Efficient and seamless DNA recombineering using a thymidylate synthase A selection system in *Escherichia coli*

Queenie N. Y. Wong¹, Vivian C. W. Ng, Marie C. M. Lin¹, Hsiang-fu Kung¹, Danny Chan* and Jian-Dong Huang

Department of Biochemistry and ¹Institute of Molecular Biology, The University of Hong Kong, Pokfulam, Hong Kong SAR, China

Received as resubmission March 6, 2005; Accepted March 9, 2005

ABSTRACT

λ-Red system-based recombinogenic engineering is a powerful new method to engineer DNA without the need for restriction enzymes or ligases. Here, we report the use of a single selectable marker to enhance the usefulness of this approach. The strategy is to utilize the thymidylate synthase A (*thyA*) gene, which encodes an enzyme involved in the synthesis of thymidine 5'-triphosphate, for both positive and negative selection. With this approach, we successfully created point mutations in plasmid and bacterial artificial chromosome (BAC) DNA containing the mouse *Col10a1* gene. The results showed that the *thyA* selection system is highly efficient and accurate, giving an average of >90% selection efficiency. This selection system produces DNA that is free from permanent integration of unwanted sequences, thus allowing unlimited rounds of modifications if required.

INTRODUCTION

Recent advances in homologous recombination-based DNA engineering technology, termed recombinogenic engineering or recombineering, have led to the development of highly efficient procedures with which chromosomal or plasmid DNA can be modified in *Escherichia coli* by the introduction of mutations, such as single base substitutions, deletions and insertions. These methods are based upon the rac-encoded RecET system or the bacteriophage λ-Red recombination system (1–6), eliminating the need for *in vitro* manipulations using restriction enzymes or DNA ligases (7,8). The three proteins of the Red system, Exo, Beta and Gam, mediate recombination between a linear double-stranded DNA donor and its homologous target sequence by promoting double-strand break repair (9–15).

This system, while powerful, suffers from a relatively low rate of recombination events, so that screening of a large number of bacterial colonies is still required in most cases. This limitation can be overcome by incorporating a selectable marker to assist in selection of the desired recombinants. Selection protocols generally use antibiotic resistance genes flanked by loxP or frt sites, such that the selectable marker can later be removed by cre- or flp-mediated recombination (10). This method is highly efficient but unavoidably leaves at least one loxP or frt sequence behind. Alternatives include antibiotic-selectable marker approaches, such as *SacB*–neo, which have been used in a two-step modification procedure to avoid unwanted residual DNA (4,16,17). In the first round of recombination, cells are transformed with the *SacB*–neo fusion cassette and are selected for their resistance to kanamycin. Subsequently, an appropriate DNA cassette is introduced to replace the entire *SacB*–neo cassette to create the desired change in DNA sequence. Cells retaining the *SacB* marker gene will not survive in 7% sucrose. However, these methods can result in unwanted rearrangement (18) and require labor-intensive screening procedures to distinguish clones with the desired recombineered product from cells that survived owing to mutational events that prevented the expression of the counter-selectable gene.

Here, we describe a novel selection approach in *E.coli* utilizing the λ-Red recombineering system. It is a single selectable marker approach with selection criteria based on previous work performed in *Bacillus subtilis* (9,19). In brief, the selectable marker is the enzyme encoded by the

*To whom correspondence should be addressed. Tel: +852 2819 9482; Fax: +852 2855 1254; Email: chand@hkusua.hku.hk
Present address: Hsiang-fu Kung, The Center for Emerging Infectious Diseases, Faculty of Medicine, Chinese University of Hong Kong, Hong Kong SAR, China

The authors wish it to be known that, in their opinion, the first two authors should be regarded as joint First Authors

© The Author 2005. Published by Oxford University Press. All rights reserved.

The online version of this article has been published under an open access model. Users are entitled to use, reproduce, disseminate, or display the open access version of this article for non-commercial purposes provided that: the original authorship is properly and fully attributed; the Journal and Oxford University Press are attributed as the original place of publication with the correct citation details given; if an article is subsequently reproduced or disseminated not in its entirety but only in part or as a derivative work this must be clearly indicated. For commercial re-use, please contact journals.permissions@oupjournals.org
thymidylate synthase A (thyA) gene, which is involved in the de novo synthesis of dTTP from dUMP. Without thyA, the cell is unable to synthesize DNA and, therefore, will not grow in minimum growth media. Thus, in a thyA-null E.coli mutant (∆thyA), recombinants containing an exogenous thyA gene can be selected for (positive selection) by culture in growth medium in the absence of thymine. When thymine is provided, de novo dTTP synthesis can proceed without the need for ThyA function.

