many important nonstandard indicators of patient care—can easily be extended to hand hygiene surveillance. Because log-ins linked to computers in patient rooms correlate with actual visits by HCWs vis-à-vis hand hygiene opportunities arising from HCW/patient contact, they can also be used to estimate temporal patterns appropriate for effectively monitoring hand hygiene activity levels.

To validate our new method, we used 660 days of UIHC MICU log-in data (September 1, 2006, through June 21, 2008), restricted to those log-ins linked to patient rooms (a total of 1,757 unique users). We then counted the number of unique users who log in for every hour for each day in our data set. For each day and night shift, we then rank ordered each hour on the basis of the number of unique individual log-ins observed (the choice of this metric was motivated by our simulations of hand hygiene compliance, which show that methodologies that favor observing more unique individuals rather than more events results in a better overall estimate of unit compliance, in essence by reducing sample bias in population selection). The resulting distribution of each hour's respective rank is then calculated across the entire data set and validated against a similar rank-order statistic derived from the sensor-mote data, where each hour in the shift is ranked by median number of captured hand hygiene events.

Overall, we found that the observed hourly, unique HCW log-ins in our sensor data set are highly correlated with the same measure in our log-in data, with a Spearman's ρ of 0.86 ($P < .001$).

Choosing a single observation hour on the basis of log-in rank results in selecting the single best hour 22% and 29% of the time for the day and night shift, respectively, a 2.5–3-fold improvement over simply selecting an hour at random. If we instead select the top quartile of hours per shift, it will contain the best hour 47% and 60% of the time for the day and night shift, respectively, a 1.5–2.5-fold improvement over uniform random selection. More generally, because this approach calculates qualitative rankings for each hour, we can both identify alternate candidate hours for observation (eg, the second-best hour to observe) and identify candidates that are consistently the best hours for observation compared with other, more variable candidate hours. By examining the variability (ie, entropy) of a given hour's rankings, we find that the best hours for observation tend to be those with lower variability for a shift—that is, their rankings are more stable across any given day. As a last point, all these results assume a static choice of observation hour across the entire data set. An obvious improvement would be a dynamic schedule in which an algorithm uses a window of recent log-in data to propose different candidate hours, providing real-time guidance to observers on which hours to monitor. We leave this idea for exploration in future work.

Data-driven approaches are being applied to problems in health care with increasing regularity. Improving hand hygiene observation is one such application. Our results show that human observation schedules can be effectively and inexpensively operationalized using data that healthcare facilities already have on hand.

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Acinetobacter calcoaceticus–Acinetobacter baumannii Complex Is Not Equal to *A. baumannii*

To the Editor—We read with great interest the article by Kang et al[1] that investigated the epidemiology and clinical features of community-onset *Acinetobacter baumannii* infections in a medical center in Korea. In this study, Kang and colleagues provide some significant findings to help clinicians better understand the clinical manifestations of *A. baumannii* in-

fections. However, we are seriously concerned that the lack of molecular methods to identify the different genospecies of *Acinetobacter* in this study makes the conclusions doubtful.

A. baumannii is just one genospecies of the group *Acinetobacter calcoaceticus–A. baumannii* complex (ACB complex), which also includes genospecies *A. calcoaceticus*, *A. nosocomialis*, and *A. pittii*.[2] As they are phenotypically similar and difficult to distinguish using routine laboratory methods, they have been proposed as a group. After the introduction of molecular methods to accurately identify each genospecies, the clinical characteristics of each have been clarified, and it has been better realized that every genospecies has its own distinct features. For example, in the latest study by Lee et al,[3] patients with *A. baumannii* pneumonia were more likely to have abnormal hematological findings, lobar pneumonia, significantly higher Acute Physiology and Chronic Health Evaluation II scores, and higher mortality than those with *A. nosocomialis* pneumonia. Thus, they concluded that *A. baumannii* and *A. nosocomialis* nosocomial pneumonia are 2 distinct clinical entities.

In conclusion, we suggest that molecular methods to precisely identify the ACB complex should be conducted in studies of *A. baumannii* infections.

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Reply to Su and Chao

To the Editor—We appreciate the interest of Su and Chao[1] in our study.[2] As *Acinetobacter calcoaceticus*, *Acinetobacter baumannii*, *Acinetobacter* genomic species 3, and *Acinetobacter* genomic species 13TU are very closely related, it has been proposed to refer to these species as the *A. calcoaceticus–A. baumannii* complex (ACB complex). We agree with the comment that molecular methods to precisely identify the ACB complex should be conducted in studies of *A. baumannii* infections. Since the clinically relevant members of the ACB complex cannot be separated by currently available commercial identification systems, such as the Vitek 2, Phoenix, and Microscan systems, *A. baumannii* isolates in our study represent the ACB complex.[2] Species identification with commercial identification systems that are currently used in clinical microbiology laboratories remains problematic, and molecular methods have been developed and validated for identification of *Acinetobacter* species.[3]

Given that *A. baumannii*, *Acinetobacter* genomic species 3, and *Acinetobacter* genomic species 13TU share important clinical and epidemiological characteristics, the need for species identification of the ACB complex in clinical microbiology laboratories is questionable.[3,4] Moreover, *A. calcoaceticus* is the environmental species that has frequently been recovered from soil and water, and the designation "ACB complex" may be misleading and not appropriate if used in a clinical context.[3] The majority of studies that have addressed epidemiological and clinical issues related to *Acinetobacter*, including ours, have not employed identification methods for the ACB complex.[2,3] However, further clinical studies using proper methods for species identification of *Acinetobacter* are warranted to increase our knowledge of the epidemiology, pathogenicity, and clinical implications of the various species of this diverse genus.

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