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Emergence and Characterization of Community-Associated Methicillin-Resistant *Staphyloccocus aureus* Infections in Denmark, 1999 to 2006[▽]

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The epidemiology of methicillin-resistant *Staphylococcus aureus* (MRSA) infections has changed worldwide. From being strictly nosocomial, MRSA is now frequently found as a community-associated (CA) pathogen. Denmark has been a low-prevalence country for MRSA since the mid-1970s but has in recent years experienced an increasing number of CA-MRSA cases. The aim of this study was to describe the emergence of CA-MRSA infections in Denmark. All Danish MRSA specimens and corresponding clinical data from 1999 to 2006 were investigated. Isolates were analyzed by antibiotic resistance and molecular typing and were assigned to clonal complexes (CC). Clinical data were extracted from discharge summaries and general practitioners' notes, from which assessments of community association were made for all infected cases. CA-MRSA cases constituted 29.4% of all MRSA infections (n = 1,790) and an increasing proportion of the annual numbers of MRSA infections during the study period. CA-MRSA was associated with a young age, skin and soft tissue infections, and non-Danish origin. Transmission between household members was frequently reported. Molecular typing showed >60 circulating clones, where 89.4% of the isolates belonged to five CC (CC80, CC8, CC30, CC5, and CC22), 81.2% carried staphylococcal cassette chromosome *mec* IV, and 163/244 (69.4%) were positive for Panton-Valentine leukocidin. Clinical and microbiological characteristics indicated that import of MRSA occurs frequently. Resistance to ≥3 antibiotic classes was observed for 48.8% of the isolates. The emergence of CA-MRSA in Denmark was caused by diverse strains, both well-known and new CA-MRSA strains. The results suggest multiple introductions of MRSA as an important source for CA-MRSA infections in Denmark.

Methicillin-resistant *Staphylococcus aureus* (MRSA) was until recently predominantly a nosocomial problem. Cases of community-associated MRSA (CA-MRSA) infections were first reported in the late 1980s and early 1990s (12, 19, 37). However, the general perception of a change in MRSA epidemiology came in 1999, when four fatal infections were reported for American children without health care-related risk factors for MRSA, followed by multiple reports of CA-MRSA worldwide (8, 17).

This change in epidemiology has been concomitant with the appearance of new MRSA strains characterized by carrying the small staphylococcal cassette chromosome *mec* (SCC*mec*) type IV or V and the Panton-Valentine leukocidin (PVL) genes *lukS-PV* and *lukF-PV* (20, 28, 39). Attempts to define CA-MRSA have been hampered by the nature of MRSA colonization, which necessitates a detailed epidemiological investigation to determine exactly where a given MRSA was acquired. Health care-associated MRSA (HA-MRSA) with a community onset (HACO) tends to mix with true CA-MRSA, especially in countries with high incidences of HA-MRSA (2, 32). Furthermore, CA-MRSA has been defined differently in different publications, based on either the bacteriological or clinical characteristics of the infections and depending on the information available (10). In this respect, low-incidence countries such as Denmark may provide important settings for studying CA-MRSA, since the low prevalence of HA-MRSA provides less potential for confusion and the overall low number of MRSA cases allows close surveillance of each case.

In Denmark, staphylococcal infections have been surveyed nationally at the Statens Serum Institut (SSI) since 1957. MRSA isolates from all cases have, since 1986, been systematically referred to the SSI for characterization. Since 1999, clinical and epidemiological data have also been collected consecutively on all MRSA cases. Historically, the prevalence of MRSA has been below 2% among bacteremia isolates since the mid-1970s (3), and sporadic outbreaks have mostly been limited to a few individuals.

The first CA-MRSA infections in Denmark were recognized in 1997 in two independent cases with isolates of sequence type 80 (ST80) (15). Since then, a substantial increase in the annual number of new MRSA cases has been observed (1). The aim of this study was to characterize the emergence and epidemiology of CA-MRSA infections, as well as the bacterial isolates, based on data from national surveillance between 1999 and 2006.

