Engaging Scientists, Clinicians, Community Health Workers and Patients to Conduct a CER Study of Home-based Interventions to Reduce CA-MRSA Recurrence and Household Transmission

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CDN N² -PBRN: Building a Network of Safety Net PBRNs

A collaboration among:
- Access Community Health Network (ACCESS)
- Alliance of Chicago (ALLIANCE)
- Association of Asian Pacific Community Health Organization (AAPCHO)
- Center for Community Health Education Research and Service (CCHERS)
- Clinical Directors Network (CDN) [Lead PBRN]
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Principal Investigator: Jonathan N. Tobin, PhD (CDN)

Program Officers: Rebecca A. Roper, MS, MPH & Theodore G. Ganiats, MD - AHRQ PBRN Initiative

- 9 Established PBRNs
- 3 “Incubator” PBRNs
- 600+ Practices
- 4.5 million patients
The Rockefeller University

- Unique structure
  - 82 heads of labs
  - 100+ year tradition of translational research
  - 40 bed JCAHO-accredited research-only hospital
  - AAHRPP-accredited

- 250 protocols
  - 80% investigator - initiated
  - 20% phase I, II, III or device trials

- Center for Clinical Translational Science 2006 -
  - Community Engaged Research Core
Recurrent Furunculosis Caused by a Community-Acquired \textit{Staphylococcus aureus} Strain Belonging to the USA300 Clone

Shirish Balachandra, MD (CDN/Urban Health Plan FQHC) and Maria Pardos, MD PhD (Rockefeller)

Case Study of MRSA Infection Recurrence

**(T3 Clinician Investigator Expertise/Interest)**

Recurrent Furunculosis Caused by a Community-Acquired \textit{Staphylococcus aureus} Strain Belonging to the USA300 Clone

Background: A 24-year-old female with recurrent skin and soft tissue infections (SSTI) was enrolled as part of a multicenter observational cohort study conducted by a practice-based research network (PBRN) on community-acquired methicillin-resistant \textit{Staphylococcus aureus} (CA-MRSA). \textbf{Methods:} Strains were characterized by pulsed-field gel electrophoresis (PFGE), \textit{spa} typing, and multilocus sequence typing. MRSA strains were analyzed for SCC\textit{mec} type and the presence of the Panton-Valentine leukocidin (PVL) and arginine catabolic mobile element (ACME) using PCR. \textbf{Results:} In the first episode, \textit{S. aureus} was recovered from the wound and inguinal folds; in the second, \textit{S. aureus} was recovered from a lower abdomen furuncle, inguinal folds, and patellar fold. Molecular typing identified CA-MRSA clone USA300 in all samples as \textit{spa}-type t008, ST8, SCC\textit{mec}IVa, and a typical PFGE pattern. The strain carried virulence genes \textit{pvl} and ACME type I. Five SSTI episodes were documented despite successful resolution by antibiotic treatment, with and without incision and drainage. \textbf{Conclusions:} The source of the USA300 strain remains unknown. The isolate may represent a persistent strain capable of surviving extensive antibiotic pressure or a persistent environmental reservoir may be the source, possibly in the patient’s household, from which bacteria were repeatedly introduced into the skin flora with subsequent infections.
CAMP1 Findings:

Convergence of CER/PCOR Interests

- **Patients**: Responses from the RPPS patient focus group indicated that many patients participated in the CAMP study in order to contribute to knowledge about CA-MRSA transmission and recurrence. Outcomes that patients were most concerned about include: *recurrence*, pain and inability to work.

- **Clinicians**: “[It is assumed that] colonization is ongoing, because we’ve had patients return with recurrent infections. ...If you just use systemic antibiotics, the nasal colonization persists. Another question to consider is if the source is in the house. We can take all measures to decolonize the person but if the infection is still in the house (pet, towel, sheets, etc), then it’s a huge factor.” – Dr. Balachandra

- **Laboratory Investigators**: “Does the MRSA recurrent phenotype reflect a single or multiple genotypes?

