# Genetic Basis of Tetracycline Resistance in Clinical Isolates of *Listeria monocytogenes*

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The genetic basis of tetracycline resistance was studied in 25 clinical isolates of Listeria monocytogenes. Resistance to tetracycline was associated with resistance to minocycline and due to the presence of the tet(M) gene in 24 strains. Association of tet(M) with *int-Tn*, the gene encoding the protein required for the movements of Tn1545-like conjugative transposons, was found in all strains. Cotransfer of tet(M) and *int-Tn* among L. monocytogenes cells and from L. monocytogenes to Enterococcus faecalis was detected in 7 of the 12 strains studied at frequencies similar to those obtained with the prototype element Tn1545. tet(L), the secondmost prevalent tetracycline resistance gene in enterococci and streptococci, was detected in the remaining strain, where it was borne by a 5-kb plasmid. These observations indicate that two types of movable genetic elements, transposons and plasmids, in enterococci and streptococci are responsible for emergence of drug resistance in L. monocytogenes.

Listeria monocytogenes is a gram-positive opportunistic pathogen responsible for severe infections (septicemia, meningitis, and meningoencephalitis) primarily in immunocompromised hosts, the elderly, neonates, and fetuses. Infections caused by L. monocytogenes are likely to be food borne and the intestinal tract is the most initial probable site of invasion (16). Prognosis of listeriosis remains serious, and even with appropriate antibiotic therapy, listeriosis is fatal in approximately one-third of all cases (10). Most strains of L. monocytogenes are uniformly susceptible to antibiotics (18, 19). Acquired resistance to chloramphenicol, erythromycin, streptomycin, and tetracycline in two clinical isolates of L. monocytogenes has been reported (27, 30). It is likely that the emergence of multiple-antibiotic resistance in this species results from acquisition of self-transferable plasmids originating in the genera Enterococcus and Streptococcus (27). Recently, the involvement of enterococcal and streptococcal Tn1545-like conjugative transposons in the acquisition of antibiotic resistance by L. monocytogenes was anticipated (7). All these transposons contain the tetracycline resistance (Tc<sup>r</sup>) gene tet(M) alone (Tn916, Tn918, Tn919, and Tn925) or associated with other resistance genes (Tn1545) (3). These elements possess a broad host range of conjugal transposition and are responsible for acquired antibiotic resistance in Streptococcus pneumoniae (5, 29). We have demonstrated that a transposon-encoded protein designated Int-Tn is essential for transposition and conjugation of Tn1545 and related elements (28, 37). By using probes specific for int-Tn (the gene encoding the integrase of Tn1545 [28] and Tn916 [4]), and tet(M) and dot blot hybridization, we have studied the distribution of this class of transposons and of this resistance gene in clinical isolates of L. monocytogenes resistant to tetracycline. The distribution of three other  $Tc^r$  determinants [tet(K), tet(L), and tet(O)] already found in gram-positive bacteria was also studied.

#### MATERIALS AND METHODS

Bacterial strains. Strains from 1,288 cases of human listeriosis which had occurred in the United Kingdom were collected in the Division of Microbiological Reagents and Quality Control of the Central Public Health Laboratory. The isolates were identified by using the following criteria: gram strain positive; motile at room temperature; hemolytic on horse blood agar; catalase positive; oxidase negative; Voges-Proskauer positive; urease negative; esculin positive; no reduction of nitrates to nitrites; production of acid but not gas from D-glucose; and production of acid from D-salicin, L-rhamnose, and  $\alpha$ -methyl-D-mannitol but not from D-mannitol or D-xylose. All strains were serotyped in the Division of Microbiological Reagents and Quality Control. L. monocytogenes L017RF (26), resistant to fusidic acid and rifampin, L. monocytogenes EGDSmR (9), and Enterococcus faecalis BM4110 (5), both resistant to streptomycin, were used as recipients in conjugation experiments. Escherichia coli JM83 (22) was used in transformation experiments.

Media. Brain heart infusion (BHI) broth and agar (Difco Laboratories, Detroit, Mich.) were used for bacterial cultures. Sensitivity tests were done on Mueller-Hinton agar (Diagnostics Pasteur, Marnes-la-Coquette, France). All incubations were at 37°C.

Antibiotic susceptibility testing. Susceptibility to antibiotics was determined by either agar diffusion with disks impregnated with antibiotics (Diagnostics Pasteur) or a breakpoint multipoint inoculation technique. The method of Steers et al. (36) with  $10^4$  CFU per spot was used to determine the MICs of antibiotics.

