Influence of Amino Acid Substitutions in the Nisin Leader Peptide on Biosynthesis and Secretion of Nisin by Lactococcus lactis*

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Jan Roelof van der Meer, Harry S. Rollema, Roland J. Siezen, Marko M. Beerthuyzen, Oscar P. Kuipers, and Willem M. de Vos

From the Department of Biophysical Chemistry, NIZO, P. O. Box 20, 6710 BA Ede, The Netherlands

Structural genes for small lanthionine-containing antimicrobial peptides, known as lantibiotics, encode N-terminal leader sequences which are not present in the mature peptide, but are cleaved off at some stage in the maturation process. Leader sequences of the different lantibiotics share a number of identical amino acid residues, but they are clearly different from sec-dependent protein export signal sequences. We studied the role of the leader sequence of the lantibiotic nisin, which is produced and secreted by Lactococcus lactis, by creating site-directed mutations at various positions in the leader peptide sequence. Mutations at Arg-4 and Ala, but not at the conserved Pro-2, strongly affect the processing of the leader sequence and resulted in the extracellular accumulation of a biologically inactive precursor peptide. Amino acid analysis and 1H NMR studies indicated that the precursor peptide with an Ala-4 → Asp mutation contained a modified nisin structural part with the (mutated) unmodified leader sequence still attached to it. The Ala-4 → Asp precursor peptide could be activated in vitro by enzymatic cleavage with trypsin, liberating nisin. These results confirmed that cleavage of the leader peptide is the last step in nisin maturation and is necessary to generate a biologically active peptide. Several mutations, i.e. Pro-2 → Gly, Pro-2 → Val, Asp-7 → Ala, Lys-9 → Leu, Ser-10 → Ala/Val-11 → Asp/Val-12 → Glu in the leader peptide did not have any detectable effect on nisin production and secretion, although some of them affected highly conserved residues. When mutations were created in the 18 to 15 region of the nisin leader peptide (i.e. Phe-18 → Leu, Leu-18 → Lys, Asp-15 → Ala), no secretion or intracellular accumulation could be detected of nisin or its precursors. This suggested that these conserved residues are involved in the maturation process and may interact with lantibiotic-specific modifying enzymes.

The antimicrobial peptide nisin, which is produced and secreted by several strains of Lactococcus lactis, is a highly modified peptide with several characteristic features, such as dehydrated Ser and Thr residues (Dha and Dhb, respectively), and five intramolecular thioether ring structures called (β-methyl)lanthionine residues (Gross and Morell, 1971). Peptides with molecular structures similar to nisin have been found in several other Gram-positive bacteria, and together they have been named lantibiotics (Schnell et al., 1988; for a review see Jung, 1991). Nisin is ribosomally synthesized, and the primary translation product of 57 amino acids is presumed to undergo a number of modifications, catalyzed by specific enzymes, before finally being secreted into the extracellular medium in a bioactive form (Buchmann et al., 1988). The bioactive peptide nisin is composed of the 34 C-terminal amino acid residues of the primary translation product, which are modified in a sequence of events in which specific Ser and Thr residues become dehydrated to form dehydroalanine and dehydrobutyryl, which, in five cases, form intramolecular thioether bridges with the Cys residues present in this part of the precursor peptide (Fig. 1A). Intermediate precursor peptides in different stages of dehydration have been isolated from Staphylococcus epidermidis strains producing the lantibiotic Pep5, which suggested that sequential dehydration of Ser and Thr residues takes place as a first step in maturation (Weil et al., 1990).

