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Antibiotic Resistance in Food-Borne Bacterial Contaminants in Vietnam▽

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This study was conducted to examine the rate of contamination and the molecular characteristics of enteric bacteria isolated from a selection of food sources in Vietnam. One hundred eighty raw food samples were tested; 60.8% of meat samples and 18.0% of shellfish samples were contaminated with *Salmonella* spp., and more than 90% of all food sources contained *Escherichia coli*. The isolates were screened for antibiotic resistance against 15 antibiotics, and 50.5% of *Salmonella* isolates and 83.8% of *E. coli* isolates were resistant to at least one antibiotic. Isolates were examined for the presence of mobile genetic elements conferring antibiotic resistance. Fifty-seven percent of *E. coli* and 13% of *Salmonella* isolates were found to contain integrons, and some isolates contained two integrons. Sequencing results revealed that the integrons harbored various gene cassettes, including *aadA1*, *aadA2*, and *aadA5* (resistance to streptomycin and spectinomycin), *aacA4* (resistance to aminoglycosides), the dihydrofolate reductase gene cassettes *dhfrXII*, *dfrA1*, and *dhfrA17* (trimethoprim resistance), the beta-lactamase gene bla_{PSE1} (ampicillin resistance), and *catB3* (chloramphenicol resistance). Plasmids were also detected in all 23 antibiotic-resistant *Salmonella* isolates and in 33 *E. coli* isolates. Thirty-five percent of the *Salmonella* isolates and 76% of the *E. coli* isolates contained plasmids of more than 95 kb, and some of the isolates contained two large plasmids. Conjugation experiments showed the successful transfer of all or part of the antibiotic resistance phenotypes among the *Salmonella* and *E. coli* food isolates. Our results show that enteric bacteria in raw food samples from Vietnam contain a pool of mobile genetic elements and that the transfer of antibiotic resistance can readily occur between similar bacteria.

Food contamination with antibiotic-resistant bacteria can be a major threat to public health, as the antibiotic resistance determinants can be transferred to other bacteria of human clinical significance. The prevalence of antimicrobial resistance among food-borne pathogens has increased during recent decades (9, 15, 18, 56), possibly as the result of selection pressure created by the use of antimicrobials in food-producing animals (1, 4, 11, 55, 59). The coexistence of resistance genes with mobile elements such as plasmids, transposons, and integrons facilitates the rapid spread of antibiotic resistance genes among bacteria (53). Molecular analysis of antibiotic resistance genes and antibiotic-resistant mobile elements has shown that identical elements were found in bacteria that colonize both animals and humans, suggesting a role for raw foods in the dissemination of resistant bacteria and resistance genes to humans via the food chain (33, 44, 55).

Information on the phenotypes and genotypes of antimicrobial resistance in food-borne microorganisms is largely restricted to first-world countries, and there is a paucity of information on what is happening in developing countries. Where they are reported, rates of resistance to antibiotics of bacteria originating from meat were high in developing countries (2, 3, 16, 37, 54), possibly as the result of the inappropriate or uncontrolled use of antibiotics in farming practices. Therefore, the study of antibiotic resistance in developing countries is important as the information could enhance prudent use of antibiotics in food production. In Vietnam, antibiotic resistance has been reported to occur in human bacterial isolates, including *Salmonella enterica* serovar Typhi and other diarrhea-causing pathogens (5, 12, 22, 26, 40). However, as far as we are aware, there has been very little published about the occurrence of antibiotic-resistant bacteria in raw food samples in Vietnam and even less about the molecular characteristics of these antibiotic-resistant bacteria. This study was conducted to address some of these issues and to provide a current baseline of information on molecular characteristics of antibiotic resistance of *Salmonella* and *Escherichia coli* isolates from foods commonly sold in the marketplace in Vietnam. The isolates were investigated for the presence of class 1 integrons and their associated gene cassettes and for the presence of plasmids. The transferability of antibiotic resistance was examined by conjugation.

