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Functional characterization of Tn*1331* gene cassettes

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***Objectives*: The transposon Tn*1331* possesses a region including three antibiotic resistance genes with the structure *aac(6′)-Ib-attC-aadA1-attI1*-bla*$_{OXA-9}$*-attC*, which potentially includes four gene cassettes. Experimental data on the mobility of fusion cassettes as well as those on mobility of cassettes in a genetic environment such as Tn*1331*, which lacks an integrase gene, are limited. Therefore, experiments using pJHCMW1, a plasmid harbouring this transposon, in the presence of IntI1 supplied *in trans* were carried out to define which cassettes are mobile *in vivo*.**

***Methods*: *In vivo* excision of resistance genes was investigated in *Escherichia coli* cells harbouring pJHCMW1 and in a recombinant clone that included the *intI1* gene under the control of the P_{tac} promoter. Plasmid DNA was purified and subjected to PCR analysis, and DNA sequencing of PCR products was performed to determine whether excision had occurred.**

***Results and conclusions*: *In vivo* recombination experiments showed that the fused *aadA1-attI1*-bla*$_{OXA-9}$*-attC* gene cassette was excised in the presence of IntI1. The excision of a DNA fragment including *aadA1-attI1** was also detected but at a lower frequency. The analysis of the latter recombination reaction showed that, although *attI1** includes only a small fraction of the complete *attI1* sequence, it is still used as a substrate by IntI1, albeit in a very inefficient manner.**

Keywords: integron, integrase, site-specific recombination

Introduction

Antibiotic resistance genes have the potential to reach most, if not all, bacterial cells through a combination of mechanisms that facilitate dissemination at the cellular and molecular levels. Some of these genes are found in structures known as gene cassettes, which consist of the structural gene and a target for site-specific recombination.[1,2] These gene cassettes are usually part of the integrons, which include an integrase gene that mediates excision or integration of gene cassettes.[3] This results in a highly versatile mechanism for the dissemination of antibiotic resistance genes at the molecular level. The spread of these resistance genes is enhanced when integrons are included within transposons and plasmids.

The transposon Tn*1331*, found in numerous multiresistance plasmids from Enterobacteriaceae including pJHCMW1,[4–7] harbours a 2438 bp DNA fragment (coordinates 7302–9740, accession number AF479774) with the general structure of the variable region of class 1 integrons, but lacking the 3′- and 5′-conserved sequences.[8] This region contains three resistance genes with the following genetic structure: *aac(6′)-Ib-attC-aadA1-attI1*-bla*$_{OXA-9}$*-attC* (Figure 1a).[8,9] In integrons, the gene located at the 5′ end of the variable region is preceded by an *attI* recombination site,[3,10,11] which is located adjacent to the *intI* gene within the 5′-conserved region.[12,13] In the case of Tn*1331*, *attI* is missing upstream of the *aac(6′)-Ib* gene (Figure 1a). Instead, an 8 bp sequence known as *attI1** (AAACAAAG) is found at the beginning of the structural gene, at the location where a gene fusion between a *bla*$_{TEM}$ gene and a precursor of *aac(6′)-Ib* is believed to have occurred (Figure 1a).[9,14] The complete *attI1* site is 65 bp and includes the so-called 'simple site', which consists of a pair of IntI1-binding domains separated by a 7 bp spacer and two directly oriented IntI1-binding sites known as DR1 and DR2.[13] The 8 bp *attI1** site includes the 7 bp spacer (underlined earlier) and the nucleotide preceding it.[13]

At the 3′ end of the *aadA1* gene, instead of the usual *attC* site (also known as 59 base element[10]), there is a copy of *attI1** (Figure 1a), which may have been formed by an illegitimate recombination event between *attC* located 3′ of *aadA1* of an integron and *attI1* located 5′ of *bla*$_{OXA-9}$ of another integron in which the *bla*$_{OXA-9}$ gene cassette is adjacent to the 5′-conserved sequence.[8,15,16]

