
PETER V. ADRIAN,1,2* CHRISTOPHER J. THOMSON,2 KEITH P. KLUGMAN,1 AND SEBASTIAN G. B. AMYES3

Department of Medical Microbiology, University of the Witwatersrand, and the South African Institute for Medical Research, Johannesburg, South Africa,1 and Molecular Chemotherapy, Department of Medical Microbiology, University of Edinburgh, Edinburgh, United Kingdom2

Received 11 June 1999/Returned for modification 23 August 1999/Accepted 3 November 1999

In a previous survey of 357 trimethoprim-resistant isolates of aerobic gram-negative bacteria from communal fecal flora, hybridization experiments showed that 25\% (90 of 357) of the isolates failed to hybridize to specific oligonucleotide probes for dihydrofolate reductase types 1, 2b, 3, 5, 6, 7, 8, 9, 10, and 12. Subsequent cloning and sequencing of a plasmid-borne trimethoprim resistance gene from one of these isolates revealed a new dihydrofolate reductase gene, \textit{dfr13}, which occurred as a cassette integrated in a site-specific manner in a class 1 integron. The gene product shared 84\% amino acid identity with \textit{dfr12} and exhibited a trimethoprim inhibition profile similar to that of \textit{dfr12}. Gene probing experiments with an oligonucleotide probe specific for this gene showed that 12.3\% (44 of 357) of the isolates which did not hybridize to probes for other dihydrofolate reductases hybridized to this probe. Immediately downstream of \textit{dfr13}, a new cassette, an aminoglycoside resistance gene of the class AADA [\textit{ANT}(3\textsuperscript{0})-I], which encodes streptomycin-spectinomycin resistance, was identified. This gene shares 57\% identity with the consensus \textit{aadA1} (\textit{ant(3\textsuperscript{0})-Ia}) and has been called \textit{aadA4} (\textit{ant(3\textsuperscript{0})-Id}). The 3' end of the \textit{aadA4} cassette was truncated by IS\textsubscript{26}, which was contiguous with a truncated form of \textit{Tn3}. On the same plasmid, pUK2381, a second copy of IS\textsubscript{26} was associated with \textit{sul2}, which suggests that both integrase and transposase activities have played major roles in the arrangement and dissemination of antibiotic resistance genes \textit{dfr13}, \textit{aadA4}, \textit{bla\textsubscript{TEM}-I\textsuperscript{a}}, and \textit{sul2}.

Class 1 integrons are DNA elements that encode a site-specific recombinase (\textit{intI1}) of the \textlambda family of integrases and are capable of catalyzing the insertion and recombination of mobile DNA elements (gene cassettes) at specific sites (core site) with a consensus sequence, GTTRRRY. The integron also provides a 5' conserved core site, \textit{attI1}, into which gene cassettes are preferentially inserted, and the promoters responsible for expression of the cassette-encoded genes (10, 19). Gene cassettes are identified by a 59-base element which occurs at the 3' end of the cassette and which consists of an inverted imperfect repeat of between 50 and 150 bp which has an inverse core site at the 5' end of the inverted repeat and a core site at the 3' end. The insertion of a gene cassette into the \textit{attI1} site results in the formation of a secondary site (\textit{attC}) downstream of the cassette. The \textit{attI1} site differs from \textit{attC} sites in that the inverse core site and secondary structure are missing 5' of the \textit{attI1} core site (21). The majority of published cassettes contain genes for resistance to various antimicrobial agents including trimethoprim and aminoglycosides (41). Trimethoprim selectively inhibits the bacterial dihydrofolate reductase (DHFR), thus preventing reduction of dihydrofolate to tetrahydrofolate (11). The most common mechanism of resistance to trimethoprim in enterobacteria is the production of an additional plasmid-mediated DHFR which, unlike the chromosomal enzyme, is less sensitive to inhibition by trimethoprim (6). Sixteen trimethoprim-resistant enzymes have been identified in enterobacteria and have been characterized and grouped on the basis of their sequences. With the exception of the phylogenetic group comprising DHFR types 1, 5, 6, 7, 14, and 15 and the unusual type 2 DHFRs, the trimethoprim-resistant DHFRs remain as diverse as chromosomal prokaryotic DHFRs in general (1, 45). The genes for the majority of resistant DHFRs occur as gene cassettes that are site specifically inserted into the recombinationally active site of class 1 and class 2 integrons (28). The high incidence of trimethoprim resistance gene cassettes inserted into class 1 integrons which normally harbor \textit{sul1} (sulfonamide resistance) at the 3' end is most likely driven by the use of trimethoprim-sulfonamide combinations, which exert strong selection pressure for co-resistance (28).