- **Clinical Investigators**: 31% of MRSA+ wounds and 28% of MSSA+ wounds are *recurrent*

**S. aureus Recurrence**

- MRSA+ (n=61)
  - Both Prospective & Retrospective: 3%
  - Prospective Only: 23%
  - Retrospective Only: 17%

- MSSA+ (n=30)
  - Both Prospective & Retrospective: 15%
  - Prospective Only: 7%
  - Retrospective Only: 7%

*This convergence of interests led us to focus on laboratory & clinical correlates of infection recurrence and to prioritize the study of prevention of infection recurrence*
The lack of association between S. aureus nasal colonization and serious skin infection underscores the need to explore alternative venues or body sites that may be crucial to transmission. Moreover, the magnitude of colonization and infection within the household suggests that households are an underappreciated and substantial community reservoir.

Figure. Proportion of Households Contaminated With an Environmental Stratification Type of Staphylococcus aureus Correlating With the Participants’ Baseline Colonizing or Infecting Strain Type, by Household Surface

Repetitive sequence-based polymerase chain reaction queries the entire chromosome but is not specific to the mecA locus; thus, a methicillin-resistant determined by whether the surface was available for testing and whether there was at least 1 baseline isolate (colonizing or infecting strain) obtained from the

Universal decolonization resulted in a significantly greater reduction in the rate of all bloodstream infections than either targeted decolonization or screening and isolation.

Figure 2. Effect of Trial Interventions on Outcomes.

Shown are group-specific hazard ratios and 95% confidence intervals (indicated by vertical lines) for outcomes attributable to the intensive care unit. Results are based on unadjusted proportional-hazards models that accounted for clustering within hospitals. Analyses were based on the as-assigned status of hospitals. Panel A shows hazard ratios for clinical cultures that were positive for methicillin-resistant Staphylococcus aureus (MRSA) infection. Panel B hazard ratios for MRSA bloodstream infection, and Panel C hazard ratios for bloodstream infection from any pathogen. Bubble plots of hazard ratios (predicted random effects or exponentiated frailties) from individual hospitals relative to their group effects are shown. The size of the bubble indicates the relative number of patients contributing data to the trial.

Targeted versus Universal Decolonization to Prevent ICU Infection


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The Rockefeller University Hospital

Center for Clinical and Translational Sciences

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INFECTION VS COLONIZATION: RESERVOIRS

Staphylococcus aureus in the Community: Colonization Versus Infection

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EFFECTIVE INTERVENTIONS TO PREVENT INFECTION
CAMP2 Specific Aims

- **Aim 1:** To evaluate the **comparative effectiveness of a CHW/Promotora-delivered home intervention** (Experimental Group) as compared to Usual Care (Control Group) on the primary patient-centered and clinical outcome (SSTI recurrence rates) and secondary patient-centered and clinical outcomes (pain, depression, quality of life, care satisfaction) using a **two-arm randomized controlled trial (RCT)**

- **Aim 2:** To understand the **patient-level factors** (CA-MRSA infection prevention knowledge, self-efficacy, decision-making autonomy, prevention behaviors/adherence) and environmental-level factors (household surface contamination, household member colonization, transmission to household members) that are associated with differences in SSTI recurrence rates

- **Aim 3:** To understand **interactions of the intervention with bacterial genotypic and phenotypic** variables on decontamination, decolonization, SSTI recurrence, and household transmission

- **Aim 4 [Exploratory]:** To explore the **evolution of stakeholder engagement and interactions** among patients and other community stakeholders with practicing community-based clinicians and academic laboratory and clinical investigators over the duration of the study period
CAMP1 & CAMP2 Stakeholders and Partners

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University of California Irvine

Denny Moe’s Superstar Barbershop
*Denis “Denny Moe” Mitchell
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CAMP2 Logic Model

**INTERVENTION**
- Medical Treatment for SSTIs
- Control (Usual Care)
- Experimental Intervention (Home/Environment)
- I& D +/- Antibiotics as per CDC guidelines

