Ribosome-controlled transcription termination is essential for the production of antibiotic microcin C

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ABSTRACT

Microcin C (McC) is a peptide–nucleotide antibiotic produced by Escherichia coli cells harboring a plasmid-borne operon mccABCDE. The heptapeptide MccA is converted into McC by adenylation catalyzed by the MccB enzyme. Since MccA is a substrate for MccB, a mechanism that regulates the MccA/MccB ratio likely exists. Here, we show that transcription from a promoter located upstream of mccA directs the synthesis of two transcripts: a short highly abundant transcript containing the mccA ORF and a longer minor transcript containing mccA and downstream ORFs. The short transcript is generated when RNA polymerase terminates transcription at an intrinsic terminator located in the intergenic region between mccA and mccB genes. The function of this terminator is strongly attenuated by upstream mcc sequences. Attenuation is relieved and transcription termination is induced when ribosome binds to the mccA ORF. Ribosome binding also makes the mccA RNA exceptionally stable. Together, these two effects—ribosome-induced transcription termination and stabilization of the message—account for very high abundance of the mccA transcript that is essential for McC production. The general scheme appears to be evolutionary conserved as ribosome-induced transcription termination also occurs in a homologous operon from Helicobacter pylori.

INTRODUCTION

Microcins are a group of peptide antibiotics synthesized by enterobacteria (1). These compounds are produced under stress conditions and are effective against bacteria closely related to the producing strain. As a group, microcins are characterized by their small size (<10 kDa) and synthesis by ribosomes. The mechanisms of toxicity and targets vary for different microcins. While some microcins depolarize the cell membrane (2), others act on intracellular targets. For instance, microcin B targets DNA gyrase (3), microcin J targets the DNA-dependent RNA polymerase (4), while microcin C targets aspartyl-tRNA synthetase (5). Microcins acting on intracellular targets are extensively posttranslationally modified and have unusual chemical structures (6).

Typically, microcin gene clusters are located on plasmids and contain genes coding for microcin precursor peptide, self-immunity proteins and modification enzymes (7). Microcin C (McC), the smallest microcin known, is produced by Escherichia coli cells harboring a plasmid-borne gene cluster mccABCDE (Figure 1A). Mature McC (Mw = 1178 Da) is a heptapeptide with covalently attached C-terminal adenosine monophosphate and a propylamine group attached to the phosphate (Figure 1B). McC enters susceptible E. coli cells through the YejABEF inner-membrane transporter (8). Inside the cell, the peptide part is processed by intracellular aminopeptidases (9) to release processed McC—a non-hydrolysable analog of aspartyl-adenylate, which specifically inhibits aspartyl-tRNA synthetase (Asp-RS), leading to cessation of translation (5).

The product of mccA, the first gene of the McC biosynthesis operon, is a heptapeptide MRTGNAN that is converted into biologically active McC maturation intermedi-
ate in an adenylation reaction catalyzed by the MccB enzyme (10–11). Aminopropylation of the product of MccB-catalyzed reaction requires MccD and MccE and increases the biological activity ca. 10-fold (11). MccE is also responsible for detoxification of processed McC that accumulates in the producing cell (12). The mccC gene encodes a pump that exports produced McC and its maturation intermediate and also renders the producing cells resistant to external McC (13).

The transcription of the mcc operon initiates from a CAP (catabolite activator protein)-dependent promoter located upstream of the mccA gene when the producer enters stationary phase or is nutrient deprived (14,15). Since both the mccA transcript, which codes for precursor peptide substrate, and the mccB transcript, which codes for the MccA peptide adenylation enzyme, are produced from the same promoter, there is likely a mechanism that regulates the substrate (MccA) to enzyme (MccB) ratio, so that a necessary level of McC production is achieved. In this work we uncover two mechanisms responsible for preferential synthesis of MccA compared to other products of the mcc operon. First, an intrinsic transcription terminator located between the mccA and mccB leads to the production of excess of monocistronic mccA transcripts. The function of this terminator requires ribosome binding to the mccA ORF. Second, ribosome binding leads to dramatic stabilization of the monocistronic mccA transcript. Together, these two effects lead to ca. 20-fold overproduction of mccA mRNA compared to mccB mRNA, so that a sufficiently high amount of substrate for McC synthesizing enzyme is achieved.

**MATERIALS AND METHODS**

**Bacterial strains and DNA**

*E. coli* strain BW25113 K-12 (16) was used if not indicated otherwise. *E. coli* BL21(DE3) was used as a sensitive strain for McC sensitivity tests. The pp70 plasmid is pBR322-based and bears a ∼6000 bp DNA fragment with the mcc gene cluster. To create pp70, a BstXI-AraLI fragment of plasmid pBM43 (17) was ligated in the EcoRI-AvaI fragment of the pBAD vector (Life Technologies). Both the vector and the insert were blunt ended before the ligation. The pp70 derivatives carrying mccA ATG¹→TTA or Shine–Dalgarno ATAGGAGG→CCCTACTT (SD) mutations, as well as plasmid pp70Δ51 lacking nucleotides +59/+109 (the mcc transcription start is designated as +1) from the mccA–mccB intergenic region, were constructed by site-specific mutagenesis of pp70.

