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Cloning and Characterization of the DNA Region Responsible for Megacin A-216 Production in *Bacillus megaterium* 216

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Megacins are bacteriocins produced by certain strains of the gram-positive spore-forming bacterium *Bacillus megaterium* (13, 17, 36, 39). Megacinogeny was first described in 1954 (17). It was observed that some cells in a growing culture of *B. megaterium* 216 spontaneously produced a substance that lysed cells of other *B. megaterium* strains but did not affect most other bacterial species. Production of this substance, later termed megacin A-216, is inducible by UV light (17), N-methyl-N′-nitro-N-nitrosoguanidine (28), or mitomycin C (23). Induction of megacin A-216 synthesis leads to lysis of the culture in 2 to 3 h (17). Cell-free supernatants of an induced culture of *B. megaterium* 216 kill sensitive cells even in 10^4-fold dilutions, whereas the producer strain 216 exhibits relative immunity to the bacteriocin (17). Like bacteriocins in general, megacin A-216 has a rather narrow antibacterial spectrum: besides *B. megaterium*, it is active against some strains of *Bacillus subtilis, Bacillus anthracis, Micrococcus aurantiacus*, and *M. cinnabareus* (17, 18, 28).

Many observations indicate that megacin A-216 acts by impairing the cell membrane integrity of sensitive bacteria. Microscopic pictures show that the cell content is partially released from the killed bacteria, while the cell wall appears to stay intact and the shape of the cells is retained (19). Megacin A-216 is active against protoplasts of megacin-sensitive strains (13, 28). In isosmotic medium, the cell material of the protoplasts becomes less dense after megacin treatment, but the cell contours remain visible for a long time. These observations suggest that megacin A-216 somehow damages the membrane permeability barrier but does not destroy the membrane completely. The bacteriocidal effect of megacin A-216 is inhibited by low temperature, suggesting involvement of enzymatic activity in megacin A-216 action (13).

Megacin A-216, first purified by Holland, was found to be an acidic protein precipitating around pH 4.0 (14). Later studies determined that it has a native molecular mass of ~66 kDa, contains two different subunits with molecular masses of 30 and 15 kDa, respectively, and displays phospholipase A2 (PLA2) activity (27, 28, 39).

A specific inhibitor of megacin A-216, purified from cultures of *B. megaterium* 216, was suggested to confer immunity to the self-produced bacteriocin. The partially purified substance, whose chemical nature was not identified, inhibited the toxic effect as well as the phospholipase activity of megacin A-216 (26).

After recognition of bacteriocin production in other *B. megaterium* strains, a classification of megacins was proposed (types A, B, and C). Based on its inducibility by a low level of UV irradiation or mitomycin C treatment, megacin A-216 was classified as type A (15). In a broader context, its physical properties and enzymatic activity place megacin A-216 in class III of bacteriocins produced by gram-positive bacteria (12, 20). There are only a few bacteriocins (megacin A-216, megacin
Megacin assay. Five-microliter aliquots of overnight cultures were pipetted and allowed to dry onto the surface of LB agar plates. After incubation at 30°C for 6 h, the plates were overlaid with LB-kanamycin soft agar (0.4 to 0.5%) containing 1/100 vol of a dense culture of the Km′ mutant of B. megaterium strain TH7 and incubated at 30°C overnight. Kanamycin was added to the soft agar to inhibit growth of the colonies tested. A clear zone surrounding the colony identified clones producing megacin.

To study UV light induction of megacin A-216 production, the agar plates with the dried test cultures were incubated at 30°C for 2 h and then irradiated with UV light (germicid lamp) for 15 s. After the UV treatment, the plates were returned to 30°C for 4 h and then megacin production was assayed as described above.

Immunity to megacin A-216 was estimated by titrating a cell-free lysate of a mitomycin C-induced B. megaterium 216 culture on the clone tested and, as a control, on the sensitive strain B. megaterium KM(pHY301). Five-microliter aliquots of serial dilutions of the lysate were pipetted onto the surface of a 3-mL soft agar layer containing 10 μL of a dense B. megaterium culture. After an overnight incubation at 30°C, the level of resistance was assessed by determining the highest dilution that caused a clear spot in the bacterial lawn. Under the conditions of the assay, the 10-fold dilution still caused lysis of the sensitive KM strain, whereas clones carrying the intact meg4 region were not affected even by the undiluted lysate.

Protein purification. Megacin A-216 was purified by a modification of methods described previously (14, 39). An overnight culture of B. megaterium 216 was diluted 1:100 into fresh LB medium. After shaking at 30°C for 2 h, mitomycin C was added to a concentration of 0.5 mM and shaking was continued for 3 to 4 h until lysis occurred.