Another class of genes frequently found as cassettes in the variable region of integrons encode aminoglycoside-modifying enzymes which modify aminoglycosides by acetylation, adenylation, or phosphorylation (41, 43). The adenylylating enzymes comprise a phylogenetically diverse group, of which only the classes \textit{ANT}(3\textsuperscript{0}) and \textit{ANT}(9) are related (31, 6, 30\% identity) (31, 35, 43). The \textit{ANT}(3\textsuperscript{0}) enzymes confer streptomycin-spectinomycin resistance by adenylation of the 3'-hydroxyl position of streptomycin and the 9-hydroxyl position of spectinomycin, whereas the \textit{ANT}(9) class lack 3' activity and confers resistance only to spectinomycin (43). The most frequently encountered \textit{ant(3\textsuperscript{0})} in enterobacteria is \textit{aadA1}, also called \textit{(ant(3\textsuperscript{0})-Ia)} (27, 43). Gene types for two other enzymes in this class have also been established in gram-negative bacteria: \textit{aadA2} \textit{(ant(3\textsuperscript{0})-Ib)}, which is found on \textit{pSa} in \textit{Agrobacterium tumefaciens} (9) and which shares 82\% identity with \textit{aadA1}, and an \textit{aadA}, which is found in \textit{Salmonella enterica} serovar Choleraesuis and which shares 44\% identity with \textit{aadA1} (32). The genes \textit{aadA1} and \textit{aadA2} occur as gene cassettes and are flanked by a core sequence at the 5' end and a 59-base element at the 3' end (9, 17).
In a survey of trimethoprim resistance in South Africa, 357 isolates of gram-negative aerobic commensal fecal flora were probed with oligonucleotide probes to determine the prevalence within the population of DHFR genes that encode trimethoprim resistance (3, 4). An isolate from these studies which expressed high-level trimethoprim resistance (MIC, \( \geq 1.024 \) mg/liter) and which did not hybridize to any of the DHFR probes was selected for further study. This paper reports on the molecular epidemiology, nucleotide sequence, and biochemical properties of a new DHFR gene for trimethoprim resistance and its surrounding genetic structures which include a new gene for streptomycin-spectinomycin resistance.

**MATERIALS AND METHODS**

**Resistance determination.** The MICs of trimethoprim were determined by the agar dilution method; and the antibiotic sensitivity tests for detection of resistance to tetracycline, ampicillin, chloramphenicol, spectinomycin, streptomycin, and sulfisoxazole were performed by the disk diffusion method according to the guidelines set by the National Committee for Clinical Laboratory Standards (36).

**Bacterial strains and plasmids.** A fecal *Escherichia coli* isolate, RA33-2, was selected for this study from a group of 52 of 357 isolates which could transfer their trimethoprim resistance determinants by conjugation to an *E. coli* J62-2 recipient strain (5) and which failed to hybridize to probes for *intI1*, dfr5, dfr6, dfr13, and aadA4, the positions of insertion sequences IS1 and IS26, and the truncated transposons Tn21 and Tn3. The core elements of the gene cassettes and the inverted repeats (IRs) of the insertion sequence elements are indicated.

**Preparation and assay of adenyltransferase.** Cells from logarithmic-phase cultures of *E. coli* JM109 were harvested, washed, and resuspended in 2\% assay buffer (38). Cell extracts (50 \( \mu \)g of protein) from ultrasonically disrupted cells were assayed for adenyltransferase activity by a phosphocellulose paper binding method described previously (38). Positive and negative controls were pUK2412 (1) with *aadA1* and pGEM-3Zf(+), respectively. Estimates of the protein concentrations in crude lysates were obtained by the method of Waddel (50).