Genetic techniques. Mating on filters was performed as described previously (38), and transfer frequencies were expressed as the number of transconjugants per donor CFU after the mating period. Transformation of  $E. \ coli$  (34) and

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TABLE 1. Probes used for hybridization

Probe	Reference
tet(K) (870-bp HincII fragment of pT181)	Khan and Novick (15)
tet(L) (310-bp ClaI-HpaII fragment of	
pBC16)	Hoshino et al. (13)
tet(M) (850-bp ClaI-HindIII fragment	
of Tn1545)	Martin et al. (20)
tet(O) (1,458-bp HindIII-NdeI fragment	
of pIP1433)	Sougakoff et al. (35)
int-Tn (830-bp TaqI fragment of Tn1545)	Poyart-Salmeron et al.
	(28)
inlA (3.3-kb HincII chromosomal DNA	
fragment of L. monocytogenes	
EGDSmR)	Gaillard et al. (8)

electrotransformation of *E. faecalis* (6) were performed as described previously. The antibiotics and concentrations used for selection of transcipients were as follows: fusidic acid (Leo, Montigny-Le-Bretonneux, France), 10  $\mu$ g/ml; rifampin (Merell Dow, Neuilly-sur-Seine, France), 20  $\mu$ g/ml; streptomycin (Pfizer, Paris-la-Défense, France), 500 and 1,000  $\mu$ g/ml of *L. monocytogenes* EGDSmR and *E. faecalis* BM4110, respectively; and tetracycline (Rhône-Poulenc, Vitry, France), 8  $\mu$ g/ml.

Preparation of DNA. Total DNA from Listeria and Enterococcus cells was prepared as follows: cells from 5 ml of a culture grown overnight were harvested, suspended in 1 ml of TE buffer (0.01 M Tris-hydrochloride [pH 8.0], 0.001 M EDTA) containing 25% sucrose and lysozyme (25 mg/liter), and incubated at 37°C for 1 h. The resulting protoplasts were lysed by phenol-chloroform extraction. Total DNA was recovered from the supernatant by ethanol precipitation and dissolved in 100 µl of TE buffer. The presence of DNA was monitored by agarose gel electrophoresis. Aliquots (10 µl) were denatured for 10 min at 100°C and spotted on Nytran membranes (Amersham S.A., Les Ulis, France). Purification of plasmid DNA from L. monocytogenes (27) and E. faecalis (5) by ultracentrifugation in cesium chloride-ethidium bromide was performed as described previously. Plasmids from E. coli were purified by rapid alkaline lysis as described previously (34).

DNA-DNA hybridization. The probes used for hybridization experiments are listed in Table 1. Fragments were extracted from low-gelling-temperature agarose type VII (Sigma S.A., La Verpillière, France) as described previously (34). Purified restriction endonuclease-generated DNA fragments were labeled with  $[\alpha^{-32}P]dCTP$  (Amersham S.A.) by nick translation (34). Dot blot hybridization under stringent conditions was performed as follows: prehybridization and hybridization for 5 and 18 h, respectively, at 65°C in a solution consisting of  $6 \times$  SSC (1× SSC is 0.15 M sodium chloride plus 0.015 M sodium citrate), 0.5% sodium dodecyl sulfate (SDS), and 0.05% nonfat dry milk, two washings in  $2 \times$  SSC-0.1% SDS at room temperature for 30 min each, and two washings in 0.2× SSC-0.1% SDS at 68°C for 45 min. Hybridization under low-stringency conditions was done in  $6 \times$  SSC-0.5% SDS-0.05% nonfat dry milk at 37°C for 18 h, and then the probes were washed twice in  $2 \times$  SSC-0.1% SDS at 45°C for 1 h. In dot blot experiments, self-hybridization of the probe and hybridization of the probe with total DNA from L. monocytogenes L017RF were used as positive and negative controls, respectively.

## RESULTS

Antibiotic sensitivity testing and strain characteristics. Thirty-three (2.5%) of the 1,288 isolates of L. monocytogenes collected from cases occurring over the time periods 1967 to 1981, 1983 to 1986, and 1987 to 1990 were found to be resistant to tetracycline (Tc<sup>r</sup>). The numbers of cases yielding strains resistant to tetracycline for these time periods were 13 of 265 (5%), 7 of 405 (2%), and 13 of 618 (2%), respectively. The results of antibiotic susceptibilities for the final group of strains (1987 to 1990) have been published previously (19). There was no obvious temporal or geographical clustering of cases due to the Tcr L. monocytogenes. Twenty-five of the Tc<sup>r</sup> strains were selected for further study. One strain was serovar 1/2a, one strain was serovar 1/2c, and the remaining 23 were serovar 4b, which is the most common cause of human listeriosis (21). Twenty-four of these strains were resistant to both tetracycline (MIC, 64 to 128  $\mu$ g/ml) and minocycline (MIC > 4  $\mu$ g/ml) (Tc<sup>r</sup> Mc<sup>r</sup>) (24). The remaining strain was resistant to tetracycline (MIC, 64  $\mu$ g/ml) only (Tc<sup>r</sup> Mc<sup>s</sup>). The strains were uniformly susceptible to ampicillin, chloramphenicol, cotrimoxazole, erythromycin, gentamicin, imipenem, kanamycin, penicillin, rifampin, streptomycin, and vancomycin (24).

