Characterization of Methicillin-Resistant \textit{Staphylococcus aureus} Isolates from Food and Food Products of Poultry Origin in Germany\footnote{Published ahead of print on 1 July 2011.}

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During a survey of fresh chicken and turkey meat as well as chicken and turkey meat products for the presence of methicillin-resistant \textit{Staphylococcus aureus} (MRSA) isolates in Germany, 32 (37.2\%) of 86 samples were MRSA positive. Twenty-eight of these MRSA isolates belonged to clonal complex 398 (CC398), which is widespread among food-producing animals. These CC398 isolates carried SCCmeC elements of type IV or V and exhibited \textit{spa} type 1011, 1034, 8599, 12346 or 16574 and either the known \textit{dru} types dt2b, dt6j, dt10a, dt10q, dt11a, dt11r, and dt11ab or the novel \textit{dru} types dt6m, dt10as, and dt10at. In addition, two MRSA sequence type 9 (ST9) isolates with a type IV SCCmeC cassette, \textit{spa} type 14436, and \textit{dru} type dt10a as well as single MRSA ST5 and ST1791 isolates with a type III SCCmeC cassette, \textit{spa} type 1002, and \textit{dru} type dt9v were identified. All but two isolates were classified as multiresistant. A wide variety of resistance phenotypes and genotypes were detected. All isolates were negative for the major virulence factors, such as Panton-Valentine leukocidin, toxic shock syndrome toxin 1, or exfoliative toxins. In contrast to the MRSA CC398 isolates, the four ST9, ST5, or ST1791 isolates harbored the \textit{ege} gene cluster for enterotoxin G, I, M, N, O, and U genes. Although the relevance of contamination of fresh poultry meat or poultry products with MRSA is currently unclear, the presence of multiresistant and, in part, enterotoxigenic MRSA emphasizes the need for further studies to elucidate possible health hazards for consumers.

Methicillin-resistant \textit{Staphylococcus aureus} (MRSA) isolates in livestock have gained particular attention during recent years (38). The identification of livestock-associated MRSA in food-producing animals has raised questions regarding the presence of MRSA in food of animal origin. Several studies were conducted in different parts of the world (i) to screen food of animal origin intended for human consumption for the presence of MRSA and also (ii) to identify the MRSA types present. A study from The Netherlands identified MRSA isolates in 11.9\% of 2,217 samples tested (3). Differences in the prevalence of MRSA were detected with respect to the animal origin of the meat samples. MRSA was most prevalent in turkey (35.3\%), followed by chicken (16.0\%), veal (15.2\%), and pork (10.7\%), and beef (10.6\%). About 85\% of the MRSA isolates were assigned to multilocus sequence type 398 (ST398) (3). Another study from The Netherlands focused on the detection of MRSA in pork and beef raw meat samples purchased from retail stores (34). Among 79 samples, only two MRSA isolates were found, one (1.3\%) of which was identified as an ST398 isolate. MRSA was not identified in a study conducted in Switzerland examining 100 pooled neck skin swabs from chicken carcasses and 460 food samples of animal origin. In Spain, Lozano et al. (24) identified only five MRSA isolates in 318 raw food samples. Of these, ST398 isolates were found in single samples of veal and pork, ST125 isolates in single chicken and rabbit samples, and an ST217 isolate in a sample from a wild boar. During a prevalence study of MRSA contamination of retail pork in Canada, Weese et al. detected MRSA in 31 (7.7\%) of 402 samples. Ten of the 31 isolates were classified as ST398 by their nontypeability in Smal pulsed-field gel electrophoresis and their \textit{spa} type t034 (37).

In addition to these livestock-associated MRSA isolates, MRSA isolates that corresponded to types commonly found in humans were also detected in food of animal origin. This observation suggested that there is potential for contamination of food either at the slaughterhouse or during food processing, with humans being a likely source of contamination. Pu et al. (30) identified only two MRSA isolates in 120 retail meat samples sourced from 30 grocery stores in Baton Rouge, LA. One of them, however, was a Panton-Valentine leukocidin (PVL)-positive USA300 isolate known to be associated with community-associated MRSA infections, while the other was a PVL-negative USA100 isolate commonly found in health care-associated MRSA infections in the United States (30). In a Canadian study, Weese et al. (36) found 32 MRSA isolates in 678 food samples (pork, ground beef, and chicken) purchased at retail outlets. All 32 isolates were classified as Canadian epidemic MRSA-2 (= ST5-MRSA-II [26]), a human MRSA strain recognized as the most common cause of health care-associated infections in Canada but which has also been identified in pigs and pig farm personnel in that country (36). Two MRSA isolates, which displayed characteristics of community-associated MRSA isolates, were also detected among 444 retail raw chicken meat samples in Japan (19). MRSA ST72 from beef and pork as well as MRSA ST692 was...
identified at low frequencies (0.3 to 1.0%) in Korea (23). In addition, MRSA ST5 has also been identified from retail chicken in Korea (22).

