2</sub>O<sub>2</sub> production (274).

**Resistance to neutrophil extracellular traps.** NETs are DNA-based structures containing microbicidal effectors, including histones, the granule proteases elastase and myeloperoxidase, and cathelicidin antimicrobial peptide LL-37, that are released by neutrophils at the site of infection to ensnare and kill bacteria (275). Serotype MIT1 GAS secretes the bacteriophage-encoded DNase Sda1, also known as SdaD2 (276), which degrades NETs and protects serotype MIT1 strains from neutrophil-mediated killing (277, 278). Sda1 also suppresses Toll-like receptor 9 (TLR9)-mediated innate immune responses and macrophage bactericidal activity by inhibiting the release of alpha interferon (IFN-α) and TNF-α (279).

Cell wall-anchored nuclease A (SpnA) also degrades NETs, promotes survival in whole human blood and neutrophil assays, and is required for full virulence in a mouse model of infection (280). The expression of the M protein and hyaluronic acid cap-



**FIG 2** The interplay between host and bacterial factors leads to tissue destruction, vascular leakage, and hyperinflammation in invasive GAS disease. Plasminogen is recruited to the GAS cell surface directly (PAM/Prp, SEN, and GAPDH) or indirectly (fibrinogen receptors). Activation of plasminogen is mediated by bacterial (Ska) or host (uPA/tPA) plasminogen activators. Subsequent plasmin activity contributes to fibrin degradation, tissue destruction, and vascular leakage. Complexes of soluble M protein and fibrinogen cross-link to  $\beta 2$ -integrins on the neutrophil surface, triggering the release of proinflammatory mediators. Soluble M protein fragments also mediate the activation of the extrinsic pathway of coagulation by triggering tissue factor synthesis and platelet aggregation. Contact activation at the GAS cell surface (M protein, fibrinogen, and kininogen) leads to the formation of a fibrin network and bradykinin generation, contributing to vascular leakage. The secreted toxins SLO and SLS trigger apoptosis of host cells, leading to tissue destruction. SLO also mediates neutrophil platelet aggregation. Secreted superantigens (Sags, Spes, and SmeZ) bind to the beta-chain of antigen-presenting cells (APC) and  $CD4^+$  T cells, triggering the release of proinflammatory mediators and overstimulation of the immune response.

sule enhances GAS survival within NETs by increasing bacterial resistance to the antimicrobial peptide LL-37 (201).

### MOLECULAR MECHANISMS OF INVASIVE DISEASE

Severe GAS infection results from the ability of the organism to migrate to normally sterile sites, such as the bloodstream and deep tissues. The interplay between host and pathogen factors underlies the coordinated expression of multiple GAS virulence factors, ultimately leading to tissue destruction, bacterial dissemination, and hyperinflammation (Fig. 2). The mechanisms underlying invasive GAS disease, central to which are the processes of bacterial transcriptome modification, virulence factor expression, and dysregulation of host immune homeostasis, remain the subject of intense research.

### Types of Invasive Infections Caused by GAS

Invasive infection is defined as the entry of GAS into usually sterile sites of the body (e.g., blood or organs). Invasive GAS infections range from less severe forms (e.g., cellulitis) to diseases with high mortality rates (e.g., necrotizing fasciitis or STSS).

**Cellulitis and bacteremia.** Cellulitis and bacteremia are the most common invasive infections caused by GAS, each accounting for 20 to 40% of invasive disease cases. In addition to impetigo (pyoderma), GAS infection of the skin may penetrate the epider-

mis to cause cellulitis or erysipelas. Cellulitis is an infection of the subcutaneous tissues and is characterized by redness and inflammation of the skin with associated pain and swelling, while a well-circumscribed infection that does not extend beyond the superficial layers is termed erysipelas (6, 281). Bacteremia is the presence of GAS in the bloodstream and is often characterized by high fever, nausea, and vomiting as a result of a robust proinflammatory cytokine response. GAS strains may be introduced directly into the bloodstream as a result of childbirth (puerperal sepsis) or injury or may be introduced transiently as a consequence of superficial infection or colonization of the throat or skin (282).

**Necrotizing fasciitis.** Necrotizing fasciitis is a severe GAS infection of the skin, subcutaneous and deep soft tissue, and muscle. Due to the rapidly progressive nature of the disease, mortality rates associated with necrotizing fasciitis are high. In the United States and Europe, case fatality rates are reported to be 24% and 32%, respectively (7, 81), while in developing countries, the rates may be even higher (283). Furthermore, in the absence of surgical treatment, mortality rates are as high as 85.7% (284). This “flesh-eating” disease occurs as a result of rapid GAS growth and spread along the fascial sheaths that separate adjacent muscle groups, which in turn are breached, resulting in severe necrosis of the adjacent tissues (285). The pathogenesis of necrotizing fasciitis is



thought to involve host and bacterial proteases (plasmin and SpeB), spreading factors (e.g., phospholipase), tissue-damaging enzymes released by activated host neutrophils, and a proinflammatory cytokine cascade arising from uncontrolled T-cell responses to superantigens (20, 61, 85, 282, 286). Blunt trauma is a major risk factor for the development of necrotizing fasciitis, presumably as a result of increased vimentin expression, which is thought to tether circulating GAS to the injured muscle (287, 288). Epidemiologically, host major histocompatibility complex (MHC) class II haplotype DR11/DQ3 is associated with necrotizing fasciitis, while haplotype DR3/DQ2 may protect against disease (289, 290).

**Streptococcal toxic shock syndrome.** STSS can occur in conjunction with other GAS invasive diseases in response to superantigen production, resulting in a rapidly progressing illness characterized by high fever, rapid-onset hypotension, and accelerated multiorgan failure (291). In STSS, GAS superantigens simultaneously engage T-cell receptor beta-chain variable regions and MHC class II, activating large numbers of T cells in an antigen-independent manner. The result is a massive cytokine response by T cells (lymphotoxin- $\alpha$ , IL-2, and IFN- $\gamma$ ) and antigen-presenting cells (TNF- $\alpha$ , IL-1 $\beta$ , and IL-6), which causes widespread tissue damage, disseminated intravascular thrombosis, and organ dysfunction (7, 81, 291, 292). There is strong epidemiological and genetic evidence that the host MHC class II haplotype influences host susceptibility, with haplotype DR15/DQ6 being less commonly associated with STSS disease and haplotype DR14/DQ5 being more commonly associated with this disease (289, 290).

### Role of Gene Regulators in GAS Invasive Infections

There are approximately 13 two-component regulatory systems (TCSs) and >100 putative standalone transcriptional regulators in the GAS genomes sequenced to date (34, 35, 39, 293). Both *ex vivo* and *in vivo* studies demonstrate that controlled expression of bacterial genes in response to changes in the host environment facilitates the transition from superficial to invasive infection (20, 294, 295).

**The *ihk-irr* two-component regulatory system.** The *ihk-irr* two-component regulatory system is comprised of the *isp*-adjacent response regulator (*irr*) and the *isp*-adjacent histidine kinase (*ihk*) (296). Exposure of GAS to neutrophil reactive oxygen species (ROS) or antibacterial peptides results in the activation of *ihk-irr*, which regulates approximately 20% of the GAS genome (297). Inactivation of this system in an M6 background significantly reduces GAS virulence in a mouse model of bacteremia (298). The contribution of *ihk-irr* to GAS invasive disease is likely due to the control of genes involved in cell wall synthesis and oxidative stress resistance, rendering GAS less susceptible to neutrophil and macrophage killing and promoting bacterial dissemination (298).