MATERIALS AND METHODS

Setting. During the period from 1999 to 2006, Denmark had an average population of 5.4 million (approximately 1.2 million in the Greater Copenhagen area); 3% were Danes of foreign origin (www.statbank.dk). Clinical microbiology services were performed by 14 regional laboratories processing all microbiological specimens from hospitals, outpatient clinics, and general practitioners (GPs).

MRSA surveillance in Denmark. The regional laboratories systematically referred isolates from all MRSA-positive individuals to the SSI. At the SSI, the isolates were confirmed as *mecA* positive (29, 34), tested for antimicrobial sus-

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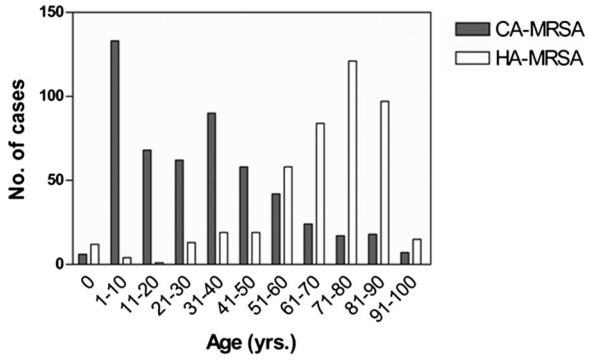

FIG. 1. Age distribution of patients with CA- and HA-MRSA infections in Denmark, 1999 to 2006.

ceptibility, typed by various molecular methods, and stored. The referral was voluntary, but compliance was nearly 100%, based on feedback from the regional laboratories on yearly summaries of the registrations.

Clinical and epidemiological information was obtained consecutively by requesting discharge summaries from hospitals or notes from outpatient clinics and GPs for each case at the time of initial diagnosis. A case was defined as a person found positive for MRSA for the first time or when molecular typing documented that a second finding of MRSA involved a different strain (i.e., with a difference greater than what could be explained by one genetic event).

In November 2006, MRSA became a notifiable disease, and submission of MRSA isolates and clinical information became mandatory.

Clinical and epidemiological information. The following clinical and epidemiological data were extracted from discharge summaries and registered for each MRSA case: age, sex, rationale for specimen collection (e.g., infection or screening for MRSA colonization), type of infection, hospitalization or residency in a long-term care facility, household members with a history of MRSA, history of travel directly related to the MRSA diagnosis, and other factors regarded as significant by the reporting physician.

Non-Danish origin (defined as being born outside of Denmark or having a parent who was born outside of Denmark) and any hospitalization within the 12 months prior to diagnosis were investigated through the Danish civil registration system and the national patient registry, respectively. Infections were categorized into four different groups: (i) import (MRSA infections with onset abroad), (ii) HA (hospital onset >48 h after admission), (iii) CA (community onset or onset <48 h after admission to hospital, with no stay in a hospital or long-term care facility within the previous year), and (iv) HACO (community onset for a person associated with a hospital environment, e.g., a person living in a residential home, a health care worker, a dialysis patient, or an individual with a history of hospitalization within the previous year) (21).

Strain characterization. All MRSA isolates were typed by pulsed-field gel electrophoresis (PFGE) (27) and analyzed by BioNumerics (version 4.61; Applied Maths, Belgium) using Dice coefficients and the unweighted-pair group method with arithmetic means. A similarity coefficient of ≥80% defined major clusters of PFGE types (14, 25) that were assigned to clonal complexes (CC) based on *spa* gene (encoding *S. aureus* protein A) typing and/or multilocus sequence typing (MLST) of representative isolates from each major PFGE cluster (13, 18). Furthermore, international reference strains (the Harmony collection and USA100 to USA1100) were included in the analysis (25, 27).