To create pFD_mcc_dir and pFD_mcc_rev plasmids, two pairs of oligonucleotides were annealed to yield two ds-DNA fragments containing, in direct either inverted orientation, the mcc terminator hairpin along with 7 bp upstream and 13 bp downstream DNA flanked by AvaI (upstream) and EcoRV (downstream). The mcc part of resulting double-stranded DNA fragments corresponded to positions +71/+114 with respect to the mcc transcription start point. These fragments were ligated in the AvaI-EcoRV fragment of the pFD100 plasmid (18), between the lacUV5 promoter and the galK gene. To test galK gene expression, *E. coli* HB101 cells (ATCC33694) lacking functional galK gene were transformed with pFD-derivatives and streaked on McConkey indicator medium containing 1% galactose. The results were recorded after an overnight growth at 37°C.
RNA purification and differential RNA-seq

An aliquot of overnight culture was diluted hundred times with LB containing 100 µg/ml carbenicillin and grown for 4 h at 37°C until OD600 reached 2.0. Cells from 0.5 to 3 ml culture aliquots were collected by centrifugation, the supernatant was discarded, and cell pellets frozen in liquid nitrogen and stored at −70°C until further use. Cell pellets were resuspended in 30–50 µl of 20 mM Tris-HCl, pH 8.0, 1 mM EDTA, treated with 10 mg/ml lysozyme, mixed with 500 µl of TRIzol reagent (Invitrogen) and incubated for 5 min at room temperature. Hundred microliter of chloroform was added next and the samples were incubated for 15 min on ice until phase separation occurred. After 15-min centrifugation at 13,000×g the aqueous phase (~300 µl) was transferred to a fresh tube. RNA was ethanol precipitated and then redissolved in 20–50 µl of DEPC-treated water. RNA concentration was determined using the NanoDrop spectrophotometer.

For whole transcriptome analysis by differential RNA-seq (dRNA-seq) (19) total RNA samples purified as described above were treated with DNase I (New England Biolabs) according to manufacturer’s protocol to remove residual DNA from the samples. For depletion of processed transcripts, RNA was treated with Terminator™ 5’-phosphate-dependent exonuclease (TEX) (Epicentre) as previously described (19). cDNA libraries were constructed by vertis Biotechnology AG, Germany as described in (19). Sequencing of cDNA libraries was performed on an Illumina HiSeq2000 machine. In total, 1.8–2.4 million cDNA reads for each cDNA library were sequenced. The reads were mapped to the pp70 plasmid sequence. For data visualization, graphs representing the number of mapped reads per nucleotide were calculated and visualized using the Integrated Genome Browser (IGB) version 6.5.3 software from Affymetrix (http://genoviz.sourceforge.net/). The whole transcriptome dataset as well as further details of read mapping and sequencing statistics will be published elsewhere.

Northern blot hybridization

The RNA samples were diluted to a final concentration of 0.25 µg/µl with formamide loading buffer (95% formamide, 0.025% xylene cyanol, 0.025% bromophenol blue), and 1 µg of RNA was loaded on a 10% (19:1) denaturing polyacrylamide gel. After separation at 10W for 15–20 min, RNA was electroblotted to Hybond XL membrane. After thawing on ice, samples were centrifuged for 5 min at 5000xg and RNA was purified as described above.

In vivo transcript stability measurements

Cells were grown as described above. After 4 h of growth, 100 µg/µl rifampicin was added and growth was continued. Five hundred microliter culture aliquots were taken before and 2, 5, 10 and 20 min after rifampicin addition. Samples were immediately mixed with 100 µl stop solution (95% ethanol, 5% phenol) and snap-frozen in liquid nitrogen. After thawing on ice, samples were centrifuged for 5 min at 5000xg and RNA was purified as described above.

Estimation of in vivo termination efficiency

The monocistronic transcript (that we here denote A after mecA) and the polycistronic transcript (that we denote B after mecB) are generated from the same promoter, and their transcription rate is denoted as \( \varphi \). Change of concentration for the two transcripts with time can be described by the following equations:

\[
\frac{dA}{dt} = \varphi - k_A A
\]

\[
\frac{dB}{dt} = \varphi (1 - k) - \lambda_B B
\]

In the equations above, A and B are the concentration of the transcripts. \( k \) is the termination efficiency, which is defined as the ratio between the initiated transcripts that are terminated, and the total number of initiated transcripts (note that \( k < 1 \)). \( \lambda_A \) and \( \lambda_B \) are, respectively, the decay rates of transcripts A and B. Consequently, the first terms on the right-hand sides of the equations describe the transcript generation, while the second terms describe the decay of the transcript concentration. In the steady state, we have \( dA/dt = 0 \) and \( dB/dt = 0 \), and by solving the two equations above for \( k \) we obtain:

\[
k = \frac{1}{1 + \frac{\lambda_B}{\lambda_A} \frac{B}{A}}
\]

Furthermore, the decay rate \( \lambda \) and the half-life are related by \( \lambda = \ln(2)/T \), where \( T \) is transcript half-life time, so that:

\[
k = \frac{1}{1 + \frac{\lambda_B}{\lambda_A} \frac{B}{A}}
\]

Primer extension reactions

1–6 µg RNA was reverse-transcribed using MuMLV reverse transcriptase (Invitrogen) according to manufacturer’s instructions. Briefly, primers were annealed to RNA for 10 min at 65°C followed by transfer on ice. MuMLV reverse transcriptase was added to make up a total volume of 10 µl and a final MuMLV concentration of 10 u/µl in 1x reaction buffer (50 mM Tris-HCl, pH 8.3, 75 mM KC1, 3 mM MgCl2, 10 mM DTT); reactions were allowed to proceed at 37°C for 55 min. Reactions were terminated by the addition of an equal volume of formamide loading buffer and loaded on 8% denaturing polyacrylamide gel.
**5′-RACE**