**Preparation and assay of adenyltransferase.** Cells from logarithmic-phase cultures of *E. coli* JM109 were harvested, washed, and resuspended in 2\% assay buffer (38). Cell extracts (50 \( \mu \)g of protein) from ultrasonically disrupted cells were assayed for adenyltransferase activity by a phosphocellulose paper binding method described previously (38). Positive and negative controls were pUK2412 (1) with *aadA1* and pGEM-3Zf(+), respectively. Estimates of the protein concentrations in crude lysates were obtained by the method of Waddel (50).

**Preparation and assay of adenyltransferase.** Cells from logarithmic-phase cultures of *E. coli* JM109 were harvested, washed, and resuspended in 2\% assay buffer (38). Cell extracts (50 \( \mu \)g of protein) from ultrasonically disrupted cells were assayed for adenyltransferase activity by a phosphocellulose paper binding method described previously (38). Positive and negative controls were pUK2412 (1) with *aadA1* and pGEM-3Zf(+), respectively. Estimates of the protein concentrations in crude lysates were obtained by the method of Waddel (50).

**Preparation and assay of adenyltransferase.** Cells from logarithmic-phase cultures of *E. coli* JM109 were harvested, washed, and resuspended in 2\% assay buffer (38). Cell extracts (50 \( \mu \)g of protein) from ultrasonically disrupted cells were assayed for adenyltransferase activity by a phosphocellulose paper binding method described previously (38). Positive and negative controls were pUK2412 (1) with *aadA1* and pGEM-3Zf(+), respectively. Estimates of the protein concentrations in crude lysates were obtained by the method of Waddel (50).

**PCR.** To determine the association between the novel *dfr* cassette and the class 1 integron, intragenic primers for *intI1* (5'-CGTTCCATAAGAGACGGTG-3') and *dfr13* (5'-CATACAGGCCATTTGGCCT-3') were used to amplify the region between the two genes. DNA amplification was performed in 50-\( \mu \)l volumes with 2 \( \mu \)l of Taq DNA polymerase (Promega), 1 mM MgCl\(_2\), and 0.1 mM dNTPs. The amplified 320-bp DNA fragment was analyzed by agarose gel electrophoresis. The nucleotide sequence data reported here have been assigned the accession no. Z50802 by EMBL.
FIG. 2. Nucleotide sequence and translated peptides of the PvuII-BamHI fragment of pUK2381 showing the class I integron context of gene cassettes dfr13 and aadA4 and the position and flanking sequences of IS26. The 235 and 210 promoter regions of the 5′CS are underlined, the oligonucleotide probe for dfr13 is underlined, the points of insertion of the gene cassettes are marked (.), the imperfect inverted repeat of the 5′-9-base element of the dfr13 cassette is underlined and the direction is marked (.), the inverted repeats of IS26 are in boldface type, and asterisks indicate stop codons.
}

Downloaded from http://aac.asm.org/ on October 29, 2017 by guest
exponentially defined as a weak promoter system and is iden-
tical to the promoters found within the 5’ CSs of pLMO20 and
Tn5086 (46, 47). The translated polypeptide sequence was
compared with other amino acid sequences in the SwissProt
database. The 31 sequences with the best scores were all
dHFR sequences. The amino acid sequence of the new dfr
shared the highest degree of amino acid identity with dfr12
(82.4%). The degrees of identity between the dfr13 sequence
and the sequences of other resistance and chromosomal
dHFR genes ranged between 15 and 36%, thus placing dfr12
and dfr13 in an indisputable monophyletic group. The trans-
lated polypeptide for the DHFR gene is shown in Fig. 2. The
novel DHFR gene has been named dfr13, and the encoded
polypeptide has been named the type 13 DHFR. The nucleo-
tide sequence immediately 3’ of the end of dfr13 encoded a
structure of 86 nucleotides which was recognizable as an attC
site (59-base element) in that it begins with the inverse core site
CTAAC and terminated with the consensus core sequence
GTAGGCC. The sequence between the two core sites differed
from the sequence found between the core sites of the con-
sensus attC site in that it encoded a relatively short imperfect
inverted repeat which was positioned 15 bases to the left of the
axis of symmetry within the element and which is similar in
structure to the dfr12 cassette (24). The attC site flanking dfr13
is shown underlined in Fig. 2.

