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The Deoxyribonucleases of Pathogenic Lancefield Streptococci

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Abstract

Deoxyribonucleases (DNases) are abundant among the pathogenic streptococci, with most species harbouring genes for at least one. Despite their prevalence, however, the role for these extracellular enzymes is still relatively unclear. The DNases of the Lancefield group A *Streptococcus*, *S. pyogenes* are the best characterised, with a total of eight DNase genes identified so far. Six are known to be associated with integrated prophages. Two are chromosomally encoded, and one of these is cell-wall anchored. Homologues of both prophage-associated and chromosomally encoded *S. pyogenes* DNases have been identified in other streptococcal species, as well as other unique DNases. A major role identified for streptococcal DNases appears to be in the destruction of extracellular traps produced by immune cells, such as neutrophils, to ensnare bacteria and kill them. These traps are composed primarily of DNA which can be degraded by the secreted and cell wall anchored streptococcal DNases. DNases can also reduce TLR-9 signalling to dampen the immune response and produce cytotoxic deoxyadenosine to limit phagocytosis. Upper respiratory tract infection models of *S. pyogenes* have identified a role for DNases in potentiating infection and transmission, possibly by limiting the immune response or through some other unknown mechanism. Streptococcal DNases may also be involved in interacting with other microbial communities through communication, bacterial killing and disruption of competitive biofilms, or control of their own biofilm production. The contribution of DNases to pathogenesis may therefore be wide ranging and extend beyond direct interference with the host immune response.

Introduction

A number of clinically significant eukaryotic and prokaryotic microorganisms produce deoxyribonucleases (DNases) as virulence factors. These include Gram-positive bacterial pathogens such as *Staphylococcus aureus* and streptococcal species such as *Streptococcus pyogenes* [1, 2]. Gram-negative pathogens such as *Helicobacter pylori* and *Shigella flexneri,* in addition to members of the genera *Salmonella* and *Yersinia*, also implement these enzymes in a similar manner [3, 4]. Further, the opportunistic fungal pathogens *Candida albicans* and *Cryptococcus neoformans* and the malarial parasites of the genus *Plasmodium* are also known to utilise DNases in pathogenesis [5-7].

The genus *Streptococcus* comprises a multitude of obligate and opportunistic pathogens of both humans and animals [8]. A classification system identified by Rebecca Lancefield in the 1930s is still used to classify the beta-haemolytic streptococci based on their type specific carbohydrate antigen [8]. *S. pyogenes,* the Lancefield Group A *Streptococcus* (GAS) is a major human pathogen responsible for a diversity of clinical manifestations and considerable global disease burden exceeding 700 million infections per annum [9]. Clinical manifestations include superficial infections such as pharyngitis, non-bullous impetigo and scarlet fever in addition to potentially lethal invasive manifestations such as streptococcal toxic shock syndrome, necrotising fasciitis and puerperal sepsis [10]. Furthermore, *S. pyogenes* is associated with serious post-infectious sequelae, notably post-streptococcal glomerulonephritis and rheumatic fever [11]. *Streptococcus agalactiae*, the Lancefield group B *Streptococcus* (GBS) is another major human pathogen and, although present as a commensal in the gastrointestinal and genitourinary tract, it is a leading cause of neonatal morbidity and mortality worldwide, often associated with neonatal meningitis, pneumonia and sepsis [12]. *Streptococcus dysgalactiae* sbsp. *equisimilis* (SDSE) can carry the Lancefield group C or G antigens and has only relatively recently been recognised as a major human pathogen, increasing in incidence and prevalence [13]. The spectrum of symptoms associated with SDSE infection are similar to those observed with *S. pyogenes*, indeed the two species share many virulence factors and significant DNA sequence similarity [13]. Other Lancefield group C streptococci include *Streptococcus equi* subsp. *equi*

(hereafter referred to as *S. equi*) and *S. equi* subsp. z*ooepidemicus* (hereafter referred to as *S. zooepidemicus*). *S. equi* is almost exclusively a pathogen of horses and is believed to be descended from an ancestral strain of *S. zooepidemicus,* which will readily colonise and infect humans in addition to a vast spectrum of domestic and livestock animals. Both species share in excess of 80% DNA sequence similarity with *S. pyogenes* [14].

