An easily modifiable conjugative plasmid for studying horizontal gene transfer

Wang, Qinqin; Olesen, Asmus Kalckar; Maccario, Lorrie; Madsen, Jonas Stenløkke

Published in:
Plasmid

DOI:
10.1016/j.plasmid.2022.102649

Publication date:
2022

Document version
Publisher's PDF, also known as Version of record

Document license:
CC BY

Citation for published version (APA):
An easily modifiable conjugative plasmid for studying horizontal gene transfer

Qinlin Wang, Asmus Kalckar Olesen, Lorrie Maccario, Jonas Stenløkke Madsen

Section of Microbiology, Department of Biology, University of Copenhagen, 2100 Copenhagen, Denmark

ARTICLE INFO

Keywords:
Conjugative plasmid
Genetic engineering
red recombination system
Tn7 transposons

ABSTRACT

Horizontal gene transfer (HGT) is an important mechanism in bacterial evolution and can occur at striking frequencies when mediated by mobile genetic elements. Conjugative plasmids are mobile genetic elements that are main drivers of horizontal transfer and a major facilitator in the spread of antibiotic resistance genes. However, conjugative plasmid models that readily can be genetically modified with the aim to study horizontal transfer are not currently available. The aim of this study was to develop a conjugative plasmid model where the insertion of gene cassettes such as reporter genes (e.g., fluorescent proteins) or antibiotic resistance genes would be efficient and convenient. Here, we introduced a single attTn7 site into the conjugative broad-host-range IncP-1 plasmid pKJK5 in a non-disruptive manner. Furthermore, a version with lower transfer rate and a non-conjugative version of pKJK5-attTn7 were also constructed. The advantage of having the attTn7 sites is that genes of interest can be introduced in a single step with very high success rate using the Tn7 transposition system. In addition, larger genetic fragments can be inserted. To illustrate the efficacy of the constructed pKJK5 plasmids, they were complemented with sfGFP (a gene encoding superfolder green fluorescent protein) in addition to seven different β-lactamase genes representing the four known classes of β-lactamases.

1. Introduction

Horizontal gene transfer (HGT) is an important facilitator of bacterial evolution and when mediated by mobile genetic elements, such as conjugative plasmids, HGT can occur at striking frequencies (Sørensen et al., 2005). Conjugative plasmids are especially known for their role in spreading antibiotic resistance genes (Che et al., 2021) and virulence factors (Ghigo, 2001), however, while this underlines their importance, there are still many unknowns about the biology of plasmids and HGT in general. Here we constructed a conjugative plasmid which easily can be complemented with genetic cassettes to investigate various aspects of HGT including plasmid biology, transfer dynamics, accessory genes, stability, etc. Molecular engineering of conjugative plasmids can have numerous objectives such as, complementing conjugative plasmids with reporter genes that can be used to study transfer dynamics at the single cell level (Pinilla-Redondo et al., 2018), testing what genes can be transferred stably by conjugation, factors that affect the success of HGT, and metagenome engineering and cargo delivery by conjugation. Though, many other applications can be imagined.

Tn7 transposons have been widely used in bacterial genome engineering enabling gene complementation and expression (Peters and Craig, 2001). When transposition is mediated by Tn7 transposon can be inserted specifically into chromosomes at an attTn7 site, which typically is located downstream of the bacterial glutamine synthetase (glmS) gene of gram-negative bacteria which is highly conserved (Peters and Craig, 2001). Choi et al. constructed the widely used mini-Tn7 system where the genetic material one wishes to transpose is flanked by inverted repeats named Tn7L and Tn7R on a transfer plasmid. Tn7L and Tn7R are recognized by the transposase complex TnsABCD, encoded on the helper plasmid, and then inserted at the chromosomal attTn7 (Kyoung Hee Choi et al., 2005). The bacterial Tn7 transposon is that genes of interest can be introduced in a single step with very high success rate using the Tn7 transposition system. In addition, larger genetic fragments can be inserted. To illustrate the efficacy of the constructed pKJK5 plasmids, they were complemented with sfGFP (a gene encoding superfolder green fluorescent protein) in addition to seven different β-lactamase genes representing the four known classes of β-lactamases.

* Corresponding author at: Section of Microbiology, Department of Biology, University of Copenhagen, Universitetsparken 15, DK-2100 Copenhagen Ø, Denmark.
E-mail address: jsmadsen@bio.ku.dk (J.S. Madsen).

https://doi.org/10.1016/j.plasmid.2022.102649
Received 17 May 2022; Received in revised form 3 September 2022; Accepted 7 September 2022
Available online 11 September 2022
0147-619X/© 2022 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).
complex TnsABC-D were integrated into a single temperature-sensitive vector, which furthered the ease by which Tn7-based gene complementation can be done (McKenzie and Craig, 2006).

Another widely used gene integration system is the \( \lambda \) phage derived Red recombination system, a mutagenesis method that through homologous recombination allows defined insertions of genes, deletions, or point mutations in bacteria and fungi (Chaveroche, 2000; Datosenko and Wanner, 2000). With this method, efficient recombination can be achieved between polymerase chain reaction (PCR) products and a target replicon by induction of the Tn7 phage Red operon, provided that the linear DNA obtained by PCR has up to 36 nt or larger flanking extensions that are homologous to the target DNA. The Red operon encodes three genes, \textit{gam}, \textit{exo} and \textit{beta}. \textit{Gam} prevents the intracellular exonucleases from digesting the linear DNA introduced into the bacteria. \textit{Exo} will degrade linear dsDNA starting from the 5′ end and generate ssDNA, and \textit{Beta} protects the ssDNA produced by the \textit{Exo} and promotes its annealing to the complementary ssDNA target in the replicon (Datosenko and Wanner, 2000). The great advantage of the Red recombination system is that mutagenesis can be done specifically at any genomic site (Datosenko and Wanner, 2000).

