

## Microreview

# Streptococcal toxins: role in pathogenesis and disease

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### Summary

**Group A *Streptococcus* (*Streptococcus pyogenes*), group B *Streptococcus* (*Streptococcus agalactiae*) and *Streptococcus pneumoniae* (pneumococcus) are host-adapted bacterial pathogens among the leading infectious causes of human morbidity and mortality. These microbes and related members of the genus *Streptococcus* produce an array of toxins that act against human cells or tissues, resulting in impaired immune responses and subversion of host physiological processes to benefit the invading microorganism. This toxin repertoire includes haemolysins, proteases, superantigens and other agents that ultimately enhance colonization and survival within the host and promote dissemination of the pathogen.**

### Introduction

The genus *Streptococcus* comprises several important species of human and animal pathogens, most specifically adapted to survive within a single host species. As host-adapted pathogens, streptococcal species have evolved distinctive repertoires of protein and non-protein toxins

that play crucial roles in colonization, pathogenesis and dissemination. While there are examples of streptococcal toxins that are represented across species boundaries, many streptococcal toxins are species specific or even limited to certain clonal lineages within an individual species. A number of these toxins have found utility as vaccine antigens or as novel therapeutics. In this review, we divide our examination of streptococcal toxins into four groups: haemolysins, proteases, superantigens (SAGs) and miscellaneous toxins. The best-studied individual examples from each class from across the genus *Streptococcus* are used to illustrate the function of these toxin molecules and their contribution to the disease process.

### Haemolysins

The complete lysis of red blood cells by streptococci, known as  $\beta$ -haemolysis, was first observed in 1895 and is embodied by the characteristic zone of clearing surrounding bacterial colonies on the surface of blood agar medium (Ayers and Rupp, 1922; Molloy *et al.*, 2011). This section summarizes our current understanding of streptococcal  $\beta$ -haemolysins/cytolysins ( $\beta$ -h/c) and their key role in pathogenesis (Table 1).

#### *Streptolysin S*

The potent membrane-active haemolysin streptolysin S (SLS) is secreted by 99% of all group A *Streptococcus* (GAS) isolates at stationary phase (Yoshino *et al.*, 2010) and is related to the class I bacteriocin family of proteinaceous toxins and antimicrobial peptides (Nizet *et al.*, 2000; Cotter *et al.*, 2005). SLS belongs to the thiazole/oxazole-modified microcin class of natural products, a family of diverse ribosomally produced peptides that are post-translationally modified to contain thiazole and (methyl)oxazole heterocycles from cysteine, threonine and serine residues (Mitchell *et al.*, 2009; Melby *et al.*, 2011). The activity of SLS is both temperature and concentration dependent and is principally responsible for the characteristic zone of  $\beta$ -haemolysis surrounding GAS colonies cultured on blood agar plates (Betschel *et al.*, 1998; Nizet *et al.*, 2000). SLS is encoded by the chromosomal SLS-associated gene (*sag*) locus, a conserved nine-gene operon comprised of contiguous genes *sagA* to *sagI* (Nizet *et al.*, 2000). The mature SLS is a

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**Table 1.** Streptococcal haemolysins.

Haemolysin	Streptococcal species	Virulence role	References
Streptolysin S family haemolysins			
Streptolysin S	<i>Streptococcus pyogenes</i>	Lysis of erythrocytes, lymphocytes, neutrophils, platelets, sub-cellular organelles	(Sierig <i>et al.</i> , 2003; Miyoshi-Akiyama <i>et al.</i> , 2005; Lin <i>et al.</i> , 2009)
	<i>Streptococcus dysgalactiae</i> ssp. <i>equisimilis</i>	ND	(Humar <i>et al.</i> , 2002; Hashikawa <i>et al.</i> , 2004)
	<i>Streptococcus equi</i> ssp. <i>equi</i>	ND	(Flanagan <i>et al.</i> , 1998; Hashikawa <i>et al.</i> , 2004)
	<i>Streptococcus iniae</i>	Lysis of erythrocytes, neutrophils, lymphocytes	(Locke <i>et al.</i> , 2007)
	<i>Streptococcus canis</i>	ND	(Richards <i>et al.</i> , 2012)
	<i>Streptococcus anginosus</i> ssp. <i>anginosus</i>	ND	(Tabata <i>et al.</i> , 2013; Asam <i>et al.</i> , 2015)
	<i>Streptococcus constellatus</i> ssp. <i>constellatus</i>	ND	(Tabata <i>et al.</i> , 2014)
Cholesterol-dependent cytolysins			
Streptolysin O	<i>S. pyogenes</i>	Disrupts cytoplasmic integrity of erythrocytes, leukocytes, macrophages, platelets, epithelial cells	(Limbago <i>et al.</i> , 2000; Sierig <i>et al.</i> , 2003; Brosnahan <i>et al.</i> , 2009; Timmer <i>et al.</i> , 2009)
		Translocates NAD-glycohydrolase ( <i>Streptococcus pyogenes</i> NAD-glycohydrolase) toxin into epithelial cells	(Madden <i>et al.</i> , 2001)
	<i>S. canis</i>	ND	(Richards <i>et al.</i> , 2012)
	<i>S. dysgalactiae</i> ssp. <i>equisimilis</i>	ND	(Tanaka <i>et al.</i> , 2008)
Pneumolysin	<i>Streptococcus pneumoniae</i>	Contributes to proliferation in whole blood, and colonization of the nasopharynx and lungs	(Berry <i>et al.</i> , 1989b; Kadioglu <i>et al.</i> , 2000; Reiss <i>et al.</i> , 2011)
Suilyysin	<i>Streptococcus suis</i>	Cytotoxic to endothelial cells, epithelial cells, macrophages and neutrophils	(Allen <i>et al.</i> , 2001; Lun <i>et al.</i> , 2003)
$\beta$ -Haemolysin/cytolysin	<i>Streptococcus agalactiae</i>	Induces proinflammatory responses by human brain microvascular endothelial cells, neuronal and hepatocyte apoptosis, promotes intrauterine colonization	(Ring <i>et al.</i> , 2002; Doran <i>et al.</i> , 2003; Liu <i>et al.</i> , 2004; Reiss <i>et al.</i> , 2011)
Intermedilysin	<i>Streptococcus intermedius</i>	Forms cytotoxic pores in CD59-positive cells, promotes adherence to and invasion of human liver cells	(Sukeno <i>et al.</i> , 2005)

ND, not determined.

~2.7 kDa oxygen-stable and broad-spectrum cytolytic toxin that forms hydrophilic pores in cholesterol-containing cytoplasmic membranes to induce irreversible osmotic lysis of host cells (Todd, 1938; Bernheimer, 1967; Ginsburg, 1999; Carr *et al.*, 2001). The plasma membrane damage caused by pore-forming toxins induces signalling cascades in the host cell to promote membrane repair, metal ion homeostasis and a low-energy state whereby protein synthesis is arrested (Gonzalez *et al.*, 2008, 2011).

The *sagA* gene encodes pre-SLS, while the downstream genes are required for post-translational modifications, heterocycle formation, processing and export of the mature SLS exotoxin (Nizet *et al.*, 2000; Nizet, 2002; Molloy *et al.*, 2011). SLS enhances GAS pathogenicity by

lysing a broad spectrum of host cells including erythrocytes (red blood cells), lymphocytes, neutrophils, platelets, sub-cellular organelles (e.g. lysosomes and mitochondria) and several other mammalian cell types (Ofek *et al.*, 1970; Betschel *et al.*, 1998), but not bacteria with intact cell walls (Bernheimer, 1966). In a murine model of cutaneous infection, GAS strains lacking SLS activity were less virulent than the wild-type (WT) isogenic parental strain (Betschel *et al.*, 1998; Mitchell *et al.*, 2009). Soft tissue damage in mice associated with bacterial proliferation, inflammation, vascular injury and formation of necrotic lesions also depends on the activity of SLS in GAS, group G *Streptococcus* (GGs) and *Streptococcus iniae* (Betschel *et al.*, 1998; Limbago *et al.*, 2000; Fuller *et al.*,

2002; Humar *et al.*, 2002; Sierig *et al.*, 2003). SLS may interact synergistically with other virulence factors (e.g. M protein and streptolysin O (SLO)) and host factors (e.g. neutrophil proteases and reactive oxygen species) to induce tissue necrosis and promote the development of necrotizing fasciitis in humans (Humar *et al.*, 2002).