A new spectinomycin-streptomycin resistance determinant.
From pUK2408 and pUK2409, the region 3’ to the DHFR
gene cassette was sequenced. Twelve nucleotides downstream
of the consensus core sequence (GTAGGCC) which marked
the end of the dfr13 cassette, an ORF of 262 amino acids was
identified. Like many other gene cassettes, there were no rec-
ognizable promoters or ribosome binding sites between the
core sequences and the first codon, and on the basis of previous
experimental evidence (15), it is presumed that the promoters
in the 5’ CSs are adequate to ensure gene expression. The amino
acid sequence of the ORF shared 57.6% identity with AADA1,
54.6% identity with AADA2, and 44.3% identity with the
AADA from Salmonella enterica serovar Choleraesuis. The new enzyme
also shared 37 and 27% identities with the AAD(9) adeny-
transferases of Staphylococcus aureus and Enterococcus faeca-
lis, respectively (31, 35). The new resistance gene had adeny-
ating activity similar to that of aadA1 and was 31% more
efficient at adenylating spectinomycin (Table 1). The sequence
identity and the 3’(9)-O-adenylating activity suggest that this
enzyme is of the AADA class and has been named aadA4
(anti(3’)-Id). The translated polypeptide has been named
AAD4 (ANT(3’)-Id). The MIC of spectinomycin was signif-
ically higher for the pUK2408 clone (512 µg/ml) than for the
original pUK2381 transconjugant (64 µg/ml), and this differ-
ence is most likely due to increased expression as a result of the
strong promoter and the high copy number of the cloning vec-

## Table 1. Comparison of adenyltransferase activities of aadA1 and aadA4 on different antibiotic substrates

<table>
<thead>
<tr>
<th>Plasmid</th>
<th>Streptomycin (activity with various antibiotics (cpm))</th>
<th>Spectinomycin</th>
</tr>
</thead>
<tbody>
<tr>
<td>pGEM-3Zf (none)</td>
<td>4,500 ± 74</td>
<td>3,520 ± 190</td>
</tr>
<tr>
<td>pUK2408 (aadA4)</td>
<td>4,540 ± 140</td>
<td>2,420 ± 150</td>
</tr>
</tbody>
</table>

a. Plasmids were expressed in E. coli JM109.
b. The reported values are the average ± standard deviation for samples tested in triplicate.

to the expression of a functional cassette with a 59-base element located more than
39 bases downstream from the 3’ end of the ORF, prior to its
interruption by the insertion of IS26. An analysis downstream of the
IS26 element showed that no sequences resembled a putative
59-base element and suggests that the 59-base element
may have been deleted from pUK2381 through recombination
with other IS26 elements.

### Insertion sequences IS26 and IS1. The 3’ conserved sequence
(3’ CS) is usually found downstream of the variable region of
class 1 integrons and contains genes that confer resistance to
intercalating dyes and quaternary ammonium compounds
(gaacΔE1) and sulfonamides (sulI) (39). To determine whether
the 3’ CS was disrupted by IS26 and is still present on pUK2381,
the nucleotide sequence downstream of IS26 was determined and
was shown to be identical to the sequence of part of the
resolvase gene (tnpR) previously identified on Tn3 and Tn1331
(14, 22). Hybridization studies of pUK2381 with gene probes
consisting of the HindIII-PstI fragment sulI and the
HindIII fragment of gaacΔE1 showed that neither of these two
probes hybridized to the plasmid, and therefore, the 3’ CS was
absent. Southern analysis with a gene probe for sulI revealed that
two copies of the element were present on pUK2381 and
suggests that this element has played a significant role in the
arrangement of resistance genes in pUK2381 through transpos-
ion or incoGinate formation with IS26. The determinant for
sulfonamide resistance was cloned into pGEM-3Zf(+)+. A
partial sequence of this clone identified sul2 as the sulfonamide
resistance determinant. The second copy of IS26 was located
approximately 2 kb upstream of sul2. Partial sequencing and
restriction mapping 3’ of intII revealed that the integrase was
contiguous with tnpM of Tn21 and that the downstream tnpR
was truncated by the insertion of IS1, 270 bp after the start of
tnpR (29).

