Molecular cloning and sequence analysis of the clorobiocin biosynthetic gene cluster: new insights into the biosynthesis of aminocoumarin antibiotics

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The biosynthetic gene cluster of the aminocoumarin antibiotic clorobiocin was cloned by screening of a cosmid library of Streptomyces roseochromogenes DS 12.976 with two heterologous probes from the novobiocin biosynthetic gene cluster. Sequence analysis revealed 27 ORFs with striking similarity to the biosynthetic gene clusters of novobiocin and coumermycin A₁. Inactivation of a putative aldolase gene, cloR, by in-frame deletion led to the abolishment of the production of clorobiocin. Feeding of the mutant with 3-dimethylallyl-4-hydroxybenzoic acid (Ring A of clorobiocin) restored clorobiocin production. Here, it is suggested that the formation of Ring A of clorobiocin may proceed via a retro-aldol reaction catalysed by CloR, i.e. by a mechanism different from the previously elucidated benzoic acid biosynthetic pathway in Streptomyces maritimus. A comparison of the gene clusters for clorobiocin, novobiocin and coumermycin A₁ showed that the structural differences between the three antibiotics were reflected remarkably well by differences in the organization of their respective biosynthetic gene clusters.

Keywords: coumermycin A₁, novobiocin, aldolase, retro-aldol reaction

INTRODUCTION

Aminocoumarin antibiotics, such as novobiocin, clorobiocin and coumermycin A₁ (Fig. 1) (Berger & Batcho, 1978), are produced by various Streptomyces strains and are very potent against Gram-positive pathogenic bacteria, including methicillin-resistant Staphylococcus strains. Novobiocin is licensed in the USA as an antibiotic for use in humans (Albamycin; Pharmacia & Upjohn).

Bacterial DNA gyrase is the target of the aminocoumarin antibiotics (Hooper et al., 1982; Maxwell, 1999). X-ray crystallographic examinations (Ali et al., 1993; Lewis et al., 1996; Maxwell, 1993; Tsi et al., 1997; Lafitte et al., 2002) have demonstrated that as well as the aminocoumarin moieties, the substituted deoxysugar moieties, the prenylated 4-hydroxybenzoate moieties of clorobiocin and novobiocin are essential for the binding of these compounds to the B subunit of gyrase.

The affinity of the aminocoumarin antibiotics for bacterial gyrase is extremely high. The inhibition constant ($K_i$) values of these antibiotics are in the 10 nM range, i.e. two orders of magnitude lower than those of modern fluoroquinolones. This makes the aminocoumarins very interesting starting materials for the development of new antibacterial compounds.

Previously, our group has identified the biosynthetic gene clusters for novobiocin from Streptomyces spheroides NCIMB 11891 (Steffensky et al., 2000a) and for coumermycin A₁ from Streptomyces rishiriensis DSM 40489 (Wang et al., 2000). In the present study, we report the identification of the clorobiocin biosynthetic gene cluster from Streptomyces roseochromogenes DS 12.976. A comparison of the gene clusters for clorobiocin, novobiocin and coumermycin A₁ showed that the structural differences between the three antibiotics corresponded well to the differences in the organization of their respective biosynthetic gene clusters. Furthermore, the very stringent organization of the biosynthetic genes encoding the three different aminocoumarin antibiotics into ‘modules’, each of which carries the complete genetic information required for the biosynthesis of the respective antibiotic, offers excellent prospects for

The GenBank accession number for the sequence of cosmid K1F2 is AF329398.
the production of novel aminocoumarins using a combinatorial biosynthetic approach.

METHODS

Bacterial strains, plasmids and culture conditions. *S. roseochromogenes* var. *oscitans* DS 12.976 (kindly provided by Aventis) was routinely cultivated at 28 °C for 2 days in HA medium containing 1-0 % malt extract, 0-4 % yeast extract, 0-4 % glucose and 1-0 mM CaCl₂ (pH 7-3). For the production of clorobiocin and other secondary metabolites, wild-type and mutant strains of *S. roseochromogenes* were cultured in 500 ml baffled flasks containing 50 ml pre-culture medium (Mancy *et al*., 1974). After growth of these cultures for 48 h at 33 °C and 210 r.p.m., 5 ml of the cultures were inoculated into 500 ml baffled flasks containing 50 ml production medium (Mancy *et al*., 1974). After inoculation into the production medium, cells were cultured at 33 °C and 210 r.p.m. for 7 days.