Recently, SLS and SLO have been shown to induce endoplasmic reticulum (ER) stress and an unfolded protein response (UPR) in host cells to reduce the surplus of unfolded proteins. The activation of UPR plays a key role in cellular defences against bacterial pore-forming toxins and is an important downstream target of the p38 mitogen-activated protein kinase pathway (Bischof *et al.*, 2008), a central pathway of cellular immunity. In a mechanism that is yet to be fully understood, UPR results in the transcriptional upregulation of *asns*, a gene encoding for asparagine synthetase, and the release of asparagine into the extracellular environment. The extracellular asparagine sensed by GAS triggers a reduction in SLS and SLO transcription and stimulates bacterial growth (Baruch *et al.*, 2014). Similarly, the pore-forming toxin listeriolysin O (LLO) produced by *Listeria monocytogenes*, a facultative intracellular bacterial pathogen, induces ER stress and is required for UPR activation (Pilllich *et al.*, 2012). LLO is activated within the acidic phagosome, allowing the bacterium to degrade the phagosome and escape to the cytosol (Dramsai and Cossart, 2002).

#### Groups C and G streptococci streptolysin S homologues

Group C *Streptococcus* (GCS) and GGS comprise several species of streptococci, with the significant human pathogen *Streptococcus dysgalactiae* ssp. *equisimilis* responsible for throat, skin and soft tissue infections and invasive infections including endocarditis, bacteremia and toxic shock. Nine-gene SLS-like loci are present in GCS and GGS. The SagA peptides of GCS and GGS share 89% amino acid identity with SagA from GAS (Humar *et al.*, 2002) and are responsible for the prototypical  $\beta$ -haemolytic phenotype on the surface of blood agar plates (Flanagan *et al.*, 1998; Hashikawa *et al.*, 2004). Heterologous expression of GAS SagA in a non-haemolytic *sagA* mutant in GGS restored  $\beta$ -haemolytic activity on blood agar (Humar *et al.*, 2002).

#### *Streptococcus iniae* streptolysin S homologue

*Streptococcus iniae* is an emerging zoonotic pathogen responsible for sporadic human infections through soft tissue injuries suffered during the handling and preparation of infected fish (Weinstein *et al.*, 1997; Koh *et al.*, 2009). The nine-gene *S. iniae* *sag* operon is 73% homologous to the *sag* operon from GAS and shares the same gene order (Fuller *et al.*, 2002). Encoded by the *sagA* gene, the cytolysin of *S. iniae* shares 73% identity

with GAS SLS (Fuller *et al.*, 2002; Locke *et al.*, 2007) and lyses erythrocytes, neutrophils, lymphocytes and several tissue culture cell lines. Heterologous expression of the *S. iniae* *sagA* gene in a non-haemolytic  $\Delta$ *sagA* mutant of serotype M49 GAS restored haemolytic activity (Fuller *et al.*, 2002; Locke *et al.*, 2007). *S. iniae* SLS promotes neither adherence and invasion of epithelial cells nor resistance to opsonophagocytosis (Locke *et al.*, 2007). However, a SagA-deficient mutant is highly attenuated for virulence (Locke *et al.*, 2007).

#### Intermedilysin

*Streptococcus intermedius*, *Streptococcus constellatus* and *Streptococcus anginosus* are members of the Anginosus group of streptococci (AGS) that colonize the oral cavity, upper respiratory, gastrointestinal and female genitourinary tracts (Whiley *et al.*, 1992; Jacobs *et al.*, 1995). AGS are opportunist human pathogens capable of causing liver and brain abscesses, dentoalveolar infections and endocarditis (Jacobs *et al.*, 1995). The secreted intermedilysin (ILY) of *S. intermedius* binds complement receptor CD59 on human cells and forms cytotoxic pores, but only in the presence of sufficient levels of cholesterol (Nagamune *et al.*, 1996; Farrand *et al.*, 2008; Heuck *et al.*, 2010; Johnson *et al.*, 2013). ILY damages host tissues and immune cells to promote bacterial survival and dissemination (Nagamune *et al.*, 1996, 2000). ILY is considered to be a major virulence factor required for adherence to and invasion of human liver cells (Sukeno *et al.*, 2005).

#### Streptolysin O

The oxygen-sensitive, 57 kDa thiol-activated SLO exotoxin is encoded by the highly conserved *slo* gene and secreted by nearly all GAS isolates during exponential and early stationary growth phases. SLO is a cholesterol-dependent cytolysin that disrupts the cytoplasmic membrane integrity of numerous eukaryotic cell types, including erythrocytes, leukocytes, macrophages, platelets, epithelial cells and various tissue culture cell lines (Limbago *et al.*, 2000; Sierig *et al.*, 2003). SLO contributes to GAS  $\beta$ -haemolysis under the surface of blood agar medium and, in contrast to SLS, contributes negligibly to  $\beta$ -haemolytic activity on the surface of blood agar (Molloy *et al.*, 2011). The *slo* gene is co-transcribed with the *nga* gene encoding NAD-glycohydrolase (NADase), also known as *Streptococcus pyogenes* NADase, which is actively translocated into the cytosol of human epithelial cells by SLO to deplete energy stores and promote host cell injury (Madden *et al.*, 2001; Bricker *et al.*, 2005; Michos *et al.*, 2006). Cathelicidin antimicrobial peptide LL-37 has been shown to upregulate the expression of *slo* and hyaluronan capsule, which promotes GAS resistance to killing by human epithelial cells, neutrophils and

macrophages (Love *et al.*, 2012). SLO blocks the clathrin-dependent pathway for GAS internalization through disruption of the keratinocyte cell surface (Logsdon *et al.*, 2011) and induces keratinocyte apoptosis through the dysregulation of calcium signalling (Cywes Bentley *et al.*, 2005). SLO expression by intracellular GAS also contributes to the inhibition of dendritic cell maturation by inducing apoptosis (Cortes and Wessels, 2009). Upon macrophage phagocytosis, SLO damages the phagolysosome membrane, preventing phagolysosome acidification and resulting in the translocation of NADase into the macrophage cytosol (Bastiat-Sempe *et al.*, 2014). SLO and NADase also inhibit the autophagic killing of GAS in pharyngeal keratinocytes (O'Seaghda and Wessels, 2013). The toxic effects of NADase are further discussed below.

In subcutaneous, intravenous and intraperitoneal murine models of invasive disease, *slo*-deficient GAS mutants have decreased virulence compared with WT parental strains (Limbo *et al.*, 2000; Ato *et al.*, 2008; Timmer *et al.*, 2009). A recent study showed that SLO binding to A549 epithelial cells does not require cholesterol, suggesting that cholesterol is not the membrane receptor for SLO (Mozola *et al.*, 2014). In support of this hypothesis, SLO binding to a glycan on the surface of human erythrocytes is essential for pore formation (Shewell *et al.*, 2014), and the haemolytic activity of SLO can be inhibited with a specific galactose-binding lectin (Hasan *et al.*, 2014). Similarly, an exposed F-type lectin domain at the N-terminus of lectinolysin (LLY), a cholesterol-dependent cytolysin from *Streptococcus mitis*, promotes binding of LLY to fucose-rich sites on target cell membranes (Farrand *et al.*, 2008; Bouyain and Geisbrecht, 2012). SLO and an enzymatically inactive derivative are immunogenic and protective against GAS challenge in mouse vaccination models (Bensi *et al.*, 2012; Chiarot *et al.*, 2013).

