Invasive *Staphylococcus aureus* Infection in Utah Children; Continued Dominance of MSSA over MRSA


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**Abstract**

**Background:** *Staphylococcus aureus* is an invasive pathogen causing significant disease in children. Methicillin-resistant *S. aureus* (MRSA) dominates in many US institutions, but our institution continues to see predominantly methicillin-sensitive *S. aureus* (MSSA) disease. We sought to characterize the clinical and molecular epidemiology of invasive *S. aureus* in our population.

**Methods:** All invasive *S. aureus* isolates from children 0-18 years treated at Primary Children's Hospital (PCH; Salt Lake City, Utah) were collected from 2006-2012. Medical records were queried for clinical and laboratory data associated with invasive disease. Next generation sequencing (NGS) was performed on all available isolates (3613). Multi-locus sequence type (MLST) was determined in selected isolates using previously published primers. MLST was used to identify genetically distinct clusters, suggesting a possible role for novel virulence factors contributing to invasive *S. aureus* disease in children.

**Results**

- **MLST Distribution of *S. aureus* Isolates**

<table>
<thead>
<tr>
<th>MLST Type</th>
<th>MSSA</th>
<th>MRSA</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bone, joint infection</td>
<td>11/17 (65)</td>
<td>20/28 (71)</td>
<td>p = 0.009</td>
</tr>
<tr>
<td>Bone and Joint infection (n=137)</td>
<td>108/168 (64%)</td>
<td>8/16 (5%)</td>
<td>14 (10%)</td>
</tr>
<tr>
<td>Pneumonia (n=40)</td>
<td>13/40 (33%)</td>
<td>2/40 (5%)</td>
<td>12 (30%)</td>
</tr>
<tr>
<td>CLABSS (n=68)</td>
<td>55/68 (81%)</td>
<td>2/68 (3%)</td>
<td>3 (5%)</td>
</tr>
<tr>
<td>ICU Admission (n=129)</td>
<td>92/129 (71%)</td>
<td>6/129 (5%)</td>
<td>17 (13%)</td>
</tr>
</tbody>
</table>

  **Table 1. Demographic and clinical characteristics of all 362 patients with invasive MSSA or MRSA disease from 2009 to 2012 at PCH.**

- **Table 3. Common multi locus sequence types and the relative risk for selected disease phenotypes and clinical severity indicators. ST30 is associated with an increased risk for ostearticular infections, while ST8 is associated with an increased risk for pneumonia and severe sepsis. ST5, ST15 and ST87 are associated with an increased risk for ICU admission.**

- **Table 2. Number of patients with MSSA, MRSA and PVL in selected infections and clinical severity indicators. The majority of invasive *S. aureus* infections at PCH are PVL (-) MSSA.**

**Conclusions**

- Invasive *S. aureus* disease at PCH has distinct epidemiology, with continued dominance of PVL (-) MSSA.
- These MSSA are concentrated in a small number of genetically distinct clusters and some STs appear to be associated with specific disease phenotypes suggesting a possible role for novel virulence factors in these isolates leading to invasive infections.
- Further study of these isolates could increase our understanding of the virulence factors contributing to invasive *S. aureus* disease in children.

**References**


**Figure 1. MLST distribution of invasive *S. aureus* infections by year from 2009 to 2012. Overall rates of invasive disease are relatively unchanged and are predominantly MSSA. MSSA is predominantly ST30, while MRSA is predominately ST8.**

**Methods**

- Invasive *S. aureus* isolates and associated patient information were identified through a search of the Intermountain Healthcare Enterprise Data Warehouse (EDW) and PCH microbiology records. Methicillin sensitivity was determined using disk diffusion. Proton (Thermo-Fisher). Multi-locus sequence type (MLST) was extracted from NGS data. PCR was performed and all isolates to determine the presence or absence of PVL, using previously published primers.

- **Invasive *S. aureus* disease at PCH has distinct epidemiology, with continued dominance of PVL (-) MSSA.**

- **These MSSA are concentrated in a small number of genetically distinct clusters and some STs appear to be associated with specific disease phenotypes suggesting a possible role for novel virulence factors in these isolates leading to invasive infections.**

- **Further study of these isolates could increase our understanding of the virulence factors contributing to invasive *S. aureus* disease in children.**