Here we utilized the Red recombination system to insert an \textit{attTn7} site into a model conjugative plasmid pKJK5, in a non-disruptive manner. pKJK5 belongs to the IncP-1 incompatibility group (Bahl et al., 2007a) and has a very broad host range (Klümper et al., 2015). It transfers at high frequencies to many proteobacteria but has also been reported to transfer to gram-positive bacteria (Klümper et al., 2015) and IncP-1 plasmids have been demonstrated to transfer even to eukaryotes (Hayman and Bolten, 1993). After successful insertion of \textit{attTn7} into pKJK5, generating pKJK5-\textit{attTn7}, we demonstrate the ease at which genes can be complemented into pKJK5-\textit{attTn7} where only a few PCR and screening steps are needed to achieve the desired results. In brief, the model conjugative plasmid presented here can be engineered easily and reliably to advance research on HGT and plasmid biology.

## 2. Material and methods

### 2.1. Plasmids and strains

The bacterial strains and plasmids used in this study are listed in Table 1. \textit{Escherichia coli} strains were grown in Luria-Bertani (LB) medium (VWR Life Science) at 30 °C, 37 °C or 42 °C. Antibiotics (Sigma-Aldrich) were used at the following concentration: Ampicillin (Amp, 100 \( \mu \)g/mL), kanamycin (Kan, 50 \( \mu \)g/mL), tetracycline (Tet, 15 \( \mu \)g/mL), gentamicin (Gen, 15 \( \mu \)g/mL), rifampicin (Rif, 100 \( \mu \)g/mL), nalidixic acid (Nal, 100 \( \mu \)g/mL), chloramphenicol (Chl, 30 \( \mu \)g/mL), Cefotaxime (Ctx, 2 \( \mu \)g/mL), and Meropenem, (Mem, 0.5 \( \mu \)g/mL). Plasmid DNA was extracted from overnight cultures using the Plasmid Mini AX kit (A&A Biotechnology). Primers (TAG Copenhagen A/S) used in this study are in Table 2.

### 2.2. Electroporation

5 ml of \textit{E. coli} cultures were grown to mid-log phase (OD\textsubscript{600} approximately 0.6) at 30 °C and washed twice with 1 ml of ice-cold 10% v/v glycerol. Cells were then resuspended in 50 ml of ice-cold 10% glycerol. DNA (100–150 ng PCR fragment or 10 ng plasmid) was added to the cell suspension and electroporated in a 0.1 cm Gene Pulser® cuvette (Bio-Rad) at 1.8 kV for ~ 5 ms on a MicroPulser Electroporator (Bio-Rad). 1 ml of LB medium was added immediately after electroporation and the cells were incubated for 1.5 h at 30 °C. Finally, the cells were plated on LB agar plates containing selective antibiotics and incubated overnight at 30 °C.

### 2.3. Construction of plasmid pKJK5-\textit{attTn7}

Plasmid p-\textit{attTn7} was synthesized by Thermofisher Scientific based on a provided design, as further described in the results section (Fig. 1). Using p-\textit{attTn7} as template, the \textit{attTn7-FRT-\textit{aac3}-FRT} fragment was amplified by PCR using primers \textit{attTn7Gen}\textsubscript{R} and \textit{attTn7Gen}\textsubscript{F}. These primers included overhangs with 40 bp homology to the pKJK5 target region. The two tandem flippase recognition target (FRT) sites are used for later flippase (FLP) to delete the DNA sequence between these two sites (Schlake and Bode, 1994). 100–150 ng of the linear PCR product was transformed by electroporation into competent \textit{E. coli} DH5\( ^{\alpha} \) cells already harboring both the helper plasmid pKD46 and the target plasmid pKJK5. Here the \( \lambda \) Red recombinant protein expressed by the helper plasmid pKD46 recombined the \textit{attTn7-FRT-\textit{aac3}-FRT} fragment into pKJK5 by homologs recombination. Successfully integration of \textit{aac3} rendered strains resistant to gentamicin. Selection was thus done on LB agar medium containing Amp, Tet, and Gen. Growing colonies were screened by colony PCR using the \textit{attTn7Gen}\textsubscript{F} and \textit{attTn7Gen}\textsubscript{R} primers. Positive colonies were grown in LB with Tet and Gen at 42 °C overnight to remove pKD46. Post plasmid curing, it was ensured that colonies were sensitive to Amp.

Hereafter, to remove the antibiotic resistance selection marker \textit{aac3}, the helper plasmid pFLP2 expressing the FLP recombinase was introduced (Young Hee Choi and Schweizer, 2005). Plasmid pFLP2 was transformed into the \textit{E. coli} DH5\( ^{\alpha} \) cells containing the now constructed pKJK5-\textit{attTn7-FRT-\textit{aac3}-FRT} by electroporation, to obtain plasmid pKJK5-\textit{attTn7}. FLP excised the gene \textit{aac3} between the two inversely repeated FRT sites by cleavage and re-ligation, leaving a single FRT site (Fig. 1c and d). Clones that grew on LB agar medium with Tet but did not grow in the presence of Gen were selected and verified by colony PCR with primers \textit{attTn7Gen}\textsubscript{R} and \textit{attTn7Gen}\textsubscript{F}. After flippase mediated removal of \textit{aac3}, LB agar plates containing 5% w/v sucrose were used to counter-select against pFLP2 which encoded \textit{sacB}. Cells containing only pKJK5-\textit{attTn7} were whole-genome sequenced by Nanopore sequencing

