
Christopher J. Crnich, MD PhD 1,2#

Megan Duster, MT (ASCP) 1

Simone Warrack 1

Dennis Maki, MD 1

Nasia Safdar, MD PhD 1,2

Short Title: MRSA genotyping

# Corresponding author, email: cjc@medicine.wisc.edu; phone: 1-608-262-4558; fax: 1-608-263-4464; address: 1685 Highland Avenue, MFCB 5217, Madison, WI, 53705

1 University of Wisconsin, School of Medicine and Public Health, Madison, WI

2 William S. Middleton Veterans Affairs Hospital, Madison, WI
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Abstract: Pulsed-field gel electrophoresis (PFGE) is a common method used to type methicillin-resistant Staphylococcus aureus (MRSA) in nosocomial investigations and epidemiological studies but is time consuming and methodologically challenging. We compared typing results obtained using a commercial repetitive-element PCR (rep-PCR) system with PFGE in a sample of 86 unique MRSA isolates recovered from subjects in an academic referral hospital and two nursing homes in the same geographic region. Both methods reliably assigned isolates to the same Centers for Disease Control and Prevention (CDC) pulsotype. PFGE was significantly more discriminatory (Simpson’s Index of Diversity = 0.92 at the 95% strain similarity threshold) than the commercial rep-PCR system (Simpson’s Index of Diversity = 0.58). The global (Adjusted Rand coefficient = 0.10) and directional congruence (Wallace_{repPCR \parallel PFGE} = 0.06; Wallace_{PFGE \parallel repPCR} = 0.52) between the two methods was low. MRSA strains recovered from study nursing homes that were clonal when typed by the commercial rep-PCR method were frequently noted to be genetically distinct when typed using PFGE. These data suggest that the commercial rep-PCR has less utility than PFGE in small-scale epidemiological assessments of MRSA in healthcare settings.
Introduction:

Methicillin-resistant Staphylococcus aureus (MRSA) is an important cause of nosocomial infections in healthcare facilities (1-3). Strain typing of MRSA isolates has become an indispensable epidemiological tool used to identify reservoirs as well as the routes and patterns of transmission of MRSA in these settings (4, 5). Pulsed-field gel electrophoresis (PFGE), a macro-genomic strain typing approach, is the most commonly employed method used for identifying MRSA clusters in healthcare facilities (6). Nevertheless, PFGE remains an effort-intensive and technically demanding procedure with a long turn-around time (2-4 days) prompting a search for alternatives.

Recently, an automated repetitive-element-based PCR (rep-PCR) method that amplifies non-coding repetitive sequences interspersed within the MRSA genome has been commercialized (DiversiLab System™, bioMérieux, Marcy l'Étoile, France) and marketed as an alternative to PFGE. This commercial rep-PCR typing method employs microfluidic technology to automate separation and detection of amplified genomic DNA and is paired with a software platform that facilitates interpretation and reporting of typing data (7). Typing data generated by the commercial rep-PCR typing method are generally available within 24 hours and results are highly reproducible across different lab settings.

While shorter result turnaround and improved inter-laboratory reliability are potential advantages of rep-PCR, its capacity to discriminate between genetically distinct MRSA isolates relative to PFGE remains poorly understood. Comparisons of PFGE and rep-PCR based on collections of MRSA isolates recovered during outbreaks have demonstrated reasonable congruence between the two typing methods (8-12). Conversely, comparative studies based on more diverse
collections of MRSA isolates that one might expect to encounter in non-outbreak conditions have found that rep-PCR is less discriminatory than PFGE (13-15). Based on these findings, several authors have recommended that MRSA isolates assigned to the same cluster by rep-PCR undergo confirmatory typing by PFGE (10, 13, 15). This recommendation assumes that rep-PCR is discriminatory enough to obviate a need for PFGE in most situations and that there is directional congruence with PFGE (i.e., isolates clustered by PFGE are also clustered by rep-PCR). Whether these assumptions are valid and whether a tiered typing strategy is practical (rep-PCR □ PFGE | clustering by rep-PCR) for examining patterns of MRSA in non-outbreak situations has not been examined in detail.