**PROCESS**
- Patient Reported Measures
  - MRSA Knowledge
    - Infection Prevention Knowledge and Hygiene Behaviors Assessment (CDN)
  - Prevention self-efficacy
    - Self-Efficacy Assessment (Jones et al, 2010)
  - Decision-making autonomy
    - Decision Self-Efficacy Scale (O’Connor et al, 1995)
- Intervention Uptake
- Environmental Reservoir
  - Colonization
    - Surveillance cultures from consenting household members and index patient (Bacterial genotypic and phenotypic measures)
  - Environmental Contamination
    - Household environmental surface samples (Bacterial genotypic and phenotypic measures)
- Prevention Behaviors
  - 1) Medication Adherence Scale (Morisky)
  - 2) Hygiene Score (Miller 2007 Clin Infect Dis)

**OUTCOMES**
- Clinical Outcomes
  - SSTI Recurrence
    - 1) Clinical Response Questionnaire (CDN)
    - 2) Case Report and Chart Review Form (CDC and DHHS)
- Patient-Centered Outcomes
  - Quality of Life
    - 1) Pain Interference Short Form (PROMIS)
    - 2) Depression Short Form (PROMIS)
    - 3) 36 Item SF Health Survey Instrument (RAND)
  - Patient Satisfaction
    - 1) Satisfaction with Participating in Social Roles (PROMIS)
    - 2) CAHPS APQ 1.0 (AHRQ)
- Public Health Outcomes
  - Household Transmission
    - Household members SSTI/MRSA Infection (SSTI Self-Report)
CAMP1 and CAMP2 Study Designs

**CAMP-1**
- Patients present to clinics with skin or soft tissue infections (SSTIs) on routine visits
- Clinicians provide information about the study & explain informed consent procedure
- Patients are enrolled if they meet inclusion criteria, and provide informed consent to participate in the study

**Visit 1 (T1)**
- Clinicians Complete:
  - Dermatological Symptoms Instrument
  - Physical Examination including ruled digital photo of lesion(s)
  - Obtain Purulent Material Sample after incision and drainage (if available)
  - Obtain Nasal Sample via nasal swab
  - Schedule a follow-up interview with CDN within 2 days

**CDN Phone Interview Complete:**
- (within 48 hours of clinic visit)
  - Medical History
  - Demographics
  - Co-Morbidities
  - Healthcare Utilization Scale
  - Antibiotic Adherence Scale
  - Social Network & Environmental Exposure

**Visit 2 (T2)**
- 4 weeks after T1, completed by CDN interviewers
  - Telephone Interview (15 min)
  - Obtain interim history regarding:
    - Antibiotic adherence
    - Clinical response
    - Request photograph
  - Patient takes ruled digital photo of (former) infection site(s)

**Follow-up Chart Review (T3)**
- 3 months after T1, completed by CDN and RU research staff
  - Standardized review of Electronic Health Records (EHRs) of all enrolled patients
    - Complete Active Bacteria Core Surveillance Case Report Form
    - Identify subsequent follow-up CHC visits for SSTIs & related problems
    - Assess follow-up laboratory tests/antibiotic prescriptions

**Inclusion Criteria**
- The patient is between 7 to 70 years of age
- The patient is fluent in English or Spanish
- The patient plans on receiving care in this health center during the next year
- The patient presents with signs and symptoms of a skin or soft tissue infection

**Exclusion Criteria**
- The patient is unwilling to provide informed consent
- The patient is acutely sick (for example, crying, wheezing, bleeding, screaming or shaken) and unable to participate in a discussion about the study
- The patient is unable to understand the information shared about the study

**CAMP-2**
1. Home visits with Community Health Workers/Promotoras (patient and household assessment/swabs) [Exp + UC]
2. Patient and household member decolonization [EXP]
3. Household decontamination [EXP]
**CDC Guidelines:**
Incision & Drainage
+ Oral Antibiotics

**Assessment of Household Environmental Contamination & Household Members Colonization**

**Patient & Household Members**
- Decolonization

**Home Environment**
- Environmental Decontamination

*(after S. Huang, 2014)*
1) Nasal Mupirocin
2) Chlorhexidine Baths on Skin
3) Chlorine Bleach Cleaning of Household Surfaces
Home Visit Assessment: Household Surface Sampling

Collected from index patients (n=278), consenting household members, and home environment surfaces.