### Table 1

<table>
<thead>
<tr>
<th>Strains and plasmids used in this study.</th>
<th>Growth temperature</th>
<th>Antibiotic resistance</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>\textit{Escherichia coli DH5( ^{\alpha} )}</td>
<td>37 °C</td>
<td>#</td>
<td>Invitrogen</td>
</tr>
<tr>
<td>\textit{Escherichia coli K-12 MG1655}</td>
<td>37 °C</td>
<td>Kan( ^{\beta} ), Rif( ^{\beta} ), Nat( ^{\beta} )</td>
<td>(Madsen et al., 2016)</td>
</tr>
<tr>
<td>\textit{Escherichia coli K-12 MG1655}</td>
<td>37 °C</td>
<td>Kan( ^{\beta} )</td>
<td>(Klümper et al., 2015)</td>
</tr>
<tr>
<td>pGRG36</td>
<td>30 °C, temperature-sensitive replicon</td>
<td>Amp( ^{\beta} )</td>
<td>Addgene plasmid #16666 (Datosenko and Wanner, 2000)</td>
</tr>
<tr>
<td>pKD46</td>
<td>30 °C, temperature-sensitive replicon</td>
<td>Amp( ^{\beta} )</td>
<td>Addgene plasmid #54519 (Pedelaar et al., 2006)</td>
</tr>
<tr>
<td>pKD3</td>
<td>37 °C</td>
<td>Amp( ^{\beta} ), cat (Chl( ^{\beta} ))</td>
<td>(Datosenko and Wanner, 2000)</td>
</tr>
<tr>
<td>pFLP2</td>
<td>37 °C</td>
<td>Amp( ^{\beta} )</td>
<td>(Hoang et al., 1998)</td>
</tr>
<tr>
<td>p-\textit{attTn7}</td>
<td>37 °C</td>
<td>\textit{aac3} (Gen( ^{\beta} ))</td>
<td>This study</td>
</tr>
<tr>
<td>p-sfGFP</td>
<td>37 °C</td>
<td>\textit{tetA}(Tet( ^{\beta} ))</td>
<td>Addgene plasmid #53219 (Pedelaar et al., 2006)</td>
</tr>
</tbody>
</table>
Table 2
Oligonucleotide primers used in this study.

<table>
<thead>
<tr>
<th>Primers</th>
<th>Sequence</th>
<th>Product size (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>attTn7Gen(^{a})-F</td>
<td>5′-GGGTGGATCTCGTTGAGAT-3′</td>
<td>1501 bp</td>
</tr>
<tr>
<td>attTn7Gen(^{a})-R</td>
<td>5′-CCAGATTGGAATAACAGGAAAG-3′</td>
<td>1113 bp</td>
</tr>
<tr>
<td>CD-cat-F</td>
<td>5′-TTGATGTCGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCTGGTGGTGATGGGAGTGTCGCT-3′</td>
<td>1113 bp</td>
</tr>
<tr>
<td>CD-cat-R</td>
<td>5′-CGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG-3′</td>
<td>1113 bp</td>
</tr>
<tr>
<td>NC-cat-F</td>
<td>5′-TGGGTGGATCTCGTTGAGAT-3′</td>
<td>1501 bp</td>
</tr>
<tr>
<td>NC-cat-R</td>
<td>5′-GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG-3′</td>
<td>1113 bp</td>
</tr>
<tr>
<td>psfGFP-F</td>
<td>5′-GGGTGGATCTCGTTGAGAT-3′</td>
<td>1501 bp</td>
</tr>
<tr>
<td>psfGFP-R</td>
<td>5′-GGGTGGATCTCGTTGAGAT-3′</td>
<td>1501 bp</td>
</tr>
<tr>
<td>pGRG36-F</td>
<td>5′-ATCCTGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT-3′</td>
<td>257 bp</td>
</tr>
<tr>
<td>pGRG36-R</td>
<td>5′-ATCCTGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT-3′</td>
<td>257 bp</td>
</tr>
<tr>
<td>blaTEM1-F</td>
<td>5′-ATCCTGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT-3′</td>
<td>257 bp</td>
</tr>
<tr>
<td>blaTEM1-R</td>
<td>5′-ATCCTGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT-3′</td>
<td>257 bp</td>
</tr>
<tr>
<td>blaCTXM15-F</td>
<td>5′-ATCCTGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT-3′</td>
<td>257 bp</td>
</tr>
<tr>
<td>blaCTXM15-R</td>
<td>5′-ATCCTGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT-3′</td>
<td>257 bp</td>
</tr>
<tr>
<td>blaCMY2-F</td>
<td>5′-ATCCTGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT-3′</td>
<td>257 bp</td>
</tr>
<tr>
<td>blaCMY2-R</td>
<td>5′-ATCCTGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT-3′</td>
<td>257 bp</td>
</tr>
<tr>
<td>blaNDM5-F</td>
<td>5′-ATCCTGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT-3′</td>
<td>257 bp</td>
</tr>
<tr>
<td>blaNDM5-R</td>
<td>5′-ATCCTGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT-3′</td>
<td>257 bp</td>
</tr>
<tr>
<td>blaKPC2-F</td>
<td>5′-ATCCTGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT-3′</td>
<td>257 bp</td>
</tr>
<tr>
<td>blaKPC2-R</td>
<td>5′-ATCCTGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT-3′</td>
<td>257 bp</td>
</tr>
<tr>
<td>blaampC-F</td>
<td>5′-ATCCTGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT-3′</td>
<td>257 bp</td>
</tr>
<tr>
<td>blaampC-R</td>
<td>5′-ATCCTGGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT-3′</td>
<td>257 bp</td>
</tr>
</tbody>
</table>

Fig. 1. Stepwise engineering of pKJK5-attTn7. (a) The backbone of the conjugative broad-host-range IncP-1 plasmid pKJK5 and the region of insertion. (b) Schematic diagram of the attTn7 fragment used. (c) Schematic diagram of the plasmid pKJK5-attTn7-aac3 after insertion of the attTn7-aac3 cassette into plasmid pKJK5. (d) Schematic diagram of the plasmid pKJK5-attTn7 after removal of resistance gene aac3. (e) Colony PCR used to verify insertions. The primers attTn7Gen\(^{a}\)-F/R were used for PCR here. Lane M is DNA maker (NEB 1 Kb DNA Ladder), lane N shows the PCR product from negative control (ddH\(_2\)O), lane P shows the PCR product from plasmid pKJK5-attTn7-aac3, lanes 1 and 2 show the PCR products from two clones of pKJK5-attTn7. Figures (a), (b), (c) and (d) were generated with SnapGene software 6.0.2 (GSL Biotech).
carried out on R9.4 MiNiON flowcells (Oxford Nanopore Technologies) for up to 48h. Libraries were prepared using the Rapid Barcoding Sequencing Kit (Oxford Nanopore Technologies, SQK-RBK004) following the manufacturer’s instructions.

