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Gene cluster for biosynthesis of thermophilin 1277 – a lantibiotic produced by Streptococcus thermophilus SBT1277, and heterologous expression of TepI, a novel immunity peptide

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Introduction

Lantibiotics are synthesized as precursor peptides and subsequently undergo post-translational modifications (Kupke and Gotz 1996). Lanthionine and β-methylthionine in these molecules are produced from the reaction of sulfhydryl groups of cysteine residues with dehydroalanine and dehydrobutyryl, after dehydration of serine and threonine residues, respectively. Jung (1991) divided the lantibiotics into two groups, type A (linear) and type B (globular), on the basis of their secondary structures. Sahl and Bierbaum (1998) further divided each group into three subgroups, the nisin (AI), lacticin 481 (AII) and lactococcin S (AIII) types, on the basis of the primary structural similarities of the peptides. Major lantibiotic gene clusters have been clarified, which include the structural gene (lanA), modification enzyme genes (lanB and lanC, or lanM), the secretion ABC-type transporter gene (lanT), the leader peptidase gene (lanP), self-protection (immunity) genes (lanFEG and lanI, or lanH) and regulatory genes (lanR and lanK). The gene cluster for nisin A is arranged in the sequence nisABTCPRKFG (McAuliffe et al. 2001).

Nisin A, an AI-type lantibiotic, is the most widely investigated, because it is the first found for bacteriocin and it is the only lantibiotic approved as a food preservative (Chatterjee et al. 2005). The successful application of
nisin as a safe food preservative has attracted much attention over the 50 countries (Delves-Broughton et al. 1996). So far, streptococcal lantibiotics have been reported in the oral cavities and upper respiratory tracts of humans and animals. However, they may also be isolated from almost any type of clinical specimen. Some examples include salivaricin A produced by Streptococcus salivaricus 20P3 (Ross et al. 1993), mutacin 1140 produced by Streptococcus mutans JH1000 (Hillman et al. 1998) and streptococcin SA-M49 produced by Streptococcus pyogenes (Hynes et al. 1994). Lantibiotic-producing oral streptococci is pathogenic; therefore, it is obvious that they cannot be used in foods. Streptococcus macedonicus ACA-DC 198, which was isolated from the cheese and nonpathogenic streptococcal species, produced a lantibiotic, macedocin (Papadelli et al. 2007).

There are numerous reports and reviews on LAB bacteriocins produced by lactococci, lactobacilli, pediococci, leuconostocs and enterococci; however, to date, only three class IIa bacteriocins produced by Streptococcus thermophilus strains have been cloned and sequenced – thermophilin 13 (produced by Strep. thermophilus Sfi 13) (Marciset et al. 1997), thermophilin A (produced by Strep. thermophilus ST134) (Ward and Somkuti 1995; Whitford et al. 2001) and thermophilin 9 (produced by Strep. thermophilus LMD-9) (Fontaine and Hols 2008). Furthermore, lantibiotics produced by Strep. thermophilus strains have never been reported. Streptococcus thermophilus is one of the most widely used bacteria in the manufacture of dairy products (yoghurt and cheese) and is considered to be a generally recognized as safe (GRAS) organism. Recently, the complete genome sequences of three Strep. thermophilus strains were published, and comparative genome analyses were performed (Hols et al. 2003; Bolotin et al. 2004). Comparative genomics and multiocic sequencing analyses suggest that this species is undergoing a process of regressive evolution, to adapt to growth in milk. While pathogenic streptococci are recognized for their high capacity to expose proteins at the cell surfaces to achieve cell adhesion or to escape host immune systems, Strep. thermophilus has lost these features, along with many virulence-related functions. These results are strongly suggestive of the safety status of Strep. thermophilus and the bacteriocins it produces.

Thermophilin 1277, produced by Strep. thermophilus SBT1277, is an AII-type lantibiotic, which contains two β-methylallantionines and a disulfide bridge. Thermophilin 1277 is identical in terms of primary amino acid sequence to bovicin HJ50 from Streptococcus bovis HJ50 (Xiao et al. 2004). Furthermore, the structural gene tepA has been cloned (Kabuki et al. 2009).