Two natural variants of nisin have been found among lactococcal strains, which have been named nisin A (Gross and Morell, 1971) and nisin Z (Mulders et al., 1991; de Vos et al., 1993). The structural genes for both nisin A (nisA) (Buchmann et al., 1988; Kaletta and Entian, 1989; Dodd et al., 1990) and nisin Z (nisZ) (Mulders et al., 1991; de Vos et al., 1993) have been cloned and sequenced, and it was shown that the two mature peptides differ in only one amino acid residue (His27 in nisin A and Asp27 in nisin Z). In L. lactis NIZ O the production of nisin A is encoded by the 70-kilobase pair conjugative transposon Tn5276 (Rausch and de Vos, 1992). A recently cloned DNA fragment from Tn5276 was cloned from L. lactis R5, which contained the gene cluster nisABTCIPR (van der Meer et al., 1993, Kuipers et al., 1993a). The genes nisABTC have also been found in strain L. lactis 6F3 (Engelke et al., 1992), whereas the nisAB genes have been reported in L. lactis 11454 (Steen et al., 1991). It is assumed that NisF is involved in transport of (precursor) nisin across the cytoplasmic membrane, since it shares significant homology with ATP-dependent translocator proteins (Engelke et al., 1992; Kuipers et al., 1993a). It can be hypothesized that nisA and nisC encode the enzymes needed for modification of the lantibiotic precursor peptides (Steen et al., 1991; Engelke et al., 1992; Kuipers et al., 1993a). The nisI gene encodes a putative lipoprotein, which was shown to be involved in immunity to nisin (Kuipers et al., 1993a). The nisP gene was shown to encode a subtilisin-like serine protease, involved in cleavage of the leader peptide sequence from the final precursor peptide (van der Meer et al., 1993a).
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**Fig. 1.** A, primary translation product of the nisZ gene and schematic drawing of the primary structure of the mature nisin. The arrow in the primary translation product indicates the site for cleavage of the leader peptide from the structural region. Residues in the precursor nisin, which are dehydrated only, are dotted, whereas those residues which subsequently form lanthionine bridges are shaded. B, comparison of leader peptide sequences of nisin, subtilin, epidermin, and Pep5, as deduced from the gene sequences (Banerjee and Hansen, 1988; Buchmann et al., 1988; Kaletta et al., 1989; Schnell et al., 1988). Residues conserved in all four sequences are shown in black; residues with a conservative replacement or conserved in three out of four sequences are represented in dark grey; other less conserved sites or residues which are conserved but do not occur at identical positions in all sequences are drawn in light grey shading. The site of cleavage of the leader peptide from the mature peptide is indicated with an arrow.

Finally, nisR encodes a positive regulator protein needed for activation of expression of the nis genes (van der Meer et al., 1993).

Research on the structure/function relationships and on biosynthesis of nisin has mainly focused on the mature (active) nisin, and several features of the peptide have been proposed to be important for its biological activity. For instance, it was shown that an intact Dha residue is important for antimicrobial activity of nisin (Chan et al., 1989) and that changing the Dha residue at position 5 to a Dhb reduced the antimicrobial properties of nisin 2–10-fold depending on the indicator species (Kuipers et al., 1992). The lanthionine rings are assumed to be of critical importance to maintain the rigid structure of nisin to allow it to insert into the target membrane and form pores therein. In contrast to the function of nisin and the effect of different residues on the antimicrobial activity of nisin, little is known about the role of the leader peptide. The leader peptide is formed by the 23 N-terminal residues of the deduced primary translation product, but it does not undergo dehydration (van der Meer et al., 1993; Kuipers et al., 1993b), and it is absent in mature nisin (Fig. 1A). Leader peptides of different lantibiotics, such as nisin, subtilin, epidermin, and Pep5, exhibit a clear similarity in size and primary structure (Fig. 1B). This suggests a critical role of the leader in the process of lantibiotic maturation, which thus may be largely similar in the different lantibiotic producing strains. It has been proposed that the leader peptide is involved in the biosynthetic process (Jung, 1991) for instance (i) by functioning as a recognition or binding part of the molecule for the biosynthetic enzymes, (ii) by interacting with residues of the mature part to keep the molecule in a favorable conformation for the necessary enzymatic reactions and in this way preventing nonspecific modifications, (iii) by keeping the maturing peptide biologically inactive and thus contributing to immunity of the host cell, or (iv) by assisting transport of the precursor peptide across the cytoplasmic membrane.

