The Sequence of a 1.8-Mb Bacterial Linear Plasmid Reveals a Rich Evolutionary Reservoir of Secondary Metabolic Pathways

Marnix H. Medema1,2, Axel Trefzer3, Andriy Kovalchuk1, Marco van den Berg3, Ulrike Müller3, Wilbert Heijne3, Liang Wu3, Mohammad T. Alam2, Catherine M. Ronning4, William C. Nierman4, Roel A. L. Bovenberg3,5, Rainer Breitling2,6, and Eriko Takano*,1

1Department of Microbial Physiology, Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, Haren, The Netherlands
2Groningen Bioinformatics Centre, Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, Haren, The Netherlands
3DSM Biotechnology Center, DSM Food Specialties B.V., Delft, The Netherlands
4J. Craig Venter Institute, Rockville, Maryland
5Centre for Synthetic Biology, University of Groningen, Groningen, The Netherlands
6Faculty of Biomedical and Life Sciences, University of Glasgow, Glasgow, United Kingdom

*Corresponding author: E-mail: e.takano@rug.nl.

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The Whole Genome Shotgun project of S. clavuligerus strain ATCC 27064 has been deposited at DDBJ/EMBL/GenBank under the accession ADGD00000000. The version described in this paper is the first version, ADGD01000000.

Abstract

Plasmids are mobile genetic elements that play a key role in the evolution of bacteria by mediating genome plasticity and lateral transfer of useful genetic information. Although originally considered to be exclusively circular, linear plasmids have also been identified in certain bacterial phyla, notably the actinomycetes. In some cases, linear plasmids engage with chromosomes in an intricate evolutionary interplay, facilitating the emergence of new genome configurations by transfer and recombination or plasmid integration. Genome sequencing of Streptomyces clavuligerus ATCC 27064, a Gram-positive soil bacterium known for its production of a diverse array of biotechnologically important secondary metabolites, revealed a giant linear plasmid of 1.8 Mb in length. This megaplasmid (pSCL4) is one of the largest plasmids ever identified and the largest linear plasmid to be sequenced. It contains more than 20% of the putative protein-coding genes of the species, but none of these is predicted to be essential for primary metabolism. Instead, the plasmid is densely packed with an exceptionally large number of gene clusters for the potential production of secondary metabolites, including a large number of putative antibiotics, such as staurosporine, moenomycin, β-lactams, and enediyynes. Interestingly, cross-regulation occurs between chromosomal and plasmid-encoded genes. Several factors suggest that the megaplasmid came into existence through recombination of a smaller plasmid with the arms of the main chromosome. Phylogenetic analysis indicates that heavy traffic of genetic information between Streptomyces plasmids and chromosomes may facilitate the rapid evolution of secondary metabolite repertoires in these bacteria.

Key words: genome sequence, chromosomal evolution, natural products, Streptomyces clavuligerus.

Introduction

Prokaryotic chromosomes were originally thought to lack many of the features that characterize eukaryotic chromosomes, such as linearity and the possession of telomeres (Bendich and Drlica 2000). However, during recent decades, a few bacterial taxa have been shown to have linear chromosomes that contain telomere-like structures (Hinnebusch and Tilly 1993). Among these are the high-GC, Gram-positive, soil-dwelling Streptomyces bacteria (Chen et al. 1994; Hopwood 2006), renowned for their capacity to produce a vast array of natural products. Their linear chromosomes are relatively long (8–10 Mb) and consist of
A conserved "core" of 5–6 Mb and variable "arm" regions (Hopwood 2006). Nearly all genes that are likely to be unconditionally essential are located within the core. Interestingly, besides possessing linear chromosomes, streptomycetes also often contain linear plasmids, extrachromosomal DNA molecules that replicate independently from the main chromosome and contain their own telomere-like structures (Chater and Kinashi 2007; Chen 2007). Evidence is accumulating that the evolution of streptomycete chromosomes and plasmids can be very dynamic because of their relative instability (Volf and Altenbuchner 1998; Chen et al. 2002; Widenbrant et al. 2007).