These data show that different types of MRSA are present in food of animal origin in different countries. For Germany, very limited data about MRSA in food of animal origin are currently available. This applies in particular to MRSA in poultry and food of poultry origin (5). To gain insight into the MRSA types present in raw poultry meat and poultry meat products available from retail stores in the federal state Rhineland-Palatinate in Germany, a small-scale study focusing on chicken and turkey meat as well as the corresponding products was performed. The MRSA isolates obtained during this study were subjected to molecular analysis with particular reference to their genotypic characteristics, their virulence, and their antimicrobial resistance patterns.

**MATERIALS AND METHODS**

**Bacterial isolates.** Eighty-six samples from food and food products of poultry origin were obtained from individual retail stores in the federal state Rhineland-Palatinate in the western part of Germany between May 2009 and December 2009. These included 22 samples from fresh turkey meat (15 from Germany, three from Italy, two from France, one from Austria, and one of unknown origin), 21 samples from turkey meat products (18 from Germany and three from Austria), 24 samples from fresh chicken meat (21 from Germany, two from Austria, and one from Hungary), and 19 samples from chicken meat products (17 from Germany, 1 from The Netherlands, and 1 of unknown origin). From each sample, 25 g of meat or meat product was minced, added to 225 ml Mueller-Hinton broth (supplemented with 6.5% [wt/vol] sodium chloride), homogenized for 1 min, and incubated at 35 to 37°C for 16 to 20 h. For selective enrichment of MRSA, 1 ml of this mixture was added to 9 ml of tryptone soya broth (Oxoid, Wesel, Germany) supplemented with 3.5 µg/ml cetaxin and 75 µg/ml aztreo- nam. After another incubation at 35 to 37°C for 16 to 20 h, an aliquot of 10 µl was streaked on chromogenic MRSA selective agar (Brilliance MRSA agar; Becton Dickinson, Heidelberg, Germany) supplemented with 3.5 µg/ml cetaxin and 75 µg/ml aztreomycin. For this, the primers tcpC-fw (5′-TCGTTCGAGGAAATCCCTTA-3′) and radC-rv (5′-TCAAAACC ACACTCTTCAACC-3′) were used and an amplicon of 972 bp was expected. The PCR program included an initial denaturation step at 94°C for 2 min, followed by 30 cycles of 94°C for 1 min, 52°C for 1 min, and 72°C for 1 min and a final extension at 72°C for 5 min. One of the amplicons was sequenced for confirmation. For the detection of van(B), the primers vgaB-fw (5′-GAATAA GCCGCAGAAAGTGA-3′) and vgaB-rv (5′-TAGCTTGCGAAAGACCCAAC-3′) were used to generate a 601-bp amplicon. The PCR program was the same as described above, except that the annealing temperature was set at 54°C.

**Antimicrobial susceptibility testing.** All MRSA isolates were tested for their antimicrobial susceptibility by broth microdilution according to the recommendations given in document M31-A3 of the Clinical and Laboratory Standards Institute (1). For this, custom-made microtiter plate panels were used (MCS Diagnostics, Swalmen, The Netherlands), which included 10 to 12 concentrations of 30 antimicrobial agents in 2-fold dilution series. The tested compounds included penicillins (penicillin G, ampicillin, amoxicillin-clavulanic acid [2:1], and oxacillin), cephalexin, cefotaxime, ceftazidime, cefquinome, and cefetiazuromycin), tetracyclines (tetracycline and doxycycline), macrolides (erythromycin, spiramycin, tilmicosin, tulathromycin, and tylosin), lincomycines (clindamycin and pirlimycin), folate pathway inhibitors (trimethoprim and sulfamethoxazole-trimethoprim [19:1]), (fluoro)quinolones (nalidixic acid and enrofloxacin), phenicol (chloramphenicol and florfenicol), aminopenicillins (ampicillin and spectinomycin), an aminoglycoside (gentamicin), a streptogramin (quinupristin-dalfopristin), a glycopeptide (vancomycin), and a pleuro- mulltin (tiamulin). For selected isolates which proved to be positive for the aminoglycoside resistance genes vanA-vanB and/or aadD in the microarray analyses, kanamycin MICs were determined by broth microdilution (1). The reference strain S. aureus ATCC 29213 served as quality control strain in the MIC determinations.