Here we describe studies to determine the role of the nisin leader peptide sequence in the biosynthetic process of nisin maturation. We created site-directed mutations in conserved residues of the leader sequence to alter the nature of the original residue at that particular position. Some mutations in a region close to the cleavage site prevented the cleavage of the leader peptide from the final precursor. This precursor peptide was secreted into the extracellular medium by the mutant L. lactis cells and contained the mutated nisin leader peptide still attached to the fully matured nisin. This result showed that residues critical for leader cleavage and recognition by the leader protease are present in this part of the leader sequence. Another set of mutations, created in a strongly conserved region of different lantibiotic leader peptides, resulted in an almost complete blockade of nisin biosynthesis, without any detectable secretion or intracellular accumulation of precursors. This demonstrates that the leader peptide is indeed involved in nisin biosynthesis.
L. lactis wild-type and mutant strains were analyzed in the supernatant. For primer 4 we used a mixed synthesized oligonucleotide. Previously (Kuipers et al., 1993a), a transconjugant of the plasmid-free strain MG1614 containing a single copy of Tn5276 (Rauch and de Vos, 1992) and N29700, a derivative of N29700 in which the nisA gene has been exchanged by replacement recombinant with a modified nisA gene containing a 4-base pair deletion in the pronisin-encoding part and which is therefore no longer able to produce nisin A (Kuipers et al., 1993a). Lactococci were cultivated without aeration at 30 °C in M17 broth (Difco), supplemented with 0.5% (w/v) glucose or sucrose. When analyzed for nisin production, cells were grown in SPYS medium, containing 1% sucrose, 1% bactopepton (Difco), 1% yeast extract (Difco), 0.2% NaCl, 0.002% MgSO4·7H2O and 1% KH2PO4, pH 7.0. Bacterial Strains, Plasmids, Media, and Growth Conditions—L. lactis strains used in this study are: NIZO R5, harboring the nisin A gene (De Vuyst and Vandamme, 1992). For L. lactis strains harboring nisZ genes were cloned in expression plasmid pNZ9019 containing a modified nisA gene containing a 4-base pair deletion in the pronisin-encoding region and hybridization with a nisA gene probe were performed as described previously (van der Meer et al., 1992). The wild-type nisZ gene was taken from plasmid pNZ9013 (Kuipers et al., 1992), which contains a 280-base pair PstI-HindIII fragment, carrying the nisZ gene of L. lactis. Site-directed mutagenesis, DNA Techniques, and DNA Sequence Analysis—Site-directed mutagenesis of DNA sequences encoding the nisin leader peptide region involved a two-step polymerase chain reaction amplification and was performed as described above (Kuipers et al., 1991). Mutant polymerase chain reaction fragments were digested with PstI and HindIII and ligated with plasmid pNZ9019, previously digested with the same enzymes, and subsequently used to transform E. coli MC1061. E. coli transformants were analyzed for their plasmid DNA content, and the DNA sequence of the nisZ region was determined on the double-stranded plasmid DNA with the HindIII-primer (primer 2, see below) by a modified dideoxy chain termination method (Sanger et al., 1977) as described elsewhere (van der Meer et al., 1993). Plasmids carrying the proper mutation were then introduced by electroporation into L. lactis NZ29700 or NZ9800. Plasmid DNA content was subsequently isolated from chloramphenicol-resistant L. lactis transformants and analyzed on the restriction enzyme level.

To obtain site-directed mutations in the region of nisZ encoding the leader peptide, we used the primers listed in Table 1. Restriction enzymes and other DNA modifying enzymes were purchased from Life Technologies, Inc., or United States Biochemical Corp., and used as recommended by the manufacturer. DNA isolation, Northern blotting, and hybridization with a nicked gene probe were performed as described previously (Kuipers et al., 1993a).