Hybridization. Five classes of tetracycline resistance determinants, tet(K), tet(L), tet(M), tet(O), and tet(P), have been detected in gram-positive bacteria (17). We tested the listerial strains for the presence of nucleotide sequences that were structurally related to int-Tn, tet(K), tet(L), tet(M), and tet(O) by dot blot hybridization using intragenic probes. The tet(P) gene, which is apparently specific for the anaerobic species *Clostridium perfringens* (1), was not included in this study. Homology with tet(M) and int-Tn was detected in the 24 Tc<sup>r</sup> Mc<sup>r</sup> strains and the Tc<sup>r</sup> Mc<sup>s</sup> strain, BM4212, hybridized with tet(L) only (data not shown). None of the probes hybridized with the susceptible strain L. monocytogenes L017RF. The presence of DNA on the membranes was assessed by using as a probe the 3.3-kb HincII fragment containing the gene encoding InIA, a protein involved in the entry of L. monocytogenes into epithelial cells (8).

Genetic support of Tc<sup>r</sup> in L. monocytogenes. The transferability of Tc<sup>r</sup> Mc<sup>r</sup> from 12 strains of L. monocytogenes containing tet(M) was tested by filter mating. Seven strains transferred the resistance determinant to plasmid-free strains L. monocytogenes L017RF and E. faecalis BM4110 at frequencies of  $10^{-5}$  and  $10^{-6}$ , respectively. E. faecalis BM4110 transconjugants corresponding to the seven donors were able to retransfer Tc<sup>r</sup> Mc<sup>r</sup> to L. monocytogenes L017RF at frequencies ranging from  $10^{-6}$  to  $10^{-7}$ . Total DNA extracted from L. monocytogenes and E. faecalis transconjugants hybridized with tet(M) and int-Tn and no plasmid DNA was detected in these strains by ultracentrifugation in cesium chloride-ethidium bromide and by agarose gel electrophoresis of crude bacterial lysates (data not shown).

L. monocytogenes BM4212 containing tet(L) transferred tetracycline resistance by conjugation to L. monocytogenes L017RF at a frequency of  $1.6 \times 10^{-8}$  but not to E. faecalis BM4110 (< $10^{-9}$ ). A transconjugant, BM4213, was selected for further studies. Retransfer of Tc<sup>r</sup> from BM4213 to L. monocytogenes EGDSmR and to E. faecalis BM4110 was not detected (< $10^{-9}$ ). Plasmid DNA of strains BM4212 and BM4213 was purified by ultracentrifugation in cesium chloride-ethidium bromide and electrophoresed after digestion with EcoRI and HindIII endonucleases (Fig. 1). Comparative analysis revealed that two plasmids designated pIP812

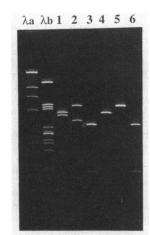


FIG. 1. Analysis of plasmid DNA from L. monocytogenes BM4212 (lanes 1 to 3) and BM4213 (lanes 4 to 6) by agarose (0.8%) gel electrophoresis. Plasmid DNA (2 to 3  $\mu$ g) was digested with EcoRI (lanes 1 and 4), HindIII (lanes 2 and 5), or EcoRI plus HindIII (lanes 3 and 6). Bacteriophage  $\lambda$  DNA digested by HindIII ( $\lambda$ a) and PstI ( $\lambda$ b) was used as a molecular size standard.

and pIP813 were present in L. monocytogenes BM4212, whereas pIP813 was detected only in BM4213. The molecular sizes of pIP812 and pIP813 were estimated to be 4 and 5 kb, respectively. Nucleotide sequences homologous to tet(L) were detected in pIP813 DNA by dot blot hybridization (data not shown), whereas pIP812 remained cryptic. Plasmid pIP813 was introduced by electrotransformation in E. faecalis BM4110 and by transformation in E. coli JM83, where it was able to replicate and confer resistance to tetracycline. Taken together, these results indicate that the tet(L) gene of BM4212 is carried by pIP813. The failure to transfer this plasmid by mating from L. monocytogenes BM4213 to L. monocytogenes EGDSmR indicate that it is not self-transferable. Therefore, it is likely that transfer of pIP813 from the wild-type strain L. monocytogenes BM4212 to L. monocytogenes L017RF occurred by mobilization, although we did not detect any large, potentially conjugative, plasmid in the donor.