Here, we sequenced the biosynthesis gene cluster of thermophilin 1277 and examined the heterologous expression of a small hydrophobic immunity peptide, TepI, which shows no similarity to other lantibiotic accessory proteins.

**Materials and methods**

**Bacterial strains, plasmids and culture conditions**

The strains and plasmids used in this study are listed in Table 1. The bacteriocin-producing strain Strep. thermophilus SBT1277 was isolated from raw milk (Kabuki et al. 2007). All strains were maintained as frozen stocks at −80°C. M17 medium (Becton, Dickinson & Co., Sparks, MD, USA) with 0·5% (w/v) glucose (GM17) was routinely used for culturing Strep. thermophilus SBT1277 at 37°C, and Lactococcus lactis ssp. cremoris MG1363 at 30°C. To select and maintain transformants, erythromycin (Sigma, Tokyo, Japan) was used at a concentration of 5 μg ml⁻¹ in GM17 for L. lactis ssp. cremoris MG1363.

**Molecular cloning and nucleotide sequencing**

Molecular cloning techniques were performed as described by Sambrook et al. (1989). Chromosomal DNA was prepared using a previously reported method (Pospiech and Neumann 1995). PuReTaq Ready-To-Go PCR Beads (GE Health Bioscience, Tokyo, Japan) were used for the PCR, which was performed in a GeneAmp PCR System 9700 (PE Applied Biosystems, Tokyo, Japan) using standard PCR conditions. PCR products were purified using a QIAquick Spin Column (Qiagen, Tokyo, Japan). Plasmid extraction from L. lactis ssp. cremoris MG1363 was performed using a Plasmid Miniprep kit (Bio-Rad, Tokyo, Japan). DNA sequencing was performed by an industrial sequence commission (Hokkaido System Science, Sapporo, Japan). The nucleotide sequence surrounding tepA was determined by primer walking, using

**Table 1 Bacterial strains and plasmids used in this study**

<table>
<thead>
<tr>
<th>Strains and plasmids</th>
<th>Description</th>
<th>Source or reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Strains</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Strep. thermophilus</td>
<td>Thermophilin 1277 producer</td>
<td>SBT</td>
</tr>
<tr>
<td>SBT1277</td>
<td>Plasmid-free derivative of NCD0712</td>
<td>Gasson (1983)</td>
</tr>
<tr>
<td>Lactococcus lactis</td>
<td>Emr: pIL253 derivative with P32 promoter</td>
<td>Kemperman et al. (2003)</td>
</tr>
<tr>
<td>ssp. cremoris MG1363</td>
<td>Emr: pIL253-P32 derivative carrying tepA</td>
<td>This study</td>
</tr>
<tr>
<td>Plasmids</td>
<td></td>
<td></td>
</tr>
<tr>
<td>pIL253-P32</td>
<td></td>
<td></td>
</tr>
<tr>
<td>pTEPI</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
the total DNA of *Strep. thermophilus* SBT1277 as the template.

**Computer analysis**

Open reading frames (ORFs) were identified using an ORF finder (http://www.ncbi.nlm.nih.gov/gorf/gorf.html). Sequence similarity searches of nucleotide or protein sequences were performed using the BLAST program in the DDBJ databases. Transmembrane regions in peptides and proteins were deduced using the SOSUI program (http://bp.nuap.nagoya-u.ac.jp/sosiu/) (Hirokawa et al. 1998). G+C content was calculated using a web tool (http://www.bioinformatics.org/JaMBW/3/1/9/index.html).

