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Abstract (oral session)

What are we missing? Typing of Staphylococcus aureus protein A (spa) mutants

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Objectives: Spa-typing of Staphylococcus aureus is commonly used to distinguish different strain genotypes in clinical and community studies. However, for individuals who carry strains with rearrangements in the spa gene, conventional spa-typing gives an incomplete picture of colonizing strains. Here we investigate (i) the nature of rearrangements, (ii) the proportion of community and hospital-associated non-typeable strains with rearrangements, and (iii) the impact of rearrangements on the quality of spa-typing. Methods: 2205 clinical and 3905 community S. aureus strains from Oxfordshire were spa-typed using a modified protocol that enables identification of multiple strain colonization. For strains that failed to amplify with the standard set of primers (1095F/1517R), we developed a new forward primer (spaT3-F) with multisite binding within the spa-gene, with which all previously non-typeable samples were successfully amplified. To identify rearrangements that did not affect spa-typing, the whole spa-gene was sequenced for a subset of 99 previously typed strains. Results: We found 8 novel spa gene variants with rearrangements in the IgG-binding region, together with one variant previously described by Baum et al. in 2009. 3 insertions/deletions that affect conventional spa-typing (ie would have led to strains being called “non-typeable” in other studies) were present in 1.8% (72/3905) of carriage samples from 1.8% (8/442) of healthy carriers and 0.6% (14/2205) of clinical samples from 0.7% (9/1273) of inpatients. Patients with mixed infections with strains with and without spa gene variants would previously have been classified as single strain carriers. 11% (11/99) of randomly chosen strains from 11% (11/97) of individuals carried ‘hidden’ deletions that do not affect spa-typing. Spa-types associated with ST398, common among domestic animals, had a higher proportion of strains with deletions (35%) than other groups of spa-types with deletions (1-4%) ($p<0.0001$) and are therefore likely to be underrepresented in most human studies based on spa-typing. Conclusions: A modified spa-typing protocol with a novel forward primer identified previously non-typeable strains in 2% of healthy carriers and 1% of hospital inpatients. Groups of related spa-types with a high proportion of rearrangements are likely to be overlooked in most epidemiological studies based on conventional spa-typing, potentially leading to bias.