### Biochemical properties of DHFR type 13. The specific activ-
ities of DHFRs from crude extracts of wild-type E. coli
RA33-2 and the pUK2381 transconjugant were 4.0- and 2.6-
fold higher than that for E. coli K-12, respectively. The high
copy number and strong promoters of pGEM-3Zf(+) resulted in
an 1,000-fold increase in the level of production of DHFR
in the pUK2410 clone in comparison to that in the host chromo-
somal DHFR. The peak fraction of the type 13 DHFR from
the Sephadex G75 column was assayed in the presence of
increasing concentrations of trimethoprim and methotrexate.
The trimethoprim concentration required to inhibit the activity of
the type 13 DHFR by 50% (ID50; ID50 = 800 µM) was
100,000-fold higher than that for the E. coli JM109 chromo-
somal DHFR (ID50 = 0.007 µM). This value is similar to that
to the type 12 DHFR (ID50 = 700 µM) (24). The type 13

transconjugant (128 µg/ml) was higher than that for the pUK2408
clone (64 µg/ml). A possible explanation for this discrepancy is
the presence of an additional gene for streptomycin resistance
located on pUK2381, such as strA, which is often associated with
sulII (40). The pUK2381 transconjugant was sensitive to
gentamicin, netilmicin, tobramycin, and amikacin.

aadA4, a truncated gene cassette. A truncation due to IS26
(34) was noticed 39 bases (nucleotides 2091 to 2130 in Fig. 2)
downstream of aadA4. An analysis of the sequence between the
3’ end of aadA4 and IS26 suggests that aadA4 is an atypical
cassette, since an inverse core site YYAAGC, which occurs im-
mediately downstream of related cassettes aadA1 and aadA2
was absent. It is likely that aadA4 may have originally been a
functional cassette with a 59-base element located more than
39 bases downstream from the 3’ end of the ORF, prior to its
interruption by the insertion of IS26. An analysis downstream
of the IS26 element showed that no sequences resembled a
putative 59-base element and suggests that the 59-base element
may have been deleted from pUK2381 through recombination
with other IS26 elements.

Downloaded from http://aac.asm.org/ on October 29, 2017 by guest
DHFR was 1,700 times more resistant to inhibition by methotrexate (ID<sub>50</sub> = 5 μM) than the chromosomally encoded DHFR of <i>E. coli</i> JM109 (ID<sub>50</sub> = 0.003 μM). However, the ID<sub>50</sub> of methotrexate was low enough relative to those of the type 2 DHFRs (ID<sub>50</sub> = 1,000 μM) to suggest that the active site for dihydrofolate (FH<sub>2</sub>) was not dissimilar to those of other DHFR genes. From the Lineweaver-Burk plots, the Michaelis constant (K<sub>M</sub>) for the type 13 DHFR was calculated to be 33.3 μM FH<sub>2</sub>, which is one of the highest values for a resistant DHFR determined and which suggests that this DHFR has a 10-fold lower affinity for FH<sub>2</sub> than the <i>E. coli</i> chromosomal DHFR (K<sub>M</sub> = 3.2 μM FH<sub>2</sub>). The inhibitor constants (K<sub>i</sub>) at trimethoprim concentrations of 250 and 500 μM were 178 and 182 μM, respectively (mean K<sub>i</sub> = 180 μM FH<sub>2</sub>), which is the highest K<sub>i</sub> recorded for non-type 2 DHFRs. The duration of exposure to 45°C required to inhibit DHFR activity by 50% (TD<sub>50</sub>) for the lower affinity for FH<sub>2</sub> than the which is one of the highest values for a resistant DHFR de-