Cloning of recombinant carrying putative immunity peptide for thermophilin 1277

The *tepI* region was amplified using PuReTaq Ready-To-Go PCR Beads (GE Health Bioscience) with the primers 5’CGCGGATCCTAGGGCTGAAAATGGGTTA3’ and 5’GCAGGACGTCCTCCCAATCGCTAAAGCTAC3’ (the BamHI and PstI sites were underlined in the primer sequences, respectively), and the genomic DNA of *Strep. thermophilus* SBT1277 was used as a template. After digestion of the PCR products with BamHI and PstI, the *tepI* fragment was ligated into pIL253-P32 and digested with the same restriction enzymes. The ligation mixture was used to transform pIL253-P32 into *L. lactis* ssp. *cremoris* MG1363, and the resultant plasmid was named pTEPI.

**Broth-based assay with recombinants of Lactococcus lactis ssp. cremoris**

Bacteriocin tolerance was assayed using the agar well diffusion methods (Kabuki et al. 2007), which are briefly described later. The GM17 culture supernatant of *Strep. thermophilus* SBT1277 containing thermophilin 1277 was serially diluted by the 50 mmol l⁻¹ sterile phosphate buffer (pH 6.8). The GM17 agar plate was overlaid with a soft agar lawn (15 ml), which was inoculated with the diluted overnight culture of each indicator strain at 1% (v/v). Wells, 6·88 mm in diameter, were cut from the plates, and 40 μl of serially diluted bacteriocin sample was added to each well. *Lactococcus lactis* ssp. *cremoris* MG1363, MG1363 (pIL253-P32) and MG1363 (pTEPI) were used as indicator strains. The diameters of the halos around wells of GM17 agar plates were measured after incubation at 30°C for 18 h. The experiments were performed in triplicate.

**Nucleotide sequence accession number**

The nucleotide and protein sequences of the thermophilin 1277 region have been assigned GenBank accession number AB434921.

**Results**

Cloning and sequencing of the gene cluster for thermophilin 1277 production

The nucleotide sequence of a 16 402-bp region flanking the structural gene of thermophilin 1277 (*tepA*) was determined using a primer-walking method. The G+C content (33%) of the total region was different from the average G+C content of *Strep. thermophilus* (39%) (Hols et al. 2003; Bolotin et al. 2004). Using computer analysis, 15 ORFs were detected; nine ORFs were designated *tepM*, *tepT*, *tepF*, *tepE*, *tepG*, *tepK*, *tepR*, *tepI* and *ORF4* in a 9-kb region containing *tepA*. The amino acid sequences of the seven *tep* gene (*tepAMTEGKR*) products among nine putative thermophilin 1277 biosynthesis genes show the highest similarity (98–100%) with those of the respective gene products of bovicin HJ50 produced by *Strep. bovis* HJ50 (Liu et al. 2009) (Fig. 1, Table 2).

TepM (837 amino acids), which is present downstream of *tepA*, showed 99% similarity to *bovM* (AC51935) of *Strep. bovis* HJ50. The gene clusters of AII- and AIII-type lantibiotics contain a *lanM* (-like) gene encoding 900–1000 amino acid residues, which has been proposed to be involved in post-translational modification of lantibiotics such as lactosin S and lacticin 481. The function of LanM for AII- and AIII-type lantibiotic is dehydration of amino acid length. Predicted promoters and a terminator are represented by angled arrows and an omega-like symbol, respectively.

![Figure 1](image_url) Comparison of the gene clusters for thermophilin 1277 and bovicin HJ50. The names of genes and a protein are shown with the amino acid length. Predicted promoters and a terminator are represented by angled arrows and an omega-like symbol, respectively.
acid and formed the thioether bridges in the molecule. On the other hand, the function of Lan C for AI-type lantibiotic is to form the thioether bridges in the molecule. Uguen et al. (2000) identified 11 and eight conserved domains (N1–11 and C1–8) in the N- and C-terminal parts of LanM containing those from lacticin 481 groups, respectively. The LanM and LanC gene products shared some structural motifs, such as GXAHG, WCXG and CHG, in which histidine and cysteine residues are well conserved. These motifs might have some relevance in the catalytic function of these enzymes (Paul et al. 2007). The N-terminal region of TepM showed homology between six conserved domains of LanM proteins (positions 222–261, 274–284, 350–372, 385–398, 437–459 and 467–495). The C-terminal regions of TepM showed high similarity to the five domain motifs (positions 547–558, 661–673, 703–715, 752–758 and 787–816) including the consensus sequences of GXAHG (position 662), WCXG (position 706) and CHG (position 753) of LanM and lanC, which are predicted to form a thioether bridge-forming enzyme for lantibiotics (Li et al. 2006; Li and van der Donk 2007; Zhang et al. 2007). These findings suggest that TepM catalyses the reaction of prelantibiotic post-translation modification, which results in the formation of $\beta$-methyllanthionine residues.