**DNA microarray analysis.** A previously described diagnostic DNA microarray (StaphyType; Alere Technologies, Jena, Germany) was used to characterize the MRSA isolates (25, 26). This microarray-based assay is able to detect a total of 330 different sequences (~180 genes and alleles thereof), including S. aureus-specific genes, accessory gene regulator (agr) alleles, genes coding for virulence factors (toxins, enterotoxins, putative toxins, hemolysins, protocase, and biofilm formation molecules) and microbial surface components recognizing adhesive matrix molecules (MSCRAMMs), capsule type-specific genes, and numerous antimicrobial resistance genes. Performance of the microarray analyses followed the recommendations of the manufacturer. Analysis of the recorded hybridization patterns was conducted using a designated reader and software (ArrayMate and IconoClust, both by Alere Technologies). Microarray analysis was supplemented by specific PCRs for recently identified antimicrobial resistance genes which have not yet been included in the microarray, such as dfrK (15), vgrG (16), erm(T) (17), and aapNA (7). Moreover, specific PCRs to confirm the linkage of the genes tet(L)-dfrK and erm(A)-spp were applied (8).

For isolates that carried tet(L) and dfrK but were negative for the PCR confirming linkage of the two genes, as well as for isolates that carried only dfrK without tet(L), a PCR assay was established to confirm the location of dfrK as part of transposon Tn559 (18) in the chromosomal DNA. For this, the primers tcpC-fw (5′-TCGTTCGAGGAAATCCCTTA-3′) and radC-rv (5′-TCAAAACC ACACTCTTCAACC-3′) were used and an amplicon of 972 bp was expected. The PCR program included an initial denaturation step at 94°C for 2 min, followed by 30 cycles of 94°C for 1 min, 52°C for 1 min, and 72°C for 1 min and a final extension at 72°C for 5 min. One of the amplicons was sequenced for confirmation. For the detection of van(B), the primers vgaB-fw (5′-GAATAA GCCGCAGAAAGTGA-3′) and vgaB-rv (5′-TAGCTTGCGAAAGACCCAAC-3′) were used to generate a 601-bp amplicon. The PCR program was the same as described above, except that the annealing temperature was set at 54°C.

**RESULTS**

**MRSA detection and characterization.** In total, 32 (37.2%) of the 86 samples were MRSA positive. These included 6 (25.0%) of the 24 samples from fresh chicken meat, 4 (21.1%) of the 19 samples from chicken meat products, 11 (50.0%) of the 22 samples from fresh turkey meat, and 11 (52.4%) of the 21 samples from turkey meat products. Among the MRSA-positive samples detected, only four, two from fresh turkey meat and two from turkey meat products, originated from the area where the samples had been taken (Table 1).

Twenty-eight of the 32 MRSA isolates reacted positively in both of the CC398-specific PCR assays described by van Wamel et al. (35). Isolates which were negative in these PCR were subjected to multilocus sequence typing (MLST) according to the protocol of Enright et al. (6). The sequences obtained for the seven housekeeping genes were compared to those deposited in the MLST database (http://saureus.mlst.net/). All MRSA isolates were subjected to spa sequence typing in accordance with the Ridom StaphyType standard protocol (http://spasever.ridom.de). In addition, two PCR-directed typing methods applicable exclusively to mecinillin-resistant staphylococci, dru typing and SCCmec typing, were applied. The dru amplicons were sequenced and compared with the dru sequences and dru types stored in the dru typing database (http://dru-typing.org) (8, 9). For SCCmec typing, the multiplex PCRs as described by Kondo et al. (21) were used. The discriminatory value for each typing method was calculated as an index of discrimination (D) as described by Hunter and Gaston (12).

**MRSA detection and characterization.** In total, 32 (37.2%) of the 86 samples were MRSA positive. These included 6 (25.0%) of the 24 samples from fresh chicken meat, 4 (21.1%) of the 19 samples from chicken meat products, 11 (50.0%) of the 22 samples from fresh turkey meat, and 11 (52.4%) of the 21 samples from turkey meat products. Among the MRSA-positive samples detected, only four, two from fresh turkey meat and two from turkey meat products, originated from the area where the samples had been taken (Table 1).