All steps of purification were performed at 4°C. Cell debris was removed by centrifugation. Proteins were precipitated from the supernatant by adding ammonium sulfate to 80% saturation. The precipitated material was dissolved in PC buffer (20 mM sodium phosphate [pH 6.0], 10 mM 2-mercaptoethanol, 0.1 mM EDTA, 5% glycerol) and dialyzed against the same buffer. Proteins precipitated during dialysis were removed by centrifugation. The solution was treated with 2% streptomycin sulfate to remove nucleic acids. After centrifugation, the supernatant was dialyzed against PC buffer and loaded onto a DE52 (Whatman) anion-exchange column equilibrated with the same buffer. Proteins were eluted with a 0 to 0.5 M linear NaCl gradient in PC buffer. Fractions were assayed for megacin A-216 activity by titration on B. megaterium KM strain. Pooled active fractions were dialyzed against PC buffer and loaded onto a hydroxyapatite column equilibrated with PC buffer. Proteins were eluted with a 20 to 400 mM sodium phosphate (pH 6.0) gradient containing 10 mM 2-mercaptoethanol, 0.1 mM EDTA, and 5% glycerol. Peak megacin-containing fractions were pooled, and the protein was precipitated with ammonium sulfate (80% saturation). The precipitate was dissolved in a minimal volume of buffer S (20 mM sodium phosphate [pH 7.4], 150 mM NaCl, 10 mM 2-mercaptoethanol, 0.1 mM EDTA) and further purified by gel filtration on a Sephacryl S-200 column in buffer S.

Purified megacin preparations were dialyzed against PC buffer and stored at −80°C for several months with only slight loss of biological activity. Protein concentration was determined by the Bradford reaction, using Bio-Rad protein assay reagent with a bovine serum albumin calibration curve.

Estimation of native molecular weight by gel filtration. A sample of purified megacin A-216 (450 μL, 7.5 mg/mL) was loaded onto a 1-by-50-cm Sephacryl S-200 column in S buffer. Dextran blue 2000 was used for determination of the exclusion volume, and aldolase, bovine serum albumin, chymotrypsinogen A, and RNase A (with molecular masses of 158, 67, 25, and 13.7 kDa, respectively) were used for calibration.

Electrophoresis of proteins. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) of proteins was performed in 12% gels using Coomasie brilliant blue R-250 staining.

For electrophoresis under non-denaturing conditions, SDS and 2-mercaptoethanol were omitted. Megacin samples migrated toward the anode. Proteins were extracted from non-denaturing gels by electroelution. Gel pieces containing unstained bands were cut out using adjacent gel slices with stained megacin bands and prestained molecular weight markers as guide. Electrophoresis was performed in Little Blue Tank gel electroelution equipment (ISCO) using 1X Tris-glycine (25 mM Tris, 192 mM glycine [pH 8.3]) in the tank and 0.2X Tris-glycine in the sample-holding chamber. Two hundred volts (1 to 2 mA per sample holder) was applied for 7 h.

Molecular mass was prepared for MS by in-gel digestion (http://ms-facility.ucsf.edu/in-gel.html). Brieﬂy, disulﬁde bridges were reduced by dithiothreitol, and then the free Cys residues were alkylated by iodoacetamide. Samples were incubated with side-chain-protected porcine trypsin (Promega) for 4 h at 37°C. Unfractionated digests were analyzed on a Bruker Reflex III matrix-assisted
laser desorption ionization–time of flight (MALDI-TOF) mass spectrometer in reflection mode. One microliter of 10 μl of digest solution was loaded with 1 μl 2,5-dihydroxybenzoic acid solution (Sigma-Aldrich) as a matrix for the MS analysis. External calibration was applied. Post-source decay (PSD) analysis was performed in order to obtain sequence information for selected peptides.

Bioinformatic methods. DNA and protein sequence similarity searches were performed using the BLAST program package (1, 2), pairwise comparison of sequences by the BLAST 2 Sequences program (37), conserved domain searches by the CD-Search program (22), and PROSITE signature searches by the ScanProsite program (6). In all cases, default settings were used.

Nucleotide sequence accession number. Nucleotide sequence data have been deposited in GenBank under accession no. EU014074.