MATERIALS AND METHODS

Isolation and identification of *E. coli* and *Salmonella* spp. One hundred eighty samples of meat, consisting of beef ($n = 50$ samples), chicken/poultry ($n = 30$ samples), pork ($n = 50$ samples), and shellfish ($n = 50$ samples), were purchased from various markets and supermarkets around Ho Chi Minh City between February and June 2004 for the isolation and identification of *Salmonella* spp. and *E. coli*. Forty-three samples from chicken feces were also collected for *E. coli* isolation from chickens less than 1 month old. The procedures for the isolation of *Salmonella* spp. and *E. coli* were based on the Nordic Committee on Food Analysis methods (41, 42). *Salmonella* isolates were further grouped with commercial monovalent sera (Remel, Inc.), used according to the manufacturer's instructions. The representative salmonella isolates were further serotyped by the Microbiological Diagnostic Unit, Melbourne University, Australia.

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Antibiotic susceptibility tests. Antibiotic resistance of *E. coli* and *Salmonella* isolates was determined by the disk diffusion method using the standard procedure of the Clinical and Laboratory Standards Institute (CLSI, formerly NCCLS) (39). The isolates were classified as susceptible, intermediate, or resistant according to interpretation of the zone diameter standards recommended by CLSI (17). The concentration of the discs (Oxoid, Australia) and the abbreviations of antimicrobial agents used throughout this report are ampicillin (AMP), 10 μg; amoxicillin (AMX), 10 μg; amoxicillin-clavulanic acid (AMC), 30 μg; cephalothin (CEF), 30 μg; chloramphenicol (CHL), 30 μg; ciprofloxacin (CIP), 5 μg; enrofloxacin (ENR), 5 μg; tetracycline (TET), 30 μg; gentamicin (GEN), 10 μg; kanamycin (KAN), 30 μg; nalidixic acid (NAL), 30 μg; norfloxacin (NOR), 10 μg; sulfafurazole (SUL), 300 μg; streptomycin (STR), 10 μg; and trimethoprim (TMP), 5 μg. The reference strains *Escherichia coli* ATCC 25922 and *Staphylococcus aureus* ATCC 25923 were used to verify the quality and accuracy of the testing procedures.

Detection of class 1 integrons. Twenty-three antibiotic-resistant *Salmonella* isolates and 35 *E. coli* isolates, which showed the highest degree of resistance among the collection, were examined for the presence of class 1 integrons by PCR using primers and conditions as described previously (36). PCRs were carried out in a total volume 50 μl containing 2 μl of boiled bacterial suspension, each deoxyribonucleotide at a concentration of 0.25 mM, 2 mM $MgCl_2$, 1 U of AmpliTaq Gold DNA polymerase (Roche, Germany), and 0.4 μM of each primer. Thermal cycler reaction conditions included an initial denaturation at 95°C for 5 min, followed by 35 cycles, each of which consisted of denaturation at 95°C for 30 s, annealing time at 56°C for 30 s, and a final 7-min extension at 72°C. *Salmonella enterica* serovar Typhimurium strain DT104, which contained 1.0-kb and 1.2-kb integrons, was used as a positive control. PCR products were digested with at least three separate restriction endonucleases. Isolates with the same PCR amplicon sizes and identical restriction patterns were randomly chosen for complete sequence analyses using an ABI Prism BigDye Terminator cycle sequencing Ready Reaction kit (Perkin-Elmer Corp.) according to the manufacturer's protocol and were sequenced at Monash University, Victoria, Australia. The sequences obtained were analyzed using BLAST (http://www.ncbi.nih.gov) and compared with those registered in GenBank.