Substantial effort in the study of streptomycetes is focused on the secondary metabolites they produce. Many bacterial secondary metabolites or their derivatives are used as antimicrobial agents, whereas some are used as anti-tumor drugs, immunosuppressive agents or cholesterol-lowering drugs (Bode and Muller 2005; Gullo et al. 2006; Newman and Cragg 2007). More than half of all known antibiotics originate from the streptomycetes (Berdy et al. 1995; Challis and Hopwood 2003), and many more clearly remain to be discovered. A statistical analysis of antibiotic discovery has predicted that streptomycetes may have the capacity to produce as many as $10^5$ secondary metabolites (Wawn et al. 2001). The finding that a single genus can carry such a massive number of secondary metabolism biosynthetic gene clusters is correlated with the location of many of them in the arm regions of the chromosome, which are extremely variable between species. In a few cases, such clusters have been shown to be plasmid-borne. Thus, the 365-kb plasmid SCP1 of \textit{Streptomyces coelicolor} carries the biosynthetic gene cluster for methylenomycin A (Kirby and Hopwood 1977; Bentley et al. 2004), and the 210-kb plasmid pSLA-2 of \textit{Streptomyces rochei} carries the biosynthetic gene cluster for tunicamycin (Kenig and Reading 1979; Sandagar et al. 2008). Clavulanic acid is widely used in combination with the semisynthetic \beta-lactam amoxicillin to treat various bacterial infections (Brogden et al. 1981). The biosynthetic genes for both compounds are encoded by a single intensively studied gene supercluster (Liras et al. 2008). Clavulanic acid is widely used in combination with the semisynthetic \beta-lactam amoxicillin to treat various bacterial infections (Brogden et al. 1981). The biosynthetic genes for both compounds are encoded by a single intensively studied gene supercluster (Liras et al. 2008).

One of the most important industrial streptomycete species is \textit{Streptomyces clavuligerus}. Multiple natural products from this organism have been structurally and functionally characterized, and two of these are used in the clinic, the \beta-lactam antibiotic cephamycin C (Alexander and Jensen 1998), and the \beta-lactamase inhibitor clavulanic acid (Saudagar et al. 2008). Clavulanic acid is widely used in combination with the semisynthetic \beta-lactam amoxicillin to treat various bacterial infections (Brogden et al. 1981). The biosynthetic genes for both compounds are encoded by a single intensively studied gene supercluster (Liras et al. 2008). Several clavam antibiotics closely related to these \beta-lactam ring-containing compounds are also produced by \textit{S. clavuligerus} and are encoded by separate gene clusters (Evans et al. 1983; Tahlan, Anders, and Jensen 2004; Tahlan, Park, and Jensen 2004; Tahlan, Park, Wong, et al. 2004; Tahlan et al. 2007; Zelyas et al. 2008). At least three additional antibiotics have been reported to be produced by \textit{S. clavuligerus}, although no biosynthetic genes for these have been described: the pyrroline class antibiotic holomycin (Kenig and Reading 1979; Oliva et al. 2001), a tacroliimus-like macrolide (Kim and Park 2008), and a compound related to the nucleoside antibiotic tunicamycin (Kenig and Reading 1979).

Here, we describe the genome sequence of \textit{S. clavuligerus} ATCC 27064 and show that this species has a unique 1.8-Mb linear megaplasmid, which is densely packed with 25 putative secondary metabolite gene clusters, in addition to its 6.8-Mb chromosome, which also contains 23 such clusters. Some of these clusters strongly resemble known antibiotic gene clusters, others appear to be completely novel, and a number show extravagant features that have never been observed before. The megaplasmid found in \textit{S. clavuligerus} is by far the largest linear megaplasmid ever sequenced, and its gene complement sheds light on the rapid and dynamic evolution of secondary metabolite repertoires in bacteria, in addition to being a rich and compact potential source of novel bioactive metabolites.

**Materials and Methods**

**Genome Sequencing and Assembly**

The genome of \textit{S. clavuligerus} ATCC 27064 was sequenced and assembled by random shotgun sequencing. Sanger sequencing of shotgun libraries with insert sizes of 3, 10, and 50 kb was accomplished using ABI 3700 sequencers as described by Venter et al. (2001). Sequences were assembled using Celera Assembler (Levy et al. 2007). Genome assembly was facilitated and validated with an optical restriction map (Latreille et al. 2007) acquired from OpGen (Madison Wisconsin). Finally, as many gaps as possible were filled using sequences from a cosmid library created in-house at the DSM Biotechnology Center. We estimate the final genome assembly to be $>99.7\%$ complete.