RESULTS

Cloning of the DNA region responsible for megacinogeny. Plasmid pBM309 carrying the genetic determinants of megacin A-216 production and immunity (32) was purified from B. megaterium AL, a strain harboring only this plasmid. We chose to clone the ∼10-kb PstI fragment, which, in a previous study (30), was shown to carry the megA genes. To obtain a plasmid shuttle vector with a unique PstI site, pHY300PLK (Ap r Tcr), originally developed as a B. subtilis-E. coli shuttle vector (16), was modified to yield pHY301, as described in Materials and Methods. PstI fragments of pBM309 were ligated to PstI-digested pHY301, and the ligated DNA was used to transform protoplasts of the plasmid-less B. megaterium THT strain. Transformed cells were regenerated in a tetracycline-containing batch culture. It was assumed that the acquired capacity of megacin A-216 production would endow clones carrying the megA genes with a very strong selective advantage. Restriction analysis of the plasmids purified from Tc + clones revealed that all contained the same ∼10-kb PstI fragment. One plasmid (pMGCl) was selected for further analysis. In the overlay assay, B. megaterium THT colonies harboring pMGCl produced a narrow clear zone around the colony, which became wider when the colonies were briefly exposed to UV irradiation; this indicated that the cloned PstI fragment contained the genetic elements associated with the MegA phenotypes (Fig. 1). Interestingly, pMGCl conferred the MegA’s phenotype also to E. coli ER1821 cells, although the zone of growth inhibition was smaller than around MegA’s B. megaterium colonies (not shown).

A 5.5-kb HindIII fragment of the pMGCl insert was sub-cloned in pHY301 to yield pMGCl3 and was subjected to further analysis.

Sequence analysis of the DNA region responsible for megacinogeny. The nucleotide sequence (5,494 bp) of the cloned HindIII fragment was determined (GenBank accession no. EU014074). Nine open reading frames (ORFs) starting with ATG, encoding a protein longer than 50 amino acids and nonoverlapping with other ORFs, were identified (Fig. 2 and Table 1). Translated sequences of all ORFs were used to search the GenBank database for similar amino acid sequences. Start and stop coordinates of the ORFs and results of the BLASTP search are listed in Table 1. Going from left to right on the map of Fig. 2, the translated product of ORF59 showed a medium level of similarity to a hypothetical protein of Bacillus cereus AH1134 and weaker similarity to a number of other hypothetical bacterial proteins in the database. The predicted protein (P91) encoded by the next ORF showed marginal sequence similarity to a single protein, a hypothetical protein of Enterococcus faecalis. Conceptual translation of ORF293A yielded a protein with moderate level of similarity to proteins with PLA2 activity. Moreover, the BLAST search identified conserved phospholipase domains (PLA2_plant, PLA2_bee_venom_like, Phospholip_A2_2, PLA2c, and PLA2_like) matching the C-terminal 30% of P293A. In the light of previous results demonstrating phospholipase activity of purified megacin A-216 (28, 39), detection of sequence similarity to proteins with phospholipase activity suggested that ORF293A is the gene encoding megacin A-216. P62, determined by the next ORF, showed very low level of similarity to hypothetical proteins from diverse sources and a medium level of similarity to a hypothetical protein of the taxonomically closely related B. thuringiensis. The neighboring gene (ORF85) encodes a protein with medium level of similarity to glutaredoxins and related proteins. The BLAST search also identified an NrdH conserved domain in P85. The predicted product of the next ORF (ORF293B) shares high sequence identity with a large number of serine proteases. The putative ORF188 product is very similar to bacterial RNA polymerase sigma factors containing the Sigma70_r4 conserved domain. The translational start point of P188 is somewhat ambiguous, because there is an in-frame ATG 9 bp upstream of the ATG at 3361. However, there is no appropriately positioned ribosomal binding site in
front of the upstream start codon; thus, ATG3361 (Table 1) is more likely to be the initiator codon for this protein. Hypothetical translation of the next ORF (ORF73) yields a protein displaying a low level of similarity to hypothetical proteins of different Bacillus species. Finally, the predicted ORF185 product is highly similar to several bacterial cell wall hydrolases with N-acetylmuramoyl-L-alanine amidase activity.

Gram-positive bacteria are characterized by strong ribosomal binding sites (24, 25, 31). Sequences located immediately upstream of the ORFs were screened for putative Shine-Dalgarno sequences. All ORFs have preceding sequences with similarity to consensus Bacillus ribosomal binding sites (34) and to a consensus sequence deduced from the 3' ends of B. megaterium 16S rRNAs (Table 2). The potentially strongest ribosomal binding sites (showing the highest similarity to the consensus sequence) were detected before ORF293A, ORF91, and ORF293B (Table 2). A consensus Shine-Dalgarno sequence was detected before ORF59, but the distance between the “core” GGAGG motif and the start codon is probably too long for efficient function (24, 25).