The activity of ThyA requires the cofactor tetrahydrofolate (THF), which is converted to dihydrofolate (DHF) in the process. THF is also an important cofactor for many other essential cellular reactions and is replenished from DHF by the action of dihydrofolate reductase, which can be inhibited by trimethoprim. Thus, recombination events in which the thyA gene is removed can then be selected for (negative selection) using growth media containing thymine and trimethoprim. Under these culture conditions, cells with functional thyA can be grown without thymine; thus, these cells will grow.

Cells were grown in a modified M9 minimal medium in the absence of thymine. When thymine is provided, de novo dTTP synthesis can proceed without the need for ThyA function.

Materials and Methods

Bacterial strains and growth media

Two bacterial strains, DY380 and QW1, were used in this study. DY380 is a gift from Dr Don Court (10) and is a modification of DH10B [F− mcrA ∆(mrr-hsdRMS-mcrBC) 80d lacZΔM15 lacY74 deoR recA1 endA1 araD139 (ara, leu) 7649 galU galK rpsL supG] that includes the Red genes [kcl857 (cro-bioA) · tet] as a prophage. QW1 is a further modification of DY380 created in the current study with the thyA gene deleted (∆thyA).

Preparation of DNA fragment for recombineering procedures

All linear DNA fragments were generated by PCR amplification and the appropriate primers are shown in Table 1. Primers thyAF1 and thyAR1 were used to amplify a 1470 bp DNA fragment (Figure 2A) containing the full-length thyA gene (thyA-FL) using DY380 chromosomal DNA as template. The amplified DNA was cloned into pBluescript KS II (+) (Stratagene) to generate the plasmid, pThyA-FL.

A 744 bp DNA fragment (Figure 2A) containing a truncated ‘inactive’ version of the thyA gene (∆thyA) was generated by overlapping PCR using pThyA-FL plasmid DNA as a template. The primers used to generate the two overlapping fragments were thyAF1 and thyAR2, and thyAF2 and thyAR1 (Table 1). The resultant amplification fragments were purified and used as templates in the second round of overlapping PCR with primers thyAF1 and thyAR1. In Table 1, the nucleotides in bold represent the overlapping regions where the two fragments will anneal to one another. A 1124 bp DNA fragment (Figure 2A) containing an ‘active’ version of the thyA gene (∆thyA) was generated by overlapping PCR using pThyA-FL plasmid DNA as a template. The primers used to generate the two overlapping fragments were thyAF1 and thyAR2, and thyAF2 and thyAR1 (Table 1). The resultant amplification fragments were purified and used as templates in the second round of overlapping PCR with primers thyAF1 and thyAR1. In Table 1, the nucleotides in bold represent the overlapping regions where the two fragments will anneal to one another.

For site-directed mutagenesis in a plasmid containing the mouse collagen X gene (Col10al), two PCR-amplified DNA fragments were generated, X-thyAΔ3′-X and ColIX-G18D. The X-thyAΔ3′-X fragment was amplified using primers thyAF1 and thyAR3 (Table 1) with plasmid pThyA-FL as a template. This fragment was cloned into pBluescript KS II (+) to generate the plasmid, pThyA-Δ3′.

Polymerase chain reaction

PCR was used for the amplification of DNA fragments with the GeneAmp PCR System 9700 (Applied Biosystems). The high-fidelity Pfx DNA polymerase (Invitrogen) was used in all the reactions, prepared as specified by the supplier. The general condition included an initial denaturation at 94°C for 5 min, followed by 30 cycles of denaturation at 94°C for 45 s, annealing at 55°C for 45 s and extension at 72°C for 45 s to 1 min 30 s, depending on the length of the DNA to be amplified. PCR products were gel-purified and recovered using the gel purification kit from Qiagen. The quality and concentration of DNA were analyzed by gel electrophoresis and UV spectrophotometry, respectively.
Table 1. Normal and mutant primers for PCR site-directed mutagenesis