SCC*mec* types I to IV were annotated primarily by using the multiplex PCR strategy described by Oliveira and de Lencastre (29). Isolates that were nontypeable (NT) by this method were further investigated by PCR to assess the *ccrA*, *ccrB*, and *ccrC* recombinase genes and the *mec* class (20, 28) or by multiplex PCR to distinguish SCC*mec* subtypes IVa to IVh (26).

PVL genes (*lukS-PV* and *lukF-PV*) were detected as described previously (11).

Susceptibility testing for penicillin, cefoxitin, streptomycin, gentamicin, kanamycin, erythromycin, clindamycin, tetracycline, fusidic acid, rifampin (rifampicin), and norfloxacin was performed by using Neo-Sensitabs (Rosco, Denmark) on Danish blood agar (SSI Diagnostica, Denmark). The interpretation of the results was based on the manufacturer's guidelines and on studies of *S. aureus* population structures (www.ssi.dk/sw3425.asp). Susceptibility to glycopeptides was tested using the Etest (AB Biodisk, Sweden) for screening and the PAP-AUC (population analysis profile–area-under-the-curve ratio) method for confirmation (40, 41). Antimicrobial multiresistance was defined as resistance to ≥3 different classes of non-beta-lactam antimicrobials.

Statistics. Statistical significance was assessed using the Mann-Whitney and chi-square tests, with a P value of <0.05 indicating significance.

RESULTS

A total of 2,692 new MRSA cases, involving 2,663 individuals, were reported from 1999 to 2006 in Denmark. Epidemiological information was lacking in two cases. In an additional 18 cases, information regarding the onset of infection was absent, leaving 2,672 cases with complete epidemiological records. Of these, 1,790 (67%) represented infections and 882 (33%) were found by screening healthy carriers. The total number of MRSA cases rose exponentially, from approximately 100 cases per annum between 1999 and 2002 to 851 new MRSA cases in 2005 (1, 23). The infective isolates were grouped into the CA (n = 526), HACO (n = 582), HA (n = 443), and import (n = 239) categories on the basis of the available epidemiological information. Isolates obtained from healthy carriers, HACO cases, and imported cases were not investigated further in this study.

CA-MRSA cases constituted 29.4% (526/1,790) of all MRSA infections in the study period. The number of CA-MRSA infections increased from 11 in 1999 to 153 in 2006, corresponding to an increase in incidence from 0.21/100,000 inhabitants to 2.81/100,000 inhabitants. Thus, in 2006 the incidence of CA-MRSA infections exceeded that of HA-MRSA infections (1.34/100,000). During the study period, the geographical spread of CA-MRSA cases also increased. The largest increase was observed in the Greater Copenhagen area, from 4 cases in 1999 to 72 cases in 2006 (an incidence of 5.95/100,000 inhabitants).

Demographic data. For CA-MRSA patients, the female-to-male ratio was 0.84 and the median age was 30 years (range, newborn to 96 years), with children (1 to 10 years old) constituting 25.3% (133/526) of all cases (Fig. 1; Table 1). The median age of CA-MRSA patients was significantly lower than that of HA-MRSA patients ($P < 0.0001$ by the Mann-Whitney test). In total, 35.6% (187/526) of the patients were of non-Danish origin. The proportion of patients of non-Danish origin and the female-to-male ratio differed significantly between the CA-MRSA and HA-MRSA cases ($P = 0.0001$ and $P = 0.03$, respectively, by the chi-square test).

Patients of non-Danish origin originated from 39 foreign

TABLE 1. Demographic data on patients with HA- and CA-MRSA infections in Denmark, 1999 to 2006

Type of MRSA (no. of patients)	Incidence per 100,000 inhabitants (1999/2006)	Age (yr)[a]	Female/male ratio	No. (%) of foreign origin[b]
HA (443)	0.15/1.34	71 (58–81)	0.60	39 (8.8)
CA (526)	0.21/2.81	30 (10–46)[c]	0.84[d]	187 (35.6)[d]

[a] Given as the median (25th to 75th percentile).
[b] Defined as being born in a foreign country or having at least one parent born in a foreign country.
[c] Significantly different from the value for HA-MRSA infections ($P < 0.05$) by the Mann-Whitney test.
[d] Significantly different from the value for HA-MRSA infections ($P < 0.05$) by the chi-square test.