A BLASTN search identified a short, approximately 70-bp region, located between nucleotide positions 4279 and 4345, that shows strong similarity to tRNA_Cys genes of gram-positive bacteria. The highest sequence similarity (94%) was detected with the tRNA_Cys gene of Bacillus thuringiensis serovar konkukian strain 97-27 (NC_005957, positions 969811 to 969884) of the B. thuringiensis genome. An inverted repeat was found between nucleotides 4488 and 4521 (within ORF185).

The GC content of the sequenced region is 30.85%, lower than the average GC content of B. megaterium DNA (37%) (29) and lower than that of two B. megaterium plasmids, pBM300 (35.2%) and pBM400 (36.5%), whose sequences have become available recently (21, 34).

To our knowledge, transcription signals of B. megaterium have not been systematically analyzed, making promoter assignment difficult. A sequence resembling the B. subtilis sigma A promoter consensus sequence TTGACA (35), TATAAT (11), was found to precede ORF91.

**Functional mapping of the megA region.** Detection of a conserved PLA2 domain strongly suggested that ORF293A is the structural gene of megacin A-216. To corroborate this assignment and identify other genes that might play a role in megacin A-216 production and immunity, deletion derivatives of pMGC3 were constructed by removing restriction fragments or by subcloning fragments of the original HindIII insert in pHY301. The plasmids were constructed in E. coli and subsequently introduced into B. megaterium THT to test MegA production and immunity.
phenotypes. Extension of the deletions and their phenotypic effects are shown in Fig. 1 and 2.

With regard to megacin production, pMGC1 and its deletion derivatives can be classified into four types. (i) The B. megaterium THT clone harboring pMGC1 with the ~10-kb PstI insert produced a narrow zone of growth inhibition, which increased substantially upon UV light irradiation. This phenotype was similar to that of the parental B. megaterium 216 strain (Fig. 1). (ii) pMGC3 carrying the sequenced 5.5-kb HindIII fragment and its deletion derivatives (pMGC21, pMGC20, and pMGC23), in which only ORF293B or ORF185 was inactivated either alone or in combination, produced a wider inhibitory zone around uninduced colonies than pMGC1 (Fig. 1 and 2). The diameter of the inhibitory zone around UV-irradiated colonies was similar to that around induced colonies harboring pMGC1. The effect of UV light was especially evident when samples from young cultures were tested and the cells, dried onto the surface of the agar plate, were allowed to grow for only a short period of time (2 h) before the UV treatment. (iii) Clones belonging to the third class in some experiments produced a narrow clear zone around the colony. This was more often detected with pMGC6 and pMGC10, than with pMGC24, but the phenomenon was, in general, not reproducible. UV irradiation did not increase megacin production (Fig. 1). These plasmids (pMGC6, pMGC10, and pMGC24) carried shorter or larger deletions affecting several genes located on the 5.5-kb HindIII fragment, but ORF293A was always intact (Fig. 2). (iv) Clones categorized in the fourth class did not show megacin production. Some of the plasmids belonging to this class (pMGC26, pMGC17, and pMGC30) lacked intact ORF293A, while others (pMGC28, pMGC4, and pMGC29) had intact ORF293A but carried deletions affecting ORF73 and the tRNA2 gene (pMGC28, pMGC24, and pMGC29) (Fig. 2).

Megacin immunity was tested by a plate assay using a high-titer cell extract prepared from B. megaterium 216. A large deletion removing all ORFs but ORF91 and ORF59 (pMGC30) did not impair megacin immunity, whereas deletions inactivating ORF91 (pMGC24, pMGC17, and pMGC40) led to loss of megacin immunity, suggesting that the putative 91-amino-acid protein is responsible for the relative resistance of the producer strain to megacin A-216.

Analysis of the phenotypes of the deletion derivatives allowed us to test whether, in addition to ORF293A and ORF91, other genes have a role in megacinogony. The lack of phenotypic change associated with the deletion of ORF293B and ORF185 (see above) suggested that neither the putative protease nor the cell wall amidase plays a role in megacin production. A deletion extending into ORF188 led to severe reduction (pMGC6), whereas deletion of ORF73 and the tRNA2 gene alone (pMGC28), or in combination with ORF188 (pMGC4 and pMGC29), abolished megacin production. All deletions affecting ORF188 or ORF73/tRNA2 led to