**Gene Prediction, Functional Annotation, and Comparative Analysis**

Straightforward gene prediction by Glimmer3 (Delcher et al. 2007) appeared to give a large number of false positives and negatives. The high GC content of \textit{Streptomyces} species leads to the presence of many long open reading frames (ORFs) which are not actual genes but only exist by coincidence because of the low number of AT-rich stop codons. These long reading frames often are not actual genes. Therefore, we complemented Markov model-guided prediction by Glimmer3 with mapping of BlastP searches of all putative ORFs to the nonredundant (nr) protein database (using an in-house Python script) and by analysis of the GC frame plots in Artemis (Rutherford et al. 2000) to manually identify all putative genes accurately.

Transfer RNA (tRNA) and tmRNA genes were identified using ARAGORN, and ribosomal RNAs (rRNAs) were
identified using the RNAmmer tool. For functional annotation, all proteins were first processed with the AutoFACt automatic annotation pipeline (Koski et al. 2005) through hierarchical information transfer from the best hits in the Uniref90, NCBI nr, COG, KEGG, CDD, PFAM, and SMART databases. A round of manual re-annotation followed to ascertain the accuracy of the annotation.

Genome alignment of the DSM and Broad Institute draft genomes was performed using the Mauve genome alignment program (Darling et al. 2004). Clusters of orthologous groups were constructed using the OrthoMCL software (Li et al. 2003), using cutoffs of e value <1 × 10−5 and identity >60%. Dotplots for genome comparison were created with Gepard (Krumseck et al. 2007). GC skew plots were created using GenSkew (http://mips.gsf.de/services/analysis/genskew/).

Phylogenetic analysis of plasmid-encoded transposase proteins was performed as follows. The S. clavuligerus transposase sequences were blasted against the nr protein database with BlastP. For each query sequence, the 25 best blast hits were aligned using Muscle 3.6 (Edgar 2004), the alignment was quality trimmed with Gblocks 0.91b (Talavera and Castresana 2007), and an approximate maximum likelihood phylogenetic tree was generated using FastTree 2.1.1 (http://www.microbesonline.org/fasttree/). Finally, all the hits incorporated in the trees were blasted against a self-assembled database of Streptomyces chromosomes to identify transposases from Streptomyces chromosomal termini (distance <1 Mb to either end of the chromosome) using BlastX. Query sequences present in a monophyletic taxon comprised of at the most three proteins, in which at least one of the two other proteins was a transposase from a Streptomyces chromosomal terminus, were considered as positive hits.

**Results and Discussion**

**Architecture of the S. clavuligerus Genome**

Pulse-field gel electrophoresis of restriction-digested fragments in the nineteen leads to an estimated size of 6.8 Mb for the chromosome of S. clavuligerus (Chen et al. 1994). Genome sequencing and assembly confirmed this estimate but, remarkably, a second large contig of 1.8 Mb was identified as well.

The optical restriction map that we obtained indicated that this second contig represents a separate replicon. This was confirmed by almost perfectly symmetrical cumulative GC skew plots of both contigs (supplementary fig. S1, Supplementary Material online), characteristic for bacterial chromosomes and plasmids (Grigoriev 1998). Origins of replication (Oris) were identified near the peak of the plots for both replicons on the basis of homology.

The identification of the two large contigs was later independently confirmed by a prepublishing draft sequence from the Broad Institute (GenBank accession number ABJH00000000), although our assembly of the 6.8-Mb replicon differed from theirs by a large inversion at virtually identical rRNA operons (supplementary fig. S2, Supplementary Material online). The optical restriction map that we obtained and our GC skew analysis indicated that our assembly is most probably correct.

The discovery of a second large replicon in S. clavuligerus is not altogether surprising, as Kirby (1978) suspected the presence of a plasmid when he found that a genetic element without linkage to the chromosome influenced holomycin production. Intriguingly, pulse-field gel electrophoresis in the closely related S. clavuligerus strain NRRL 3585—the type strain which should be identical to strain ATCC 27064—has shown the presence of three plasmids (pSCL1–3) ranging in size between 11 and 430 kb (Netolitzky et al. 1995). However, only a 7-kb replicon matching to the smallest of these plasmids—the 11-kb plasmid pSCL1 (Wu and Roy 1993)—was identified in our assembly. No replicons of the sizes reported for plasmids pSCL2 or pSCL3 were identified in our assembly, and the nucleotide sequence of pSCL2 (Wu et al. 2006) did not match to any part of our contigs in a BlastN analysis. This implies that the evolution of streptomycete genomes by plasmid acquisition, loss, or recombination is extremely dynamic.