The primary objectives of this study were to: 1) assess the discriminatory power of a rep-PCR typing method and PFGE; 2) measure the global and directional congruence of these two typing methods; and 3) assess the practicality of using a tiered approach (rep-PCR □ PFGE | clustering by rep-PCR) to type MRSA isolates recovered from healthcare facilities not currently experiencing an outbreak. To achieve these objectives, we prospectively typed MRSA isolates recovered from two epidemiological studies of MRSA in three regional healthcare facilities (1 hospital and 2 nursing homes) using the commercial rep-PCR typing method and PFGE. Discriminatory power and congruence between the two typing methods were calculated in aggregate using MRSA isolates recovered from study subjects in all three healthcare facilities. Further analyses based on MRSA isolates recovered from subjects in study nursing homes were performed to assess the performance of the typing methods at a facility-level and assess the practicality of typing MRSA isolates using a tiered approach (rep-PCR □ PFGE | clustering by rep-PCR).

Materials and Methods:
**Bacterial Isolates:** A total of 86 MRSA isolates were included in the analyses. 36 MRSA isolates were collected over a 4-year period (May 2002 – May 2006) from hospitalized subjects participating in a longitudinal cohort study of antibiotic-resistant bacteria in a 566-bed teaching hospital in the Midwest. In this study, 486 adult subjects (age > 17) with an anticipated length of stay ≥ 72 hours were randomly recruited from all eligible admissions. 95% of the eligible subjects approached by research staff provided consent and underwent multi-anatomical sampling to detect MRSA colonization. The overall prevalence of MRSA colonization identified in this cohort study was 7.5%. An additional 50 MRSA isolates were recovered from subjects participating in a longitudinal study of MRSA colonization in two nursing homes in the same region. Cohort inception in this study occurred in 2008 in one facility and 2009 in the other facility. Specimen collection in each of these two facilities occurred over a period of one week. MRSA isolates in both studies were recovered by swabbing subject nares, skin of the axilla and groin and skin of the peri-rectal region using sterile Dacron-tipped swabs (BBL™ CultureSwab™ Liquid Stuart, Becton Dickenson, Franklin Lakes NJ). Additional surface cultures of open wounds and insertion sites of indwelling medical devices were performed when present. Only the first non-duplicate MRSA isolate recovered from a participating subject was included in this study. All isolates collected from subjects enrolled in both cohort studies were processed and analyzed at the University of Wisconsin Infectious Disease Research Laboratory.

**Bacteriology:** Swab specimens were vortexed in trypticase soy broth (TSB, Remel, Lenexa, KS) supplemented with 6.5% NaCl and allowed to incubate at 37°C for 24 hours (16). 50 mL of broth was then plated onto mannitol salt agar (Remel, Lenexa, KS) containing cefoxitin (4 mg/mL) (MSFOX) and allowed to incubate for an additional 48 hours and examined for growth (16). S. aureus isolates were identified using standard microbiological methods,
including Gram stain, catalase test and coagulase test. The Kirby Bauer Disk Diffusion method was used to confirm resistance to cefoxitin (17). Isolates were stocked in TSB containing 20% glycerol and stored at -80°C until typing.