The ability for Lancefield streptococci to cause a wide range of disease may be due to an extensive arsenal of virulence factors. Some of these factors, which include DNases, are associated with mobile genetic elements and can transmit between strains and even species. The function of DNases during pathogenesis is still relatively unclear and the potential for DNases to be virulence factors has only recently been explored.

DNase history & nomenclature

Historically, it was believed that *S. pyogenes* produced only four DNases and these were serologically classified as DNase A, DNase B, DNase C and DNase D. Anti-DNase B titres have been used as a serological biomarker of streptococcal infection and post-streptococcal immune sequalae since at least the 1970s [15, 16]. However, the identity of DNase B would not be truly known for over a decade when it was demonstrated that the chromosomally encoded DNase *spdB* or mitogenic factor (*mf*; then thought to be a streptococcal superantigen) was in fact DNase B [17]. It would be many years subsequent to the initial use of DNase B in the clinical laboratory before it was established that these enzymes could contribute to the pathogenesis of *S. pyogenes* [2]. DNase C is now known to be Spd3, and DNase D has been identified as Sda2 (SdaD2) [2], however, the identity of DNase A in the original serological system is not currently known.

Since their discovery, the classification, nomenclature and role of the DNases found in streptococci has been a confusing topic. With advances in molecular biology and the application of whole genome sequencing, it is now apparent that a number of variants exist for the majority of DNases and there is homology between DNases of different streptococcal species.

Genetic identification and classification of streptococcal DNases

DNases of the Lancefield group A Streptococcus

The DNases of group A *Streptococcus* are by far the best characterised and currently eight have been identified; *spnA*, *spdB*, *sda1*, *sda2*, *spd1*, *spd3*, *spd4* and *sdn*. Both *spn*A and *spdB* are encoded on the chromosome and have been shown to be common to all *S. pyogenes* isolates tested, existing as different alleles related to the *emm* genotype of the isolate [18, 19]. We confirmed the presence of both *spnA* and *spdB* in all available completed *S. pyogenes* genomes (NCBI, n=54) representing 25 different *emm* genotypes. SpnA is the only *S. pyogenes* DNase to be identified that is cell wall anchored via an LPXTG motif [19].

The other six *S. pyogenes* DNases are associated with prophages or prophage-like elements (Table 1). *S. pyogenes* has a close evolutionary relationship with temperate bacteriophage as most strains are polylysogenised, and prophage and prophage-like-elements account for ~10% of the *S. pyogenes* genome [20, 21]. Bacteriophages are transmissible between hosts, carrying genes for bacterial virulence factors; the streptococcal superantigens, DNases and a secreted phospholipase. Different bacteriophages may carry the same virulence factor and each factor may exist as a different allele, as has been shown for the streptococcal superantigens [22]. By mining the 54 available genomes of *S. pyogenes* we identified that at least two different DNA sequence alleles exist for each of the six prophage associated DNases (Table 1). The most prolific prophage-associated DNase genes were *spd1* and *spd3*. The other four prophage-associated DNase genes were restricted to isolates belonging to only 2-5 different *emm* genotypes, which may be reflective of host-specificity or functionality of the associated prophage. Twelve isolates did not carry any prophage-associated DNases and they belonged to the *emm* genotypes *emm*44, 59, 71, 82, 83, 89 and 101. Although other *emm*89 isolates did carry prophage-associated DNases, two *emm*89 isolates (H293 and MGAS23530) have been shown not to have any prophage elements integrated into their chromosomes, and therefore only carry chromosomal DNase genes [23, 24].