TepT (680 aa) is deduced to possess an N-terminal proteolytic domain for cleavage of the leader sequence from ORF1

<table>
<thead>
<tr>
<th>ORF</th>
<th>Length (amino acids)</th>
<th>Proposed function</th>
<th>Best homologue [identities (%), no. of amino acids], GenBank accession no.</th>
<th>Localization (TMS no)*</th>
<th>pl</th>
<th>Molecular weight (kDa)</th>
</tr>
</thead>
<tbody>
<tr>
<td>ORF1</td>
<td>347</td>
<td>Unknown</td>
<td>Helicase, Streptococcus equi ssp. zooepidemicus (95%, 2281 aa), YP002745281</td>
<td>Soluble (0)</td>
<td>5.30</td>
<td>41.0</td>
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<tr>
<td>ORF2</td>
<td>99</td>
<td>Unknown</td>
<td>Conserved domain protein, Streptococcus suis 89/1591 (88%, 99 aa), ZP03624205</td>
<td>Soluble (0)</td>
<td>4.15</td>
<td>12.0</td>
</tr>
<tr>
<td>ORF3</td>
<td>96</td>
<td>Unknown</td>
<td>Membrane protein, Strept. equi ssp. zooepidemicus (73%, 89 aa), YP002745279</td>
<td>Membrane (3)</td>
<td>6.07</td>
<td>10.9</td>
</tr>
<tr>
<td>tepA</td>
<td>58</td>
<td>Prethermophilin 1277</td>
<td>Bovicin HJ50, Streptococcus bovis HJ50 (100%, 58 aa), AAP23217</td>
<td>Soluble (0)</td>
<td>4.44</td>
<td>6.1</td>
</tr>
<tr>
<td>tepM</td>
<td>837</td>
<td>Post-translational modification</td>
<td>BovM, Strep. bovis HJ50 (99%, 837 aa), ACA51935</td>
<td>Soluble (0)</td>
<td>5.71</td>
<td>97.6</td>
</tr>
<tr>
<td>tepT</td>
<td>680</td>
<td>Processing and secretion ABC transporter.</td>
<td>BovT, Strep. bovis HJ50 (99%, 311 aa), ACA51936, BovE, Strep. bovis HJ50 (98%, 292 aa), ACA51937</td>
<td>Membrane (6)</td>
<td>8.38</td>
<td>77.3</td>
</tr>
<tr>
<td>tepF</td>
<td>302</td>
<td>Subunit of ABC transporter involved in immunity. ATP-binding protein</td>
<td>Lantibiotic transport ATP-binding protein, Strep. suis SC84 (63%, 304 aa), YP003024866</td>
<td>Soluble (0)</td>
<td>5.70</td>
<td>33.8</td>
</tr>
<tr>
<td>tepE</td>
<td>240</td>
<td>Subunit of ABC transporter involved in immunity. ATP transporter</td>
<td>Unknown, Strep. bovis HJ50 (98%, 240 aa), ACA51938</td>
<td>Membrane (7)</td>
<td>9.30</td>
<td>27.4</td>
</tr>
<tr>
<td>tepG</td>
<td>238</td>
<td>Subunit of ABC transporter involved in immunity. ATP transporter</td>
<td>Unknown, Strep. bovis HJ50 (98%, 238 aa), ACA51939</td>
<td>Membrane (6)</td>
<td>9.11</td>
<td>27.3</td>
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<tr>
<td>tepK</td>
<td>503</td>
<td>Histidine kinase</td>
<td>BovK, Strep. bovis HJ50 (99%, 503 aa), ACA1940</td>
<td>Membrane (8)</td>
<td>8.06</td>
<td>58.1</td>
</tr>
<tr>
<td>tepR</td>
<td>208</td>
<td>Response regulator</td>
<td>BovR, Strep. bovis HJ50 (98%, 198 aa), ACA1941</td>
<td>Soluble (0)</td>
<td>4.99</td>
<td>24.1</td>
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<tr>
<td>tepI</td>
<td>52</td>
<td>Immunity protein</td>
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<td>Membrane (2)</td>
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<tr>
<td>ORF4</td>
<td>161</td>
<td>Unknown</td>
<td>Sdb1, Strep. bovis HJ50 (100%, 161 aa), ACA1942</td>
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<tr>
<td>ORF5</td>
<td>216</td>
<td>Unknown</td>
<td>Unknown, Strep. bovis HJ50 (99%, 216 aa), ACA1943</td>
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<td>24.4</td>
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<tr>
<td>ORF6</td>
<td>362</td>
<td>Unknown</td>
<td>DNA primase. Strep. suis BM407 (78%, 358 aa), NP735785</td>
<td>Soluble (0)</td>
<td>5.97</td>
<td>41.7</td>
</tr>
</tbody>
</table>