---

### Table 1. Results of amino acid sequence similarity search with proteins encoded by the meg4 region^a^

<table>
<thead>
<tr>
<th>ORF no.</th>
<th>Start coordinate</th>
<th>Stop coordinate</th>
<th>Conserved domain with highest similarity^b^</th>
<th>Characteristic of protein with highest sequence similarity^c^</th>
</tr>
</thead>
<tbody>
<tr>
<td>59</td>
<td>259</td>
<td>80</td>
<td>None</td>
<td>Hypothetical protein</td>
</tr>
<tr>
<td>91</td>
<td>396</td>
<td>671</td>
<td>None</td>
<td>Hypothetical protein</td>
</tr>
<tr>
<td>293A</td>
<td>1593</td>
<td>712</td>
<td>PL22_plant</td>
<td>Hypothetical protein</td>
</tr>
<tr>
<td>62</td>
<td>1885</td>
<td>1807</td>
<td>None</td>
<td>Hypothetical protein</td>
</tr>
<tr>
<td>85</td>
<td>2145</td>
<td>1888</td>
<td>NrdH</td>
<td>Probable DNA-directed RNA polymerase sigma subunit FilA</td>
</tr>
<tr>
<td>293B</td>
<td>3158</td>
<td>2277</td>
<td>Peptidase_S8</td>
<td>Possible DNA-directed RNA polymerase sigma subunit FilA</td>
</tr>
<tr>
<td>188</td>
<td>3361</td>
<td>3927</td>
<td>Sigma70_r4</td>
<td>Bacillus thuringiensis serovar konkukian strain 97-27</td>
</tr>
<tr>
<td>73</td>
<td>3971</td>
<td>4192</td>
<td>None</td>
<td>Bacillus cereus AH1134</td>
</tr>
<tr>
<td>185</td>
<td>4381</td>
<td>4938</td>
<td>Amidase_3</td>
<td>Bacillus sp. strain SG-1</td>
</tr>
</tbody>
</table>

^a^ ORFs starting with ATG, longer than 50 amino acids, and nonoverlapping with other ORFs are shown. ORFs are identified by the number of the encoded amino acids and are listed in their order of location from left to right as shown on Fig. 2. Start and stop coordinates define nucleotide positions within the sequenced 5,494-bp fragment. Proteins encoded by ORF91 through ORF185 have GenBank identifiers ABS44966 through ABS44973.

^b^ Identified by BLAST search of the nonredundant protein database (March 2008).

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### Table 2. Putative ribosomal binding sites

<table>
<thead>
<tr>
<th>ORF no.</th>
<th>Shine-Dalgalno sequence^c^</th>
</tr>
</thead>
<tbody>
<tr>
<td>59</td>
<td>AAGGAGGTGATGTagcATG</td>
</tr>
<tr>
<td>91</td>
<td>GAGGAGGAGttttttAG</td>
</tr>
<tr>
<td>293A</td>
<td>atAGGAGGAGAaatATG</td>
</tr>
<tr>
<td>62</td>
<td>tttGAGTailaatATG</td>
</tr>
<tr>
<td>85</td>
<td>AagGttGaaGtttaATG</td>
</tr>
<tr>
<td>293B</td>
<td>gaaGAGGAGaGtaaatATG</td>
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<tr>
<td>188</td>
<td>AaAGGAGGAtaATggatATG</td>
</tr>
<tr>
<td>73</td>
<td>tggGAGGAGGaagatATG</td>
</tr>
<tr>
<td>185</td>
<td>agAAGGgtGaaagatATG</td>
</tr>
</tbody>
</table>

^c^ The ATG start codons are shown in boldface. Nucleotides matching the consensus B. megaterium sequence (5'-AAGGAGGTGATG) derived from two GenBank entries (DQ660362 and AY180964) for 16S rRNA are printed in capital letters.
loss of UV inducibility of megacin production. These observations point to the crucial role of the predicted sigma-factor-like protein (P188) in megacin expression and especially in high-level expression after UV treatment. ORF73 and/or the tRNA\textsubscript{Cys} gene seems to be even more important, because their inactivation had more drastic effect than deletion of ORF188. The available deletions did not allow separate testing of ORF73 and the tRNA\textsubscript{Cys} gene. Puzzlingly, pMGC10 and, in some assays, pMGC24, which lack both ORF188 and ORF73/tRNA\textsubscript{Cys}, showed signs of weak megacin production, but inducibility was lost also in these cases.