**The *mga* regulon.** The standalone multiple-gene regulator (*mga*) activates the transcription of several virulence genes, including the M protein family (*emm*, *mrp*, *arp*, and *enn*), *scpA*, *sof*, *sic*, and *sclA* (299–304). The role of Mga in GAS virulence has been demonstrated in numerous models of GAS disease, including several invasive disease models (143, 305). Mga activity has been linked to carbohydrate metabolism (143, 303, 305), and variation in the phosphorylation of Mga in response to differences in sugar availability alters Mga function (306). Phosphorylation of Mga *in vivo* by the GAS phosphotransferase system (PTS) inactivates

Mga, effectively downregulating the expression of key GAS colonization factors. In a carbohydrate-rich setting, where a colonization phenotype is desirable, PTS phosphorylation of sugars may prevent Mga phosphorylation, promoting the expression of key adherence factors. In contrast, low carbohydrate availability may signal GAS to disseminate into deep tissue sites; thus, phosphorylation of Mga would result in a downregulation of Mga-regulated adherence factors (306). The inhibition of Mga phosphorylation significantly decreased virulence in a mouse model of invasive infection (306), and thus, the ability to modulate Mga activity appears to contribute to invasive disease initiation.

**The *covRS* two-component system and SpeB expression.** The control of virulence regulatory system (*covRS*), also known as the capsule synthesis regulon (*csrRS*) (296, 307, 308), encodes a membrane-bound sensor kinase (CovS) and a DNA binding response regulator (CovR) (309). CovS appears to mediate a general stress response in GAS, whereby specific environmental stimuli such as increased temperature, acidic pH, high salt concentrations, and supraphysiological concentrations of Mg<sup>2+</sup> signal CovS to alter the phosphorylation state of CovR (309–311). CovR binds upstream of specific genes, thereby repressing gene expression. It has been hypothesized that phosphorylated CovR represses the expression of certain genes (*speA*, *hasA*, and *ska*), while nonphosphorylated CovR represses the expression of another, distinct set of genes, including *speB* and *grab* (312). The *covRS* regulon directly or indirectly regulates the expression of ~10 to 15% of genes in the GAS genome (294, 295, 313) and is required for GAS survival under general environmental stress conditions (309). CovRS positively regulates the expression of the secreted cysteine protease SpeB and negatively regulates multiple virulence factors, including hyaluronic acid capsule, streptokinase (Ska), SLO, IgG-degrading enzyme of *S. pyogenes* (IdeS), and the DNase Sda1 (294, 308). Spontaneous and unidirectional mutations within *covRS* affect the expression of numerous virulence factors important for impeding the host innate immune response (294, 314) and the initiation and progression of GAS invasive disease (20, 277, 294). Multiple neutrophil resistance factors are upregulated in *covRS* mutants, including the hyaluronic acid capsule, SIC, IdeS/Mac-1/MspA, Sda1, SpeA, Ska, and C5a peptidase (294). Consequently, GAS isolates with mutations in either *covR* or *covS* are more resistant to phagocytosis and killing by human neutrophils (294) and are hypervirulent in mouse models of systemic GAS infection (277, 315). Less frequently, mutations in the standalone regulator *ropB* (alternatively known as *rsg*) have also been identified in invasive GAS isolates (316, 317). SpeB expression is strongly downregulated in both *covRS* mutants (277, 294) and *ropB* mutants (316, 318). The loss of SpeB activity prevents the degradation of key host proteins (plasminogen and fibrinogen) and GAS virulence factors (Ska, M protein, GAPDH, and SEN), allowing the sequestration of human plasmin protease activity on the GAS cell surface (255, 314). The surface accumulation of plasmin activity allows the pathogen to degrade host tissue barriers and spread systemically (255, 277). Serotype M1T1 GAS is the most frequently isolated serotype from severe invasive human infections worldwide (103), but strains of non-M1 serotypes also cause invasive GAS infections (319, 320). The frequency of *covRS* mutations in strains of non-M1T1 GAS serotypes is lower than that in M1T1 strains, which may explain why strains of non-M1 serotypes are less frequently isolated from human invasive infections (314). It is important to note that SpeB expression is required for



full virulence in mouse models of invasive GAS disease (254, 255, 316, 321, 322), and *covRS* mutants of GAS are less able to establish infection due to enhanced capsule expression, which may explain the maintenance of the wild-type allele in the GAS population (323, 324).

### Subversion of the Plasminogen Activation System

GAS has evolved numerous mechanisms to interact with the host plasminogen activation system. Epidemiological studies suggest that GAS strains associated with invasive disease bind plasminogen more avidly than those associated with benign infection (319), and the ability to accumulate cell surface plasmin is a prerequisite for systemic infection by multiple GAS serotypes (255, 258, 325). The glycoprotein plasminogen is found in plasma and extracellular fluids at concentrations of approximately 2  $\mu$ M. Plasminogen activation generates the serine protease plasmin, which can degrade fibrin clots, connective tissue, ECM components, and adhesion proteins. Additionally, plasmin activation of prometalloproteases results in the degradation of the collagen structural components of the ECM, further facilitating widespread tissue destruction (326). Conversion of plasminogen to plasmin in the host is mediated by urokinase plasminogen activator (uPA) and tissue-type plasminogen activator (tPA). The broad proteolytic activity of plasmin necessitates tight regulation of this system. The major circulating inhibitor of plasmin is  $\alpha_2$ -antiplasmin; however, plasmin bound to cell surface receptors, or surfaces such as fibrin, is partially protected from inactivation by  $\alpha_2$ -antiplasmin (327). Sequestration of the proteolytic activity of plasmin by GAS can facilitate fibrinolysis, thus promoting the release of bacteria from a formed clot or preventing clot formation (328, 329). Plasmin degradation of fibrinogen can also initiate the release of products that enhance blood vessel permeability and the accumulation of inflammatory cells (330, 331). Thus, a major pathogenic consequence of plasminogen acquisition by GAS is unregulated tissue destruction and overstimulation of the inflammatory response.

**Streptokinase.** GAS secretes the plasminogen activator streptokinase (Ska), which is highly specific for human plasminogen (332). Ska is a single-chain, 414-amino-acid protein composed of three distinct domains (333). Phylogenetic studies of the most divergent *ska* sequences have revealed two main sequence clusters (cluster types 1 and 2), with evidence of smaller subclusters observed in cluster type 2 sequences (cluster types 2a and 2b) (174, 175). Ska variants display significant functional differences, with cluster type 2, but not type 1, streptokinase requiring fibrinogen to efficiently activate plasminogen (175). The species specificity of Ska impacts the design and utility of small-animal models of GAS infection (334). To overcome this, a humanized plasminogen mouse model of GAS infection has been developed to clearly demonstrate that GAS exploits plasminogen in invasive disease. Following subcutaneous infection with a *covS* mutant GAS isolate, humanized plasminogen mice displayed 75% mortality, compared with 20% mortality for wild-type mice. In contrast, infection of humanized plasminogen mice with a *ska* deletion mutant resulted in only 27% mortality, clearly demonstrating the importance of Ska expression in this model (258). Ska expression is negatively regulated by *covRS*, and SpeB readily degrades and inactivates streptokinase (255, 294). Thus, *covRS* mutations enhance the ability of an isolate to activate plasminogen (255). In addition, it has recently been demonstrated that serotype M1T1 GAS strains utilize the host activator uPA to acquire cell surface

plasmin in the absence of Ska and that this interaction also plays a role in a mouse model of invasive GAS disease (335).