Plasmid extraction. The plasmid extraction method used was based on the Kado and Liu method, with some modifications (28). Strains were grown in 10 ml of Luria-Bertani (LB) broth containing appropriate antibiotic at 37°C with shaking to exponential stage. Cells from 1.5 ml of culture were harvested, and the pellet was resuspended in 200 μl of Tris-EDTA buffer. The cells were lysed by the addition of 400 μl of lysis solution (containing 3% [wt/vol] sodium dodecyl sulfate and 50 mM Tris [pH 12.6]). The mixture was incubated at 60°C for 1 h. Proteins and chromosomal DNA were then precipitated by the addition of 900 μl of 1:1 (vol/vol) phenol-chloroform, and the precipitate was removed by centrifugation. The aqueous DNA solution was then freed of phenol by extraction with 1 volume of chloroform. The upper aqueous layer containing the plasmid DNA was collected and was either loaded on a gel for electrophoresis or stored at −20°C. The gel was prepared at 0.7% in 1× Tris-acetate-EDTA buffer, and electrophoresis was carried out at 70 V for 2.5 h. *Salmonella* serovar Typhimurium strain 82/6915, which contained a single 95-kb plasmid, was used as a control. Sizes of the plasmids were compared using a BAC-Tracker supercoiled ladder, with sizes ranging from 8 to 165 kb (Epicenter). Isolates used for integron detection (except for isolates E/C/15a and E/SF/29) were evaluated for the presence of plasmids.

Conjugation study. Spread-plate mating and liquid mating methods (30) were used in the conjugation experiments with different donor-recipient combinations. Selected strains which contained plasmids of more than 95 kb were used, including S/C/5 (*Salmonella* serovar Havana, chicken isolate), S/C/9b (*Salmonella* serovar Havana, chicken isolate), S/P/24 (*Salmonella* serovar Anatum, pork isolate), E/C/4a (*E. coli*, chicken isolate), and E/C/5a (*E. coli*, chicken isolate). Recipient laboratory strains and strains isolated for this study included E/P/8a (*E. coli*, pork isolate), E/F/13 (*E. coli*, chicken feces isolate), E/F/16 (*E. coli*, chicken feces isolate), *E. coli* HB101 (*E. coli*, laboratory strain), *E. coli* JM109 (*E. coli*, laboratory strain), S/P/9 (*Salmonella* serovar Typhimurium, pork isolate), and S/P/13 (*Salmonella* serovar Anatum, pork isolate). For the spread-plate mating, the donor and recipient strains were grown separately overnight with appropriate antibiotics, and then 100 μl of donor and 100 μl of recipient strains at different concentrations were spread plated onto LB agar plates containing both of the selected antibiotics. In liquid mating, 0.5 ml and 1.0 ml of overnight-incubated donor and recipient broth cultures, respectively, were mixed in 10 ml of LB broth. The mixtures were then incubated overnight without shaking. Then, 0.2-ml volumes of each mixture at different concentration were spread onto LB-agar plates containing both of the selected antibiotics. Colonies from the selector plates were picked off and identified again after plates were incubated at 37°C for 24 h and their antibiotic resistance phenotypes were determined.

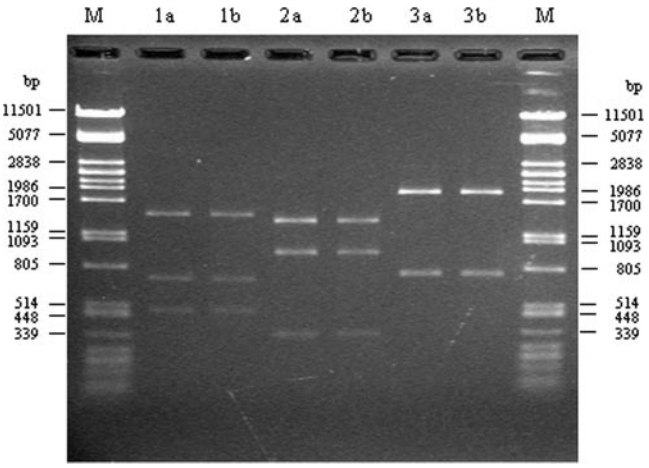

FIG. 1. Restriction fragment length polymorphism analysis of 2.65-kb class 1 integron PCR product of isolates E/C/16a and E/C/21a. Lanes M, lambda DNA PstI marker; 1a, 2a, and 3a, digestion of integron PCR product of isolates E/C/16a with HincII, SspI, and SacII enzymes, respectively; 1b, 2b, and 3b, digestion of integron PCR product of isolate E/C/21a with HincII, SspI, and SacII enzymes, respectively.

