J. Bangladesh Acad. Sci. 49(2); 179-188: December 2025 DOI:https://doi.org/10.3329/jbas.v49i2.80908

Journal of Bangladesh Academy of Sciences

Journal homepage: http://www.bas.org.bd/publications/jbas.html

Research Article

Genome mining reveals the prevalence of Bsa lantibiotic and its variants in *Staphylococcus aureus* strains

Suvroto Kormokar[1], Md. Amzad Hossain[2], M. Aftab Uddin[1] and Mohammad Riazul Islam[2*]

[1]*Department of Genetic Engineering and Biotechnology, University of Dhaka, Dhaka, Bangladesh*

ARTICLE INFO

Article History

Received: 14 April 2025
Revised: 08 July 2025
Accepted: 19 August 2025

Keywords: Genome mining, Lantibiotic, Class-I lanthipeptide, AntiSMASH, Bsa.

ABSTRACT

With rising antibiotic resistance, the discovery of novel antimicrobial compounds has become increasingly crucial. *In silico* genome mining is widely used to predict secondary metabolite production prior to laboratory testing. In this study, 505 *Staphylococcus aureus* genomes from the NCBI database were analyzed using antiSMASH 7.0, which identified a class I lanthipeptide gene cluster in 206 strains. Although antiSMASH annotated this gene cluster as hyicin 3682 and the RefSeq genome database classified it as a 'gallidermin- or nisin-family lantibiotic', the prepeptide sequence encoded by the cluster is identical to that of the *S. aureus* bacteriocin (Bsa) lantibiotic. Moreover, other genes within the cluster share the same number and orientation as the Bsa loci found in community-acquired *S. aureus* strains. Variations in prepeptide sequences and gene numbers revealed four distinct Bsa variants. Overall, this analysis supports the presence of lantibiotic gene clusters in pathogenic strains and highlights the potential of genome mining to reduce time, cost, and labor in antimicrobial discovery.

Introduction

Scientists have discovered a bunch of new antibiotics, and sooner or later new antibiotic-resistant pathogens have emerged as a result. So, the search for new and novel antibiotics continues from every possible source, e.g., animals, insects, plants, and bacteria. Among several alternative options, lanthipeptides from bacteria show potential as future therapeutic agents due to their ability to kill antibiotic-resistant pathogens and their broad antimicrobial spectrum (van Staden et al., 2021).

Lanthipeptides are ribosomally synthesized and post-translationally modified peptides. They contain specific amino acids, including lanthionine (Lan) and (2S,3S,6R)-3-methyllanthionine (MeLan) (Arnison et al., 2013). The lanthipeptide is produced from a precursor peptide known as LanA, which is then subjected to post-translational changes to yield the mature, bioactive lanthipeptide. After serine (Ser) and threonine (Thr) residues are dehydrated to form dehydroalanine (Dha) and dehydrobutyrine (Dhb), the thiol groups of cysteine (Cys) residues are added to Dha and Dhb to form thioether cross-links, which yield the Lan and MeLan residues, respectively (Arnison et al., 2013). Enzymes responsible for these modifications, lanthipeptide synthetases, show different features that classify the lanthipeptides into 4 subfamilies: class-I – class-IV (Arnison et al., 2013). While Class-I lanthipeptides (such as nisin) have been extensively studied, the prevalence of other classes (III and IV) is gaining attention.

Lantibiotics are produced by the members of the Gram-positive bacteria with a length of usually 19 to 34 amino acids (Willey and van der

*Corresponding author:<mriazulislam@du.ac.bd>

[2]*Department of Biochemistry and Molecular Biology, University of Dhaka, Dhaka, Bangladesh*

Donk, 2007). Some of the reported lantibiotics are Pep5 from *S. epidermidis* 5 (Kaletta et al., 1989), epidermin (Epi) from *S. epidermidis* Tü3298 (Allgaier et al., 1985), gallidermin (Gdm) from *S. gallinarum* DSM 4616 (Kellner et al., 1988), Bsa_{COL} from *S. aureus* COL1881 (Daly et al., 2010), nisin J from *S. capitis* APC2923 (O'Sullivan et al., 2020), homicorcin from *S. hominis* MBL_AB63 (Uddin et al., 2021), etc. Although many lantibiotics are produced by food-grade bacteria or bacteria generally regarded as safe, there have also been a few examples of antibiotic production by pathogens (Cox et al., 2005). One such pathogen is *Staphylococcus aureus*, a frequent opportunistic pathogen of humans and animals. To date, 4 lantibiotics have been reported to be produced by *S. aureus*: Staphylococcin Au-26 (Scott, 1992), Staphylococcin C55 (Navaratna et al., 1998), BacCH91 (Wladyka et al., 2013), and Bsa (bacteriocin of *Staphylococcus aureus*) (Daly et al., 2010). As a member of the *Staphylococcus* genus, the *S. aureus* genome holds the promise of harboring novel antimicrobial compound gene clusters.