#### *Suilysin*

*Streptococcus suis* is a pathogen of swine that is responsible for numerous diseases (meningitis, septicaemia and endocarditis) and important economic losses to the porcine industry worldwide (Fittipaldi *et al.*, 2012). This species is also an emerging zoonotic agent of meningitis and streptococcal toxic shock-like syndrome in humans. *S. suis* expresses the haemolysin suilysin (SLY), a secreted 54 kDa thiol-activated exotoxin that binds cholesterol and forms pores in eukaryotic cell membranes (Gottschalk *et al.*, 1995; Palmer, 2001). It is closely related to both GAS SLO and the pneumolysin (PLY) of *Streptococcus pneumoniae* and is cytotoxic to endothelial cells, epithelial cells, macrophages and neutrophils (Charland *et al.*, 2000; Lalonde *et al.*, 2000; Segura and Gottschalk, 2002; Chabot-Roy *et al.*,

2006). SLY allows *S. suis* to evade the innate immune response by interfering with the complement cascade and activating phagocytic cells to release proinflammatory cytokines (Lun *et al.*, 2003; Segura *et al.*, 2006). SLY-deficient mutants are attenuated for virulence in a systemic mouse infection model (Allen *et al.*, 2001), but SLY is not required for full virulence in a piglet infection model (Lun *et al.*, 2003). Recently, SLY has been shown to promote *S. suis* adherence to and invasion of human HEp-2 epithelial cells (Seitz *et al.*, 2013).

#### *β-Haemolysin/cytolysin*

*Streptococcus agalactiae* (group B *Streptococcus*, GBS) is the leading cause of meningitis, sepsis and pneumonia in human newborn infants and a significant agent of invasive infections among immunocompromised adults (e.g. diabetes and cancer patients) and pregnant women worldwide (Farley, 2001). The  $\beta$ -h/c of GBS is a non-immunogenic oxygen-stable pore-forming cytolysin and a major virulence factor expressed by most clinical isolates, with a predicted size of 78.3 kDa (Dal and Monteil, 1983; Nizet *et al.*, 1996; Spellerberg, 2000). First described in 1934 (Todd, 1934), cell surface-associated  $\beta$ -h/c is encoded by the *cyIE* gene in the *cyI* locus, a unique 12-gene operon involved in fatty acid biosynthesis (Pritzlaff *et al.*, 2001) that is expressed by almost all strains of GBS. CylE expression is invariably associated with the production of an orange to brick-red carotenoid pigment (Tapsall, 1987; Spellerberg *et al.*, 2000) and is primarily regulated by the two-component system *covR/S* (control of virulence) (Tapsall, 1987); some have recently suggested the pigment itself may convey the haemolytic activity (Whidbey *et al.*, 2013). CylE expression is required for GBS survival in mouse and human blood *ex vivo* (Liu *et al.*, 2004). Animal studies with WT and isogenic  $\beta$ -h/c mutants demonstrate that haemolysin expression has proapoptotic, proinflammatory and cytotoxic effects and is necessary for full GBS virulence in multiple *in vivo* systems, including mouse models of GBS arthritis (Puliti *et al.*, 2000), meningitis (Doran *et al.*, 2003) and ascending chorioamnionitis (Randis *et al.*, 2014), a rat model of experimental GBS meningitis (Reiss *et al.*, 2011), and rabbit models of GBS septicaemia (Ring *et al.*, 2002) and pneumonia (Hensler *et al.*, 2005).

#### *Pneumolysin*

*Streptococcus pneumoniae* (pneumococcus) is the causative agent of pneumococcal pneumonia, meningitis, sepsis, otitis media and other less serious infections. PLY is a 53 kDa (471-amino-acid) (Walker *et al.*, 1987) cholesterol-dependent pore-forming toxin with four functional domains (Mitchell and Dalziel, 2014). In a recent study, binding of PLY domain 4 to the sialyl LewisX glycolipid cellular receptor on the surface of human



erythrocytes was shown to be an essential step before membrane insertion and pore formation (Shewell *et al.*, 2014). PLY is a cytoplasmic thiol-activated toxin with cytolytic and complement-activating properties (Lucas *et al.*, 2013). PLY is localized primarily to the cell wall compartment in the absence of detectable cell lysis (Price *et al.*, 2012). However, unlike other cholesterol-binding cytolysins, PLY lacks secretion signal sequences and is not actively secreted into the extracellular milieu (Cassidy and O'Riordan, 2013). The cytolytic activity of PLY and its release into the extracellular milieu are inhibited by branched stem peptides in the peptidoglycan cell wall (Greene *et al.*, 2015). PLY is released into the alveolar compartment upon bacterial lysis induced by autolysis (Berry *et al.*, 1989a, 1992) or by antibiotic treatment of pneumococcal pneumonia patients (Anderson *et al.*, 2007). However, in the absence of cell lysis, PLY is exported from the cytoplasm and attached to the cell wall by a yet-to-be-characterized mechanism (Price *et al.*, 2012). PLY is directly toxic for a wide variety of host cells and tissues and also elicits strong inflammatory responses at the site of infection, triggering signalling via TLR4 (Malley *et al.*, 2003), as well as activation of the NLRP3 inflammasome (McNeela *et al.*, 2010). Circulating PLY also induces myocardial injury in a mouse model of invasive pneumococcal disease and dose-dependent damage to cardiomyocytes *in vitro* (Alhamdi *et al.*, 2015). In pneumococcal meningitis, the majority of the damage to the blood–brain barrier has been attributed to PLY (Zysk *et al.*, 2001; Mitchell and Dalziel, 2014). Structural homology to the Fc region of immunoglobulin G (IgG) also allows PLY to activate the classical complement pathway away from intact bacteria to deplete host serum complement levels and promote survival and spread (Paton *et al.*, 1984; Mitchell *et al.*, 1991; Rossjohn *et al.*, 1998; Alcantara *et al.*, 2001). Recently, PLY was also shown to contribute to the assembly of pneumococcal biofilms (Shak *et al.*, 2013). PLY activates p38 *in vitro* (Ratner *et al.*, 2006) and the NLRP3 inflammasome in macrophages to stimulate the production of type I interferons following pneumococcal phagocytosis (Koppe *et al.*, 2012). In murine infection models, PLY-deficient mutants have reduced proliferation in whole blood (Benton *et al.*, 1995), diminished capacity to colonize the nasopharynx, induce less lung inflammation and neutrophil recruitment and are rapidly cleared from the lung, compared with WT (Berry *et al.*, 1989b; Kadioglu *et al.*, 2000). Genetically inactivated PLY toxoids are immunogenic and protective against lethal pneumococcal challenge in mouse vaccination models (Paton *et al.*, 1991; Alexander *et al.*, 1994; Kirkham *et al.*, 2006). Phase I clinical trials demonstrated that PLY toxoid PlyD1 is safe and elicits functional neutralizing antibodies against the pneumococcus (Kamtchoua *et al.*, 2013).

## Proteases

Proteases (or peptidases) are enzymes that catalyse the hydrolysis of peptide bonds. The genus *Streptococcus* possesses a wide array of proteases that have diverse functions, including nutrient acquisition, protein maturation and quality control, and various host interactions. For the purposes of this review, however, we will focus only on those surface-exposed or secreted proteases that have direct effects on pathogenesis through their activities on host proteins and tissues.

### *Group A Streptococcus cysteine protease (SpeB)*

The GAS cysteine protease SpeB is encoded in the genomes of essentially all GAS strains (Bohach *et al.*, 1988; Yu and Ferretti, 1991); homologous proteins, albeit uncharacterized, are encoded in the genomes of the closely related species *Streptococcus didelphis*, *Streptococcus porcinus* and *Streptococcus pseudoporcinus*. Expression of this protein is tightly regulated at the transcriptional level, as well as post-transcriptionally through the maturation of the inactive zymogen to the active mature enzyme (for a review, see Carroll and Musser, 2011). With diverse functions in pathogenesis, including direct action on host tissues as well as roles in the maturation and surface display of other surface-exposed GAS proteins, SpeB is a veritable 'Swiss army knife' of GAS biology.