DNases of other streptococci

Literature search and BLAST analyses identified DNases in other streptococcal species that are similar to those found in *S. pyogenes*. Despite the prevalence of *spd1* and *spd3* among *S. pyogenes* isolates, we only identified three potential homologues of either of these genes (Figure 1). Homologues of *spd1* were identified by BLAST analysis (sharing ≥90% identity over 75% or more of the sequence length) in isolates of *S. iniae* and *S. porcinus*, pathogens of fish and swine respectively, although they may also cause disease in humans. A third gene, similar to *spd1* was identified in *S. zooepidemicus* MGCS1056, and is one of three inferred DNases in this genome termed *sdzA* (the *spd1* homologue), *sdzB* and *sdzD* [25]. The gene *sdzA* was unique to MGCS1056 but the other two DNases were identified in the other three *S. zooepidemicus* genomes and the two genomes of the closely related equine pathogen *S. equi.* Alleles of the *sdzD* gene cluster with *sda* genes of *S. pyogenes* and SDSE, suggesting they are homologous. Although in *S. pyogenes*, *sda* is associated with prophages, no such elements were identified associated with the *sda*-like genes of *S. zooepidemicus* [25], *S. equi* or SDSE. This was also the case for the third DNase gene of *S. zooepidemicus* and *S. equi*, *sdzB,* although it shares some similarity to the *S. pyogenes* chromosomally encoded *spdB* as well as the prophage associated *spd4*. Recently, two further DNases were identified in *S. zooepidemicus* that are cell wall anchored, termed ENuc and 5Nuc [26]. The *enuc* alleles identified in both *S. zooepidemicus* and *S. equi* clustered with other identified cell surface anchored DNases (Figure 1) that include *spnA*-like alleles from SDSE. The SDSE *spnA*-like alleles all have a cell wall anchor motif, except *spnA.5* carried by the SDSE strain GGS_124, which has a truncation mutation resulting in the loss of the far C-terminal region including the LPXTG anchor motif. Other cell surface anchored DNases that have been identified include the *S. sanguinis* cell wall anchored nuclease, SWAN and the *S. suis* SsnA. *S. suis* does not have a Lancefield antigen and is a pathogen of swine, but can cause severe zoonotic infection in humans. SsnA of *S. suis* has been previously identified as a functional DNase [27, 28] along with EndAsuis, although EndAsuis is membrane anchored and shows homology to *endA* of *S. pneumoniae* which may play a role in competence [29]. The gene *endAsuis* did not show any homology to other streptococcal DNases

analysed (Figure 1) although similar DNases with a role in competence may exist in other streptococcal species. The *nucA* gene of *S. agalactiae* also appeared unrelated to any other identified streptococcal DNases, but has confirmed DNase activity [30]. It seems likely that other DNases exist in *S. agalactiae* but have yet to be identified.

We did identify two prophage-associated DNases genes in SDSE. One was in strain GGS_124 and associated with a prophage element that shares ~90% identity to prophage 315.3 from *S. pyogenes* *emm*3 genome MGAS315 [31]. Although in *S. pyogenes,* the prophage 315.3 is associated with the DNase *spd4*, the gene found in GGS_124 (SDSE167_1285, SDSE *sdn*) is 100% identical to a different prophage-associated *S. pyogenes* DNase, *sdn.5* (Figure 1). Another SDSE strain, 167 also has a prophage-like element associated with a DNase gene [32]. The prophage is most closely related to a prophage-element found in *emm*1 NCTC8198 *S. pyogenes,* although this prophage is not associated with any virulence factors, the prophage element in the SDSE strain 167 is associated with an *sda*-like gene (SDEG_1103, SDSE *sda*2). However, in this strain, the gene carries a mutation that would truncate the protein. These findings suggest an exchange of prophages and associated virulence factors between *S. pyogenes* and SDSE.

The Role of DNases

Immune evasion

Originally it was thought that DNases facilitated dissemination of streptococci through tissue planes in the human host by liquefying purulent exudate produced during infection [33]. It has also been speculated that in reducing the viscosity of the microenvironment, DNases expedite transmission of progeny phage particles between bacterial hosts, potentially conferring a selection advantage to both bacteriophage and bacterium [34]. Although this may still be the case, a recently described role for DNases is in the evasive strategy implemented by *S. pyogenes* to prevent neutrophil activation and degradation of neutrophil extracellular traps (NETs) (Figure 2) [35]. NETs are composed of chromatin,

164 histones, proteolytic enzymes and other peptides, and produced by neutrophils on degranulation
165 whereupon they bind to invading microorganisms by charge interaction [36]. Once entrapped,
166 secreted cationic antimicrobial peptides attack the offending agent and neutralise virulence factors.
167 Similar extracellular trap structures have been described in association with mast cells [37] and
168 eosinophils [38], all of which can be degraded by DNases [39].