* TMS, transmembrane segment number, deduced using the SOSUI program.

Table 2  Deduced peptides and proteins derived from tep
the prepeptide at the two conserved sequence motifs: QX4D/ECX2AX3MX3MX4Y/FGX4/L and HY/FY/VV-X10L/LXDP (Havarstein et al. 1995) at positions 10 and 88, respectively. TepT also contains an ATP-binding domain, with Walker A motifs, GXXGXXGK/(position 498), and Walker B motif, hhhhhDEP/A (l: a hydrophobic amino acids; positions 621) in a C-terminal domain (Fath and Kolter 1993). tepT has 99 and 98% similarity with bovT (ACAS1936) and bovE (ACAS1937) containing the conserved thioredoxin motif (CXXC). The formation of a disulfide bond in thermophilin 1277 might be related to the function of ORF4 (Sdb1). The ORF5 encoding 216 amino acid residues was 99% similarity to unknown protein from *Strep. bovis* HJ50. ORF5 and ORF6 (both downstream of ORF4), which had no similarity to protein by lantibiotic gene cluster reported, appeared to be unrelated to the biosynthesis of thermophilin 1277.

A putative promoter was located upstream of tepA (Kabuki et al. 2009). A deduced terminator was predicted to be present downstream of tepA. However, deduced terminator sequences were not found downstream of other regions related to bacteriocin synthesis. The G+C content of the area between ORF1 and ORF3 and that between tepA and orf4 was 39 and 29%, respectively. ORF4, which is downstream of the putative tep operon, contained 33% G+C. On the other hand, the downstream region of ORF4 exhibited 37% G+C content.

**Heterogenous expression of the putative immunity peptide for thermophilin 1277**

*In silico* analysis indicated that TepI – a novel hydrophobic peptide with the cationic region – is the immunity-like peptide for thermophilin 1277. Figure 2 shows the primary sequence and deduced transmembrane regions of the small immunity peptides for the lantibiotics. The peptides, TepI (for thermophilin 1277), EciI (for epicidin 280), PepI (for Pep5), LtnI (lacticin 3147) and NukI (nukacin ISK-1), ranging in size from 52 to 116 amino acid residues, have two or three transmembrane segments.

![Figure 2](image-url)
tepI was cloned downstream of the lactococcal P32 promoter in pIL253-P32, and heterologous expression of tepI from the resulting plasmid, pTEPI (Fig. 3), was examined in L. lactis ssp. cremoris MG1363. The recombinant strain, L. lactis ssp. cremoris MG1363 (pTEPI), was at least 1.3 times more resistant to the GM17 culture supernatant of Strep. thermophilus SBT1277 than the control strain carrying pIL253-P32 (Fig. 4).