**Plasminogen binding proteins.** Approximately 15% of GAS isolates express plasminogen binding M proteins (PAM/Prp), and similar proteins have been identified in other streptococcal species (319, 336). These proteins bind plasminogen and plasmin directly with high affinity (337–339). Plasminogen binding to GAS M proteins is dependent on the presence of an internal plasminogen binding repeat domain comprised of positively charged lysine, arginine, and histidine residues (339–341). Once bound to the M protein, plasminogen can be readily activated to plasmin by both host activators (tPA and uPA) and Ska (337). For GAS strains that express a plasminogen binding M protein, targeted elimination of plasminogen binding reduces the capacity of GAS to cause lethal infection in the humanized plasminogen mouse model (258, 325, 342).

In addition to specialized plasminogen receptors, GAS bacteria secrete the glycolytic pathway enzymes  $\alpha$ -enolase/SEN (343) and GAPDH/Plr/SDH (152), which themselves display plasminogen binding abilities. While the mechanisms underlying the translocation of glycolytic proteins, which lack secretion and surface-anchoring signals, to the GAS cell surface are not defined, it has been confirmed in multiple bacterial species (152, 344–346). Due to the metabolic function of these enzymes, their role as plasminogen receptors in invasive disease has been difficult to characterize using traditional molecular biology techniques involving gene deletion. For GAS strains expressing plasminogen binding M proteins, the contribution of glycolytic enzymes to plasmin recruitment appears to be limited (325). However, a number of GAS strains demonstrate human plasminogen-dependent virulence in the absence of a plasminogen binding M protein (255, 258), and  $\alpha$ -enolase/SEN and GAPDH/Plr/SDH may provide an alternate pathway of plasminogen recruitment for these strains.

**Fibrinogen binding proteins.** The acquisition of plasmin activity by some GAS isolates requires human fibrinogen in addition to plasminogen and Ska. According to this model, fibrinogen bound to the GAS cell surface provides a target for the lysine-dependent binding of a preassembled plasminogen-Ska complex (328). The trimolecular complex of plasminogen, fibrinogen, and Ska possesses plasmin activity, in addition to activating fluid-phase plasminogen in the presence of host inhibitors (347). Thus, plasminogen acquisition via the fibrinogen-dependent pathway results in the creation of an unregulated surface protease and an immobilized plasminogen activator (348). For GAS strains that do not possess high-affinity plasminogen binding proteins but do express fibrinogen binding proteins such as PrtF1 and PrtF2 variants (349), M protein variants (141), and the lipoprotein Spy0591 (350), this mechanism of plasmin acquisition may be central to plasminogen-mediated virulence. The interaction between GAS, fibrinogen, Ska, and plasminogen confers a stable cell-associated enzymatic activity which can lyse fibrin clots despite the presence of the plasmin inhibitor  $\alpha_2$ -antiplasmin (328). It has been demonstrated that GAS isolates associated with invasive infection bind significantly higher levels of plasminogen via the indirect pathway than do isolates associated with noninvasive infection (319).

Fibrinogen binding M proteins also mediate inflammation and vascular leakage via direct interactions with fibrinogen and fibrinogen fragments. Cleavage of the M protein from the GAS cell surface by SpeB results in the presence of soluble M protein fragments at the site of infection (351). Binding of soluble M1 to

fibrinogen promotes neutrophil activation following cross-linking of  $\beta$ 2-integrins on the neutrophil surface. Subsequent neutrophil degranulation leads to the release of heparin binding protein and other inflammatory mediators (352). This process mimics the hyperinflammatory state that is characteristic of invasive GAS infections, and M1 protein/fibrinogen complexes have been identified in biopsy specimens from patients with necrotizing fasciitis and septic shock (352).

### GAS Superantigens

Severe GAS infections such as necrotizing fasciitis and STSS are hyperinflammatory states mediated in part by streptococcal superantigens (353). Clinical features of these conditions include increases in levels of inflammatory markers such as interleukin-1 $\beta$ , -2, and -6; IFN- $\gamma$ ; and TNF- $\alpha$  (354). Serum levels of proinflammatory mediators are strongly linked to the severity of infection (282, 289, 354). Multiple GAS superantigens have been identified. These include the streptococcal pyrogenic exotoxins (SpeA, SpeC, and SpeG to SpeM), the streptococcal superantigen (SSA), and streptococcal mitogenic exotoxin Z (SmeZ). Of these superantigens, SpeG and SmeZ are chromosomally encoded, while the remaining superantigen genes are located on prophages in the GAS genome (355). These low-molecular-weight, secreted proteins have a highly conserved tertiary structure consisting of an N-terminal  $\beta$ -barrel globular domain, a  $\beta$ -grasp motif located within the C terminus, and 2 conserved amino acid motifs at the interface between the N- and C-terminal domains of the molecule (356). Superantigens bind to the beta-chain of CD4<sup>+</sup> T cells and MHC class II molecules on B cells, monocytes, and dendritic cells, resulting in the overstimulation of the inflammatory response and subsequent systemic toxicity, tissue necrosis, organ failure, and shock (357). Each superantigen is specific for a distinct repertoire of V $\beta$  gene products and can therefore activate up to 20% of circulating naive T cells (358). Rampant T-cell activation has also been shown to occur following the uptake of superantigens by dendritic cells *in vivo*, further contributing to the proinflammatory cascade (359). In addition, *in vitro* studies suggest that SpeS can induce a strong proinflammatory response from stratified, squamous epithelial cells (225), suggesting a broader role for superantigens in amplifying the host inflammatory response to GAS. Most superantigens contain a low-affinity N-terminal binding site that recognizes the  $\alpha$ -chain of MHC class II molecules. In addition, binding of SpeA and SSA to the  $\beta$ -chain of MHC class II molecules may be mediated by a high-affinity zinc binding site located in the C terminus (356, 360–362). Finally, SpeA, SpeI, SSA, SmeZ, SpeH, and SpeO contain a conserved CD28 binding site that recognizes the CD28 molecule on T cells (363, 364).

Numerous retrospective studies have attempted to make associations between specific GAS superantigens and disease severity. Early studies of STSS in which GAS serotypes M1 and M3 were associated significantly with infection suggested that there may be an association between the superantigen gene repertoire and invasive GAS disease (365–367); however, targeted mutagenesis of SpeA has a limited effect on the mitogenic activity of toxigenic GAS *in vitro* (368), and several recent studies indicate that there is no association between superantigen gene profile and disease outcome (369–371). Numerous allelic variants have been identified for SpeA, SpeC, SpeG, SSA, and SmeZ (355). This variation may have confounded early studies that screened clinical isolates for the superantigen repertoire, as primer sequences may not have

been optimized to detect multiple allelic variants of the one superantigen. Thus, the large amount of functional redundancy between superantigens both highlights the biological importance of these molecules and suggests that host factors contribute significantly to the outcome of GAS infection, as discussed above in the context of MHC class II variation and susceptibility to STSS.

