

Unraveling the Dynamics of Community-Associated Methicillin-Resistant *Staphylococcus aureus*

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(See the Major Article by Popovich et al on pages 1067–74.)

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Since the first description of the community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) strain USA300 [1] in the 1990s, this pathogen has emerged worldwide [2]. Within a decade, USA300 has become the most prevalent cause of community-acquired *S. aureus* infections in many settings in the United States [3]. Originally causing infections mainly in individuals without recent healthcare exposure, USA300 is increasingly causing hospital-acquired infections. There is, therefore, an urgent need for infection control measures. Although person-to-person transmission in the community must be the driving force of this epidemic [4], transmission dynamics and risk factors for colonization are still not well understood [5]. The study of Popovich et al in this issue of *Clinical Infectious Diseases* [6] is a next step in

elucidating the dynamics of USA300. In their study they demonstrate that, compared to individuals not infected with human immunodeficiency virus (HIV), patients with HIV are more likely to be colonized with USA300 at hospital admission and that they are carrying USA300 at multiple body sites, such as the nares, throat, axillae, inguinal regions, and perirectal area, and in wounds, if present. Importantly, 38.5% of the USA300 carriers would have remained undetected if only nasal cultures had been obtained.

This study emphasizes 2 important aspects in the transmission dynamics of USA300. First, there are patient groups with a higher risk of colonization, but whether this results from more activities with increased transmission risk, higher bacterial load of carriers, and/or a longer duration of carriage is still unknown. Second, there is huge variation in colonization patterns between carriers, but it remains unknown if and how colonization at different sites is related, and whether the duration differs between sites.

These aspects are important for our understanding of the transmission dynamics and for the design of effective infection prevention strategies. For many pathogens (eg, for hospital-associated

MRSA), mathematical models have been used to provide both theoretical and quantitative estimates for intervention strategies [7–9]. If the most important transmission routes are known, such models are cheap and fast alternatives to large-scale intervention studies for comparing the relative effects of different interventions. The few available models for USA300 [10–13] are restricted to subpopulations, either incarcerated persons or hospitalized patients, and assume that all individuals in the population are equally susceptible to acquire USA300. More complex models, integrating spread in the community and within healthcare and other relevant settings, are not available, reflecting our lack of knowledge of the transmission dynamics. There are at least 5 important unknowns in the USA300 transmission dynamics: (1) the duration of carriage with USA300 at different body sites; (2) the interaction between USA300 and other *S. aureus* genotypes (both MRSA and methicillin-susceptible *S. aureus*); (3) the modes of spread of USA300, that is, the relative importance of sexual contacts, use of shared equipment, or transmission through temporarily contaminated hands of healthcare workers; (4) heterogeneity

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between different groups of individuals; and (5) interaction between these different groups.

The duration of infectiousness is unknown. Two studies in young healthy persons revealed that 4% of new military recruits carried CA-MRSA, including USA300, and 33%–35% were still colonized after 8–10 weeks [14, 15]. Others have reported infections that developed immediately after acquisition (ie, bypassing the colonization state) [16, 17]. However, a mean duration of colonization of several weeks would require high transmission rates to prevent USA300 from going extinct. If that is not the case, the USA300 epidemic could still be explained if the average duration of colonization is much longer and has been underestimated in studies because of misclassification (ie, too-low test sensitivity or screening restricted to the nares), or if there is substantial heterogeneity in transmission capacity of USA300 in subgroups (ie, there are certain core groups that drive the epidemic). Transmission also occurs frequently within sporting teams, among men having sex with men [18], in daycare centers, and in jails [13, 19], which implies that mathematical models for USA300 should incorporate nonhomogeneous mixing patterns.

Only 80% of the human population seems susceptible to colonization with *S. aureus*, and only half of them are persistently carrying *S. aureus* in the nares [20]. Whether this also applies to USA300 is currently unknown. Another aspect that is not well understood is immunity against USA300, or any other *S. aureus* genotype. Antibodies against *S. aureus* and immunological memory seem insufficient to prevent reinfection. Yet, *S. aureus* carriers had lower mortality from subsequent bacteremia caused by other *S. aureus* genotypes than noncarriers, suggesting immune modulation of the inflammatory response in carriers [21]. Yet, to the best of our knowledge, no evidence exists that immunity affects carriage with *S. aureus*.