We identified 7,281 putative protein-encoding genes on the two large replicons, as well as six rRNA operons, 72 tRNA genes, and 14 pseudogenes (table 1). Strikingly, the sum of all genomic features of the two replicons matches very well to the typical make-up seen in other Streptomyces genomes.
The 1.8-Mb Replicon Has the Hallmarks of a Giant Linear Plasmid

We set out to characterize and compare the two replicons. First of all, the central region of the 6.8-Mb replicon had very large regions of conserved synteny to the chromosomes of the four completed Streptomyces genomes, whereas the smaller replicon had no regions with significant homology to these chromosomes (supplementary fig. S3, Supplementary Material online). Moreover, the large replicon had an origin of replication typical of Streptomyces chromosomes, including dnaA and dnaN (SCLAV_2911–2912). The 6.8-Mb replicon thus appears to represent a typical Streptomyces chromosome. Interestingly, it is significantly smaller than other published Streptomyces chromosomes, which range in size between 8.5 and 9.0 Mb (Bentley et al. 2002; Ikeda et al. 2003; Ohnishi et al. 2008) (table 1). Comparative analysis shows that the conserved core region of Streptomyces chromosomes is present in S. clavuligerus, yet the typical large chromosomal arms are not (supplementary fig. S3, Supplementary Material online).

As stated in the previous section, the smaller replicon appeared to have its own Ori, highly homologous to those of the S. coelicolor plasmid SCP1 and the S. rochei plasmid pSLA2-L, two Streptomyces plasmids that are known to harbor secondary metabolite gene clusters. The Ori lies at around 945 kb, adjacent to close homologues of the plasmid-type DNA primase/repli- 
cation proteins Orf1 and Orf2 (SCLAV_p0889 and SCLAV_p0888) from the S. coelicolor SCP1 plasmid (Redenbach et al. 1999) and an additional DNA primase/polymerase (SCLAV_p0890).

Both replicons have genes that encode ParAB chromosome partitioning proteins near their predicted Ori (<10 kb). The parAB genes of the 6.8-Mb replicon (SCLAV_2901–2902) strongly resemble the S. griseus and S. avermitilis chromosome parAB genes, whereas the parAB genes of the 1.8-Mb replicon (SCLAV_p0884–0885) are plasmid-type and strongly resemble the parAB genes on the SCP1 plasmid of S. coelicolor A3(2) (supplementary fig. S4, Supplementary Material online).

The smaller replicon also has its own tap and tpg genes, which encode proteins necessary for telomere replication of Streptomyces chromosomes and plasmids (Bao and Cohen 2001, 2003). No tap or tpg genes were identified on the main chromosome, as for the Rhodococcus sp. RHA1 genome (McLeod et al. 2006). The chromosome therefore seems to depend on the tap/tpg genes of the smaller replicon. However, there could also be a different, unknown, system for telomere replication; the recent identification of the tac/tpc system (not present on the S. clavuligerus chromosome) of the S. coelicolor SCP1 plasmid shows that the tap/tpg system is not universal for streptomycete chromosomes and plasmids (Huang et al. 2007).

Genes for conjugative transfer were also detected on both replicons. Again, although the chromosome carries typical chromosomal-type traAB genes (SCLAV_4235–4236), the smaller replicon has plasmid-type traAB genes (SCLAV_p0254–0255) similar to those of the S. coelicolor plasmid SCP2 (Brolle et al. 1993).

Based on these observations, we conclude that the 1.8-Mb replicon has all the hallmarks of being a giant version of a typical Streptomyces linear plasmid.

The Smaller Replicon Is a Megaplasmid Predicted to be Dispensable for the Core Metabolism of S. clavuligerus

Extrachromosomal genetic elements of bacteria can have quite different functions compared to the chromosomes. In some cases, they encode only accessory functions, whereas in others they have evolved to encode essential cellular functions as well. Although megaplasmids and chromosomes are part of a continuous spectrum, Bentley and Parkhill (2004) have proposed to distinguish chromosomes from megaplasmids not by their replication genes but by whether they are essential for growth of the organism and whether they carry rRNA operons. We therefore set out to predict whether the 1.8-Mb replicon is essential for growth of S. clavuligerus.