169 By secreting DNases, such as Sda1, *S. pyogenes* is able to escape these bactericidal traps by degrading
170 their chromatin backbone, thus surviving and spreading (Figure 2) [2, 35]. The ENuc and 5Nuc DNases
171 of *S. zooepidemicus* also have the capacity to degrade NETs, both synergistically and alone, and
172 enabled *S. zooepidemicus* to spread systemically in a murine model of infection [26]. The *S.*
173 *agalacatiae* DNase NucA is also able to degrade NETs and its loss results in reduced virulence [30].

174 Cell wall anchored DNases have also been associated with NET degradation. The first description of a
175 cell wall located DNase was the discovery of SsnA of *S. suis* [40]. *S. pyogenes,* further to secreting
176 extracellular DNases, is also able to implement the cell wall anchored DNase SpnA to escape these
177 traps [41]. The SWAN (Sanguinis cell wall anchored nuclease) of *S. sanguinis,* an opportunistic
178 periodontal pathogen, has been shown to degrade NETs [42]. *S. pneumoniae* also produces a cell wall
179 located nuclease, EndA, which is capable of degrading NETs [43] and a homologue of this enzyme,
180 EndAsuis, can be found in *S. suis.* EndAsuis is reported to increase survival in NETs and is produced in
181 addition to the aforementioned secreted nuclease [29]. Although it is unclear why streptococci might
182 implement both cell-wall anchored and secreted DNases, they may provide necessary localised DNase
183 activity in the immediate environment as well as more wide-spread activity [44]. *S. pyogenes* remained
184 attenuated following deletion of the cell-wall anchored DNase SpnA, despite complementation with a
185 secreted form of the enzyme [44]. SpnA may also have an additional role in pathogenesis that is not
186 related to its enzymatic activity [44] and this may well extend to other streptococcal cell wall anchored
187 DNases.

Another method by which *S. pyogenes* is able to evade innate immunity is by degrading its own nucleic acids. Indeed, depolymerisation of bacterial DNA by DNases has been shown to prevent killing of *S. pyogenes* by reducing TLR-9 signalling and subsequent recognition of un-methylated CpG-rich DNA by macrophages [45]. The ENuc and 5Nuc DNases of *S. zooepidemicus* too have a dual action against the innate immune system. Both nucleases degrade extracellular traps but also possess 5'-nucleotidase activity and produce cytotoxic deoxyadenosine as a substrate, that impedes phagocytosis by macrophages [26]. A similar mechanism was also identified in *S. pyogenes* whereby a cell wall anchored 5' nucleotidase (S5nA) acted synergistically with the DNase SpnA to cleave NETs and generate the cytotoxic deoxyadenosine [46]. S5Na and SpnA are closely related to 5Nuc and ENuc of *S. zooepidemicus*, respectively (Figure 1). Other streptococcal species also express 5' nucleotidases and so similar mechanisms may exist for DNase synergy.

Nutrient scavenging

Elimination of DNA during infection may also have an indirect impact on pathogenesis, serving more than one purpose. For certain strains of *S. pyogenes*, nucleic acid derivatives are essential for growth. Indeed, efforts to standardise a laboratory method for sulphonamide sensitivity testing in the 1940s were hindered by this necessity [47]. Scavenging nucleic acids during infection or colonisation by implementing may therefore provide nutrients during both colonisation and infection. In addition, extracellular trap formation by neutrophils and mast cells ultimately leads to death of these phagocytes [39], and could provide further nutrients for the bacteria. This may also explain why *S. pyogenes* and other streptococci possess both secreted and cell-wall- anchored DNases, to retain DNase activity close to the bacterium for nutrition.

Role of DNases during infection

Experimental infection data obtained using a genotype *emm*1 strain with three DNases revealed that sequential inactivation of these genes, most importantly SdaD2, significantly impeded the capacity of the strain to establish pharyngeal infection in cynomolgus macaques [2]. Similarly, the acquisition of

the Spd1 DNase by ST15 *emm*3 *S. pyogenes* was associated with increased nasal and airborne shedding in a murine nasopharyngeal infection model [48]. While not inherently more invasive, nor more lethal, the *emm*3 strains that had acquired Spd1 were found to be overrepresented in an upsurge of disease, and their emergence was coincident with a dramatic but transient spike in invasive *emm*3 disease in the United Kingdom [49]. The exact role DNase play during upper-respiratory tract infection has yet to be elucidated but these findings support the potential for DNases to contribute directly to infection. DNases have also been shown to contribute to the disease progression in murine skin and soft tissue infections [2,19,35] and the *Galleria mellonella* model of invasive disease [46], which may be due to their role in preventing NET-mediated killing as well as some other as yet un-identified role [46].