TABLE 2. Results of typing of Danish CA-MRSA strains, 1999 to 2006 (n = 526)

CC	No. of isolates	PFGE synonym(s)[a]	Result of the following typing method[b]:			PVL testing (n = 244)	
			MLST (n = 28)	*spa* (n = 231)	SCC*mec*	No. of isolates tested	% Positive
CC80	206	European CA-MRSA	ST80	t042, t044, t131, t376, t455, t1109	IV, IVc, NT	65	100
CC8	101	Brazilian/Hungarian, EMRSA-5, Iberian, USA300, USA500	ST8, ST239, ST247	t008, t024, t026 t037, t051, t052, t068, t211, t304, t591, t844	I-IV, Iva, NT	66	62.1
CC30	80	Western Pacific CA-MRSA, EMRSA-16	ST30	t019, t253, t318, t974, t1347	II, IV, V	38	92.1
CC5	61	New York/Japan clone, Pediatric, USA100-II, USA800-IV	ST5, ST225	t002, t003, t105, t653, t688, t2008	II, III, IV, V, NT	10	40
CC22	22	EMRSA-15	ST22	t005, t032, t432, t436, t541, t852	IV	12	16.7
CC1	10	USA400	ST1	t127, t175	IV, NT	10	10
CC45	10	Berlin IV, USA600	ST45	t015, t026	IV	9	0
CC59	10	USA1000		t216, t413, t437	IV, V	10	70
CC398	6	Pig strain		t034	V, NT	6	16.7
CC88	5			t186, t1339	IV, NT	5	20
CC72	4	USA700		t324	IV	4	0
CC152/377	4		ST152	t355	V	4	100
Other CCs	7			t267, t991, t1379, t1387	IV, V, NT	5	40

[a] EMRSA, epidemic MRSA.
[b] n, number of isolates tested.

countries, including countries in the Greater Middle East (41.2% [77/187]), Europe (especially the Balkan area) (24.1% [45/187]), Southeast Asia (primarily the Philippines) (12.8% [24/187]), and Northern Africa (4.8% [9/187]). Furthermore, 3% of infected individuals reported recent travel to areas of high endemicity (the United States, Thailand, the Philippines, and Mediterranean countries). Probable transmission routes reported by the physicians included household members (68 cases [12.9%]), kindergartens (3 cases), workplaces (3 cases), and intravenous drug abuse (1 case).

Infections. Skin and soft tissue infections (SSTI) were predominant (476 cases [90.5%]), followed by infections in the ear (12 cases [2.3%]), respiratory tract (9 cases [1.7%]), and eye (6 cases [1.1%]), invasive infections (e.g., arthritis and osteomyelitis) (6 cases [1.1%]), bacteremia (4 cases [0.8%]), urinary tract infections (4 cases [0.8%]), and other infections (8 cases). In 320 (67.2%) cases, SSTI was associated with an abscess.

Typing. CA-MRSA isolates clustered into 14 CC groups, including 54 *spa* types and 10 MLST types (Table 2). Five CC groups encompassed 89.4% of the isolates (Fig. 2). CC80 was the only lineage found each year of the study period, reaching a level of 38 to 48 annual cases in 2004 to 2006 (Fig. 2). Pronounced diversity was observed among CC8 isolates (ST8, ST239, and ST247), but the majority of isolates were related to USA300 (t008) or a PVL-negative variant (t024).

The CA-MRSA CC22, SCC*mec* type IV (CC22-IV) isolates had PFGE profiles and *spa* types (t005, t032, t436, t541, t852) differing from the those of the CC22, *spa* type t022, SCC*mec* type IV (CC22:t022-IV) clone, which caused a larger nosocomial outbreak from 2003 to 2005 in Denmark (1).