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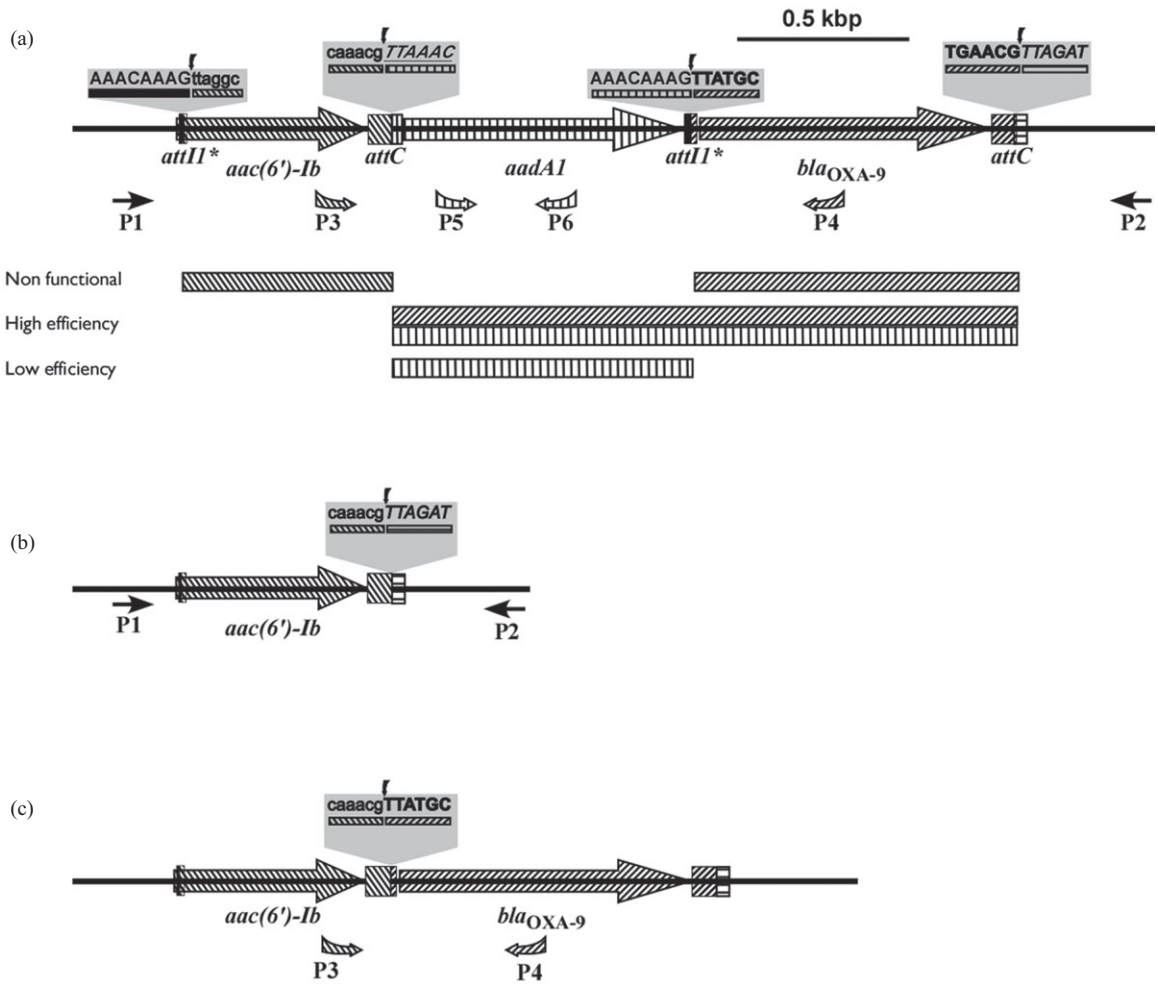

