Major West Indies MRSA Clones in Human Beings: Do They Travel With Their Hosts?

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Background. Descriptions of the epidemiology of methicillin-resistant Staphylococcus aureus (MRSA) have seldom been produced in the Caribbean, which is a major tourism destination.

Materials and Methods. Using DNA microarrays and spa typing, we characterized 85 MRSA isolates from human skin and soft-tissue infections from five different islands.

Results. In the French West Indies (n = 72), the most frequently isolated clones were the same clones that are specifically isolated from mainland France [Lyon (n = 35) and Geraldine (n = 11) clones], whereas the clones that were most frequently isolated from the other islands (n = 13) corresponded with clones that have a worldwide endemic spread [Vienna/Hungarian/Brazilian (n = 5), Panton Valentine leukocidin-positive USA300 (n = 4), New York/Japan (n = 2), and pediatric (n = 1) clones].

Conclusion. The distribution of the major MRSA clones in the French (Guadeloupe and Martinique) and non-French West Indies (Jamaica, Trinidad, and Tobago) is different, and the clones most closely resemble those found in the home countries of the travelers who visit the islands most frequently. The distribution might be affected by tourist migration, which is specific to each island.

The Caribbean region is composed of more than 7,000 islands in the Caribbean Sea, which is located southeast of the Gulf of Mexico east of Central America and north of South America; because of their remarkable geographic position (ie, their presence at a crossroads), the Caribbean islands have associated with different countries throughout history. For instance, Guadeloupe and Martinique are currently two overseas French departments, Jamaica and Trinidad and Tobago are parts of the Commonwealth, and the Dominican Republic is part of the Great Antilles, with Spanish as its official language. The Caribbean islands are also known to be a major tourism destination, having drawn an estimated 23.8 million tourists from various geographical origins in 2011 (Table 1).1

It has been shown that the prevalence of methicillin resistance in Staphylococcus aureus is increasing in these regions.2–6 Akpaka and colleagues studied 60 randomly selected methicillin-resistant S aureus (MRSA) isolates from hospitalized patients in three hospitals in Trinidad and Tobago and found that all of the isolates exhibited a similar pulsed field gel electrophoresis (PFGE) banding pattern, which is related to a Canadian strain named CMRSA-6, and all of the isolates were Panton Valentine leukocidin (PVL)-negative (−).7 Monecke and colleagues found that in MRSA isolated from Trinidad and Tobago, the ST239-MRSA-III clone represented 76 of 80 isolates.8 Uhlemann and colleagues studied 22 MRSA strains from the Dominican Republic...
and 56 strains from Martinique and found that the predominating sequence types (STs) were ST5, ST30, and ST72 in the Dominican Republic, and ST8 (spa t304) in Martinique.9

In this study, we aimed to evaluate the possible relationship between human migration and local MRSA epidemiology by analyzing (with spa typing and DNA microarrays) and comparing MRSA isolates that have been implicated in skin and soft-tissue infections (SSTIs) from five different islands of the Caribbean and using data from the literature.

Materials and Methods

Bacterial Strains and Clinical Data

Between 2004 and 2009, 65 MRSA strains were gathered in the laboratory of a hospital in Martinique. These strains were subsequently sent to the National Centre for Staphylococci in Lyon, France, for further characterization. In 2010 and 2011, this collection was completed with four more strains from Martinique, three from Guadeloupe, five from Tobago, five from Trinidad, and three from Jamaica. All of the strains were isolated from patients with SSTIs.

The following clinical and demographic information was retrospectively obtained for the patients infected in Martinique between 2004 and 2009: age and gender of each infected patient, type of infection, and date and site of isolation of the bacterial strains. The 65 bacterial strains from Martinique were isolated from 35 men and 30 women. The mean age of the patients was 55.8 years. All but four of the patients were inpatients. The infections were mostly healthcare-associated (85%, 55/65), even those isolated from outpatients (75%, 3/4). These infections were hospital-associated (85%, 55/65), even those isolated from outpatients. The infections were mostly healthcare-related procedures and protocols have been previously described.12 Using the nomenclature described on the Ridom website (http://spa.ridom.de/).