### Dysregulation of the Coagulation System

Coagulopathy is another well-recognized clinical feature of invasive human infections, and clot formation may prevent bacterial dissemination. Transgenic mice lacking clotting factor V, deficient for thrombin generation, or lacking fibrinogen are more susceptible to invasive disease following subcutaneous challenge with GAS (372), highlighting the protective effect of proper coagulation in GAS infection. However, vascular thrombosis can promote hypoxia-induced tissue damage in necrotizing fasciitis (373). GAS activates the clotting cascade via both the intrinsic (contact activation) and extrinsic (tissue factor) pathways. Activation of the intrinsic pathway at the bacterial cell surface is mediated by the M protein, which facilitates the recruitment of clotting factors, including kininogen and fibrinogen (374). Kininogen binding has been demonstrated for the M1, M6, and M46 proteins (374). Activation of these clotting factors leads to the formation of a fibrin network, the generation of the proinflammatory peptide bradykinin, vasodilation, and vascular leakage (375). Activation of the intrinsic coagulation pathway occurs in animal models of severe streptococcal infection and also in patients suffering from invasive infection (376–378).

Serotype-dependent activation of the extrinsic pathway of coagulation has been demonstrated *in vitro*, with heat-killed serotype M1 and M3, but not serotype M6, GAS strains triggering tissue factor synthesis on isolated human monocytes and cultured human umbilical vein endothelial cells, resulting in subsequent induction of procoagulant activity (373, 379). Unlike the activation of the intrinsic pathway, which occurs at the cell surface, the activation of the extrinsic pathway is thought to occur via the interaction of the M protein with TLR2 following the release of M protein from the bacterial cell wall by bacterial or host-derived proteases (380–382). Soluble M protein also mediates platelet activation and aggregation *in vitro* (383), which may contribute to the aggregated platelet deposition seen in invasive GAS infections (383, 384). In an invasive model of GAS infection, disease severity was significantly reduced in platelet-depleted mice, implying a role for platelets in the migration of GAS from the local site of infection or in the survival of bacteria in the blood (384). Mutation of the *mga* regulon significantly reduced the ability of serotype M1 GAS bacteria to form complexes with platelets and decreased bacterial dissemination in this model. It was hypothesized that GAS may utilize platelet binding to facilitate passage through the blood to other organs or that bacteria in complex with platelets may be protected from the host immune response (384).

Soluble M protein may also initiate the activation of coagulation by both the intrinsic and extrinsic pathways following the release of procoagulant microvesicles from peripheral blood mononuclear cells (385). The level of procoagulant microvesicles increases significantly in a mouse model of invasive streptococcal infection, and these microvesicles appear to bind to the streptococcal surface, leading to the entrapment of the bacteria within a dense fibrin network (386). Thus, the coagulation system and the early immune response to GAS infection are tightly linked, and

dysregulation of this system by GAS appears to contribute significantly to invasive pathogenesis.

### MOLECULAR MECHANISMS OF IMMUNE SEQUELAE

GAS infection is associated with several immune-mediated conditions affecting a diverse set of organs and tissues, including the heart, kidneys, joints, brain, eyes, and skin.

#### Heart

Major criteria for diagnosis of ARF include carditis, migratory polyarthritis, Sydenham chorea, erythema marginatum, and subcutaneous nodules. In addition to one or two of these major clinical conditions, evidence for antecedent GAS infection is one of the important laboratory diagnostic criteria for ARF. Due to the latency of 1 to 5 weeks between infection and the onset of ARF, evidence for antecedent streptococcal infection often relies on serological investigation. If untreated, ARF may progress to RHD. It is well known that the host genetic makeup contributes to a predisposition for developing ARF and RHD. Individuals with certain class II human leukocyte antigens (e.g., DRB1, DRB4, and DQA1) and certain single-nucleotide polymorphisms for TNF- $\alpha$  and mannan binding lectin genes were found to exhibit a greater predilection for ARF and RHD (6, 387, 388).

There is strong support for ARF as an autoimmune disease with an involvement of cross-reactive antibodies and T-cell clones (387–389). Several polyreactive streptococcal antibodies have been shown to react with host tissue autoantigens. For instance, monoclonal antibodies to streptococcal antigens were found to react with both M proteins and sections of myocardium, and the major autoantigen was found to be myosin (390, 391). In the M5 and M6 proteins, the epitope responsible for eliciting this response was found to be the amino acid sequence QKSKQ (390). Likewise, a subset of antistreptococcal monoclonal antibodies was found to cross-react with *N*-acetyl- $\beta$ -D-glucosamine (GlcNAc) in the GAS cell wall constituent group A carbohydrate (GAC) and heart proteins including myosin in the endothelium at the valve surface (392). Collectively, these findings provide strong evidence for antibody-mediated deleterious autoimmune reactions as possible primary triggers in the pathogenesis of RHD.

In addition, several lines of investigation revealed an involvement of cross-reactive T-cell clones in the pathogenesis of RHD (6, 393). Epitopes within M proteins as well as cardiac myosin are capable of activating these T-cell clones. An array of chemokines is expressed in myocardium and valvular tissue lesions, among which CXCL9/Mig was shown to play a role in mediating T-cell recruitment to the site of inflammation in the heart (394). Cunningham proposed that antibody mimics trigger oligoclonal T-cell expansion, followed by their extravasation into the valve through valvular endothelial cells (395). This endothelial damage in ARF patients exposes valve collagen, which, on its own or after aggregating on ARF-associated GAS isolates, elicits elevated anti-collagen responses (396, 397). Consistent with this hypothesis, several GAS M proteins, notably those associated with ARF and RHD, are known to bind collagen IV through a motif called PARF (peptide associated with rheumatic fever) (397). PARF-containing M or M-like proteins stimulate an immune response to collagen IV. Interestingly, these antibodies are distinct populations from anti-M-protein antibodies (398) and hence are not likely to be cross-reactive. Although it is possible that not all aspects of ARF/RHD disease pathogenesis could be attributable to cross-

reactivity (399), it is believed that the anticollagen antibodies and recurring stimulation of T cells at the valve may result in tissue scarring. Taken together, both humoral and cellular immune responses to streptococcal antigens may contribute to the pathogenesis of RHD (389).

#### Brain

Sydenham chorea, an immune-mediated neurological disorder, is a definitive manifestation of ARF and RHD. Monoclonal antibodies produced by human hybridomas derived from Sydenham chorea patients are known to cross-react with GlcNAc and neuronal gangliosides (400). A similar group of neurological disorders, called pediatric autoimmune neuropsychiatric disorders associated with streptococcal infections (PANDAS), is hypothesized to be a consequence of GAS infection. The diagnostic criteria for PANDAS include obsessive-compulsive disorder (OCD) or tic disorder, prepubertal onset of symptoms, abnormal choreiform movements, and a temporal relationship between GAS infection and exacerbated OCD behavior. In the early stages of PANDAS onset, it is difficult to differentiate this disorder from Sydenham chorea. However, chorea is associated with RHD, whereas PANDAS is not associated with RHD. The literature on whether GAS infection has a role in PANDAS and related neurological disorders has recently been critically reviewed (401). A definitive association between PANDAS and antecedent GAS infection is still quite debatable (402, 403). Although there may be an overlap in the immunopathogenic mechanisms of Sydenham chorea and the hypothesized PANDAS (reviewed in reference 404), a large number of studies suggest that these two neuropsychiatric diseases are separate entities (405–408).