Genome mining is a fast, high-throughput technique that exploits genomic information to discover natural products, their biosynthetic pathways, and potential interactions. The possibility of predicting novel putative lanthipeptide gene clusters in bacterial genomes has increased steadily over the last decade, driven by greater genomic data availability and advances in genome-mining tools. One of these tools is antiSMASH (antibiotics and secondary metabolite analysis shell), which analyzes genome sequences, identifies putative lanthipeptide biosynthetic gene clusters, provides information on their post-translational modifications and determines the class of the detected lanthipeptide (Blin et al., 2023). Another one is BAGEL, a web tool that identifies gene clusters in prokaryotic DNA involved in the biosynthesis of Ribosomally synthesized and post-translational modified Peptides (RiPPs) and bacteriocins (van Heel et al., 2018). There are numerous studies on the identification of lanthipeptide gene clusters through *in silico* screening of bacterial genomes, reflecting the growing interest in secondary metabolites (Begley et al., 2009; Singh and Sareen, 2014).

In this study, more than 500 *Staphylococcus aureus* complete genome sequences available in NCBI were screened using antiSMASH 7.0 to examine the pattern of secondary metabolite prediction by *S. aureus*. In 206 strains, a complete lanthipeptide class I gene cluster was identified. Initially, this gene cluster was identified as hyicin 3682 and annotated as a gallidermin or nisin family lantibiotic in the RefSeq genome database. However, analysis of gene arrangement within the cluster and its sequences confirmed that it is a Bsa locus, and its multiple variants were identified. As this is an *in silico* study, this presumption must be validated by experimental analysis.

Methods

Selection of genome sequences and identification of gene clusters using antiSMASH7.0

From the Genome database of NCBI (https://www.ncbi.nlm.nih.gov/genome), the first 505 *S. aureus* complete genome sequences were selected out of 1716 publicly available sequences until October 2023. The accession numbers of these sequences were used as input in 'antibiotics and secondary metabolite analysis shell—antiSMASH' version 7.0 (Blin et al., 2023) (https://antismash.secondarymetabolites.org/) for identification, annotation, and analysis of secondary metabolite biosynthesis gene clusters.

Comparison of the identified lantipeptide cluster genes with corresponding genes of other lantipeptides of the same class

The individual genes of the identified lantipeptide cluster were aligned with corresponding biosynthesis genes of other well-studied class-I lantibiotics using the NCBI Nucleotide BLAST tool (https://www.ncbi.nlm.nih.gov/geo/query/blast.html).

Phylogenetic tree construction

To study the evolutionary relationship among the Seq 1 prepeptide and to compare class I lantipeptides, a phylogenetic tree was constructed in MEGA11 using the neighbour-joining method, with the Poisson model as the substitution model (Tamura et al., 2021). An outgroup sequence of *S. aureus*, glyceraldehyde-3-phosphate dehydrogenase (GPD) was used to determine the root of the sequences.

Results

The lanthipeptide class-I gene cluster was the most prevalent gene cluster in the studied genomes

In the 505 *S. aureus* genomes screened, 7 different types of gene clusters were identified, i.e., lanthipeptide-class-I, non-ribosomal peptide synthetase (NRPS), cyclic lactone autoinducer, siderophore, ribosomally synthesized and post-translationally modified peptides (RiPP) like opine-like-metallophore and terpene. While the other 6 gene clusters were found in more than 500 genomes, the lanthipeptide class I gene cluster was found in only 206 genomes. The most similar gene cluster to this lanthipeptide was predicted to be hyicin 3682. Of these, 161 gene clusters were 100% similar, and 45 were 87% identical to the hyicin 3682 gene cluster.

The lantipeptide cluster identified as the Bsa biosynthesis gene cluster is revealed through gene-by-gene sequence comparison

The identified gene clusters of the class-I lanthipeptide in 206 *S. aureus* strains contain 4 different types of prepeptide sequences at different frequencies, arranged in 5 different arrangements in the clusters. The most prevalent of these types (found in 197 strains out of 206) contains 20 genes of varying lengths in most cases, of which 9 genes (Fig. 1) are supposed to be involved in lantibiotic production and transport according to their annotations by antiSMASH 7.0. Among the 9 genes, two genes code for two different prepeptide sequences (A, A'), three genes code for modification enzymes (B, C, D), one codes for a cleavage enzyme (P), while the other three are involved with transport and immunity (F, E, G). The genes were identified as the most identical genes in the NCBI database, and their roles in lanthipeptide production and transport were determined.