Strikingly, all stable RNAs necessary for primary metabolism (rRNA and tRNAs) are encoded on the main chromosome (table 1). A few putative tRNAs are encoded on the 1.8-Mb replicon, but these appear functionally redundant compared with those on the chromosome according to their

### Table 1

<table>
<thead>
<tr>
<th></th>
<th>S. clavuligerus</th>
<th>Streptomyces coelicolor</th>
<th>S. avermitilis</th>
<th>S. griseus</th>
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<tbody>
<tr>
<td><strong>Chromosome</strong></td>
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<tr>
<td>Sequence length</td>
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<td>8.556 Mb</td>
<td>8.668 Mb</td>
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<tr>
<td>GC%</td>
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<td>6%</td>
<td>72%</td>
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<tr>
<td>Coding sequences</td>
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<tr>
<td>Coding sequences</td>
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<tr>
<td>Secondary metabolite clusters</td>
<td></td>
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<td>30</td>
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Feist et al. 2007), and subsequent gap filling (table 2). This has been experimentally verified on the chromosome, which has been experimentally verified using standard carbon and nitrogen sources without amino acid specificity and anticodon sequence. To investigate whether the protein-coding genes of the replicon are likely to be involved in essential cellular functions, a Streptomyces core genome (Ussery et al. 2008) of 976 genes was defined, with each gene representing a cluster of orthologous genes present in all four completed Streptomyces genomes. This core genome had only 14 significant BlastP hits (e value < 1 x 10^-05 and identity >60%) to the 1.8-Mb replicon, distributed throughout its length, with none appearing to be required for crucial cellular processes (see supplementary table S1, Supplementary Material online). Furthermore, all 21 out of the 24 Streptomyces-specific signature genes (Ohnishi et al. 2008) that are present in the S. clavuligerus genome are located on the S. clavuligerus chromosome. Therefore, the 1.8-Mb replicon does not seem to encode any of the essential genetic complement of S. clavuligerus ATCC 27064. This is corroborated by the fact that almost all the genes with the highest codon adaptation indexes and third codon GC percentages (GC3s)—which are likely to have housekeeping functions (Wu et al. 2005)—lie on the chromosome (supplementary fig. S5, Supplementary Material online).

In order to predict whether S. clavuligerus could grow normally using standard carbon and nitrogen sources without the help of enzymes encoded on the 1.8-Mb replicon, we constructed a metabolic model based on our functional annotation, comparisons with known metabolic models from other organisms (Duarte et al. 2004; Borodina et al. 2005; Feist et al. 2007), and subsequent gap filling (table 2). This model successfully simulated growth of S. clavuligerus on various carbon and nitrogen sources. In silico knock-outs of all enzyme-coding genes specific to the 1.8-Mb replicon resulted in no growth defects when growth was simulated using glycerol as a carbon source. This suggests that no essential genes of primary metabolism lie on the megaplasmid.

Nonetheless, a few enzymes for primary metabolism were found to be encoded on the 1.8-Mb replicon. Among them are malate synthase and isocitrate lyase, enzymes of the glyoxylate pathway required for bacteria to grow on acetate. However, there is a malate synthase isoenzyme gene on the chromosome, which has been experimentally verified before (Chang and Sim 1998), and copies of alternative acclinozyme glyoxylate pathway genes (cccmeA and mcl1; Akopiants et al. 2006) were also detected on the main chromosome, possibly making the plasmid-encoded copies redundant. Therefore, we predict that, even when growing on alternative carbon sources, the 1.8-Mb replicon is dispensable for primary metabolism. Experimental analysis by either curing of the whole replicon or constructing multiple targeted knock-outs should confirm this.