RESULTS

Presence of class 1 integrons and resistance gene cassettes in *Salmonella* spp. and *E. coli* isolates. When 180 food samples were examined for *Salmonella* spp., 60.8% of the meat and 18.0% of the shellfish samples were positive, yielding 91 *Salmonella* isolates. *E. coli* was present in more than 90% of all food sources. Isolates were screened for antibiotic resistance against 15 antibiotics, and 50.5% of the *Salmonella* isolates were found to be resistant to at least one antibiotic, and 78 to 89% of these isolates from pork and poultry displayed this characteristic. On the other hand, 83.8% of *E. coli* isolates were resistant to at least one antibiotic, and the resistance rates for this group were 100% for pork, chicken, and chicken feces isolates, and the rates for beef isolates and shellfish isolates were 65% and 55%, respectively. In addition, multiresistance (resistance to at least three different classes of antibiotics) was detected in 20.9% of *Salmonella* isolates and in 61.6% of *E. coli* isolates. When 23 *Salmonella* isolates and 35 *E. coli* isolates were screened for class 1 integrons by PCR, 3/23 (13%) of the *Salmonella* isolates and 20/35 (57.1%) of the *E. coli* isolates were positive for the PCR amplification product of class 1 integrons, with six patterns (2,650, 2,000, 1,700, 1,500, 1,250, and 1,200 bp) detected. Restriction fragment length polymorphism analysis of the PCR products showed that isolates having the same amplicon sizes had the same restriction patterns, suggesting that the gene cassettes in these strains were likely to be identical (Fig. 1). Sequence analysis of the integron PCR products showed the presence of classic gene cassettes in the integrons, including *aadA1*, *aadA2*, and *aadA5* (which confer resistance to streptomycin and spectinomycin), *aacA4* (which confers resistance to aminoglycosides), the dihydrofolate reductase gene cassettes *dhfrXII*, *dfrA1* and *dhfrA17*

TABLE 1. Features of the *E. coli* and *Salmonella* isolates carrying class 1 integrons