*Escherichia coli* XL-1 Blue MRF' (Stratagene) was grown in liquid or on solid Luria–Bertani medium at 37 °C (Sambrook & Russell, 2001). SuperCos-1 was purchased from Stratagene. pBSKT, an integrative vector carrying carbenicillin and thiostrepton resistances, was described by Lombo *et al*. (1997). Carbenicillin (50 µg ml⁻¹) and thiostrepton (50 µg ml⁻¹) were
used in the medium for selection of recombinant plasmids and strains.

**Genetic procedures.** Standard methods for DNA isolation and manipulation were performed as described by Kieser et al. (2000). DNA fragments were isolated from agarose gels using a NucleoSpin 2 in 1 extraction kit (Macherey-Nagel). Isolation of cosmids and plasmids was carried out with ion-exchange columns (Nucleobond AX kit; Macherey-Nagel). Genomic DNA was isolated from *Streptomyces* strains by lysozyme treatment and phenol/chloroform extraction.

**Construction and screening of the cosmid library.** Chromosomal DNA of *S. roseochromogenes* was partially digested with Sau3A1, dephosphorylated and then ligated into the BamHI sites of SuperCos-1. The ligation products were packaged with Gigapack III XL (Stratagene, Heidelberg; Germany) and transduced into *E. coli* XL-1 Blue MRF’. Southern blot analysis was performed on Hybond-N membranes (Amersham) with digoxigenin-labelled probes by using the DIG high prime DNA labelling and detection kit II (Roche Molecular Biochemicals). Two probes, one containing part of the dTDP-glucose 4,6-dehydratase gene *novT* (Steffensky et al., 2000a) and the other containing a 1·58 kb *SphI–BamHI* fragment of the novobiocin operon DNA, were used for hybridizations.

**DNA sequencing and computer-assisted sequence analysis.** Double-stranded sequencing of the entire cosmid KIFF2 (carrying an insert of 42291 bp) was performed by the dideoxy-nucleotide chain termination method on a LI-COR automated sequencer (MWG-Biotech) using a shotgun library with DNA fragments of approximately 1·5–2·0 kb in length. The *dnasis* software package (version 2.1; Hitachi Software Engineering) was used for sequence analysis. Amino acid sequence homology searches were carried out in the GenBank database by using the BLAST program (release 2.0).

**Construction of pFP02 for in-frame gene inactivation.** For inactivation of *cloR* in *S. roseochromogenes*, the fragments *cloR*-1 (1282 bp) and *cloR*-2 (1301 bp) were amplified by PCR. Primer pair *cloR*-1/*HindIII* (5’-GTACCCGGAACCTTGCCTG-3’) and *cloR*-1/*PstI* (5’-GCATGGTTCTCAGAGCC-TTG-3’) was used to amplify *cloR*-1; primer pair *cloR*-2/*PstI* (5’-GCCTGCACTGAGGCCAAA-3’) and *cloR*-2/*BamHI* (5’-TCGTAGGACTCCCCGTCGC-3’) was used to amplify *cloR*-2. Restriction sites introduced into the primers are shown in bold in the aforementioned sequences. *cloR*-1 was digested with *HindIII* and *PstI* and cloned into the corresponding sites of vector pBSKT, a pBluescript SK(+) derivative containing carbenicillin and thiostrepton resistances, resulting in pFP01. *cloR*-2 was digested with *PstI* and *BamHI* and ligated into the same sites of pFP01 to give pFP02.

**Transformation of *S. roseochromogenes* and selection of recombinant mutants.** Transformation of *S. roseochromogenes* with pFP02 was carried out by polyethylene glycol-mediated protoplast transformation (Kieser et al., 2000). For the preparation of protoplasts, mycelia of *S. roseochromogenes* were grown in CRM medium containing 10·3% sucrose, 20% tryptic soy broth, 1·0% MgCl₂, 6H₂O, 1·0% yeast extract and 0·75% glycine (pH 7·0) for 48 h. The mycelia were then harvested and incubated in 5 ml P (protoplast) buffer (g mycelium)⁻¹ containing 1 mg lysozyme ml⁻¹ for 30–60 min at 30°C.

For transformation of *S. roseochromogenes*, pFP02 was mixed with 200 µl P-buffer containing 1·0×10⁹ *S. roseochromogenes* protoplasts and 500 µl T (transformation) buffer containing 50% (w/v) polyethylene glycol 1000 (Roth). The resulting suspension was plated onto R2YE agar. After incubation for 20 h at 30°C, the plates were overlaid with 3 ml of soft R2YE agar containing a total of 500 µg thiostrepton, for selection of the recombinant mutants. After the transformation of *S. roseochromogenes* protoplasts with pFP02, thiostrepton-resistant colonies were obtained.