Pulsed Field Gel Electrophoresis (PFGE): Preparation of chromosomal DNA and Smal endonuclease restriction was performed using previously described methods (18, 19) with slight modifications; isolates were grown in TSB rather than brain heart infusion broth. PFGE was performed using a contour-clamped homogeneous electric field (CHEF) apparatus (GenePath System, Bio-Rad, Hercules, CA) using the following run parameters: 200v (6 v/cm); temperature, 14°C; initial switch, 5.3 seconds; final switch, 34.9 seconds; and total time, 20 hours. Salmonella serotype Braenderup strain H9812 was loaded onto gels as a bacteriological molecular size standard to facilitate comparisons of banding patterns across gels (20). After the electrophoresis run was completed, gels were stained with ethidium bromide (Promega H5041, 10 mg/ml; Promega, Corporation, Madison, WI), photographed and digitized as a TIFF image using a Gel Doc 2000 and Quantity One Software, version 4.6.3 (Bio-Rad Life Sciences, Hercules, CA). Analyses of gel images were performed using Gel Compar II, version 6.5 (Applied Maths, Austin, TX). An unweighted pair group method with arithmetic mean (UPGMA) clustering algorithm (20) was used to create a hierarchical dendrogram and the genetic similarity between isolates was calculated using the Dice coefficient (21). Band position tolerance and optimization were set at 1.25% and 0.5%, respectively (19). Study isolates were assigned a numerical code based on genetic similarity (at the 100%, 95% and 80% similarity thresholds) to isolates maintained in the University of Wisconsin Infectious Disease Research Laboratory.
Repetitive-Element PCR: Typing of MRSA isolates was performed using the DiversiLab System™ (bioMérieux, Marcy l’Etoile, France) according to manufacturer instructions. Microbial DNA from study isolates was extracted using an Ultraclean Microbial DNA Isolation kit (Mo Bio Laboratories, Carlsbad, CA). Rep-PCR was performed using a Staphylococcus Fingerprinting kit (bioMérieux, Marcy l’Etoile, France) with Ampli-Taq DNA polymerase (Applied Biosystems [ABI], Foster City, CA). Thermal cycling parameters were as follows: initial denaturation at 94°C for 2 minutes; 35 cycles of denaturation at 94°C for 30 seconds, annealing at 45°C for 30 seconds, and extension at 70°C for 90 seconds; and a final extension at 70°C for 3 minutes. The resulting product was loaded onto a microfluidics chip containing a fluorescent gel-dye matrix and product amplicons were separated using a 2100 Bioanalyzer instrument (Agilent Technologies, Palo Alto, CA) so that each fluorescent peak represents a single amplified region of the isolate genome. The fluorescence and corresponding banding patterns for all isolates were analyzed using the Diversilab System™ Software, version 3.4. The Kullbeck-Leibler Divergence estimator (22) was used to determine the similarity between the overlaid pattern peaks and UPGMA (20) was used to create dendrograms of study isolates. The Diversilab System™ software’s pattern overlay function was used to assign MRSA isolates to pattern groups for comparisons with PFGE.

Comparison of PFGE and rep-PCR typing: A comparison of PFGE with rep-PCR was performed using all 86 MRSA isolates recovered from subjects in the three study healthcare facilities. Comparisons were performed according to the framework proposed by Çarrico (23) using an online tool available on the Comparing Partitions website (accessible at: http://darwin.phyloviz.net/ComparingPartitions/index.php?link=Home). 80%, 95% and 100% Dice coefficient thresholds were used to determine strain relatedness by PFGE. The 95% (1 to 4
band differences) and 80% (5 to 8 band differences) similarity thresholds were of particular interest as these typically reflect isolates that differ by ≤1 versus ≥2 mutational events involving the restriction endonuclease site (24). These thresholds are consistent with guidelines published by the European Society of Clinical Microbiology and Infectious Diseases (25). The Diversilab System™ software’s pattern overlay function was used to determine strain relatedness by rep-PCR. By this approach, isolates with identical banding and fluorescent intensity patterns were assigned to the same group, otherwise they were assigned to a unique group.

The extent to which PFGE and rep-PCR assigned study MRSA isolates to the same CDC pulsotype was performed. Using the K-Nearest Neighbor clustering algorithm (26), each isolate was assigned to a Centers for Disease Control and Prevention (CDC) PFGE pulsotype (19) based on the resulting PFGE banding pattern relationship to a library of MRSA isolates maintained by the CDC. The Diversilab System™ Software independently assigned study isolates to a CDC pulsotype using a reference MRSA library maintained by the manufacturer.