The most prevalent whole gene cluster (Fig. 1) was compared with the other lantibiotic gene clusters to find similarity in terms of gene number, function and orientation (Fig. 2). It is clearly visible that the lanthipeptide class I gene cluster is identical to the Bsa gene cluster (Daly et al., 2010) and hyicin 3682 gene cluster (Carlin et al., 2017) having 8 genes, all of which are in the same orientation. The epidermin gene cluster (Schnell et al., 1992), the 181 allidermin gene cluster (Valsesia et al., 2007), and the nisin A gene cluster (Trmčić et al., 2011) show notable differences in the number of genes (both have 11 genes), their orientation, and their function. Moreover, sequences of all similar genes in the most prevalent cluster were compared (using the NCBI BLAST algorithm) with those of the rest to determine similarity (Table 1). Except for one, all the genes in the identified lanthipeptide gene cluster show significant similarity to the corresponding genes in Bsa.

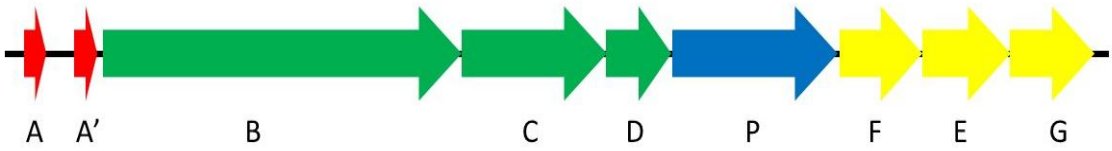

Fig. 1. Arrangement of biosynthetic genes in the most prevalent lanthipeptide class-I gene cluster in *S. aureus*. The function of each gene product is indicated by colors: red, precursor peptide (A, A'); green, modification enzyme (B, C, D); blue, cleavage enzyme (P); and yellow, transport and immunity protein (F, E, G).

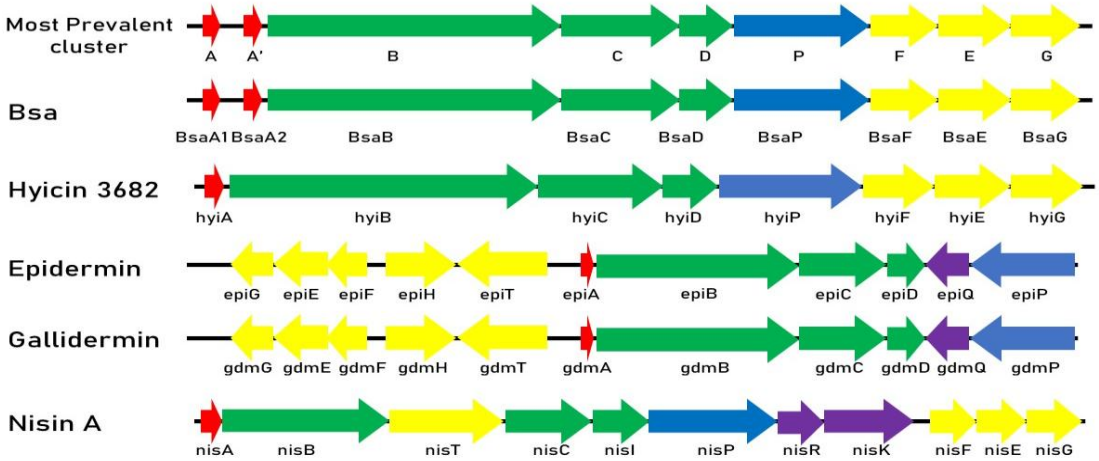

Fig. 2. Comparison of the whole gene cluster of the identified class I lanthipeptide with other lantibiotics. The function of each gene product is indicated by colors: red, precursor peptide; green, modification enzyme; blue, cleavage enzyme; yellow, transport and immunity protein; and purple, response regulator.

Table 1. Sequence comparison (% identity) of different biosynthetic genes of Bsa from different clusters with the corresponding genes of the identified class I lanthipeptide.

	Class-I lanthipeptide genes						
Lantipeptide	**LanB**	**LanC**	**LanD**	**LanP**	**LanF**	**LanE**	**LanG**
Bsa	99.7	100	100	100	100	100	100
Hyicin	60.28	58.21	72.67	64.44	82.46	67.06	56.28
Epidermin	44.87	46.34	53.49	49.34	72.89	50.99	49.34
Gallidermin	43.5	44.47	51.16	46.97	76.37	50.6	48.91
Nisin A	23.08	28.2	...	43.5	46.61	22.12	*

(... indicates absence of corresponding gene and * indicates no significant similarity).

Based on sequence comparisons and gene arrangements within the cluster, it is evident that the identified class-I lanthipeptide gene clusters in 206 *S. aureus* strains are Bsa gene clusters.

Prepeptide sequences in the identified lantipeptide resemble Bsa variants

The 4 different prepeptide sequences have been termed Seq 1, Seq 2, Seq 3, and Seq 4, with frequencies of 197, 194, 8, and 6, respectively, across 206 identified gene clusters.