#### Joints

Migratory polyarthritis is one of the major presentations of ARF. However, nonmigratory polyarthritis can also occur as a complication of poststreptococcal infection independent of ARF (409, 410). The disease is referred to as poststreptococcal reactive arthritis and is a distinct entity from ARF (411). Unlike ARF, poststreptococcal reactive arthritis is rarely associated with carditis; a long-term follow-up study (412) did not reveal cardiac involvement in poststreptococcal reactive arthritis patients. The latency period after the antecedent GAS infection is shorter than that for ARF. Finally, poststreptococcal reactive arthritis is less responsive to treatment than arthritis in ARF and is persistent. Occasionally, poststreptococcal reactive arthritis can co-occur with APSGN (413). There is also evidence for an association between poststreptococcal reactive arthritis and antecedent *Streptococcus dysgalactiae* subsp. *equisimilis* infection (414). The molecular mechanism for the pathogenesis of poststreptococcal reactive arthritis is poorly understood. However, epitopes shared between GAS M proteins and antigens in cartilage and synovium (415) suggest a role for autoimmunity in poststreptococcal reactive arthritis.

#### Kidneys

The clinical presentation of APSGN includes hematuria, proteinuria, edema, hypertension, elevated serum creatinine levels, hypocomplementemia, and general malaise. Antecedent GAS infections and increased titers to streptococcal antigens are other diagnostic criteria. The time lag between GAS infection and the onset of APSGN (1 to 6 weeks), high antibody titers to several GAS antigens in acute-phase sera, and the presence in the early stages of



APSGN of glomerular deposits of IgG, complement C3, and immune complexes containing GAS antigens are consistent with an immune-mediated etiology of APSGN. However, the pathogenic mechanism of APSGN remains incompletely understood (416). Furthermore, despite several excellent correlations between outbreaks of APSGN and community-wide spread of specific GAS types (417), the identity of nephritogenic components in GAS are still undefined.

GAPDH (also referred to as nephritis-associated plasminogen receptor [NAPlr]), SpeB, and streptokinase have been claimed to be possible nephritis-associated antigens (416, 418–420). However, for each of these proteins, there are counterarguments expressing doubts over their involvement in APSGN pathogenesis (421). Interestingly, the unifying feature of all the above-mentioned proteins is the ability to bind plasmin and plasminogen. It is possible that multiple factors potentially initiate glomerular damage through the acquisition of plasmin activity. Such a mechanism has been proposed (422, 423).

The prognosis of APSGN is excellent among children, with long-term complications being rare. However, there have been reports (424–427) suggesting that a history of APSGN is an independent and strong risk factor for chronic kidney disease and end-stage renal disease. In the indigenous Australian population, the mean age of onset of overt albuminuria for GAS-seropositive patients is 15 to 30 years earlier than that for GAS-seronegative patients (428), suggesting that past GAS infection is a risk factor for chronic kidney disease in this population.

Four of the major nephritis-associated GAS serotypes (serotypes M1, M12, M55, and M57) produce highly antigenic secretory proteins called streptococcal inhibitor of complement (SIC) and distantly related to SIC (DRS). Moreover, antibodies against these proteins are persistent (209, 217, 429–431). In the indigenous Australian population, a greater proportion of individuals with a history of APSGN than those without were seropositive for DRS (431). A similar study showed an association between APSGN and SIC seropositivity in a Swedish pediatric population (432). More recently, such serological observations were extended to chronic kidney disease and end-stage renal disease patients in India (Mumbai), where both GAS diseases and chronic renal disease are endemic (433). Interestingly, in this population, SIC seropositivity was associated with chronic kidney disease and end-stage renal disease. Moreover, the prognosis of chronic kidney disease for SIC-seropositive patients was worse than that for SIC-seronegative patients.

## TREATMENT OF GROUP A STREPTOCOCCAL INFECTIONS

### Treatment of GAS Pharyngitis

Although GAS pharyngitis is typically a self-limiting disease, antibiotic treatment is recommended for individuals with symptomatic pharyngitis once GAS has been confirmed by throat culture or a rapid antigen detection test (RADT) (e.g., latex agglutination), to prevent progression to ARF (434). Additional benefits of treatment of GAS pharyngitis include amelioration of clinical symptoms, a rapid decrease in contagiousness for close contacts, and prevention of suppurative complications, including peritonsillar abscess, cervical lymphadenitis, and, possibly, invasive infections (434).

Where clinical and epidemiological findings strongly suggest GAS, antibiotic treatment can be started pending microbiological

confirmation, provided that such treatment is discontinued if culture or RADT results are negative. Antibiotics shorten the clinical course of GAS pharyngitis (435); however, most signs and symptoms spontaneously resolve within 3 to 4 days, even without antibiotic treatment (436). Furthermore, the start of antibiotic treatment can be delayed for up to 9 days after the onset of pharyngitis and can still prevent the development of ARF (437). Thus, there is flexibility in the initiation of antibiotic treatment during careful evaluation of a patient with suspected GAS pharyngitis.

Most advisory groups recommend penicillin as the treatment of choice for GAS pharyngitis (434, 438), because of its narrow spectrum and because GAS has remained exquisitely susceptible to  $\beta$ -lactam drugs (439). Amoxicillin, with efficacy equal to that of penicillin, is often used in children because of the acceptable taste of suspension formulations. Orally administered macrolides, e.g., clarithromycin and azithromycin, are often effective. First-generation cephalosporins have excellent activity and are acceptable in patients who are allergic to penicillin and who do not manifest immediate-type hypersensitivity to  $\beta$ -lactam antibiotics or may be appropriate for patients at high risk for complications, with severe symptoms, or with a suspected treatment failure or relapse. Trimethoprim-sulfamethoxazole and tetracyclines are not effective and should not be used for GAS pharyngitis.

Penicillin resistance has not occurred in GAS anywhere in the world (440), and the baseline level of macrolide resistance is approximately 5 to 10%, although significant outbreaks of macrolide-resistant strains have appeared in specific communities (441–444), such that clinicians should be aware of local resistance patterns. Oral penicillin must be administered 2 to 4 times a day for 10 days in order to achieve maximal rates of GAS eradication (445). Several antimicrobial agents, including clarithromycin, cefuroxime, and cefixime, can successfully eradicate GAS from the pharynx when administered for  $\leq 5$  days (446, 447), and effective eradication with once-daily dosing has been described for amoxicillin, azithromycin, and various cephalosporins (448, 449). Importantly, the endpoints of these studies are generally the eradication of GAS and not symptomatic improvement or prevention of ARF, the two main clinical reasons for treatment. Also, such antibiotic alternatives tend to be more expensive than standard therapy and, with broader spectra of activity than penicillin, may produce greater perturbations to the normal flora (450).

