



Characterization and Comparative Analysis of the *Staphylococcus aureus* Genomic Island *vSaβ*: an *In Silico* Approach

Anita J. Kläui,^a Renate Boss,^b Hans U. Graber^a

^aFood Microbial Systems, Agroscope, Bern, Switzerland

^bRisk Assessment Division, Federal Food Safety and Veterinary Office, Bern, Switzerland

ABSTRACT *Staphylococcus aureus* is a widespread opportunistic pathogen to humans and animals. Of its genome, 20 to 25% varies between strains and consists of phages, pathogenicity islands, transposons, and genomic islands. *S. aureus* harbors up to three genomic islands, *vSaα*, *vSaβ*, and *vSaγ*. The *vSaβ* region of *S. aureus* can encode a number of virulence-associated factors, such as serine proteases, leukocidins, enterotoxins, bacteriocins, or a hyaluronate lyase. In this study, the *vSaβ* regions of 103 clinically relevant *S. aureus* strains were characterized *in silico* and compared to the three predefined *vSaβ* types. We here suggest a superordinate system of 15 different *vSaβ* types, of which 12 were newly defined. Each *vSaβ* type has a distinct structure with a distinct set of genes, which are both highly conserved. Between the different types, gene content and composition vary substantially. Based on our data, a strain's *vSaβ* type is strongly coupled with its clonal complex, suggesting that *vSaβ* was acquired in an ancestral *S. aureus* strain, arguably by phage mediation, before differentiation into clonal complexes. In addition, we addressed the issue of ambiguous nomenclature in the serine protease gene cluster and propose a novel, phylogeny-based nomenclature of the cluster contained in the *vSaβ* region.

IMPORTANCE With the rapid increase of available sequencing data on clinically relevant bacterial species such as *S. aureus*, the genomic basis of clinical phenotypes can be investigated in much more detail, allowing a much deeper understanding of the mechanisms involved in disease. We characterized in detail the *S. aureus* genomic island *vSaβ* and defined a superordinate system to categorize *S. aureus* strains based on their *vSaβ* type, providing information about the strains' virulence-associated genes and clinical potential.

KEYWORDS *Staphylococcus aureus*, genomic islands, *in silico* characterization, comparative analysis

Staphylococcus aureus is a commensal colonizer of the skin and mucous tissue of up to two-thirds of the human population (1, 2). It is an opportunistic pathogen in humans and animal hosts (3, 4), and its pathogenic potential ranges from being relatively harmless to causing potentially deadly infections (5). The *S. aureus* genome consists of the core genome and the accessory (or auxiliary) genome. The core genome, representing about 75%, is conserved in all *S. aureus* strains and consists largely of genes related to metabolism or other housekeeping functions. The accessory genome, about 20 to 25%, consists of mobile (or formerly mobile) genetic elements (MGE), such as bacteriophages, chromosomal cassettes, pathogenicity islands, transposons, and genomic islands (6). Its genes differ between strains (7–9) and are often related to virulence and antibiotic resistance. Therefore, they have important clinical implications, especially when considering their potential to spread horizontally (6, 7). The combination of these variable regions is the key to the high phenotypic variability in *S. aureus*.

S. aureus strains carry three different classes of genomic islands, *vSaα*, *vSaβ*, and the

Citation Kläui AJ, Boss R, Graber HU. 2019. Characterization and comparative analysis of the *Staphylococcus aureus* genomic island *vSaβ*: an *in silico* approach. *J Bacteriol* 201:e00777-18. <https://doi.org/10.1128/JB.00777-18>.

Editor Michael J. Federle, University of Illinois at Chicago

Copyright © 2019 Kläui et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Hans U. Graber, hansulrich.graber@agroscope.admin.ch.

Received 8 January 2019

Accepted 25 July 2019

Accepted manuscript posted online 26 August 2019

Published 21 October 2019

substantially smaller vSa γ . These genomic islands are extremely stable and have highly conserved genes. However, the gene compositions of each of the islands can vary substantially between some strains and are yet identical between others (8, 10).

In 2008, when Baba et al. (8) classified 12 sequenced *S. aureus* strains into 4 vSa α types and 3 vSa β types, the comparison of the genomic islands was rather limited. To date, over 10,000 *S. aureus* whole genomes (including contigs and scaffolds) are available in the NCBI database. Such an enormous increase in sequencing data calls for a new, superordinate system to classify *S. aureus* strains based on genomic islands. The genomic island vSa β is of particular interest, as it carries two genes belonging to the type I staphylococcal restriction-modification (RM) system (*hsdM* and *hsdS*) and harbors a number of virulence-associated genes, such as a hyaluronate lyase precursor gene (*hysA*), a lantibiotic gene cluster (bacteriocins of *S. aureus* [*bsa*]), two leukocidin genes (*lukD* and *lukE*), an enterotoxin gene cluster (EGC), and a cluster of serine protease genes (serine protease like [*spl*] genes).

First characterized in 2001, the *spl* cluster was described as an operon containing 6 genes (*splA*, *splB*, *splC*, *splD*, *splE*, and *splF*) with DNA sequence similarities ranging from 42% to 94% (11). For listing new *spl* genes, the existing alphabetical nomenclature is not ideal. Therefore, we establish an approach to unambiguously name the genes in the *spl* cluster, including new ones, based on their phylogenetic relationships.

To our knowledge, the findings of Baba et al. (8) have not been proceeded. Hence, we extended their vSa β listing to a total number of 15 types by adding 12 new types obtained by analysis of the vSa β islands of 103 clinical *S. aureus* strains. Thus, striking conservation of the virulence-associated genes was found within each type.

RESULTS

Of the 103 analyzed strains, 37 strains showed known vSa β types (I to III), and 66 strains showed novel vSa β types (IV to XV) (see Table 1; also see File S2 in the supplemental material).

vSa β type I ($n = 11$) originated mostly from humans, with the exception of 1 strain originating from a bovine mammary infection. vSa β type I is found commonly and included well-studied clinical strains, such as strains N315, 502A, Mu3, Mu50, and JH1. vSa β type II ($n = 17$) comprised 8 human isolates with the well-known strain COL and strain DSM 20231^T. The remaining isolates originated from bovine mastitis. Of the vSa β type III strains ($n = 9$), 7 originated from humans (including the hospital-acquired MRSA252 and the quality control strain ATCC 25923), and 2 strains were of unknown origin. All vSa β type IV strains ($n = 8$) were isolated from bovine mastitis. Of vSa β type V ($n = 9$), one host was unknown, and the other 8 strains originated from humans. vSa β type VI ($n = 11$) were all isolated from either humans or cattle.

Only a few strains harbored vSa β types VII to XI. vSa β type VII ($n = 5$) contained 4 human isolates and 1 bovine mastitis isolate, and for vSa β type VIII, only a single isolate was found. vSa β types IX ($n = 5$) and X ($n = 2$) were uniquely isolated from ovine mastitis. The two vSa β type XI strains were bovine mastitis strains. From vSa β type XII strains ($n = 6$), 2 originated from cattle and 4 from humans. Out of 9 vSa β type XIII strains, 5 originated from human hosts and 2 from cattle, and for 2 strains, no information was available. One vSa β type XIV ($n = 6$) strain was isolated from Swiss cattle and 5 from human hosts. The two strains with type XV were both bovine mastitis isolates.

Structure of vSa β and highly conserved regions. All vSa β islands were enclosed by 2 distinct genes coding for hypothetical proteins (*hp* genes). In the strain Mu50 (reference strain for vSa β type I [see below]) the *hp* with the locus tag SAV1803 marks the 5' terminus of vSa β , and SAV1831 marks the 3' terminus. These two *hp* genes could be found in nearly all vSa β islands (see Fig. 1 and Table 1). For convenience, we refer to these sequences as *sav1803* and *sav1831*, respectively. These *hp* genes were highly conserved among all strains, with product amino acid identities of >95% in SAV1803 and >98% in SAV1831. In all strains, *sav1831* directly followed a cluster of 8 tRNAs (tRNA^{Met}, tRNA^{Asp}, tRNA^{Phe}, tRNA^{His}, tRNA^{Gly}, tRNA^{Asn}, tRNA^{Glu}, and tRNA^{Ser}).