As the 1.8-Mb replicon does not seem to encode any functions essential to primary metabolism, the definition of Bentley and Parkhill supports the labeling of the 1.8-Mb replicon as a megaplasmid. As it is the fourth S. clavuligerus plasmid to be described, we name it pSCL4. It is the largest linear plasmid ever sequenced (Moh et al. 2003). If the above definition is strictly applied, pSCL4 is actually the largest plasmid ever sequenced, as the only larger plasmid (the circular plasmid pHG1000MP from Ralstonia solanacearum Salanoubat et al. 2002) should then be classified as a chromosome: it contains an important part of the metabolic core (an RNA locus with two tRNA genes, a gene coding for the alpha subunit of DNA polymerase III, a gene for the protein elongation factor G, as well as several important enzymes of primary metabolism, including amino acid and cofactor biosynthesis), and thus is probably essential under many growth conditions (Salanoubat et al. 2002).

### The Megaplasmid Is Packed with Secondary Metabolite Gene Clusters

As the pSCL4 megaplasmid does not appear to harbor any housekeeping genes, we were interested in predicting the biological role of such a giant replicon. To our surprise, pSCL4 is packed with gene clusters putatively encoding the biosynthesis of secondary metabolites. No fewer than 25 such gene clusters, a number on the same order as observed in the chromosomes of other Streptomyces genomes, are dispersed throughout the plasmid (fig. 1). Together with the clusters identified on the chromosome, the total number of putative secondary metabolite gene clusters (SMC) identified in S. clavuligerus is 48, a number unprecedented in any bacterium (fig. 2 and 8). These include 10 putative nonribosomal peptide synthetase (NRPS) gene clusters, eight putative PKS gene clusters, and six gene clusters putatively encoding NRP and PKS hybrids, as well as 12 clusters putatively encoding one or more terpene synthases or cyclases. An overview of all clusters encoding putative NRPS and PKSs is shown in figure 2, and further details are given in supplementary table S2 (Supplementary Material online).

As expected, the three known antibiotic gene clusters of S. clavuligerus were identified in our genome assembly. Although the supercluster encoding the clavulanic acid and cephamycin C biosynthetic pathways (SMC10-11) and one of the clavam clusters (Tahlan et al. 2007) (SMC9) lie on the main chromosome, the alanyclavam:

<table>
<thead>
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<th>Table 2 Genome-Scale Metabolic Model of Streptomyces clavuligerus</th>
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<tr>
<td><strong>Number of reactions</strong></td>
</tr>
<tr>
<td><strong>Number of metabolites (internal/external)</strong></td>
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<tr>
<td><strong>Dimensions of S (metabolites by reactions)</strong></td>
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<tr>
<td><strong>Number of internal fluxes</strong></td>
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<td><strong>Number of exchange fluxes</strong></td>
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<td><strong>Number of chromosomal genes included</strong></td>
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<td><strong>Number of plasmid genes included</strong></td>
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<td><strong>Total number of genes included</strong></td>
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<td><strong>Number of essential genes</strong></td>
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cluster (SMCp13) (Zelyas et al. 2008) is located on the megaplasmid. The latter cluster has been called a “paralogous cluster” of the clavulanic acid gene cluster (Tahlan, Park, Wong, et al. 2004) and was thought to have arisen through a recent gene duplication. Interestingly, a previously unknown third cluster of genes (SMCp25) containing a more distant homolog of the clavaminate synthase gene was also identified on pSCL4. This cluster might encode the production of yet another β-lactam antibiotic.

We could not predict with certainty which gene clusters are responsible for the production of holomycin and the tuamicamycin-related antibiotic, given the paucity of knowledge on their biosynthesis. For the tacrolimus-like macrolide, we identified a potential gene cluster: the only macrolide PKS cluster detected, consisting of 11 modules. It is positioned near the end of one of the chromosomal arms (SMC1).

Interestingly, we also identified gene clusters potentially encoding unknown products were also identified on both the megaplasmid and the chromosome. These include two enediyne-type PKS clusters on the megaplasmid (SMCp16 and SMCp21), which have the typical unbLVU genes encoding the biosynthetic machinery for the core enediyne structure. The clusters are quite similar to the biosynthetic gene clusters of C-1027 (Liu et al. 2002) and calicheamycin (Ahlert et al. 2002). Both S. clavuligerus clusters fall into the phylogenetic subgroup of nine-membered enediyne polyketides that was recently identified (Udwary et al. 2007) (supplementary fig. S7, Supplementary Material online), although we should note that recombination might have occurred between the two clusters (we observed some extremely similar regions in the multiple sequence alignments of these PKSs) which might distort the phylogenetic analysis.