Index Patients and Household Members
(n=3 per participant)
Baseline and 3-Months

Environment
(n=13 surfaces per household)
Baseline and 3-Months

<table>
<thead>
<tr>
<th>Swab Category</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Front doorknob</td>
<td>Kitchen floor</td>
</tr>
<tr>
<td>TV remote</td>
<td>Bathroom sink handle</td>
</tr>
<tr>
<td>Telephone</td>
<td>Hair brush</td>
</tr>
<tr>
<td>Kitchen light switch</td>
<td>Toilet seat</td>
</tr>
<tr>
<td>Kitchen countertop</td>
<td>Bedroom floor</td>
</tr>
<tr>
<td>Refrigerator door handle</td>
<td>Favorite child's toy (non-plush)</td>
</tr>
<tr>
<td>Kitchen sink handle</td>
<td></td>
</tr>
</tbody>
</table>
Assessed for eligibility (n=602)

Excluded based on negative lab result (n=235)

Allocated to Usual Care Group (n=89)
- Received allocated intervention (n=58)
- Did not receive allocated intervention (n=31)

Allocated to Experimental Group (n=97)
- Received allocated intervention (n=62)
- Did not receive allocated intervention (n=35)

Excluded based on eligibility criteria (n=181)
- Declined to participate (n=141)
- Not meeting inclusion criteria (n=40)
  - Over or under age limit (n=10)
  - On antibiotics (n=3)
  - Acutely ill (n=3)
  - Did not speak English or Spanish (n=7)
  - Does not meet probable diagnostic criteria for CA-MRSA (n=7)
  - No lesion to culture (n=4)
  - Not planning to continue receiving care at site (n=6)

Consented; Baseline Visit Conducted (n=421)

Randomized (n=186)

Allocation

3-Month Home Visit
- Complete (n=47)
- Pending (n=7)

6-Month Interview and Chart Review
- Complete (n=)
- Pending (n=)
**Results: Baseline Demographic Data**

We have recruited *421 patients with SSTIs* to participate; 
*44.1% (n=186) have been eligible* for the study 
[Wound culture: MRSA+ (22.3%) or MSSA+ (22.3%)]

120 baseline home visits and 95 three-month home visits have been completed

### Age

- **Mean:** 38 ± 14.9 years
- **Range:** 9 – 70 years

### Gender

- **Male:** 59%
- **Female:** 41%

### Ethnicity

- **Hispanic or Latino:** 11%
- **Not Hispanic or Latino:** 59%
- **Prefer not to Answer:** 30%

### Race

- **Black or African American:** 22%
- **More than one race:** 1%
- **Prefer not to answer:** 18%
- **White:** 22%
- **American Indian or Alaska Native:** 16%
- **Asian:** 44%
- **Native Hawaiian or Other Pacific Islander:** 0%

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Results: Baseline Clinical Data
Dermatological Symptoms and Treatment (n=186)

Signs and Symptoms of SSTI

- Redness: 91%
- Swelling: 89%
- Warmth: 75%
- Pain/Tenderness: 93%
- Complaint-Spider Bite: 3%

Lesion Type

- Folliculitis: 10%
- Abscess: 76%
- Furuncle/Boil: 4%
- Carbuncle: 3%
- Cellulitis: 26%

Treatment

- Antibiotics Only: 37.1%
- I&D Only: 9.7%
- Antibiotics and I&D: 47.8%
- No Treatment: 5.4%
Results: Baseline Microbiological Data

ANTIBIOTIC CULTURE & SENSITIVITY (n=121)
**Results: Baseline Data – Staph Infection**