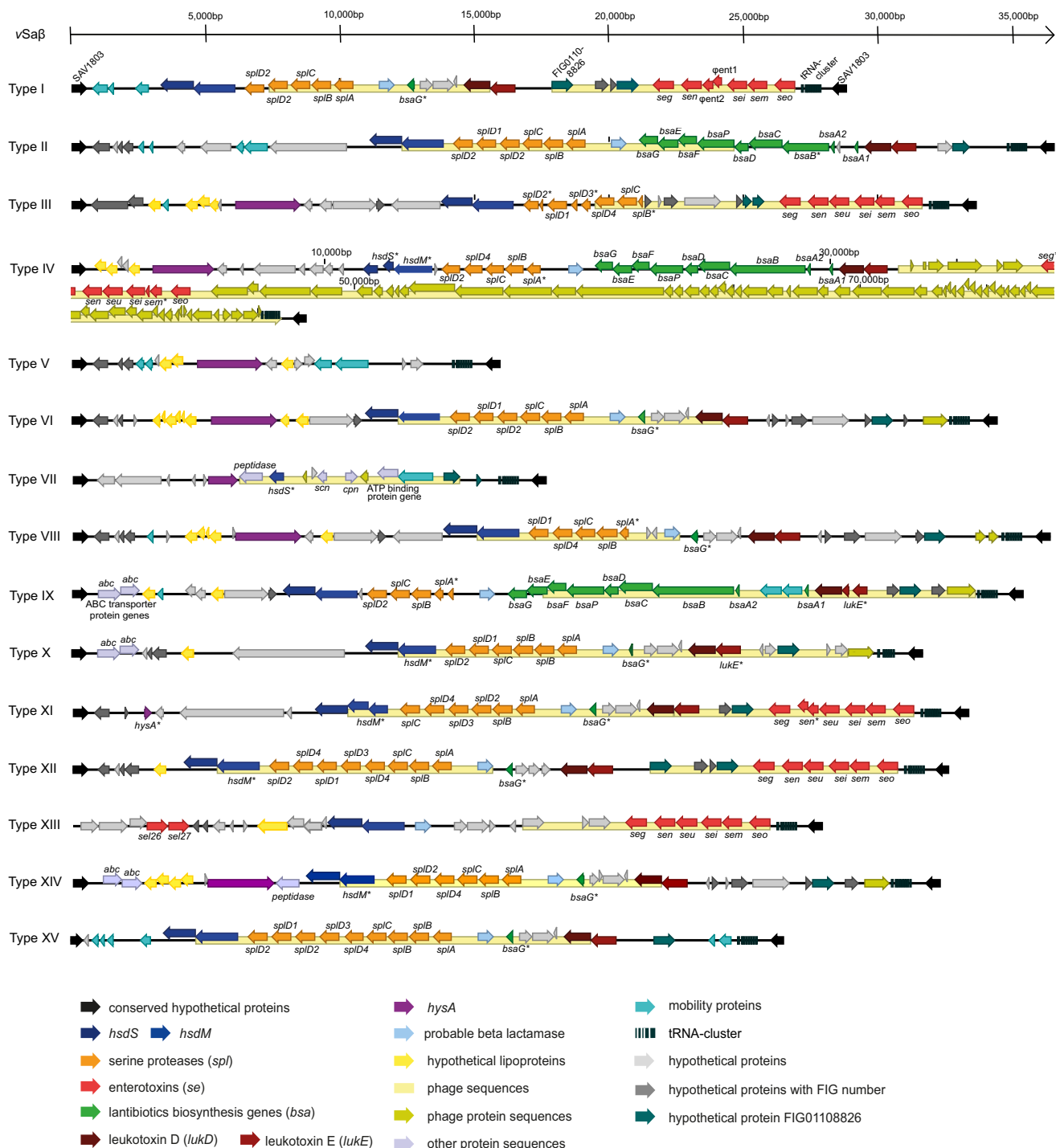


FIG 1 Representation of all *Staphylococcus aureus* genomic island *vSaβ* types I to XV, their virulence-associated genes, and other hypothetical genes located on *vSaβ*. For each *vSaβ* type, one reference strain is shown. Arrows show orientation of open reading frames. Asterisks indicate truncated or fragmented genes. Note that *vSaβ* IV is substantially longer due to the presence of a complete phage. All other sequences are scaled relative to each other.

Most *vSaβ* types followed a similar structural design (with exceptions of types V, VII, and XIII) carrying a distinct set of virulence genes (Fig. 1). They included *hysA*, the lipoprotein (*lpn*) genes, the RM genes *hsdM* and *hsdS*, a cluster of *spl* genes (*splA*, *splB*, *splC*, *splD1*, *splD2*, *splD3*, and *splD4*), a probable beta-lactamase gene (*bla*), a cluster of 9 *bsa* genes (*bsaA1*, *bsaA2*, *bsaB*, *bsaC*, *bsaD*, *bsaE*, *bsaF*, *bsaG*, and *bsaP*), the *lukD* and *lukE* genes, as well as an EGC consisting of the *seg*, *sei*, *sem*, *sen*, *seo*, and *seu* genes. In some

cases, the *seu* gene was replaced by the two truncated genes, *φent1* and *φent2*. The compositions of these genes and gene clusters varied substantially between different vSaβ types but were highly conserved within the same vSaβ type (Fig. 1 and Table 1). In addition to these core vSaβ genes, a number of *hp* genes were found of which some were assigned to a FIG number by the RAST (Rapid Annotations using Subsystem Technology) pipeline.

By typing the vSaβ islands and aligning all related sequences, a consensus structure for each vSaβ type could be defined. vSaβ type I possessed the genes of the type I RM system, an *spl* cluster (*splA*, *splB*, *splC*, and two copies of *splD*₂), *lukD*, *lukE*, and a complete EGC. The amino acid sequences were, with only very few exceptions, highly similar within this vSaβ type (>95%) (Table 1). The exceptions were truncated genes, the lack of a second *splD*₂ gene, and a lower sequence identity of the *splD*₂ protein in three strains (Table 1). Furthermore, 3 sequences for mobile element proteins (*mep*), a *bsaG* fragment, *bla*, and remnants of phages were detected (Table 1; Fig. 1). Comparing the structures of all 11 vSaβ type I genomic islands, Mu50 showed consensus and hence was used as a reference for this vSaβ type. The consensus of vSaβ type II was best represented by *S. aureus* strain TW20. It harbored the type I RM genes, an *spl* cluster (*splA*, *splB*, *splC*, *splD*₁, and two copies of *splD*₂), a *bla*, a *bsa* cluster, and the *lukD* and *lukE* genes. Exceptions were some strains that harbored truncated *hsdM*, *basE*, and *lukE* genes. Moreover, vSaβ type II comprised sequences for two *mep* genes, *bla*, a number of *hp* genes, and a partial phage (Table 1). The consensus on vSaβ type III was strain MRSA252. It harbored *hysA*, *hsdM*, *hsdS*, an *spl* cluster (*splB*, *splC*, *splD*₁, *splD*₂, *splD*₃, and *splD*₄), and an EGC. Besides three *spl* genes being all pseudogenes (*splB*, *splD*₂, and *splD*₃), vSaβ type III lacked *lukD* and *lukE* but had additional genes in its 5' region (a number of putative *lpn* genes, a *hysA*, and a lipase gene). vSaβ type III carried sequences for *mep*, *hp*, and remnants of a phage. In most of the type III strains, the core proteins were highly conserved, showing an identity of ≥99% when *S. aureus* strain MRSA252 was used as a reference. Deviations thereof could be found in the *spl* cluster and in *hsdM* (Table 1). The vSaβ type IV was best represented by strain M3783C and was, with over 85,000 bp, substantially longer than the other vSaβ types. It harbored a number of *hp* genes, a *hysA* gene, an *spl* cluster (*splB*, *splC*, *splD*₂, *splD*₄, and a truncated *splA*), a complete *bsa* cluster, an EGC (with truncated *seg* and *sem*), *lukD*, *lukE*, and the *bla* gene. *hsdM* and *hsdS* were either missing or had premature stop codons. The amino acid sequences of all other vSaβ key genes were highly conserved (≥99%) among strains, with only a small number of exceptions (Table 1). Furthermore, a 50.4-kb intact mosaic phage closest to Ipla88 (NCBI RefSeq accession no. [NC011614](#)) was detected in 6 vSaβ type IV strains, coding for approximately 75 proteins including those encoded by the EGC also found in other vSaβ types. In contrast, the strains M2323C and Sa110 harbored only remnants of two phages; hence, the vSaβ islands of these two strains were shorter than the other type IV islands. The structure of vSaβ type V differed substantially from the other types and was only 15,965 bp long and highly conserved, showing a nucleotide sequence identity of ≥99% when using strain 50385 as a reference. From the typical genes, vSaβ type V harbored only *hysA*. However, it carries a total of 4 transposons, as well as a number of *hp* genes, some of which were related to FIG numbers, or they were identified as *lpn* genes. Within vSaβ type VI, strain K2R was a suitable representative. It comprised *hysA*, *hsdS*, *hsdM*, an *spl* cluster (*splA*, *splB*, *splC*, *splD*₁, and two copies of *splD*₂), *bla*, a *bsaG* fragment, *lukD*, *lukE*, a phage integrase, as well as a number of *hp* genes, some of which were assigned a FIG number, and others were identified as *lpn* genes. In addition, a partial phage was detected encompassing the entire *spl* cluster. Four strains (M0443, Newbould, G071, and Lodi4R) had a frameshift in the beginning of *lukE*, leading to a truncated protein. Additionally, G071 and Lodi4R also lacked the *splD*₁ and the second *splD*₂ gene. Except for these very few special cases, all genes of vSaβ type VI were highly conserved between strains, showing an amino acid identity of ≥98%. The low overall nucleotide identity of 76% in strain Lodi4R compared to the reference was based on the insertion of the transposon Tn554 within *hysA*. This strain was, therefore, considered a special case of vSaβ type VI. Tn554