**Fig. 2.** Inactivation of *cloR* of the clorobiocin biosynthetic gene cluster. (a) Schematic presentation of the gene inactivation experiment. *thio*, Thiostrepton-resistance gene. (b) Southern blot analysis of the wild-type and mutant strains. Genomic DNA was digested with *SacI*. The indicated 1122 bp *SacI* fragment containing part of *cloR* in (a) was used as the probe.
### Table 1. Identified ORFs in the biosynthetic gene cluster of clorobiocin

<table>
<thead>
<tr>
<th>ORF</th>
<th>Size of the product (aa)</th>
<th>Similar entity/entities*</th>
<th>Identity with similar entity/entities (%)</th>
<th>Accession no.</th>
</tr>
</thead>
<tbody>
<tr>
<td>ORF1</td>
<td>306</td>
<td>Fkbl (lysine cyclodeaminase) from <em>Streptomyces hygroscopicus</em></td>
<td>37</td>
<td>AAF86391</td>
</tr>
<tr>
<td>ORF2</td>
<td>197</td>
<td>Sarcosine oxidase γ-subunit from <em>Corynebacterium</em> sp.</td>
<td>44</td>
<td>Q46338</td>
</tr>
<tr>
<td>ORF3</td>
<td>962</td>
<td>Sarcosine oxidase α-subunit from <em>Corynebacterium</em> sp.</td>
<td>59</td>
<td>Q46337</td>
</tr>
<tr>
<td>ORF4</td>
<td>93</td>
<td>Sarcosine oxidase δ-subunit from <em>Corynebacterium</em> sp.</td>
<td>66</td>
<td>Q46336</td>
</tr>
<tr>
<td>ORF5</td>
<td>406</td>
<td>Sarcosine oxidase β-subunit from <em>Corynebacterium</em> sp.</td>
<td>80</td>
<td>P40875</td>
</tr>
<tr>
<td>ORF6</td>
<td>406</td>
<td>Serine hydroxymethyltransferase from <em>S. coelicolor</em></td>
<td>75</td>
<td>O86565</td>
</tr>
<tr>
<td>ORF7</td>
<td>218</td>
<td>Putative transcriptional regulator from <em>S. coelicolor</em></td>
<td>45</td>
<td>AL596248.1</td>
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<tr>
<td>ORF8</td>
<td>149</td>
<td>Unknown protein</td>
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<td>AL109949.1</td>
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<tr>
<td>ORF9</td>
<td>78</td>
<td>Transposase from <em>S. coelicolor</em></td>
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<td>T36310</td>
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<tr>
<td>cloE</td>
<td>217</td>
<td>norE (217 aa)</td>
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<td>S44974</td>
</tr>
<tr>
<td>cloF</td>
<td>362</td>
<td>Prephenate dehydrogenase from <em>Streptomyces lavendulae</em></td>
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<td>AAK81837</td>
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<tr>
<td>cloG</td>
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<td>norG (318 aa)/couG (319 aa)</td>
<td>79/80</td>
<td>S44506</td>
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<tr>
<td>cloY</td>
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</tr>
<tr>
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<td>75/80</td>
<td>AAG34184.1</td>
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<tr>
<td>cloI</td>
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<td>norI (407 aa)/couI (407 aa)</td>
<td>90/95</td>
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<td>norJ (262 aa)/couJ (258 aa)</td>
<td>72/77</td>
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<td>norK (244 aa)/couK (245 aa)</td>
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<td>AAG34182</td>
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<tr>
<td>cloL</td>
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<td>norL (527 aa)/couL (529 aa)</td>
<td>86/86</td>
<td>AAG34183</td>
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<tr>
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<td>78/78</td>
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</tr>
<tr>
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<td>86</td>
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<td>couN4 (501 aa)</td>
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<tr>
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<td>89</td>
<td>couN5 (89 aa)</td>
<td>91</td>
<td>AAG34183</td>
</tr>
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<td>561</td>
<td>couN6 (560 aa)</td>
<td>94</td>
<td>AAG34183</td>
</tr>
<tr>
<td>cloN7</td>
<td>278</td>
<td>couN7 (281 aa)</td>
<td>82</td>
<td>AAG34183</td>
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<tr>
<td>clo–hal</td>
<td>524</td>
<td>Non-haem halogenase from <em>S. lavendulae</em></td>
<td>34</td>
<td>CAB95984</td>
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<tr>
<td>cloP</td>
<td>277</td>
<td>norP (262 aa)/couP (276 aa)</td>
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<td>AAG34183</td>
</tr>
<tr>
<td>cloQ</td>
<td>324</td>
<td>norQ (323 aa)/hypothetical protein</td>
<td>84</td>
<td>AAG34183</td>
</tr>
<tr>
<td>cloR</td>
<td>277</td>
<td>norR (270 aa)</td>
<td>95</td>
<td>AAG34183</td>
</tr>
<tr>
<td>cloS</td>
<td>288</td>
<td>norS (288 aa)/couS (288 aa)</td>
<td>84/87</td>
<td>CAB82026</td>
</tr>
<tr>
<td>cloT</td>
<td>336</td>
<td>norT (336 aa)/couT (336 aa)</td>
<td>82/87</td>
<td>AAF13998</td>
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</table>