| Primers          | Primer sequence (5' to 3')                                                                 | Position          | Orientation |
|------------------|-------------------------------------------------------------------------------------------|-------------------|-------------|
| thyA-F1          | GCTGCTGCTGAGAGTGTG                                                                         | −277 to −257      | Forward     |
| thyA-R1          | CCTCCCTGTATAACGCTGTA                                                                       | +1193 to +1173    | Reverse     |
| thyA-F2          | GTTTAATCCGCACATGTCGCGGCAATCTCTCGAGACC                                                   | +104 to +122     | Forward     |
| thyA-R2          | GGCCTCGAAGATTTAAGGCGGCACTCTTGACGTGTTAAC                                                  | +869 to +849     | Reverse     |
| thyA-R3          | GGTTAATCCGCACATGTCGCGGCAATCTCTCGAGACC                                                   | +847 to +826     | Reverse     |
| thyA-R2          | GGCCTCGAAGATTTAAGGCGGCACTCTTGACGTGTTAAC                                                  | −223 to −202     | Forward     |
| thyA-F2          | GCCGCGTGAGGCGGCAATCTCTCGAGACC                                                           | −33 to +17       | Forward     |
| thyA-F1          | GCTGCTGCTGAGAGTGTG                                                                         | +156 to +107     | Reverse     |
| thyA-R1          | CCTCCCTGTATAACGCTGTA                                                                       | +55 to +53       | Reverse     |
| thyA-R2          | GGCCTCGAAGATTTAAGGCGGCACTCTTGACGTGTTAAC                                                  | +49 to +72       | Forward     |

The positions of the primers are relative to the start codon of the mouse Col10a1 or the thyA genes. The sequences in bold letters are overlap regions. In primers ColX-thyAF and ColX-thyAR, Col10a1 sequences are in bold and thyA sequences are in italics. The sequences that are in both bold and italics in primers ColX-mF and ColX-mR represent the codon to be mutated in the mouse Col10a1 gene. Sequence assignment numbers for the collagen X primers are taken from Kong et al. (27) and for thyA from Belfort et al. (28).

previous mutagenesis of the human COL10A1 gene (20). In brief, two overlapping DNA fragments were generated using primers ColX-F and ColX-mR, ColX-mF and ColX-R. The overlap fragment contained a 2 bp substitution changing the codon GGG for glycine at residue 18 (relative to the start of translation) to GAT for aspartate in the precollagen X α-chain, analogous to a mutation in the signal peptide cleavage site (21).

For site-directed mutagenesis in a Col10a1 containing BAC, primers (ColX-F and ColX-R) were used to amplify a 566 bp PCR fragment from a plasmid (pG18D-Flag) containing a different variant of the G18D mutation (GGG to GAC) and an in-frame insertion of the Flag K sequence (5'-GACGACGATGACAAAGGTTGCGGCCGCGCATGACAA-3') at the 3' region of exon 2 (Figure 2C).

Electroporation of DNA into bacterial cells

Appropriate bacterial cells were prepared for electroporation as described previously. The Red gene function was induced at 42°C for 15 min to allow the expression of Exo, Bet and Gam as the temperature-sensitive repressor falls off at this high temperature. Cells grown at 32°C without induction were used as a control (5). In brief, 50 μl of ‘competent’ cells were mixed with 2–8 μg of the PCR-amplified DNA in a pre-cooled 0.1 cm Gene Pulser cuvette (Bio-Rad Laboratories) and electroporated using the Bio-Rad Gene Pulser with conditions set at 1.8 kV, 25 μF and 200 ohms. Following electroporation, the cells were grown in 1 ml of LB broth at 32°C for 1–1.5 h, collected by centrifugation and plated at various dilutions onto M9 minimal medium agar plates with appropriate supplements for selective growth, and incubated at 32°C for 48–72 h.

Generation of a thyA-null bacterial strain (QW1)

The thyA-null strain (QW1) was constructed by electroporating the 744 bp ‘inactive’ ΔthyA DNA fragment (created by overlapping PCR as described above) into DY380 following activation of the λ-Red recombinase system. Clones with the appropriate homologous recombination event inactivating the endogenous thyA gene were selected for culturing electroporated cells on modified M9 minimal growth agar plates supplemented with 0.79 mM thymine and 10 μg/ml trimethoprim.