Twenty microgram of total RNA was treated with DNase I (New England Biolabs) according to manufacturer’s instructions. To half of the sample (10 μg) five units of TAP (Tobacco Acid Pyrophosphatase, Epicentre) (+TAP reaction) was added. An equal amount of water was added instead of enzyme to another half, making control-TAP reaction. Reactions were incubated for 1 h at 37°C in 25 μl reaction volume in the presence of 20 units of RNaseOUT (Invitrogen). RNA was next phenol/chloroform extracted and ethanol precipitated. The pellet was resuspended in 50 μl ligation buffer (50 mM Tris-HCl pH 7.5, 10 mM MgCl₂, 1 mM DTT) with 120 units of T4 RNA ligase I (New England Biolabs) and 50 pmoles of RNA primer (5′ GGUAU-UCCGGUACCCUUUGUACGC 3′), and ligation was performed overnight at 16°C. Following phenol/chloroform extraction and ethanol precipitation, the RNA/primer pellet was resuspended in 10 μl of water, heated at 65°C for 10 min and immediately transferred on ice. The cDNA synthesis was carried out with 100 units of Super Script III from the First-Strand Synthesis System for RT-PCR (Invitrogen) according to manufacturer’s instructions for 50 min at 55°C using a primer complementary to the beginning of mccB gene. Two microliter aliquots of cDNA synthesis reactions were used as templates for PCR (for one primer was identical to RNA primer, another was complementary to the beginning of the mccB gene). PCR products were resolved on 2%/agarose gels. Amplified fragments of expected length were excised from the gel and cloned into the pT7Blue cloning vector from the pT7Blue Perfectly Blunt Cloning Kit (Novagen). Inserts in several recombinant plasmids were sequenced using standard T7-promoter oligonucleotide primer. The 5′ ends of transcripts were determined by the position of the junction site between the sequence corresponding to the RNA primer and mcc sequences.

**3′-RACE**

Ten microgram of total RNA was mixed with 40 pmol of 5′ pre-adenylated DNA-adapter (New England Biolabs) and 200 units of truncated T4 RNA ligase 2 (New England Biolabs) in 50 mM Tris-HCl, pH 7.5, 10 mM MgCl₂, 1 mM DTT, 10% PEG. Reactions proceeded at 25°C for 1 h and were terminated by incubation at 60°C for 25 min. Five microliter of reaction mixtures was used as templates for cDNA strand synthesis with 100 units SuperScript III reverse transcriptase (Invitrogen) according to the manufacturer’s protocol using 1 pmoles of primer complementary to the DNA adapter. Two microliter of reverse transcription reactions was used as a template for PCR amplification (one primer was complementary to the DNA adapter, another to the template strand of the mccA gene). The product of PCR amplification was cloned directly to the pGEM-T easy vector (Promega) using pGEM-T easy PCR ligation kit (Promega) according to the manufacturer’s protocol. Plasmids from insert-positive clones were purified and insert sequences were determined.

**In vitro transcription**

Promoter complexes were allowed to form for 10 min at 37°C in 10 μl reactions containing 40 mM Tris-HCl, pH 8.0, 40 mM KCl, 10 mM MgCl₂, 100 nM E. coli RNA polymerase σ⁷₀ holoenzyme (Epicentre) and 10 nM DNA templates. Reactions were supplemented with 10 μM CpApUpCp, 25 μM ATP and GTP, and 0.33 μM α⁻³²P-CTP (3000 Ci/mmole) and stalled elongation complexes were allowed to form for 5 min 37°C and reactions were diluted 10-fold with a chase mix that resulted in the final concentrations of 500 mM KCl, 2.5 μM of ATP and GTP, and 10 μM of UTP and CTP. Reactions were incubated for 15 min at 25°C and terminated by the addition of formamide loading buffer.

For chase reactions coupled with in vitro translation, stalled elongation complexes were formed as described above except that 50 mM NaCl was used instead of KCl. Stalled elongation complexes were diluted 10-fold with in vitro translation mix (In Vitro Protein Synthesis, ΔRibosome, or Δ(aa, rRNA) PURExpress kit, New England Biolabs) and reactions were allowed to proceed for 15 min at 25°C. Reaction volume was made up to 100 μl with ASE buffer (0.3 M NaAc, 0.5% SDS, 5 mM EDTA, pH5.3) and reactions were extracted twice with acid phenol/chloroform, precipitated with ethanol and dissolved in formamide loading buffer.

For single-round in vitro transcription promoter complexes were allowed to form for 10 min at 37°C in 10 μl reactions containing 40 mM Tris-HCl, pH 8.0, 40 mM KCl, 10 mM MgCl₂, 100 nM E. coli RNA polymerase σ⁷₀ holoenzyme (Epicentre) and 10 nM DNA templates. Reactions were supplemented with 50 μg/ml heparin, 100 μM ATP, 100 μM GTP, 100 μM UTP, 10 μM CTP and 0.33 μM α⁻³²P-CTP (3000 Ci/mmole). Reactions were incubated for 15 min at 37°C to allow single-round RNA synthesis and terminated by addition of 10 μl formamide loading buffer.

**Isolation of ribosomal fractions**

Cells were resuspended in 25 mM Tris, pH 8.0, 60 mM KCl, 10 mM MgCl₂, 20% sucrose and lysed by five cycles of freezing in liquid nitrogen—thawing at 37°C. The suspension was next diluted 4-fold by the same buffer and supplemented with 0.5% Brij58, 10 u/ml DNase I, 0.15% deoxycholic acid and 3 mM MgSO₄. The suspension was incubated on ice for 30 min and cell debris was pelleted by 30-min centrifugation at 30,000xg. The lysate was loaded onto a 10–40% sucrose gradient (in 25 mM Tris, pH 7.8, 50 mM KCl, 10 mM MgCl₂, 3 mM DTT) and centrifuged for 16 h at 18,000 rpm in SW38Ti rotor. Fractions were collected by dripping from percolated bottom of centrifuge tube.