Among the remaining 10% of the CA-MRSA isolates, CC45, CC59, CC88, CC152/377, and CC398 lineages were encountered, which included PFGE variants of USA400, Berlin IV/USA600, and USA1000 strains (Table 2). An increasing diversity was noticed during the study period, with the introduction of new genetic lineages (CC72, CC97, CC101, and CC398) from 2004 onward.

Isolates from patients whose families were of foreign origin showed strong correlations between the bacterial lineage and the geographic origin of the patient, i.e., 79.2% (19/24) of patients of Eastern Asian origin (mainly the Philippines) carried CC30:ST30-IV, whereas 79.2% (61/77) of patients of Middle Eastern origin and 66.7% (6/9) of those of North African origin carried CC80:ST80-IV MRSA.

SCC*mec*. SCC*mec* type IV was found in 81.9% (431/526) of isolates and in all CC groups except for CC152/377. SCC*mec*

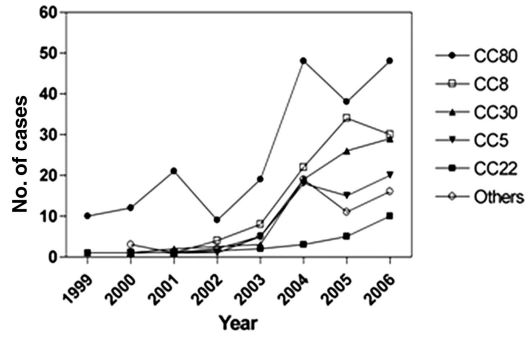

FIG. 2. Annual numbers of CA-MRSA infections in Denmark and associated CC, 1999 to 2006.

TABLE 3. Antimicrobial susceptibilities of all CA-MRSA strains and the major CA-MRSA CC in Denmark, 1999 to 2006

Characteristic	% of strains with the indicated characteristic					
	Total (n = 526)	CC80 (n = 206)	CC8 (n = 101)	CC5 (n = 61)	CC30 (n = 80)	CC22 (n = 22)
Susceptible to all drugs listed	18.8	0.5	12.0	11.6	74.6	22.7
Resistant to:						
Tetracycline	43.8	84.7	15.2	21.7	12.7	4.5
Fusidic acid	44.4	92.6	10.2	36.7	2.5	9.1
Rifampin	2.0	0.5	4.0	1.7	1.3	0
Fluoroquinolones	18.0	0.8	57.6	23.1	3.4	52.9
Streptomycin	37.1	84.7	8.1	1.7	3.8	0.5
Kanamycin	53.6	90.6	41.4	48.3	3.8	27.2
Erythromycin	27.0	5.4	69.7	33.3	10.1	45.5
Clindamycin	18.8	4.4	31.7	27.9	11.25	36.6
Mupirocin	0	0	0	0	0	0
Linezolid	0	0	0	0	0	0
Glycopeptides[a]	0.5	0	2.7	0	0	0

[a] Resistance was confirmed by Etest. Intermediate resistance MICs for vancomycin (4 to 8 mg/liter) and/or teicoplanin (16 mg/liter) were found.

type V (n = 15) was found in CC5, CC30, CC59, CC152/377, and CC398. SCC*mec* types I/IA (n = 4), II (n = 10), and III (n = 5) were identified in the CC5 and CC8 groups (e.g., CC8-I, CC8:ST247-IA, CC5-ST225-II, and CC8-ST239-III). The remaining 11.0% (58/526) of isolates were NT and were related to at least seven CC groups.

PVL. The presence of the PVL genes was investigated in 244 isolates, including all CC groups (Table 2). PVL was detected in 163 (66.8%) of the isolates and was distributed among all major CC groups—CC80 (65/65 isolates tested), CC8 (41/66), CC30 (35/38), CC5 (4/10), and CC22 (2/12)—but was not found in CC45 (n = 9) or CC72 (n = 4). In CC398, all isolates except one were PVL negative.