2.4. Construction of conjugation deficient plasmid pKJK5-attTn7 and non-conjugative plasmid pKJK5NC-attTn7

The λ Red homologous recombination method was also used to construct two additional versions of pKJK5-attTn7. One that transfers at lower frequencies, referred to as pKJK5NC-attTn7, and a non-conjugative version referred to as pKJK5NC-attTn7. Plasmid pKD3 (Datsenko and Wanner, 2000) was used as template to amplified the chloramphenicol acetyltransferase gene (cat) including FRT sites flanked by 40 bp homology overhangs (1113 bp). The primers CD-cat-F/R and primers NC-cat-F/R were used here respectively. The cat fragment was integrated into the traC gene (pKJK5 nt position 36,168–37,226, AM261208) of pKJK5-attTn7 using λ Red homologous recombination as described above. Hereafter, the plasmid pLP2 was used to remove the traC region including the cat gene (pKJK5 nt position 33,431–37,226) hereby obtaining pKJK5–attTn7. Similarly, to obtain pKJK5NC–attTn7, the cat fragment was integrated upstream of the traC gene (pKJK5 nt position 43,767–45,046) of pKJK5–attTn7, hereafter, the same approach was used to remove the traC–tra1 region including the cat gene (pKJK5 nt position 33,431–45,046). Colony PCR with primer sets attTn7Gen5-F and CD-cat-F/R-NC-cat-R were used to screen candidate colonies for pKJK5–attTn7 and pKJK5NC–attTn7, respectively. pKJK5–attTn7 specific PCR products were purified and confirmed by Sanger sequencing (Eurofins Genomics). pKJK5–attTn7 was whole-genome sequenced using the Illumina MiSeq platform. Sequencing libraries were prepared using the Nextera XT DNA Library Preparation Kit (Illumina, FC-131-1096) and sequenced with 2 x 250 base paired-end reads on the Illumina MiSeq platform (Illumina) according to the manufacturer’s protocol. Sequencing results were analyzed in CLC Genomic Workbench V7.5.1.

2.5. Construction of mini-Tn7 pGRG36-based delivery vectors for blgf expression complementation

To verify that integration could be done at the attTn7-site of the plasmids, the superfolder green fluorescent protein (sfGFP) gene and seven different β-lactamase genes were cloned into helper plasmid pGRG36 to subsequently be used as delivery into pKJK5-attTn7 and pKJK5NC–attTn7. sfGFP flanked by tetA was amplified by PCR from pSF-GFP, using primers psfGFP-F and psfGFP-F/R. This fragment was cloned into pGRG36 at the site of the lacI gene cassette, ensuring that Tn7 transposition inserts the blaf-sfGFP cassette into the attTn7 site of pKJK5–attTn7 and pKJK5NC–attTn7.

2.6. Insertion of different bla-sfGFP cassettes into pKJK5-attTn7 and pKJK5NC-attTn7 using Tn7 transposition

Firstly, the plasmids pKJK5–attTn7 and pKJK5NC–attTn7 were transformed by electroporation to Escherichia coli MG1655-lacI-mcherry (Klümper et al., 2015) competent cells, where the chromosomal attTn7-site is blocked by the lacI-mcherry gene cassette, ensuring that Tn7 transposition inserts the blaf-sfGFP cassettes into the attTn7 site of pKJK5–attTn7 and pKJK5NC–attTn7. Secondly, vectors pGRG36-sfGFP and pGRG36-sfGFP-bla (100–150 ng) were transformed by electroporation to E. coli MG1655-lacI-mcherry competent cells containing the conjugative plasmid pKJK5–attTn7 or pKJK5NC–attTn7. pGRG36 is a convenient Tn7 transposon vector that encodes transposition genes msc/ABC under the control of the arabinose-inducible regulator araC and Pbad promoter. pGRG36 also carries the temperature sensitive pC101 replication origin and an ampicillin resistance gene (McKenzie and Craig, 2006). For each of the 14 constructs, three colonies that grew on LB agar medium with Amp and Tet at 30 °C, single colonies were grown in LB broth supplemented with 0.1% w/v L-arabinose overnight at 30 °C with shaking. Hereafter, cultures were re-streaked onto LB agar medium and incubated overnight at 42 °C with the aim of curing the different pGRG36 vectors after the blaf-sfGFP cassettes insertion. Finally, clones were screened and verified by colony PCR with primers psfGFP-F/R and primers pGRG36-F/R.

2.7. Solid surface filter conjugation assay

Overnight cultures of donor strains (E. coli MG1655/pKJK5, E. coli MG1655/pKJK5–attTn7, E. coli MG1655/pKJK5NC–attTn7, and E. coli MG1655/pKJK5NC–attTn7) and a recipient strain (E. coli MG1655-KanR, RifR-NalR) were washed twice with PBS, and the OD600 of all cultures were adjusted to 0.5 with PBS. Donors and recipients were mixed at a ratio of 1:1 and immediately 50 μl was added onto a 0.2 μm mixed cellulose ester filter which was placed on top of LB agar medium. These were incubated for 20 h at 37 °C. After incubation, cells were transferred to a tube with 5 ml PBS by repeatedly pipetting cells off the filter. 100 μl of each of these suspensions were spread evenly onto agar plates with antibiotics as detailed below and incubated overnight at 37 °C. Transfer efficiencies were calculated as transconjugants per donor (Sørensen et al., 2005). LB agar plates containing Tet were used to count CFUs of the donors. LB agar plates containing Tet, and Rif were used to count CFUs of transconjugants. Three biological replicates were performed for each experiment and three technical replicates were made for each biological replicate.