SpeB is a broad-spectrum cysteine protease structurally related to papain and has been shown to degrade numerous host proteins *in vitro*, including immunoglobulins, complement components, chemokines, cytokines, extracellular matrix proteins and numerous other host proteins (for a review, see Nelson *et al.*, 2011). However, despite these studies, it has recently been shown that SpeB does not cleave immunoglobulins under physiologically relevant conditions (Persson *et al.*, 2013), and thus, the true *in vivo* substrate profile might be considerably smaller. Multiple lines of evidence suggest that SpeB is important for GAS pathogenesis: passive immunization of mice with anti-SpeB antibodies or a synthetic protease inhibitor protects against infection, and low-milligram amounts of SpeB are lethal when injected into mice (Bjorck *et al.*, 1989; Kapur *et al.*, 1994; Nelson *et al.*, 2011). Furthermore, isogenic  $\Delta speB$  mutant GAS strains are avirulent in mice following subcutaneous (Lukomski *et al.*, 1999; Cole *et al.*, 2006; Terao *et al.*, 2008) and intraperitoneal (Lukomski *et al.*, 1997; Hollands *et al.*, 2008) infection and exhibit decreased survival in human whole blood (Chiang-Ni *et al.*, 2006) and serum (Honda-Ogawa *et al.*, 2013).

*Role in superficial infections.* SpeB expression has a strong epidemiological association with isolates from superficial disease (Ikebe *et al.*, 2010; Cole *et al.*, 2011).

While the exact role of this enzyme during superficial GAS disease was presumed to involve its degradation of host immune components, two recent reports have suggested alternative or complementary functions. In the first report (Barnett *et al.*, 2013), SpeB conferred the ability of GAS strains to replicate in the cytosol of infected epithelial cells. SpeB was shown to degrade the host proteins that direct intracellular bacteria to the autophagy pathway, a host system for degrading cytosolic components in lysosomes that constitutes an important immune defence against intracellular bacteria. Consequently, SpeB-expressing GAS strains are able to evade this pathway and replicate in the cytosol of infected cells. In a separate study, SpeB was shown to promote the translocation of GAS across epithelial barriers by degrading occludin and E-cadherin (Sumitomo *et al.*, 2013). Thus, SpeB may aid in the establishment of an epithelial replicative niche and dissemination of GAS into deeper tissues.

**Role in invasive disease.** Epidemiological studies have demonstrated that SpeB expression is inversely related to disease severity (Kansal *et al.*, 2000; Ikebe *et al.*, 2010). Loss of SpeB expression, through the accumulation of mutations in the regulatory genes *covR/S* and to a lesser extent *ropB*, leads to the abolishment of *speB* expression. This genetic switch has multiple consequences that lead to a hypervirulent invasive state: loss of SpeB production spares several GAS virulence factors (e.g. M protein, various SAGs and streptokinase) from proteolytic degradation, and *covR/S* mutations lead to the up-regulation of multiple virulence factors required for the invasive disease phenotype (for a review, see Cole *et al.*, 2011).

While SpeB expression is strongly linked to GAS isolates from superficial disease, immunohistochemical analysis has shown that human tissues from necrotizing fasciitis cases are strongly positive for SpeB, suggesting that SpeB is elaborated during the establishment or progression of this disease (Johansson *et al.*, 2008). Similarly, SpeB is required for full virulence in invasive infection models in mice (Lukomski *et al.*, 1999; Cole *et al.*, 2006; Hollands *et al.*, 2008; Olsen *et al.*, 2010) and nonhuman primate animal models (Olsen *et al.*, 2010). While these results seemingly contradict other studies that have clearly demonstrated a genetic switch from a SpeB-positive phenotype to a SpeB-negative phenotype during invasive disease (Aziz *et al.*, 2004; Cole *et al.*, 2006; Sumbly *et al.*, 2006; Walker *et al.*, 2007), it is possible that a mixed population of SpeB-positive and SpeB-negative bacteria contribute to the overall pathology of GAS invasive disease and penetration into deeper tissues (Cole *et al.*, 2006).

In addition to regulation through *covR/S* and *ropB* mutations, it has also been recently demonstrated that SpeB activity can be inhibited by the divalent cations of

zinc and copper (Chella Krishnan *et al.*, 2014). While the physiological consequence of this inhibition is currently unknown, it was postulated that reversible inhibition of SpeB activity may reversibly preserve critical virulence factors required during certain stages of the infectious process.

#### *Immune-modulating proteases*

**C5a peptidase.** C5a peptidase (ScpA), is a serine endopeptidase that specifically cleaves and inactivates the C5a complement factor and has been implicated to play a role in inhibiting the recruitment of phagocytes to the infectious site (Ji *et al.*, 1996; Collin and Olsen, 2003). While recombinant ScpA is very potent in inhibiting phagocyte chemotaxis *in vitro*, the effects of  $\Delta scpA$  mutations in mice infections *in vivo* are much less dramatic (Ji *et al.*, 1996), possibly as a result of alternative chemoattractants, such as interleukin (IL)-8, and GAS proteases that inhibit them, such as SpyCEP (below). C5a peptidase is a cell wall-anchored enzyme but can be released from the surface of GAS as a functionally active enzyme by SpeB and can thus inactivate C5a at some distance from the bacterium (Berge and Bjorck, 1995). C5a peptidase is expressed by strains of GAS (ScpA; Chen and Cleary, 1990), GBS (ScpB; Cleary *et al.*, 1992) and *Streptococcus equi* ssp. *zooepidemicus* (ScpZ; Wei *et al.*, 2013) and is encoded in the genomes of several other streptococcal pathogens, including *S. dysgalactiae*, *S. iniae*, *Streptococcus sanguinis*, *S. mitis* and *Streptococcus canis* (GGS). In addition to its endopeptidase activity, the C5a peptidase proteins from GAS, GBS and *S. equi* ssp. *zooepidemicus* have also been suggested to function as an invasin (Cheng *et al.*, 2002b; Purushothaman *et al.*, 2004; Wei *et al.*, 2013). Vaccination against ScpA is protective for GAS (Park and Cleary, 2005), GBS (Cheng *et al.*, 2002a; Santillan *et al.*, 2008) and *S. equi* ssp. *zooepidemicus* (Wei *et al.*, 2013).

**SpyCEP.** Group A *Streptococcus* SpyCEP is a subtilisin-like serine protease that can cleave human CXC chemokines. In its mature form, SpyCEP exists as a dimer composed of two subunits (30 and 150 kDa) generated by intramolecular autocatalytic cleavage (Zingaretti *et al.*, 2010). Substrates include granulocyte chemotactic peptide-2 (CXCL6), growth-related oncogene- $\alpha$ ,  $\beta$ ,  $\gamma$  (CXCL1, 2, 3), neutrophil-activating peptide-78 (CXCL5), GRB2-related adapter protein 2 and IL-8 (CXCL8), which correspond to the murine CXC chemokines MIP-2 and KC (Hidalgo-Grass *et al.*, 2004; Sumbly *et al.*, 2008; Chiappini *et al.*, 2012). As a result of this activity, SpyCEP impairs the recruitment of neutrophils, monocytes and eosinophils to the site of infection (Zinkernagel *et al.*, 2008; Chiappini *et al.*, 2012). SpyCEP also promotes resistance to neutrophil killing by reducing

the production of neutrophil extracellular traps (Zinkernagel *et al.*, 2008). SpyCEP-producing GAS strains are more virulent in murine models of invasive disease, and SpyCEP production is up-regulated in human invasive GAS isolates (Edwards *et al.*, 2005; Hidalgo-Grass *et al.*, 2006; Zinkernagel *et al.*, 2008; Turner *et al.*, 2009a). Furthermore, immunization with SpyCEP protects mice against GAS nasopharyngeal (Alam *et al.*, 2013), intramuscular and intranasal infection (Turner *et al.*, 2009b) and intramuscular infection with *S. equi* (Turner *et al.*, 2009b), demonstrating that a vaccine based on SpyCEP may provide cross-protection against multiple streptococcal species. While SpyCEP is cell wall anchored, it can be shed into the supernatants of bacterial cultures during stationary-phase growth (Chiappini *et al.*, 2012), presumably as a result of protease processing. In addition to these protease activities, SpyCEP also promotes the uptake of GAS into endothelial, but not epithelial, cells (Kaur *et al.*, 2010). Homologous proteases have also been characterized in *S. iniae* (Zinkernagel *et al.*, 2008) and *S. equi* (Turner *et al.*, 2009b) and are present in the genomes of several other *Streptococcus* species (*S. dysgalactiae*, *S. canis*, *S. didelphis*, *Streptococcus phocae*, *S. porcinus*, *S. pseudoporcinus* and *Streptococcus thermophilus*).