The second enediyne-type PKS cluster lies very close to an NRPS gene cluster (SMCp20) with a very unusual feature that has not been observed before: the module containing the thiоesterase is fused C-terminally to a major facilitator-type transporter. This may be used to export the end product from the cell immediately after assembly. Such a mechanism could have the advantage that the transport efficiency of the substance is much higher, and the cell can synthesize highly toxic compounds without these poisoning the producing cell.

Yet another remarkable cluster (SMC14) on the chromosome has one of its putative NRPS modules fused to a β-lactamase domain (PFAM number PF00144). No significant resemblance of this domain to any experimentally studied protein was detected, so we can only speculate about its function: it might, for example, act as a transpeptidase or bind to, but not hydrolyze, a β-lactam compound that is then attached to the peptide synthesized by
the NRPS. Generally, these domains are of high importance in β-lactam producing organisms, as they can catalyze the opening and hydrolysis of the β-lactam ring of β-lactam antibiotics and can thus provide resistance to the strain’s own antibiotics. Twenty-two proteins carrying a predicted β-lactamase domain were detected on the chromosome or plasmid (supplementary table S3, Supplementary Material online).

Cross-regulation Takes Place between the Megaplasmid and the Chromosome

Expression of secondary metabolite genes can be regulated in a variety of ways. One important regulatory mechanism involves small signaling molecules called γ-butyrolactones (Takano 2006). In S. clavuligerus, a gene encoding a γ-butyrolactone receptor protein (Scαr/Brp) was recently identified and shown to regulate clavulanic acid and cephamycin C production (Kim et al. 2004; Santamarta et al. 2005). We identified this gene as the megaplasmid-encoded SCLAV_p0894, which appeared to be the only γ-butyrolactone receptor protein-encoding gene in the entire genome. However, four ScβA/AsfA-like putative butyrolactone biosynthetic proteins were detected: three on the chromosome (SCLAV_0463, SCLAV_0471, SCLAV_2310) and one on the megaplasmid (SCLAV_p0812). Based on phylogenetic analysis (supplementary fig. S8, Supplementary Material online), SCLAV_2310 is the most likely candidate for being involved in butyrolactone biosynthesis. The fact that the only γ-butyrolactone receptor protein is encoded on the megaplasmid is remarkable, as all other characterized γ-butyrolactone receptors are chromosomally encoded. Moreover, it means that Brp transregulates several factors on the chromosome (at least the cephamycin C and clavulanic acid gene clusters). Because in a phylogenetic analysis, Brp was shown to cluster together with all known chromosomally encoded γ-butyrolactone receptors (Nishida et al. 2007), one is tempted to speculate that this gene was originally derived from the main chromosome and became plasmid-borne through recombination or transposition. Interestingly, two of the AsfA domain-containing butyrolactone biosynthetic proteins (SCLAV_0463 and SCLAV_0471) lie in a PKS gene cluster (SMC5), which consequently might be regulated by butyrolactone signaling.

Other regulatory genes were also identified. Fifty sigma factor genes were found, of which 43 lie on the chromosome and seven on pSCL4. Fifty-one paired two-component regulatory systems were identified, of which 44 are encoded on the chromosome and seven on the megaplasmid. Also, 21 orphan response regulator genes and eight orphan hisidine kinase genes were identified. The two-component systems include at least five (chromosomally encoded) very close homologues of systems that have been observed to be involved in the regulation of antibiotic biosynthesis: AfsQ12 (SCLAV_3812–3813) (Ishizuka et al. 1992), CutRS (SCLAV_4778–4779) (Chang et al. 1996), RapA12 (SCLAV_4312–4313) (Lu et al. 2007), AbrB12 (SCLAV_1381–1382) and AbiA123 (SCLAV_3595–3597). Additionally, 26 serine/threonine kinase genes were detected, of which only two are on the megaplasmid. Finally, 20 Streptomyces antibiotic regulatory protein (SARP) genes were detected, of which eight...
are on the megaplasmid. Seven SARPs are encoded in or very near secondary metabolism gene clusters.

The vast array of potential regulatory mechanisms suggests that the production of secondary metabolites in *S. clavuligerus*—as in other streptomycetes—is under complex regulation, being highly tuned to the specific needs of the organism. It is striking that for all classes of regulators, the plasmid seems to encode considerably fewer compared with the chromosome, reinforcing the view that it is a highly specialized genetic element.