When the most prevalent prepeptide (Seq 1) of the identified lanthipeptides was aligned with the mentioned lantibiotics (Fig. 3), it showed total identity with Bsa being identical in all 47 residues. Hyicin 3682, a lantibiotic with the same length of prepeptide sequence, is similar to the query and Bsa at 40 positions. The query sequence shows significant dissimilarity to epidermin, gallidermin, and nisin A, with the lengths of the prepeptides also being notably different.

When the structural peptides (without leader sequences) of Seq 1, Seq 2, Seq 3, and Seq 4 were compared with Bsa variants, they showed identity with BsaA2, BsaA1, $BsaA2_{ET3\text{-}1}$, and $BsaA1_{ET3\text{-}1}$, respectively (Fig. 4).

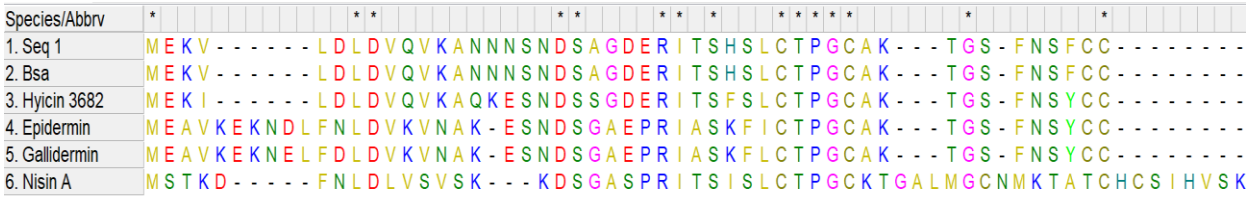

Fig. 3.Amino acid sequence alignment of the prepeptide sequence of Seq 1 with Bsa, Hyicin 3682, Epidermin, Gallidermin and Nisin A. (*) indicates conserved residues. The alignment was performed using MEGA11.

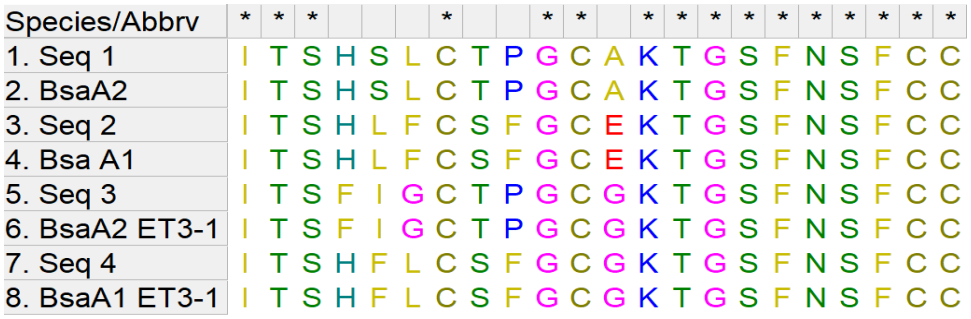

Fig. 4. Amino acid sequence alignment of the 4 different identified structural peptides with different Bsa variants. Seq 1, Seq 2, Seq 3 and Seq 4 are the identified structural peptides with different frequencies. BsaA2, BsaA1, $BsaA2_{ET3-1}$ and $BsaA1_{ET3-1}$ are the 4 variants of Bsa. The alignment was performed using MEGA11.

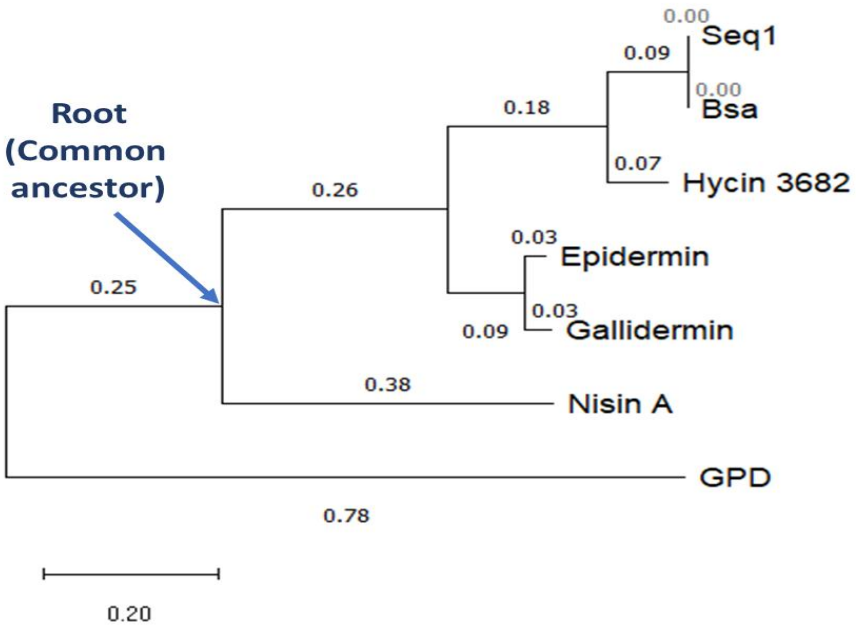

Fig. 5. Phylogenetic tree comprising the most prevalent prepeptide (Seq 1) and other comparable class I lantipeptides. Seq 1 and Bsa are identical showing 0.00 branch length from a common ancestor. Nisin A is the most diverged prepeptide in the group. To identify the common ancestor (root) of the sequences, the glyceraldehyde-3-phosphate dehydrogenase (GPD) sequence of *S. aureus* was used as the outgroup.