Discrimination and congruence comparisons between rep-PCR and PFGE at the 80% (PFGE-80) and 95% (PFGE-95) strain similarity thresholds were performed. Simpson’s Index of Diversity (SID) was used to measure each typing method’s ability to discriminate between genetically unique MRSA strains in the study sample (27, 28). Probabilities of finding differences between SID’s as or more extreme than those observed for rep-PCR, PFGE-80 and PFGE-95 were calculated using a jackknife pseudo-values resampling method (29). Global (adirectional) congruence between rep-PCR, PFGE-80 and PFGE-95 was assessed using the Adjusted Rand coefficient (30). The Adjusted Rand coefficient is conceptually similar to a Kappa coefficient as it provides the overall concordance taking into account that agreement between typing methods may arise by chance alone. Directional congruence between the typing
methods was assessed using the Adjusted Wallace (W) coefficient (31, 32). While also a measure
of congruence, the Adjusted Wallace coefficient differs from the Adjusted Rand coefficient in
that it reflects the probability that isolates clustered together by one method will also cluster
together when typed by a second method. By this approach, isolates clustered together by a
highly discriminatory typing method will generally cluster together when typed using a less
discriminatory method (high coefficient). Typing isolates in the opposite sequence usually results
in a lower coefficient, hence the directional nature of this measure. Confidence intervals for the
Adjusted Rand and Wallace coefficients were estimated using a jackknife pseudo-values
resampling method (29). Facility-level comparisons between rep-PCR and PFGE-95 were
performed using MRSA isolates contemporaneously recovered from subjects in the two study
nursing homes.

Results:

PFGE Typing: 83 of 86 study isolates were assigned to one of four genetically related
clusters using the 80% strain similarity threshold (PFGE-80) with three isolates exhibiting a
unique banding pattern (number of partitions = 7; Table 1). As expected, using a more stringent
threshold for strain similarity identified significantly more diversity in study facilities. 64 of the
86 isolates were assigned to one of 12 clusters using a 95% strain similarity threshold (PFGE-95;
number of partitions = 34; Table 1) and 53 of 86 isolates were assigned to one of 12 clusters
using a 100% strain similarity threshold (PFGE-100; number of partitions = 45; Table 1). When
comparing study MRSA isolates to the CDC MRSA library, 70 of 86 (81.3%) isolates were
assigned to the USA100 CDC pulsotype group and 9 of the 86 isolates (10.5%) were assigned to
the USA300 pulsotype group. The remaining 7 isolates were assigned to the USA500/Iberian (n
= 2), USA700 (n = 2), USA400 (n = 1), USA800 (n =1), and Group D (n = 1) pulsotype groups.
Rep-PCR Typing: 82 of the 86 isolates were assigned to one of 7 genetically related clusters using rep-PCR and four MRSA isolates were considered genetically unique by this typing method (number of partitions = 11, Table 1). Rep-PCR assigned 71 (82.6%) of the isolates to the USA100 pulsotype and 11 (12.8%) to the USA300 pulsotype. The remaining 4 isolates were assigned to the USA700 (n = 2), USA400 (n = 1), and USA800 (n = 1) pulsotype groups. Overall, 83 of the 86 (96.5%) study isolates were assigned to the same CDC pulsotype by rep-PCR and PFGE. Two isolates assigned to the USA300 pulsotype by rep-PCR were assigned to the USA500/Iberian pulsotype group by PFGE; this has been previously reported (11). One isolate assigned to the USA100 pulsotype group by rep-PCR was assigned to the Group D pulsotype by PFGE.