**Toeprinting**

The mcc RNA (+1/+146 with respect to the natural transcription start site) was transcribed in vitro using T7 High Yield RNA Synthesis Kit (New England Biolabs) and an appropriate DNA template generated by PCR, and purified with RNA Clean&Concentrator 25 kit (ZymoResearch).

One pmol of purified in vitro transcribed mcc RNA was mixed in a total volume of 5 μl, with 2 pmoles of
RESULTS

An abundant short mccA transcript is required for McC production

To get an overview of the mccABCDE operon transcription, total RNA was prepared from E. coli cells harboring the McC-production plasmid. Cells were grown in LB broth to late exponential phase, a condition, when the culture was actively synthesizing McC (14) and data not shown. Total RNA was purified from a culture aliquot and subjected to the differential RNA-seq (dRNA-seq) procedure that allows one to identify the 5’ ends of transcripts (19). During dRNA-seq, half of the RNA sample is subjected to TAP treatment prior to library construction, while another half is treated with 5’-phosphate-dependent exonuclease (TEX), an enzyme that destroys RNA molecules containing 5’-monophosphates, followed by TAP treatment and library construction. Sequencing reads present in libraries prepared from TEX treated RNA (+TEX) are enriched with sequences whose 5’ ends correspond to transcription initiation start points, while the TAP-only (−TEX) treated samples contain reads corresponding to both transcription initiation start points and exo- and endonucleolytic processing/degradation events. The results of dRNA-seq analysis for RNAs synthesized from the mcc operon are shown in Figure 2A. As can be seen, at conditions of McC production high coverage corresponding to the beginning of the mcc operon was observed in the −TEX library. Coverage was decreased ca. 30-fold in samples treated with TEX. The location of 5’ ends of these reads corresponds to the published location of the start point of Pmcc, a CAP-cAMP-dependent promoter located upstream of mccABCDE (14,15). Inspection of Figure 2A also reveals the apparent absence of other strong transcription initiation points within the mccABCDE operon, indicating that transcription from Pmcc is primarily responsible for operon expression at conditions tested. Several potential minor start points within the mccB and mccE gene are apparent. These start points are not preceded by recognizable promoter consensus elements and their significance is unknown. The mRNAs initiated from these hypothetical start points do not contain full-sized mccB ORF and so can have no influence on the MccA/MccB ratio in the producing cell, which is the subject of this study.

Northern-blotting analysis using an oligonucleotide complementary to the mccA ORF was also performed. A prominent ~100 nt long RNA was present in McC-producing cells (Figure 2B, left, top panel, lane 1) but not in control cells lacking the mcc plasmid (data not shown). This RNA was also not detected in cells harboring an mcc plasmid with a deletion that removed the putative terminator in the intergenic region between the mccA and mccB genes (Figure 2B, left, top panel, lane 2). The amount of control transcript from plasmid-borne bla gene was unaltered by the deletion (Figure 2B, left, bottom panel, compare lanes 1 and 2).

The 5’ and 3’ ends of the mccA RNA were identified using RACE. A single 5’ end located 29 nt upstream of the mccA ATG codon was detected, coinciding with the previously reported Pmcc start point (15) and dRNA-seq data (above).
The 3′ ends of the mccA transcripts mapped to three consecutive adenine residues downstream of the stem-loop formed by the putative intergenic transcription terminator hairpin. Thus, the size of the short mccA transcript is \(~105–107\) nt. It contains the entire mccA ORF as well as a 52–54-nt 3′ untranslated region.

To monitor the polycistronic (mccA and downstream genes) mcc transcript, primer extension reactions with a primer annealing in the mccB gene were performed. A single primer extension product was observed (Figure 2B, left, middle panel, lane 1) and its 5′ end matched the transcription start point of the monocistronic mccA transcript (data not shown). The amount of polycistronic transcript appears to be unchanged in cells harboring a plasmid with deletion of the putative terminator (Figure 2B left, middle panel, compare lanes 1 and 2).

Semi-quantitative analysis using in vitro transcribed mono- and polycistronic mce RNA as markers allowed us to estimate that there are ca. 20 molecules of monocistronic transcript for every polycistronic mce transcript molecule present in Mcc-producing cells (data not shown). Cells harboring an mce plasmid with disrupted putative terminator produced ca. 30 times less Mcc than cells harboring the wild-type plasmid (Figure 2B, right). The result thus suggests that the short mccA transcript is required for high Mcc production, presumably by allowing the synthesis of sufficient amounts of the MccA peptide to be converted into Mcc by MccB. The results of mccA transcript mapping are summarized in Figure 2C.

**Short mccA transcript is highly stable and is ribosome-bound**

The data presented above can be explained by either transcription termination or transcript processing between the mccA and the mccB ORFs. A processing event would be expected to generate a new 3′ end that should be detectable by primer extension with oligonucleotides annealing to mccB. No such primer extension product was detected (data not shown), suggesting that transcription termination is likely responsible for the appearance of the short mccA transcript. The high ratio of monocistronic to polycistronic mceA transcripts may result from very efficient transcription termination in the intergenic region or it may be caused by differential transcript stability (a combination of these two effects is also possible). To determine transcript stabilities, Mcc-producing cells were treated with rifampicin, an inhibitor of transcription initiation, and decay of mce RNA abundance was followed over time by Northern blotting (for mceA transcript) and primer extension (for polycistronic transcript). The results are presented in Figure 3A. As can be seen, the half-life of polycistronic transcript was several minutes, i.e. comparable to half-lives of most E. coli mRNAs (20). In contrast, the short mccA transcript was exceedingly stable (almost no change in transcript abundance after a 20-min incubation with rifampicin). The exceptional stability of the mccA transcript may be responsible for the abnormally low (∼3%) ratio of TEX-resistant transcripts revealed by dRNA-seq (Figure 2A), since transcripts that persist for a long time could lose their 5′ triphosphate moiety (21).