Phylogenetic study indicates that Bsa is the most evolved prepeptide within the comparative group

A phylogenetic tree was constructed comprising the most frequent prepeptide (Seq 1) and other class I lantipeptides using the neighbour-joining method (Fig. 5). The *S. aureus* glyceraldehyde-3-phosphate dehydrogenase (GPD) sequence was employed as the outgroup to identify the common ancestor (root) of the sequences. The tree illustrates that Seq 1, identified as Bsa, is the most evolved prepeptide and is significantly closer to hyicin 3682, forming the most divergent clade in the tree. Epidermin and gallidermin constitute an additional clade that has a common ancestor with the previously stated clade. Nisin A is the most divergent prepeptide derived from the root, exhibiting the greatest branch length (0.38) among the comparative group.

Genes from various clusters, aside from prepeptides, also exhibit a notable degree of similarity

The 4 different prepeptide sequences are arranged in 5 different types of biosynthesis gene clusters named CT1 (Cluster type 1), CT2, CT3, CT4 and CT5 having found in 197, 2, 2, 4 and 1 strains respectively (Fig. 6). The most prevalent cluster type (CT1) contains two genes encoding BsaA1 and BsaA2, whereas CT2 only contains $BsaA2_{ET3-1}$ followed by other genes of the clusters for lanthipeptide modification, cleavage and transportation. Like CT1, CT3 contains two successive genes encoding $BsaA1_{ET3-1}$ and $BsaA2_{ET3-1}$. A different picture is seen in CT4, where there are also two genes like CT3 but intervened by a transposase. The transposase gene is also observed in CT5 which separated the gene for BsaA1 and the modifying enzymes.

The genes of the clusters other than the prepeptides were compared with the corresponding genes of the other 5 clusters using the NCBI BLAST algorithm to understand the variability of their roles in producing and transporting the lanthipeptide (Table 2). All genes but one in CT4 and CT5 were identical with the genes of CT1. CT2 shows a little bit of dissimilarity in some of the genes while CT3 shows the most with none of the genes being identical with CT1.

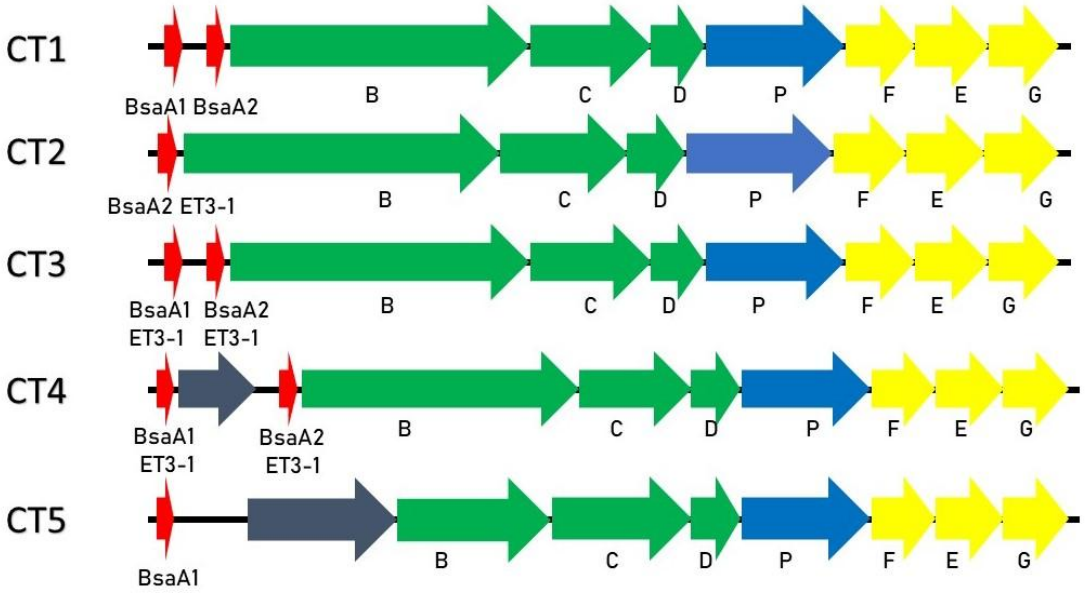

Fig. 6. Variation of Bsa lantibiotic gene clusters identified in *S. aureus* strains. Cluster types (CT) are differentiated by the presence of a single or two genes and a transposase gene. The prepeptide sequences have been labeled by identical matches with various Bsa variants. Functions of the rest of the genes are indicated by colors: red, precursor peptide; green, modification enzyme; blue, cleavage enzyme; yellow, transport and immunity protein; blue gray, uncharacterized protein.

