New trimethoprim-resistant dihydrofolate reductase cassette, dfrXV, inserted in a class 1 integron

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New Trimethoprim-Resistant Dihydrofolate Reductase Cassette, *dfrXV*, Inserted in a Class 1 Integron

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Trimethoprim is an antimicrobial agent used on its own or in combination with sulfamethoxazole in the treatment of infections caused by gram-negative organisms. Trimethoprim selectively inhibits the bacterial dihydrofolate reductase (DHFR), thus preventing the reduction of dihydrofolate to tetrahydrofolate (8). 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 (5). Sixteen trimethoprim resistance enzymes have been identified in enterobacteria and have been characterized and grouped on the basis of their nucleotide sequences and kinetic properties. The largest of these groups and by far the most prevalent are the type I-like enzymes, which include *dfrI, dfrIb, dfrV, dfrVI, and dfrVII* (14). This enzyme group is characterized by an open reading frame (ORF) of 157 amino acid residues, and the members of this group share between 64 and 88% amino acid sequence identity in this ORF (14). The majority of these enzymes have been found as gene cassettes inserted into the recombinationally active sites of integrons (22). 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 of DHFR resistance genes within the population (2, 3). Hybridization experiments revealed that contrary to all previous data, the most prevalent DHFR was type Ib (21.8%), followed by types VII (18.8%), I (14.6%), VIII (12.9%), XIII (12.3%), V (7.8%), and XII (0.3%) (1, 3). Forty-six of 357 isolates did not hybridize to any of the DHFR probes. One of these isolates, *Escherichia coli* UI14, which is highly resistant to trimethoprim (MIC, >2,048 μg/ml), was shown to transfer a 101-kb plasmid (pUK2317) which confers resistance to trimethoprim, spectinomycin, tetracycline, and sulfanamides to a recipient strain, *E. coli* J62-2, by conjugation (4).

The nucleotide sequence of a plasmid-borne trimethoprim resistance gene from a commensal fecal *Escherichia coli* isolate revealed a new dihydrofolate reductase gene, *dfrXV*, which occurred as a gene cassette integrated in a site-specific manner in a class 1 integron. The new gene shows 84% nucleotide identity and the predicted protein shows 90% amino acid identity with *dfrI* and DHFR type I, respectively. Genes for spectinomycin resistance, *aadA1* (ant (3′)-Ia), and sulfonamide resistance, *sulI*, were located downstream of *dfrXV* in a manner identical to that in pLMO229.

**RESULTS AND DISCUSSION**

Figure 1 shows the restriction map, gene map, and direction of sequencing of pUK2412. From the partial sequence and restriction map, the trimethoprim resistance gene was shown to be preceded by the *intI1* gene associated with a class 1 integron, as reported previously (12, 16, 19, 24). A primer (5′-AA CGATGTTACGCAGCAG-3′) based on the sequence which occurs between the integrase ORF and the start of the first gene cassette (12, 16, 19, 24) was used to sequence the complementary strand upstream of the integrase gene. Upstream of the integrase ORF and its flanking structures, the nucleotide sequence revealed the DHFR ORF of 471 bp on the complementary strand. The DHFR ORF encoded 157 amino acids and was identified by its close nucleotide sequence homology with *dfrI* (84.4%) and the close amino acid homology (90 to 63%) that it shared with the trimethoprim-resistant type I-like DHFRs encoded by *dfrI, dfrIb, dfrV, dfrVI, and dfrVII* (11, 24, 26, 29, 31). The ORF begin with the atypical *E. coli* start codon GTG at positions 357 to 359 (Fig. 2). Despite the unusual start codon which normally codes for valine, it is the only codon, which is preceded by a plausible Shine-Dalgarno sequence (TAAGGAAGT). Since the ATG codon that is located five amino acids downstream of the GTG codon is not preceded by such a sequence, it is unlikely that this is the start codon. Furthermore, the use of alternative *E. coli* start codons GTG