**IdeS.** IdeS (also known as Mac) is a 35 kDa secreted cysteine protease produced by strains of GAS that specifically cleaves between the two glycine residues in positions 236 and 237 in the lower hinge region of the IgG heavy chain, resulting in the separation of the Fc and Fab fragments (von Pawel-Rammingen *et al.*, 2002; Vincents *et al.*, 2004; von Pawel-Rammingen, 2012). As a homologue of CD11b, IdeS has been proposed to also inhibit phagocytosis by inhibiting Fc receptor (CD16) recognition of IgG and/or complement deposition (Lei *et al.*, 2001). This is hypothesized to prevent the recognition of antibody-opsonized bacteria by Fc receptors of immune cells and by the complement system (von Pawel-Rammingen *et al.*, 2002). Protease activity is considerably higher against soluble IgG and IgG bound in an antigen-specific manner at the Fab region than to IgG bound non-specifically to GAS M protein at the Fc region, suggesting that this enzyme has evolved to allow GAS to resist Ig-mediated phagocytosis and cytotoxicity while still allowing non-immune IgG interactions, which are believed to contribute to GAS pathogenesis (Su *et al.*, 2011). However, IdeS was recently found to not be essential for phagocyte resistance or mouse virulence, and thus, the exact role of this protein in human disease remains to be identified (Okumura *et al.*, 2013). The human protease inhibitor cystatin C can act as a cofactor for IdeS and greatly increase enzymatic activity (Vincents *et al.*, 2008). All GAS strains examined possess one of two identified variants of IdeS (IdeS and Mac-2), with

considerable amino acid sequence divergence in the middle third of the proteins but with indistinguishable enzymatic activity, with the exception of the Mac-2 protein from M28 strains that displays only weak endopeptidase activity (Lei *et al.*, 2001; von Pawel-Rammingen *et al.*, 2002; Soderberg *et al.*, 2008; von Pawel-Rammingen, 2012). IdeS homologues that cleave IgG have also been identified in several other *Streptococcus* species, including *S. equi* ssp. *equi* and *S. equi* ssp. *zooepidemicus* (Lannergard and Guss, 2006; Hulting *et al.*, 2009). Additionally, an IdeS homologue that cleaves porcine IgM has recently been found in *S. suis* (Seele *et al.*, 2013).

#### *Zinc metalloproteases*

*Streptococcus pneumoniae* strains encode various combinations of four zinc metalloproteases: IgA1 protease, ZmpB, ZmpC and ZmpD. An unusual characteristic of all of these proteins is the presence of an LPXTG cell wall-anchoring motif near their N-terminus (Bek-Thomsen *et al.*, 2012), which in the case of IgA1 protease has been shown to be important for proper localization and enzymatic function (Bender and Weiser, 2006).

IgA1 protease specifically cleaves the IgA1 hinge region, resulting in separation of the Fc and Fab fragments (Senior and Woof, 2005a,b). This cleavage abrogates the protective effects of IgA1 in mediating complement-dependent killing of pneumococci by phagocytes (Fasching *et al.*, 2007; Janoff *et al.*, 2014) and promotes the adherence of this bacterium to respiratory epithelial cells (Weiser *et al.*, 2003). It is likely that IgA1 protease has additional roles in virulence, as mutants have reduced virulence in mice yet murine IgA1 is not a substrate for this enzyme (Chiavolini *et al.*, 2003; Janoff *et al.*, 2014). Homologous IgA1 proteases have been characterized in *S. suis*, which is important for virulence in pigs (Zhang *et al.*, 2011), and *S. sanguinis* (Gilbert *et al.*, 1988). IgA1 protease is encoded by all strains of *S. pneumoniae*, *Streptococcus pseudopneumoniae*, *Streptococcus oralis* and *S. sanguinis* and is variably present in *S. mitis* and *Streptococcus infantis* (Bek-Thomsen *et al.*, 2012).

In contrast to IgA1 protease, the ZmpC protease has multiple targets and is an important virulence factor in experimental pneumonia (Oggioni *et al.*, 2003). ZmpC has been shown to activate human matrix metalloprotease 9, a host zinc protease involved in neutrophil migration and wound repair of the respiratory epithelium (Oggioni *et al.*, 2003). ZmpC inhibits neutrophil flux by degrading the N-terminal region of P-selectin glycoprotein 1 (Surewaard *et al.*, 2013). In addition, ZmpC induces specific epithelial cell shedding of both mucin 16, a vital defence barrier of ocular epithelial cells (Govindarajan *et al.*, 2012; Menon and Govindarajan, 2013), and syndecan-1, a surface proteoglycan with diverse roles in cell–cell and cell–matrix binding, cell signalling and cytoskeletal organization

(Chen *et al.*, 2007). Genes encoding ZmpC are variably present in *S. pneumoniae*, *S. pseudopneumoniae*, *S. mitis*, *S. oralis* and *Streptococcus gordonii* and present in all strains of *S. sanguinis* (Bek-Thomsen *et al.*, 2012).

In contrast to IgA1 protease and ZmpC, ZmpB and ZmpD have not been well characterized, and their substrates have not been identified. ZmpB induces tumour necrosis factor- $\alpha$  production in the respiratory tract, and a *zmpB* mutant was attenuated in pneumonia and septicaemia models of infection (Blue *et al.*, 2003; Chiavolini *et al.*, 2003). Genes encoding ZmpB are present in all *S. pneumoniae* strains as well as several other *Streptococcus* species, including *S. pseudopneumoniae*, *S. mitis*, *S. oralis*, *S. sanguinis*, *S. gordonii*, *Streptococcus vestibularis* and *Streptococcus salivarius*. Genes encoding ZmpD are sporadically distributed among *S. pneumoniae*, *S. pseudopneumoniae* and *S. mitis* (Bek-Thomsen *et al.*, 2012).

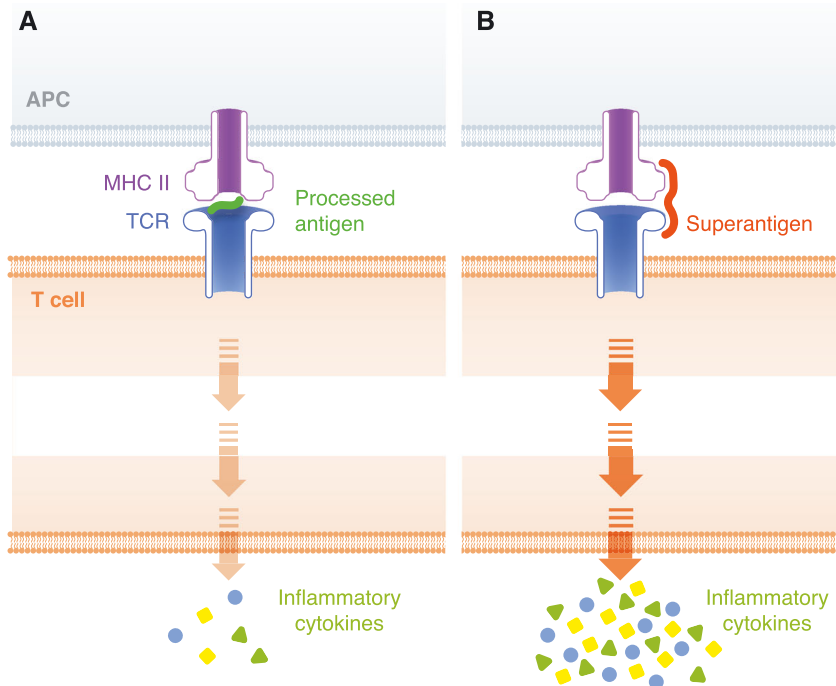
### SspA

Strains of *S. suis* encode a cell wall-anchored subtilisin-like serine protease termed SspA, which is important for disease in pigs (Bonifait *et al.*, 2010; Hu *et al.*, 2010). SspA cleaves fibrinogen, preventing subsequent fibrin formation by thrombin. Purified SspA protease is toxic when added to brain microvascular endothelial cells (Bonifait *et al.*, 2011b) and induces a proinflammatory response in macrophages through a non-proteolytic mechanism (Bonifait and Grenier, 2011a). Homologous genes are present in the genomes of several other *Streptococcus* species, including *S. thermophilus*, *S.*

*canis*, *S. agalactiae*, *S. dysgalactiae*, *S. gordonii*, *S. mitis*, *S. sanguinis* and *S. intermedius*.

