Objectives: Over the last 2 decades, the prevalence of MRSA bacteraemia in England has declined from >40% of all *Staphylococcus aureus* bacteraemias to only ~9%. Throughout this period, two clones of MRSA were responsible for 95% MRSA bacteraemias nationally (EMRSA-15, CC22-IVh and EMRSA-16, ST36-II); PVL-MRSA causing bacteraemia have been reported rarely. As the reservoirs of MRSA become more apparent (healthcare, community, livestock and wildlife), the need to monitor for emergence of high risk clones is evident. We sought to probe for changes in the molecular epidemiology of MRSA from bacteraemia cases in England.

Methods: Between October 2012 and September 2013, isolates of MRSA from bacteraemia cases throughout England were characterised by both *spa* and SCC*mec* typing; key virulence and resistance markers were sought by PCR (*luk-PV*, *meca*, *mecC*) and MICs of a range of antibiotics were determined by agar dilution (BSAC method). Patient level demographic, clinical and geographic data were obtained by linking to the national Mandatory Enhanced Surveillance System.

Results: During the study period, 910 MRSA bacteraemia episodes were reported and 433 isolates were received from patients throughout England. Most of the isolates (359; 82.9%) were able to be deterministically linked to mandatory case reports, giving a national sampling proportion, for this study, of 39.5% of all cases. Isolate sampling varied across NHS England area-teams geographies, with the proportions ranging from 15.8 – 88.2% of all cases. Patient demographics for the isolate collection were similar to that seen for all cases. Of the successfully linked cases, 188 (52.4%) were hospital onset. Patient ages ranged from 0 to 103y (median 72y); 62.4% were male. Based on 30 day all-cause mortality data, 103 (28.7%) cases were fatal. Overall, 118 different *spa* types belonging to 16 different MLST clonal complexes were identified, including 5 different SCC*mec* types; 38 (8.8%) were PVL-positive and included representatives of 10 different lineages. CC22 (EMRSA-15) and CC5 predominated (63.5% and 9% respectively); both lineages were frequently resistant to ciprofloxacin and erythromycin. Others included other internationally recognised clones (CC1, 8, 30 and 59).

Conclusion: This molecular epidemiological study of MRSA bacteraemia cases is more comprehensive than those published previously and the data contrast sharply with analyses from earlier years. Against a background of falling MRSA rates, a marked increase in genetic diversity is apparent. Whilst EMRSA-15 remains predominant, its prevalence has decreased from >85% to 64% and this decline has been associated with an increase in diversity. CC5 has displaced EMRSA-16 as the second most frequent lineage. The penetration of CC5 (a lineage known to acquire *vanA*) and multiple PVL-MRSA clones is cause for public health concern. Effective ongoing surveillance of this genetically diverse reservoir is warranted to probe for trends and facilitate the early detection of emerging clones.