Mutagenesis of the mouse Col10a1 gene

A plasmid, pKM2-ColX, containing 10 kb of the mouse Col10a1 gene was first transformed into QW1. Next, 4 μg of X-thyA3'-'X DNA fragment (constructed as described above) was electroporated into ‘competent’ QW1 cells harboring pKM2-ColX. Appropriate clones with a functional thyA gene were selected by growth on modified M9 minimal medium growth agar media (acinetobacter agar in the absence of thymine). Thymine (10 μg/ml) was used as a control (5). In brief, 50 μl of ‘competent’ cells derived from QW1-pKM2-ColX-ThyA cloning vector contained the mouse Col10a1 gene, except that in the final mutagenesis step, between 2 and 8 μg of a PCR product, FColX-G18D (Figure 2C) was electroporated into ‘competent’ cells derived from QW1 containing the RP23-19413 BAC with thyA introduced at the appropriate site for subsequent mutagenesis.

RESULTS

Generation of a thyA-null bacterial strain (QW1)

Utilizing the λ-Red recombination function present in DY380, the thyA gene was inactivated through homologous recombination between DY380 chromosomal DNA and a PCR-amplified DNA fragment, ΔthyA. The overall strategy is outlined in Figure 1A. Growth selection for the absence of ThyA function resulted in >250 colonies when the λ-Red
recombination system was activated (42°C) prior to electroporation as compared with only two colonies without prior activation (maintained at 32°C) (Table 2). Twelve colonies were selected for analysis; deletion of the thyA gene from the bacterial genome was confirmed by PCR amplification using primers flanking the thyA gene in eleven of the twelve colonies (Table 2 and Figure 1B). One colony with the correct recombination was selected as the newly generated thyA-null strain (QW1), where sequencing of the PCR product confirmed the expected deletion in the gene (data not shown).

Establishment and confirmation of selective growth conditions

To establish that QW1 can be utilized to facilitate the selection of homologous recombination events between exogenous DNAs, a number of ‘rescue’ assays were performed to test the newly designed thyA selection system. The introduction of a full-length functional thyA gene in a plasmid (pThyA-FL) restored ‘normal’ cell function in QW1. Under the appropriate growth selection for the presence of ThyA function, >1300 colonies were observed (Table 2). A similar result was obtained for the introduction of plasmid pThyA-Δ3' (Table 2), indicating that DNA sequence encoded in thyA Δ3' is also fully functional. The use of thyAΔ3' is preferred for subsequent mutagenesis experiments as it lacks 347 bp 3' to the terminator of the thyA gene, minimizing potential recombination events where the thyA gene may recombine back into the original position in the bacterial chromosome, introducing false positives. Furthermore, we have shown that transformation of linear PCR DNA fragments, thyA-FL or thyAΔ3' (Figure 2A), did not result in ThyA function, indicating that during the selective growth period, the linear DNAs are likely to be degraded and will not contribute to false positives. This is supported by the very low frequency or absence of colonies in transformation of QW1 with thyA-FL or thyAΔ3' PCR-amplified DNA fragments when the λ-Red recombination system is not active (Table 2).

Site-directed mutagenesis of the mouse Col10a1 gene

As a proof of principle experiment, we utilized the ThyA selection system in QW1 to introduce a specific 2 bp mutation in a plasmid containing the mouse Col10a1 gene relying solely on the λ-Red recombination system. The overall strategy is illustrated in Figure 3A. It involves two rounds of homologous recombination in QW1. The first round is between a plasmid containing the normal Col10a1 sequence (pKM2-ColX) and a PCR-generated DNA fragment containing ΔthyA sequence flanked by 50 bp of Col10a1 sequences, corresponding to the 5' and 3' regions of the intended site of mutagenesis, respectively. When the λ-Red recombination system is activated, the 50 bp flanking sequences of homology to normal Col10a1 sequence are sufficient to allow homologous recombination in QW1 to promote the incorporation of the ΔthyA gene into pKM2-ColX, with an efficiency of 1.32 × 10^4 recombinants/µg DNA when growth was selected in conditional medium lacking thymine (Table 2). Of the 13 colonies selected, 1 colony showed only the parental plasmid, while 12 colonies showed a varying mixture (~1:2) of parental and correctly recombinated plasmids by PCR amplification of the region corresponding to the site of ΔthyA integration. Colonies containing only the recombinant plasmid were obtained by retransformation in QW1 and selected for ThyA function. A representation of the respective PCR product with (1565 bp) and without (530 bp) ΔthyA integration is shown in Figure 3B.