Chronic carriers have GAS in their pharynx but are asymptomatic and have little or no immunologic response to the organism. Carriers are unlikely to spread GAS to their close contacts and are at very low, if any, risk for developing suppurative or nonsuppurative complications (451, 452). Treatment is generally not recommended for the carrier state, although it may be considered for close contacts in scenarios such as invasive disease outbreaks (453). Tonsillectomy is not recommended solely for the purpose of reducing GAS pharyngitis (434).

### Impetigo/Pyoderma Management

Superficial GAS skin infections are managed with gentle cleansing, using an antibiotic soap and a washcloth to remove the honey-colored crust, along with antibiotic treatment, either topically or topically, in combination with oral therapy. Empirical therapy should recognize that *Staphylococcus aureus*, including methicillin-resistant *S. aureus* (MRSA), is also a potential cause of impetigo. Topical mupirocin or retapamulin ointments are effective for focal disease, but systemic antibiotics are indicated for diffuse in-



volvement and outbreaks among athletic teams, child care centers, or multiple family members (454). Clindamycin and linezolid provide dual coverage, including MRSA, but a  $\beta$ -lactam antibiotic is preferred when GAS is the proven infectious agent (434).

### Treatment of Invasive Disease

Initial management of severe invasive GAS infection includes hemodynamic stabilization and specific antimicrobial therapy (455). When necrotizing fasciitis is suspected, prompt surgical exploration is required, and debridement or fasciotomy is almost always necessary (456). Parenteral antimicrobial therapy should include coverage of both GAS and *S. aureus* until the results of bacteriological studies are available. Once GAS has been identified, intravenously (i.v.) administered penicillin G (3 to 4 million units i.v. every 4 h) plus clindamycin (600 to 900 mg i.v. every 6 to 8 h) for 10 to 14 days is the drug regimen of choice (457, 458). A mouse model of streptococcal myositis indicated that clindamycin can be more effective than penicillin in eradicating GAS in severe, invasive infections; in part, this may result from the “Eagle effect,” wherein GAS reduces the expression of penicillin binding proteins (PBPs) during the stationary growth phase (459). As an additional potential benefit, clindamycin is a protein synthesis inhibitor that may limit the production of important GAS virulence factors such as the M protein or superantigens. A number of case reports and small series have described the use of intravenous immunoglobulin (IVIG) therapy in patients with severe invasive GAS infections. An observational cohort study in Canada reported reduced mortality among patients treated with IVIG (460), and a European, multicenter, placebo-controlled trial designed to evaluate the efficacy and safety of IVIG showed a slight trend (not statistically significant) toward reduced mortality rates (461). While IVIG is sometimes considered for patients with invasive GAS who do not respond promptly to other therapeutic measures, current Infectious Diseases Society of America guidelines remind us that the levels of toxin-neutralizing antibodies vary considerably among different IVIG preparations and that additional studies of efficacy are needed before a definitive recommendation for IVIG therapy can be made (457).

### Management of ARF

The management of ARF includes antibiotic and anti-inflammatory therapy, symptomatic treatment, and prophylaxis to prevent further GAS infections (73). Following a diagnosis of ARF, an antibiotic is used to eradicate GAS from the upper respiratory tract, regardless of throat culture results. Patients should receive either a single intramuscular injection of benzathine penicillin, 10 days of orally administered penicillin or amoxicillin, or a macrolide for patients allergic to penicillin. Salicylate therapy (50 to 75 mg/kg of body weight/day) should be initiated for 2 to 4 weeks and then tapered over the next 4 to 6 weeks for patients with definite arthritis and those who have carditis without cardiomegaly or congestive heart failure. The response of ARF arthritis to salicylates is usually rapid, and other nonsteroidal anti-inflammatory drugs have not demonstrated greater efficacy. Corticosteroids (e.g., oral prednisone at 2 mg/kg/day for 2 weeks, with a slow taper over 4 to 6 weeks) are often used to treat patients with carditis and cardiomegaly or congestive heart failure, but the benefits of anti-inflammatory therapy for cardiac outcomes remain unproven (462, 463). Additional supportive therapies for patients with carditis include fluid and salt restriction, diuretics, oxygen, angioten-

sin-converting enzyme inhibitors, or digoxin. If the lesions of RHD are persistent and hemodynamically significant, catheterization or surgery may be required to repair or replace defective valves (463).

### Secondary Prevention of Rheumatic Heart Disease

Antibiotic prophylaxis is used to avoid recurrences of GAS pharyngitis that increase the likelihood and severity of RHD (464). Such prophylaxis may be required into adulthood and perhaps for life for patients who have had carditis with the initial episode of ARF. Antibiotic prophylaxis can be discontinued for patients who have a relatively low risk of carditis after 5 years or when they reach the age of 21 years, whichever comes later. However, the discontinuation of antibiotic prophylaxis should include careful consideration of epidemiological factors that may influence the risk of further GAS infections. The treatment of choice for secondary prevention of GAS infection is a single injection of 1.2 million units of benzathine penicillin G every 4 weeks or continuous oral prophylaxis (e.g., penicillin twice daily) for patients who are likely to be compliant (465).

### Treatment of Glomerulonephritis

Antibiotic therapy does not affect the clinical course of APSGN. However, antibiotic treatment may clear the nephritogenic GAS strain and reduce the risk of patient-to-patient transmission. Penicillin is the antibiotic of choice, but a macrolide is usually prescribed for patients who are allergic to penicillin. Similarly to ARF, immunosuppressant or anti-inflammatory therapy has not been shown to influence the resolution of APSGN renal lesions. Consequently, treatment is directed at the complications of the disease and involves supportive measures. More than 95% of children with APSGN spontaneously and completely resolve symptoms and edema and regain renal function. Urinalysis results are normal for >95% of patients 15 years following the acute episode (466).

## ANTIBIOTIC RESISTANCE

### Penicillin Sensitivity

GAS remains exquisitely sensitive to penicillin despite being the drug of choice for most GAS infections. The penicillin susceptibility of GAS has not altered significantly in over 50 years of use of penicillin as a treatment for GAS infection (467). Reported MIC<sub>90</sub> values of penicillin are a median of 0.016 mg/liter and a range of 0.0025 to 0.032 mg/liter (467–471). There has been only a single report of naturally occurring penicillin-tolerant GAS (472); however, this report has not been independently confirmed. Despite universal sensitivity to penicillin, GAS infections may fail to respond to penicillin therapy, leading to persistent throat carriage and recurrent infections (473, 474). It has been suggested that GAS may escape penicillin treatment by entering epithelial cells, which are poorly penetrated by penicillin (475–477), or by forming a biofilm (478, 479), or alternatively, failure of penicillin treatment may possibly be due to the protection of GAS by other  $\beta$ -lactamase-producing bacterial species; however, this has not been proven (480, 481).