Molecular epidemiology of dfr13. On the basis of the most significant heterogeneity, a 30mer oligonucleotide probe (5'-AAGCCTGTATACGCTCCTGTTGTGCAG-3') was derived from a comparison of the nucleotide sequences of the closely related dfr12 and dfr13 (nucleotides 929 to 958; Fig. 2). This heterogeneous region encodes a predicted loop between β-sheets C and D which is based on homology with the <i>E. coli</i> DHFR crystal structure (8) and overlaps the region from which the other dfr probes were selected (3). Of the 90 of 357 isolates of gram-negative commensal fecal flora which did not hybridize to probes for dfr1, dfr2b, dfr3, dfr5, dfr6, dfr7, dfr8, dfr9, dfr10, dfr12, and dfr14 (3, 4), 49% (44 of 90) hybridized to the probe for dfr13 and represented all the samples from rural and urban populations in South Africa. Fifty-eight percent (30 of 52) of self-transmissible plasmids hybridized to the probe for dfr13. Of the isolates which did not transfer trimethoprim resistance to recipient strain <i>E. coli</i> J62-2, 37% (14 of 38) hybridized to the probe for dfr13.

The EcoRI restriction profiles of the plasmids from the transconjugants which harbored dfr13 showed that the majority of the plasmids exhibited unique restriction profiles; however, identical restriction fragments of the sequence which represent the resistance region were common to most of the plasmids, which suggests that a significant amount of transfer and rearrangement is associated with the element that harbors dfr13. The antibiograms of the plasmids that harbor dfr13 showed that multiple drug resistance was extremely prevalent. Most of these plasmids conferred resistance to five or more antimicrobial agents. Resistance to ampicillin, tetracycline, sulphonamides, and streptomycin was virtually ubiquitous. Spectinomycin resistance was found on 23 of 30 of the plasmids, and resistance to chloramphenicol was found on 17 of 30 of the plasmids. The MICs of trimethoprim conferred by these plasmids were ≥0.048 mg/liter. To determine the association and position of dfr13 within the integron, the region between the two genes was amplified by PCR with a primer pair whose sequence was from within the sequences of intI1 and dfr13. PCR products of about 700 bp were obtained from 29 of 30 of the isolates that harbored transferable plasmids and 12 of 14 of the isolates that did not transfer resistance. The size of the PCR product suggests that the dfr13 cassette is inserted at the intI1 site in all these isolates.

To determine the location of dfr13 in the isolates which did not transfer resistance, plasmid and total DNAs from the hybridization-positive isolates were run on an agarose gel, Southern blotted, and then hybridized to the dfr13 probe. dfr13 was located on the chromosomes of 10 of 14 of these isolates and occurred on nontransferable plasmids in the remaining 4 isolates. DNAs from isolates that harbored nontransferable tri-

methoprim resistance were restricted with BamHI, Southern blotted, and probed with the dfr13-specific probe. More than half of the isolates (8 of 14) hybridized to a restriction fragment of 3.5 kb which corresponds to that of the pUK2381 control and which suggests that intI1, dfr13, dfrA4, and the truncated version of Tn3 are arranged on the chromosome in a manner similar to that in pUK2381. The restriction fragment sizes of the remaining hybridization-positive isolates, which included the PCR-negative isolates, were variable. The differences in the sizes of the restriction fragments indicate that different flanking sequences surround dfr13.