*Accession numbers (in parentheses) for similar entities.*
The single-cross-over mutant RSCO2 was grown in the absence of thiostrepton, allowed to sporulate and then examined for loss of resistance to thiostrepton due to double-cross-over events. Two mutants, named RDCO30 and RDCO32, were examined further. Chromosomal DNA from wild-type S. roseochromogenes, as well as from mutants RSCO2, RDCO30 and RDCO32, was digested with SacII and hybridized with a probe containing part of cloR. A band of approximately 1·1 kb in size was detected upon hybridization of the wild-type S. roseochromogenes DNA with the probe, whereas hybridization of the chromosomal DNA from mutant strain RDCO30 with the probe produced the expected 2·2 kb band, which corresponded to the in-frame deletion of cloR (Fig. 2).

Table 1 (continued).

<table>
<thead>
<tr>
<th>ORF</th>
<th>Size of the product (aa)</th>
<th>Similar entity/entitiesa</th>
<th>Identity with similar entity/entities (%)</th>
<th>Accession no.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>cloU</strong></td>
<td>420</td>
<td><em>novU</em> (420 aa)/<strong>couU</strong> (420 aa)</td>
<td>88/90</td>
<td>CAB96549</td>
</tr>
<tr>
<td><strong>cloV</strong></td>
<td>296</td>
<td><em>novV</em> (297 aa)/<strong>couV</strong> (296 aa)</td>
<td>89/92</td>
<td>AAD31796</td>
</tr>
<tr>
<td><strong>cloW</strong></td>
<td>198</td>
<td><em>novW</em> (207 aa)/<strong>couW</strong> (198 aa)</td>
<td>86/91</td>
<td>S44236</td>
</tr>
<tr>
<td><strong>cloZ</strong></td>
<td>253</td>
<td>Hypothetical protein</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td><strong>gyrB</strong></td>
<td>Partial sequence</td>
<td><em>gyrB</em>-<strong>nov</strong> (novobiocin cluster)/<strong>gyrB</strong>-<strong>cou</strong> (coumermycin cluster)</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

a *nov* genes are from the novobiocin biosynthetic gene cluster of *S. spheroides* (accession no. AF170880); *cou* genes are from the coumermycin *A* biosynthetic gene cluster of *S. rishiriensis* (accession no. AF235030).

RESULTS

Cloning and sequencing of the clorobiocin biosynthetic gene cluster

We have previously cloned the novobiocin (Steffensky et al., 2000a) and coumermycin *A* (Wang et al., 2000) biosynthetic gene clusters (Fig. 1). In the novobiocin cluster, *novT* encodes a dTDP-glucose 4,6-dehydratase involved in the biosynthesis of the deoxyugar moiety of novobiocin; *novL* encodes the novobiocin acid synthase that catalyses the formation of the amide bond between Ring A and Ring B of novobiocin (Fig. 1) (Steffensky et al., 2000b). Similar reactions to these were expected to be involved in clorobiocin biosynthesis. Therefore, Southern hybridizations of genomic DNA from the clorobiocin producer *S. roseochromogenes* were carried out with probes for *novT* and *novL*; each hybridization resulted in a single band.
Fig. 3. Hypothetical biosynthetic pathway for clorobiocin.
ORFs were arranged in exactly the same order and oriented in the same direction (Fig. 1).

Table 1 lists the homologies found between the genes in cosmid K1F2 and the genes of the novobiocin and coumermycin \( A_1 \) clusters, as well as the homologies of the K1F2 genes to other sequences found in GenBank. The sequence of cosmid K1F2 has been deposited in GenBank under accession no. AF329398.