Figure 1. (a) Genetic map of the Tn*1331* region including genes *aac(6′)-Ib*, *aadA1* and bla_{OXA-9}. The genes are shown in different patterns. Boxes with patterns represent *attC* loci and black boxes represent *attI1** loci. The points of potential crossover reactions are indicated (downward arrows). Possible gene cassettes are indicated below the genetic map by bars of different patterns. The gene cassette including *aadA1-attI1*-*bla_{OXA-9}*-attC* is identified by a double box with two patterns. The primers are indicated by arrows of different patterns. The genetic map is at scale, but the primers and boxes are not. (b) Genetic map of the product of excision of the *aadA1-attI1*-*bla_{OXA-9}*-attC* gene cassette. (c) Genetic map of the product of excision of the *aadA1-attI1** gene cassette.

The Tn*1331* 2438 bp DNA region described in the preceding paragraphs has the potential to include four gene cassettes, assuming that the excision of a gene cassette requires at least one intact *attC* site at one boundary. Three of the potential gene cassettes include a single resistance gene, whereas the fourth includes *aadA1* and bla_{OXA-9} (Figure 1a). However, the characteristics discussed earlier suggest that not all of them may be excised in the presence of the IntI1 integrase. To define which ones are mobile *in vivo*, we performed excision experiments in *E. coli* cells carrying pJHCMW1 and in a recombinant plasmid that included the *intI1* gene under the control of the P_{tac} promoter.

Materials and methods

Bacterial strains and plasmids

E. coli TOP10 (Invitrogen) cells were used for all assays. Plasmid pJHCMW1 was originally isolated from *Klebsiella pneumoniae* JHCK1.[4] Plasmid pLQ369 is a recombinant clone that includes the *intI1* gene under the control of the P_{tac} promoter.[17]

In vivo recombination assays

Recombination assays to detect excision of resistance genes were performed using *E. coli* TOP10 cells harbouring pJHCMW1 and pLQ369, following the protocol described by Gravel *et al.*,[17] with slight modifications. The assays were carried out by inducing the expression of the *intI1* gene in the presence of 0.5 mM isopropyl-β-D-thiogalactopyranoside followed by incubation of the cell suspension at 37°C for 3 h in Luria broth (0.5% yeast extract, 1.5% tryptone and 0.5% NaCl) with shaking. To determine whether recombination had occurred, plasmid DNA was extracted from the cells using the QIAspin miniprep kit (Qiagen) and used as template in the PCR analysis. PCR reactions were carried out using the QIAGEN *Taq* master mix, and the products were detected by agarose gel electrophoresis. PCR reactions were carried out using the primers shown in Table 1. Control assays were performed using *E. coli* TOP10 that carried only pJHCMW1.

Table 1. Nucleotide sequences of the primers used for PCR

Oligonucleotide	Sequence	Coordinates (accession number AF479774)
P1	5′-GCCTCGTGATACGCCTATTTT	7111-7131
P2	5′-GCCCTTCTGATGAAGCGTC	10080-10061
P3	5′-GCAAGGTACCGTAACCACCC	7820-7839
P4	5′-GCTGCGAGAACCAGACAACAG	9168-9148
P5	5′-TGCTGGCCGTACATTTG	8057-8073
P6	5′-TCATTGCGCTGCCATTC	8321-8305

DNA sequencing

Prior to sequencing, the PCR products were cloned into the pCR2.1 vector as recommended by the supplier (Invitrogen). The recombinant clones were purified using the QIAspin miniprep kit (Qiagen) and used as templates for sequencing reactions. Sequencing was performed on both DNA strands using an ABIPrism 3100 BioAnalyzer and Taq FS Terminator Chemistry (Taq FS, Perkin-Elmer) at the Utah State University sequencing facility. Sequences were examined and assembled with Sequencher 4.7 software (Gene Codes Corp.).