### Superantigens

Bacterial superantigens (SAGs) are potent microbial secreted toxins produced by GAS, group C/G *S. dysgalactiae* ssp. *equisimilis*, *Staphylococcus aureus*, *Yersinia pseudotuberculosis* and *Mycoplasma arthritidis* (Fraser and Proft, 2008). Their importance in disease pathogenesis resides in their ability to bypass the regular antigen presentation process and overstimulate immune activation. Conventional antigen presentation by antigen-presenting cells (APCs) to T cells is mediated by the interaction of the major histocompatibility complex (MHC) molecules and the T-cell receptor (TCR). TCRs are formed by five variable elements ( $V\beta$ ,  $D\beta$ ,  $J\beta$ ,  $V\alpha$  and  $J\alpha$ ), which are responsible for a highly specific immune response to a vast number of foreign antigens. All five variable elements from the TCR are needed to recognize the complex formed by the MHC and the processed antigen in order to stimulate T-cell proliferation (Fig. 1). As a result of this specificity, conventional processed antigens are only able to stimulate approximately 0.01% of the T-cell repertoire (Davis and Bjorkman, 1988). Conversely, unprocessed SAGs bind directly to the MHC II molecules on the surface of APCs and to the  $V\beta$  variable region of the TCR, which is present in up to 25% of the T-cell population (Fig. 1). When this simultaneous binding occurs, stimulated T cells and APCs secrete a vast amount of proinflammatory cytokines such as IL-2,



**Fig. 1.** A. T-cell stimulation mediated by conventional major histocompatibility complex (MHC) II antigen presentation, where large antigens are processed by antigen-presenting cells (APCs) into linear epitopes and presented by MHC II; specific recognition of the MHC–antigen complex by T-cell receptor (TCR) on the surface of T cells has to occur in order to trigger production of inflammatory cytokines. B. Superantigen direct binding to MHC II and TCR, where binding occurs in a less specific manner, thus stimulating a significantly higher number of T cells and producing an uncontrollable cytokine release.



interferon- $\gamma$  and tumour necrosis factor- $\alpha$  (Jupin *et al.*, 1988; Fast *et al.*, 1989; Müller-Alouf *et al.*, 1996). This uncontrollable cytokine release is then thought to be responsible for the characteristic manifestations of streptococcal toxic shock syndrome (STSS), such as systemic vasodilatation, hypotension and multi-organ failure (Lappin and Ferguson, 2009). In addition, recent published data suggest that for some SAGs, binding to the CD28 receptor on the surface of T cells is required for the expression of Th1 cytokines (Arad *et al.*, 2011). It has been hypothesized that SAGs dysregulate the host immune response and therefore increase the chance of pathogen survival (Spaulding *et al.*, 2013). In the case of GAS, an outside-in signalling mechanism has been proposed to explain the ability of GAS to trigger STSS from mucosal surfaces, where SAGs together with SLO act synergistically to penetrate the mucosal epithelium, recruit lymphocytes to the site of infection and initiate SAG stimulation of T cells (Fig. 2) (Brosnahan, 2009; Brosnahan and Schlievert 2011). Additional new evidence suggests that SAGs provide an advantage for nasopharyngeal colonization in a humanized mouse model (Kasper *et al.*, 2014).

#### Structure of superantigens

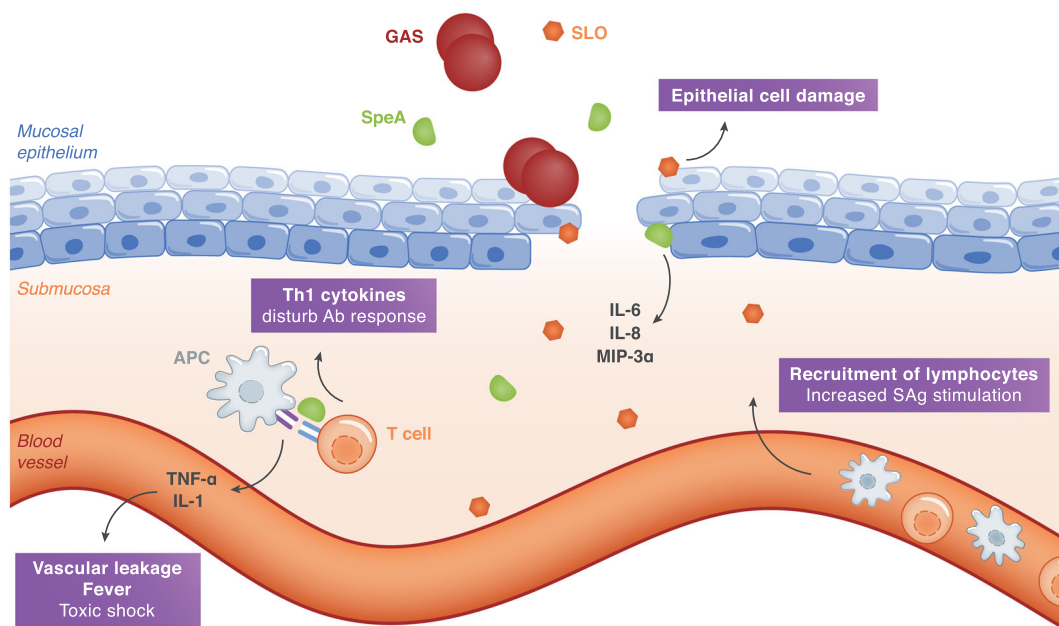
Since their discovery in GAS in 1924, numerous streptococcal SAGs have been identified, particularly since the expansion of whole-genome sequencing technologies. In

total, 91 unique sequences encoding complete streptococcal SAGs have been reported and a uniform nomenclature proposed (Commons *et al.*, 2014), which has been used in this review (Table 2).

Superantigens are small non-glycosylated proteins between 22 and 29 kDa. Despite low DNA sequence homology, they share a common two-domain architecture formed by the N-terminal and C-terminal domains, which are separated by a long accessible  $\alpha$ -helix. Hydrophobic residues in solvent-exposed regions characterize the N-terminal domain, while a four-stranded  $\beta$ -sheet capped by a central  $\alpha$ -helix constitutes the C-terminal domain. Most of the streptococcal SAGs contain a zinc binding site in the C-terminal domain, and the presence of zinc has been shown to be critical for MHC II binding (Proft *et al.*, 1999). In addition, the majority of streptococcal SAGs bind to the  $\beta$ -chain of MHC II with the exception of SpeA and SSA, which bind to the  $\alpha$ -chain. The TCR binding site is located in a shallow cavity between the two protein domains, and different SAGs show preference for different TCR V $\beta$  chains (Table 2) (Papageorgiou and Acharya, 1997; Proft and Fraser, 2007). Some streptococcal SAGs (SSA, SpeA, SpeI, SpeH and SmeZ) contain a CD28 binding motif situated in the SAG  $\beta$ -strand/hinge/ $\alpha$ -helix domain (Arad *et al.*, 2011; Commons *et al.*, 2014).