**Genes involved in the biosynthesis of the deoxysugar moiety (Ring C)**

At the 3′ end of the clorobiocin gene cluster, five ORFs with high homology to genes involved in the deoxysugar biosynthesis were discovered (cloSTUVW) (Table 1). Homologous genes are found in the same position in the gene clusters of novobiocin (novSTUWV) and coumermycin \( A_1 \) (couSTUWV) (Fig. 1). Based upon their homology to known genes involved in deoxysugar biosynthesis, we previously assigned these genes to the five steps required for the biosynthesis of the deoxysugar moiety (Fig. 3); functional proof for this hypothesis was provided by an inactivation experiment with \( novT \) in the novobiocin producer \( S. spheroides \) (Steffensky et al., 2000a). The presence of these genes in the clorobiocin gene cluster provides additional support to our previous functional assignment of these genes.

O-Methylation at position 4 of the deoxysugar moiety is regarded as the last step in aminocoumarin biosynthesis (Fig. 3) (Queener et al., 1978). The genes cloP, novP and couP, situated in the same relative position of their respective gene clusters, show homology to genes encoding O-methyltransferases and may be assigned to this reaction. CouP has recently been proven to be responsible for the methylation of 4-OH of the deoxysugar (Li et al., 2002).

**Genes presumably involved in the formation of the pyrrole ring**

Clorobiocin and coumermycin \( A_1 \) contain pyrrole carboxylic acid rings attached to position 3 of their deoxysugar moieties (Fig. 1). Novobiocin contains a carbamyl group at the corresponding position.

These structural similarities and differences between the three antibiotics are reflected in the organization of their respective gene clusters (Fig. 1). Downstream of the glycosyltransferase gene \( novM \), the novobiocin cluster contains a gene (\( novN \)) with homology to those encoding carbamoyl transferases, whereas in the same relative position of the clorobiocin and coumermycin clusters, a group of seven genes is found (\( cloN1–N7 \) or \( couN1–N7 \), respectively) which show very high homology between the two clusters (on average 87% identity). These genes can be assigned to pyrrole biosynthesis, which has been elucidated on the genetic and biochemical level: \( cloN3, cloN4 \) and \( cloN5 \) show sequence similarities to \( pltE, pltF \) and \( pltI \), respectively, which are involved in the biosynthesis of the pyrrole moiety of pyoluteorin in \( Pseudomonas fluorescens \) Pf-5 (Nowak-Thompson et al., 1999) and to \( redW, redM \) and \( redO \), respectively, which are involved in the biosynthesis of the pyrrole moiety of undecylprodigiosin in \( Streptomyces coelicolor \) (Cerdeno et al., 2001). PltE and RedM convert l-proline into its acyl adenylate (Fig. 3) and the small proteins PltL and RedO act as peptidyl carrier proteins (PCPs) (Thomas et al., 2002). Therefore, the same functions may be assigned to the homologous proteins CloN4 and CloN5, respectively. CloN3, like CouN3, PltE and RedW, shows homology to flavine-dependent acyl-coenzyme A dehydrogenases. PltE and RedW catalyse the dehydrogenation of the PCP-bound proline (Thomas et al., 2002). The resulting pyrrole derivative (presumably \( \Delta^4 \)) undergoes spontaneous oxidation to the aromatic pyrrole derivative (Fig. 3).

CloN6 (CouN6) belongs to the BchE-like/methyltransferase subgroup of radical SAM proteins, which has recently been identified using bioinformatic techniques (Sofia et al., 2001). We suggest that CloN6 catalyses the transfer of a methyl group to position 5 of the pyrrole-2-carboxylic acid. cloN2 (couN2) shares homology with \( dpcC \), which encodes an enzyme with acyltransferase activity. cloN7 and/or cloN2 may be involved in the transfer of the activated pyrrole-2-carboxylic acid to the 3-OH of the deoxysugar moiety. The small ORF \( cloN1 \) (encoding 95 aa) does not show homology to other database entries, and its function remains unknown at present.

**Genes presumably involved in the biosynthesis of the aminocoumarin ring (Ring B)**

The genes for the biosynthesis of the characteristic aminocoumarin ring must be present in all three gene clusters; hence, a comparison of the three gene clusters presents an obvious method for identifying possible candidate genes involved in the biosynthesis of this ring. In the clorobiocin cluster, \( cloHIJK \) showed, on average, 85% homology to the corresponding genes in the novobiocin (\( novHIJK \)) and coumermycin \( A_1 \) (\( couHIJK \)) clusters (Table 1). It appears likely that the products of these genes are involved in the formation of the aminocoumarin ring from tyrosine (see Discussion).