Strain Discrimination and Concordance of Typing Methods: PFGE was highly discriminatory at the 95% similarity threshold (Simpson’s Index of Diversity = 0.92; Table 1) but demonstrated poor discrimination between study isolates at the 80% strain similarity threshold (Simpson’s Index Diversity = 0.33; Table 1). Rep-PCR was more discriminatory than PFGE-80 (Simpson’s Index of Diversity = 0.58; Table 1) and this difference was statistically significant (P-value < 0.001). Rep-PCR was considerably less discriminatory than PFGE-95 and this difference was also statistically significant (P-value < 0.001).

Global congruence between rep-PCR and PFGE at different similarity thresholds (80% and 95%), as determined by the Adjusted Rand coefficient was low (Table 2). The Adjusted Rand coefficient from the comparisons between rep-PCR and PFGE dropped from 0.47 for PFGE-80 to 0.10 for PFGE-95. The directional congruence going from rep-PCR to PFGE-80 was high (Adjusted Wallace = 0.89; Table 3) suggesting that isolates assigned to a cluster by rep-PCR had a high probability of being assigned to the same cluster when typed by PFGE-80.
However, directional congruence with PFGE-95 was substantially lower (Adjusted Wallace = 0.06; Table 3). When examined in the other direction, there was a low to moderate probability that isolates assigned to the same cluster by PFGE-80 (Adjusted Wallace = 0.32; Table 3) and PFGE-95 (Adjusted Wallace = 0.52; Table 3) would be assigned to the same cluster when typed by rep-PCR.

Facility-Level Comparisons: A total of 50 MRSA isolates recovered from subjects in the two study nursing homes were typed using rep-PCR and PFGE-95 (Figures 1 and 2). In general, patterns of discrimination and congruence identified in the overall study sample were re-demonstrated at the facility-level. The ability of rep-PCR to discriminate between different strains of MRSA in the first nursing home was moderate (SID = 0.77; Figure 1) but was low in the second (SID = 0.21; Figure 2). PFGE-95 performed equally well in both settings (SID = 0.90; Figures 1 and 2). Global and directional congruence between the two measures was generally low although the probability that isolates assigned to the same cluster by PFGE-95 also being assigned to the same cluster by rep-PCR was high in second nursing home (Adjusted Wallace = 0.93; Figure 2). While both methods consistently assigned strains to the same CDC pulsortype (48/50 [96%] of isolates were assigned to the same pulsortype by both methods), strains identified as genetically related (i.e., clustered) by rep-PCR were frequently identified as genetically distinct by PFGE-95. For example, in the second study nursing home (Figure 2), rep-PCR assigned 32 of the 36 recovered isolates to a single cluster (designated pattern “A”). However, PFGE-95 assigned these 32 isolates to 12 different clusters, the largest of which contained 10 isolates (designated pattern “0113”). Isolates assigned to the same cluster by PFGE-95 were rarely assigned to different clusters by rep-PCR. For example, four isolates were assigned to the same cluster by PFGE-95 (designated pattern “0100”) in the first study nursing home (Figure 1)
but segregated out as a unique patterns (designated as patterns “A” and “B”) when typed by rep-PCR.

Discussion:

Strain typing is an important tool for investigations of nosocomial outbreaks and research studies that focus on determinants of MRSA spread in different healthcare settings. PFGE has long been considered the “gold standard” of strain typing methods but it remains a time-consuming procedure that requires considerable levels of laboratory expertise. Rep-PCR is a typing method with several attractive features, including shorter turn around times, high degrees of reproducibility and greater methodological simplicity.

In the current study, we found that rep-PCR performed as well as PFGE in assigning MRSA isolates to respective CDC clonal groups and was marginally more discriminatory than PFGE when using liberal thresholds of genetic relatedness between isolates (>80% similarity). However, rep-PCR was significantly less discriminatory than PFGE when more rigorous thresholds were employed (>95% similarity). These findings are consistent with other published studies that have examined the discriminatory power of both typing methods (9, 10, 13-15).