Antimicrobial susceptibility. Antimicrobial susceptibility in total and for each of the major CC is shown in Table 3. In total, 48.8% of CA-MRSA isolates were multiresistant, whereas 18.8% remained susceptible to all non-beta-lactam antimicrobials.

Antimicrobial susceptibility was strongly influenced by the genetic background of the distinct strains studied, e.g., 78.2% of CC80 versus 6.1% of CC30 isolates were multiresistant.

DISCUSSION

The emergence of CA-MRSA has caused global concern during the past decade. However, several different definitions of CA-MRSA, including clinical and/or bacteriological aspects, have been used (10, 16). This has led to confusion in the literature and to debate about whether CA-MRSA is a separate category, exemplified by Salgado et al., who proposed that CA-MRSA infections were likely to represent unrecognized "overflow" from hospitals due to improper assessment of risk factors, especially concerning contact with hospitals and health care settings, in defining "true" CA-MRSA infections (32). In the present study, HACO patients constituted the largest group, indicating the difficulties in identifying true CA-MRSA isolates. However, by exclusion of HACO infections, this study clearly confirmed the separate identity of CA-MRSA, as proposed by others (5, 7, 21). CA-MRSA accounted for 29.4% of all new MRSA infections in Denmark from 1999 to 2006. These findings are consistent with those from Finland, another country with low endemicity, where a high proportion of CA-MRSA infections (21%) was also found (33). This study confirmed both demographic and bacteriologic aspects of CA-MRSA cases that distinguish them from HA-MRSA cases: the patients are younger; SSTI is the predominant type of infection; and the majority of isolates belong to lineages associated with CA-MRSA by others, are PVL positive, and carry SCC*mec* type IV (17).

Children (1 to 10 years old) constituted the largest group of CA-MRSA patients in this study, followed by younger adults (30 to 40 years old); in many cases, these were children and their parents. However, the true frequency of family and other routes of transmission cannot be estimated from this type of study.

Patients of non-Danish origin were highly overrepresented, suggesting that regular contact with areas of high endemicity is a source of initial colonization and subsequent infections. This is in accordance with the results found in a Danish case-control study performed in 2004, where having parents of non-Danish origin was a significant risk factor associated with CA-MRSA (odds ratio, 30.5 [95% confidence interval, 3.6 to 257.3]) (6). Furthermore, travel to countries of high endemicity was specifically mentioned in the GP's notes on several occasions. Thus, contact with community members from high-prevalence countries may constitute a previously unrecognized risk factor associated with CA-MRSA. A number of proposed risk factors, such as imprisonment, military attendance, and sports activities, were not observed in this study, and only one case related to intravenous drug use was seen. These proposed risk factors may thus be more related to general acquisition of *S. aureus* infections (due to crowding, breach of the skin barrier, or poor hygiene, for example) than to CA-MRSA.

CC80-IV strains constituted more than one-third of all CA-MRSA strains during the study period. A detailed description of the epidemiology of these Danish isolates has recently been published (23). The increase in the number of CA-MRSA strains showed a high diversity dominated by globally disseminated PVL-positive CA-MRSA lineages (CC1, CC8, CC30, CC59, and CC80, including USA400 [ST1], USA300 [ST8], South Pacific clone [ST30], and USA1000 [ST59]). Although a large majority (>80%) of CA-MRSA isolates contained the small SCC*mec* type IV or V, a remarkable and increasing genetic diversity was seen during the study period, with more than 60 combinations of *spa* and SCC*mec* types, supporting the clinical data in suggesting numerous introductions of CA-MRSA into Denmark. In addition, 11.1% of the SCC*mec* cassettes were NT; these could represent new cassette types or variants.

Correlations between strain types and non-Danish origins of patients were also observed, i.e., ST152-IV from the Balkan area, CC80-IV from the Middle East/Northern Africa, and CC30-ST30-IV from East Asia, as reported by others (4, 31, 36, 39). The CC398 isolates, which have been emerging rapidly in pig farming environments, appeared in Denmark in 2003 (42). Denmark has a large pig industry, and working with pigs has been shown to constitute a new risk factor associated with CA-MRSA (24).