We next wondered what could be the reason of exceptional stability of the mccA transcript, an obviously important part of the mechanism that contributes to preferential accumulation of the mccA message in the cell. The short transcript could be intrinsically stable (for example, there are known cases of 3′ end stem-loops stabilizing bacterial RNA (22–25)) or it could be stabilized by ribosome binding to and/or translation of the mccA ORF (26) (since the mccA ORF is only seven codons long, only one ribosome can bind to mccA RNA). Using sucrose gradient centrifugation, we showed that the mccA transcript is only present in the ribosome-containing fraction and is undetectable in the free RNA fraction (Figure 3B), consistent with idea that ribosome-binding and/or translation may have a stabiliz-

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**Figure 2.** In vivo analysis of the mce operon transcripts. (A) Analysis of the mceABCDE operon of E. coli using differential RNA-Seq. RNA was extracted from E. coli cells harboring the MccC-production plasmid pp70 and grown to late exponential phase in LB medium. Half of RNA was treated with Terminator™ 5′-phosphate-dependent exonuclease (TEX) (+TEX), while another half was left untreated (−TEX) and then converted into a cDNA library, which was subjected to high-throughput Illumina sequencing. cDNA sequencing reads were aligned to the mce operon and visualized as coverage plots representing the number of reads per nucleotide (‘k’ for thousands of reads) in the IGB (Affymetrix). In the IGB screenshot shown plasmid coordinates are indicated in the middle; gray arrow represent annotated ORFs, black arrow denotes Pmcc, and the ORF of the small peptide mceA is shown as a red arrow. (B) At the left-hand side, results of detection of mce transcripts in cells harboring the wild-type MccC-production plasmid pp70 and its derivative pp70Δ51 harboring a deletion in the mce–mccB region are shown: top—Northern blotting with an mccA-specific probe. Positions of Decade™ RNA Markers are indicated on the right. Middle—primer extension using a primer annealing at the beginning of the mceB gene. Bottom—primer extension using a primer annealing to plasmid-borne bla gene. At the right-hand side, the levels of Mcc production by cells harboring the wild-type or mutant MccC-production plasmids and used for transcript analysis are shown. (C) Summary of mceA transcript mapping. A fragment of the mceABCDE operon DNA (in black) and the short mceA transcript (in blue) are schematically shown, arrows in the end of mceA transcript indicate residues of 3′ end mapping by 3′-RACE. SD sequences of mceA and mceB ORFs are shown in green.
the result hinted that the free short transcript is unstable or, more interestingly, that ribosome binding may somehow stimulate short transcript production. To address this issue, in vitro transcription and transcription-translation experiments were performed. Since mccA promoter has very low basal transcription activity in vitro (data not shown), we used a chimeric transcription template containing a strong T7 A1 promoter with modified initial transcribed sequence (extending from positions −67 to +30, 5′-tcagatccgagagggccacggcaacagcaaccca-3′, the promoter consensus elements are underlined, the +1 position is capitalized) fused to a fragment of mccDNA from position +1 to +154 with respect to the mccA promoter transcription start point. Transcription templates containing mutations at the mccA initiating codon and/or its SD sequence (above) were also created. Transcription templates were combined with E. coli RNA polymerase ς70 holoenzyme and transcription was initiated with a C−1pApA+1pUpC+2pC+3 primer, ATP, GTP and radioactive CTP. Since the first adenine in the template strand is located in position +35 of the template, transcription is stalled before this position. The stalled transcription complexes contain a radioactive nascent 34-nt long RNA whose extension can be monitored upon the addition of UTP. As can be seen from Figure 4A, lane 2, very little, if any, transcription termination was detected with the wild-type template. However, when elongation of the nascent 34-mer RNA was performed in the presence of defined PURExpress in vitro translation system, a new transcript whose 3′ end matched the 3′ end of mccA RNA observed in vivo was produced on the wild-type template (Figure 4A, lane 5). The PURExpress system used in Figure 4A, lane 5, contains all components of the translation machinery and ribosomes. To determine whether transcription termination in the mccA–mccB intergenic region requires translation of the mccA gene, in vitro transcription of wild-type template was performed in the presence of PURExpress (Δaa, tRNA) system lacking amino acids and tRNA (Figure 4A, lane 4), or in the presence of PURExpress ΔRibosome system that lacks ribosomes but contains all other translation system components (Figure 4A, lane 3). As can be seen, transcription termination required the presence of ribosomes but was not dependent on the presence of amino acids and tRNA.

Our data suggest that the presence of ribosomes, even in the absence of translation, stimulates transcription termination in the mccA–mccB intergenic region. To detect ribosome binding to the mccA transcript, a toeprinting experiment was conducted using purified monocistronic mccA mRNA prepared by in vitro transcription with T7 RNA polymerase from an appropriate DNA template. In the absence of ribosomes reverse transcriptase stalled at several points along the transcript (Figure 4B, lane 1). The stalling apparently increased in the presence of PURExpress ΔRibosome system compared to what was observed with just pure RNA (Figure 4B, compare lanes 2 and 1). In the presence of PURExpress (Δaa, tRNA) system, a prominent toeprint was observed (Figure 4B, lane 3). The major toeprints were located 17/20 nt downstream of the mccA ORF start point, corresponding to the ribosome location at the first and
second codons of mccA (27). Additional minor toeprints were located further downstream (up to position +31) and correspond to ribosome binding within the mccA ORF. A toeprinting experiment with PUREExpress full system was also conducted (Figure 4B, lane 4). At these conditions, which support the synthesis of the MccA heptapeptide, a change in the toeprinting pattern was observed. In addition to toeprints corresponding to ribosome bound at the beginning and within the mccA ORF, another toeprint, at position +36, which corresponds to ribosome stalled at the last sense codon of mccA, was detected. The addition of thiostrepton, an antibiotic that inhibits ribosome translocation (28), to reactions containing full system led to accumulation of the toeprint at position +17 corresponding to ribosome bound at the initiating codon and eliminated the downstream toeprints (Figure 4B, lane 5).