Production, Purification, and Analysis of Nisin and Precursor Nisin Species—Production and secretion of nisin or nisin precursor species by L. lactis wild-type and mutant strains were analyzed in the supernatant of cultures grown to early stationary phase on SPYS medium (100 г/л) (10 ml). Cultures (20 ml) were centrifuged for 10 min at 6,000 × g to remove the lactococcal cells. The supernatant was subsequently filtrated over a 0.45-μm membrane, 0.10 volume of 100% (w/v) trichloroacetic acid was added, and the mixture was incubated on ice for 16 h to precipitate the protein fraction in the supernatant. The precipitate was then pelleted by centrifugation for 15 min at 6,000 × g and the supernatant removed. The pellet was redissolved in 400 μl of 50 mM sodium acetate, pH 5.5, and, when necessary, the pH was adjusted with NaOH to pH 5.5. The protein fraction was then analyzed for the presence of nisin by electrophoresis through 10% Tricine-SDS-PAGE gels (Schägger and Jagow, 1987), which were stained with silver nitrate, and further by examination on RP-HPLC to discriminate between nisin A and nisin Z (see below). Purified 6-kDa precursor of nisin A (van der Meer et al., 1993) was used as a standard on Tricine-SDS-PAGE gels. Large scale isolation of nisin species was performed from the supernatant of 10-liter cultures of L. lactis by chromatography on Fractogel TSK gel 650-S. Preparative RP-HPLC and lyophilization of the Ala4-Asp mutant nisin precursor were performed essentially as described previously (Kuipers et al., 1992), with an altered elution gradient of 5–27% buffer B in buffer A during 35 min at a flow rate of 10 ml·min⁻¹. N-terminal sequencing of precursor nisin species was performed at the Stichting Scheikundig Onderzoek in Nederland sequencing facility (Dr. R. Amons, Department of Medical Biochemistry, Sylvius Laboratory, Leiden, The Netherlands) by using an automated gas-phase sequencer (Applied Biosystems Inc, Foster City, Ca). A chemically synthesized nisin leader peptide was kindly provided by Dr. A. Beck-Sickinger of Tübingen University, Tübingen, Germany. Antibodies raised against nisin A and against the synthetic leader peptide were used for Western blotting as described previously (van der Meer et al., 1993).

Analysis of Nisin Species by HPLC—Nisin-containing samples were examined by analytical RP-HPLC, using a Hi Pore RP-318 column (Bio-Rad Laboratories Inc., Brussels, Belgium) at a temperature of 20 °C. Proteins were eluted using a linear gradient from 10 to 23% buffer B (90% aqueous acetonitrile, 0.07% trifluoroacetic acid) in buffer A (10% aqueous acetonitrile, 0.1% trifluoroacetic acid) during 10 min, followed by a 40-min linear gradient from 23 to 28% buffer B in buffer A, at a flow rate of 1.0 ml·min⁻¹. The absorbance of the effluent was monitored at 220 nm. NMR Experiments—1H NMR spectra were taken at 400.13 MHz on a Bruker AM400 spectrometer interfaced to an Aspect 3000 computer. Experimental conditions were: 1–2 mM protein, dissolved in 10% D,O, 90% H2O, pH 3.5, 25 °C. The solvent resonance was suppressed by presaturation. The spectra were referenced to external 3-(trimethylsilyl)-2,3,3-tetradesuteropropionic acid sodium salt (British Drug House).

RESULTS AND DISCUSSION

Effect of Site-specific Mutations in the Nisin Z Leader Peptide on Production and Secretion of Nisin—To analyze the role of specific residues in the leader peptide sequence on nisin biosynthesis, we created a number of site-specific mutations in the leader-encoding region of the nisZ gene, resulting in altered amino acid residues in the nisin Z leader peptide (Fig. 2). The mutations were chosen primarily at residues or motifs conserved among the four related antibiotic leader peptides (Fig. 1B) and generally applied in such a way that the nature of that particular residue would be altered drastically. Mutated nisZ genes were cloned in pNZ9019 and expression was established

| Table 1 | Primers used in this study |
|---|---|
| **Primers** | **Mutation** |
| Primer 1 | 5'-GATTAAATTCGCAATTTGGCTAG-3' |
| Primer 2 | 5'-CCTCTTACTGCAATTAGTAAAGTACG-3' |
| Primer 3 | 5'-GACTTACCCAAATTACAGTTATCCCC-3' |
| Primer 4 | 5'-CAAGCCATTACCAGCTACATAGTCCGAC-3' |
| Primer 5 | 5'-CAAGGACAGGATCTGCTGCCAC-3' |
| Primer 6 | 5'-CCGAAGAGGCTGCTGCACTGAC-3' |
| Primer 7 | 5'-GGCTTTCTGTTGAAGTCTGCAGGTGGTACC-3' |
| Primer 8 | 5'-GGCTTTCTGTTGAAGTCTGCAGGTGGTACC-3' |
| Primer 9 | 5'-GGCTTTCTGTTGAAGTCTGCAGGTGGTACC-3' |
| Primer 10 | 5'-GGCTTTCTGTTGAAGTCTGCAGGTGGTACC-3' |
| Primer 11 | 5'-GGCTTTCTGTTGAAGTCTGCAGGTGGTACC-3' |
| Primer 12 | 5'-GGCTTTCTGTTGAAGTCTGCAGGTGGTACC-3' |
| Primer 13 | 5'-GGCTTTCTGTTGAAGTCTGCAGGTGGTACC-3' |
in *L. lactis* strain NZ9700. This strain is a nisin A producer, but will simultaneously produce nisin Z when the *nisZ* gene is present on the expression plasmid pNZ9013 (Kuipers et al., 1992).