2.8. Growth curves

E. coli strains carrying plasmids pKJK5, pKJK5–attTn7, pKJK5NC–attTn7, or pKJK5NC–attTn7 were cultured overnight in LB broth with Tet at 37 °C. Then LB broth was used to make 10-fold dilutions of the overnight cultures, and 200 μl diluted cultures were added to wells of a 96-well microtiter plate. Finally, the plate was incubated in a spectrophotometer (Bio Tek ELx808™ Absorbance Microplate Reader) at 37 °C overnight, with continuously shaking, and OD600 was measured every 15 min. Nine replicates were done for each strain (three biological replicates each with three technical replicates).

2.9. Flow cytometry

Flow cytometry was conducted to verify sfGFP expression using a BD FACS AriaIIa (BD Biosciences) with a 488 nm excitation laser and FITC (530/30 nm band-pass filter) detector. Wild-type strain E. coli MG1655 was used as a negative control. For sample treatment, 5 μl of the overnight cultured bacterial solution was added to 1 ml of PBS to ensure reaching ~3000 evt/s. The threshold for forward scatter (FSC) was 1200, for side scatter (SSC) was 200, and the gating strategy was
consistent with our previous study (Olesen et al., 2022). Data was acquired and analyzed using the BD FACSDiva software v.6.1.3.

2.10. Antibiotic sensitivity

Inhibitory concentrations of antibiotics for all strains were determined using the agar dilution method (Wiegand et al., 2008). Overnight cultures were diluted to 10^4 CFU/ml. 10 μl from each suspension were spotted onto LB agar plates containing a series of antibiotics (0–10 μg/ml MEM, 0–10 μg/ml CTX, 0–200 μg/ml AMP) to determine the minimum inhibitory concentration. The agar plates were incubated at 37°C for 16 h and the lowest antibiotic concentration that inhibited visible bacterial growth was regarded as inhibitory. These experiments were repeated independently three times.

2.11. Statistical analysis

All the comparisons of mean values between conditions (e.g., OD_{600}) were performed using one-way ANOVA with post-hoc Tukey tests calculated using R 4.0.0 (Team, 2013). Growth curves were analyzed with the R package Growthcurver (Sproufske and Wagner, 2016).

3. Results

3.1. Engineering an easily modifiable conjugative plasmid pKJK5-attTn7

Here, an attTn7-site was introduced into conjugative IncP-1 plasmid pKJK5 (Fig. 1a). Based on the genome sequence of pKJK5, we chose to insert the attTn7-site between nt 33,431–33,440 (Fig. 1a), as this was at the interface between plasmid backbone and accessory genes with little risk of functional disruption. The region may have encoded a terminator associated with traC, however, a new terminator was added with the attTn7 fragment (Fig. 1b). The inserted attTn7-FRT-aac3-FRT fragment was flanked on both sides with strong terminators to diminish expression spillover both from flanking genes and from genes to be inserted into the attTn7-site (Fig. 1c). aac3 was introduced alongside the attTn7-site and was subsequently removed by FLP recombinase-mediated excision via the flippase recognition target sites that flanked aac3 (Fig. 1d and Fig. 2a). Colony PCR and full genome sequencing verified pKJK5-attTn7 had been constructed successfully (Fig. 1e).

3.2. Conjugation deficient plasmid pKJK5_{CD}-attTn7 and non-conjugative plasmid pKJK5_{NC}-attTn7

In addition to the conjugative pKJK5-attTn7 plasmid, two additional versions of pKJK5-attTn7 were constructed. One that transfers at lower frequencies, referred to as pKJK5_{CD}-attTn7, and a non-conjugative version referred to as pKJK5_{NC}-attTn7. These were made as they can be used as comparative controls in various experimental setups. Previous studies have shown that making a knock-out in traF, which is in operon and upstream of traC, reduces the conjugation transfer frequency of pKJK5 (Bahl et al., 2007b; Roder et al., 2021). Therefore, it was assumed that deleting traC would in a similar manner create a conjugation deficient version of pKJK5-attTn7. To create a version that was not able to conjugate the traC-I region was deleted. This region encodes core proteins for relaxosome formation which is essential for the transfer of plasmid DNA during conjugation (Adamczyk and Jagura-Burdzy, 2003; Bahl et al., 2007a). An FRT-cat-FRT fragment was introduced upstream of traC to create pKJK5_{CD}-attTn7 (Fig. 3a) and upstream of traK to create pKJK5_{NC}-attTn7 (Fig. 3b) using λ Red recombination. Hereafter, FLP recombination was used to remove the regions between the FRT-site associated with attTn7 and those introduced with cat. This resulted in the deletion of the traC-FRT-cat-FRT region constructing pKJK5_{CD}-attTn7 and the deletion of traCDEFGHL-FRT-cat-FRT region constructing pKJK5_{NC}-attTn7.