Clorobiocin contains a chlorine atom at position 8 of the aminocoumarin ring, whereas novobiocin and coumermycin \( A_1 \) contain a methyl group at the same position (Fig. 1). This structural difference of the antibiotics is perfectly reflected in the organization of their gene clusters: the novobiocin and coumermycin clusters contain a C-methyltransferase gene, \( novO \) or \( couO \), respectively, whereas in the clorobiocin cluster, \( clo–bal \), a homologue of non-haem halogenase genes, is found at the same relative position.

**Genes presumably involved in the biosynthesis of the 3-dimethylallyl-4-hydroxybenzoic acid (Ring A)**

Clorobiocin and novobiocin contain a prenylated 4-hydroxybenzoate moiety (Ring A). Coumermycin \( A_1 \)
contains a pyrrole dicarboxylic acid moiety instead, linking the two aminocoumarin rings of this molecule (Fig. 1). The aromatic nucleus of Ring A of clorobiocin and novobiocin is derived from tyrosine (Bunton et al., 1963; Kominek & Sebek, 1974), but the exact reaction sequence is unknown.

Sequencing of the clorobiocin gene cluster revealed two genes that are also present in the novobiocin cluster, but which are not present in the coumermycin cluster, i.e. cloQ and cloR. This fact drew us to the hypothesis that these genes may be involved in Ring A biosynthesis.

cloQ and cloR, like novQ and novR, show transcriptional coupling (i.e. the stop codon of cloQ is fused with the start codon of cloR) and are likely to be transcribed as a single operon. Unusually large intergenic regions are found upstream and downstream of cloQR (1001 and 830 bp, respectively). CloR has 47% identity to a putative aldolase from S. coelicolor. cloQ did not show homologies to other genes in the database, with the exception of novQ.

**Generation of a cloR-defective mutant**

To test whether cloR was indeed involved in Ring A biosynthesis, a gene inactivation experiment was carried out. An inactivation vector carrying a thiostrepton-resistance gene (pFP02) was constructed, in which the structural gene cloR was disrupted by an in-frame deletion (Fig. 2). The deletion mutant, RDCO30, was subsequently cultured and the ethyl acetate extract of the culture was examined by HPLC for secondary metabolites. As shown in Fig. 4, the production of clorobiocin was abolished in this mutant. Another thiostrepton-sensitive strain obtained in the screening for double-cross-over mutants, RDCO32, represented a reversion to the wild-type (Fig. 2), and showed clorobiocin production identical to that of the wild-type strain (data not shown).

**Feeding of Ring A to the cloR-defective mutant**

To restore clorobiocin biosynthesis in the cloR-defective mutant strain RDCO30, Ring A (3-dimethylallyl-4-hydroxybenzoic acid) was added to the culture medium of this strain. This led to the reconstitution of clorobiocin production (Fig. 4), to one-third the level of the wild-type strain. The identity of this product was confirmed by MS and ^1^H-NMR, in a comparison with authentic clorobiocin.

Besides the major peak for clorobiocin (peak A in Fig. 4), a minor peak of identical mass (peak B) was detected both in the wild-type and the complemented mutant strain. This substance is likely to represent an isomer of clorobiocin, possibly carrying the pyrrole carboxylic acid moiety in position 2 instead of position 3 of the deoxysugar. Such isomers have been reported previously for novobiocin (Hinman et al., 1957).

**Genes involved in the linkage of Rings A, B and C of clorobiocin**

Attachment of the deoxysugar to the 7-OH group of the aminocoumarin ring requires very similar glycosyl transferases in clorobiocin, novobiocin and coumermycin A₁ biosynthesis; indeed, three very similar putative glycosyltransferase genes, cloM, novM and couM, are found at the same relative position in all three gene clusters.

In clorobiocin and novobiocin, the aminocoumarin moiety (Ring B) and the prenylated 4-hydroxybenzoate moiety (Ring A) are linked by an amide bond (Fig. 1). It has been demonstrated that the enzyme NovL catalyses...
this reaction, i.e. the adenylation of the substituted benzoyl moiety and its transfer to the amino group (Steffensky et al., 2000b). cloL shows high homology to novL and is most probably involved in the formation of the amide bond of clorobiocin.

**Resistance and regulatory genes**

Downstream of the deoxysugar biosynthesis genes cloSTUVW in the clorobiocin cluster, and similarly at the corresponding position of the novobiocin and coumermycin clusters, a gene encoding an aminocoumarin-resistant gyrase B subunit (gyrB\(^B\)) is located. This gene has previously been identified as the principal novobiocin-resistance gene in the novobiocin producer *S. spheroides* (Thiara & Cundliffe, 1988).