PVL genes were detected in 69.4% of the CA-MRSA isolates tested, including all the major CC groups (CC5, CC8, CC22, CC30, and CC80). Whereas our understanding of the

impact of PVL production on clinical manifestations awaits further investigations, the wide distribution of PVL may indicate an advantage for the bacteria. Either PVL is easily transduced into many different genetic backgrounds of MRSA, or, alternatively, several introductions of SCC*mec* type IV in existing PVL-positive methicillin-sensitive isolates have occurred, as proposed by others (9, 17, 30). CA-MRSA strains have been proposed to be less resistant to antimicrobials than HA-MRSA strains (17). However, we found that 48.8% of CA-MRSA strains were multiresistant, with differences correlating with the various genetic lineages. Consequently, the dominance of CC80 isolates in Denmark probably increases multiresistance in total.

Although increasing numbers of CA-MRSA cases have been detected, CA-MRSA isolates (USA300 and CC80-IV) have only occasionally entered Danish hospitals and have not caused large nosocomial outbreaks (22, 23). This is in contrast to the experience in the United States, where USA300 isolates are causing both community and nosocomial outbreaks (35). The strict Danish MRSA guidelines may be an important factor in this difference (www.sst.dk/publ/publ2008/CFF/MRSA/MRSA_vejl_en_19mar08.pdf).

A significant reservoir of MRSA in the community is a threat for the control of MRSA in hospitals, since unknown MRSA carriers can cause intrahospital transmission. Furthermore, the Danish guidelines for HA-MRSA (with preemptive isolation of all suspected MRSA carriers when hospitalized), which have kept the incidence of HA-MRSA low for 3 decades, have obviously not been able to prevent the increase in the incidence of CA-MRSA. Thus, new initiatives for preventing the spread of CA-MRSA seem to be crucial for the future control of MRSA. It has previously been shown that CA-MRSA can be controlled but demands extensive efforts (38).

In November 2006, new guidelines for MRSA control were implemented in Denmark, and MRSA became a notifiable disease. The primary aim of the new guidelines was to protect hospitals from MRSA. However, following the reasoning discussed above, the new infection control guidelines also relate to transmission in the community. Consequently, all members of MRSA-positive households are offered decolonization therapy using nasal mupirocin, chlorhexidine body showers, and advice on decontamination of the household environment.

The present study was limited by the epidemiological information, which was not obtained from structured forms; only matters judged to be important by the treating physician were reported. Recent travel, sport activities, imprisonment, and military service may therefore be underreported.

MRSA infections, particularly CA-MRSA infections, may have been underestimated, since MRSA cases were registered only by their first isolate, so healthy carriers subsequently infected would not have been included. Furthermore, the use of the CDC criteria in the definition of CA-MRSA in countries with low prevalences of HA-MRSA may underestimate the number of CA-MRSA cases, since the majority of hospitalized patients are not per se at risk for MRSA exposure but are by definition classified as HACO. However, the data were obtained prospectively, and this study is strengthened by the valid demographic information about previous hospitalizations and the Danish/non-Danish origin of patients obtained from national registries.

In conclusion, we have seen an increase in the incidence of CA-MRSA infections from 1999 to 2006, making CA-MRSA infections more prevalent than HA-MRSA infections in Denmark. CA-MRSA predominantly caused SSTI in children, and abscesses were the most frequently encountered indication. Well-known CA-MRSA strains, such as CC80-IV (European CA-MRSA), CC8:ST8-IV (USA300), and CC30:ST30-IV (Western Pacific CA-MRSA), were found. However, a large diversity, including CC398, the newly emerging CA-MRSA clone related to pigs and pig farming, was also found. Transmission between household members was the most frequently encountered risk factor associated with CA-MRSA infections, and patients of non-Danish origin were highly overrepresented. Clinical and microbiological evidence suggests import and subsequent transmission as the most likely sources of many of the new CA-MRSA cases.

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