## DISCUSSION

We have studied the genetic basis of tetracycline resistance in 25 strains of *L. monocytogenes* isolated in the United Kingdom from human listeriosis between 1967 and 1990 (18, 19). Among these strains, 24 were  $Tc^r Mc^r$  and contained sequences related to tet(M). The remaining strain, BM4212, was  $Tc^r Mc^s$  and harbored tet(L).

The tet(M) gene is common in enterococci and streptococci (39) and has also been found in *Staphylococcus* spp. (2), *Clostridium difficile* (12, 23), cell wall-less bacteria (32), and gram-negative pathogens (33). Dissemination of this resistance gene may reflect the fact that it is carried by broad-host-range conjugative transposons such as Tn1545 and Tn916. Our results suggest that the presence of tet(M) in *L. monocytogenes* is secondary to acquisition of Tn1545-like elements. This proposal is based on (i) the association, in all the Tc<sup>r</sup> Mc<sup>r</sup> strains, of tet(M) with *int-Tn*, the gene encoding the protein required for the movements of this class of transposons, and (ii) the cotransfer of tet(M) and *int-Tn* among *L. monocytogenes* cells and from *L. monocytogenes* to *E. faecalis* at frequencies similar to those of the prototype element Tn1545 (5; also unpublished results). The failure to transfer tet(M) in 5 of the 12 strains studied may result from rearrangements in genes or cis-active sequences essential for conjugal transposition. Derivatives of Tn916 defective for conjugation have been found in Gardnerella vaginalis and in commensal Neisseria spp. (33). Since these transposons are rare in staphylococci (29) but are widespread in enterococci and streptococci (39), it is therefore likely that their presence in L. monocytogenes is due to acquisition of genetic information originating in enterococci and streptococci. It has been shown that the transfer frequency of Tn1545 from E. faecalis to L. monocytogenes can be significantly enhanced, both in vitro and in vivo, by subinhibitory concentrations of tetracycline in the mating medium (7). It is therefore tempting to speculate that the therapeutic use of tetracycline has favored the dissemination of this class of transposons and hence of Tcr in and among L. monocytogenes strains.

In L. monocytogenes BM4212, tet(L) is carried by a 5-kb plasmid designated pIP813. In gram-positive bacteria, this determinant is frequently borne by small (<10 kb) and interrelated plasmids that replicate by using a singlestranded DNA intermediate (11). These plasmids generally possess a broad host range of replication which includes gram-positive and gram-negative bacteria. The fact that pIP813 can replicate in L. monocytogenes, E. faecalis, and E. coli suggests that it belongs to this plasmid family. As a consequence of their mode of replication, these replicons are highly recombinogenic and this might favor their intra- and intergeneric dissemination (11). The presence of tet(L) on this type of plasmids among evolutionarily distant grampositive bacteria such as Staphylococcus, Enterococcus, Streptococcus, Bacillus, and Listeria spp. is consistent with this notion. tet(L) is the second most prevalent  $Tc^{r}$  gene in enterococci and streptococci but is rarely detected in staphvlococci (39). It is therefore likely that pIP813 also originated in Enterococcus and Streptococcus species.

The results presented here, combined with a previous report (27), indicate that two types of movable genetic elements (plasmids and transposons) in enterococci and streptococci are responsible for the emergence of drug resistance in L. monocytogenes. L. monocytogenes is a frequent inhabitant of the gastrointestinal tracts of humans and animals (14) where various Enterococcus and Streptococcus species harboring conjugative resistance plasmids or transposons are also common. The demonstration that direct exchange of genetic information from E. faecalis to L. monocytogenes can occur in the digestive tracts of animals (7) is additional support for the notion that the intestinal ecosystem is the most probable site for intergeneric transfer between these two bacterial genera. The treatment of choice for listeriosis is benzylpenicillin or ampicillin combined with gentamicin. E. faecalis strains that harbor conjugative plasmids or transposons encoding β-lactamases and enzymes conferring high-level resistance to gentamicin have been described (25, 31). Acquisition by L. monocytogenes of resistance to these antibiotics can thus be predicted.

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