Comparison of Proportions of Infected Body Sites between MRSA and MSSA Infection

<table>
<thead>
<tr>
<th>Body Site</th>
<th>MRSA (%)</th>
<th>MSSA (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Breast</td>
<td></td>
<td>10%</td>
</tr>
<tr>
<td>Groin</td>
<td>5%</td>
<td></td>
</tr>
<tr>
<td>Back</td>
<td>15%</td>
<td></td>
</tr>
<tr>
<td>Arm</td>
<td>20%</td>
<td></td>
</tr>
<tr>
<td>Hand/Finger</td>
<td>25%</td>
<td></td>
</tr>
<tr>
<td>Thigh</td>
<td>30%</td>
<td></td>
</tr>
<tr>
<td>Head/Neck</td>
<td>35%</td>
<td></td>
</tr>
<tr>
<td>Lower Leg</td>
<td>40%</td>
<td></td>
</tr>
<tr>
<td>Abdomen/Torso</td>
<td>45%</td>
<td></td>
</tr>
<tr>
<td>Axilla</td>
<td>50%</td>
<td></td>
</tr>
<tr>
<td>Buttock</td>
<td>55%</td>
<td></td>
</tr>
</tbody>
</table>

*MRSA vs. MSSA: p<0.05

**Note:**
- TOR: Torso
- LL: Lower Limbs
- UL: Upper Limbs
- HG: Head/Neck
- AM: Arm
- FA: Foot/Ankle
- G: Groin
- B: Breast
**Results: Baseline Data – Staph Colonization**

**Index Patient S. aureus Positivity Rate (n=120)**

- Armpit: 10.8% (MRSA) 10.0% (MSSA)
- Groin: 10.8% (MRSA) 9.2% (MSSA)
- Nasal: 10.8% (MRSA) 18.3% (MSSA)

**Household Member S. aureus Positivity Rate (n=105)**

- Armpit: 4.8% (MRSA) 6.7% (MSSA)
- Groin: 7.6% (MRSA) 4.8% (MSSA)
- Nasal: 13.3% (MRSA) 20.0% (MSSA)
Results: Baseline Data – Staph Contamination

Surface contamination similar between MRSA and MSSA (15% vs 17.2%, respectively; \( p=0.22 \)). MRSA and MSSA contamination were most prevalent on the Kitchen Floor, Bedroom Floor, and Toilet Seat.

### Household Contamination Score (n=120)

<table>
<thead>
<tr>
<th>Contamination Level</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>No Contamination (0 surfaces)</td>
<td>46.2%</td>
</tr>
<tr>
<td>Moderate Contamination (1-3 surfaces)</td>
<td>36.1%</td>
</tr>
<tr>
<td>High Contamination (&gt;4 surfaces)</td>
<td>17.6%</td>
</tr>
</tbody>
</table>

Mean: 1.64 ± 2.36
Range: (0, 12)
**Results: Baseline Housing Density & Contamination**

- The relationship between infection type and household density may be confounded by birthplace, since non-USA born participants had both significantly higher household density and MSSA positivity.

### Household Density vs. Surface Contamination

![Graph showing the relationship between household density and surface contamination](image)

- **p=0.59**

### Household Density and Wound Infection Type vs. Birthplace

<table>
<thead>
<tr>
<th>Household Density</th>
<th>Infection Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>Low</td>
<td>High</td>
</tr>
<tr>
<td>Non-USA</td>
<td>58.0%</td>
</tr>
<tr>
<td>USA</td>
<td>57.3%</td>
</tr>
</tbody>
</table>

Household Density= # residents/# rooms; median=1.37

Birthplace vs. Infection Type: P=0.0502

Household Density vs. Infection Type, controlling for Birthplace:
- MRSA: P=0.56
- MSSA: P=0.55
Summary of Baseline Colonization & Contamination Results

- 47.5% of 120 index patients and 38.1% of 105 household members were positive for *S. aureus* colonization in one or more body sites.
- 53.8% of households had at least one surface contaminated with *S. aureus* (MRSA: 44.3%, MSSA: 55.7%).
- MRSA and MSSA surface contamination showed similar patterns of contamination, most common in the kitchen (38.5%) and bathroom (23.3%), followed by bedroom (15.4%), living room (15.4%) and entryway (7.7%).
- Those who were not born in the USA had a higher proportion of MSSA infection as compared to those born in the USA (p=0.05).
- There are high levels of colonization and contamination of surfaces in households of patients with confirmed MRSA/MSSA SSTIs suggesting the importance of these reservoirs for controlling infections.
Next Steps: National Outreach