With ΔthyA integrated, the strategy is to remove it in a second recombination event whereby the desired 2 bp substitution mutation is introduced into the plasmid. The base
changes were first introduced into a PCR product (ColX-G18D) containing Col10a1 sequence by overlapping PCR as shown schematically in Figure 2B. Through homologous recombination of this PCR with pKM2-ColX-DΔthyA, the ΔthyA integration was removed and the 2 bp substitution introduced precisely. When selected in culture conditions for cells without ThyA function, we obtained on average >1200 colonies (Table 2) when the λ-Red recombination system was activated. Of the 16 colonies selected, 14 showed the correct recombination event confirmed by PCR amplification of the region containing the 2 bp substitution with only trace amounts of parental plasmids. Thus, this indicates that the recombination can be very efficient as previously reported (8), and that the counter selection process is sufficient to differentiate growth of cells with significant differences in the level of ThyA function. Furthermore, there will be a selection pressure for the enrichment of progenies with reducing ThyA function through random segregation.

Because the base pair changes also introduced a new BspHI restriction enzyme site, the presence of the mutation was monitored by BspHI digestion of the PCR product (Figure 3C), and confirmed by DNA sequencing of the plasmids isolated from the appropriate clones (Figure 3D). Together with the data from the generation of the thyA-null strain (QW1), this shows that the selectivity of the system is extremely high with ~90% of the colonies exhibiting the expected phenotype with respect to ThyA function.

To demonstrate that the ThyA recombineering system can be applied to BACs, we performed mutagenesis in a 317 kb BAC (RP23-194I3) containing the mouse Col10a1 gene. Compared with plasmid DNA, the total number of colonies was lower for BACs, in the order of 5–10, 10–20 and 30–40 colonies using 2, 4 and 8 μg of PCR product for transformation, respectively. However, the selection efficiency remained high with >90% of the colonies contained the appropriate recombination event for the insertion of thyA into the BAC (9 from 9 colonies selected), or its subsequent removal (9 from 10 colonies selected). Introduction of thyA into the BAC was monitored by PCR as described above (data not shown), and confirmed by Southern blot analysis (Figure 4A). The DNA sequence of a final modified BAC (FColX-BAC-G18D) containing the G18D mutation with the Flag® sequence in exon 2 is shown in Figure 4B.

### DISCUSSION

With the completion of many genome projects, the next step is to understand the function and regulation of genes that are discovered. Functional genomics will play a major role. There is a need for the ability to manipulate DNA for expression studies, to create targeting vectors for making transgenic organisms and to investigate the regulation of gene expression and gene function through site-specific mutagenesis.

Recently, the development of recombineering procedures utilizing homologous recombination in bacteria has allowed DNA manipulation without the need for restriction enzymes, large plasmid DNA fragments or vectors carrying large DNA inserts, such as BACs, P1-derived or yeast artificial chromosomes. However, the efficiency is generally low and recovering the appropriate clones requires the screening of hundreds to thousands of colonies, or having to engineer a gene for growth selection, such as an antibiotic gene (22,23). Furthermore, some approaches retain unwanted residual DNA sequences that may interfere with gene function or are limited to a single manipulation. Here, we have developed a unique selection system in E.coli to enhance the usefulness and efficiency of the recombineering technique, utilizing a positive–negative selection system based on a single marker, the thyA gene, allowing seamless multiple manipulations of DNA.

With the thyA selection system, as a proof of principle experiment, we have successfully created a 2 bp mutation in exon 2 of the mouse collagen X gene, Col10a1. Overall, this system showed an average selection efficiency of >90%, requiring the screening of fewer than 10 colonies to ensure a successful outcome. This is a valuable improvement of the bacteriophage λ-Red recombination system, with advantages over existing systems. Its greatest advantage is that the selection of clones with or without ThyA function is based on growth of the bacteria concerned, with minimal background ranging from 0.01 to 0.08%.

Under optimal conditions, the efficiency of the bacteriophage λ-Red recombination system without selection has been reported at best to be only 0.1% (5) and 0.17% (10) of surviving cells. Therefore, although this is a single step without further manipulations, more than 1000 colonies need to be screened to obtain one or two recombinants. With appropriate selection using the ThyA system, we have obtained 14 recombinants from 16 colonies.
Our system is superior to similar ones that positively select for growth of the desired recombinants, such as the use of a selection cassette containing the EcoRI endonuclease and an antibiotic gene that allows selection of the desired clone at an efficiency of only 0.35% (2 recombinants from 570 colonies) (24). In this system, expression of EcoRI endonuclease, which is toxic to cells in the absence of the corresponding methylase, is induced by the addition of isopropyl-β-d-thiogalactopyranoside to kill unwanted clones. Despite the high killing efficiency of EcoRI endonuclease, there is still a high background with >95% false-positive clones. The same group, wanting to improve the efficiency, altered the selection cassette to contain a rarer cutter, I-SceI endonuclease, and an antibiotic gene. However, the efficiency was