**Purification and analysis of the megacin A-216 protein in vitro.** DNA sequence analysis and deletion mapping described above identified a single gene (ORF293A) that encodes megacin A-216. This finding was surprising in the light of previous results, which showed the presence of two different subunits in purified megacin A-216 preparations (39). To address this question, megacin A-216 was purified from lysates of mitomycin C-induced cultures of B. megaterium 216 and B. megaterium THT(pMGC3). Estimations using the biological assay indicated that megacin activity in lysates of the native host was at the same level expression after UV treatment. ORF73 and/or the tRNA\textsubscript{Cys} gene seems to be even more important, because their inactivation had more drastic effect than deletion of ORF188. The available deletions did not allow separate testing of ORF73 and the tRNA\textsubscript{Cys} gene. Puzzlingly, pMGC10 and, in some assays, pMGC24, which lack both ORF188 and ORF73/tRNA\textsubscript{Cys}, showed signs of weak megacin production, but inducibility was lost also in these cases.

To study their relationship, unfraccionated trypsin-digested samples of the three proteins purified from the B. megaterium 216 lysate were subjected to MALDI-TOF MS analysis. Measured masses were compared with calculated masses of predicted tryptic peptides deduced from the sequences of ORF293A, -293B, -191(188), and -185. Peptides detected in the 30-kDa sample matched parts of the N-terminal half of the 293A sequence, whereas peptides of the 15-kDa sample matched the C-terminal part of P293A (Fig. 4). The unfraccionated trypsin-digested protein with the apparent molecular mass of ~40 kDa featured tryptic peptides characteristic for both shorter proteins. However, an abundant component with MH\textsuperscript{+} at m/z 2,501.7, not matching any predicted peptide, was detected only in the 15-kDa sample (Fig. 4). These data indicate that all three proteins of the purified megacin preparation are products of the same gene (ORF293A) and suggest that the α and β polypeptide chains are cleavage products of the full-length γ chain.

In the MALDI-TOF mass spectra of the trypsin digests of the 40- and 30-kDa protein, masses representing peptides [1-14] and [2-14] of P293A were detected, which indicated that the initiating methionine residue was posttranslationally excised from a fraction of the molecules. MALDI-TOF measurements yielded an average molecular mass of 11,832 Da for the intact β chain (data not shown). Assuming that the C terminus of the peptide was intact, this value suggested that the β chain starts at Val-186. The calculated mass for the 108-amino-acid polypeptide beginning with Val-186 and ending with Met-293 is 11,855, which differs only by 0.2% from the experimental value. The predicted MH\textsuperscript{+} (VKLVPVPCFNSTGCCTFSN NGK) of the unique tryptic peptide (m/z 2,501.7, with carbamidomethyl Cys) was indeed detected in the trypsin-digested tryptic chain. Its identity was confirmed by PSD analysis of the peptide (Fig. 5). These data indicated that the α and β polypeptides were products of proteolytic cleavage between Gln-185 and Val-186 of the full-length γ chain.

The calculated molecular masses (32,855, 21,018, and 11,855 Da for the γ, α, and β chains, respectively) are lower than the values derived from SDS-PAGE (~40, ~30, and ~15 kDa, respectively). There are no signs of posttranslational modifications other than the removal of the N-terminal methionine. Analysis of the amino acid sequence shows that megacin A-216 is a hydrophilic molecule and that the γ chain probably consists of two different domains, with their boundary at the hypothetical cleavage site between the α and β chains. The α chain is rich in acidic residues, resulting in a calculated pI of 3.92, while the β chain contains many Lys and Arg residues and has a theoretical pI of 9.05.

The native molecular weight of megacin A-216 was estimated by gel filtration on a Sephacryl S-200 column. Megacin A-216 eluted in fractions corresponding to 66 to 68 kDa (not shown), which is in accordance with earlier estimates (39). To test the composition of native megacin, purified megacin was electrophoresed in a 12% polyacrylamide gel under nondenaturing and nonreducing conditions. Two major bands, a more intense, slow-moving band and a less intense, fast-moving band, were detected (Fig. 6A, lanes 1 and 2). Proteins from both bands were electroeluted and analyzed by SDS-PAGE (Fig. 6B). The upper (slow) band contained all three chains detected in the purified megacin preparation, whereas the