Since the PUREExpress (Δaa, tRNA) system causes efficient transcription termination (Figure 4A, lane 3) and appearance of a toeprint (Figure 4B, lane 3), we infer that ribosome binding to the mccA ORF in the absence of translation stimulates downstream transcription termination. The fact that efficient transcription termination is observed in the presence of the full system and thiostrepton (Supplementary Figure S1) is also consistent with this inference. Further support to the idea that ribosome binding is sufficient to induce transcription termination came from in vitro transcription termination analysis using mutant mccA templates. As can be seen (Figure 4C, compare lanes 4 and 5) transcription termination in the presence of PUREExpress full system was unaffected by a mutation in the initiating codon of mccA but was strongly reduced by the SD sequence mutations (Figure 4C, lane 6). In the latter case, a diffuse band migrating just above a sharp band corresponding to the transcription termination event was observed. This band is caused by nucleolytic degradation of the full-sized transcript since it is also observed when phenol-extracted full-sized in vitro transcribed RNA is combined with transcription/translation reactions components (Supplementary Figure S2).

A toeprinting experiment with purified mccA mRNAs containing mutations in the initiating codon of mccA or in the SD sequence was next conducted in the presence of PUREExpress (Δaa, tRNA) system (Figure 4D). A toeprint at positions corresponding to ribosome binding at the first and second mccA codons was seen with the wild-type template (Figure 4D, lane 2) while no toeprint was detected with mRNA containing substitutions in the SD sequence (Figure 4D, lane 6). The substitution of the initiating codon decreased the intensity of toeprint corresponding to ribosome bound at the initiating codon of mccA but led to a strong toeprint at position +31 (Figure 4D, lane 4), corresponding to ribosome bound at internal AUG codon located in the +1 reading frame within the mccA ORF.

We infer from these data that a ribosome bound upstream of or within mccA stimulates the formation of transcription terminator responsible for formation of the short mccA transcript that is required for MccC synthesis. It therefore follows that the part of mccA RNA that is covered by the bound ribosome participates in interactions that inhibit the formation of the transcription terminator hairpin. Two types of experiments support this view. First, when transcription elongation was performed in the presence of an oligonucleotide annealing to mccA transcript positions +69/+91 (oligo 1) and thus covering the left arm of the putative stem-loop structure of the terminator (Figure 5D), transcription termination was low even in the presence of
34-nt long radioactively labeled RNA were formed on a DNA template containing deletions in the mce part were performed in the absence of ribosomes (Figure 5C). As can be seen, removal of up to 29 nt of the initial transcribed mce sequence had no effect on transcription termination. Removal of 44 nt caused weak termination, while removal of first 59 or 73 nt strongly stimulated transcription termination in the absence of ribosomes. Overall, the results of this analysis demonstrate that mce RNA positions +30 to +60 inhibit the terminator function in nascent mce RNA.

We next wished to probe the structure of the mce RNA and determine whether this structure could be affected by ribosome binding. Both wild-type mce RNA and mutant versions with substitutions in the initiating codon and the SD sequence were probed with RNases T1 and T2, which are specific to unpaired Gs (T1) and all unpaired nucleotides (T2). RNA digested with RNase T1 under denaturing conditions was used as a size marker. The results, presented in Figure 6A, are consistent with a structure presented in Figure 6B, showing the existence of two prominent stem-loop structural elements. The first element is located immediately downstream of bound ribosome, and contains an RNase T2 hypersensitive loop (loop 1), which is resistant to RNase T1 because it contains only A and U residues. Another stem-loop structure corresponds to the transcription terminator hairpin. Its loop, loop 2, is sensitive to both RNase T2 and RNase T1 (the sensitivity to the latter enzyme is due to the presence of G88). The two mutant RNA structures appear to be the same as that of the wild-type mce RNA.

We next performed the probing experiment in the presence of PURExpress full system. While ribosomes seem to have generally protected mce RNA from RNase T2 digestion, the hypersensitivity in both loops persisted (Figure 6A, compare lanes 7 and 8, and lanes 10 and 11). The result either suggests that changes caused by bound ribosome are not sensed by the probing method used (for example, they may involve a tertiary, rather than secondary structure change) or, that such changes only occur in the context of shorter nascent RNAs, which fold co-transcriptionally.