Integron size(s) (kb)	Isolate (species)	Source	Genes identified within integrons	Resistance phenotype pattern	
				Full	Intermediate
2.0	S/SF/8a (*Salmonella* serovar Typhimurium)	Shellfish	*dhfrXII-orfF-aadA2*	TET, TMP, KAN	STR
2.0	S/P/9 (*Salmonella* serovar Typhimurium)	Pork	*dhfrXII-orf-aadA2*	AMP, TET, GEN, SUL, TMP, STR, KAN, AMX	
2.0	E/C/24a (*E. coli*)	Chicken	N/A[a]	AMP, TET, GEN, SUL, TMP, AMX, CHL, STR	CEF, AMC, NAL, ENR
2.0	E/SF/29 (*E. coli*)	Shellfish	N/A	AMP, TET, GEN, SUL, CEF, TMP, STR, NAL, AMX, CEF, AMC	CHL, ENR
2.0	E/F/2 (*E. coli*)	Chicken feces	N/A	AMP, TET, GEN, CHL, SUL, TMP, AMX	STR, KAN, NAL, ENR, AMC
2.0	E/F/8 (*E. coli*)	Chicken feces	N/A	AMP, TET, GEN, CHL, SUL, TMP, KAN, NAL, ENR, AMX	CEF, AMC, STR
2.0	E/F/25 (*E. coli*)	Chicken feces	N/A	TET, CHL, SUL, TMP, NOR, NAL, ENR, CIP	CEF, STR
2.0	E/P/18a (*E. coli*)	Pork	*dhfrXII-orf-aadA2*	AMP, TET, GEN, SUL, NAL, ENR, AMX, STR	CEF, NOR
2.0	E/P/27a (*E. coli*)	Pork	N/A	CIP, TET, GEN, SUL, TMP, NOR, NAL, ENR, STR	CEF, AMC, AMP, AMX
2.0	E/P/43a (*E. coli*)	Pork	N/A	AMP, TET, GEN, SUL, TMP, AMX, STR	CHL
1.5	E/C/29a (*E. coli*)	Chicken	*dfrA1-aadA1*	AMP, TET, SUL, TMP, AMX	CEF, AMC, STR
1.5	E/P/25a (*E. coli*)	Pork	N/A	AMP, CIP, TET, CHL, SUL, TMP, NOR, STR, NAL, ENR, AMX	CEF, AMC
1.7	E/SF/1a (*E. coli*)	Shellfish	*dhfr17-aadA5*	AMP, TET, CHL, SUL, TMP, STR, NAL, AMX	CEF, AMC, ENR
1.7	E/C/15a (*E. coli*)	Chicken	N/A	AMP, TET, SUL, TMP, STR, NAL, ENR, AMX	CEF, AMC
1.7	E/C/17a (*E. coli*)	Chicken	*dhfr17-aadA5*	AMP, TET, GEN, CHL, SUL, TMP, NOR, KAN, NAL, ENR, AMX, STR	CEF, CIP, AMC
1.7	E/F/9 (*E. coli*)	Chicken feces	N/A	AMP, TET, GEN, CHL, SUL, TMP, NAL, AMX, CEF	AMC, STR, ENR
1.7	E/F/13 (*E. coli*)	Chicken feces	N/A	TET, GEN, CHL, SUL, TMP, KAN, NAL	CEF, STR, ENR
1.7	E/F/16 (*E. coli*)	Chicken feces	N/A	TET, GEN, CHL, SUL, TMP, KAN, NAL	CEF, STR, ENR
1.7	E/F/20 (*E. coli*)	Chicken feces	N/A	TET, GEN, CHL, SUL, TMP, KAN, NAL	STR, ENR
2.65	E/C/16a (*E. coli*)	Chicken	*aacA4-catB3-dfrA1*	AMP, CIP, TET, GEN, CHL, SUL, TMP, NOR, NAL, ENR, AMX, CEF, AMC	KAN
2.65	E/C/21a (*E. coli*)	Chicken	N/A	AMP, CIP, TET, GEN, CHL, SUL, TMP, NOR, STR, NAL, ENR, AMX, CEF	AMC, KAN
1.2, 1.25	S/C/21a (*S.* Albany)	Chicken	bla_{PSE1}, *dfrA1*	AMP, TET, CHL, SUL, TMP, NAL, AMX	
2.0, 1.5	E/F/3 (*E. coli*)	Chicken feces	*dhfrXII-orf-aadA2, dfrA1-aadA1*	AMP, TET, GEN, CHL, SUL, TMP, STR, NAL, ENR, AMX	CEF, NOR

[a] N/A, not applicable.

(which confer resistance to trimethoprim), the beta-lactamase gene bla_{PSE1} (which confers resistance to ampicillin), and *catB3* (which confers resistance to chloramphenicol). When isolates contained a gene cassette, the corresponding antibiotic resistance phenotypes were detected in most of the cases, except for the E/P/18a isolate, which contained the *dhfrXII* gene cassette with sensitivity to trimethoprim. Resistance to streptomycin in the presence of the *aadA* gene varied from full resistance to intermediate susceptibility (Table 1).

Plasmid content of *Salmonella* and *E. coli* isolates. The Kado and Liu method (28) was used to examine *Salmonella* and *E. coli* isolates for plasmids. The plasmid extraction of 23 antibiotic-resistant *Salmonella* isolates and 33 *E. coli* isolates showed that all of the isolates tested contained plasmids, and sizes ranged from less than 8 kb to more than 165 kb. Thirty-five percent of the *Salmonella* isolates and 76% of the *E. coli* isolates contained plasmids of more than 95 kb, and some of the isolates contained two large plasmids.