Fig. 2. Schematic diagram of the construction of plasmids pKJK5-attTn7, pKJK5_{CD}-attTn7 and pKJK5_{NC}-attTn7. (a) λ Red homologous recombination was used when constructing plasmid pKJK5-attTn7. The helper plasmid pKD46 encoding the Red homologous recombinases was used to integrate the PCR product attTn7-FRT-aac3-FRT into pKJK5. The fragment attTn7-FRT-aac3-FRT contained the gentamicin resistance gene (aac3) and facilitated the selection of positive clones. Vector pFLP2 which facilitates FLP recombination of FRT-sites eliminated the gentamicin resistance gene. (b) λ Red homologous recombination was used when constructing plasmid pKJK5_{CD}-attTn7 and pKJK5_{NC}-attTn7. Insertion of the fragment FRT-cat-FRT into the plasmid pKJK5-attTn7 was performed in a similar way as (a). With the help of the FRT-site left in pKJK5-attTn7, FLP recombination removed traC-cat from pKJK5_{CD}-attTn7 and the traC-traA-cat region from pKJK5_{NC}-attTn7. Figures were created with BioRender.com. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)
Fig. 3. Stepwise engineering of plasmids pKJK5_{CD}-attTn7 and pKJK5_{NC}-attTn7. (a) FRT-cat-FRT was inserted into pKJK5-attTn7 upstream traC. Hereafter, Fpl recombination was used to remove traC-FRT-cat-FRT constructing conjugation deficient plasmid pKJK5_{CD}-attTn7. (b) FRT-cat-FRT was inserted into pKJK5-attTn7 upstream traI. Fpl recombination was used to remove traCDEFGHI-FRT-cat-FRT constructing non-conjugative plasmid pKJK5_{NC}-attTn7. (c) Schematic diagram of the FRT-cat-FRT fragment. (d) Colony PCR to verify the construction of pKJK5_{CD}-attTn7 and pKJK5_{NC}-attTn7. Lanes M are 1 kb DNA ladders (Thermo Scientific™ GeneRuler™ 1 kb Plus DNA Ladder). Lanes 1, 2, 3, and 4 show the PCR product from negative control (ddH₂O), plasmid pKJK5-attTn7, pKJK5_{CD}-attTn7-cat, and pKJK5_{CD}-attTn7 with primers CD-cat-F/R, respectively. Lanes 5, 6, and 7 show the PCR product from plasmid pKJK5_{CD}-attTn7-cat, pKJK5_{CD}-attTn7, and negative control (ddH₂O) with primers attTn7Gen⁸-F and CD-cat-R, respectively. Lanes 8, 9, 10, and 11 show the PCR product from negative control (ddH₂O), plasmid pKJK5_{attTn7}, pKJK5_{NC}-attTn7-cat, and pKJK5_{NC}-attTn7 with primers NC-cat-F/R, respectively. Lanes 12, 13, and 14 show the PCR product from plasmid pKJK5_{NC}-attTn7-cat, pKJK5_{NC}-attTn7, and negative control (ddH₂O) with primers attTn7Gen⁸-F and NC-cat-R, respectively. Figures (a), (b) and (c) were generated with SnapGene software 6.0.2 (GSL Biotech).
constructing pJK5\textsubscript{NC-attTn7} (Fig. 2b). Removal of tra\textsubscript{C} in pJK5\textsubscript{CD-attTn7} and tra\textsubscript{C-I} in pJK5\textsubscript{NC-attTn7} was verified by colony PCRs (Fig. 3d).

3.3. Growth and conjugal transfer frequencies

To investigate if the genetic modification applied to the plasmids had an immediate effect on their host, growth curves of the same host complemented with the different plasmids were done. Growth curves were made of strains \textit{E. coli} MG1655/pJK5, \textit{E. coli} MG1655/pJK5\textsubscript{attTn7}, \textit{E. coli} MG1655/pJK5\textsubscript{CD-attTn7}, and \textit{E. coli} MG1655/pJK5\textsubscript{NC-attTn7} (Fig. 4a). No significant difference was found between growth rates or the doubling times between the strains (\(P < 0.05\), one-way ANOVA with post-hoc Tukey test).

Next, we compared conjugal transfer frequencies of the different constructed plasmids in addition to the unmodified pJK5 plasmid. We used the strains \textit{E. coli} MG1655/pJK5, \textit{E. coli} MG1655/pJK5\textsubscript{attTn7}, \textit{E. coli} MG1655/pJK5\textsubscript{CD-attTn7}, and \textit{E. coli} MG1655/pJK5\textsubscript{NC-attTn7} as donors, and strain \textit{E. coli} MG1655-Kan\textsubscript{R}-Rif\textsubscript{R}-Nal\textsubscript{R} as recipient (Fig. 4b-c). We found that the insertion of the attTn7-site did not affect conjugal transfer as transfer frequencies of wildtype plasmid pJK5 and pJK5\textsubscript{attTn7} were similar (\(P = 0.739\), one-way ANOVA with post-hoc Tukey test). The transfer frequency of tra\textsubscript{C} deletion plasmid pJK5\textsubscript{CD-attTn7} was significantly reduced (\(P < 0.05\), one-way ANOVA with post-hoc Tukey test) rendering it conjugation deficient. No transconjugants were observed in transfer experiments with pJK5\textsubscript{NC-attTn7} showing that this plasmid had lost its ability to conjugate.

3.4. Gene complementation at the attTn7-site of the constructed plasmids

To test the efficacy of the attTn7 complemented plasmids, 7 different \(\beta\)-lactamase genes (\(\text{bla}_{\text{TEM-1}}, \text{bla}_{\text{CTX-M-15}}, \text{bla}_{\text{CMY-2}}, \text{bla}_{\text{NDM-5}}, \text{bla}_{\text{KPC-2}}, \text{bla}_{\text{SOX-19}}, \text{bla}_{\text{AMP}}\)) flanked by sfGFP were inserted into pJK5\textsubscript{attTn7} using the mini-Tn7 delivery vector pGRG36. Since the attTn7 site typically also exists in the bacterial chromosome, \textit{E. coli} MG1655-lac\textsuperscript{P-}\text{mcherry} (Klümpер et al., 2015) was used as background when performing complementation. In \textit{E. coli} MG1655-lac\textsuperscript{P-}\text{mcherry} the chromosomal attTn7-site was occupied by the lac\textsuperscript{P-}\text{mcherry} cassette preventing further chromosomal transposition events. PCR, gel electrophoresis, and Sanger sequencing was used to verify that the plasmids has been successfully constructed (Fig. 5a).