Production of nisin and its secretion into the extracellular medium by the different mutant strains was characterized first by analyzing the supernatant of late-log cultures on SDS-PAGE gels (Fig. 3, A and B). All mutants were found to produce and secrete peptides of approximately 3.5 and/or 6.0 kDa. Using SDS-PAGE it cannot be distinguished whether nisin A, nisin Z, or both are present in the 3.5-kDa band. By using HPLC we could detect the presence of nisin A and nisin Z separately in the culture supernatants of mutant strains, and we compared this to the production of nisin A and nisin Z by strain NZ9700 harboring pNZ9013 (*nisZ*). Changing the leader peptide sequence of nisin Z at several unique positions showed strong effects on the production and secretion of nisin Z (Fig. 2). Two mutant strains (carrying the leader mutations Arg→Gln and Ala→Asp) produced and secreted an extra peptide with an apparent molecular mass of 6 kDa on SDS-PAGE (Fig. 3A, lanes 1 and 4). On RP-HPLC the 6-kDa peptide appeared as an additional peak with a shorter retention time than nisin A and Z; a peak eluting at exactly the same position as nisin Z was observed in both cases, suggesting a slow processing of the secretion of nisin Z by the lactococcal cells, although differences in production levels of mutants were found in some cases, e.g. higher production of the Ser→Ala/Ser→Ala mutant (Fig. 4B) and lower production of Lys→Glu. It was unchanged that changing the highly conserved Pro residue at position -2 to a Gly or Val had no obvious effect on nisin Z biosynthesis or processing. The only effect we found was that strains with these mutations (Pro→Gly and Pro→Val), and with the Asp→Ala mutation in the leader peptide, showed a 2-fold slower growth on SPYS medium than did strain NZ9700 harboring pNZ9013. However, the final production and secretion levels of nisin A and of nisin Z in cells harvested at an A600 of 1.0 were not different (results not shown). In strains containing one of the following mutations, Ser→Leu, Asp→Ala, Leu→Lys and Phe→Leu in the leader peptide, the production of mutant Z, but not of nisin A, was drastically reduced or not detectable at all on HPLC. An example of the elution pattern of such a mutant (Phe→Leu), deficient in nisin Z production in strain NZ9700, is shown in Fig. 4B. When we screened the cytoplasmic protein fraction of these mutant strains (i.e. mutations at positions -18, -16, -15, or -6) for intermediate (mutant) precursor nisin peptides by Western blotting and immunological staining techniques with antibodies raised against the nisin leader peptide, we did not find any intracellular accumulation of precursor nisins, whereas in the case of wild-type *nisZ* expression in strain NZ9700, a 6-kDa precursor band was visible. Therefore, we...
which did not result in any detectable nisin Z production (Fig. 4A). Arrows mark changes was demonstrated by the Phe-I8 to Ile1, which is strongly conserved among the different leader sequences. The sensitivity of residues in this region even for relatively conservative hydrophobic interactions. The Ala4-Asp mutant was purified from the supernatant of strain producing the kg'-Gln mutant, it seems likely that this peptide is a precursor form of nisin Z, which results in the release of a peptide from the Ala4-Asp mutant nisin Z. These results indicated that the Ala4-Asp precursor peptide by Asp mutation was purified from the supernatant of 10-liter culture by hydrophobic interaction chromatography and RP-HPLC. The different peaks in the chromatogram of the Ala4-Asp mutant (Fig. 4A) were collected, lyophilized, and analyzed by SDS-PAGE (not shown). This confirmed that the major peak with a retention time of 23 min on analytical RP-HPLC (Fig. 4A) and 20 min on preparative RP-HPLC (Fig. 6) was a 6-kDa peptide species. About 10 mg of lyophilized peptide was obtained and further analyzed by N-terminal sequencing, collagenolytic activity, and by an in vitro enzymatic cleavage assay to determine the possible biological activity of this peptide. N-terminal sequencing gave the following sequence for the purified peptide: STKDFNLIDIVSISKDGDSPRI. This is identical to the primary sequence of the leader peptide deduced from the mutated nisZ gene, except for the absence of the N-terminal methionine, which is usually cleaved off in bacterial cells. This suggests that this peptide is a precursor form of nisin in which the leader sequence is still attached to the nisin part (in some stage of modification). The apparent molecular mass of 6 kDa is in good agreement with such a precursor nisin peptide of 56 amine acids. The N-terminal sequencing stopped after Ile1, indicating that Thr2 is converted to Dhb, which blocks further Edman degradation. The N-terminal analysis further showed that Ser and Thr residues in the leader peptide itself are not modified, as was found likewise for the leader peptides of Pep5 (Weil et al., 1990), of nisin A (van der Meer et al., 1993), and of subtilin, which had been fused to the pronisin part (Kuijpers et al., 1993b).