Bacterial competition and communication

Spd1 is also reported to have ribonuclease (RNase) activity [50]. A number of secreted eukaryotic RNases are known to be bactericidal; human RNases, such as the eosinophil cationic protein (also known as RNase 3) and the keratinocyte-derived RNase 7 have been shown to play an important role in innate immunity and defence against both Gram-positive and Gram-negative pathogens, by attacking the bacterial cell wall [51-53]. It may be the case, therefore, that the duality of some of the streptococcal DNases in their ability to also degrade RNA, may serve a similar offensive purpose. Microbial RNases have also been reported to have the capacity to damage eukaryotic cells both directly and indirectly of their ribonucleolytic activity, targeting various cellular components, leading to altered gene expression, cellular dysfunction and cell death [54].

The contact-dependent growth inhibition (CDI) toxin of *Yersinia kristensenii* was recently identified as a novel bacterial RNase of the RNase A superfamily with a key role in bacterial competition and growth [55]. The RNase activity of streptococcal DNases may therefore also serve to mediate cell-cell interactions within and between bacterial species, coordinating microbial communities such as those observed in non-sterile sites and biofilm.

It is also possible that these enzymes may be used by streptococci to compete with commensal microorganisms in non-sterile sites, such as in the nasopharynx or on the skin. Indeed, nucleic acids are a fundamental component of many microbial biofilms [56], and streptococcal DNases may be able to effectively eliminate biofilms formed by other bacteria or regulate the formation of its own biofilm.

The EndA nuclease of *S. pneumoniae* plays a role in immune evasion, virulence and competence [43, 57]. EndA degrades double-stranded DNA to single-stranded DNA during transformation for the purposes of uptake and recombination [57, 58]. Although no such mechanism has been described in *S. pyogenes,* it is possible that streptococcal DNases could reduce the potential for competing bacterial cells in the environment to be transformed by degrading extracellular DNA.

Summary

The prevalence of DNases suggests an important role in the biology of many streptococci, particularly *S. pyogenes*, with at least two being found in all strains tested. With the increased use of whole genome sequencing it may be that more DNases are identified and it will be important to maintain a consistent classification system across streptococcal species, similar to that proposed for the streptococcal superantigens [22].

It has been demonstrated experimentally that acquisition of prophage–associated DNases does not necessarily increase the virulence of a strain, and the genetic background of the bacterial host may play a role [59]. Although this could also be dependent on the types of virulence assays used and the sensitivity of both *in-vitro* and *in-vivo* disease models which are required to build a more complete picture of how DNases function. Indeed, DNase production has been shown previously to require interaction with eukaryotic cells or induction by other external triggers [34].

Both chromosomally-encoded and prophage-associated DNases have also been shown to be under the control of the extensive regulatory systems used by streptococci. This includes the control of virulence system (CovR/S or CsrR/S), which negatively regulates *sdaD2* but positively regulates *spdB*

in M1 strains [60] and Rgg, which negatively controls *spdB* and *spd3* [61]. Other regulators such as PerR, Ihk/Irr and CodY have also been shown to influence expression of DNases [62-64]. Further work is required to fully understand the complex regulation of DNase expression, which could also be influenced by genotype and associated prophage.

Interestingly, Walker et al demonstrated that *sda*1 (*sdaD2*) expression during disease is essential for *emm*1 strains and places a selective pressure upon CovR/S to mutate, not only to de-repress *sda1* expression but to down-regulate the protease SpeB which degrades Sda1 [65]. Sda1 can therefore influence the infection potential of isolates not only through direct means of protection against NETs, but also by indirectly promoting the development of 'hyper-virulent' CovR/S mutant strains.