#### Evolution and genetic mobility of superantigen genes

Most of the streptococcal SAGs are located on prophage regions within the genome. Only *speG*, *speJ* and *smeZ*,



**Fig. 2.** Outside-in mechanism proposed by Brosnahan and Schlievert (2011), where streptolysin O (SLO) and SpeA act synergistically to cause streptococcal toxic shock syndrome (STSS) from a mucosal surface. SLO produces damage to epithelial cells allowing SpeA to access the submucosa. SpeA in turn stimulates epithelial cells to secrete chemokines that recruit lymphocytes to the site of infection where they are targets for superantigen (SAG) stimulation. Secretion of Th1 cytokines by SAG-stimulated T cells and antigen-presenting cells (APCs) skews the host's immune response, interfering with its ability to effectively combat infection. The uncontrolled release of proinflammatory cytokines can then cause vascular leakage and fever leading to STSS.

**Table 2.** Streptococcal superantigens.

Superantigen	Streptococcal species	Major histocompatibility complex II binding $\alpha/\beta$	T-cell receptor V $\beta$ specificity	Clinical association	References
SpeA	<i>Streptococcus pyogenes</i> <i>Streptococcus dysgalactiae</i> ssp. <i>equisimilis</i>	+/-	2.1, 12.2, 14.1, 15.1	Scarlet fever	(Eriksson <i>et al.</i> , 1999; Hartwig <i>et al.</i> , 1994; Musser <i>et al.</i> , 1991; Silva-Costa <i>et al.</i> , 2014)
SpeC	<i>S. pyogenes</i> <i>S. dysgalactiae</i> ssp. <i>equisimilis</i> <i>S. dysgalactiae</i> ssp. <i>dysgalactiae</i>	-/+	2.1, 3.2, 12.5, 15.1	Streptococcal toxic shock syndrome Scarlet fever Kawasaki Disease	(Li <i>et al.</i> , 1997; Silva-Costa <i>et al.</i> , 2014; Davies <i>et al.</i> , 2015; Yoshioka <i>et al.</i> , 2003)
SpeG	<i>S. pyogenes</i> <i>S. dysgalactiae</i> ssp. <i>equisimilis</i> <i>S. dysgalactiae</i> ssp. <i>dysgalactiae</i> <i>Streptococcus minor</i> <i>Streptococcus canis</i>	-/+	2.1, 4.1, 6.9, 9.1, 12.3	ND	(Proft <i>et al.</i> , 1999; Sachse <i>et al.</i> , 2002)
SpeH	<i>S. pyogenes</i> <i>S. dysgalactiae</i> ssp. <i>equisimilis</i> <i>Streptococcus equi</i> ssp. <i>equi</i>	-/+	2.1, 4.1, 6.9, 9.1, 12.3	ND	(Proft <i>et al.</i> , 1999)
SpeI	<i>S. pyogenes</i> <i>S. equi</i> ssp. <i>equi</i>	-/+	6.9, 9.1, 18.1, 22	ND	(Proft <i>et al.</i> , 2001)
SpeJ	<i>S. pyogenes</i>	-/+	2.1	ND	(Proft <i>et al.</i> , 2001; McCormick <i>et al.</i> , 2001)
SpeK	<i>S. pyogenes</i> <i>S. dysgalactiae</i> ssp. <i>equisimilis</i> <i>S. equi</i> ssp. <i>equi</i>	-/+	1, 5.1, 23	Acute rheumatic fever	(Beres <i>et al.</i> , 2002; Proft <i>et al.</i> , 2003b)
SpeL	<i>S. equi</i> ssp. <i>zooepidemicus</i> <i>S. pyogenes</i> <i>S. dysgalactiae</i> ssp. <i>equisimilis</i> <i>S. equi</i> ssp. <i>equi</i>	-/+	1, 5.1, 23	Acute rheumatic fever	(Smoot <i>et al.</i> , 2002)
SpeM	<i>S. pyogenes</i> <i>S. dysgalactiae</i> ssp. <i>dysgalactiae</i>	ND	1, 23	Acute rheumatic fever	(Smoot <i>et al.</i> , 2002; Miyoshi-Akiyama <i>et al.</i> , 2003)
SpeN	<i>S. equi</i> ssp. <i>zooepidemicus</i>	ND	ND	ND	(Paillot <i>et al.</i> , 2010)
SpeO	<i>S. equi</i> ssp. <i>zooepidemicus</i>	ND	ND	ND	(Paillot <i>et al.</i> , 2010)
SpeP	<i>S. equi</i> ssp. <i>zooepidemicus</i>	ND	ND	ND	(Paillot <i>et al.</i> , 2010)
SSA	<i>S. pyogenes</i>	+/-	1, 3, 15	Scarlet fever	(Mollick <i>et al.</i> , 1993; Igwe <i>et al.</i> , 2003; Silva-Costa <i>et al.</i> , 2014; Davies <i>et al.</i> , 2015)
SmeZ	<i>S. dysgalactiae</i> ssp. <i>equisimilis</i> <i>S. pyogenes</i>  <i>S. canis</i>	-/+	2.1, 4.1, 7.3, 8.1	Streptococcal toxic shock syndrome Streptococcal toxic shock syndrome	(Kamezawa <i>et al.</i> , 1997; Igwe <i>et al.</i> , 2003; Proft <i>et al.</i> , 2003a; Vlamincx <i>et al.</i> , 2003)

ND, not determined.

which are usually flanked by transposon-like elements, are located within the main chromosome external to prophages. The hypothesis that SAg genes can be horizontally transferred through phages was validated by performing *in vitro* and *in vivo* lysogenic transfer of *speC* between two different GAS isolates (Broudy and Fischetti, 2003). Moreover, lysogenic transfer of phage-carrying toxins between different streptococcal species has also been reproduced *in vitro* (Vojtek *et al.*, 2008). Despite the fact that horizontal transfer of SAg genes has been demonstrated, little is known about the evolution of these

genes within streptococcal species. A multi-step model for the evolution of SAgS was proposed based on genome sequence analysis of GAS, *S. dysgalactiae* ssp. *equisimilis* and *S. aureus*. In step 1, ancestral bacteria acquired the ancestors of streptococcal SAgS, staphylococcal enterotoxins and staphylococcal SAg-like proteins (SSLs). In step 2, ancestral *smeZ* was likely to be deleted from the *S. dysgalactiae* ssp. *equisimilis* genome soon after the speciation of GAS and *S. dysgalactiae* ssp. *equisimilis*. In step 3, ancestral SAgS and SSLs were potentially incorporated into phages that were then transferred in between

bacterial strains. In the final step, staphylococcal SAGs (potential ancestors of streptococcal SAGs such as SSA and SpeA) were then horizontally transferred to *Streptococcus* bacteria (Okumura *et al.*, 2012).

#### *Streptococcal superantigens and disease correlation*

Clinical manifestations of disease have been linked to the presence of SAGs in streptococcal pathogens. Cases of scarlet fever have been correlated with the carriage or acquisition of *ssa*, *speA* and *speC* in different studies (Silva-Costa *et al.*, 2014; Davies *et al.*, 2015). Additionally, *speA* and *ssa*, together with *speK*, and *smeZ* have been associated with invasive disease and STSS (Eriksson *et al.*, 1999; Chatellier *et al.*, 2000; Beres *et al.*, 2002; Ikebe *et al.*, 2002). A strong correlation has been observed between M18 isolates expressing *speL* and *speM* and acute rheumatic fever (Smoot *et al.*, 2002). M89 isolates harbouring the *speK* gene have also been associated with acute rheumatic fever (Proft *et al.*, 2003b).

A controversial correlation between *speC* and Kawasaki disease, a sporadic childhood inflammatory arthritis that can affect the coronary vessels (Shulman and Rowley, 2015), has been proposed (Abe *et al.*, 1992; Curtis *et al.*, 1995); however, contradicting epidemiological studies render a direct correlation questionable (Yoshioka *et al.*, 2003). Research on the causative agents of Kawasaki disease is still ongoing. In addition, *speC* has also been correlated to psoriasis in susceptible individuals (Leung *et al.*, 1993; Lewis *et al.*, 1993); however, the evidence is not strong enough for a direct correlation, and the role of SAGs in disease manifestations remains unclear (Travers *et al.*, 1999; Thomssen *et al.*, 2000).