TABLE 2. Transfer of resistance phenotypes of selected conjugation tests

Donors (species)	Resistance phenotype of donor	Resistance phenotype (plasmid size [kb])	
		Transferred to *E. coli* JM109 E/P/8a, E/F/13, or E/F/16	Transferred to *E. coli* HB101
S/C/5 (*Salmonella* serovar Havana)	AMP, AMX, GEN, CHL, SUL	AMP, AMX (115)	N/A
S/C/5 (*Salmonella* serovar Havana)	AMP, AMX, GEN, CHL, SUL	AMP, AMX, GEN, CHL, SUL (140)	N/A
E/C/4a (*E. coli*)	AMP, AMX, CIP, TET, GEN, CHL, SUL, NOR, NAL, ENR	N/A[c]	AMP, AMX, GEN, CHL, SUL (120)[a]
E/C/5a (*E. coli*)	AMP, AMX, CIP, TET, SUL, TMP, NOR, STR, NAL, ENR, AMC, CEF	N/A	AMP, AMX, SUL (120)[b]

[a] Transfer of the tetracycline phenotype could not be measured as the recipient was also resistant to this antibiotic before the conjugation experiment.
[b] Transfer of the tetracycline and streptomycin resistance phenotypes could not be measured as the recipient was also resistant to these antibiotics before the conjugation experiment.
[c] N/A, not applicable.

Transfer of antibiotic resistance genes in *E. coli* and *Salmonella* isolates by conjugation. The antibiotic susceptibility test of transconjugants showed that the donors could transfer all or part of their resistance phenotypes to the recipients. The plasmid profiles of the donor, the recipient, and the transconjugants were studied for selective donor-recipient combinations. When isolate S/C/5a (*Salmonella* serovar Havana), which contained plasmids of 115 kb and 140 kb, was used as a donor, it was observed that transconjugants acquired either an AMP/AMX resistance phenotype or an AMP/AMX/SUL/GEN/CHL resistance phenotype, depending on whether the recipients obtained the 115-kb plasmid or the 140-kb plasmid from the donor. Similarly, when the E/C/4a and E/C/5a isolates, which both contained the 120-kb plasmid, were used as donors, the transconjugants were found to acquire the 120-kb plasmid and the corresponding antibiotic resistance phenotype (the AMP/AMX/SUL/GEN/CHL resistance phenotype or the AMP/AMX/SUL resistance phenotype, respectively) (Table 2 and Fig. 2). Therefore, these large plasmids were conjugative and contained many antibiotic resistance genes. It was also noticed in this study that in conjugation, the recipients could acquire plasmids from donors regardless of whether the recipients harbored their own plasmids or not; this observation shows furthermore that conjugation mechanisms could easily occur among the bacterial population.

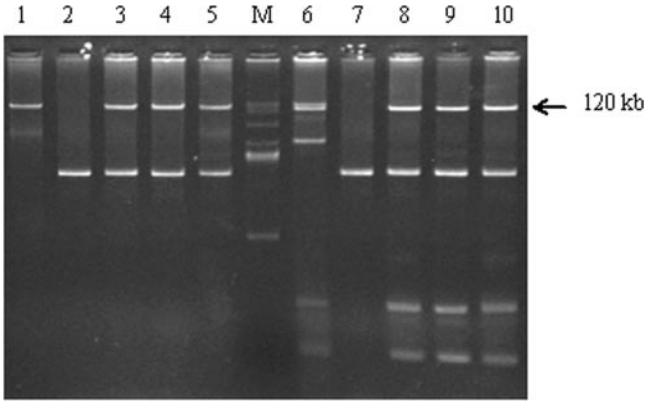

FIG. 2. Transfer of plasmid DNA in conjugation experiments. Lanes M, BAC-Tracker supercoiled DNA ladder; 1, strain E/C/4a (donor); 2, *E. coli* HB101 (recipient); 3 to 5, transconjugation of E/C/4a with *E. coli* HB101; 6, strain E/C/5a (donor); 7, *E. coli* HB101 (recipient); 8 to 10, transconjugation of E/C/5a with *E. coli* HB101.