Results and discussion

Plasmid DNA extracted from *E. coli* cells harbouring pJHCMW1 and pLQ369, after inducing expression of *intI1*, was used as a template in an amplification reaction with primers P1 and P2. Figure 2(a) shows the agarose gel electrophoresis analysis of the products of this reaction. There were two amplicons: one with the size expected of amplification of the region encompassing *aac(6′)-Ib-attC-aadA1-attI1*-bla*$_{OXA-9}$*-attC* (Figure 1a), and the other had the size expected of a region lacking the *aadA1* and *bla*$_{OXA-9}$ genes (schematically shown in Figure 1b). The nature of the latter amplicon was confirmed by nucleotide sequencing. Figure 2(b) shows that the region encompassed by the IntI1 recombination site within the *attC* site located downstream of *aac(6′)-Ib* and that by the recombination site within the *attC* site located downstream of *bla*$_{OXA-9}$ were missing from the template. Furthermore, the nucleotide sequence of this amplicon shows that the excision occurred at the expected sites for an IntI1-mediated site-specific recombination event between two *attC* sites (Figure 2a), a result consistent with the IntI1-mediated excision of a gene cassette consisting of *aadA1-attI1*-bla*$_{OXA-9}$*-attC*.

Amplification reactions using primers P1 and P6 or P5 and P2 (Figure 1a) each showed a unique band consistent with intact pJHCMW1 DNA (data not shown), indicating that the excision of the putative gene cassettes *aac(6′)-Ib-attC* and *bla*$_{OXA-9}$*-attC* was not detected in these experiments.

To detect the product of excision of the *aadA1-attI1** gene cassette, an amplification reaction was carried out using the P3 and P4 primers (Figure 1a). Figure 2(c) shows that a faint band corresponding in size to a fragment amplified from a template missing the *aadA1-attI1** gene cassette was detected (see a map detailing this excision in Figure 1c). The band intensity indicates that this template is present in a small fraction of the plasmid molecules. This experiment was repeated several times, and in