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**FIG. 3.** Purification of megacin A-216 from B. megaterium THT (pMGC3) and B. megaterium 216. Shown are the results of SDS gel electrophoresis of protein samples obtained in different stages of purification. M, molecular mass markers (Fermentas); lane 1, lysate; lane 2, after DEAE-cellulose and Sephacryl-S 200 chromatography; lane 3, lysate; lane 4, after ammonium sulfate precipitation, streptomycin-sulfate precipitation of nucleic acids, and dialysis; lane 5, after DEAE-cellulose chromatography; lane 6, after hydroxyapatite chromatography.
lower band contained only the α chain. In biological activity tests, only the sample extracted from the slow band had megacin activity. If 2-mercaptoethanol was added to megacin samples prior to electrophoresis in the nondenaturing gel, the slow band disappeared (Fig. 6A, lanes 3 and 4), suggesting that native megacin contains intrachain disulfide bonds characteristic for phospholipase 2 enzymes, and these bonds may be important for maintaining its structure. The α chain does not contain Cys residues, which can explain why reduction did not have a big effect on its mobility. The β chain, dissociated by 2-mercaptoethanol treatment from the rest of the megacin molecule, probably did not enter the gel because its pI is higher (9.05) than the pH of the gel buffer. It is less clear why the γ chain disappeared after treatment with the reducing agent. A possible explanation is that disruption of the disulfide bonds yielded a heterogeneous population of molecules with different

FIG. 4. MALDI-TOF MS spectra of the unfractionated tryptic digests of 40-kDa (a), 30-kDa (b), and 15-kDa (c) proteins. Peptides confirmed by PSD analysis are labeled with asterisks. Mass of the predicted N-terminal peptide is underlined.
similar to those observed with the parental primary clone carrying the recombinant plasmid pMGC1 were types (megacin production and effect of UV irradiation) of the involved in megacin A-216 production and immunity. Present work was the cloning and characterization of the genes strain (14, 17, 19, 28, 30, 32, 39–41). The main goal of the phenomenon of megacin A-216 production and location of the inhibited a wider inhibitory zone around noninduced colonies. It 5,494-bp HindIII subfragment of the original 10 kb insert ex-

B. megaterium strain (Fig. 1). The B. megaterium strain (14, 28).

Previous studies described several aspects of megacinogeny in the B. megaterium strain, including the microbiological phenomenon of megacin A-216 production and location of the megA genes on one of the large plasmids present in the host strain (14, 17, 19, 28, 30, 32, 39–41). The main goal of the present work was the cloning and characterization of the genes involved in megacin A-216 production and immunity. Phenotypes (megacin production and effect of UV irradiation) of the primary clone carrying the recombinant plasmid pMGC1 were similar to those observed with the parental B. megaterium strain (Fig. 1). The B. megaterium clone (pMGC3) carrying the 5,494-bp HindIII subfragment of the original 10 kb insert exhibited a wider inhibitory zone around noninduced colonies. It remains to be determined whether this difference is due to a gene present on the PstI fragment but missing from the shorter HindIII fragment or to the higher copy number of pMGC3. The observation that both pMGC1 and pMGC3 expressed megacin also in E. coli supports the interpretation that all genes playing a role in megacinogeny are present on the HindIII fragment. An ORF encoding a 293-amino-acid protein (ORF293A) was identified as the gene encoding megacin A-216. This assignment was based on three lines of evidence: (i) deletion mapping, which showed that deletion of ORF293A invariably resulted in a MegA− phenotype; (ii) amino acid sequence similarity between the protein encoded by ORF293A and several known proteins with PLA2 activity; and (iii) MS analysis of tryptic peptides obtained from purified megacin A-216.

Megacin preparations purified from B. megaterium 216 contained two main proteins with apparent molecular masses of 30 and 15 kDa and a copurifying 40-kDa protein. These results were in accordance with previous observations (39). MS analysis proved that all three polypeptides are encoded by ORF293A and that there is a precursor-product relationship between them. The largest protein (termed γ chain) is the full-length product of ORF293A, whereas the shorter α and β chains appear to be products of proteolytic cleavage between Gln-185 and Val-186 of the γ chain. The calculated molecular masses of the γ, α, and β chains (32,855, 21,018, and 11,855 Da, respectively) are substantially lower than the values deduced from electrophoretic mobility in denaturing gels. The likely reason of the anomalous migration, at least in the cases of the α and γ chains, is the highly acidic composition (pI 3.92 and 4.51, respectively).

Our purified megacin preparations contained all three chains. The α and β subunits were always present in approximately equal amounts, whereas the amount of the γ chain was variable. In preparations purified from the parental strain B. megaterium 216, the two shorter chains were more abundant, whereas preparations purified from B. megaterium THT(pMGC3) were dominated by the γ chain (Fig. 3). Biologically active megacin ran in one band in native polyacrylamide gel and contained all three chains. The most likely interpretation of these results is that the full-length protein, as well as the cleavage products, can form active megacin A-216. The native molecular mass of megacin A-216 estimated by gel filtration (∼66 kDa) is consistent with an αβγ, αβγ, or γ composition. The hypothetical protease cleaving the primary product has not been identified. It also remains to be determined what role the protease cleavage has in megacin A-216 activity. Preliminary observations suggest that the specific activity of megacin purified from B. megaterium 216 is higher than that of megacin purified from B. megaterium THT(pMGC3), suggesting that the specific protease cleavage leads to an increase in specific activity.