Despite lower levels of discrimination, initial studies demonstrated a reasonable congruence between rep-PCR and PFGE (8, 9). However, MRSA isolates in these studies were selected based on their inclusion in clusters that had previously been identified by PFGE. As shown in this study and others (15, 23), the extent of congruence between two typing methods can be influenced by the order in which they are performed. Pre-selecting isolates using a more discriminating typing method introduces a systematic bias that increases the probability that isolates will be clustered when typed by a second, perhaps less discriminatory, method. In the
current study, higher Wallace coefficients were observed when assessing directional congruence
from PFGE to rep-PCR and this may partially explain the high degrees of concordance between
these typing methods in earlier studies.

The level of global congruence between rep-PCR and PFGE has not been well studied. In the
current study, Adjusted Rand coefficients for rep-PCR and PFGE were low, regardless of the
strain similarity threshold employed. These findings are consistent with a recent study of MRSA
isolates recovered from patients hospitalized in a single academic facility over a 12-year period
(15). In this study, global congruence between rep-PCR and PFGE as determined by the
Adjusted Rand coefficient was only 0.08. Global congruence between rep-PCR and PFGE was
higher (Adjusted Rand = 0.56) in a recent study performed using MRSA isolates recovered from
patients receiving care at a VA medical center (33). Patients in this study submitted paired nasal
and wound isolates, which may explain discrepancies with our findings.

Due to its lower level of discrimination, it has been recommended that MRSA isolates
that are clustered by rep-PCR undergo additional typing using a more discriminating method (10,
However, in our study, rep-PCR ruled out clustering in a minority of cases and a majority of
isolates clustered by rep-PCR were found to be genetically distinct by PFGE. For example, 92%
of the 50 MRSA isolates recovered from subjects in the two nursing homes were clustered when
typed using the rep-PCR and 32 of the 36 (89%) isolates recovered from one of these facilities
were assigned to a single cluster (Figure 2). Generalizing our results to similar facilities, it seems
far more efficient to rely on PFGE given its superior capacity to discriminate between genetically
distinct strains of MRSA despite the longer turnaround time with this method. That rep-PCR
may rarely discriminate between strains found to be clonal by PFGE (Figures 1 and 2) suggests
that combining the results of these two typing methods may have some adjunctive value in
research studies (34).

Our study has several limitations that bear mention. Our study was performed in facilities
dominated by hospital-associated MRSA. Rep-PCR may be an efficient alternative to PFGE in
environments experiencing more frequent introductions of community-acquired MRSA given its
capacity to reliably differentiate between USA100 and USA300 strains. Additionally, we did not
perform a formal economic comparison of the two typing methods. While costs of consumables
for PFGE are cheaper than those employed in rep-PCR, it does entail more bench time which
may make overall costs of this typing method higher. A formal analysis that takes these factors
into consideration would be a useful contribution to the literature.

To conclude, rep-PCR proved to be a reasonably easy typing method to employ in our
laboratory and it readily assigned MRSA isolates to appropriate CDC pulsotype groups.
However, rep-PCR was substantially less discriminatory than PFGE and overall congruence
between these methods was poor. Rep-PCR may ultimately prove to be an efficient tool for
assessing the large-scale epidemiology of MRSA but PFGE, based on its greater flexibility and
discriminatory power, appears to be better suited for small-scale epidemiological investigations.
Whether rep-PCR can be combined with PFGE to further enhance the discrimination of MRSA
isolates in highly clonal settings deserves additional study.