carried 3 transposase genes, as well as a *bla* operon carrying the *blaI*, *blaR1*, and *blaZ*. If Tn554 was disregarded, the nucleotide sequence identity increased to 93%. vSaβ type VII, similar to type V, was short (about 17,460 bp) and lacked the typical vSaβ genes, except for *hysA* and a *hdsS* fragment. Furthermore, all vSaβ type VII strains showed a partial phage with genes for proteins targeting the host's immune response (chemotaxis-inhibiting protein Cpn and extracellular complement-binding protein Scn), as well as genes for a peptidase, a phage lysine, an ATP-binding protein, and a transposase. The amino acid sequences of these phage-encoded proteins were identical, with the exception of M3386D that was lacking a part of the phage containing genes coding for the ATP-binding protein and the transposase. The vSaβ type VIII included only the JKD6159 strain. It comprised *hysA*, *hdsM*, *hdsS*, an *spl* cluster (a truncated *splA*, *splB*, *splC*, *splD₁*, and *splD₄*), *bla*, a *bsaG* fragment, *lukD*, *lukE*, a partial phage, a number of *hp* and phage-related genes, and a number of *lpn* genes in the 5' region. For vSaβ type IX, ED133 served as the reference harboring the vSaβ key genes *hdsM* and *hdsS*, an *spl* cluster (a truncated *splA*, *splB*, *splC*, and *splD₂*), *lukD*, *lukE* (truncated), *bla*, and a complete *bsa* cluster, as well as a number of *hp* genes, some of which were identified as *lpn* genes and others that were assigned a FIG number. In addition, vSaβ type IX carried 2 genes encoding ATP-binding cassette (ABC) transporter proteins, and a gene encoding a phage integrase. Despite the isolates being from 3 different countries, they shared an overall nucleotide sequence identity of $\geq 95\%$ in their vSaβ. The only small difference in the vSaβ key genes was found in *hdsM* and *lukD*, which showed lower similarities in some strains (Table 1). vSaβ type X showed 93% nucleotide sequence identity. The vSaβ consisted of an *spl* cluster (*splA*, two copies of *splB*, *splC*, *splD₁*, *splD₂*), a *bla*, a *bsaG* fragment, *lukD*, *lukE*, a complete *hdsS* gene and an *hdsM* gene with a premature stop codon. In addition to a number of *hp* and FIG-assigned genes, *lpn*, two genes encoding an ABC transporter, and a phage integrase gene could be found, similar to vSaβ type IX. The amino acid identity in the key genes were $\geq 98\%$, with the exceptions of *lukE* being truncated in O11, *splD₁* lacking in strain O46, and a slightly lower identity in *splD₂* (93% amino acid identity). vSaβ type XI consisted of two strains with an amino acid identity of $\geq 99\%$ in the vSaβ key genes and a nucleotide identity of 99% over the entire vSaβ region. Their vSaβ consists of *hdsM* and *hdsS*, but *hdsM* has a premature stop codon. Furthermore, vSaβ type XI was characterized by an *spl* cluster (*splA*, *splB*, *splC*, *splD₂*, *splD₃*, and *splD₄*), a *bla*, a *bsaG* fragment, *lukD*, *lukE*, a complete EGC (with a truncated *sen*), several *hp* genes (some of which with assigned FIG numbers), and a short *hysA* fragment. The most striking feature of vSaβ type XII was the enlarged *spl* cluster consisting of *splA*, *splB*, *splC*, *splD₁*, *splD₂*, *splD₃*, and 2 copies of *splD₄*. It further harbored both RM genes (*hdsM* with premature stop codon), *bla*, a *bsaG* fragment, *lukD*, *lukE*, and a complete EGC along with several *hp* genes, some with assigned FIG numbers. The strains categorized as vSaβ type XIII had a typical vSaβ structure in the 3' end, yet a clear beginning could not be defined for this vSaβ type, as it lacked the conserved 5'-end *sav1803*. Instead, there were three *hp* genes as well as two recently discovered enterotoxin sequences, *sel26* and *sel27*. These were followed by several *hp* genes (some with assigned FIG number) and genes typical for vSaβ, such as *lpn*, *hdsM*, *hdsS*, *bla*, the EGC followed by the tRNA cluster, and *sav1831*, typically marking the 3' end. vSaβ type XIV harbored *hysA*, both RM genes (*hdsM* and *hdsS*), an *spl* cluster (*splA*, *splB*, *splC*, *splD₁*, *splD₂*, and *splD₄*), *bla*, a *bsaG* fragment, *lukD*, and *lukE*. When strain G08M was used as a reference, most proteins showed an amino acid identity of 100%, with the exceptions being three strains with truncated *hdsM* genes. vSaβ type XV consisted of both RM genes (*hdsM* and *hdsS*), an *spl* cluster (*splA*, two copies of *splB*, *splC*, *splD₁*, two *splD₂*, *splD₃*, and *splD₄*), *bla*, a *bsaG* fragment, *lukD*, and *lukE*. When strain Lodi11bM was used as a reference, the only differences were *lukE* being truncated and *splD₄* having a lower amino acid identity in strain 4185.

In summary, all vSaβ types had the same basic structural design. The design was minimal for types V, VII, and XIII and was more complex for the other types, as they harbored a distinct set of virulence factors and gene clusters. Also common to all vSaβ

types, except to type XIII, was the pervasive flanking by the same conserved sequences with the locus tags SAV1803 and SAV1831. Variation among the *vSaβ* types was observed for the *spl* cluster in gene number and composition. Furthermore, some types were characterized by truncated RM genes and/or *bsa* or *spl* genes. Within each *vSaβ* type, they were highly conserved, at the structural and the protein levels.

HsdS. Inspection of the HsdS sequences with a phylogenetic approach (Fig. 2A) revealed that the HsdS sequence alone does not provide sufficient resolution for inference of gene content or virulence determinants of the entire *vSaβ*. Hence, categorization of *vSaβ* based on the nucleotide sequence identity of the entire genomic island can be considered the method of choice when the entire sequence of the genomic island is available.

Serine proteases. All *vSaβ* islands, with the exceptions of types V, VII, and XIII, carried an *spl* cluster, harboring between 4 and 9 *spl* genes. Phylogenetic analyses using the maximum-likelihood method confirmed the existing Spl family members SplA, SplB, SplC, and SplD, but with SplD having 4 different variants (SplD₁, SplD₂, SplD₃, and SplD₄) (Fig. 2B). SplD₁ replaces the former SplE, and SplD₂ replaces the former SplD and SplF. The SplD₃ and SplD₄ clades include Spl proteins that could not be assigned into any of the preexisting Spl variants. Furthermore, the presence of multiple *splD* variants per strain points to a relatively recent gene duplication.

Clonal complexes and *spa* types. *spa* typing showed that one *vSaβ* type can harbor a number of *spa* types, but each *spa* type is limited to one *vSaβ* type. Highly striking was the consistency of a *vSaβ* type with the strains' clonality. The predominance of a single clonal complex (CC) per *vSaβ* type underlined the concept that *vSaβ* acquisition and its diversification happened prior or simultaneously to the clonal diversification of ancestral *S. aureus* strains.