• Add whole genomic sequencing/metagenomics

• National CA-MRSA Surveillance System with Practice Based Research Networks (PBRNs) using a network of networks (N²-PBRN)

• Comparative Effectiveness Research (CER) Studies using Pragmatic Individual-level (RCTs) and Cluster Randomized Controlled Trials (cRCTs)

• Surveillance and educational outreach directly to the public

• Enduring partnerships to disseminate, implement and evaluate evidence-based practices, including:
  • Understanding the Role of the microbiome and commensals
  • Carriage/Chronic Carriers
  • Decolonization Strategies
  • Antibiotic Stewardship
  • Environmental Decontamination Strategies to eliminate reservoirs of resistance (ARBs & ARGs)
CA-MRSA Project (CAMP) Rockefeller-CDN-CHC Team

Bi-Directional Community Engaged Research Partnership

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Rockefeller/CDN Model:
To Simultaneously Study Effectiveness and Mechanisms so as to Answer the Questions:

1) What works? [Comparative Clinical Effectiveness]
2) For whom does it work? [Heterogeneity of Tx Effects/Precision Medicine]
3) How does it work? [Mechanisms]
Translational Research, NIH “Blue Highways” & The Rockefeller/CDN Model

T1 Laboratory Investigation
Pathogen Virulence Factors (MRSA)
Laboratory of Microbiology & Infectious Diseases

T2 Human Clinical Research

T3 Dissemination & Implementation Research
Host Defense Factors (Patients, Households, Communities)
Laboratory of Community-based Comparative Effectiveness Research

T4 Public Health Impact

T5 Policy
**T₅: Translation into Policy**

Reducing Antibiotic Resistant Bacteria (ARBs) and Antibiotic Resistant Gene Fragments (ARGs) in the Environment

- Antibiotic Stewardship
  - Clinical
  - Livestock
- Livestock/Feed/Antibiotics
  - Food Supply
- Environmental Waste Management
  - Soil microbiome
  - Water microbiome
MRSA has been recovered from:

- Companion Animals/Pets (dogs, cats)
- **HUMANOSIS ↔ ZOONOSIS**
- Farm/Food Animals (cows, pigs)
- **Livestock Acquired MRSA (LA-MRSA)**
  - Meat (beef, pork)
  - Dairy (cow milk)
  - Fish (tilapia)
- Aquaculture
- Occupational Settings (healthcare, veterinarians, agriculture, livestock, fishermen, athletes)
- Environment (high touch surfaces, public transportation, soil, water table, Ocean, Lakes, Wastewater pools)

T₅: Why is this Important?
N² PBRN: Network of Networks

- Clinical Directors Network (CDN)
- Lutheran Family Health Centers (LFHCs)
- Access Community Health Network (ACCESS)
- South Texas Ambulatory Research Network (STARNet)

NYC/Westchester:
- Hudson River Health Care
- Brookdale Family Care Center
- Open Door Family Health Center
- Urban Health Plan
- Manhattan’s Physician Group 95th Street
- Manhattan’s Physician Group 125th Street

Brooklyn:
- Park Slope Family Health Care

Chicago:
- Kling Adult Medicine
- Madison Family Health

San Antonio:
- Trevino Family Clinic
- University Health System

Funded by AHRQ Grant (P30) HS 021667, NCATS 8 UL-1 TR-000043 & Rockefeller CCTS Pilot Grants

4 PBRNs
12 CHCs
319 Patients
318 Specimens

Links: [www.pbrn.ahrq.gov/pbrn-profiles/P30-Centers](http://www.pbrn.ahrq.gov/pbrn-profiles/P30-Centers)
[http://pbrn.ahrq.gov/sites/default/files/docs/page/N2.pdf](http://pbrn.ahrq.gov/sites/default/files/docs/page/N2.pdf)
Clonal Distribution of Nasal and Wound Isolates, MRSA and MSSA Results

Molecular Types of Methicillin-Resistant Staphylococcus aureus and Methicillin-Sensitive S. aureus Strains Causing Skin and Soft Tissue Infections and Nasal Colonization, Identified in Community Health Centers in New York City