Twenty-eight of the 32 MRSA isolates reacted positively in both of the CC398-specific PCR assays described by van Wamel et al. (35) and were considered to belong to clonal complex 398 (CC398). Of the remaining four MRSA isolates, two exhibited ST9 (allelic profile 3-3-1-1-1-10), which belongs to CC9 (26). Another one was assigned to ST5 (allelic profile 1-4-1-4-12-1-10), whereas the last one was a single-locus variant of ST5, designated ST1791 (allelic profile 1-4-184-4-12-1-10). It should be noted that the glpF alleles 1 and 184 differ by a single nucleotide exchange (C at position 217 in allele versus T in allele 184). Both ST5 and ST1791 belong to CC5 (26). The spa typing identified seven different spa types among the 32 isolates, each of them consisting of 5 to 10 repeats (Table 1; Fig. 1). Both ST9 isolates showed spa type t1430, while the ST5 and ST1791 isolates had spa type t002. The remaining five spa types were found in the CC398 isolates, with
t011 (n = 16) and t034 (n = 9) seen most frequently. SCCmec typing revealed the presence of SCCmec types III (n = 2), IV (n = 11), and V (n = 19). The dru typing identified 11 different dru types composed of 2 to 11 repeats (Table 1; Fig. 1). Three novel dru types, dt6m, dt10as, and dt10at, were identified for the first time during this study. Calculation of the discriminatory indices showed that dru typing had the highest discriminatory power (D = 0.863), followed by spa typing (D = 0.681), SCCmec typing (D = 0.542), and MLST (D = 0.236).

**Virulence properties.** Microarray analysis revealed a rather uniform virulence gene pattern among the MRSA isolates included in this study. All isolates were positive for the genes hla and hld, coding for α and β hemolysins, for genes indicative of capsule type 5, and for the icaACD genes, whose products are involved in biofilm formation. Moreover, all MRSA isolates carried a similar set of genes for microbial surface components recognizing adhesive matrix molecules (MSCRAMMs), including clfA and clfB (encoding clumping factors A and B), fnbA and fnbB (encoding fibronectin binding proteins A and B), and ebpS (encoding elastin binding protein) among others. All isolates were negative for the PVL genes lukF-PV and lukS-PV, the toxic shock syndrome toxin 1 tst alleles, the exfoliative toxin genes eta, etb, and etd, the arginine catabolic mobile element (ACME), and the genes edin-A, edin-B, and edin-C, encoding epidermal cell differentiation inhibitors.

Differences in the carriage of enterotoxin genes were seen between the ST9, ST5, and ST1791 isolates on one hand and the CC398 isolates on the other hand. The enterotoxin gene cluster eeg, which comprises genes for the staphylococcal enterotoxins G, I, M, N, O, and U, was detected in the two ST9 isolates, the single ST5 isolate, and the single ST1791 isolate, whereas the CC398 isolates were negative for all enterotoxin genes tested. In addition, the single ST5 and ST1791 isolates were positive for the leukotoxin genes lukD and lukE. The ST9, ST5, and ST1791 isolates also differed in the carriage of specific MSCRAMM genes. These non-CC398 isolates were negative for cna (encoding collagen binding protein) but positive for the regular fib (encoding fibrinogen binding protein) allele present in S. aureus Newman (accession no. AP009351) and other S. aureus strains. The CC398 isolates were instead positive for the fib allele detected in MRSA 252 (accession no. BX571856) (Table 1). Moreover, these four isolates were also positive for the gene hlb, coding for the β hemolysin.

**Antimicrobial resistance phenotypes and genotypes.** As MRSA isolates, all carried the mecA gene and exhibited oxacillin MICs of 4 to ≥32 μg/ml. Thirty isolates exhibited a
Recent findings showed that amides, and streptogramin B (MLSB) antibiotics in 28 (87.5%), in 31 (96.9%), combined resistance to macrolides, lincosamides, and tetracycline resistance was found in 31 (96.9%) antimicrobial agents (Table 2). Among the most common multidrug resistance phenotype with resistance to ≥3 classes of antimicrobial agents (Table 2). The most common additional resistance properties, tetracycline resistance was found in multidrug-resistant isolates. The variable nucleotides in the dru repeats are shaded.