DISCUSSION

With the rapid advancement of sequencing technologies and the decreasing costs thereof, the amount of *S. aureus* sequences deposited in databases is growing exponentially. These databases offer a powerful information source for studying the variabilities and consistencies between different isolates and their potential ability to cause disease. As opposed to the slow accumulation of point mutations, acquisition of larger parts of DNA through horizontal gene transfer leads to a rapid genetic change. This can be crucial in survival under certain selection pressures (antibiotics) or in novel niches (new host) (10, 12, 13). The mechanism of how *S. aureus* acquired its genomic islands is not fully understood, yet here, we have elaborated why phage mediation has played a crucial role.

Viral origin of *vSaβ*. Throughout all *vSaβ* types, the strains belonging to one *vSaβ* type almost exclusively harbor the same virulence genes. In addition to the gene composition, an amino acid sequence identity of 95% or higher is another characteristic within each type, and in many cases, even 100% over all strains of a *vSaβ* type (Table 1).

Despite the range of hosts and geographical origins covered in this study, the *vSaβ* islands were always located in between SAV1803 and SAV1831 at the 5' and 3' ends, respectively. This highly precise location together with the tRNA cluster preceding SAV1831 as observed throughout all *vSaβ* types strongly indicates that these sites may be key for the presence of the *vSaβ* islands in *S. aureus*. Indeed, tRNAs are known to harbor a conserved attachment site (14) for integrating prophages and other foreign DNA (15, 16).

It is widely accepted that *S. aureus* genomic islands were acquired through horizontal gene transfer, but the exact mechanism and their current mobility status have been questioned (8, 10, 17). Our data show the presence of partial phages in almost all *vSaβ* types, with the exceptions of type V, where no phages were predicted, and type IV, where a complete prophage was predicted by PHASTER. In addition, *vSaβ* type IV also harbors all virulence-related key features of *vSaβ*, as follows: the type I RM system, the *spl* cluster, the *bsa* cluster, the leukocidin genes, and the EGC. Other *vSaβ* types

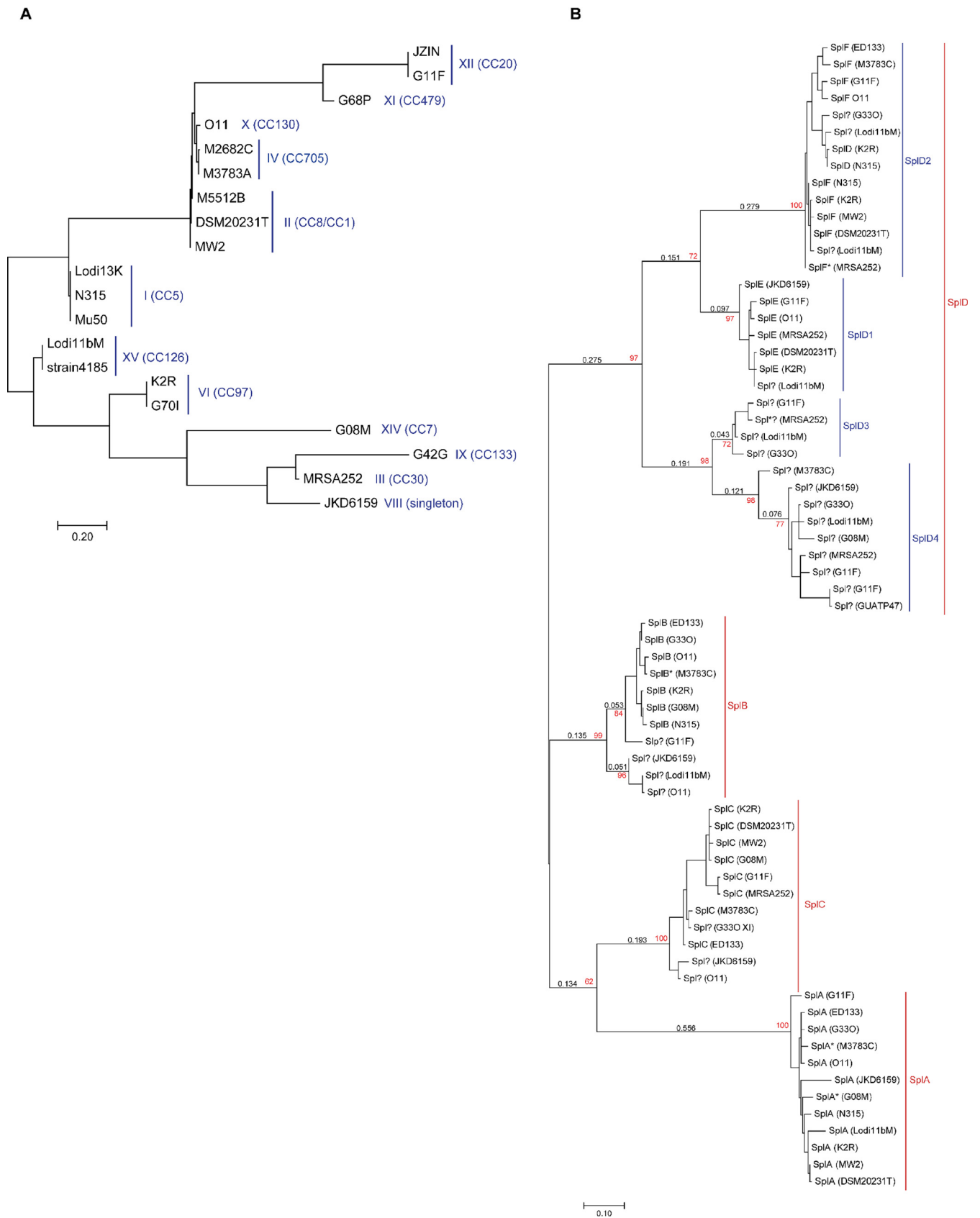


FIG 2 (A and B) Phylogeny of the 20 HsdS (A) and 68 Spl (B) amino acid sequences of *Staphylococcus aureus*. For both trees, protein sequences that differed in at least one amino acid were aligned, and a phylogenetic tree was reconstructed using maximum likelihood. For each tree, a scale indicates the relative (Continued on next page)

possess the EGC only (types I, III, XI, XII, and XIII), the *bsa* cluster only (II and IX), or lack both. In this sense, vSa β type IV can be considered the most complete of all vSa β types regarding virulence-related gene content and phage. Moon et al. (14) showed that this very phage of strain RF122 (vSa β type IV) can be mobilized *in vitro*, resulting in heterogeneous, yet overlapping particles that integrated sequentially through recombination into the host; in some cases, it even resulted in the transfer of the almost-complete vSa β (14).

Our results also demonstrate that all vSa β islands containing the key virulence factors also harbored partial phages, suggesting that vSa β originated in an ancestral *S. aureus* strain through a phage integration event. In the course of evolution, multiple recombination, integration, and excision events may have occurred, resulting in various combinations of the virulence genes that we now observe in the different vSa β types. To our knowledge, vSa β type IV is the only type to harbor a complete phage that has been shown to be mobilized, suggesting that the phages of the other vSa β types are likely to have lost their mobility in the course of evolution.

The unequivocal location, the demonstrated mobility (14), and the ubiquitous presence of phage particles in vSa β islands, as well as a conserved phage attachment site, strongly support the hypothesis that vSa β was mediated by a phage, followed by diversification into the types observed today.

vSa β and clonality. In total, vSa β typing of 103 *S. aureus* strains revealed 15 different types. They correlated strongly with the CCs and were always linked to one specific vSa β type. Therefore, the CC of *S. aureus* allows the link to virulence-associated vSa β key genes. This link has been made previously (18), but by assessing and categorizing the novel 12 vSa β types, we confirmed this observation to be a general principle. Indeed, all studied strains follow this pattern, indicating that the horizontal acquisition of vSa β in an ancestral *S. aureus* strain happened before divergence into the clones occurred. It is evident that the primordial vSa β underwent multiple genetic changes (e.g., recombination and duplications), likely just prior or simultaneously to clone formation, resulting in the types observed today.