![Figure 2. Schematic representation of the PCR DNA fragments ThyA-F, ThyA-Δ3', ΔThyA and X-thyAΔ3'-X']. (A) PCR amplification using primers thyA-F1 and thyA-R1 (Table 1) amplifies a 1470 bp fragment (thyA-FL) of the thyA gene containing the promoter, Factor Sigma 54 binding site and the transcription termination flanking the start and stop codons for translation. The 1124 bp product, thyA-Δ3', amplified using primers thyA-F1 and thyA-R3 (Table 1), lacks 347 bp 3' of the transcription terminator. ΔthyA is a 744 bp product generated by overlapping PCR (see Materials and Methods for details) with most of the coding sequence deleted (+123 to +848, relative to the translational start site), and Δ in the diagram represents the deleted region. X-thyAΔ3'-X' is a fusion product amplified using primers ColX-thyAF and ColX-thyAR with 5' and 3' overhang sequences for the regions of the Col10a1 gene for homologous recombination. (B) Schematic representation of the strategy for the generation of the ColX-G18D fragment. Two PCR products were first generated using primer sets, ColX-F/ColX-mR and ColX-mF/ColX-R. These products, containing complementary sequences from primers ColX-mF and ColX-mR, were used in an overlapping PCR to produce ColX-G18G using primers ColX-F and ColX-R. (C) Schematic representation for the amplification of a PCR product from a plasmid, pG18D-Flag, using primers ColX-F and ColX-R. pG18D-Flag contains mutations (bold and underlined) around the signal peptide cleavage site of collagen X, and a Flag sequence inserted at the 3' region of exon 2 (shaded region).
Mutagenesis of the mouse collagen X gene (Col10a1) using QW1. (A) A schematic presentation of selective growth for thyA gene replacement and removal through two rounds of homologous recombination events to introduce a 2 bp substitution in exon 2 of Col10a1, pKM2-ColX is a plasmid containing the normal Col10a1 gene with GGG as the codon for Gly18. pKM2-ColX was first transformed into a thyA-null strain (QW1). This was followed by a second transformation with a PCR product (X-thyA∆3′-X') containing flanking sequences homologous to the Col10a1 gene (shaded region). Through homologous recombination, a specific region of the Col10a1 gene in pKM2-ColX is replaced with thyA and this event is selected for by growth in defined medium (see Materials and Methods for details) that requires ThyA function. A selected colony is then transformed with a PCR product containing Col10a1 sequence with a 2 bp mutation at codon 18 (GGG to GAT), representing a G18D amino acid substitution. Activation of homologous recombination will remove the thyA∆3′ sequence and introduce the G18D mutation to produce plasmid pFColX-G18D; growth conditions are used that select for the absence of ThyA function. (B) Confirmation of thyA∆3′ integration in pKM2-ColX following the first round of homologous recombination. Colonies derived from growth selection for the reintroduction of ThyA function in QW1 were analyzed by PCR amplification of the resultant plasmid using primers ColX-F and ColX-R (Table 1). Lanes 1 and 2 show the amplification products from pKM2-ColX (530 bp) and pKM2-ColX-ThyA (1565 bp), respectively. M is a DNA molecular size marker (1 kb GeneRuler, MBI Fermentas). (C) Confirmation of thyA∆3′ removal and introduction of a 2 bp substitution in pKM2-ColX following the second round of homologous recombination. The 2 bp substitution mutation introduces a new BspH1 restriction enzyme site in the 530 bp PCR product and will result in two fragments of 271 and 259 bp following digestion. M is a DNA molecular size marker (100 bp GeneRuler, MBI Fermentas); lanes 1 and 2 are the PCR fragments from pKM2-ColX and pColX-G18D digested with BspH1, respectively. (D) DNA sequencing of pFColX-G18D showing that the codon GGG (glycine) has been specifically changed to GAT (aspartate) following the two rounds of homologous recombination using the thyA selection system.
improved to only 7.5% (7 recombinants from 93 colonies) upon counter selection (25).