multidrug resistance phenotype with resistance to ≥3 classes of antimicrobial agents (Table 2). Among the most common additional resistance properties, tetracycline resistance was found in 31 (96.9%), combined resistance to macrolides, lincosamides, and streptogramin B (MLSB) antibiotics in 28 (87.5%), and trimethoprim resistance in 24 (75.0%) isolates. In contrast, resistance to enrofloxacin or apramycin was detected in only one of the remaining six isolates. The genetic basis of trimethoprim resistance in these cases remains to be clarified. Apramycin resistance was recorded in only a single isolate and was shown to be due to the presence of the gene \( apmA \). Two aminoglycoside resistance genes, \( aacA-apfH \), known to mediate resistance to gentamicin and kanamycin, and \( aadD \), known to confer resistance to kanamycin and neomycin, were detected either alone or in combination in isolates that displayed resistance to gentamicin and/or kanamycin. In contrast, the isolate Chi-1 from chicken meat, with a gentamicin MIC of 16 μg/ml, did not exhibit the presence of a gene for gentamicin resistance. Ten of the 16 isolates with tiamulin MICs of ≥16 μg/ml carried any of the genes \( vga(A) \) (n = 5) or \( vga(C) \) (n = 5), both of which code for ABC transporters that confer combined resistance to streptogramin A antibiotics, lincosamides, and pleuromutilins. Since none of the remaining six isolates carried the \( vga(B) \) gene, the genetic basis of tiamulin resistance in these cases remains to be determined. All isolates were negative in the microarray for the lincosamide resistance gene \( lnu(A) \), the macrolide resistance genes \( msr(A), mph(C) \), and \( mef(A) \), the streptogramin A resistance genes \( vat(A) \), and \( vat(B) \), the streptogramin B resistance gene \( vat(B) \), and the kanamycin/neomycin resistance gene \( aphB3 \).

DISCUSSION

The occurrence of MRSA not only in food-producing animals but also in food of animal origin might represent a relevant issue with regard to food safety and consumer protection. For eradication, it is important to identify the origin of the isolates and their dissemination on the farm and along the food chain, including potential ways of transmission and the vectors involved in the spread. To evaluate potential health hazards, it is necessary to know the pathogenic potential of the MRSA isolates. Thus, molecular typing of the isolates and a comprehensive analysis of their virulence and antimicrobial resistance properties will provide relevant information for epidemiological studies and for risk analysis. The application of four different typing techniques, two applicable to \( S. aureus \) in general and two applicable only to methicillin-resistant staphylococci, identified a hierarchy in these methods with regard to their discriminatory power. The highest discriminatory value of 0.863 was calculated for \( spa \) typing. This means that two isolates randomly selected from the test population can be assigned to different \( spa \) types with a probability of 86.3%. When \( dru \) typing was combined with \( spa \) typing, the discriminatory power was increased slightly to 0.893.

The molecular characterization of the MRSA isolates from
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**TABLE 2. Antimicrobial resistance phenotypes and genotypes of the 32 MRSA isolates**

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**Abbreviations of antimicrobial agents:** APR, apramycin; BLA, beta-lactam antibiotics; ENR, enrofloxacin; GEN, gentamicin; KAN, kanamycin; MLSB, macrolides-lincosamides-streptogramin B; Q/D, quinupristin-dalfopristin; SPC, spectinomycin; TET, tetracyclines; TIA, tiamulin; TMP, trimethoprim. Parentheses indicate that based on the MICs, these isolates proved to be intermediate or borderline susceptible to the antimicrobial agent.
fresh poultry meat and poultry products identified the vast majority as livestock-associated MRSA CC398. The spa types detected among the isolates of the present study were mainly those previously seen in MRSA ST398 from swine (10, 13), cattle (8), and poultry (5, 27, 29). Only spa type i6574, identified in an MRSA isolate from turkey meat imported from Italy, appeared as a spa type that has so far not been described in MRSA CC398. Comparison of the dru types detected among the isolates in the present study with dru types determined in previous studies revealed that certain dru types may be present in different SCCmec cassettes, such as dt10a in a Type V cassette of an ST398 isolate (8) or dt11a in a Type IV cassette of a human MRSA ST22 isolate (32). Among the four non-CC398 isolates in the present study were two ST9 isolates with spa type t1430 and dru type dt10a. In a recent screening of professional food handlers and food of animal origin in The Netherlands, one MRSA isolate from a chicken meat sample belonged to ST9/t1430 (4). One of the two ST9 isolates in the present study was also from a chicken product imported from The Netherlands.