Penicillin resistance occurs in the closely related species *Streptococcus pneumoniae*, where resistance is mediated by mutations that result in conformational changes in PBPs, the targets of  $\beta$ -lactam antibiotics (482). Similar first-step mutations leading to pen-

icillin nonsusceptibility have been demonstrated in group B *Streptococcus* (483). While GAS strains express PBPs (484, 485), they have not been shown to naturally accumulate mutations in response to penicillin exposure. In the 1950s, experimental penicillin-tolerant strains of GAS were isolated following multiple passages through medium containing sublethal concentrations of penicillin. These penicillin-tolerant GAS bacteria displayed reduced M protein production and alterations of other virulence characteristics (486, 487). Ethyl methane sulfonate mutagenesis of GAS also allowed selection of penicillin-tolerant strains, with comparatively poor growth rates (488). Thus, the lack of naturally occurring penicillin-resistant GAS isolates may be due to a fitness cost associated with such mutations (489). As  $\beta$ -lactamase enzymes are often plasmid encoded (490), resistance can potentially be readily transmitted between bacteria. While no streptococcal species has been found to express  $\beta$ -lactamase activity, continued ongoing surveillance measures are recommended (489).

### Resistance to Macrolides

Macrolides (erythromycin, azithromycin, and clarithromycin) are common alternative antibiotics used for patients who are allergic to penicillin, and the lincosamide antibiotic clindamycin is commonly used for the treatment of patients with life-threatening soft tissue infections, as it may reduce exotoxin production (459, 491, 492). Macrolide resistance in GAS occurs via two mechanisms: target site modification or target drug efflux. In target site modification, *erm* (erythromycin ribosomal methylase) genes encode an enzyme that methylates a single adenine in 23S rRNA. This results in a conformational change in the ribosome, leading to reduced binding of macrolide-lincosamide-streptogramin B-type antibiotics (493). In target drug efflux, *mefA* (macrolide efflux pump) genes encode an efflux pump of 14- and 15-carbon-ring macrolides (494), conferring resistance to erythromycin only. A worldwide surveillance program conducted from 1999 to 2000 revealed geographic heterogeneity in macrolide resistance. The prevalence of macrolide-resistant isolates was high in Poland (42%), Hong Kong (28%), Italy (25%), Portugal (24%), and Spain (21%); low in the United States (6.9%), Australia (4%), Turkey (1.9%), Sweden (4%), and Switzerland (2.6%); and absent in Indonesia, Austria, Belgium, the Netherlands, and the United Kingdom (443, 495). Some countries have a high proportion of *mefA*-positive isolates, whereas in other countries, *erm* genes dominate, leading to higher levels of clindamycin resistance. There is also temporal variation in the distribution of the *mefA*-encoded and *erm*-encoded phenotypes within the same geographic region (496–500). Studies in Finland, Spain, and Italy have shown a strong correlation between macrolide usage and resistance of GAS (501–503). A rapid increase in the percentage of macrolide-resistant strains may also be due to the clonal expansion of a single resistant strain (442, 498, 504). Many countries have instituted a more restrictive use of macrolides in response to alarming reports of high rates of macrolide resistance among GAS strains. For instance, in Germany, the rate of macrolide resistance in pediatric isolates fell from 13.6% (1999 to 2003) to 2.6% (505); in Belgium, the prevalence fell from 13.5% to 3.3% during 1999 to 2006 and remained low from 2006 onward (506); and in Spain, the rate fell from 34.2% in 2001 to 2004 down to 7.4% in 2007 to 2008 (507). In South Korea, the prevalence of macrolide-resistant GAS strains fell from 44.8% in 2002 to just 4.6% in 2009; however, in this case, the decrease was more likely due to a reduction in the

prevalence of a resistant *emm* 12 GAS clone rather than a decrease in macrolide usage (496). Despite these observed declines in some countries, many other countries still have exceptionally high levels of macrolide-resistant GAS strains; for example, >96% of GAS strains isolated from Beijing, China, in 2011 were erythromycin resistant (111). However, in this case, high rates of macrolide resistance were due to the emergence of a resistant *emm* 12 clone. Variations in clonal prevalence can lead to significant temporal variations in the rates of macrolide resistance among GAS strains (111, 496, 508).

### Tetracycline Resistance

In GAS, tetracycline resistance is conferred by ribosome protection genes such as *tet*(M) or *tet*(O) (509). These proteins share homology with elongation factors EF-G and EF-Tu and possess GTPase activity that is important for the displacement of tetracycline from the ribosome (510, 511). Efflux pumps for tetracycline encoded by the *tet*(K) or *tet*(L) gene also confer tetracycline resistance; however, in contrast to macrolide resistance, these efflux pumps are relatively uncommon in streptococci (512, 513). In a cohort of GAS strains sampled globally between 1990 and 2000, 38% and 25% displayed resistance to tetracycline and erythromycin, respectively, and 15% of isolates were resistant to both classes of drugs (514). The *erm* and *mef* genes are often collocated with *tet* genes on mobile elements, and a high proportion of GAS strains are resistant to both macrolides and tetracycline (515–519); as such, tetracycline usage may also drive macrolide resistance and *vice versa*.

### Resistance to Fluoroquinolones

GAS isolates with low-level resistance to fluoroquinolones have been reported by several groups (506, 520–524). GAS strains with high-level fluoroquinolone resistance occur far less frequently (499, 521, 524–526). Low-level fluoroquinolone resistance in GAS is brought about by point mutations within the quinolone resistance-determining region (QRDR) located within topoisomerase IV (*parC* and *parE*) (499, 521, 524–526). High-level resistance results from additional point mutations in the DNA gyrase (*gyrA* and *gyrB*) genes (521). These point mutations may be acquired by spontaneous mutation within the QRDR or via horizontal gene transfer (527). The subsequent clonal expansion of resistant strains has contributed to rapid increases in the prevalences of fluoroquinolone-resistant GAS isolates in recent years (521). The rate of occurrence of fluoroquinolone resistance is increasing. For example, in Belgium in 2008, only 4.3% of isolated GAS strains were fluoroquinolone nonsusceptible, but this figure rose to 21.6% in 2010 (506). Likewise, in Spain in 2005, a 1.9% rate of fluoroquinolone nonsusceptibility among isolated GAS strains was recorded, but this rate rose to 30.8% in 2007 (521). In both of these studies, the majority of fluoroquinolone-nonsusceptible strains were *emm* 6 and *emm* 75 GAS strains, indicating the importance of clonal spread in the dissemination of fluoroquinolone nonsusceptibility.

### VACCINE CANDIDATES

A safe and effective human GAS vaccine is not yet available. A number of obstacles hinder the development of a GAS vaccine, including serotype diversity (528), antigenic variation (529), pronounced differences in the geographical distribution of serotypes (4), and, critically, the potential for GAS antigens to produce im-

munity against host tissue that triggers autoimmune sequelae (400). A diverse array of GAS proteins and molecules have been assessed as vaccine candidates, including cell wall-anchored proteins, membrane-associated proteins, secreted proteins, anchorless proteins, and the group A carbohydrate molecule (2, 31).