The different \(\beta\)-lactamase genes and sfGFP were also inserted into the non-conjugative plasmid pJK5\textsubscript{NC-attTn7}, illustrating the high efficacy of gene complementation into the attTn7-sites located on the constructed plasmids presented here (Fig. 5a).

To verify the expression of the inserted genes, the inhibitory concentrations of the different strains were tested (Table 3). The inhibitory concentrations towards relevant \(\beta\)-lactamases of all strains carrying the different \(\text{bla}\) genes in pJK5\textsubscript{attTn7}, were significantly higher than those of the wildtype \textit{E. coli} MG1655 (Table 3). To test the expression of sfGFP, green fluorescence was measured by flow cytometry using \textit{E. coli} MG1655-lac\textsuperscript{P-}\text{mcherry}/pJK5\textsubscript{attTn7}-\text{sfGFP-KPC2} as a representative (Fig. 5b-c). Here the constitutively expressed lac\textsuperscript{P-} represses the \(P\text{_{lacI}}\) promoter of sfGFP. To counteract this 1 mM Isopropyl \(\beta\)-D-1-thiogalactopyranoside (IPTG) was added to relieve the repression of sfGFP by lac\textsuperscript{P-} (Dahlberg et al., 1998; Lanzer and Bujard, 1988). Lastly, we tested if the \(\text{bla}_{\text{KPC-2}}\)-sfGFP insertion influenced conjugation frequencies of the plasmid (Fig. 4b-c). We found that the \(\text{bla}_{\text{KPC-2}}\) and sfGFP were expressed as expected and transfer frequencies were similar to the wildtype plasmid pJK5 (\(P = 0.592\), one-way ANOVA with post-hoc Tukey test).
Fig. 5. Verification of insertion of \( \text{bla-sfGFP} \) cassettes into pJK5-\( \text{attTn7} \) and pJK5\( \text{KPC-2} \)-\( \text{attTn7} \). (a) PCR verification of the correct insertion of the different \( \text{bla-sfGFP} \) cassettes into pJK5-\( \text{attTn7} \) and pJK5\( \text{KPC-2} \)-\( \text{attTn7} \). Lanes 1, 2, 3, 4, 5, 6, and 7 verifies insertion of \( \text{bla}_{\text{KPC-2}}, \text{bla}_{\text{NDM-5}}, \text{bla}_{\text{CTXM-15}} \), \( \text{bla}_{\text{CMY-2}}, \text{bla}_{\text{TEM-1}}, \) and \( \text{bla}_{\text{OXA-181}}, \) respectively, into pJK5-\( \text{attTn7} \). Lane 8 a 1 kb DNA Ladder (Thermo Scientific™ GeneRuler™ 1 kb Plus DNA Ladder). Lanes 9, 10, 11, 12, 13, 14, and 15 verifies insertion of \( \text{bla}_{\text{KPC-2}}, \text{bla}_{\text{NDM-5}}, \text{bla}_{\text{CTXM-15}}, \text{bla}_{\text{CMY-2}}, \) and \( \text{bla}_{\text{TEM-1}}, \) respectively, into pJK5\( \text{KPC-2} \)-\( \text{attTn7} \). (b) Image showing green fluorescence under ultraviolet light due to expression of the sfGFP by \( \text{E. coli} \) MG1655/pJK5-\( \text{attTn7} \)-\( \text{bla}_{\text{KPC-2}} \)-\( \text{sfGFP} \). E. coli MG1655/pJK5-\( \text{attTn7} \) was used as a negative control. (c) Green fluorescence due to expression of the sfGFP by \( \text{E. coli} \) MG1655/pJK5-\( \text{attTn7} \)-\( \text{bla}_{\text{KPC-2}} \)-\( \text{sfGFP} \) detected by flow cytometry. \( \text{E. coli} \) MG1655/pJK5-\( \text{attTn7} \) was used as a negative control. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Table 3
The minimum inhibitory concentration (MIC) of strains.

<table>
<thead>
<tr>
<th>Strains</th>
<th>Meropenem (µg/ml)</th>
<th>Cefotaxime (µg/ml)</th>
<th>Ampicillin (µg/ml)</th>
</tr>
</thead>
<tbody>
<tr>
<td>( \text{E. coli MG1655 WT} )</td>
<td>0.125 &lt; 0.05 20</td>
<td>( \text{E. coli MG1655/pJK5-attTn7} )</td>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{KPC-2}} )</td>
</tr>
<tr>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{TEM-1}} )</td>
<td>0.125 &lt; 0.05 20</td>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{CTXM-15}} )</td>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{CMY-2}} )</td>
</tr>
<tr>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{OXA-181}} )</td>
<td>&gt;10 200</td>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{KPC-2}} )</td>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{NDM-5}} )</td>
</tr>
<tr>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{KPC-2}} )</td>
<td>&lt;10 20</td>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{CTXM-15}} )</td>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{CMY-2}} )</td>
</tr>
<tr>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{OXA-181}} )</td>
<td>&gt;10 200</td>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{KPC-2}} )</td>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{NDM-5}} )</td>
</tr>
<tr>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{KPC-2}} )</td>
<td>&lt;10 20</td>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{CTXM-15}} )</td>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{CMY-2}} )</td>
</tr>
<tr>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{OXA-181}} )</td>
<td>&gt;10 200</td>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{KPC-2}} )</td>
<td>( \text{E. coli MG1655/pJK5-bla}_{\text{NDM-5}} )</td>
</tr>
</tbody>
</table>

(µg/ml), \( \sim \) means not been tested.