Important virulence factors such as PVL and toxic shock syndrome toxin 1, as well as exfoliative toxins, were not identified in any of the MRSA isolates from poultry and poultry products. This is in accordance with the findings of ST398 isolates from pigs and cattle (8, 13). Although enterotoxin genes of types B, K, and Q have previously been detected in single MRSA ST398 isolates from pigs (13), none of the MRSA CC398 isolates from poultry or poultry products was positive in the microarray for enterotoxin genes. Based on the currently available data, the carriage of enterotoxin genes seems to be rare among CC398 isolates (8, 11, 13). However, the MRSA ST9, ST5, and ST1791 isolates (Table 1) carried the egc gene cluster for enterotoxin genes seg-sei-emp-seo-seu. The presence of this gene cluster is a common feature of CC9 and CC5 isolates (26). MRSA ST1 and MRSA ST72 carrying the enterotoxin genes seg-sei or sea-seg-set, respectively, were found in raw beef and fish samples in Korea (31).

Thirty of the 32 MRSA isolates in the present study were classified as multiresistant by resistance to at least three classes of antimicrobial agents. The simultaneous occurrence of more than one tet or erm gene has previously been observed in ST398 isolates of porcine and bovine origin (8, 13). The same is true for the presence of the blaz/IIR gene cluster and the mecA gene (8, 13). The recently identified trimethoprim resistance gene dfrK (15) proved to be the dominant dfr gene in MRSA CC398 and was also found in one of the two ST9 isolates (Table 2). PCR assays confirmed that the dfrK gene was in most cases either linked to the tet(L) gene (15) or part of the transposon Tn559 (18). In staphylococci, transposon Tn559 has been identified in only a single methicillin-susceptible ST398 isolate (18). The finding that it is also present in MRSA isolates from poultry and poultry products is a novel observation. The linkage of the resistance genes erm(A) and spo strongly suggested the presence of a Tn554-like transposon (28). The isolate Chi-1 did not harbor a gene for gentamicin resistance but had a gentamicin MIC of 16 μg/ml, which classified this isolate as borderline resistant. The same isolate, however, carried the gene aprmA for apramycin resistance. Although aprmA does not confer gentamicin resistance, it has been shown to elevate the MIC of gentamicin from 0.25 to 8 μg/ml in S. aureus RN4220 transformants that carry a plasmid-borne aprmA gene (7). Thus, a contribution of aprmA to this borderline gentamicin resistance is possible. Four of the MRSA isolates were identified as resistant to the streptogramin A plus B combination quinupristin-dalfopristin by showing a MIC of 4 or 8 μg/ml, while another 11 isolates were classified as intermediate by showing a MIC of 2 μg/ml (2) (Table 2). Nine of these 15 isolates carried at least one erm gene, whose product also specifies resistance to streptogramin B antibiotics, together with a vga(A) or vgb(C) gene, whose products have been shown to mediate resistance to streptogramin A antibiotics in addition to pleuromutilins and lincosamides (14, 16). Since all isolates tested negative for vat(A), vat(B), vga(B), and vgb(A), the classification of these nine isolates as intermediate or resistant to quinupristin-dalfopristin most likely resulted from the synergistic effect of an erm gene and a vga gene.

When comparing all characteristics listed in Tables 1 and 2, a wide variety of MRSA isolates were detected among the 32 isolates tested. Only three pairs of isolates, Chi-2 and Chi-10, Chi-3 and Tur-6, and Tur-8 and Tur-10, proved to be indistinguishable or closely related. The last two pairs of isolates differed from one another only by the presence or absence of an erm(B) gene (Table 2). In general, the MRSA CC398 isolates from poultry and poultry products showed characteristics similar to those of isolates from pigs and cattle (8, 13). In addition, the ST9, ST5, and ST1791 isolates corresponded closely in their microarray patterns to human strains of CC9 and CC5 (26). As previously stated by Weese et al. (36), the relevance of MRSA contamination of retail meat is unknown and is controversial (20). Different screening studies resulted in strikingly different MRSA prevalences. This may be due to differences in the sampling plans and the MRSA detection procedures applied, but it may also reflect country-specific or food-specific true differences in the MRSA prevalence. This study presented only a time-limited snapshot of the presence of MRSA in fresh chicken and turkey meat as well as in the corresponding products sold in Germany, and it is uncertain in how far the results found in the federal state Rhineland-Palatinate can be extrapolated to other federal states in Germany or to Germany in general. Nevertheless, the observation that 37.2% of the samples tested were MRSA positive is alarming and needs further investigation. Specifically, longitudinal studies with a farm-to-fork approach are needed to identify the sources of contamination and to clarify whether isolates found as commensals in poultry are indistinguishable in their genotypic characteristics from those found in fresh poultry meat and poultry products.

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