The evolutionary link of vSa β types and CCs are in perfect agreement with the topology of the phylogenetic tree by Boss et al. (19). For that study, the authors concatenated 7 *S. aureus*-specific genes from 30 different strains and aligned these using the Needleman-Wunsch algorithm. This alignment was then used to construct a maximum parsimony phylogeny. This phylogeny showed the evolutionary relationship between some of the most common *S. aureus* CCs that all possess a vSa β and a type-specific set of virulence genes. Therefore, it is evident that the common ancestor of these CCs already carried an ancestral vSa β .

The discrepancy between the overall structures of vSa β types V and VII and all other vSa β types can be explained by an evolutionary loss of the vSa β key genes in these types during two separate events. We can still find vSa β typical elements, such as the conserved regions marking the 5' and 3' ends of vSa β or the almost ubiquitous *hp* FIG01108826 in the 3' region. Furthermore, type V harbors sequences that can be found in a number of other vSa β types, such as 3 *hp* genes with an assigned FIG number located the 5' region (FIG01108398, FIG01108644, and FIG01108514), *lpn*, and *hysA*. Interestingly, type VII encodes different virulence factors that tackle the host's immune defenses. As vSa β types V and VII have additional transposase genes, we suggest that in these two types, the vSa β key genes were replaced by a transposon, indicating that vSa β themselves may be a hot spot for inserting mobile genetic elements and potentially accumulating virulence factors.

FIG 2 Legend (Continued)

distance on the phylogenetic tree. (A) The blue line indicates a strain's vSa β type, and its clonal complex (CC) is given in parentheses. (B) The strain from which the amino acid sequence originated is shown in parentheses. Numbers in red represent bootstrap values. Question marks indicate sequences of Spl with previously uncertain or unknown nomenclature, and red and blue lines show suggested nomenclature of the corresponding branch based on phylogenetic distances of the Spl amino acid sequences. Curated sequences are marked with an asterisk.

vSaβ type XIII has a deviate structure, as it lacks the typical 5' region found in the other types. Together with types V and VII, it lacks the *spl* cluster and the *luk* genes. We cannot exactly locate the beginning of this *vSaβ* type on the genome, but interestingly, we found two very recently discovered phage-associated enterotoxin genes (*sel26* and *sel27*) in that region (20). Furthermore, we found an *hp* (FIG01108398) which is adjacent to the SAV1803 in some other types.

Virulence and *vSaβ*. The variable regions contribute to the fate of an *S. aureus* strain on a given host and its disease-causing potential, as these regions encode a number of virulence factors (6, 10). They include the pore-forming LukD and LukE, which are present on most *vSaβ* types (except III, V, VII, and XIII). Both proteins are members of the leukocidin family (21) that form pores in the lipid bilayer of host cells, particularly in neutrophils, leading to cell death and, therefore, the promotion of immune evasion and progression of the infection (22, 23).

Further virulence factors encoded on *vSaβ* are the Spl proteins that are unique to *S. aureus* and are organized in an operon (11). *vSaβ* types V, VII, and XIII lack the *spl* cluster, whereas all other types have a *spl* cluster, some of them with truncated genes. Based on our phylogenetic approach, there are 4 different *spl* genes (*splA*, *splB*, *splC*, and *splD*) and 4 gene variants of *splD* (*splD*₁, *splD*₂, *splD*₃, and *splD*₄). SplA, SplB, and SplC form their own clades and are clearly separated from the SplD clade (Fig. 2B). The former SplD and SplF are now members of the SplD₂ clade, which is unsurprising, as their amino acid identity can be as high as 94% (11, 24). The SplD₃ and SplD₄ clades consist both of Spl sequences that have not been previously studied and did not match any of the predefined *spl* genes based on sequence similarity. We observed a high conservation of the *spl* operon within but not between *vSaβ* types. The function of *spl* genes in infection and disease is still largely unclear (24–27). Studies showed that *spl* genes are expressed and secreted during host infection (25, 27) and have been linked to allergic reactions (28, 29). Interestingly, *vSaβ* can harbor multiple copies of the very same *spl* gene. The plasticity of the *spl* cluster is an evidence for its varied importance among different *vSaβ* types.

Hyaluronic acid is a major component of the connective tissue, in particular, the extracellular matrix (30). HysA is considered a virulence factor, as it can depolymerize hyaluronic acid and favoring the spreading of infection (31, 32). Many *S. aureus* genomes contain a chromosomal copy of *hysA* (33) outside of *vSaβ*. The additional copy present in the *vSaβ* region of types III to VIII and XIV may be linked to enhanced invasiveness of these clones.

Lantibiotics (or bacteriocins) are antimicrobial peptides produced by some Gram-positive bacteria against closely related species (34, 35) and are thought to play a role in colonization by outcompeting other bacteria (10, 24).

***vSaβ* typing.** In contrast to the link of CC and *vSaβ* types, it has been suggested that the *vSaβ* type is dependent on the strain's HsdS sequence (8). These predictions were not very reliable, as they were based on 3 *vSaβ* types and 12 sequenced *S. aureus* strains only. From a total of 15 *vSaβ* types, we defined 12 new types based on multiple hosts and geographical regions. Within the scope of our study, the method used for typing the *vSaβ* region proved to be a very robust procedure, as all used strains could be exclusively allocated to one *vSaβ* type, and cross-classification was never observed. Hence, we expect the specified principles to be robust enough to uphold future findings when additional *S. aureus* strains are analyzed.

In the scope of this study, we limited the data set to clinically relevant *S. aureus* strains either from human or animal infections. Strains that were not invasive (i.e., colonizers and strains isolated from foods) were excluded from the data set. Hence, our results are limited to these invasive strains only, yet we did find that a few colonizers also fit into the system proposed here (data not shown). In the future, more *vSaβ* regions need to be analyzed spanning more hosts and including noninvasive strains.

Conclusions. In general, the *vSaβ* islands harbor a number of virulence-associated and pathogenic genes with different scopes of action. While the exact functions of

many of these genes are yet to be unraveled, it is clear that they have severe effects on the host's health and are likely to play key roles in *S. aureus* adaptation to the clinical microenvironment. Our data support a viral origin of the vSa β region. As the vSa β type is strongly linked to a strain's CC, acquisition of the vSa β region happened in a very ancestral *S. aureus* strain while the transformation to the distinct vSa β subtypes occurred before or simultaneously to diversification into the different clones. The here-suggested superordinate system to classify *S. aureus* strains based on their vSa β region may be used in the future to assess the clinical potential of an *S. aureus* strain. In the future, more vSa β genomic islands need to be analyzed and categorized into this superordinate system.

MATERIALS AND METHODS

Sequencing. The in-house *S. aureus* genome collection includes 23 strains that were previously sampled from bovine mastitis (36). All strains were kept in skim milk at -20°C and were recultured at 37°C for 24 h on blood agar (bioMérieux Suisse s.a., Geneva, Switzerland). Plates were sent to Microsynth AG (Balgach, Switzerland) for DNA extraction and subsequent whole-genome sequencing (WGS), initially by the 454 (Roche, Basel, Switzerland) and later by the Illumina (Illumina, Inc., San Diego, CA) technology, as the 454 method was no longer available. For *de novo* assembly of the reads to contigs, they used the Newbler v.2.6 assembler for the 454 (Roche) technology and SPAdes v.3.1 (37) for the Illumina technology (see File S1 in the supplemental material for details). In addition, contigs of 4 bovine *S. aureus* strains after Illumina WGS were provided by M. Luini (IZSLER, Lodi, Italy) and P. Cremonesi (CNR, Lodi, Italy).

Data collection. In an attempt to characterize the vSa β islands of our 27 bovine mastitis *S. aureus* genomes as described by Baba et al. (8), it turned out that many of them did not match the 3 previously defined types proposing a much higher diversity of vSa β ; hence, an in-depth characterization based on more data was required. To do so, more sequences were collected by a BLAST search (36) of each known, presumptively novel, vSa β against the NCBI nonredundant/nucleotide (nr/nt) database (<https://www.ncbi.nlm.nih.gov/nucleotide/>) using the default BLAST settings and limiting the search to *S. aureus*. To increase the diversity of the vSa β islands, the NCBI databases were also evaluated for genomes or contigs of clinical *S. aureus* strains from hosts other than humans or cattle. This approach was selected, as invasive strains of *S. aureus* are host specific (19, 38, 39), possibly accounting for additional types of vSa β islands. For each vSa β type, ≥ 10 chromosomal sequences of clinical *S. aureus* were then attempted to be retrieved. If this was impossible, the BLAST search was further extended to the NCBI whole genome shotgun contig database (<https://www.ncbi.nlm.nih.gov/assembly/>). All available chromosomal sequences were then retrieved, including all contigs containing a complete vSa β region.