### M-Protein-Based Vaccine Preparations

GAS vaccinology has been focused largely on the cell wall-anchored M protein. Historical studies administered crude whole M protein preparations to human volunteers, which was followed by challenge with live GAS bacteria in the pharynx. While these preparations decreased GAS colonization (530–532), an increased incidence of ARF was reported for some of the immunized subjects (533). Several recent M-protein-based studies have investigated the protective efficacy of the N-terminal hypervariable region (338, 444, 534–539), as this region may not be involved in autoimmune disease. Two N-terminal M protein vaccine preparations have reached human clinical trials to date: a hexavalent preparation (444, 539, 540) and a 26-valent preparation (541, 542). These preparations were well tolerated in adult volunteers. More recently, a similar multivalent vaccine was developed, which includes N-terminal peptides representing 30 GAS serotypes (543). Sera raised against this experimental vaccine exhibited bactericidal activity against all 30 vaccine serotypes as well as 24 (of 40 tested) nonvaccine serotypes. While such preparations have been shown to have the capacity to protect against select nonvaccine serotypes, they do not protect against all globally circulating serotypes (4, 81, 544–546). The 30 serotypes included are based on those prevalent in North America and Europe (543), which often differ from the diverse serotypes isolated in regions of endemicity. An alternative approach is to target the highly conserved C-repeat region of the M protein, as this eliminates concerns regarding serotype-specific antibody responses. Protection has been observed following heterologous expression of the C-repeat region by vaccinia virus (547) and *Lactococcus lactis* (548). Conformationally restricted C-repeat-region peptides (J8 and J14 and derivatives thereof and StreptInCor, a 55-mer peptide containing B- and T-cell epitopes from the conserved region of the M5 protein) have been extensively studied and were observed to induce bactericidal and/or protective antibodies in animal-based trials (549–560).

### Other Vaccine Targets

**Group A carbohydrate.** The group A carbohydrate (GAC), composed of a polyrhamnose backbone with an immunodominant GlcNAc side chain, is present on the surface of strains of all GAS serotypes irrespective of M type and has been examined as a GAS vaccine candidate. Affinity-purified anti-GAC antibodies successfully opsonized three tested GAS serotypes (561), and mice immunized with GAC were protected against both intraperitoneal and intranasal GAS challenge (562). However, immunological cross-reactivity between anti-GAC antibodies and host heart valve proteins (563) and cytoskeletal proteins, such as actin, keratin, myosin, and vimentin (392), raises important potential safety concerns regarding the use of GAC as a GAS vaccine constituent.

**Other protein antigens.** A number of non-M-protein antigens have also been characterized as GAS vaccine candidates, although none of these have reached human clinical trials. Non-M-protein antigens that have been tested in animal models include fibronectin binding protein A (FbaA) (564), protein F1/SfbI (240), serum

opacity factor (SOF/SfbII) (565), fibronectin binding protein 54 (FBP54) (566), R28 protein (567, 568), streptococcal protective antigen (Spa) (569), C5a peptidase (ScpA) (570–572), streptococcal hemoprotein receptor (Shr) (573), streptococcal pyrogenic exotoxin B (SpeB) (574, 575), streptococcal secreted esterase (Sse) (576), streptococcal immunoglobulin protein 35 (Sib35) (577), *Streptococcus pyogenes* cell envelope protease (SpyCEP) (578), arginine deiminase (ADI) (579), and trigger factor (TF) (579). While each of these antigens exhibited protection against GAS infection in selected animal models, there are concerns regarding the incorporation of a number of these antigens into GAS vaccine preparations. Expression of FbaA, protein F1/SfbI, SOF/SfbII, and Shr is limited to a subset of serotypes, and their sequences can vary among the serotypes that do express them. For example, SOF/SfbII exhibits up to 57.1% sequence divergence (529). In addition, some antigens may exhibit protection in one animal model but not another. For example, protein F1/SfbI was observed to protect against GAS intranasal challenge (240) but did not protect against subcutaneous challenge (580). Finally, a number of these antigens exhibit toxic effects in the host or possess enzymatic activity, including SOF, ScpA, SpeB, Sse, Sib35, SpyCEP, SLO, ADI, and TF. The incorporation of the active forms of these antigens into GAS vaccine preparations may raise safety concerns, and consequently, inactive forms of these antigens have been engineered by employing site-directed mutagenesis for use in vaccine studies, including SOF (581), ScpA (571), SpeB (575), SpyCEP (578, 582), SLO (582, 583), and ADI (584).

### GAS Reverse Vaccinology

Reverse vaccinology is the identification of vaccine targets through *in silico* analysis of the genome of the target pathogen, enabling the rapid discovery and identification of all possible antigens, putative virulence factors, and surface-associated proteins (585). This technology, underpinned by proteomics, whole-genome sequencing, immunoblotting, bioinformatics, and DNA microarray analysis, has already resulted in the successful identification of a number of novel GAS antigens. For instance, one study coupled high-throughput multigenome data mining with proteomics to identify 52 potentially universal GAS vaccine candidates (586), which are yet to be tested in *in vivo* studies.

Demonstrating the robustness of this technology, SpyCEP has been identified as a protective GAS antigen in multiple studies employing GAS reverse vaccinology (582, 587, 588). One such study used trypsin to “shave” surface-exposed proteins, which were subsequently identified by proteomics (588). In this study, immunization with SpyCEP protected mice against subsequent GAS mucosal challenge. Another group produced genomic surface display libraries that were screened by using human serum samples from donors infected by GAS. This approach yielded 6 conserved antigens, including SpyCEP, each of which elicited protection against intranasal and intravenous challenge (587). Another approach used proteomics, immunoprotein array experiments, and flow cytometry to identify conserved, surface-associated, and/or secreted proteins of GAS. A combination of proteins (SpyCEP, Spy0269, and Spy0167) elicited protection against 4 GAS serotypes in intranasal and intraperitoneal challenge models (582).

In summary, these new approaches, in combination with more traditional vaccine research, hold promise for the development of a future GAS vaccine for use in humans.



## CONCLUSIONS

The last 20 years have heralded significant advances in our understanding of the molecular mechanisms by which GAS causes human disease, as exemplified by a clinical association of *covRS* mutations with invasive GAS infections that was recapitulated in experimental studies of global gene expression, targeted mutagenesis, and animal infection. The crucial role of multiple components of the innate immune system in controlling GAS infection and preventing serious disease outcomes, including epithelial barrier function, antimicrobial peptides, the complement system, and phagocytic cells, including neutrophils and macrophages, is being revealed. The ability of GAS to produce serious invasive infections in previously healthy individuals defines a robust capacity of this pathogen to counteract these multifaceted host defenses. An emerging theme is the functional redundancy of GAS virulence determinants, with individual GAS factors cooperating to resist a key innate immune clearance mechanism or with a single GAS virulence determinant (e.g., M protein) harboring distinct functional domains that interfere simultaneously with multiple host defense components. Despite intensive efforts and considerable new information, the molecular mechanisms of GAS immune sequelae such as ARF and poststreptococcal glomerulonephritis remain to be conclusively defined.

The resistance of GAS to antibiotics other than penicillins and cephalosporins is an increasing concern. Apart from requiring vigilant global molecular epidemiology studies and surveillance, the spread of antibiotic resistance determinants in the GAS population should provide a fresh impetus for the development of a safe and effective commercial human vaccine against this pathogen, which ranks among the top 10 infectious disease killers worldwide. Several GAS antigens elicit protective immunity in animal models and show promise as vaccine components. A number of factors need careful consideration when developing GAS vaccines, including the conservation and serotype coverage of antigens, the geographical distribution of serotypes, the use of antigens devoid of autoimmune epitopes, the selection of human-approved adjuvants, and the design and validity of experimental animal models. Future global eradication of GAS disease may be achieved by preparations that optimally address each of these factors.

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