**MATERIALS AND METHODS**

Purified pUK2317 DNA was restricted with *PstI*, and the fragments were ligated into *PstI*-restricted pGEM-3Zf(+) (Promega, Madison, Wis.) and electrotransformed (10) into *E. coli* JM109. A trimethoprim-resistant transformant, pUK2411, which contained a 9.4-kb *PstI* fragment was further restricted with *BamHI*, and the 6.74-kb fragment which contained the plasmid vector and a 3.54-kb cloned fragment were religated to produce trimethoprim-resistant clone pUK2412. A 1,280-bp *PstI* fragment was further subcloned in both directions into the *Smal* site of pGEM-3Zf(+) to produce trimethoprim-resistant clones pUK2413 and pUK2414. These two plasmids were then restricted with *HindIII* and were religated to produce trimethoprim-sensitive clones pUK2415 and pUK2416. Cloning was performed as described previously (23), and sequencing reactions were performed with both dGTP and dITP labels with the SEQUE- NASE, version 2.0, DNA sequencing kit (United States Biochemicals, Cleveland, Ohio). Sequence comparisons were made with the BLAST computer program (National Center for Biotechnology Information).

**Nucleotide sequence accession number.** The nucleotide sequence of the type XV DHFR has been given EMBL accession no. Z83331.

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and TTG in other type I-like DHFRs such as dfrI, dfrV, and dfrVII has previously been demonstrated by experiments involving N-terminal amino acid sequencing and site-directed mutagenesis (11, 17, 26). The ORF ended with stop codon TAA at positions 828 to 830. The translated polypeptide for the DHFR is shown in Fig. 2. The new DHFR gene has been named dfrXV, and the encoded polypeptide has been designated the type XV DHFR (EMBL accession no. Z83311).

### dfrXV as a mobile cassette.

Gene cassettes inserted into the core site of class 1 integrons are usually flanked by a consensus sequence (GTTRRRY) on the 5' end, which marks the point of insertion of the gene cassette into the integron, and an imperfect inverted repeat known as the 59-base element, situated 3' to the resistance gene ORF (22). Similarly, dfrXV was flanked by both a core element, which was located 16 nucleotides 5' to the DHFR ORF and which is presumed to mark the cassette boundary, and an inverted repeat (underlined in Fig. 2) from nucleotides 825 to 928 at the 3' end of the DHFR ORF which marks the 3' end of the gene cassette. The core element (GT TAACC) differed from the consensus sequence by a single nucleotide. Like most gene cassettes, no recognizable E. coli promoter was present between the core element and the start of the ORF. Sequence analysis of the upstream conserved element (intI1) revealed a promoter region previously identified to drive the expression of inserted gene cassettes (underlined in Fig. 2) (12, 15, 22). This particular promoter polymorphism was identified as a hybrid promoter which is a promoter with weak to moderate strength, as described previously (15). The first promoter is followed by a second promoter which has been identified in all class I integrons and which is thought to be nonfunctional due to the short spacing between the 235 and 210 hexamers (15).

Inhibition profiles of DHFR.

DHFR assays were performed by the method of Osborn and Huennekens (18) as described previously (6). From crude cell lysates (28), the specific activity of the DHFR, expressed in nanomoles of dihydrofolate (FH2) reduced per minute per milligram of protein, of E. coli UI14 was 14.3, a value 14-fold higher than the specific activity of the E. coli K-12 chromosomal enzyme. The specific activity of the

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**FIG. 1.** Restriction map, gene map, cassette boundaries, and direction of sequencing (→) of pUK2412.

**FIG. 2.** Nucleotide sequence and translated polypeptide of dfrXV. The sequence used as a gene probe is printed in boldface type. The gene cassette boundaries are marked (••), and the imperfect inverted repeat (59-base element) is underlined (interrupted lines); gaps indicate mismatched bases, asterisks denote extra bases in the left half of the element which interrupt the inverted repeat, and arrows (---) denote the direction of symmetry. The putative promoter sequences of the conserved element are underlined, and the start codon of intI1 is in italics.
resistant to trimethoprim. The type XV DHFR was 1,500 times more resistant to trimethoprim at concentrations of 10 and 25 μM (50% inhibition, ID50). In comparison to the chromosomal DHFR, these results were similar to those obtained with partially purified extracts prepared by ultrasonic disruption, followed by ammonium sulfate precipitation and, finally, Sephadex G-75 gel exclusion chromatography. The specific activity of DHFR (1,049.1 nmol of F4H2 reduced/min/mg of protein) was maintained in partially purified DHFR. Partially purified DHFR was prepared by ultrasonic disruption, followed by ammonium sulfate precipitation and, finally, Sephadex G-75 gel exclusion chromatography as described previously (28). The approximate inhibitor profiles and kinetic properties of the type XV DHFR were similar to those obtained with partially purified extracts for other DHFR enzymes of this group (Table 1). DHFR activity was assayed in the presence of increasing concentrations of trimethoprim and methotrexate to determine the concentration required to inhibit the activity of the type XV DHFR by 50% (ID50). In comparison to the chromosomal DHFR of E. coli JM109 (ID50 = 0.007 μM), the type XV DHFR (ID50 = 22.4 μM) was more than 3,000 times more resistant to trimethoprim. The type XV DHFR was 1,500 times more resistant to inhibition by methotrexate (ID50 = 4.4 μM) than the chromosomal DHFR of E. coli JM109 (ID50 = 0.003 μM). The Lineweaver-Burke plots used to determine the Michaelis constant (Km) and the inhibitor constant for trimethoprim (Ki) showed that the Km for the type XV DHFR was calculated to be 16.7 μM FH2. The Ki values for trimethoprim at concentrations of 10 and 25 μM were 16.2 and 15.6 μM, respectively (mean Ki = 15.9 μM FH2). Unlike the other enzymes of this group, the type XV DHFR was found to be extremely heat stable, even at low protein concentrations, and could survive exposure to 45°C for more than 20 min without any significant loss of activity.