Comparison of the one-dimensional 1H NMR spectrum of the Ala4-Asp precursor peptide of nisin Z with that of wild-type nisin Z (Kuijpers et al., 1992) showed that the typical vinyl-proton resonances of the dehydrated residues of the mature nisin Z peptide (i.e. Dhb2, Dha3, and Dha5S) were also present in the Ala4-Asp precursor peptide (Fig. 5). This suggested that the nisin moiety of this peptide was at least partially modified in a proper way. Further preliminary results of two-dimensional 1H NMR experiments indicated that it is likely that the nisin part is completely matured with respect to dehydration and thioether bridge formation. A complete validation of the structure of the Ala4-Asp precursor peptide by two-dimensional 1H-NMR is in preparation. The Ala4-Asp precursor peptide, which itself showed no biological activity, could be activated to its bioactive form in vitro by incubation with trypsin. This should result in cleavage of the precursor at the same position after Arg-1 as occurs during normal maturation in vivo by the protease NisP (van der Meer et al., 1993). No cleavage by trypsin occurs in the nisin mature part under these conditions (van der Meer et al., 1993). Tryptic digestion resulted in the release of a peptide from the Ala4-Asp precursor with the same retention time on RP-HPLC as nisin Z (Fig. 6). When tested in a bioassay with Micrococcus flavus, this peptide had an antimicrobial activity comparable with nisin A and nisin Z, i.e. at least 200 times higher than that of the uncleaved Ala4-Asp precursor nisin Z. These results indicated that the 6-kDa peptide secreted by the Ala4-Asp mutant strain was very likely a precursor peptide of nisin Z, which had the leader peptide sequence still attached to the completely matured nisin Z moiety. Although no attempts were made in this study to isolate and purify the 6-kDa peptide from the strain producing the Arg1-Gln mutant, it seems likely that this peptide is also an uncleaved precursor form of nisin Z similar to that of the Ala4-Asp mutant. Interestingly, the mutation at the -1 position in the nisin leader peptide results in a Glu residue as also found at that position in the subtilin leader (Fig. 1B). The finding that the Arg1-Gln precursor peptide is not efficiently cleaved by the nisin leader protease shows that a clear difference in specificity exists between the
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FIG. 5. Low field region of the 400-MHz 1H NMR spectra of wild-type nisin Z (top) and Ala→Asp precursor nisin Z (bottom). Resonances of the relevant dehydrated residues are indicated in the nisin Z spectrum. Experimental conditions: 10% D2O, 90% H2O, pH 3.5, 25 °C.