**Scenarios for the Evolution of pSCL4**

The small size of the *S. clavuligerus* chromosome and the functional similarity between pSCL4 and *Streptomyces* chromosomal arms prompted the question how a megaplasmid-like pSCL4 could have originated. Interestingly, a megaplasmid or chromosome of very similar size (1.8 Mb) has been observed in *S. coelicolor* A3(2), after a single crossover between the 365-kb SCP1 plasmid and the chromosome (Yamasaki and Kinashi 2004). However, such a simple single crossover cannot have produced a plasmid configuration as seen in pSCL4, as it would have lead to an asymmetrical replicon with the Ori located distantly from the centre (fig. 3B, upper part). The central position of the pSCL4 Ori suggests that multiple recombination events have taken place either simultaneously or consecutively. Furthermore, the small size of the main chromosome compared to those of other *Streptomyces* species suggests that the plasmid may well have been endowed with genetic regions from the chromosome arms in the recent past. Other observations that should also be taken into account are the clustering of replication genes (*parAB, tap, tpg*, plasmid primase/replicase genes) and other important genes such as the butyrolactone receptor gene *brp* close to the plasmid Ori, and the existence of a region close to the plasmid Ori (SCLAV_p0926–0939) similar to chromosomal regions of many other actinomycetes but not found on the *S. clavuligerus* chromosome. These considerations suggest three possible scenarios for the origin of pSCL4 (fig. 3).

According to the first scenario, a relatively small plasmid underwent double crossing over with the chromosomal core, to yield a core chromosome with small plasmid arms and a plasmid core with large chromosomal arms. The second scenario is a variant of the first but postulates two asynchronous recombination events: first, a smaller plasmid recombined with one chromosomal arm, yielding an asymmetrical plasmid and then this situation was stabilized by another recombination with the other chromosomal arm. In the third scenario, a small integrating plasmid would have integrated into one of the chromosomal arms, after which it would have broken off (e.g., during conjugative transfer) and become a separate replicon.

The first two scenarios both seem parsimonious, as they can explain the symmetrical GC skew plot of pSCL4 without the need for extensive subsequent evolutionary fine-tuning.
the telomeres at the very ends of chromosome and mega-plasmid might help to confirm this.

**Conclusions**

The sequencing of the genome of *S. clavuligerus* reveals the potential for producing a vast array of interesting novel secondary metabolites, some of them encoded by unusual gene configurations that have never been observed before. The fact that a major part of the secondary metabolite biosynthesis gene clusters is localized on a specialized giant linear plasmid (pSCL4), which we predict not to contain any genes essential for primary metabolism, indicates that plasmids could more often encode secondary metabolites than previously thought (Kinashi 2008). The small size of the *S. clavuligerus* chromosome and the absence of hallmarks typical for *Streptomyces* chromosomal termini, together with the remarkable presence of such terminal hallmarks on the plasmid, suggest that the megaplasmid may have originated by a double recombination of a smaller plasmid with the chromosome. There is evidence that cross-regulation of chromosomal genes by at least one plasmid-encoded regulator still occurs. Intriguingly, the deduced flow of genetic material between different replicons may not be an exception: the phylogeny of telomere replication proteins from plasmids as well as chromosomes suggests that fluxes of genetic material regularly take place between streptomycete chromosomes and plasmids. Indeed, the mobilization of secondary metabolite gene clusters onto large linear plasmids such as pSCL4, which could be vectors for horizontal gene transfer (Ravel et al. 1998, 2000), indicates that constant and extensive “open source” evolution (Frost et al. 2005) of secondary metabolite-encoding DNA regions in actinomycetes could be responsible for the large differences in secondary metabolite repertoires between different species. Approaches that “awaken” uncharacterized gene clusters will undoubtedly be pivotal to uncover the functionalities of the secondary metabolites they encode (Scherlach and Hertweck 2009). Furthermore, if the plasmid could be cured from the strain (Hsu and Chen 2010), the small
chromosome of *S. clavuligerus* may be a very interesting vehicle for synthetic biology (Keasling 2008), serving as a starting point for the construction of a “minimal streptomycete.”

**Supplementary Material**

Supplementary figures S1–S8 and tables 1 and 2 are available at Genome Biology and Evolution online (http://www.oxfordjournals.org/our_journals/gbe/).

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**Literature Cited**


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