Results

Molecular Typing Results

The characterization of the strains by DNA microarray separated the 85 isolates into four CCs (MLST}

### Table 1 Populations of five islands of the West Indies, their respective numbers of tourists per year, and the main provenances of the tourists

<table>
<thead>
<tr>
<th>Island</th>
<th>Population</th>
<th>Tourists</th>
<th>Main provenance of tourists</th>
</tr>
</thead>
<tbody>
<tr>
<td>Guadeloupe</td>
<td>401,554†</td>
<td>383,518*</td>
<td>France 92%, Europe 5.6%, other countries 1.6%, unknown &lt;1%*</td>
</tr>
<tr>
<td>Martinique</td>
<td>396,404*</td>
<td>501,491*</td>
<td>France 75.7%, other French overseas departments 10.9%, Europe 5%, other Caribbean countries 4.1%, USA 2.5%, Canada 1%, other 0.6%*</td>
</tr>
<tr>
<td>Jamaica</td>
<td>2,705,800†</td>
<td>1,957,011‡</td>
<td>USA 63.8%, Canada 19.8%, Europe 11.2%, other 5.1%‡</td>
</tr>
<tr>
<td>Trinidad and Tobago</td>
<td>1,317,714‡</td>
<td>371,889‡</td>
<td>USA 46%, other Caribbean 20%, Canada 11%, UK 10%, other Europe 5%, South America 5%‡</td>
</tr>
<tr>
<td>Dominican Republic</td>
<td>10,010,590**</td>
<td>4,491,925‡</td>
<td>USA 32.4%, Europe 25%, Canada 14.8%, other 27.8%‡</td>
</tr>
</tbody>
</table>

*Source: Institut National de la Statistique et des Etudes Economiques (INSEE)—information about Guadeloupe from the years 2009 (population and number of tourists) and 2006 (provenance) and information about Martinique from the years 2009 (population) and 2007 (tourists and provenance).
†Source: Statistique Generale de France—information about Martinique from the year 2010.
‡Source: Caribbean Tourism Organization—information from the year 2010.
**Source: Office National de la Statistique de Republica Dominicana—information from the year 2011.
assignment by microarray): CC5, CC8, CC59, and CC80. Within these CCs, there were 13 diverse and well-described clones or subclones (Table 2). These clones were either healthcare-associated [Lyon clone ($n = 35$), pediatric clone ($n = 5$), Brazilian clone ($n = 5$), and New York/Japan clone ($n = 2$)] or community-associated [ST8-MRSA-IV corresponding to PVL-positive (+) USA300 clone ($n = 9$) and its arginine catabolic mobile element (ACME)-negative variant ($n = 1$), the European PVL+ ST80 clone ($n = 7$)] or both healthcare- and community-associated clones, such as the Geraldine clone ($n = 11$). Four other clones have also been identified: the UK-EMRSA-14, a CC8-MRSA-IV clone ($n = 5$), the WA-MRSA-62, a PVL+ CC8-MRSA-IV clone ($n = 2$), the PVL-negative ST72-MRSA-IV (USA700) clone ($n = 2$), and the ST59-MRSA-V clone ($n = 1$).

Of the 10 infections that were classified as being community-associated, 3 were caused by a MRSA strain belonging to the European ST80 clone, 2 others to the American epidemic ST8-MRSA-IV USA300 PVL+ clone, and another to the ACME-negative variant of this American epidemic strain. Of the four remaining clones, one was classified as the Lyon clone and one as the Geraldine clone, whereas two strains could not be assigned to a definite clone by the software (an agrI/CC8 strain and an agrII/CC5 strain) (Table 2).

spa typing separated the 84 MRSA strains into 18 different spa types, and 1 strain was not able to be typed by this method [a CC8-MRSA-IV PVL+ (WA MRSA-62) strain from Tobago] (Table 2). Seventy-four of the strains clustered into three spa-CCs (spaCC002, spaCC0008, and spaCC044) and a fourth was clustered with no founder. Ten strains were classified as singletons.

Discussion

In this study, the characterization of MRSA isolates from the French West Indies revealed that the most frequently isolated clones were identical to those that had been isolated from mainland France in 2006 to 2007 and previously mainly described in that country. Two French clones were specifically isolated in the French islands: the Lyon clone (35 strains) and the Geraldine clone (11 strains), whereas 8 of the 13 strains collected from the other islands (Trinidad, Tobago, and Jamaica) were identified as belonging to a clone distributed worldwide, specifically the Brazilian ($n = 5$), New York/Japan ($n = 2$), and pediatric ($n = 1$) clones.

The major MRSA clones spreading in France were reported by Dauwalder and colleagues in 2008: the Lyon clone (a hospital-associated ST8-MRSA-IV clone) accounted for 69.4% of the isolates, the Geraldine clone (ST5-MRSA-I truncated) for 6.3% of the isolates, the classical pediatric clone (ST5-MRSA-IV) for 8.1% of the isolates, the new pediatric clone (ST5-MRSA-VI) for 7.2% of the isolates, and the community-associated European ST80 clone (ST80-MRSA-IV) for 3.6% of the isolates. All of these clones were detected in the French West Indies, except for the new pediatric clone. The classical description of the Lyon clone in the literature almost exclusively reports that spa t008 is its corresponding spa type (not t304, as found in this study). This t304 spa type was also detected in five strains of the CC8-MRSA-IV UK-EMRSA-14 clone, which exhibits high homology with the Lyon clone.