Other recent counter-selection strategies for BAC modifications use the fused sacB/Neo gene (26) and the rspL gene (18). However, these are negative selection systems that suffer from a high background owing to mutational events affecting the SacB protein (26) or rearrangements (18).

Apart from counter-selection systems, selective procedures like the use of antibiotics and site-specific recombinases, such as Cre, and restriction enzyme digestion are also methods for eliminating selection markers (3,10,26). However, these protocols create an end product that is not ‘clean’ in that there remains a marker or a tag within the final product. These tags may be problematic, causing unpredicted splicing, altered binding of transcription factors or affecting regulation of gene expression at distant sites that cannot be predicted from sequence analysis alone.

By combining the advantages of the λ-Red recombination and the selection of ThyA function in E.coli, we have developed a system that has high and accurate efficiency in the selection of a well-proven homologous recombination event induced by specific genes of the λ-prophage. This system should be applicable to plasmids, P1-derived artificial chromosomes or bacterial artificial chromosomes. In theory, this system can allow unlimited seamless modifications in different regions of the vectors or chromosomes concerned.

ACKNOWLEDGEMENTS

The authors thank Professor A. Danchin and Dr A. Sekowska for their expert guidance in bacteriology. This work was funded in part by a Committee on Research Conference grant from the University of Hong Kong to D.C., the Research Grants Council of Hong Kong to D.C. (7213/02), and the National Science Foundation.
Foundation of China and Research Grants Council of Hong Kong Research Scheme to J.-D.H. (NSFC/HKU 17 and N_HKU712/02). Funding to pay the Open Access publication charges for this article was provided by the Research Grants Council of Hong Kong.

Conflict of interest statement. None declared.

REFERENCES

1. Datsenko,K.A. and Wanner,B.L. (2000) One-step inactivation of chromosomal genes in *Escherichia coli* K-12 using PCR products. *Proc. Natl Acad. Sci. USA*, 97, 6640–6645.

2. Murphy,K.C. (1998) Use of bacteriophage lambda recombinon functions to promote gene replacement in *Escherichia coli*. *J. Bacteriol.*, 180, 2063–2071.

3. Murphy,K.C., Campellone,K.G. and Potetee,A.R. (2000) PCR-mediated gene replacement in *Escherichia coli* *Gene*. 246, 321–330.

4. Oswald,W., Tonpitak,W., Ohrt,G. and Gerlach,G. (1999) A single-step conjuctionse system for the introduction of unmarked deletions into Actinobacillus pleuropneumoniae serotype 7 using a sucrose sensitivity marker. *FEBS Microbiol. Lett.*, 179, 153–160.

5. Yu,D., Ellis,H.M., Lee,E.C., Jenkins,N.A., Copeland,N.G. and Court,D.L. (2000) An eficient recombinon system for chromosome engineering in *Escherichia coli*. *Proc. Natl Acad. Sci. USA*, 97, 5978–5983.

6. Zhang,Y., Buchholz,F., Muyrers,J.P. and Stewart,A.F. (1998) A new logic for DNA engineering using recombination in *Escherichia coli*. *Nature Genet.*, 20, 123–128.

7. Copeland,N.G., Jenkins,N.A. and Court,D.L. (2001) Recombineering: a powerful new tool for mouse functional genomics. *Nature Rev. Genet.*, 2, 769–779.

8. Court,D.L., Sawitzke,J.A. and Thomason,L.C. (2002) Genetic engineering using homologus recombination. *Annu. Rev. Genet.*, 36, 361–388.

9. Kiel,J.A., ten Berge,A.M., Borger,P. and Venema,G. (1995) A general method for the consecutive integration of single copies of a heterologous gene at multiple locations in the *Bacillus subtilis* chromosome by recombination. *Appl. Environ. Microbiol.*, 61, 4244–4250.

10. Lee,E.C., Yu,D., Martinez de Velasco,J., Tesserollo,L., Swing,D.A., Court,D.L., Jenkins,N.A. and Copeland,N.G. (2001) A highly efficient *Escherichia coli* based chromosome engineering system adapted for recombinogenic targeting and subcloning of *BAC* DNA. *Genomics*, 73, 56–65.

11. Li,Z., Karakousis,G., Chiu,S.K., Reddy,G. and Radding,C.M. (1998) The beta protein of phage lambda promotes strand exchange. *J. Mol. Biol.*, 276, 733–744.

