

In their letter 'Transmission of *S. aureus* in critical care' the correspondent(s) highlight several limitations of our study and argue that taken together these undermine our conclusion that healthcare workers are infrequently sources of *S. aureus* transmission. While we acknowledge the criticisms made, we do not agree with this analysis.

The key findings of our study are the very high rate of *S. aureus* carriage measured among healthcare workers with the greatest patient contact and how few instances of transmission were detected from these carriers. The correspondent is concerned that by considering directionality we have under-estimated transmission but figure 4 of our paper shows that the same subtype of *S. aureus* was only found in patients and healthcare workers on 17 occasions over the whole study, irrespective of directionality. It does not seem plausible that staff with less contact should account for substantially more transmission. The correspondent is correct that some staff carried *S. aureus* intermittently but not that we identified transient carriage. In fact, in the sub-study where nurses underwent swabbing before and after shifts, we did not identify any transient carriage.

The comprehensive prospective sampling that underpinned our study cannot be achieved across multiple centres and would not add significant value. The issue with generalisability is primarily that the study was done in the presence of robust infection control practice and low rates of MRSA. We believe our results are relevant to similar settings elsewhere but not in settings where robust infection control measures are not sustained.¹

We acknowledge that some patients left the critical care unit quickly and so were only screened once. These patients could have acquired *S. aureus* without this being detected. This would however increase both the acquisition rate and potentially the number of transmissions, rather than be expected to increase the proportion of acquisitions with identified transmissions.

We agree that identifying sources of transmission is difficult but not only because it requires intensive sampling and follow up. Nosocomial *S. aureus* strains are often closely related. We previously demonstrated that insufficiently discriminatory typing techniques are unreliable tools to measure *S. aureus* transmission.² Researchers should hesitate before applying potentially lower-resolution high throughput typing techniques unless their performance in measuring *S. aureus* transmission has been established in comparison with analysis of whole-genome sequence data.

1. Tong SY, Holden MT, Nickerson EK, et al. Genome sequencing defines phylogeny and spread of methicillin-resistant *Staphylococcus aureus* in a high transmission setting. *Genome Res* 2015; **25**(1): 111-8.

2. Price JR, Golubchik T, Cole K, et al. Whole-genome sequencing shows that patient-to-patient transmission rarely accounts for acquisition of *Staphylococcus aureus* in an intensive care unit. *Clin Infect Dis* 2014; **58**(5): 609-18.