#### **Other Toxins**

In addition to producing toxic SAGs, haemolysins and proteases, streptococcal species produce a number of other toxins including proteins, enzymes and polysaccharides such as Christie Atkins Munch-Petersen (CAMP) factor, GBS toxin, adenosine diphosphate (ADP)-ribosyltransferase and NADase.

#### *Christie Atkins Munch-Petersen factor*

The CAMP reaction was initially described as the lysis of erythrocytes during a synergistic interaction of CAMP factor produced by GBS with the  $\beta$ -toxin of *S. aureus* (Christie *et al.*, 1944). Historically, this reaction has been used for the clinical identification of GBS. The CAMP factor is best characterized in GBS, where the toxin is encoded by the *cfb* gene (Podbielski *et al.*, 1994). Other streptococcal species, including groups A, B, C, G, M, P, R and U, have also been reported to produce CAMP factor; and in GAS, CAMP factor is encoded by the *cfa* gene (Gase *et al.*, 1999). The CAMP factor of GBS binds

glycophosphatidylinositol-anchored proteins (Lang *et al.*, 2007) and subsequently functions as a pore-forming toxin, likely requiring self-oligomerization for activity (Lang and Palmer, 2003). Previously, GBS CAMP factor was called protein B, following reports that it could bind the Fc region of IgG and IgM from several mammalian species (Jurgens *et al.*, 1987). However, more recent studies could not detect a non-immune binding association between CAMP factor and human IgG, leading to the suggestion that the name protein B may be inappropriate (El-Huneidi *et al.*, 2007). CAMP factor of GBS was determined to be non-pathogenic following administration to mice (Jurgens *et al.*, 1987). Furthermore, CAMP factor was not essential for systemic virulence of GBS (Hensler *et al.*, 2008), suggesting that CAMP factor (in the absence of *S. aureus*  $\beta$ -toxin) does not play a direct role in GBS pathogenesis. Recent investigations have uncovered a novel CAMP factor in GBS, designated CAMP factor II, that has been proposed to have spread to other streptococci (*Streptococcus uberis*, *S. dysgalactiae*, *S. dysgalactiae* ssp. *equisimilis* and *Streptococcus bovis*) via integrative and conjugative elements (Chuzeville *et al.*, 2012).

#### *Group B Streptococcus toxin (CM101)*

Group B *Streptococcus* toxin, also designated CM101, is a polysaccharide exotoxin that binds to embryonic receptors expressed in the developing lung of the neonate, resulting in a strong inflammatory response (Wamil *et al.*, 1997). GBS toxin also binds to tumour neovasculature in adults and for this reason has been evaluated as an anti-cancer therapeutic. In a phase I clinical trial administering GBS toxin as an anti-neovascularization agent in human cancer therapy (Harris, 1997), 5/15 patients exhibited tumour reduction or stabilization, and sera from all patients had elevated soluble E-selectin, indicative of tumour neovasculature endothelial engagement in an inflammatory process (Wamil *et al.*, 1997). Historically, GBS toxin was purified from culture media of GBS isolates from neonates who had died because of GBS infection. GBS toxin has also been identified in plasma, urine and cerebrospinal fluid from infants with GBS disease and could be used as an additional tool to diagnose GBS infection in infants, which can sometimes prove difficult to diagnose (Sundell *et al.*, 2000).

#### *Adenosine diphosphate-ribosyltransferase (SpyA)*

Adenosine diphosphate-ribosyltransferases covalently transfer ADP-ribose from NAD<sup>+</sup> to eukaryotic proteins. SpyA is a surface-exposed membrane protein of GAS that has been described as a C3-like ADP-ribosyltransferase (Korotkova *et al.*, 2012). SpyA has been documented to modify cytoskeletal proteins including vimentin, tropomyosin and actin, and when expressed in HeLa cells

following transfection, SpyA activity resulted in a loss of actin microfilaments (Coye and Collins, 2004) and inhibited vimentin polymerization, resulting in the collapse of the vimentin cytoskeleton (Icenogle *et al.*, 2012). In a mouse subcutaneous infection model, the  $\Delta$ spyA mutant generated smaller lesions and had higher levels of mRNA encoding CXCL1 and CCL2 (both neutrophil and macrophage chemoattractants) and vimentin, compared with WT (Hoff *et al.*, 2011). Vimentin plays many roles in the cell including the organization of cellular architecture (Ivaska *et al.*, 2007), and the loss of vimentin functionality can impair wound healing (Eckes *et al.*, 2000). The findings of Hoff *et al.* (2011) suggest that SpyA delays wound healing in the subcutaneous infection model. In a mouse intravenous infection model, the  $\Delta$ spyA mutant caused higher mortality with impaired bacterial clearance, and *in vivo*, the mutant was resistant to killing by macrophages (Lin *et al.*, 2015). Lin and colleagues determined that SpyA triggers pyroptosis, a caspase-1-dependent inflammasome in macrophages, resulting in macrophage cell death and the release of proinflammatory cytokine IL-1 $\beta$ . This innate defence programme triggered in response to SpyA dramatically enhances clearance of GAS and restricts bacterial growth, attenuating disease progression.

*NAD-glycohydrolase* (*Streptococcus pyogenes* NADase or NADase)

NAD-glycohydrolase (also known as *S. pyogenes* NADase or Nga) is encoded by the *nga* gene, which is found in the same operon as *slo*. SLO and NADase act synergistically to trigger cytotoxicity. NADase is translocated through pores created by SLO and delivered into the host cell cytoplasmic compartment by a process termed cytolysin-mediated translocation (Madden *et al.*, 2001). NADase possesses both ADP-ribosyl cyclase activity and cADPR hydrolase activity (Karasawa *et al.*, 1995), and once inside the cell, NADase produces the potent second messenger cyclic ADP-ribose. Cytotoxicity mediated by the enzymatic action of NADase may be a consequence of the depletion of host cell energy stores (e.g. intracellular NAD<sup>+</sup>) (Michos *et al.*, 2006). NADase has been shown to act within human pharyngeal keratinocytes, resulting in enhanced cell membrane injury, inhibition of bacterial internalization and induction of apoptosis (Bricker *et al.*, 2002). SLO stimulates xenophagy in these cells, and the co-expression of SLO and NADase results in prolonged intracellular survival of GAS and prevents maturation of GAS-containing autophagosomes (O'Seaghdha and Wessels, 2013). In addition, SLO and NADase mediate GAS intracellular survival and cytotoxicity within macrophages, subsequently enabling persistent infection by preventing phagolysosome acidification (Bastiat-Sempe *et al.*, 2014). Recent studies have identified NADase-inactive variants that have emerged with polymorphism at multiple residues

(Chandrasekaran *et al.*, 2013). This analysis revealed an NADase-independent cytotoxic activity that was retained by the enzymatically inactive variants, suggesting another domain of NADase can mediate cytotoxicity. NADase also contributes to virulence in two mouse skin tissue infection models and a model of septicaemia, suggesting NADase plays an important role in establishing infection in the host (Bricker *et al.*, 2005; Tatsuno *et al.*, 2010).

## Conclusion

While several toxins are found across streptococcal species boundaries, each of these species expresses a specific repertoire of toxic molecules that target specific aspects of host immunity and physiology. Indeed, many clones within individual species express distinct toxin profiles. These toxins play crucial roles within the host-pathogen interaction, allowing the pathogen to colonize, proliferate and disseminate. Several of these toxins have demonstrated utility as candidate vaccine antigens, in inactive forms, and in several instances, the specificity of toxin action has been experimentally utilized in the development of novel therapeutics, such as anti-cancer agents. Deepening of our knowledge of the mode of action of these toxin molecules will aid in our efforts to prevent disease caused in humans and animals by the various streptococcal pathogens.

## Acknowledgements

The authors gratefully acknowledge the support of the National Health and Medical Research Council of Australia and the National Institutes of Health of the USA.

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