In the literature, there are few articles reporting the molecular characteristics of MRSA isolated either from outpatients from Martinique and the Dominican Republic or from Trinidad and Tobago. Among the MRSA isolates from the Dominican Republic, ST30, ST5, and ST72 predominated; we did not detect any strains of ST30 or ST72. Among the MRSA isolates from Trinidad and Tobago, the ST239-MRSA-III clone represented 76 of 80 isolates; in our study, this clone was detected only in Trinidad and Tobago. The few strains from Jamaica (three isolates) were either the USA300 clone ($n = 1$) or the New York–Japan clone ($n = 2$), which was not detected on any other island. Note that the USA300 clone was detected in Martinique, Trinidad and Tobago, and Jamaica.

The relationship between human travel and the geographic dissemination of S. aureus has been reported several times; international travel has been shown to contribute to the spread of S. aureus clones. Most of the published studies have described the epidemiology of PVL+ strains [MRSA more than methicillin-susceptible S. aureus (MSSA)]. For instance, previous studies have made the following observations: (1) importation of MRSA and MSSA through immigration to Denmark and Ireland; (2) transmission of the Queensland CA-MRSA ST93 clone from Australia to England; and (3) imported cases of SSTI, including cases of PVL+ MSSA skin infections in France, with further transmission to close contacts. Most of these studies have described the importation of strains from tropical or subtropical regions. Zanger and colleagues demonstrated that the genotypes of the PVL+ S. aureus clones detected in returnees from tropical and subtropical regions were endemic to the visited destinations. Stenhem and colleagues described imported cases of PVL− S. aureus in Sweden between 2000 and 2003; the major part of this study concerned foreign healthcare-acquired infections. After studying MSSA strains from New York and the Dominican Republic, Bhat and colleagues demonstrated a strong correlation between the two populations by PFGE (with a high frequency of ST398 MSSA), arguing for an “air-bridge link” between the two sites.

In light of the characteristics of international tourism (Table 1), it appears that there is a clear difference between the French islands (where the tourism that is almost exclusively of French origin could have contributed to the strong prevalence of French- and European-specific clones) and Jamaica and Trinidad and Tobago (where a much more mixed tourism may have contributed to the dissemination of clones that have...
Table 2  Distribution of the different isolates among the five studied islands of West Indies correlated with spa typing and strain assignment by the microarray software

<table>
<thead>
<tr>
<th>Microarrays assignment</th>
<th>spa types</th>
<th>spa CC</th>
<th>agr</th>
<th>Martinique, n = 69</th>
<th>Guadeloupe, n = 3</th>
<th>Trinidad, n = 5</th>
<th>Tobago, n = 5</th>
<th>Jamaica, n = 3</th>
<th>Total, n = 85</th>
<th>Previous main geographical description</th>
</tr>
</thead>
<tbody>
<tr>
<td>CC8</td>
<td>t304</td>
<td>008</td>
<td></td>
<td>31</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>France</td>
</tr>
<tr>
<td>CC8-MRSA-IV, Lyon clone/UK-EMRSA-2</td>
<td>t648</td>
<td>008</td>
<td>1</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>t387</td>
<td>Sgl</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>t334</td>
<td>Sgl</td>
<td></td>
<td>2</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CC8-MRSA-IV, UK-EMRSA-14/WA MRSA-5</td>
<td>t304</td>
<td>008</td>
<td>1</td>
<td>5</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Europe</td>
</tr>
<tr>
<td>ST8-MRSA-IV, USA300</td>
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<td>4</td>
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<tr>
<td>ST8-MRSA-IV, ACME-NEGATIVE variant of USA300</td>
<td>t197</td>
<td>008</td>
<td></td>
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<td></td>
<td></td>
<td></td>
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<tr>
<td></td>
<td>t681</td>
<td>008</td>
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<tr>
<td></td>
<td>t211</td>
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</tr>
<tr>
<td>WA-MRSA-62 PVL↓</td>
<td>t008</td>
<td>008</td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td>Australia</td>
</tr>
<tr>
<td></td>
<td>NT</td>
<td>NT</td>
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<td></td>
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<tr>
<td>ST239-MRSA-III, Vienna/Hungarian/Brazilian clone</td>
<td>t037</td>
<td>Sgl</td>
<td></td>
<td>3</td>
<td>2</td>
<td></td>
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<td></td>
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<td>Worldwide</td>
</tr>
<tr>
<td>ST72-MRSA-IV, USA700</td>
<td>t418</td>
<td>nf</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td></td>
<td>Germany, United Arab Emirates</td>
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<tr>
<td></td>
<td>t682</td>
<td>nf</td>
<td></td>
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<td></td>
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<td>1</td>
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<td></td>
</tr>
<tr>
<td>CC5-MRSA-SV</td>
<td>t216</td>
<td>Sgl</td>
<td></td>
<td>1</td>
<td></td>
<td></td>
<td>1</td>
<td></td>
<td></td>
<td>Worldwide</td>
</tr>
<tr>
<td>ST5-MRSA-I, Geraldine clone</td>
<td>t002</td>
<td>002</td>
<td></td>
<td>2</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>France</td>
</tr>
<tr>
<td>ST5/ST225-MRSA-II, New York–Japan clone, EMRSA/UK-EMRSA-3</td>
<td>t2164</td>
<td>002</td>
<td>1</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Worldwide</td>
</tr>
<tr>
<td>CC5-MRSA-IV, pediatric clone [sed/yr-pos. subclone]</td>
<td>t067</td>
<td>002</td>
<td></td>
<td>2</td>
<td>3</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Worldwide</td>
</tr>
<tr>
<td></td>
<td>t688</td>
<td>Sgl</td>
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<td>1</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>CC5-MRSA-IV pediatric clone PVL↓ subclone</td>
<td>t002</td>
<td>002</td>
<td></td>
<td>2</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>UK, France, Australia, Switzerland, Senegal, Ireland</td>
</tr>
<tr>
<td>CC80</td>
<td>t444</td>
<td>044</td>
<td></td>
<td>4</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Europe</td>
</tr>
<tr>
<td>CC80-MRSA-IV [PVL↓], European CAMRSA clone*</td>
<td>t434</td>
<td>044</td>
<td></td>
<td>3</td>
<td>2</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td></td>
<td>t376</td>
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</tbody>
</table>