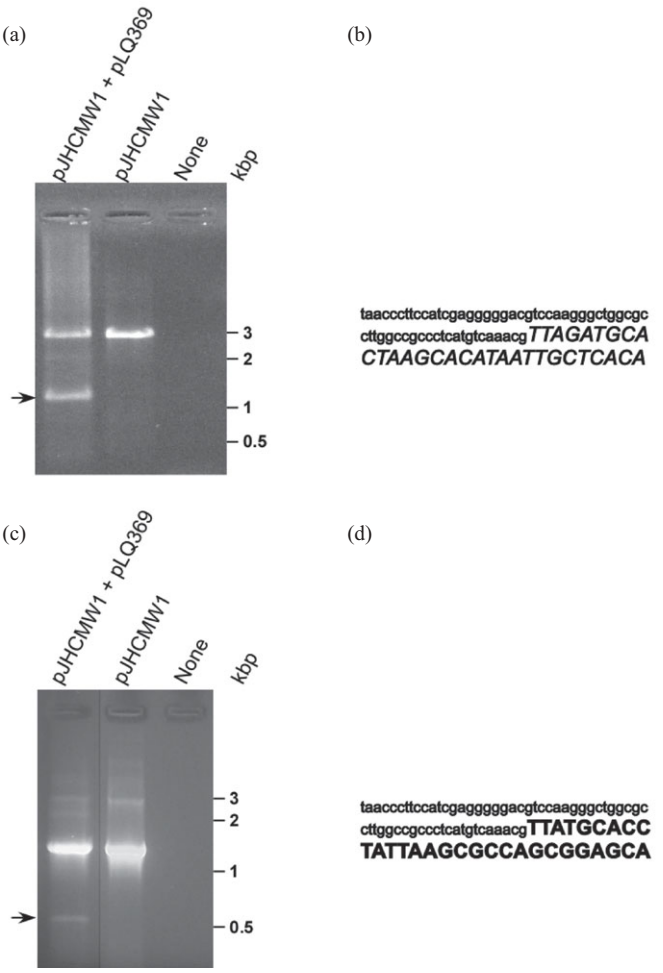

Figure 2. (a and c) Agarose gel electrophoresis of amplicons obtained using plasmid DNA extracted from cells cultured in the conditions indicated in the text as template and the primers P1 and P2 (a) or P3 and P4 (c). The 1191 bp fragment (arrow) in the gel of (a) corresponds to the amplicon obtained when excision of the fragment *aadA1-attI1*-bla*$_{OXA-9}$*-attC* has occurred. The 568 bp fragment (arrow) in the gel in (c) corresponds to the amplicon obtained when excision of the fragment *aadA1-attI1** has occurred. The line between the first and second lanes shows that they were not contiguous in the original gel. (b) Nucleotide sequence of the region surrounding the recombination site in the 1191 bp amplicon. (d) Nucleotide sequence of the region surrounding the recombination site in the 568 bp amplicon. The format of the fonts in the sequences shown in (b) and (d) corresponds to that in the genetic map shown in Figure 1(a).

all cases, the same size fragment was detected. This suggests that the excision between the *attC* locus located upstream of *aadA1* and *attI1** occurred infrequently. The fact that the deletion product is the result of IntI1-mediated site-specific recombination between *attC* and *attI1** was confirmed by nucleotide sequencing (Figure 2d). As a consequence of the overloading to detect this band, we also observed an unidentified band of 3 kb that was also present in the control that lacked pLQ369. It was somewhat surprising to observe an IntI1-mediated recombination between *attC* and *attI1**, which is a markedly truncated IntI1 recombination site. This site has been the subject of previous studies. There is a structure in Tn*1404* that consists of the prototype *aadB* gene cassette,[18] followed by an *aadA10* gene cassette that contains *attI1** instead of a complete *attC*.[19] Recombination studies failed to detect IntI1-mediated deletion of the *aadA10* cassette, suggesting that, in this environment, *attI1** is either non-functional or so inefficient that PCR analysis was unable to detect the products.[19] In the case of Tn*1331*, low but detectable recombination between *attC* and *attI1** was consistently observed, demonstrating that *attI1** is functional.

In conclusion, our *in vivo* recombination experiments show that the fused gene cassette including *aadA1-attI1*-bla*$_{OXA-9}$-*attC* and the imperfect gene cassette *aadA1-attI1** can be excised. However, the excision efficiency of the latter is much lower. Conversely, no excision of the gene cassettes containing only *aac(6′)-Ib* or *bla*$_{OXA-9}$ was observed. Although there are prototype *attC* sites downstream of both genes, the usual IntI1 target sequences located at the 5′ ends are missing. *bla*$_{OXA-9}$ is preceded by *attI1**, whereas in the case of *aac(6′)-Ib*, *attI1** is located towards the beginning, but within the gene (Figure 1a). These results suggest that the *attI1** locus does not serve as a substrate for IntI1-mediated recombination with *attC* when it is located 5′ of a gene. In contrast, it can serve as a substrate for the integrase when located 3′ of a gene, albeit inefficiently. As these experiments were designed to detect the excision of the gene cassette, the question of whether IntI1 also mediates the integration of a gene cassette with these characteristics remains unanswered.

The combination of gene exchange at the cellular and molecular levels results in the virtual elimination of barriers between bacteria, allowing antibiotic resistance genes to reach virtually all bacterial cells.[20] IntI1-mediated excision and integration of gene cassettes play a crucial role in the mobilization of antibiotic resistance genes.[3] Studies on structural[21] and mechanistic[17,22] aspects of the IntI1-mediated reaction will not only increase our understanding of the capture and spread of resistance traits, but also other genetic traits that may have an impact in genomic evolution.

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Transparency declarations

None to declare.

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