Since results presented above failed to demonstrate a conformational change in mce transcript caused by ribosome binding, we wished to prove that mce terminator alone, in the absence of interfering upstream mce sequences, can cause transcription termination in vitro. Accordingly, we cloned a fragment of mce DNA from position +71 to +114 with respect to the transcription start point in between the lacUV5 promoter and the galK gene of plasmid pFD100 (18). This fragment contains the mce terminator hairpin, the A/T-rich downstream region and a fragment of the upstream mce hairpin revealed by footprinting experiments (Figure 6B). Plasmids containing mce inserts in both orientations were constructed. E. coli galK− cells transformed with pFD100 plasmid formed purple-colored streaks on McConkey agar plates (Figure 6C) due to transcription from the lacUV5 promoter. Control cells transformed with pFD51 plasmid lacking this promoter formed white-color streaks. Cells transformed with a plasmid containing the mce insert in ‘direct’ orientation also formed white-color streaks, demonstrating that the cloned segment of mce DNA efficiently prevented galK transcription from upstream promoter. In contrast, cells transformed with a

**Figure 5.** Mapping an element of the mceA transcript that suppresses transcription termination in the mceA–mceB intergenic region. (A) Stalled E. coli RNA polymerase transcription elongation complexes containing a 34-nt long radioactively labeled RNA were formed on a DNA template containing the T7 A1 promoter fused to a fragment of mce operon extending from position +1 to position +154. Transcription elongation was allowed to resume by the addition of NTPs (lane 1), NTPs with PURExpress ΔRibosome (lane 2) or NTPs with PURExpress ΔRibosome in the presence of oligonucleotide oligo 1 (lane 3, see also panel D). An autoradiograph of a denaturing gel showing reaction product separation is shown. (B) Stalled E. coli RNA polymerase transcription elongation complexes containing a 34-nt long radioactively labeled RNA were formed on a DNA template containing the T7 A1 promoter fused to a fragment of mce operon extending from position +1 to position +154. Elongation was resumed by the addition of NTPs in the presence or in the absence of DNA oligonucleotides oligo 2 or oligo3. (C) Single-round in vitro transcription reactions were performed on a DNA containing the T7 A1 promoter fused to a fragment of mce operon extending from position +1 to position +154 (lane 1) and derivative templates that contained deletions extending from position +1 to a position, indicated in the template name (i.e. template labeled +15 lacked nucleotides +1/+14). The sites of termination are indicated by arrows. (D) The monocistronic mceA transcript. The SD sequence is shown in green, the mceA ORF in red. The area covered by a ribosome bound to the SD sequence, annealed oligos 1, 2 and 3, and the termination hairpin positions are indicated.
The ribosome-dependent mechanism of \textit{mccA} RNA production is evolutionarily conserved.

The \textit{mcc}-like operons appear to be widespread in phylogenetically diverse bacteria (6). While no production of MccC-like compounds by these operons has been shown yet, some of these compounds were recently validated by enzymatic synthesis of \textit{in vitro} using cognate pairs of MccC-like enzymes/predicted MccC-like substrates (29). It is reasonable to expect that the main features controlling the synthesis of these compounds should be conserved. Indeed, for all \textit{mcc}-like operons identified to date, a long intergenic region separating the \textit{mccA} and \textit{mccC} homologs and containing terminator-like sequences can be identified (6). In \textit{Helicobacter pylori} strain G27 (30), the \textit{mcc}-like operon is encoded on a 10,032-bp plasmid pHPG27 (NC_011334) and contains three genes, \textit{mccA}, \textit{mccB} and \textit{mccC} (Figure 7A). The intergenic region between pHPG27 \textit{mccA} and \textit{mccB} is 84 bp long (the corresponding region in \textit{E. coli} \textit{mcc} is 74 bp long, Figure 7A). To determine whether a short \textit{H. pylori} \textit{mccA} transcript is produced and, if so, whether its production can be stimulated by ribosome binding, an \textit{in vitro} transcription experiment was performed using as a template a DNA fragment containing the T7 A1 promoter fused to a fragment of \textit{H. pylori} \textit{mcc} operon extending from position +1 to position +137. Transcription elongation was allowed to resume by the addition of NTPs in the presence of PURExpress \textit{ΔRibosome} (lane 1), \textit{Δ(aa, tRNA)} (lane 2) or full (lane 3) translation systems. An autoradiograph of a denaturing gel showing reaction product separation is shown.

The \textit{mcc} insert in ‘inverted’ orientation formed purple-color streaks. We infer from this experiment that a fragment of \textit{mcc} DNA carrying the inverted repeat from the \textit{mccA–mccB} intergenic region and 7 upstream and 13 downstream base pairs functions as a unidirectional transcription terminator \textit{in vivo}.

plasmid containing the \textit{mcc} insert in ‘inverted’ orientation formed purple-color streaks. We infer from this experiment that a fragment of \textit{mcc} DNA carrying the inverted repeat from the \textit{mccA–mccB} intergenic region and 7 upstream and 13 downstream base pairs functions as a unidirectional transcription terminator \textit{in vivo}.

**Figure 6.** Structural and functional probing of \textit{mccA} transcript. (A) \textit{32P-\textit{S}-end} labeled \textit{in vitro} synthesized wild-type or mutant \textit{mccA} RNA was digested with RNase T1 or RNase T2. Reaction products were resolved by denaturing PAGE and revealed by autoradiography. Lanes labeled ‘control’ show material that was not treated with RNases. Lanes labeled ‘SEQ T1’ are marker lanes, showing digestion pattern obtained with RNase T1 under denaturing conditions (cleavages at every G). In lanes labeled ‘RNase T1’ and ‘RNase T2’ transcripts were re-folded in the presence of 10 mM MgCl2 and then digested with RNases. In lanes labeled ‘PURExpress’ \textit{wild-type} \textit{mccA} RNA was folded in the presence of PURExpress full system in the presence of thiostrepton. (B) A secondary structure of \textit{mccA} RNA produced by RNAfold software (http://rna.tbi.univie.ac.at/) and consistent with RNase probing results. Cleavage positions by RNase T1 and RNase T2 are shown, respectively, with black and white asterisks. Elements of the structure (loops, L, and hairpins, H) are also marked on the gel shown in panel A. A fragment of \textit{mccA} tested for \textit{in vivo} termination activity is indicated. (C) A DNA fragment coding for a hairpin structure and adjacent sequences shown in panel C was cloned in direct (pFD\textit{mcc} \textit{dir}) and inverted (pFD\textit{mcc} \textit{inv}) orientations between the \textit{galK} reporter and the lacUV5 promoter of plasmid pFD100. The resulting plasmids, as well as control pFD51 plasmid lacking the promoter, were transformed into \textit{E. coli} and transformants were then tested for \textit{GalK} activity on McConkey indicator agar plates. Overnight growth of cells is shown.