Using this approach, a total of 76 sequences were obtained, with 43 sequences from genomes and 33 sequences from contigs (see File S2).

Data analysis. (i) Data set. In total, 27 of our own and 76 publicly available sequences were included in the present study. From these 103 analyzed *S. aureus* strains, 58 originated from human hosts, 33 were from bovine hosts, and 7 were from ovine hosts. For 5 strains, no host information was available. Of these 103 strains, 37 strains showed known vSa β types (I to III), and 66 strains showed novel vSa β types (IV to XV) (see File S2 for details).

(ii) vSa β typing. The vSa β regions were identified on genome sequences by aligning the sequences of conserved *hp* genes flanking vSa β at the 5' end (SAV1803) and 3' end (SAV1831) (8) using the Clone Manager Professional 9 (CM9) software (Scientific & Educational Software, Denver, CO). Subtyping of the vSa β islands was then based on the initial work by Baba et al. (8). Using the *hdsS* gene of 12 clinically relevant *S. aureus* strains, Baba et al. grouped them into three vSa β types (vSa β I, vSa β II, and vSa β III [8]). We then aligned the vSa β sequences of these 12 strains in the CM9 software using the Needleman-Wunsch algorithm and found that the overall similarities within a vSa β type were $\geq 90\%$. For each of these vSa β types, a representative sequence was then selected and considered the type-specific reference sequence (Table 1). Disregarding included phages and transposons, vSa β islands showing overall sequence similarities of $< 90\%$ compared to all the existing reference sequences were then considered new vSa β types. Through the iterative process of aligning nontyped vSa β islands to each of the vSa β type reference sequences, the 103 sequences of the data set were grouped into 15 vSa β types (vSa β I to XV, Table 1).

(iii) HsdS phylogenetics. To infer the phylogeny of the HsdS proteins (37, 40), the corresponding nucleotide sequences were translated using the standard code. Proteins that differed in at least one amino acid were then used for a multiple-sequence alignment (MSA) in the CM9 software using the Needleman-Wunsch approach. The MSA was exported to the BioEdit software (<http://www.mbio.ncsu.edu/BioEdit/bioedit.html>) for visual inspection and manual curation. Afterwards, the curated MSA was imported into the MEGA X software (41) to assess a maximum likelihood (ML) phylogeny of the HsdS proteins. To do so, models using 9 different substitution matrices were computed including or leaving out modeling for invariant sites and for the evolutionary rate differences among sites by a discrete gamma distribution. The optimal model was then selected based on the lowest value of the Akaike information criterion resulting in the JTT substitution matrix (37), with specific parameters for the gamma distribution. This model was then used to construct a phylogenetic ML tree (MEGA X software [41]). Initial trees were built by applying the maximum parsimony algorithm. The topology with the highest log-likelihood value was then selected (Fig. 2A). Strains lacking the *hdsS* gene were excluded.

(iv) Multilocus and *spa* typing. Multilocus sequence typing (MLST) of seven housekeeping genes (42) and *spa* typing (43) were performed for all *S. aureus* genomes using the Center for Genomic Epidemiology online platform (<http://www.genomicepidemiology.org/>). In the eBURST V3 program, the sequence types (STs) resulting from the MLST were used to allocate each strain to a clonal complex (CC).

(v) Annotations. Annotations were assigned to the *vSaβ* regions using the RAST pipeline (44–46). RAST annotations of all genes (including *hp* genes with or without a FIG number assigned by the RAST pipeline) were verified by a BLAST search against the UniProt database (47). Where necessary, annotations were corrected manually based on the UniProt data; whenever possible, reviewed entries were used. If the RAST pipeline failed to annotate genes known to be located on *vSaβ*, these genes were searched manually by aligning the nucleotide sequences of the well-characterized strains N315 and MW2 to the *vSaβ* of interest. Transfer RNAs were identified by tRNAscan-SE 2.0 (48).

(vi) Phage detection. Phages and phage remnants were identified by the online software Phage Search Tool Enhanced Release (PHASTER) (49, 50). To ensure detection, regions 5,000 bp up- and downstream of *vSaβ* were included in the analysis.

(vii) Serine protease nomenclature. All complete and curated *spl* sequences were analyzed and translated into proteins using the standard code. Sixty-eight amino acid sequences were unique (i.e., differed in at least one amino acid) and were used to reconstruct the phylogeny using the same methods as mentioned above for the HsdS protein sequence (ML method, JTT substitution matrix, discrete gamma distribution to model evolutionary rate differences among sites) (Fig. 2A and B). As the current nomenclature of *spl* does not account for the phylogenetic relationship between their sequences and in some cases is ambiguous and arbitrary, a new nomenclature was developed using the ML phylogenetic approach based on the protein sequences. Starting from the root of the phylogenetic tree, each node along a branch is followed until a node forming a monophyletic clade is reached whose branch connecting to its predecessor is characterized by a bootstrap value (BT) of ≥ 95 and a phylogenetic distance (*d*) of > 0.10 . All leaves forming this clade obtain the same letter (e.g., “D”) added to the basic name of the protein (in this case “Spl”), resulting in the name SplD for all of these leaves. The branch is then followed toward the leaves. If a node is reached forming a monophyletic subclade whose branch connecting to the predecessor is characterized by a BT of ≥ 95 and *d* of > 0.10 , the leaves of this subclade are labeled by adding a number (e.g., “2”), resulting in the name SplD2. At this stage, further evaluation toward the leaves is stopped. If only one branch of a bifurcation fulfills these conditions, the subclade formed by the nonfulfilling branch gets a new letter or number as well.

Data availability. All whole-genome projects have been deposited in the NCBI database under the BioProject number PRJNA531079 with the accession numbers [SZYI000000000](#) (Lodi13K), [SZYM000000000](#) (G12B), [SZYO000000000](#) (G29N), [SZYT000000000](#) (Lodi10B), [VCQP000000000](#) (M2084B), [SZYY000000000](#) (M2130B), [SZZA000000000](#) (M2529B), [SZZF000000000](#) (M5512B), [VCQQ000000000](#) (M5171B), [SZZG000000000](#) (M6020B), [SZZE000000000](#) (M3783C), [SZZC000000000](#) (M2839C), [SZYW000000000](#) (M1280C), [SZYX000000000](#) (M1655C), [SZYZ000000000](#) (M2323C), [SZZB000000000](#) (M2682A), [SZYS000000000](#) (K2R), [SZYJ000000000](#) (G07I), [SZYV000000000](#) (Lodi4R), [SZZD000000000](#) (M3386D), [SZYQ000000000](#) (G42G), [SZYP000000000](#) (G33O), [SZYR000000000](#) (G68P), [SZYL000000000](#) (G11F), [SZYN000000000](#) (G19F), [SZYK000000000](#) (G08M), and [SZYU000000000](#) (Lodi11bM).

SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at <https://doi.org/10.1128/JB.00777-18>.

SUPPLEMENTAL FILE 1, XLSX file, 0.1 MB.

SUPPLEMENTAL FILE 2, XLSX file, 0.1 MB.

ACKNOWLEDGMENTS

We thank Mario Luini of the Instituto Zooprofilattico Sperimentale della Lombardia e dell’Emilia Romagna (ISZLER, Lodi, Italy) and P. Cremonesi of the Istituto di Biologia e Biotecnologia Agraria (CNR, Lodi, Italy) for providing sequencing data.

This work was financially supported by the Agroscope research program AFP REDYMO.