4. Discussion

Here we present a suite of engineered plasmids that were developed to advance research on HGT and plasmid biology. We introduced an \( \text{attTn7-site} \) into conjugative broad-host-range IncP-1 plasmid pJK5 using the \( \lambda \) phage derived Red recombination system. Hereafter, we demonstrate the ease at which genes of interest can be inserted into the \( \text{attTn7-site} \) with high efficacy using the bacterial mini-Tn7 transposon site-specific recombination system. We utilized vector \( \text{pGRG36} \) which contains a multiple cloning site for easy complementation, and it allows insertion of large fragments. It is known that Tn7 possesses transposition immunity, which counteracts Tn7 from transposing into \( \text{attTn7} \) sites already occupied by Tn7 (DeBoy and Craig, 1996), reducing the chance of at least 10\(^4\) fold (McKenzie and Craig, 2006). The construction of the 14 different plasmids with different \( \text{bla} \) genes and \( \text{sfGFP} \) (pJK5-\( \text{sfGFP-bl} \) \( \text{bla} \)) illustrates that, e.g., when wanting to study a series of functional genes in the context of a conjugative plasmid, the introduction of an \( \text{attTn7-site} \) reduced time spent engineering and overall costs.

Examples of studies where genetic complementation of plasmids has been central include those where conjugative plasmids have been complemented with fluorescent proteins such as GFP providing valuable insight into e.g. host range (Anjum et al., 2019; Olesen et al., 2022). One could imagine complementing and generating plasmids with several different fluorescent proteins, using the pJK5-\( \text{attTn7} \) plasmids presented here, to study dissemination dynamics and their impact on cell lineages and ecology in line with Jasinska et al. (Jasinska et al., 2020), or use the pJK5-\( \text{attTn7} \) plasmids when developing and assessing new reporter systems with different fluorescent proteins, promoters, and regulatory elements (Johns et al., 2018; Klümper et al., 2015; Krol et al., 2010; Rodé et al., 2021). We imagine the pJK5-\( \text{attTn7} \) plasmids will be useful in future studies investigating the horizontal and vertical transfer.
of genes. This is an important topic and studies have, for example, focused on antibiotic resistance genes (Sakamoto et al., 2022) and metal resistance genes (Cyriaque et al., 2021), but many other genes are equally relevant to study from this perspective (Jain et al., 1999; Madsen, 2020). Another use of conjugative plasmids is as delivery vectors when attempting to engineer microbial communities (sometimes referred to as metagenomic engineering) (Ronda et al., 2019). For example, Song et al. delivered a CRISPR-Cas12a system into a gut microbiome to selectively kill pathogens (Song et al., 2022). Our system could be used for similar approaches and the advantage would be that one could try many different types of CRISPR-Cas systems and/or spaces (or other systems) and compare pros and cons between them, by easily and efficiently complementation at the attTn7-site. These but a few ways we imagine the pKJK5-attTn7 plasmids could be useful for future applications but countless more are evidently possible.

The mini-Tn7-based transposon system is typically used for the insertion of single gene cassettes, however, innovative approaches such as high-throughput chromosomal-barcoding to track the evolutionary dynamics of E. coli subpopulations has recently been implemented (Jasinska et al., 2020) and illustrated the broad potential of these systems. The λ Red recombination system can also be used on its own to engineer wildtype plasmids (Anjum et al., 2018), however, the recombination efficiency is often limited by the size of the DNA insert (Doron et al., 2018). Besides, our experience is that using the λ Red recombination system can be quite challenging when attempting to engineer wildtype plasmids despite extended experience with these systems. Novel systems like INTEGRATE (Vo et al., 2021) may prove well suited for engineering wildtype plasmids.

The approach presented here can be seen as a proof-of-concept as any att-site and associated transposons/integrases could be used to generate similar systems, not only based on conjugative wildtype plasmids but any mobile genetic element. For some applications one might want to use less widespread att-site/integration systems (e.g., the CTX system), modular att-sites/integration systems (e.g., gateway systems), or others (Merrick et al., 2018; Rajeev et al., 2007). Here the attTn7-site and the mini-Tn7 system were chosen partially because it, in addition to the pKJK5 derived plasmids described here, also enables us to complement chromosomal attTn7-sites (Kyoung Hee Choi et al., 2005), which can be valuable for comparative purposes. For the same reason, we constructed the conjugation deficient plasmid pKJK5CATTn7 and non-conjugative plasmid pKJK5NC-attTn7.

5. Conclusions

Here, we constructed a number of plasmids based on the conjugative wildtype plasmid pKJK5 that efficiently can be genetically complemented. We did this by introducing an attTn7-site to pKJK5 in a non-disruptive manner. Based on this plasmid, pKJK5-attTn7, we also constructed a version that transfers at lower rates and one that cannot transfer by conjugation. We illustrated the ease at which the attTn7 plasmids can be complemented by introducing genes encoding fluorescent reporter proteins and seven different beta-lactamases. Overall, this study provides a suite of easily modifiable and convenient model plasmids for studying HGT and plasmid biology.

Data availability

Source data are provided with this paper.

Author contributions

Conceptualization, methodology, formal analysis, and validation was done by QW and JSM. AKO and LM provided resources and did data curation. QW drafted the original manuscript. QW, AKO, and JSM contributed to writing, review, and editing of the manuscript.

Declaration of Competing Interest

The authors declare that they have no competing interests.

Acknowledgements

We thank Søren J. Sørensen for his suggestions and support throughout the manuscript. We thank Valeria Bortolaia at the Technical University of Denmark for providing strains E. coli 15083205 and E. coli 15093653 used as templates for amplification of genes bla_CAR-2 and blaIMP, respectively. We thank Qie Yang and Timothy R. Walsh team from Oxford university for providing the genes blaNDM-1 and blaOXA-181. We thank Ana Filipa Silva for kindly providing the gene blaIMP. We would like to thank the China Scholarship Council for funding QW. This work was supported by the Lundbeck Foundation (JSM, R250-2017-1392) and Villum Fonden (JSM, 00028304).

References


Q. Wang et al.

Plasmid 123–124 (2022) 102649