The last column summarizes the main previously described locations (from Monecke and colleagues13). The clones colored in light gray were found only in the French islands, and those colored in dark gray only in Trinidad and Tobago and the Jamaican islands. The other clones were found in the French islands, Trinidad and Tobago, and Jamaica. Sgl = singletons; nf = no founder; NT = not able to be typed; CC = clonal complex; PVL↓ = Panton and Valentine leukocidin-positive strains.

*Described in the text as the European ST80 clone.
worldwide distribution). Nevertheless, there are other potential explanations for this difference, and tourism might only be one of several potential contributing factors. Differing medical practices, especially different antibiotic strategies, could be another major factor. Indeed, it has been established that the increase in HA-MRSA infections reflects the growing impact of medical interventions, resulting in the selection and spread of a limited number of clones. In our study, HA-MRSA strains represented the majority of isolates in Martinique (85%). Unfortunately, information could not be recovered for all of the patients from the other islands. Thus, additional risk factors (such as old age, comorbidities for HA-MRSA acquisition, or belonging to a particular community likely to acquire CA-MRSA29) were not available to support this hypothesis. Another question is related to the discriminative efficiency of the genotyping tool used to define the different MRSA clones and whether this tool is well adapted for identifying these clones. By identifying discrepancies in the results of different typing methods of 135 ST5 MSSA and MRSA isolates, Nubel and colleagues hypothesized that MRSA could have arisen on multiple independent occasions31 (and is not the result of the global spread of a small number of strains with acquired resistance capacities, as is usually argued regarding HA-MRSA32). In our study, we chose to use both spa typing and DNA microarrays, which we believe to be complementary: spa typing is a well-validated method that has an intermediate discriminatory power33 and has been shown to be useful in characterizing the global genetic evolution of an S. aureus population.34 A DNA microarray allows for the rapid identification of a large number of genes11 and the extrapolation of the ST of the studied strains.11

We established the presence of several MRSA clones from different Caribbean islands in light of their previous geographic descriptions (Table 2). We hypothesized that a link could exist between the presence of these clones and touristic migrations, but we did not explore the dynamics of their dissemination. The comparison of the strains from the French West Indies to strains collected in mainland France and the demonstration that these strains belong to the same clones using phylogenetic hierarchization (by spa typing for instance) could provide information on the evolution dynamic of MRSA over time.

The limitations of our study resulted from its design, which caused a non-negligible selection bias. Strains were collected from Martinique between 2004 and 2011, whereas strains from the other islands were collected in 2010 and 2011 only; although we gathered a larger number of strains from Martinique, we managed to recover only a few strains from the other islands. Hence, there is a bias in the timing of the strain collection when comparing the results of the isolates from Martinique with those from other islands, as the epidemiology could have changed during this time. Another bias is owing to the lack of information concerning the hospital or community acquisition of the strains, which limited the exploitation of the results. Similarly, only limited clinical information was obtained from the microbiologists who provided the strains. In particular, the proportion of HA-MRSA in the population collected in 2010 and 2011 was not known. However, as the selection of the strains was performed according to the same procedure, we consider the populations to be comparable.

**Acknowledgments**

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**Declaration of Interests**

The authors state that they have no conflicts of interest.

**References**