REFERENCES

1. Peacock SJ, De Silva I, Lowy FD. 2001. What determines nasal carriage of *Staphylococcus aureus*? Trends Microbiol 9:605–610. [https://doi.org/10.1016/S0966-842X\(01\)02254-5](https://doi.org/10.1016/S0966-842X(01)02254-5).
2. Kluytmans J, Belkum A, Verbrugh H. 1997. Nasal carriage of *Staphylococcus aureus*: epidemiology, underlying mechanisms, and associated risks. Clin Microbiol Rev 10:505–520. <https://doi.org/10.1128/CMR.10.3.505>.
3. Herrmann M, Smeltzer MS. 2016. Clinical significance in humans, p 23–43. In Somerville GA (ed), *Staphylococcus genetics and physiology*, 1st ed. Caister Academic Press, Norfolk, United Kingdom.
4. Loy JD. 2016. *Staphylococcus*: clinical significance in animals, p 45–66. In Somerville GA (ed), *Staphylococcus genetics and physiology*, 1st ed. Caister Academic Press, Norfolk, United Kingdom.
5. Lowy FD. 1998. *Staphylococcus aureus* Infections. N Engl J Med 339: 520–532. <https://doi.org/10.1056/NEJM199808203390806>.
6. Malachowa N, Deleo FR. 2010. Mobile genetic elements of *Staphylococcus aureus*. Cell Mol Life Sci 67:3057–3071. <https://doi.org/10.1007/s0018-010-0389-4>.
7. Lindsay JA, Holden M. 2004. *Staphylococcus aureus*: superbug, super genome? Trends Microbiol 12:378–385. <https://doi.org/10.1016/j.tim.2004.06.004>.
8. Baba T, Bae T, Schneewind O, Takeuchi F, Hiramatsu K. 2008. Genome

- sequence of *Staphylococcus aureus* strain Newman and comparative analysis of staphylococcal genomes: polymorphism and evolution of two major pathogenicity islands. *J Bacteriol* 190:300–310. <https://doi.org/10.1128/JB.01000-07>.
9. Fitzgerald JR, Monday SR, Foster TJ, Bohach GA, Hartigan PJ, Meaney WJ, Smyth CJ. 2001. Characterization of a putative pathogenicity island from bovine *Staphylococcus aureus* encoding multiple superantigens. *J Bacteriol* 183:63–70. <https://doi.org/10.1128/JB.183.1.63-70.2001>.
 10. Baba T, Takeuchi F, Kuroda M, Yuzawa H, Aoki KI, Oguchi A, Nagai Y, Iwama N, Asano K, Naimi T, Kuroda H, Cui L, Yamamoto K, Hiramatsu K. 2002. Genome and virulence determinants of high virulence community-acquired MRSA. *Lancet* 359:1819–1827. [https://doi.org/10.1016/S0140-6736\(02\)08713-5](https://doi.org/10.1016/S0140-6736(02)08713-5).
 11. Reed SB, Wesson CA, Liou LE, Trumble WR, Schlievert PM, Bohach GA, Bayles KW. 2001. Molecular characterization of a novel *Staphylococcus aureus* serine protease operon. *Infect Immun* 69:1521–1527. <https://doi.org/10.1128/IAI.69.3.1521-1527.2001>.
 12. Rao RT, Shofia SI, Manna A, Jayakumar K. 2016. An account of genomic islands of zoonotic origin *Staphylococcus aureus* genomes—*in silico* approach. 2016 International Conference on Bioinformatics and Systems Biology, 4 to 6 March 2016, Allahabad, India.
 13. Méric G, Miragaia M, De Been M, Yahara K, Pascoe B, Mageiros L, Mikhail J, Harris LG, Wilkinson TS, Rolo J, Lambie S, Bray JE, Jolley KA, Hanage WP, Bowden R, Maiden MCJ, Mack D, De Lencastre H, Feil EJ, Corander J, Sheppard SK. 2015. Ecological overlap and horizontal gene transfer in *Staphylococcus aureus* and *Staphylococcus epidermidis*. *Genome Biol Evol* 7:1313–1328. <https://doi.org/10.1093/gbe/evv066>.
 14. Moon BY, Park JY, Hwang SY, Robinson DA, Thomas JC, Fitzgerald JR, Park YH, Seo KS. 2015. Phage-mediated horizontal transfer of a *Staphylococcus aureus* virulence-associated genomic island. *Sci Rep* 5:9784. <https://doi.org/10.1038/srep09784>.
 15. Hacker J, Kaper JB. 2000. Pathogenicity islands and the evolution of microbes. *Annu Rev Microbiol* 54:641–679. <https://doi.org/10.1146/annurev.micro.54.1.641>.
 16. Darmon E, Leach D. 2014. Bacterial genome instability. *Microbiol Mol Biol Rev* 78:1–39. <https://doi.org/10.1128/MMBR.00035-13>.
 17. Dobrindt U, Hochhut B, Hentschel U, Hacker J. 2004. Genomic islands in pathogenic and environmental microorganisms. *Nat Rev Microbiol* 2:414–424. <https://doi.org/10.1038/nrmicro884>.
 18. Lindsay JA, Moore CE, Day NP, Peacock SJ, Witney AA, Stabler RA, Husain SE, Butcher PD, Hinds J. 2006. Microarrays reveal that each of the ten dominant lineages of *Staphylococcus aureus* has a unique combination of surface-associated and regulatory genes. *J Bacteriol* 188:669–676. <https://doi.org/10.1128/JB.188.2.669-676.2006>.
 19. Boss R, Cosandey A, Luini M, Artursson K, Bardiau M, Breitenwieser F, Hehenberger E, Lam T, Mansfeld M, Michel A, Mösslacher G, Naskova J, Nelson S, Podpečan O, Raemy A, Ryan E, Salat O, Zangerl P, Steiner A, Graber HU. 2016. Bovine *Staphylococcus aureus*: subtyping, evolution, and zoonotic transfer. *J Dairy Sci* 99:515–528. <https://doi.org/10.3168/jds.2015-9589>.
 20. Zhang DF, Yang XY, Zhang J, Qin X, Huang X, Cui Y, Zhou M, Shi C, French NP, Shi X. 2018. Identification and characterization of two novel superantigens among *Staphylococcus aureus* complex. *Int J Med Microbiol* 308:438–446. <https://doi.org/10.1016/j.ijmm.2018.03.002>.
 21. Gravet A, Colin DA, Keller D, Girardot R, Monteil H, Prévost G, Girardot R. 1998. Characterization of a novel structural member, LukE-LukD, of the bi-component staphylococcal leucotoxins family. *FEBS Lett* 436:202–208. [https://doi.org/10.1016/s0014-5793\(98\)01130-2](https://doi.org/10.1016/s0014-5793(98)01130-2).
 22. Alonzo F, Torres VJ. 2014. The bicomponent pore-forming leucocidins of *Staphylococcus aureus*. *Microbiol Mol Biol Rev* 78:199–230. <https://doi.org/10.1128/MMBR.00055-13>.
 23. Alonzo F, Ill, Benson MA, Chen J, Novick RP, Shopsin B, Torres TJ. 2012. *Staphylococcus aureus* leukocidin ED contributes to systemic infection by targeting neutrophils and promoting bacterial growth in vivo. *Mol Microbiol* 83:423–435. <https://doi.org/10.1111/j.1365-2958.2011.07942.x>.
 24. Stach N, Kaszycki P, Władyska B, Dubin G. 2018. Extracellular proteases of *Staphylococcus* spp., p 135–145. In Savini V (ed), *Pet-to-man travelling staphylococci*. Elsevier, Inc., Dublin, Ireland.
 25. Paharik AE, Salgado-Pabon W, Meyerholz DK, White MJ, Schlievert PM, Horswill AR. 2016. The Spl serine proteases modulate *Staphylococcus aureus* protein production and virulence in a rabbit model of pneumonia. *mSphere* 1:e00208-16. <https://doi.org/10.1128/mSphere.00208-16>.
 26. Kolar SL, Antonio Ibarra J, Rivera FE, Mootz JM, Davenport JE, Stevens SM, Horswill AR, Shaw LN. 2013. Extracellular proteases are key mediators of *Staphylococcus aureus* virulence via the global modulation of virulence-determinant stability. *Microbiol Open* 2:18–34. <https://doi.org/10.1002/mbo3.55>.
 27. Zdzalik M, Karim AY, Wolski K, Buda P, Wojcik K, Brueggemann S, Wojciechowski P, Eick S, Calander AM, Jonsson IM, Kubica M, Polakowska K, Miedzobrodzki J, Władyska B, Potempa J, Dubin G. 2012. Prevalence of genes encoding extracellular proteases in *Staphylococcus aureus*—important targets triggering immune response in vivo. *FEMS Immunol Med Microbiol* 66:220–229. <https://doi.org/10.1111/j.1574-695X.2012.01005.x>.
 28. Stentzel S, Teufelberger A, Nordengrün M, Kolata J, Schmidt F, van Crombruggen K, Michalik S, Kumpfmüller J, Tischer S, Schweder T, Hecker M, Engemann S, Völker U, Krysko O, Bachert C, Bröker BM. 2017. Staphylococcal serine protease-like proteins are pacemakers of allergic airway reactions to *Staphylococcus aureus*. *J Allergy Clin Immunol* 139:492–500. <https://doi.org/10.1016/j.jaci.2016.03.045>.
 29. Teufelberger AR, Nordengrün M, Braun H, Maes T, De Grove K, Holtappels G, O'Brien C, Provoost S, Hammad H, Gonçalves A, Beyaert R, Declercq W, Vandenaabeele P, Krysko DV, Bröker BM, Bachert C, Krysko O. 2018. The IL-33/ST2 axis is crucial in type 2 airway responses induced by *Staphylococcus aureus*-derived serine protease-like protein D. *J Allergy Clin Immunol* 141:549–559. <https://doi.org/10.1016/j.jaci.2017.05.004>.
 30. Necas J, Bartosikova L, Brauner P, Kolar J. 2008. Hyaluronic acid (hyaluronan): a review. *Vet Med (Praha)* 53:397–411. <https://doi.org/10.17221/1930-VETMED>.
 31. Makris G, Wright JD, Ingham E, Holland KT. 2004. The hyaluronate lyase of *Staphylococcus aureus*—a virulence factor? *Microbiology* 150:2005–2013. <https://doi.org/10.1099/mic.0.26942-0>.
 32. Ibberson CB, Jones CL, Singh S, Wise MC, Hart ME, Zurawski DV, Horswill AR. 2014. *Staphylococcus aureus* hyaluronidase is a CodY-regulated virulence factor. *Infect Immun* 82:4253–4264. <https://doi.org/10.1128/IAI.01710-14>.
 33. Farrell AM, Taylor D, Holland KT. 1995. Cloning, nucleotide-sequence determination and expression of the *Staphylococcus aureus* hyaluronate lyase gene. *FEMS Microbiol Lett* 130:81–85. <https://doi.org/10.1111/j.1574-6968.1995.tb07702.x>.
 34. McAuliffe O, Ross RP, Hill C. 2001. Lantibiotics: biosynthesis and mode of action. *FEMS Microbiol Lett* 25:285–308. <https://doi.org/10.1111/j.1574-6976.2001.tb00579.x>.
 35. Daly KM, Upton M, Sandiford SK, Draper LA, Wescombe PA, Jack RW, O'Connor PM, Rossney A, Götz F, Hill C, Cotter PD, Ross RP, Tagg JR. 2010. Production of the Bsa lantibiotic by community-acquired *Staphylococcus aureus* strains. *J Bacteriol* 192:1131–1142. <https://doi.org/10.1128/JB.01375-09>.
 36. Fournier C, Kuhnert P, Frey J, Miserez R, Kirchhofer M, Kaufmann T, Steiner A, Graber HU. 2008. Bovine *Staphylococcus aureus*: association of virulence genes, genotypes and clinical outcome. *Res Vet Sci* 85:439–448. <https://doi.org/10.1016/j.rvsc.2008.01.010>.
 37. Roberts GA, Houston PJ, White JH, Chen K, Stephanou AS, Cooper LP, Dryden DTF, Lindsay JA. 2013. Impact of target site distribution for type I restriction enzymes on the evolution of methicillin-resistant *Staphylococcus aureus* (MRSA) populations. *Nucleic Acids Res* 41:7472–7484. <https://doi.org/10.1093/nar/gkt535>.
 38. Grundmann H, Aanensen DM, Van Den Wijngaard CC, Spratt BG, Harnsen D, Friedrich AW, Sabat AJ, Muilwijk J, Monen J, Tami A, Donker T, Mittermayer H, Krziwanek K, Stummvoll S, Koller W, Denis O, Struelens M, Nashev D, Budimir A, Kalenic S, Pieridou-Bagatzouni D, Jakubu V, Zemlickova H, Westh H, Sørum M, Skov R, Laurent F, Ettienne J, Strommenger B, Witte W, Vourli S, Vatopoulos A, Vainio A, Vuopio-Varkila J, Fuzi M, Ungvári E, Murchan S, Rossney A, Miklasevics E, Balode A, Haraldsson G, Kristinsson KG, Monaco M, Pantosti A, Borg M, Van Santen-Verheul M, Huijsdens H, Marstein L, Jacobsen T, Simonsen GS, et al. 2010. Geographic distribution of *Staphylococcus aureus* causing invasive infections in Europe: a molecular-epidemiological analysis. *PLoS Med* 7:e1000215. <https://doi.org/10.1371/journal.pmed.1000215>.
 39. Leuenberger A, Sartori C, Boss R, Resch G, Oechslin F, Steiner A, Moreillon P, Graber HU. 2019. Genotypes of *Staphylococcus aureus*: on-farm epidemiology and the consequences for prevention of intramammary infections. *J Dairy Sci* 102:3295–3309. <https://doi.org/10.3168/jds.2018-15181>.
 40. Lindsay JA. 2010. Genomic variation and evolution of *Staphylococcus aureus*. *Int J Med Microbiol* 300:98–103. <https://doi.org/10.1016/j.ijmm.2009.08.013>.
 41. Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: Molecular