There may also be interaction between USA300 and other *S. aureus* strains, for example, due to colonization resistance. If colonization with USA300 would be mutually exclusive with other *S. aureus* genotypes, the total population at risk would be markedly lower, and deliberate colonization with *S. aureus* could be an effective preventive measure for spread of USA300. However, data suggest otherwise. Patients with USA300 skin and soft-tissue infection are frequently colonized in other sites than the nares [6, 22, 23], and military recruits with and without *S. aureus* colonization had similar acquisition rates of CA-MRSA [15]. Finally, parameters may change over time, such as antibiotic selective pressure or susceptibility of populations for *S. aureus* colonization (eg, due to pneumococcal vaccination).

Some countries have maintained extremely low nosocomial infection rates of MRSA by nationwide use of stringent infection-control measures. Whether such measures will be effective in countries with frequent transmission of USA300 in the community is unknown. In theory, rapid identification of carriers followed by contact precautions for carriers might be effective [7]. Extramural spread of USA300, however, may rapidly exhaust isolation capacity and nosocomial spread of USA300 will further compromise effective control strategies [24–26]. In fact, a scenario in which USA300 outcompetes other MRSA genotypes in hospital settings is far from excluded [12], especially when USA300 would acquire additional resistance traits. This could reprise the mid-20th century penicillin-resistant staphylococcal pandemic [27]. However, as the natural history of USA300 colonization and disease (eg, duration of carriage, immunity and interference with other genotypes, and the relevant network structures within the population) have not been adequately characterized, proper forecasts of the USA300 epidemiology are difficult and we strongly advocate more well-designed studies to determine these critical unknowns.

Notes

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References

1. Mediavilla JR, Chen L, Mathema B, Kreiswirth BN. Global epidemiology of community-associated methicillin resistant *Staphylococcus aureus* (CA-MRSA). *Curr Opin Microbiol* **2012**; 15:588–95.
2. Nimmo GR. USA300 abroad: global spread of a virulent strain of community-associated methicillin-resistant *Staphylococcus aureus*. *Clin Microbiol Infect* **2012**; 18:725–34.
3. Moran GJ, Krishnadasan A, Gorwitz RJ, et al. Methicillin-resistant *S. aureus* infections among patients in the emergency department. *N Engl J Med* **2006**; 355:666–74.
4. Nair N, Kourbatova E, Poole K, et al. Molecular epidemiology of methicillin-resistant *Staphylococcus aureus* (MRSA) among patients admitted to adult intensive care units: the STAR*ICU trial. *Infect Control Hosp Epidemiol* **2011**; 32:1057–63.
5. Forster AJ, Oake N, Roth V, et al. Patient-level factors associated with methicillin-resistant *Staphylococcus aureus* carriage at hospital admission: a systematic review. *Am J Infect Control* **2012** [Epub ahead of print]. doi:10.1016/j.ajic.2012.03.026.
6. Popovich KJ, Hota B, Aroutcheva A, et al. Community-associated methicillin-resistant *Staphylococcus aureus* colonization burden in HIV-infected patients. *Clin Infect Dis* **2013**; 56:1067–74.
7. Bootsma MCJ, Diekmann O, Bonten MJM. Controlling of methicillin-resistant *Staphylococcus aureus*: quantifying the effects of interventions and rapid diagnostic testing. *Proc Natl Acad Sci U S A* **2006**; 103:5620–5.
8. Robotham JV, Graves N, Cookson BD, et al. Screening, isolation, and decolonisation strategies in the control of methicillin resistant *Staphylococcus aureus* in intensive care units: cost effectiveness evaluation. *BMJ* **2011**; 343:d5694.
9. Cooper BS, Medley GF, Stone SP, et al. Methicillin-resistant *Staphylococcus aureus* in hospitals and the community: stealth dynamics and control catastrophes. *Proc Natl Acad Sci U S A*, **2004**; 101:10223–8.
10. D'Agata EM, Webb GF, Pressley J. Rapid emergence of co-colonization with community-acquired and hospital-acquired methicillin-resistant *Staphylococcus aureus* strains in the hospital setting. *Math Model Nat Phenom* **2010**; 5:76–73.