FIG. 6. Preparative RP-HPLC elution profiles of the purified Ala→Asp nisin Z precursor peptide, before (trace B) and after (trace C) incubation with trypsin in vitro. The elution pattern of wild-type nisin Z is shown by trace A. The positions of the precursor peptide, the resulting nisin Z peptide, and wild-type nisin Z are indicated. The fraction eluting at 12.5 min probably represents a tryptic fragment of the Ala→Asp leader peptide and was not further analyzed.

leader proteases of the nisin and subtilin biosynthetic pathways. This is in accordance with the finding that a gene fusion between DNA encoding the leader of subtilin and the pronisin part also results in the production of a 6-kDa peptide in L. lactis NZ9700 (Kuipers et al., 1993b). Our results demonstrate that residues in this region of the leader peptide close to the cleavage site are important for recognition by the leader protease (NisP) which removes the leader peptide from the mature nisin
(see also below).

Production of Mature Nisin Is Essential for Nisin Biosynthesis—All the experiments to screen the different leader mutations described so far were carried out in _L. lactis_ strain NZ9700, which is a nisin A-producing strain that will simultaneously produce nisin Z when the _nisZ_ gene is introduced on a plasmid. The production of nisin A by this strain, however, makes analysis of the effect of mutations in the _nisZ_ gene more laborious and may perhaps lead in some cases to competition between precursor peptides of nisin A and nisin Z for available sites on the modifying enzymes. Therefore, we analyzed a number of the mutated _nisZ_ genes in _L. lactis_ strain NZ9800, a derivative of NZ9700 which carries a 4-base pair deletion in the chromosomal _nisA_ gene, but which is otherwise not affected in any of the other known _nis_ biosynthetic genes (Kuipers _et al._, 1993a). When plasmids containing the wild-type _nisZ_ gene (such as pNZ9013) were introduced into this strain, production of nisin _Z_ was established without any nisin A present in the extracellular medium (Kuipers _et al._, 1993a). However, when plasmids carrying _nisZ_ mutations were transformed into strain NZ9800, we found remarkable differences in production and secretion of nisin _Z_ or precursor nisin _Z_ when compared with strain NZ9700. Only those mutants of _nisZ_ that gave rise to production and secretion of mature nisin _Z_ in strain NZ9700 also did so in strain NZ9800 (e.g. _Asp_→_Ala_, Fig. 3C, _lane_ 7), whereas those that blocked nisin _Z_ production in strain NZ9700 (e.g. _Phe_→_Leu_18) likewise did so in strain NZ9800 (Fig. 3C, _lanes_ 5 and 6). In contrast, the two mutants of _nisZ_ which led to the production and secretion of precursor nisin _Z_ (e.g. _Arg_→_Gln_ and _Ala_→_Asp_ in strain NZ9700 did not do so in strain NZ9800 (Fig. 3C, _lanes_ 8 and 9). In these cases no intracellular accumulation of precursor peptides could be detected by Western blotting using anti-leader-peptide antibodies. To see whether the reason for the lack of production of some of the mutants was a blockade at the level of transcription of the mutant genes, RNA was isolated and Northern blotting was performed, followed by hybridization with a radiolabeled _nisA_ gene fragment. The results revealed that all mutant genes were transcribed, since in every case a typical transcript of about 340 nucleotides was visible. Taken together, these data suggest that a defined structural characteristic of the precursor peptide is required for completion of the biosynthetic process, possibly by activating transcription of biosynthetic genes downstream of _nisA_. In strain NZ9700 mature nisin _A_ and/or its wild-type leader peptide could fulfill this function of autoregulating its own biosynthesis and (mutant) nisin _Z_ biosynthesis. Whether this possible autoregulatory effect takes place on the level of transcription or at any later stage is not known yet, but we found recently that in strain NZ9800 transcription of the _nis_ operon is blocked in the absence of a functional _nisA_ gene in trans (Kuipers _et al._, 1993a).

**Cleavage of the Leader Peptide Sequence from the Nisin Precursor Peptide Is Not Necessary for Transport across the Cell Envelope**—The different enzymatic steps that lead to full maturation of nisin and other lantibiotics are not known in detail, although the final structural characteristics of the molecule (i.e. dehydrated residues, lanthionine rings) and the partial description of intermediates in the biosynthesis of Pep5 (Weil _et al._, 1990) have provided support for the different steps in the biosynthetic process that have been postulated (Schnell _et al._, 1988). The present study shows that mutation of 2 residues in the leader peptide of nisin _Z_, _Arg_→_Gln_ and _Ala_→_Asp_, leads to secretion of a precursor peptide that most likely contains a fully matured nisin structural part into the extracellular medium. This indicates that cleavage of the leader sequence from the precursor is the last step in nisin biosynthesis and that cleavage itself is not a prerequisite for transport of this peptide across the cytoplasmic membrane.