- Evolutionary Genetics Analysis across computing platforms. *Mol Biol Evol* 35:1547–1549. <https://doi.org/10.1093/molbev/msy096>.
42. Larsen MV, Cosentino S, Rasmussen S, Friis C, Hasman H, Marvig RL, Jelsbak L, Sicheritz-Pontén T, Ussery DW, Aarestrup FM, Lund O. 2012. Multilocus sequence typing of total-genome-sequenced bacteria. *J Clin Microbiol* 50:1355–1361. <https://doi.org/10.1128/JCM.06094-11>.
 43. Bartels MD, Petersen A, Worning P, Nielsen JB, Larner-Svensson H, Johansen HK, Andersen LP, Jarløv JO, Boye K, Larsen AR, Westh H. 2014. Comparing whole-genome sequencing with Sanger sequencing for spa typing of methicillin-resistant *Staphylococcus aureus*. *J Clin Microbiol* 52:4305–4308. <https://doi.org/10.1128/JCM.01979-14>.
 44. Aziz RK, Bartels D, Best A, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <https://doi.org/10.1186/1471-2164-9-75>.
 45. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). *Nucleic Acids Res* 42:206–214. <https://doi.org/10.1093/nar/gkt1226>.
 46. Brettin T, Davis JJ, Disz T, Edwards RA, Gerdes S, Olsen GJ, Olson R, Overbeek R, Parrello B, Pusch GD, Shukla M, Thomason JA, Stevens R, Vonstein V, Wattam AR, Xia F. 2015. RASTtk: a modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. *Sci Rep* 5:8365. <https://doi.org/10.1038/srep08365>.
 47. Bateman A, Martin MJ, O'Donovan C, Magrane M, Alpi E, Antunes R, Bely B, Bingley M, Bonilla C, Britto R, Bursteinas B, Bye-Ajee H, Cowley A, Da Silva A, De Giorgi M, Dogan T, Fazzini F, Castro LG, Figueira L, Garmiri P, Georghiou G, Gonzalez D, Hatton-Ellis E, Li W, Liu W, Lopez R, Luo J, Lussi Y, MacDougall A, Nightingale A, Palka B, Pichler K, Poggioli D, Pundir S, Pureza L, Qi G, Rosanoff S, Saidi R, Sawford T, Shypitsyna A, Speretta E, Turner E, Tyagi N, Volynkin V, Wardell T, Warner K, Watkins X, Zaru R, Zellner H, Xenarios I, et al. 2017. UniProt: the universal protein knowledgebase. *Nucleic Acids Res* 45:D158–D169. <https://doi.org/10.1093/nar/gkw1099>.
 48. Lowe TM, Chan P. 2016. tRNAscan-SE On-line: integrating search and context for analysis of transfer RNA genes. *Nucleic Acids Res* 44:W54–W57. <https://doi.org/10.1093/nar/gkw413>.
 49. Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS. 2011. PHAST: a fast phage search tool. *Nucleic Acids Res* 39:W347–W352. <https://doi.org/10.1093/nar/gkr485>.
 50. Arndt D, Grant JR, Marcu A, Sajed T, Pon A, Liang Y, Wishart DS. 2016. PHASTER: a better, faster version of the PHAST phage search tool. *Nucleic Acids Res* 44:W16–W21. <https://doi.org/10.1093/nar/gkw387>.