**Figure 7.** \textit{H. pylori} \textit{mcc} operon analysis. (A) Schematic representations of \textit{E. coli} and \textit{H. pylori} \textit{mcc} operons (drawn not to scale). All designations are as in Figure 1C. The \textit{mccA–mccB} intergenic region of \textit{H. pylori} is expanded below with the stop codon of \textit{mccA}, the start codon of \textit{mccB} and the location of inverted repeat that may form a transcription terminator indicated. (B) \textit{Stalled E. coli RNA polymerase transcription elongation complexes containing a 32-nt long radioactively labeled RNA were formed on a DNA template containing the T7 A1 promoter fused to a fragment of \textit{H. pylori} \textit{mcc} operon extending from position +1 to position +137. Transcription elongation was allowed to resume by the addition of NTPs in the presence of PURExpress \textit{ΔRibosome} (lane 1), \textit{Δ(aa, tRNA)} (lane 2) or full (lane 3) translation systems. An autoradiograph of a denaturing gel showing reaction product separation is shown.
observed in *E. coli*, ribosome binding causes transcription termination in the *mccA–mccB* intergenic region of *H. pylori*.

**DISCUSSION**

In this work, we studied transcriptional control mechanisms that ensure high levels of production of peptide–nucleotide antibiotic microcin C. The transcription of the entire *mcc* operon occurs from a single upstream promoter. The activity of this promoter requires CAP-cAMP and thus McC production only occurs during nutrient deprivation (14,15). Once transcription of *mcc* genes is initiated, a proper ratio of the MccA peptide, a product of promoter-proximal gene and a substrate of promoter distal biosynthetic genes products MccB, MccD and MccE, needs to be maintained to assure continuous and high levels of McC production. We here show that the intergenic region between the *mccA* and *mccB* genes plays an important role in controlling the overall level McC synthesis. A deletion in this region dramatically reduces McC production while leaving all the codons of *mccB* intact. The deletion also abolishes the production of a highly abundant 105–107-nt transcript that contains the *mccA* ORF. Consequently, most of the MccA propeptide is synthesized from this short *mccA* RNA and the observed high abundance of this transcript evidently contributes to efficient Mcc production.

The monocistronic *mccA* RNA is produced at transcription terminator located in the intergenic region between *mccA* and *mccB*. However, the function of this terminator remains masked by secondary or tertiary interactions within the *mccA* RNA, such that in the absence of ribosome binding/*mccA* translation the RNA polymerase proceeds to transcribe downstream *mccA* genes. If a ribosome binds to the SD sequence upstream of the *mccA*, transcription termination becomes possible. While the ribosome binding is essential for transcription termination in the *mccA–mccB* intergenic region, translation of the *mccA* ORF is not. This effect appears to be due to both the very efficient interaction of ribosome with the *mccA* SD sequence and the presence of additional sites, including internal out-of-frame ATG codons within *mccA* where a ribosome can reside causing transcription termination. Presumably, a ribosome bound upstream of or within *mccA* causes a change in the nascent transcript structure that allows transcription terminator structure to form, although experiments with *in vitro* transcribed *mccA* RNA failed to reveal a structural change at least at the level of RNA secondary structure. The mechanism of short *mccA* transcript generation through ribosome-induced transcription termination may be a conserved feature of predicted *mcc*-like operons in diverse bacteria. This possibility is clearly implied by our *in vitro* analysis of transcription of *H. pylori* *mccA* operon. The result is particularly striking since sequence conservation between the *mccA* genes and untranslated regions of *E. coli* and *H. pylori* is lacking.

High (~40%) and more) termination efficiencies at the *mccA–mccB* intergenic terminator can be obtained *in vitro* in the presence of ribosomes. The large ratio in monocistronic and polycistronic *mcc* transcripts abundance observed *in vivo* suggests similarly high termination efficiencies in *vivo*. The steady-state ratio of monocistronic to polycistronic transcripts (ca. 20:1) is determined by their respective synthesis and degradation rates. Since both transcripts are synthesized from the same promoter, the ratio of their synthesis rates is determined by the termination efficiency. At steady state, the transcript synthesis has to be matched by the transcript decay; from this, it is straightforward to obtain a relationship that connects the termination efficiency with the ratio of the transcript concentrations, and the ratio of their half-lives (see Materials and Methods for derivation). The half-life of the polycistronic transcript can be estimated at ~3 min, while the monocistronic transcript is stable on the timescale of the cell division, so that its half-life is determined by the cell doubling time (~30 min). From the above it can then be estimated that the *in vivo* termination efficiency should be around 65%.

It is clear that exceptional stability of *mccA* mRNA is responsible for the large ratio of monocistronic to polycistronic transcripts observed. This stability is also due to ribosome binding, so that a ribosome bound to *mccA* ORF dramatically stabilizes the transcript. Since in the absence of translation the *mccA* transcript decays rapidly, it is very tempting to speculate that once bound to the *mccA* message, a ribosome does not dissociate from it anymore, shifting back to the beginning of the seven-codon message once translation of the MccA heptapeptide is completed. Such mechanism would provide an additional boost in the amount of MccA substrate synthesized and made available for adenylation by the MccB. Experiments aimed at testing this scenario are currently in progress in our laboratory.

**SUPPLEMENTARY DATA**

*Supplementary Data* are available at NAR Online.

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