12. Little,J.W. (1967) An exonuclease induced by bacteriophage lambda. II. Nature of the enzymatic reaction. *J. Biol. Chem.*, 242, 679–686.

13. Muyrers,J.P., Zhang,Y., Buchholz,F. and Stewart,A.F. (2000) RecE/RecT and Redalpha/Redbeta initiate double-stranded break repair by specifically interacting with their respective partners. *Genes Dev.*, 14, 1971–1982.

14. Takahashi,N. and Kobayashi,I. (1990) Evidence for the double-strand break repair model of bacteriophage lambda recombination. *Proc. Natl Acad. Sci. USA*, 87, 2790–2794.

15. Thaler,D.S., Stahl,M.M. and Stahl,F.W. (1987) Double-chain-cut sites are recombination hotspots in the Red pathway of phage lambda. *J. Mol. Biol.*, 195, 75–87.

16. Gong,S., Yang,X.W., Li,C. and Heintz,N. (2002) Highly efficient modification of bacterial artificial chromosomes (BACs) using novel shuttle vectors containing the R6Kgamma origin of replication. *Genome Res.*, 12, 1992–1998.

17. Laloti,M. and Heath,J. (2001) A new method for generating point mutations in bacterial artificial chromosomes by homologous recombination in *Escherichia coli*. *Nucleic Acids Res.*, 29, E14.

18. Imam,A.M., Patrinos,G.P., de Krom,M., Bottardi,S., Janssens,R.J., Katsantoni,E., Wai,A.W., Sherratt,D.J. and Gросveld,F.G. (2000) Modification of human beta-globin locus PAC clones by homologous recombination in *Escherichia coli*. *Nucleic Acids Res.*, 28, E65.

19. Sekowska,A. and Danchin,A. (1999) Identification of yrrU as the methylthioadenosine nucleosidase gene in *Bacillus subtilis*. *DNA Res.*, 6, 255–264.

20. Chan,D., Weng,Y.M., Hocking,A., Golub,S., McQuillan,D.J. and Bateman,J.F. (1996) Site-directed mutagenesis of human type X collagen. Expression of ot(1X)NCl, NC2, and helical mutations in vitro and in transfected cells. *J. Biol. Chem.*, 271, 13566–13572.

21. Chan,D., Ho,M.S. and Cheah,K.S. (2001) Aberrant signal peptide cleavage of collagen X in Schmid metaphyseal chondrodysplasia. Implications for the molecular basis of the disease. *J. Biol. Chem.*, 276, 7992–7997.

22. Swaminathan,S., Ellis,H.M., Waters,L.S., Yu,D., Lee,E.C., Court,D.L. and Sharan,S.K. (2001) Rapid engineering of bacterial artificial chromosomes using oligonucleotides. *Genesis*, 29, 14–21.

23. Yang,Y. and Sharan,S.K. (2003) A simple two-step, ‘hit and fix’ method to generate subtle mutations in BACs using short denatured PCR fragments. *Nucleic Acids Res.*, 31, e80.

24. Jamsai,D., Nefedov,M., Narayan,K., Orford,M., Fucharoen,S., Williamson,R. and Ioannou,P.A. (2003) Insertion of common mutations into the human beta-globin locus using GET recombination and an EcoR1 endonuclease counterselection cassette. *J. Biotechnol.*, 101, 1–9.

25. Jamsai,D., Orford,M., Nefedov,M., Fucharoen,S., Williamson,R. and Ioannou,P.A. (2003) Targeted modification of a human beta-globin locus BAC clone using GET recombination and an F-Sci counterselection cassette. *Genomics*, 82, 68–77.

26. Muyrers,J.P., Zhang,Y., Benes,V., Testa,G., Ansorge,W. and Stewart,A.F. (2000) Point mutation of bacterial artificial chromosomes by ET recombination. *EMBO Rep.*, 1, 239–243.

27. Kong,R.Y., Kwan,K.M., Lau,E.T., Thomas,J.T., Boot-Handford,R.P., Grant,M.E. and Cheah,K.S. (1993) Intron–exon structure, alternative use of promoter and expression of the mouse collagen X gene, Col10a1. *Eur. J. Biochem.*, 213, 99–111.

28. Belfort,M., Maley,G., Pedersen-Lane,J. and Maley,F. (1983) Primary structure of the *Escherichia coli* thyA gene and its thymidylate synthase product. *Proc. Natl Acad. Sci. USA*, 80, 4914–4918.