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Laboratory of Microbiology and Infectious Disease, The Rockefeller University, New York, NY, USA; Department of Biochemistry and Molecular Biology, Penn State University, University Park, Pennsylvania, USA; The Rockefeller University Center for Clinical and Translational Science, New York, New York, USA; Urban Health Center, Bronx, New York, USA; Hudson River Health Care, Poughkeepsie, New York, USA; Open Door Family Medical Center, Ossining, New York, USA; Manhattan Physicians Group—230th Street Clinic, New York, New York, USA; Laboratory of Molecular Genetics, Instituto de Tecnologia Química e Biológica (ISTQB/UL) Oeiras, Portugal

In November 2011, The Rockefeller University Center for Clinical and Translational Science (CCTS), the Laboratory of Microbiology and Infectious Disease, and Clinical Directors Network (CDN) launched a research and learning collaborative project with six community health centers in the New York City metropolitan area to determine the nature (clonal type) of community-acquired Staphylococcus aureus strains causing skin and soft tissue infections (SSTIs). Between November 2011 and March 2013, wound and nasal samples from 129 patients with active SSTIs suspicion for S. aureus were collected and characterized by molecular typing techniques. Of the 129 patients, the skin wounds were infected by S. aureus methicillin-resistant S. aureus (MRSA) was recovered from 39 wounds and methicillin-sensitive S. aureus (MSSA) was recovered from 24. Most (46 of the 63) wound isolates belonged to the CC8/Pontiac-Valentine leukocidin-positive (PVL+) group of S. aureus clonal USA300. 34 of these strains were MRSA and 12 were MSSA. Of the 63 patients with S. aureus infections, 30 were also colonized with S. aureus in the nares: 16 of the colonizing isolates were MRSA, and 14 were MSSA, and the majority of the colonizing isolates belonged to the USA300 clonal group. In most cases (79%), the colonizing isolate belonged to the same clonal type as the strain involved with the infection. In three of the patients, the identity of invasive and colonizing MRSA isolates was further documented by whole-genome sequencing.

### Table 1 Distribution of S. aureus isolates grouped by clonal complex

<table>
<thead>
<tr>
<th>MLST</th>
<th>Total</th>
<th>Wound</th>
<th>Nasal</th>
</tr>
</thead>
<tbody>
<tr>
<td>CC8</td>
<td>69</td>
<td>34</td>
<td>12</td>
</tr>
<tr>
<td>CC30</td>
<td>12</td>
<td>2</td>
<td>4</td>
</tr>
<tr>
<td>CC5</td>
<td>6</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>CC15</td>
<td>6</td>
<td>0</td>
<td>2</td>
</tr>
<tr>
<td>CC121</td>
<td>3</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>ST2</td>
<td>2</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>CC1</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>CC45</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>CC88</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>CC97</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>CC152</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>CC398</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Total</td>
<td>104</td>
<td>39</td>
<td>24</td>
</tr>
</tbody>
</table>

### Table 2 Distribution of wound isolates belonging to clonal complex CC8

<table>
<thead>
<tr>
<th>S. aureus type and clone type</th>
<th>No. of wound isolates</th>
</tr>
</thead>
<tbody>
<tr>
<td>MRSA</td>
<td>USA300 (t008/ST8/SCCmecVa/PVL+/ACME+) 21</td>
</tr>
<tr>
<td>Other spa types</td>
<td>7</td>
</tr>
<tr>
<td>PVL+</td>
<td>0</td>
</tr>
<tr>
<td>ACME+</td>
<td>2</td>
</tr>
<tr>
<td>Other</td>
<td>4</td>
</tr>
<tr>
<td>Total</td>
<td>34</td>
</tr>
<tr>
<td>MSSA</td>
<td>USA300-like (t008/ST8/PVL+/ACME+) 3</td>
</tr>
<tr>
<td>Other spa types</td>
<td>1</td>
</tr>
<tr>
<td>PVL-</td>
<td>0</td>
</tr>
<tr>
<td>ACME-</td>
<td>4</td>
</tr>
<tr>
<td>Other</td>
<td>4</td>
</tr>
<tr>
<td>Total</td>
<td>12</td>
</tr>
</tbody>
</table>