The contribution of DNases to bacterial colonisation and infection may be extensive. The main focus of DNase research so far has been on the destruction of NETs, however there are other potential roles for DNases that may facilitate infection and warrant further research.

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Conflict of Interest

The authors declare no conflict of interest.

Abbreviations

Streptococcus dysgalactiae subsp equisimilis (SDSE)

Group B *Streptococcus* (GBS)

Group A *Streptococcus* (GAS)

Neutrophil extracellular traps (NETs)

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453 **Table 1. Prophage-associated DNases in *S. pyogenes* and their alleles.**

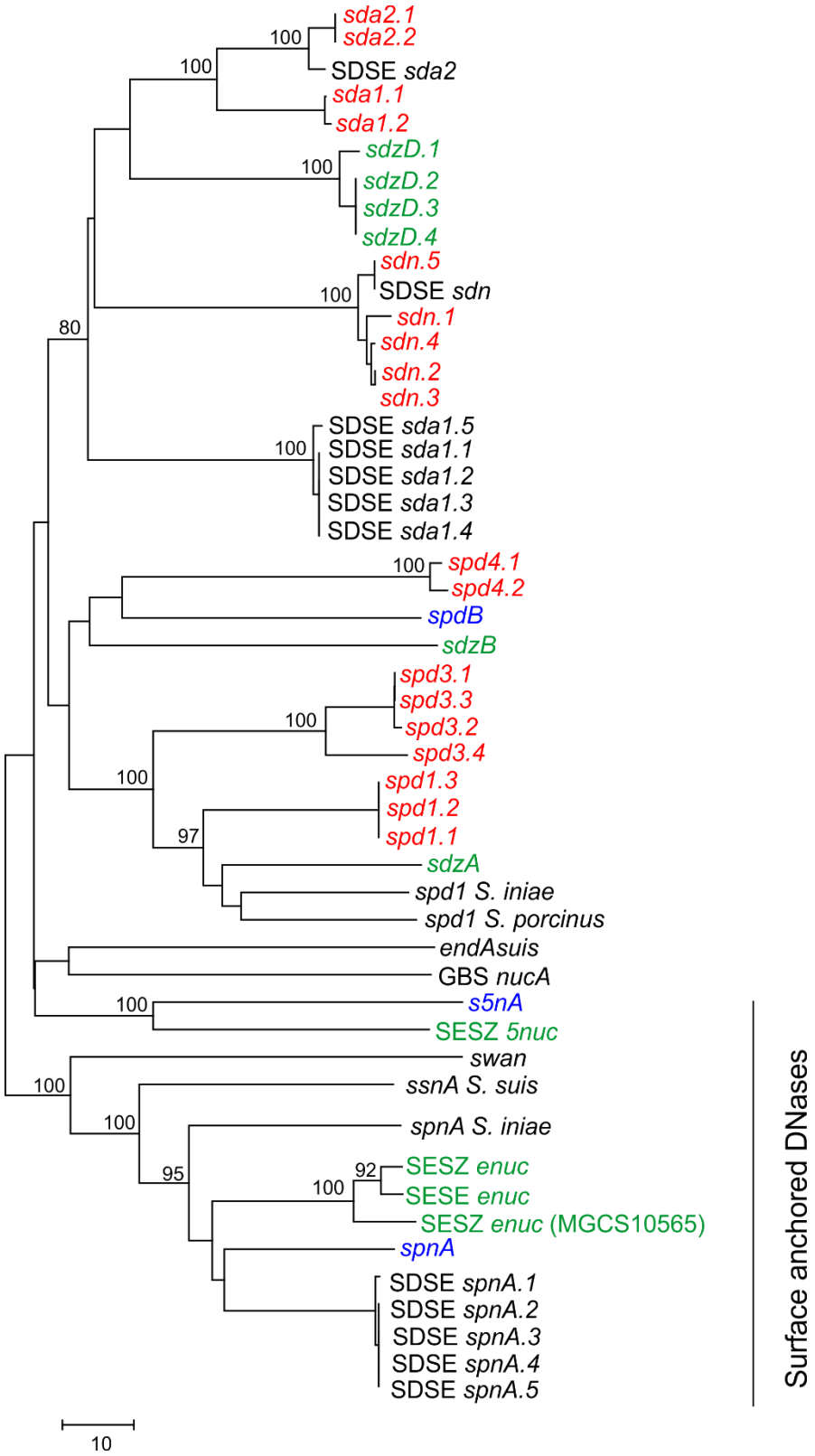
Gene	Allele*	Isolate	Locus
sda1	*sda1.1*	MGAS8232 (M18)	spyM18_1746
	sda1.2	MGAS10394 (M6), JRS4 (M6)	M6_Spy1339, SPYJRS4_1267
sda2	*sda2.1 (sdaD2)*	MGAS5005 (M1), A20 (M1), M1_476 (M1), HKU360 (M12), MGAS2096 (M12)	M5005_Spy1415, A20_1463, M1GAS476_1494, SpyOHK_02660, MGAS2096_Spy1441
	sda2.2	MGAS9429 (M12)	MGAS9429_Spy1417
spd1	*spd1.1*	SF370 (M1), MGAS10270 (M2), MGAS10750 (M4), MEW427 (M4), Manfredo (M5), MGAS9429 (M12), MGAS2096 (M12), HKU360 (M12), HKU488 (M12), MGAS8232 (M18), M23ND (M23), STAB120304 (M75), STAB14018 (M75), NGAS743 (M87), JMUB1235 (M89), MGAS27061 (M89), MGAS11027 (M89), NGAS322 (M114)	SPy0712, MGAS10270_Spy0598, MGAS10750_Spy0622, AWM58_02815, SpyM51263, MGAS9429_Spy0594, MGAS2096_Spy0602, SPYOHK_01985, HKU488_01495, spyM18_0779, FE90_0223, B5D85_03105, AYM92_03010, DI45_06730, JMUB1235_0583, MGAS27061_0582, MGAS11027_0597, SD89_06900