Table 2. Sequence comparison of genes of CT1 with the corresponding genes of other clusters in terms of percentage of identity.

Gene	CT1						
Gene	**LanB**	**LanC**	**LanD**	**LanP**	**LanF**	**LanE**	**LanG**
CT2	93.58	98.07	99.42	94.75	100	100	100
CT3	92.88	88.89	97.67	94.53	97.39	95.26	98.71
CT4	100	99.76	100	100	100	100	100
CT5	98.04	100	100	100	100	100	100

Discussion

Bacterial genome mining is a powerful bioinformatics technique used to identify novel lantibiotics by analyzing bacterial genetic blueprints (Foulston, 2019). This technique involves identifying and characterizing biosynthetic gene clusters (BGCs) in bacterial genomes that encode lantibiotics (Foulston, 2019). Genome mining has identified several bacteriocins, including new variants. Examples include miticin, a leaderless bacteriocin identified in *Streptococcus mitis* (Alkassab et al., 2024). A similar technique was used to identify BGCs for bacillaene, bacillibacin, bacilysin, subtilosin, fengycin and surfactin in *Bacillus subtilis* BDSA1 (Saikat et al., 2024). Furthermore, genome mining has uncovered the prevalent presence of bacteriocin gene clusters in cyanobacteria (Wang et al., 2011). Meanwhile, *in silico* genome mining reveals novel bacteriocins that have not yet been identified in laboratories (Uniacke-Lowe et al., 2023).

The production of lantibiotics is mainly associated with Gram-positive non-pathogenic bacteria (Kashyap, 2019). But with advances in genetic analysis and the purification of compounds from community-acquired microbes, pathogenic species, e.g., *S. mutans*, *S. pyogenes*, and *S. aureus*, are also known to produce lantibiotics (Merritt and Qi, 2012; Biswas and Biswas, 2014; Kawada-Matsuo et al., 2016). To identify additional antimicrobial compound gene clusters, *S. aureus* was selected for analysis in this study, as four lantibiotics have already been reported to be produced by this pathogenic species (Daly et al., 2010).

When the genomes of more than 500 *S. aureus* strains were analyzed with antiSMASH Ver.7 a class I lanthipeptide gene cluster was present in 206 strains, along with other gene clusters for non-ribosomal peptide synthetase (NRPS), autoinducer, siderophore, metallophore, etc. Initially, the lanthipeptide was identified as hyicin 3682 by antiSMASH, as the number of genes in the cluster and their orientation matched almost identically. The prepeptide sequence was annotated as a gallidermin/nisin family lantibiotic (epiA) in both the antiSMASH and RefSeq databases. In this stage, the identified lanthipeptide was thought to be a variant of hyicin 3682, as their prepeptide sequences differ at 7 of 47 residues and at only 2 of 22 residues in the structural peptide. To be further confirmed, when the prepeptide sequence of the identified lanthipeptide was aligned with epidermin, Bsa (an epidermin variant), gallidermin, and nisin, it showed broad identity with Bsa. The results confirmed that the identified class I gene cluster encodes Bsa, which was isolated from a community-acquired *S. aureus* strain (Daly et al., 2010).

The 206 strains of *S. aureus*, in which the Bsa lantibiotic gene cluster was identified, possess 5 different types of arrangements of prepeptide-encoding genes. In contrast, the orientation of other

genes, i.e., modifying enzymes, protease, and immunity protein, remains the same (Fig. 6). In those 5 types of arrangements, prepeptide sequences of four Bsa variants, i.e., BsaA1, $BsaA1_{ET3-1}$, BsaA2, and $BsaA2_{ET3-1}$, were observed. These variants had previously been isolated from different strains of community-acquired *S. aureus* and show very little difference in their structural sequences (Daly et al., 2010). The presence of a transposase gene upstream and between the prepeptide genes indicates different arrangements of prepeptide genes, leading to further evolution of this cluster, and supports the non-production of Bsa by many *S. aureus* isolates despite containing loci that could be due to transposition of mobile DNA (Daly et al., 2010).

The similarity of the Bsa loci's genes has led to the annotation of hyicin 3682, an epidermin or gallidermin family lantibiotic. With the enrichment of microbial genomic data and the improvement of genome mining tools, it is now easier to analyze and annotate unrecognized genes that share identity or similarity with already identified and functional genes. This study further strengthens the effectiveness of genome mining and how it could identify genes encoding compounds of interest with minimal resources and time. Before targeting a microorganism to exploit its potential to synthesize novel compounds, genome sequencing followed by genome analysis would give indications of how that organism will respond during *in vitro* culture. This would surely lessen time and labor. However, this type of predictive analysis does not always guarantee *in vitro* production of antibiotics, as the cellular environment is full of dynamic molecules that can interfere with the production process, as well as genetic modifications.