**Results: Baseline Data – Staph Contamination**

Contamination with MRSA or MSSA by Surface Material

<table>
<thead>
<tr>
<th>Household Contamination Score (n=120)</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>No Contamination (0 surfaces)</td>
<td>46.2%</td>
</tr>
<tr>
<td>Moderate Contamination (1-3 surfaces)</td>
<td>36.1%</td>
</tr>
<tr>
<td>High Contamination (&gt;4 surfaces)</td>
<td>17.6%</td>
</tr>
</tbody>
</table>

Mean: 1.64 ± 2.36

Range: (0, 12)
**What made the partnership work:**

**Aim 1:** To evaluate the comparative effectiveness of a CHW/Promotora-delivered home intervention (Experimental Group) as compared to Usual Care (Control Group) on the primary patient-centered and clinical outcome (SSTI recurrence rates) and secondary patient-centered and clinical outcomes (pain, depression, quality of life, care satisfaction) using a two-arm randomized controlled trial (RCT)

**Aim 2:** To understand patient-level factors (CA-MRSA infection prevention knowledge, self-efficacy, decision-making autonomy, prevention behaviors/adherence) and environmental-level factors (household surface contamination, household member colonization, transmission to household members) associated w/diffs in SSTI recurrence rates

**Aim 3:** To understand interactions of the intervention with bacterial genotypic and phenotypic variables on decontamination, decolonization, SSTI recurrence, and household transmission

**Aim 4**
To explore the evolution of stakeholder engagement and interactions among patients and other community stakeholders with practicing community-based clinicians and academic laboratory and clinical investigators over the duration of the study period
Conclusion:
We are Hunting an Important Microbe which serves as a Metaphor for the Best of Medicine and the Worst of Medicine

MRSA: Elusive & Rapidly Spreading & Mutating Bacteria
- Multiple clones
- Different phenotypes
- Geographic heterogeneity
  - Inappropriate Antibiotics Prescribing by Clinicians
  - Inadequate Antibiotic Medication Adherence by Patients
  - Differential Access to Care and Pharmaceuticals
  - Increasing Concentrations of Antibiotics by Pharmaceutical Manufacturing and Animal Husbandry Practices that are Flooding the Environment and Food Supply
  - Antibiotic Stewardship by the Health Care and Agriculture/Food Industries

MRSA Project: A Model System of \textit{in-vivo/in-situ} Research that combines
- Clinical and Public Health Surveillance
- Clinical Practice/Community-based Comparative Effectiveness Research
- Health and Environmental Policy
- Embedded Mechanistic Research about Evolution of Antibiotic Resistance
  \(\rightarrow\) Interactions of microbial genomics & evolution with the health care system & environment
Community-Associated Methicillin-Resistant Staphylococcus aureus (CA-MRSA) Surveillance Network CA-MRSA Project (CAMP1)

Goals:

1. Define the incidence of CA-MRSA in New York area Community Health Centers (CHCs)
2. Insure that CHCs clinicians have the training to provide optimal care to patients with CA-MRSA
3. Identify the substrains of MRSA responsible for the infections
4. Assess the relationship between MRSA colonizing a patient’s nose and the MRSA causing the clinical infection
5. Build a respectful, enduring, bidirectional partnership and network infrastructure for conducting and disseminating future studies
CA-MRSA Molecular Epidemiology:
(T1 Laboratory Investigator Expertise/Interest)

Molecular profile of USA 300 MRSA wound isolates

All MRSA wound isolates belonging to the USA 300 clone (ST 8) were:
- pvl +
- ACME type I

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The Rockefeller University Hospital
CENTER FOR CLINICAL AND TRANSLATIONAL SCIENCE

CDN CLINICAL DESIGN NETWORK
www.CDNNetwork.org
Environmental Samples vs. Isolates:
So many species where to begin...

One Codex: A Sensitive and Accurate Data Platform for Genomic Microbial Identification, Samuel S Minot, Niklas Krumm, Nicholas B Greenfield
bioRxiv 027607; doi: https://doi.org/10.1101/027607