P1400

Abstract (poster session)

Molecular characterisation of Panton-Valentine leukocidin-positive Staphylococcus aureus in southwestern England

A. Hidalgo-Arroyo*, E. Woodward, J. Leeming, A. Kearns, J. Sunderland, J. Steer, A. Lovering (Bristol, London, Plymouth, UK)

Objectives: In the last decade there has been an increase in PVL toxin-producing (PVL+) meticillin sensitive S. aureus (SA) community-acquired infections in one city in South West England. The objective of this study was to assess whether this was linked to higher nasal carriage rates compared to other cities and to determine whether molecular typing could identify clonal relationships among PVL+ nasal and clinical strains circulating in this region. Methods: In 2009-10, swabs were sent to a representative sample of adults in 3 cities of SW England. Self-taken nasal swabs were returned and cultured for SA. These strains, plus SA isolated from community-acquired infections in each location, were screened for pvl and mecA by PCR. All PVL+ SAs, MRSAs and 181 randomly selected MSSAs were genotyped by spa typing. The multilocus sequence type clonal complex (CC) was then inferred from spa types where possible. Results: SA was recovered from 553 of 1952 nasal swabs (28.3%). Six isolates (1.0%) were PVL+ with no statistically significant association with geographic locality (Chi square test $p>0.05$). In contrast, 28 of 578 (4.8%) clinical isolates were PVL+; 4.3% in city A, 0.6% in city B and 7.8% in city C ($P<0.05$). Only two PVL+ MRSA were detected; one (a nasal isolate from city C) corresponded to the CA-MRSA USA 300 clone, the other (a clinical isolate from city B) corresponded to the emerging multi-resistant CA-MRSA Bengal Bay clone. PVL+ isolates comprised 18 spa types and 9 CCs. All PVL+ nasal isolates had different spa types and CCs. Spa types t008 (CC8) and t355 (CC152) were common in both nasal and clinical PVL+ isolates. In contrast, spa type t417 (CC22) was the most common among clinical PVL+ isolates (10/28, 35.7 %), but was not found among any nasal or PVL negative isolates. Other CC22 spa types were common among both clinical and nasal isolates. Conclusions: Community-acquired infection with PVL+ SA is uncommon in SW England but rates vary geographically. However carriage rates in the nares does not reflect this variation, indicating that community-based nasal screening poorly predicts pvl rates among isolates causing infection. This is consistent with the failure to identify the spa type (t417) accounting for over a third of PVL+ SA clinical isolates among nasal isolates. This clone was not geographically restricted, and the typing data did not suggest any explanation for the high incidence of PVL associated infection in city C.