**Molecular epidemiology of dfrXV.** Dot blotting was performed as described previously (3). The nucleotide sequences of dfrI and dfrXV were aligned to determine regions of maximum heterogeneity, and a 30-mer oligonucleotide probe (5’-ATACATCTCTCATCAGGAAAGTGAGATTGTTG-3’) which contained nine nucleotide mismatches compared with the sequence of dfrI was selected for the detection of dfrXV (boldface type in Fig. 2). This region of nucleotide sequence heterogeneity encodes a predicted highly variable external loop that is located between two conserved regions of the secondary structure and that has been described previously for the discrimination and detection of closely related DHFR genes (1, 2, 31). Forty-six of 357 isolates of gram-negative commensal fecal flora did not hybridize to probes for other resistant DHFR types, and of these 26.1% (12 of 46) hybridized to the probe for dfrXV. The type XV DHFR was detected in isolates from all three regions that were sampled in South Africa: nine isolates were from urbanized communities in the province of Gauteng, two isolates were from rural populations in the Northern Province, and one isolate was from rural Mpumalanga. Of the 12 hybridization-positive isolates, an E. coli isolate from Gauteng did not transfer trimethoprim resistance to an E. coli J62-2 recipient strain. Five different EcoRI restriction profiles were obtained for the 11 plasmids from the transconjugants which harbored dfrXV. Six isolates harbored plasmids which shared identical restriction profiles (pUK2317) and resistance markers (trimethoprim, sulfamethoxazole, tetracycline, spectinomycin), and all were isolated from the same urban community in Gauteng. Two plasmids, pUK2370 and pUK2369, had similar restriction profiles, and both conferred resistance to ampicillin, trimethoprim, sulfamethoxazole, tetracycline, and spectinomycin. Plasmid pUK2370 was detected in two isolates, one from Gauteng and the other from the Northern Province, and pUK2369 was isolated from Gauteng. Plasmid pUK2403, isolated from the Northern Province, harbored another unique restriction profile and conferred resistance to ampicillin, trimethoprim, sulfamethoxazole, tetracycline, and spectinomycin. Eleven of 12 of the isolates which hybridized to the probe for dfrXV were identified as E. coli. The remaining isolate from Mpumalanga was a Klebsiella sp. which harbored a novel transferable plasmid pUK2322 which conferred resistance to trimethoprim and sulfamethoxazole. The absence of streptomycin and spectinomycin resistance determinants on this plasmid suggests that this may be a second integron context for the dfrXV cassette. The MICS of trimethoprim conferred by these plasmids were all greater than 2,048 mg/liter. To determine the association and position of dfrXV among the class 1 integrons, PCR was used to amplify the region between the intI1 and dfrXV ORFs. PCR products of 750 bp were obtained for all 11 isolates which harbored transferable plasmids. The size of the PCR product suggests that the dfrXV cassette was the most recent cassette to be inserted and was inserted immediately upstream of the integrase gene (9, 22). No PCR product was detected in the isolate which was unable to transfer resistance to the E. coli recipient strain. The use of sulfonamides in combination with trimethoprim appears to play a significant role in the selection of sulI-associated integrons and has presumably applied strong selection pressure for the uptake of new trimethoprim resistance cassettes by these elements.

**REFERENCES**