	spd1.2	MGAS10394 (M6), JRS4 (M6), MGAS6180 (M28), M28PF1 (M28), STAB9014 (M28), MEW123 (M28), STAB10015 (M28)	M6_Spy1195, SPYJRS4_1111, M28_Spy0968, ABO05_04560, VT08_04870, AWM59_04435, VU19_04860
	spd1.3	Alab49 (M53), AP53 (M53)	SPYALAB49_001168, AUQ45_1179
spd3	*spd3.1*	SF370 (M1), MGAS5005 (M1), M1_476 (M1), A20 (M1), 5448 (M1), AP1 (M1), NCTC8198 (M1), MGAS10270 (M2), MGAS10750 (M4), MEW427 (M4), Manfredo (M5), GUR (M11), HKU488 (M12), HSC5 (M14), NZ131 (M49), Alab49 (M53), AP53 (M53), STAB13021 (M66), STAB14018 (M75), STAB120304 (M75), STAB090229 (M75), NGAS743 (M87)	SPy_1436, M5005_Spy1169, M1GAS476_1231, A20_1204, SP5448_03755, SPAP1_02890, ERS445054_01298, MGAS10270_Spy0852, MGAS10750_Spy0888, AWM58_03950, SpyM50534, B2G65_01915, HKU488_01108, L897_05810, Spy49_1455, SPYALAB49_001299, AUQ45_1308, AXK13_07360, AYM92_04205, B5D85_04335, B4W66_03985, DI45_04190
	spd3.2	M23ND (M23)	FE90_0649
	spd3.3	MGAS8232 (M18)	spyM18_1446
	spd3.4	MGAS10394 (M6)	M6_Spy1541
spd4	*spd4.1*	MGAS315 (M3), SSI-1 (M3), STAB902 (M3)	SpyM3_1095, SPs0770, STAB902_04255
	spd4.2	Manfredo (M5)	SpyM50691
sdn	*sdn.1*	MGAS315 (M3)	SpyM3_1409
	sdn.2	SSI-1 (M3), STAB902 (M3)	SPs0455, STAB902_02580
	sdn.3	MGAS10394 (M6)	M6_Spy0067
	sdn.4	NGAS743 (M87), MGAS11027 (M89)	DI45_06360, MGAS11027_0659
	sdn.5	STAB90229 (M75)	B4W66_07530

454 ***** Allele based on nucleotide sequence of the entire coding region.