Discussion

By sequencing the gene cluster containing the structural gene (tepA) for a lantibiotic, thermophilin 1277, a modification enzyme gene (tepM), an ABC transporter gene (tepT), self-protection genes (tepFEGI) and two-component regulation genes (tepRK) were deduced. These ORFs (except for tepI) are commonly found in the biosynthetic gene clusters of lacticin 481-type lantibiotics (Dufour et al. 2006).

Thermophilin 1277 is identical to bovicin HJ50 of Strep. bovis HJ50 in the structural genes. The biosynthetic gene cluster of bovicin HJ50 (c. 9.9 kbp) (Liu et al. 2009) contains at least 10 ORFs (bovA, M, T, E, F, ORF1, ORF2, K, R and ORF3) involved in biosynthesis, regulation and immunity, which correspond to each gene of tepAMTFEGRK-ORF4, except for tepI. However, the putative tepT product consisted of 680 aa, instead of 311 aa from the putative bovT product. This shows that TepT has both a proteolytic domain in its N-terminal and an ATP-binding domain in the C-terminal corresponding to BovT that has a proteolytic domain and BovE (292 aa) that has an ATP-binding domain, respectively. Based on the molecular size and estimated function difference between BovT and TepT, we conclude TepT may possess the activities of both BovT and BovE. TepF, E and G are the putative immunity genes corresponding to the deduced genes of bovicin HJ50, bovF, ORF1 and ORF2, respectively. TepI product has no similarity to other bacteriocin biosynthesis protein. As the homology analysis of orf5 and orf6 products show no similarity to the bacteriocin biosyntheses protein, these protein might be not involved with thermophilin 1277 expression.

Two immunity (self-protecting) systems for lantibiotics have been reported. The first consists of individual immunity proteins (generically termed LanI or LanH) that are located in the cytoplasmic membrane or at the surface and prevent interaction of bacteriocin(s) with the membrane. The other consists of the ABC transporters (usually composed of two or three subunits, generically termed (LanFE(G)), which actively export intracellularly accumulated bacteriocins to the outside (e.g., NisFEG). LanI (LanH) and LanFE(G) may act alone, or in combination, which results in cooperative functionality (Draper et al. 2008).

A LanI immunity system has been detected in some major lantibiotics, such as nisin (NisI, 245 residues), subtilin (Spal, 165 residues), Pep5 (Pepl, 69 residues), lactacin 3147 (LtnI, 116 residues), epicidin 280 (Ecil, 62 residues).
and cytolycin (Cyll, 327 residues) (Kuipers et al. 1993; Klein and Entian 1994; Qiao et al. 1995; Paik et al. 1998; McAuliffe et al. 2000; Stein et al. 2003, 2005; Hoffmann et al. 2004; Reis et al. 2004). NisI and SpaI are lipoproteins that are anchored in the cytoplasmic membrane by their lipid motifs; they capture lantibiotics to avoid bacteriocin action. LtnI contains a leucine zipper motif and three hydrophobic domains, which suggests that it is a transmembrane protein that forms homodimers (McAuliffe et al. 2000).

LanFEG is the only immunity system for the lacticin 481 families, such as lacticin 481 (Piard et al. 1992), mutacin II (Woodruff et al. 1998) and streptococcin A-FF22 (McLaughlin et al. 1999). Aso et al. (2005) reported a novel type of lantibiotic-binding peptide, NukH, which contributes to the immunity of nukacin ISK-1. NukH (92 aa) has three putative membrane-spanning domains (Fig. 4) and is similar to the LanI peptide for lacticin 3147. Together, the two immunity systems of NukH and NukFEG provide a much greater degree of immunity function than each system alone. NukH has been referred to as an accessory factor, which acts as an ancillary protein for the assembly of the functioning ABC transporter.