We have obtained further evidence that cleavage of the leader peptide sequence is actually taking place on the outside of the cell envelope. During exponential growth of strain NIZO R5, which produces wild-type nisin _A_, we detected increasing amounts of nisin _A_ in the supernatant, but during a short period of growth, a 6-kDa peptide was also detectable (Fig. 7A). This 6-kDa peptide reacted both with antibodies raised against nisin _A_ (Fig. 7B) and with antibodies against a chemically synthesized leader peptide of nisin _A_ (results not shown). Furthermore, when analyzed by RP-HPLC this 6-kDa peptide eluted with a retention time similar to the Ala→Asp precursor peptide, suggesting that it represents precursor nisin _A_ that has escaped proteolytic cleavage and activation. This wild-type nisin _A_ precursor peptide could be isolated in large amounts from the supernatant of _L. lactis_ cells which contained the cloned _nis_ biosynthetic gene cluster _nisABTCIR_, but which did not carry a functional _nisP_ gene for the leader protease (van der Meer _et al._, 1993). The nisin _A_ precursor peptide was also found to be biologically inactive, similar to the Ala→Asp precursor peptide of nisin _Z_, and could be activated by in vitro enzymatic cleavage of the leader peptide by either trypsin or NisP (van der Meer _et al._, 1993). In _vivo_, the cleavage is supposed to be carried out by the gene product of _nisP_, which is located distal from _nis_ on Tn5276 (van der Meer _et al._, 1993). The amino acid sequence of the encoded protease suggested it to be a secreted subtilisin-like serine protease that contains a C-terminal membrane anchor (van der Meer _et al._, 1993). Modeling studies of the active site and the substrate binding region of the NisP protease, with a precursor nisin as substrate, which were based on homologies with subtilisin and thermitase com-
plexed to inhibitors, suggested that the two mutations chosen at position -1 and -4 (i.e. $\text{Arg}^{-4} \rightarrow \text{Gln}$ and $\text{Ala}^{-4} \rightarrow \text{Asp}$) indeed reduced the possibility of the substrate to fit and interact in the substrate binding cleft (Siezen, 1993). Interestingly, these modeling studies also predicted that substitutions of the conserved $\text{Pro}^{-2}$ residue to a Gly or Val would not affect cleavage of the leader sequence by the protease.

What Is the Role of the Leader Peptide Sequence in the Biosynthetic Process?—Our results show that 2 residues in the region close to the cleavage site between the leader peptide and mature nisin are essential for recognition by the leader protease, i.e. $\text{Ala}^{-4}$ and $\text{Arg}^{-1}$, whereas the conserved $\text{Pro}^{-2}$ can be exchanged by a Gly or Val without apparent effects on processing. A further critical region, which is strongly conserved among leader peptides from different lantibiotics (Fig. 1B), is located at positions -18 to -15. Substitution of residues at positions -18, -16, and -15 in this region leads to a blockade of nisin $Z$ production, even when the changes introduced are relatively conservative (e.g. Phe to Leu), by an unknown mechanism. It could be that region -18 to -15 is important for recognition by modifying enzymes, such as the possible candidates NisB and NisC (Engelke et al., 1992; Kuipers et al., 1993a) and/or by the transport system. Although we did not detect substantial amounts of precursor nisin $Z$ species intracellularly in mutants which were impaired in nisin $Z$ biosynthesis, we cannot rule out the possibility that residues in the -18 to -15 region of the leader nisin are involved in transport. Except for one other mutation generated in the leader peptide (Ser$^{-4} \rightarrow$ Leu), the rest of the leader mutations did not have a detectable effect on nisin $Z$ biosynthesis. This means that the nature of the residues at these positions (-13 to -9, -7, and -2) is not critical for the biosynthetic process. It is obvious that the pro-region modification process of the nisin structural region, and what the trigger is for translocation of the matured precursor peptide. The mutation strategy employed here appears to be useful for the elucidation of the molecular interactions during these processes.

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