*cloG*, *novG* and *coulG* are homologous to *strR*, a regulatory gene from the streptomycin cluster. Streptomycin biosynthesis is known to be regulated by \(\gamma\)-butyrolactones (Horinouchi & Beppu, 1995). It may, therefore, be speculated that \(\gamma\)-butyrolactones are involved in the regulation of the biosynthesis of clorobiocin and other aminocoumarin antibiotics.

*cloE* has homology to the *lmbU* gene of the lincomycin biosynthetic gene cluster of *Streptomyces lincolnensis* 78-11. It was suggested that *LmbU* may have a regulatory function, but no experimental evidence is available so far to support this (Peschke et al., 1995).

**Genes with unknown function**

At present, no function can be suggested for the small ORFs *cloY* and *cloN1*, which have homologies in the coumermycin A\(_1\) cluster, and for *cloZ*, which has no homologues in other clusters.

**DISCUSSION**

In this study, we have cloned and sequenced the clorobiocin biosynthetic gene cluster which spans approximately 31 kb and comprises 27 ORFs. The suggested function of these ORFs in clorobiocin biosynthesis is depicted in Fig. 3.

The primary metabolic genes found at the 5\(^{\prime}\) end of the clorobiocin cluster (Table 1) suggest that *cloE* represents the 5\(^{\prime}\) border of the cluster. The gene adjacent to *cloE*, i.e. *ORF9*, encodes a putative transposase, and it may be speculated that this gene is related to the introduction of the cluster into the *S. roseochromogenes* genome. Also at the 3\(^{\prime}\) end, downstream of *gyrB\(^B\)*, primary metabolic genes were found, suggesting that the sequence depicted in Fig. 1 comprises all biosynthetic genes of the clorobiocin cluster. However, it cannot be excluded that additional biosynthetic enzymes for clorobiocin formation are encoded at different loci of the genome.

The clorobiocin cluster contains the genes *cloHIJK*, for which homologues exist in the novobiocin cluster (novHIJK) and the coumermycin cluster (couHIJK). NovH has recently been shown to activate tyrosine by covalent binding to the 4-phosphopantetheinyl cofactor, and the P450 enzyme NovI catalyses the \(\beta\)-hydroxylation of the activated tyrosine (Chen & Walsh, 2001). A central, unresolved question in aminocoumarin biosynthesis is how activated \(\beta\)-hydroxy tyrosine is then converted to the coumarin ring, especially how the ring oxygen is introduced.

*cloJ* and *cloK*, the genes immediately downstream of *cloH* and *cloI*, are homologous to *novJK* and *coulJK* of the novobiocin and coumermycin clusters, respectively. The detection of *cloJ* and *cloK* in the clorobiocin cluster, and the homologous *simJ1* and *simK* genes in the biosynthetic gene cluster of the aminocoumarin antibiotic simocyclinone (Galm et al., 2002; Trefzer et al., 2002), now strongly supports the hypothesis that these genes are indeed related to aminocoumarin biosynthesis. *cloJ* shows homology to 3-oxo-acyl-[ACP] reductases and may likely be involved in the oxidation of a \(\beta\)-hydroxy-tyrosyl to a \(\beta\)-keto-tyrosyl intermediate (Fig. 3). Also, *cloK* shows homology to oxidoreductases, but this homology is not very high (mean of 35% on the amino acid level). Chen & Walsh (2001) speculated that *NovJ* and *NovK* may act together to oxidize the \(\beta\)-hydroxyl function to a keto group. The unresolved step in the postulated Ring B biosynthesis, however, is the hydroxylation of the activated tyrosyl derivative in position 2 of the aromatic nucleus (Fig. 3). Bunton et al. (1965) had reported that the ring oxygen of the aminocoumarin may be derived from the carboxyl group of tyrosine rather than from molecular oxygen. This was recently disproven by Holzenkampfer & Zeeck (2002), who showed that the ring oxygen of the aminocoumarin moiety of simocyclinone is in fact derived from molecular oxygen. Therefore, coumarin ring formation most likely proceeds via the 2-hydroxylation of a tyrosine derivative. Chen & Walsh (2001) had speculated that the predicted flavine dioxygenase *NovC*, encoded by a gene near the novobiocin cluster, may catalyse this reaction. An important finding of our study is that no *novC* homologue was detected in or near the clorobiocin gene cluster. Likewise, no *novC* homologue was detected in the simocyclinone cluster (Galm et al., 2002; Trefzer et al., 2002). We therefore suggest that *novC* is not related to aminocoumarin biosynthesis. The enzyme responsible for the 2-hydroxylation of the \(\beta\)-keto-tyrosyl intermediate remains unknown at present. Whether *cloK* is involved in this or another reaction of aminocoumarin biosynthesis has yet to be demonstrated.