**DISCUSSION**

It is speculated that trimethoprim-resistant plasmid-mediated DHFRs originated as chromosomal genes that have been taken up by recombinational exchange and transferred to commensal and pathogenic organisms (45). Comparison of the dfr12 and dfr13 cassettes shows that flanking cassette structures of these related gene sequences share similar homologies (81%). This suggests that the genetic divergence between these closely related genes may not be the result of recent recruitment of chromosomal dfr genes from related organisms under selective pressure from trimethoprim but, rather, that these genes existed and diverged as gene cassettes long before the introduction of trimethoprim. Cassette homology has also been observed within other phylogenetic groups of dfr cassettes such as the type 1- and type 2-like classes. Similarly, a comparison of the flanking sequences of the aadA genes found in gram-negative bacteria (Fig. 3) shows that the cassette structures of the closely related genes aadA1 and aadA2 are very similar. There is no homology between the flanking sequences of the aadA gene of <i>S. enterica</i> serovar Choleraesuis and those of aadA1 and aadA2, which suggests that aadA may have diverged early on from a common ancestor before aadA1 and aadA2 evolved as gene cassettes. In comparison, aadAA may be an intermediate in cassette evolution, bearing a core site at the 5’ end of the gene but completely lacking any homology to a 59-base element on what remains of the 3’ flanking sequence. It is possible that in aadAA a 59-base element may have been present downstream of the point of insertion IS26. This would explain the presence of this cassette in the context of a class 1 integron. This would imply that the structure of a putative cassette of aadAA is different from that of the consensus aadA cassette at the 3’ end.

Relative to phylogenetically related dfr cassettes, the class 1 integrons that harbor these cassettes are highly conserved,
which suggests that the movement of dfr cassettes into these elements is recent and is associated with the introduction of trimethoprim as a selective agent. The use of sulfonamides for three decades prior to the introduction of trimethoprim-sulfonamide combinations is most likely to have led to strong selection pressure for class 1 integrons with a 3′CS that harbors sul1. The subsequent use of trimethoprim-sulfonamide combinations has selected for the acquisition of dfr cassettes and the predominance of coresistance associated with the class 1 integrons (28). The arrangement of the genes for trimethoprim and sulfonamide resistance in pUK2381 is unusual, in that despite the association of dfr13 with the 5′CS, the 3′CS of the integron which carries sul1 is absent and has been replaced by sul2 outside of the integron context on the same plasmid. Although sul2 is most frequently found on small nonconjugative resistance plasmids, its presence on large plasmids has been observed previously (40). The presence of insert sequences IS26 and IS1 appears to have played a significant role in the evolution of pUK2381, presumably through the formation of compound transposons and/or cointegration (12). As a result, truncated forms of Tn21 and Tn3 have been combined to produce a more contiguous region of multiple resistance. In pUK2381, the potential for recombination by Tn3 and Tn21 has been substituted with insert sequences IS26 and IS1, and these elements may play a role in enhancing the prevalence of this form of multiple resistance. Southern blotting and restriction analysis of isolates that harbor dfr13 on plasmids or on the chromosome suggest that the arrangement of resistance genes, truncated transposons, and insert sequences in this element is not unique to pUK2381. dfr13 was shown to be fairly prevalent and widespread in South Africa and was detected in 12.3% (44 of 357) of the commensal fecal isolates resistant to trimethoprim. The successful spread of this DHFR may be due to a strong selection advantage provided by the high incidence of multiple drug resistance. It is difficult to predict how widely distributed dfr13 may be in other parts of the world. However, since this DHFR was extremely widespread in South Africa and was detected in all the rural and urban population groups, it is thought that this DHFR may be widely distributed in other parts of the world and may account for a proportion of the 10 to 68% of DHFR genes which were not identified in a number of studies (13, 23, 25, 30, 44, 49).

On the basis of the similarity between the sequence and inhibitor profile of the type 12 and 13 DHFRs, it is clear that these enzymes should be regarded as a monophyletic group (family 3) since they share similar degrees of homology to that found within the type I-like and type II-like DHFR enzyme families. Discrimination between resistant DHFR genes within close phylogenetic groups has often been hampered by the use of gene probes which are not representative of regions of adequate heterogeneity (52). The gene probing strategy used with the collection of isolates in this study (3, 4) targets gene regions which encode putative regions of low structural and functional significance. These regions are therefore most likely to be susceptible to genetic drift and therefore useful for the detection and discrimination of new gene types. This strategy has led to the detection of two new genes, dfr15 (1) and dfr13, both of which share high degrees of sequence homology.

ACKNOWLEDGMENTS

This work was supported in part by the Sir Samuel Scott of Yews Research Trust.

We thank Marius Teletin for technical assistance.

REFERENCES