In the C-terminal third of P293A, approximately corresponding to the β chain, a PLA2 domain was predicted by conserved domain search. A PLA2 catalytic motif, CCCnHDkC, was recognized by PROSITE search. The predicted PLA2 domain, with the presence of all conserved catalytic residues, is in agreement with the PLA2 activity measured in megacin A-216 preparations (28, 39) and with observations showing that megacin A-216 interferes with membrane integrity (13, 19, 28). A calcium-binding motif characteristic for Ca-dependent phospholipases or a signal sequence character-
istic for secreted phospholipases has not been detected in the megacin A-216 sequence.

BLAST searches of nonredundant databases of all organisms yielded proteins with low-level similarities to megacin A-216. Most of them were phospholipases or hypothetical proteins, and the similarities were mostly restricted to the C-terminal region of P293A, where the PLA2 domain is located.

This is the first case, to our knowledge, in which the sequence of a bacterial PLA2 with antibacterial activity has become known. It is known that some eukaryotic PLA2 enzymes display bactericidal activity. Also, there are bacterial PLA2 proteins that have a role in virulence (prophage-associated Sla protein in *Streptococcus pyogenes* strains and ExoU in *Pseudomonas* strains) (see the references in reference 35). In bacteria, only a few proteins with PLA2 activity have been found so far. Recently, many hypothetical protein sequences in bacterial genome projects have been predicted to contain the PLA2 domain. However, the arrangements of these genes are different in *B. megaterium* and in *B. thuringiensis*. Comparison of the two genomic regions suggests that this group of genes probably moved via lateral transfer between the two species and later evolved by recombination events.

Deletion mapping of the cloned fragment also identified the gene responsible for megacin immunity. This gene (ORF91 [*megA*]), located adjacent to the *megA* gene, encodes a short, 91-amino-acid protein. The viability of cells harboring pMGC24, which has the megacin gene (ORF293A) but lacks the immunity gene (ORF91), is somewhat surprising and probably indicates the very low level of megacin expression in the absence of ORF188 and ORF73 (see below). Previous studies found in *B. megaterium* 216 a specific inhibitor of megacin A-216, which inhibited both the bacteriocidic action and the phospholipase activity and which was suggested to mediate immunity to megacin A-216 (26). Although Ochi et al. did not determine whether the inhibitory substance was a protein, we assume that it was identical to P91. The sequence of the ribosomal binding site preceding ORF91 is more similar to the consensus than that of ORF293A (Table 2), suggesting that the immunity protein is expressed at higher level than megacin A-216.

Although the original goal of this work was cloning and characterization of the *megA* and *megA*~imm~ genes, deletion mapping revealed that at least two of three other genes located on the cloned 5.5-kb fragment are also essential for megacin production (Fig. 1 and 2). Of the three adjacent genes, the role of ORF188 and ORF73 (see below) is required for efficient expression and induction of megacin A-216. ORF188 and ORF73 are preceded by good ribosomal binding sites (especially ORF73 [Table 2]), suggesting that both encode proteins. The predicted P188 protein shares very high sequence similarity with some sigma factors of gram-positive bacteria; thus, its role might be the modification of RNA polymerase initiation specificity, leading to transcription of the megacin gene. The weak similarity detected between P73 and a few, mostly hypothetical, bacterial proteins does not allow a similar prediction for its function. Although ORF73 is more likely to be required for megacin expression than the tRNA<sup>Cys</sup> gene, the role of the latter gene cannot be excluded, given the high Cys content (14/293) of the megacin A-216 protein. In this context, it is worth mentioning that the subtle phenotypic difference observed between pMGC10, which usually produced some growth inhibition around the colony, and pMGC29, which always tested negative, suggests that the glutaredoxin-like P85 might also have some role in megacin A-216 expression. It is tempting to speculate that this effect relates to
the putative disulfide reductase activity of PS5 and the large number of cysteines in the megacin protein.

A sequence (AAAAAAGTTGGCATTTGGACACTTTTCTTT) resembling rho-independent transcriptional terminators (?) was found downstream of ORF73, between positions 4191 and 4226. The lack of a similar sequence between ORF188 and ORF73 suggests that the two genes might form an operon. Studies focusing on the genetic background of megacinogenic plasmid pHY300PLK and some properties in relation to transformation. Jpn. J. Genet. 61:515–528.

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