Halogenation of the aminocoumarin ring may occur after ring formation, as depicted in Fig. 3, or at an earlier stage.

The prenylated 4-hydroxybenzoate moiety (Ring A) of clorobiocin and novobiocin is formed from tyrosine (Kominek & Sebek, 1974) and an isoprenoid precursor, but this reaction sequence is also unknown. The biosynthesis of this moiety requires: (i) the assembly of the isoprenoid precursor (probably dimethylallyl diphosphate) via the methyerythritol phosphate pathway
(Li et al., 1998); (ii) the conversion of the phenylpropanoid compound tyrosine to a benzoic acid derivative; and (iii) the prenylation of the aromatic nucleus in a prenyltransferase reaction. The conversion of the phenylpropanoid intermediate to a benzoic acid derivative may proceed by a mechanism analogous to the oxidation of fatty acids, as demonstrated in Streptomyces maritimus (Hertweck & Moore, 2000). Alternatively, this conversion may occur by retro-aldol cleavage of a 3-hydroxylated phenylpropanoid compound, as found in P. fluorescens (Gasson et al., 1998) and Amycolatopsis sp. (Achterholt et al., 2000). Retro-aldol cleavage would result in a benzaldehyde derivative, which would subsequently be oxidized to the benzoic acid derivative.

In the clorobiocin cluster, we could not detect genes similar to those for the β-oxidation of fatty acids. We did find, however, the gene cloR which showed homology to a putative aldolase from S. coelicolor. Comparison of the gene clusters of clorobiocin, novobiocin and coumermycin A1 led to the hypothesis that this gene may be involved in Ring A biosynthesis. Inactivation of the enzyme led to an abolishment of clorobiocin production. When the mutant was complemented with the prenylated 4-hydroxybenzoate moiety (═Ring A), clorobiocin production was restored. This proved that cloR is indeed involved in Ring A biosynthesis. We suggest that the formation of Ring A of clorobiocin may proceed via a retro-aldol reaction catalysed by CloR, i.e. by a mechanism different from the elucidated benzoic acid biosynthesis in S. maritimus (Hertweck & Moore, 2000). The substrate of CloR may be an enzyme-bound prenylated β-hydroxytyrosine, as suggested by Chen & Walsh (2001) and depicted in Fig. 3. Alternatively, prenylated 4-hydroxyphenylpyruvate may be the substrate of CloR, since this compound was detected as the product of a prenyltransferase of the novobiocin producer S. spheroides (Steffensky et al., 1998). Further studies are now in progress to investigate these steps in clorobiocin biosynthesis.

The cloning and sequencing of the clorobiocin gene cluster has completed the genetic information on the biosynthesis of three ‘classical’ aminocoumarin antibiotics, namely novobiocin, clorobiocin and coumermycin A1. Comparison of the three gene clusters revealed a strikingly stringent correspondence between the structures of the antibiotics and the organization of the biosynthetic genes, unprecedented so far in any class of natural products outside the polyketide and the peptide antibiotics. For each structural moiety of the aminocoumarin antibiotics, the biosynthetic genes are grouped together, resulting in a ‘modular’ structure of the clusters. The orders of the modules and the order of the genes within each module are perfectly identical for the three ‘classical’ aminocoumarins, and nearly all of the genes within the clusters are orientated in the same direction. The comparison of the three clusters greatly facilitates the prediction of functions for the different genes. As an example, cloR was recognized by such a comparison as a candidate gene for the biosynthesis of the prenylated 4-hydroxybenzoate moiety of clorobiocin, and this was experimentally proven by an inactivation and complementation experiment. The similarity between the three clusters also provides excellent opportunities for the production of hybrid aminocoumarins by genetic methods.

**ACKNOWLEDGEMENTS**

We thank Aventis for the generous gifts of S. roseochromogenes DS 12.976 and authentic clorobiocin. This work was supported by a grant from the Deutscher Forschungsrat (to L. Heide and S.-M. Li) and by the Fonds der Chemischen Industrie.

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Received 28 May 2002; revised 29 July 2002; accepted 22 August 2002.