The presence of the Bsa lantibiotic gene cluster in more than 206 *S. aureus* strains makes it a notable producer of lantibiotics. This might give these strains survival benefits over other closely related organisms. Production and purification are necessary to confirm whether these strains produce Bsa. *S. aureus*, a pathogenic species, has the potential to serve as a commercial producer of antimicrobial compounds.

Acknowledgment

The authors would like to acknowledge Department of Biochemistry and Molecular Biology, University of Dhaka and Department of Genetic Engineering and Biotechnology, University of Dhaka.

Authors contribution

Suvroto Kormokar: Conceptualization, experiment design, experiment conduction, result interpretation and writing draft. Md. Amzad Hossain: Conceptualization, experiment design, experiment conduction, result interpretation, writing draft, review and editing. M. Aftab Uddin: Conceptualization, writing draft, review and editing. Mohammad Riazul Islam: Conceptualization, experiment design, result interpretation, writing draft, review and editing.

Conflict of interest

The authors assert that the research was conducted without any commercial or financial links that could be perceived as a potential conflict of interest.

References

Alkassab D, Sampang J, Budhwani Z, Buragina JT, And Acedo JZ. Discovery of leaderless bacteriocins through genome mining. *Can. J. Chem.* 2024; 102: 533-543.

Allgaier H, Jung G, Werner RG, Schneider U and Zähner H. Elucidation of the structure of epidermin, a ribosomally synthesized, tetracyclic heterodetic polypeptide antibiotic. *Angew. Chemie Int. Ed. Engl.* 1985; 24: 1051-1053.

Arnison PG, Bibb MJ, Bierbaum G, Bowers AA, Bugni TS, Bulaj G, Camarero JA, Campopiano DJ, Challis GL, Clardy J, Cotter PD, Craik DJ, Dawson M, Dittmann E, Donadio S, Dorrestein PC, Entian KD, Fischbach MA, Garavelli JS, Göransson U, Gruber CW, Haft DH, Hemscheidt TK, Hertweck C, Hill C, Horswill AR, Jaspars M, Kelly WL, Klinman JP, Kuipers OP, Link AJ, Liu W, Marahiel MA,

Mitchell DA, Moll GN, Moore BS, Müller R, Nair SK, Nes IF, Norris GE, Olivera BM, Onaka H, Patchett ML, Piel J, Reaney MJT, Rebuffat S, Ross RP, Sahl H-G, Schmidt EW, Selsted ME, Severinov K, Shen B, Sivonen K, Smith L, Stein T, Süssmuth RD, Tagg JR, Tang G-L, Truman AW, Vederas JC, Walsh CT, Walton JD, Wenzel SC, Willey JM and van der Donk WA. Ribosomally synthesized and post-translationally modified peptide natural products: overview and recommendations for a universal nomenclature. *Nat. Prod. Rep* .2013; 30: 108-160.

Begley M, Cotter PD, Hill C and Ross RP. Identification of a novel two-peptide lantibiotic, lichenicidin, following rational genome mining for LanM proteins. *Appl. Environ. Microbiol.* 2009; 75: 5451-5460.

Biswas S and Biswas I. A conserved streptococcal membrane protein, lsrs, exhibits a receptor-like function for lantibiotics. *J. Bacteriol* .2014;196: 1578-1587.

Blin K, Shaw S, Augustijn HE. Reitz ZL, Biermann F, Alanjary M, Fetter A, Terlouw BR, Metcalf WW, Helfrich EJN, van Wezel GP, Medema MH and Weber T. antiSMASH 7.0: new and improved predictions for detection, regulation, chemical structures and visualisation. *Nucleic Acids Res.* 2023; 51: W46-W50.

Carlin FP, Nascimento de Sousa Santos I, Silva Francisco M, Mattos AlbanoR and do Carmo de Freire Bastos M. Genetic and biochemical characterization of hyicin 3682, the first bacteriocin reported for *Staphylococcus hyicus*. *Microbiol. Res.* 2017; 198: 36-46.

Cox C, Coburn P and Gilmore M. Enterococcal cytolysin: A novel two component peptide system that serves as a bacterial defense against eukaryotic and prokaryotic cells. *Curr. protein Pept. Sci.* 2005; 6: 77-84.

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 and Tagg JR. Production of the Bsa lantibiotic by community-acquired *Staphylococcus aureus* strains. *J. Bacteriol.* 2010; 192: 1131-1142.

Foulston L. Genome mining and prospects for 2019; 51: 1-8.

Kaletta C, Entian K-D, Kellner R, JungG, ReisM and Sahl HG. Pep5, a new lantibiotic: structural gene isolation and prepeptide sequence. *Arch. Microbiol.*1989;152: 16-19.