DISCUSSION

The results demonstrated that raw food samples were heavily contaminated with enteric bacteria. The rate of *Salmonella* contamination in retail meat samples above 60% is significantly higher than that reported for other countries (16, 19, 21, 25, 27, 45, 58, 61). The antibiotic resistance susceptibility results also indicated alarming multiresistance frequencies for *Salmonella* and *E. coli* isolates from food, where multiresistance rates of 20.9% for *Salmonella* isolates and 61.6% for *E. coli* isolates were detected and most probably reflect the unregulated use of antibiotics in food-producing animals in the country (60). It was found that 78 to 89% of the *Salmonella* spp. isolated from pork and poultry were resistant to one or more antibiotics. This level was higher than that obtained by Arvanitidou et al. (7) in Greece (58.1%) or by Seyfarth et al. (50) in Denmark (9.2 to 11.1%) but lower than that reported by Carraminana et al. (14) in Spain (100%). Class 1 integrons, the mobile elements that are known for the efficient spread of antibiotic resistance genes due to mobilization capabilities of gene cassettes (24, 46, 57), were detected in *E. coli* and *Salmonella* isolates. The finding that only 13% of *Salmonella* isolates contained class 1 integrons suggests that most of the resistant *Salmonella* isolates contained resistance elements other than integrons. In contrast, integron-mediated antibiotic resistance was common among *E. coli* isolates, where more than 50% of the isolates were shown to contain integrons, with some containing two integrons. Various gene cassettes detected in *Salmonella* and *E. coli* isolates in this study, including *aadA1*, *aadA2*, *aadA5*, *aacA4*, *dhfrXII*, *dfrA1*, *dhfrA17*, bla_{PSE1}, and *catB3*, have been detected in clinical and nonclinical isolates in reports from many countries (6, 20, 29, 31, 32, 34, 35, 43, 49, 51, 52, 62, 64). The gene cassette array *aacA4-catB3-dfrA1*, which has been reported recently in Japan (31) and China (34), was also detected in *E. coli* isolates in this study, indicating that this resistance cassette is widespread in Asia.

The transfer of conjugative plasmids is considered to be the most common mechanism for genetic exchange between bacteria, as plasmid conjugation can occur at high frequency and is capable of the cotransfer of several resistance genes, and

transfer can occur both within bacterial species and between different species (13, 47). This study demonstrated that plasmids were widely distributed in *E. coli* and *Salmonella* isolates collected from food in Vietnam and that these isolates contained large conjugative plasmids which contained many antibiotic resistance determinants. The presence of large conjugative resistance plasmids has been detected in *Salmonella* and *E. coli* isolates from food and food-producing animals in many countries (8, 10, 23, 38, 63). High-molecular-weight plasmids are often attributed to virulence and antibiotic resistance (48). Therefore, the presence of the large plasmids in *E. coli* and *Salmonella* isolates detected in this study could have contributed to the spread of resistance genes. Using different combinations of donor and recipient strains, it has also been demonstrated that resistance markers can be readily transferred among the same and different species (e.g., *Salmonella* spp. and *E. coli*). These findings demonstrate the importance of plasmids in the dissemination of antibiotic resistance genes in enteric bacteria in Vietnamese food samples.

In summary, results confirm the role of raw food as a reservoir of antibiotic resistance bacteria that contained a pool of mobile genetic elements, which are ready to disseminate antibiotic resistance genes to other human pathogens and so constitute a problem for human health. The application of hygiene practices along the food chain and the prudent use of antibiotics in animal husbandry are therefore essential. To control further emergence of antibiotic resistance, studies with comprehensive collections of samples are urgently needed to increase our understanding of molecular genetic mechanisms involved in the dissemination of antibiotic resistance genes from food-borne pathogens to humans.

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