Figure Legends

Figure 1. Phylogenetic analysis of streptococcal DNases. Full length coding regions of each identified and potential DNase gene were aligned using MUSCLE and a neighbour-joining tree created. Bootstrap values greater than 80% are shown on branches. Multiple alleles were compared for all prophage-associated *S. pyogenes* DNase genes (red) but only single representative alleles for the chromosomal DNases *spnA, spnB* and *s5nA* are shown (blue). Alleles for *Streptococcus dysgalactiae subsp equisimilis* (SDSE) DNase genes were determined from five completed genomes; AC-2713 (NC_019042.1), GGS_124 (AP010935.1), RE378 (AP011114.1), 167 (AP012976.1), ATCC12394 (CP002215.1). Alleles for *Streptococcus zooepidemicus* DNase genes (green) were determined from four completed genomes; H70 (FM204884.1), CY (CP006770.1), ATCC35246 (CP002904.1), MGCS10565 (CP001129.1). Alleles for *Streptococcus equi* DNase genes (green) were determined from two completed genomes; ATCC39806 (CP021972.1), 4047 (FM204883.1). Other DNase genes comprise *endAsuis* (SSU1009) and *ssnA* (SSU1760) from *S. suis* strain P1/7 (AM946016.1), *swan* (SSA_1750) from *S. sanguinis* SK36 (CP000387.1), *spnA* (K710_1281) from *S. iniae* SF1 (CP005941.1), *spd1* (STRPO_1639) from *S. porcinus* str. Jelinkova 176 (AEUU02000001.1), group B *Streptococcus* (GBS) *nuc* (gbs0661) from *S. agalactiae* NEM316 (AL732656.1).

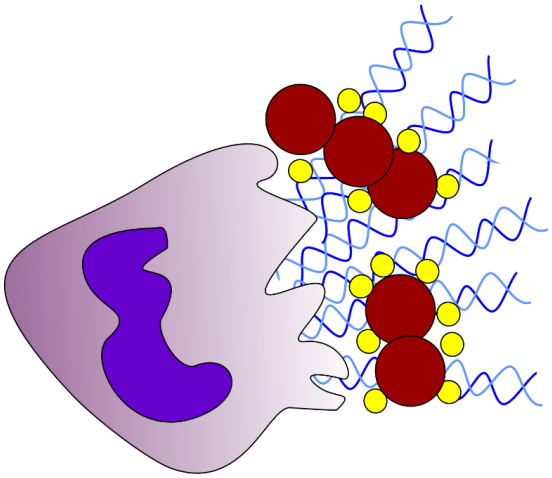
Figure 2. Streptococcal DNases can degrade neutrophil extracellular traps (NETs). NETs are composed primarily of DNA (blue strands) associated with histones and other antibacterial factors (yellow circles). Bacteria can be ensnared in the DNA traps and killed by the associated factors (left-hand figure). Streptococcal secreted and cell-anchored DNases (indicated as scissors) degrade NETs, allowing the bacteria to escape prevent killing (Right-hand figure).


sda2.1
sda2.2
SDSE sda2
sda1.1
sda1.2
sdzD.1
sdzD.2
sdzD.3
sdzD.4
sdn.5
SDSE sdn
sdn.1
sdn.4
sdn.2
sdn.3
SDSE sda1.5
SDSE sda1.1
SDSE sda1.2
SDSE sda1.3
SDSE sda1.4
spd4.1
spd4.2
spdB
sdzB
spd3.1
spd3.3
spd3.2
spd3.4
spd1.3
spd1.2
spd1.1
sdzA
spd1 S. iniae
spd1 S. porcinus
endAsuis
GBS nucA
s5nA
SESZ 5nuc
swan
ssnA S. suis
spnA S. iniae
SESZ enuc
SESE enuc
SESZ enuc (MGCS10565)
spnA
SDSE spnA.1
SDSE spnA.2
SDSE spnA.3
SDSE spnA.4
SDSE spnA.5
100
100
100
80
100
100
100
100
100
97
100
100
95
92
100
10
Surface anchored DNases

476

477

Bacteria are trapped in DNA released from neutrophils, and killed by associated factors



Streptococcal DNases degrade DNA traps freeing the bacteria and preventing killing