11. Pressley J, D'Agata EM, Webb GF. The effect of co-colonization with community-acquired and hospital-acquired methicillin-resistant *Staphylococcus aureus* strains on competitive exclusion. *J Theor Biol* **2010**; 264:645–56.
12. D'Agata EM, Webb GF, Horn MA, Moellering RC Jr, Ruan S. Modeling the invasion of community-acquired methicillin-resistant *Staphylococcus aureus* into hospitals. *Clin Infect Dis* **2009**; 48:274–84.
13. Kajita E, Okano JT, Bodine EN, Layne SP, Blower S. Modelling an outbreak of an emerging pathogen. *Nat Rev Microbiol* **2007**; 5:700–9.
14. Ellis MW, Hospenthal DR, Dooley DP, Gray PJ, Murray CK. Natural history of community-acquired methicillin-resistant *Staphylococcus aureus* colonization and infection in soldiers. *Clin Infect Dis* **2004**; 39:971–9.
15. Ellis MW, Griffith ME, Dooley DP, et al. Targeted intranasal mupirocin to prevent colonization and infection by community-associated methicillin-resistant *Staphylococcus aureus* strains in soldiers: a cluster randomized controlled trial. *Antimicrob Agents Chemother* **2007**; 51:3591–8.
16. Kazakova SV, Hageman JC, Matava M, et al. A clone of methicillin-resistant *Staphylococcus aureus* among professional football players. *N Engl J Med* **2005**; 352:468–75.
17. Hota B, Ellenbogen C, Hayden MK, Aroutcheva A, Rice TW, Weinstein RA. Community-associated methicillin-resistant *Staphylococcus aureus* skin and soft tissue infections at a public hospital: do public housing and incarceration amplify transmission? *Arch Intern Med* **2007**; 167:1026–33.
18. Diep BA, Chambers HF, Graber CJ, et al. Emergence of multidrug-resistant, community-associated, methicillin-resistant *Staphylococcus aureus* clone USA300 in men who have sex with men. *Ann Intern Med* **2008**; 148:249–57.
19. Moellering RC Jr. The growing menace of community-acquired methicillin-resistant *Staphylococcus aureus*. *Ann Intern Med* **2006**; 144:368–70.
20. Wertheim FL, Melles DC, Vos MC, et al. The role of nasal carriage in *Staphylococcus aureus* infections. *Lancet Infect Dis* **2005**; 5:751–62.
21. Wertheim FL, Vos MC, Ott A, et al. Risk and outcome of nosocomial *Staphylococcus aureus* bacteremia in nasal carriers versus non-carriers. *Lancet* **2004**; 364:703–5.
22. Eveillard M, de Lassence A, Lancien E, Barnaud G, Ricard J-D, Joly-Guillou M-L. Evaluation of a strategy of screening multiple anatomical sites for methicillin-resistant *Staphylococcus aureus* at admission to a teaching hospital. *Infect Control Hosp Epidemiol* **2006**; 27:181–4.
23. Nilsson P, Ripa T. *Staphylococcus aureus* throat colonization is more frequent than colonization in the anterior nares. *J Clin Microbiol* **2006**; 44:3334–9.
24. Seybold U, Kourbatova EV, Johnson JG, et al. Emergence of community-associated methicillin-resistant *Staphylococcus aureus* USA300 genotype as a major case of health care-associated blood stream infections. *Clin Infect Dis* **2006**; 42:647–56.
25. Popovich KJ, Weinstein RA, Hota B. Are community-associated methicillin-resistant *Staphylococcus aureus* (MRSA) strains replacing traditional nosocomial MRSA strains? *Clin Infect Dis* **2008**; 46:787–94.
26. Davis SL, Rybak MJ, Amjad M, Kaatz GW, McKinnon PS. Characteristics of patients with healthcare-associated infection due to SCCmec type IV methicillin-resistant *Staphylococcus aureus*. *Infect Control Hosp Epidemiol* **2006**; 27:1025–31.
27. Robinson DA, Kearns AM, Holmes A, et al. Re-emergence of early pandemic *Staphylococcus aureus* as a community-acquired methicillin-resistant clone. *Lancet* **2005**; 365:1256–8.