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Potential Conflicts of Interest: All authors report no conflicts of interest relevant to this
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323 References:


Table 1. Discriminatory power of rep-PCR and pulsed-field gel electrophoresis

<table>
<thead>
<tr>
<th>Method</th>
<th>No. of Partitions</th>
<th>No. of Clusters</th>
<th>No. of Singletons</th>
<th>SID (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>rep-PCR</td>
<td>11</td>
<td>7</td>
<td>4</td>
<td>0.58 (0.45 – 0.70)</td>
</tr>
<tr>
<td>PFGE-80*</td>
<td>7</td>
<td>4</td>
<td>3</td>
<td>0.33 (0.20 – 0.46)</td>
</tr>
<tr>
<td>PFGE-95**</td>
<td>34</td>
<td>12</td>
<td>22</td>
<td>0.92 (0.88 – 0.96)</td>
</tr>
<tr>
<td>PFGE-100</td>
<td>45</td>
<td>12</td>
<td>33</td>
<td>0.97 (0.95 – 0.98)</td>
</tr>
</tbody>
</table>

PFGE = pulsed-field gel electrophoresis; SID = Simpson’s Index of Diversity

* SID (rep-PCR vs. PFGE-80) significantly different (P-value <0.001)

** SID (rep-PCR vs. PFGE-95) significantly different (P-value <0.001)
Table 2. Global concordance of rep-PCR and pulsed-field gel electrophoresis

<table>
<thead>
<tr>
<th>Method</th>
<th>Adjusted Rand Coefficient (95% CI)</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>PFGE-80</td>
</tr>
<tr>
<td>PFGE-95</td>
<td>0.08 (0.03 – 0.12)</td>
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<tr>
<td>rep-PCR</td>
<td>0.47 (0.29 – 0.67)</td>
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</table>

PFGE-80 = pulsed-field gel electrophoresis at 80% strain similarity threshold; PFGE-95 = pulsed-field gel electrophoresis at 95% strain similarity threshold
Table 3. Directional concordance of rep-PCR and pulsed-field gel electrophoresis

<table>
<thead>
<tr>
<th>Method</th>
<th>Wallace Coefficient (95% CI)</th>
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<td>rep-PCR □ PFGE-80</td>
<td>0.89 (0.69 – 1.00)</td>
</tr>
<tr>
<td>rep-PCR □ PFGE-95</td>
<td>0.06 (0.00 – 0.12)</td>
</tr>
<tr>
<td>PFGE-80 □ rep-PCR</td>
<td>0.32 (0.08 – 0.57)</td>
</tr>
<tr>
<td>PFGE-95 □ rep-PCR</td>
<td>0.52 (0.27 – 0.77)</td>
</tr>
</tbody>
</table>

PFGE-80 = pulsed-field gel electrophoresis at 80% strain similarity threshold. PFGE-95 = pulsed-field gel electrophoresis at 95% strain similarity threshold.
Figure 1. Comparison of rep-PCR and pulsed-field gel electrophoresis (PFGE) at 95% strain similarity threshold in Nursing Home #1 (No. of isolates = 14). Dendrogram branches representing multiple isolates are capped by a closed circle. Measures of discrimination and congruence provided in the lower left of the figure (see text for description). The grid in the upper right of the figure demonstrates how each typing method partitioned the isolates recovered from the study facility. In this facility, three of the clusters identified by rep-PCR (A, C, & F) were further sub-divided by PFGE. In contrast, only one of the clusters assigned by PFGE (0100) was further sub-divided by rep-PCR.
Figure 2. Comparison of rep-PCR and pulsed-field gel electrophoresis (PFGE) at 95% strain similarity threshold in Nursing Home #2 (No. of isolates = 36). Dendrogram branches representing multiple isolates are capped by a closed circle. Measures of discrimination and congruence provided in the lower left of the figure (see text for description). The grid in the upper right of the figure demonstrates how each typing method partitioned the isolates recovered from the study facility. In this facility, rep-PCR assigned 32 of the 36 (89%) of the study isolates to the same cluster. PFGE separated this cluster into 12 groups when the 95% similarity threshold was employed. In contrast, a single PFGE cluster (0118) comprised of 2 isolates was further sub-divided by rep-PCR.