

Isolation and Characterization of an Epidemic Methicillin-Resistant *Staphylococcus aureus* 15 Variant in the Central United States[▼]

Epidemic methicillin-resistant *Staphylococcus aureus* 15 (EMRSA-15) and EMRSA-16 are pandemic MRSA strains which have received global attention due to their worldwide spread and increased prevalence. Both are primarily hospital-associated pathogens responsible for a myriad of diseases, ranging from uncomplicated skin infections to life-threatening bacteremia and pneumonia.

EMRSA-15 and EMRSA-16 were first identified in the United Kingdom during the early 1990s and, within a few years, became the predominant health care-associated clones in that country (11, 12, 14). One or both strains have since been detected in the health care settings of many countries, including Denmark (4, 13), Sweden (3, 18), Belgium (13), Spain (10, 15), and Kuwait (20). However, despite the global distribution of these strains, only EMRSA-16 has been found within the United States (9). In this report, we describe the isolation and characterization of an EMRSA-15 variant in the central United States.

A 10-month-old male was admitted to a local children's hospital after developing a facial rash consisting of 2- to 3-mm-size pustular lesions with some shallow ulceration accompanied by fever. MRSA strain CRG1250 was cultured from the rash. As part of a hospital surveillance study, pulsed-field gel electrophoresis (PFGE) (1) was performed and indicated that CRG1250 was related to the classic EMRSA-15 type strain (Fig. 1) with a four-band difference. Although not available for direct comparison, both the EMRSA-15 type D1 strain from Kuwait (20) and EMRSA-15 variant B3 (14) appeared to be highly related to CRG1250 with estimated one- and two-band differences, respectively.

The molecular characterization of EMRSA-15 isolates from various geographical locations has demonstrated that these isolates are multilocus sequence type (MLST) 22 (ST22), accessory gene regulator (*agr*) type 1, and staphylococcal protein A (*spa*) type t022, t032, or t223 (3, 5, 16) and harbor the SCCmec type IV element (3). Phenotypically, EMRSA-15 isolates do not typically produce urease (17) and are commonly resistant to erythromycin and/or ciprofloxacin in addition to methicillin (14). Genotypic analysis (3, 6) indicated that CRG1250 was a single-locus variant of ST22 (a 1-bp change from *glp-1* to *glp-90*), *agr* type 1, *spa* type t223, and SCCmec type IV. CRG1250 did not produce urease as determined by BBL urea agar slants (BD Diagnostic Systems, Sparks, MD) and was resistant to oxacillin, erythromycin, and ciprofloxacin by disk diffusion (2), all consistent with an EMRSA-15 designation.

Most EMRSA-15 strains produce enterotoxin C (SEC) but lack Panton-Valentine leukocidin (PVL) and toxic shock syndrome toxin 1 (TSST-1) (11, 17). However, some EMRSA-15 variants lack SEC or have acquired PVL (14, 20, 22). When screened for toxin-encoding genes by PCR (1, 21), CRG1250 was SEC negative in contrast to classical EMRSA-15 strains but similar to EMRSA-15 variants, such as strains B3 and Kuwait 2968 (14, 20). While classical EMRSA-15 strains and CRG1250 were PCR negative for PVL, CRG1250 additionally harbored the *tst* gene encoding TSST-1.

Taken together, the genotypic and phenotypic characteristics of CRG1250 strongly suggest that this strain is a SEC-

negative, *tst*-positive variant of EMRSA-15. Interestingly, studies, thus far, have failed to identify *tst* in classical or variant EMRSA-15 strains (5, 14). However, the loss of SEC and acquisition of TSST-1 are not altogether surprising since the genes encoding these toxins reside on potentially mobile genetic elements (7, 8).

To our knowledge, this report represents the first observed incidence of EMRSA-15 in the United States. The patient and his immediate family reside in the central United States and

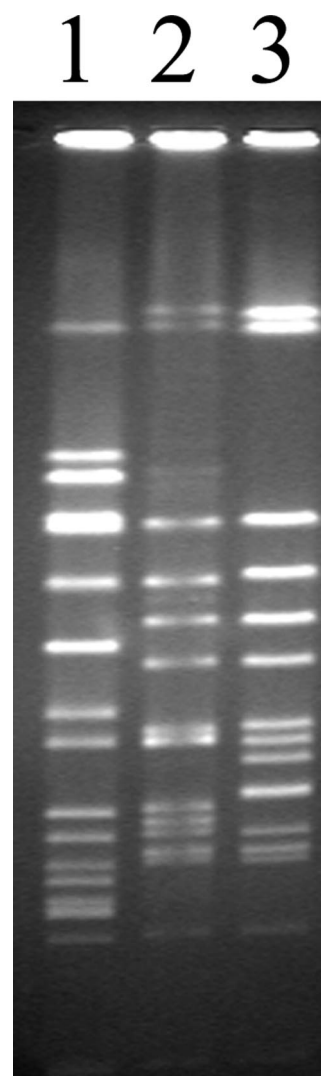


FIG. 1. PFGE analysis of *Sma*I-digested chromosomal DNA from *S. aureus* isolates NCTC8325 (size standard; lane 1), classical EMRSA-15 (lane 2), and CRG1250 (lane 3). The resulting PFGE pattern was compared with known EMRSA strain types as described previously (19) using BioNumerics version 4.6 (Applied Maths, Sint-Martens-Latem, Belgium) with unweighted-pair group arithmetic averages and the Dice coefficient.

had not recently traveled internationally. Thus, this isolate most likely does not represent a direct introduction of EMRSA-15 into the United States but rather a strain currently present in relatively small numbers, since it was the only such isolate we have encountered, which may or may not increase in incidence.

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