Kashyap DR. Microbial metabolites: peptides of diverse structure and function. In: *New and future developments in microbial biotechnology and bioengineering,* Gupta VK and Pandey A, eds., Elsevier, 2019; p. 87-101.

Kawada-Matsuo M, Shammi F, Oogai Y, Nakamura N, Sugai M and Komatsuzawa H. C55 bacteriocin produced by ETB-plasmid positive *Staphylococcus aureus* strains is a key factor for competition with *S. aureus* strains. *Microbiol. Immunol.* 2016; 60: 139-147.

Kellner R, Jung G, Horner T, Zähner H, Schnell N, Entian KD and Götz F.Gallidermin: a new lanthionine-containing polypeptide antibiotic. *Eur. J. Biochem.*1988; 177: 53-59.

Merritt J and Qi F. The mutacins of *Streptococcus mutans*: regulation and ecology. *Mol. Oral Microbiol.* 2012; 27: 57-69.

Navaratna MA, Sahl HG and Tagg JR. Two-component anti-*Staphylococcus aureus* lantibiotic activity produced by *Staphylococcus aureus* C55. *Appl. Environ. Microbiol.*1998; 64: 4803-4808.

O'Sullivan JN, O'Connor PM, Rea MC, O'Sullivan O, Walsh CJ, Healy B, Mathur H, Field D, Hill C and Ross RP. Nisin J, a novel natural nisin variant, is produced by *Staphylococcus capitis* sourced from the human skin microbiota. *J. Bacteriol.* 2020; 202(3): e00639-19.

Saikat TA, Sayem Khan MA, Islam MS, TasnimZ and Ahmed S. Characterization and genome mining of *Bacillus subtilis* BDSA1 isolated from

river water in Bangladesh: A promising bacterium with diverse biotechnological applications. *Heliyon*, 2024;10: e34369.

Schnell N, Engelke G, Augustin J, Rosenstein R, UngermannV, Götz F and Entian K-D. Analysis of genes involved in the biosynthesis of lantibiotic epidermin. *Eur. J. Biochem.*1992; 204: 57-68.

Scott J. Lantibiotic-mediated anti-lactobacillus activity of a vaginal *Staphylococcus aureus* isolate. *FEMS Microbiol. Lett.* 1992; 93: 97-102.

Singh M and Sareen D. Novel LanT associated lantibiotic clusters identified by genome database mining. *PLoS One*, 2014; 9: e91352.

Tamura K, Stecher G and Kumar S. MEGA11: Molecular evolutionary genetics analysis version 11. *Mol. Biol. Evol.* 2021; 38: 3022-3027.

Trmčić A, Samelis J, Monnet C, Rogelj I and Matijasic BB**.** Complete nisin A gene cluster from *Lactococcus lactis* M78 (HM219853) — obtaining the nucleic acid sequence and comparing it to other published nisin sequences. *Genes Genom.* 2011; 33: 217-221.

Uddin MA, Akter S, Ferdous M, Haidar B, Al Amin, Molla AHMSI, Khan H and Islam MR. A plant endophyte *Staphylococcus hominis* strain MBL_AB63 produces a novel lantibiotic, homicorcin and a position one variant. *Sci. Rep.* 2021; 11: 11211.

Uniacke-Lowe S, Collins FWJ, Hill C and Ross RP. Bioactivity screening and genomic analysis reveals deep-sea fish microbiome isolates as sources of novel antimicrobials. *Mar. Drugs*, 2023; 21: 444.

Valsesia G, Medaglia G, Held M, Minas W and Panke S. Circumventing the effect of product toxicity: development of a novel two-stage production process for the lantibiotic gallidermin. *Appl. Environ. Microbiol.* 2007; 73: 1635-1645.

van Heel AJ, de Jong A, Song C, Viel JH, Kok J and Kuipers OP. BAGEL4: a user-friendly web server to thoroughly mine RiPPs and bacteriocins. *Nucleic Acids Res.* 2018; 46: W278-W281.

van Staden ADP, van Zyl WF, Trindade M, Dicks LMT and Smith C. Therapeutic application of lantibiotics and other lanthipeptides: old and new findings. *Appl. Environ. Microbiol.* 2021; 87: e0018621.

Wang H, Fewer DP and Sivonen K. Genome mining demonstrates the widespread occurrence of gene clusters encoding bacteriocins in cyanobacteria. *PLoS One* 2011; 6: e22384.

Willey JM and van der Donk WA. Lantibiotics: peptides of diverse structure and function. *Annu. Rev. Microbiol.* 2007; 61: 477-501.

Wladyka B, Wielebska K, Wloka M, Bochenska O, Dubin G, Dubin A and Mak P. Isolation, biochemical characterization, and cloning of a bacteriocin from the poultry-associated *Staphylococcus aureus* strain CH-91. *Appl. Microbiol. Biotechnol.* 2013; 97: 7229-7239.