We demonstrated the heterologous expression of tepI with the P32 promoter in L. lactis ssp. cremoris MG1363. The recombinant strain is not completely resistant to thermophilin 1277, but is at least 1.3 times more resistant to thermophilin 1277 than the control strains carrying pIL253-P32. This result shows that the tepI product is an immunity peptide against thermophilin 1277 and might cooperate with the tepFEG products for full immunity function. This suggests that the immunity system of thermophilin 1277 slightly differs from that of bovicin HJ50.

The ORF4 downstream of tepI encodes a putative disulfide oxidase-like protein (161 aa). BlpGst of Strep. thermophilus LMD-9 (Fontaine and Hols 2008) and BdB of B. subtilis 168 (Dorenbos et al. 1998) have been reported to be disulfide oxidases involved in bacteriocin production. Bovicin HJ50, which is identical to thermophilin 1277 with regard to the primary amino acid structure, has a thiol-disulfide oxidoreductase gene in the bacteriocin loci (Liu et al. 2009). Gene disruption analysis showed that the thiol-disulfide oxidoreductase encoded by sdb1 is not involved in bovicin HJ50 biosynthesis. The inhibitory activity of the reduced form of bovicin HJ50 treated by dithiothreitol (DTT) neither decreased nor increased (Xiao et al. 2004). On the other hand, our previous result shows that the antimicrobial activity of thermophilin 1277 disappears after treatment with DTT. It can be speculated that ORF4 functions in the formation of intra- and/or intermolecular disulfide bridges between the cysteine residues of thermophilin 1277. The function of ORF4 products is being investigated.

The G+C content of tepAMTFEGRKI-ORF4 (29%) is lower than the average genome G+C content (c. 38%) of Strep. thermophilus (Hols et al. 2003; Bolotin et al. 2004). Horizontal gene transfer (HGT) can be defined as the exchange of genetic material between phylogenetically unrelated organisms (Jain et al. 2002). Mechanisms of intercellular DNA transfer include conjugation, phage transduction and transformation. HGT events can be detected using phylogenetic and compositional approaches. Information on the gene transfer mechanisms for genes, such as transposase- or phage-related genes found in the neighbourhood of the target genes, can improve the prediction of HGT events; there are many reports regarding the HGT events indicated. The operon of lacticin 481, which is 23% similar to thermophilin 1277, contains part of Tn5721 – a potentially mobile DNA sequence in a 70-kbp plasmid (Dufour et al. 2006). In contrast, no plasmids were detected in the strains of Streptococcus pyogenes and Streptococcus agalactiae producing streptococcin A-F22 and salivaricin A1 (45 and 42% similarity to thermophilin 1277, respectively). This indicates that the lantibiotic loci are chromosomal in these species (Wescombe et al. 2006). It should be noted that a transposase gene lies downstream of the streptococcin A-F22 gene cluster in Strep. pyogenes (McLaughlin et al. 1999), which might explain plasmid–chromosome and/or chromosome–plasmid exchanges. The other gene clusters of the lacticin 481 group are chromosomally located. Transposase genes have been found in the mutacin II cluster (Cheng et al. 1999), as well as between the macA and macR genes for macedocin (Papadelli et al. 2007). Consistently, the G+C content of the macedocin gene cluster (29.6%) is low compared to the average genome G+C content of Strep. macedonicus species (38%) (Papadelli et al. 2007). The surrounding region of the macedocin gene cluster is involved in the three putative mobilization elements: relaxase, transposase and resolvase; this suggests that Strep. macedonicus might be able to gain the macedocin genes by horizontal transfer of DNA from other organisms. These findings might indicate the possibility of horizontal transfer for the thermophilin 1277 gene cluster in Strep. thermophilus SBT1277.

Streptococcus thermophilus is of major importance to the food industry; it is the second most important industrial dairy starter after L. lactis (Hols et al. 2003). Streptococcus thermophilus SBT1277 is a food-grade GRAS microorganism, which is isolated from milk and is routinely used as a starter organism by various sectors of the food industry. The safety status of Strep. thermophilus SBT1277 will be of considerable advantage in the application of this bacteriocin-producing organism as a biopreservative.
References


