

**P2717 Phylogenetics of *mecA* *Staphylococcus haemolyticus* recovered from high-frequency hand-touched surfaces from the public setting in East and West London**Rory Cave\*<sup>1</sup>, Raju Misra<sup>2</sup>, Hermine Mkrtchyan<sup>1</sup><sup>1</sup> University of East London, United Kingdom, <sup>2</sup> National History Museum, United Kingdom

**Background:** *Staphylococcus haemolyticus* is an emerging opportunistic pathogen, primarily isolated from neonatal patients and care units. However, little is known about the genetic diversity and molecular epidemiology of *S. haemolyticus* recovered from general public settings. Whole genome sequencing has been instrumental in studying the genetic diversity and population structure of many important pathogens. We performed whole genome sequencing (WGS) to unveil the molecular epidemiology of *S. haemolyticus* recovered from general public settings in East and West London.

**Materials/methods:** Between November 2016 and September 2017 ten *S. haemolyticus* isolates were recovered from high-frequency hand-touched areas in general public settings and public areas in hospitals in East and West London. Isolates were speciated by MALDI-TOF and the *mecA* gene was determined by PCR. All *mecA* positive isolates were WGS using Illumina HiSeq. Sequenced samples were phylogenetically compared to 73 WGS *S. haemolyticus* isolates recovered from different biological and environmental sources. Maximal likelihood core SNP Phylogenetic tree was constructed using Varscan, which included removing recombination with gubbins and then constructing the phylogenetic tree with RaXML. Unique genes were identified using Roary and classified to specific Clusters of Orthologous Groups (COG) family. Horizontally transferred genes (HTG) were predicted from isolates recovered from public settings in London by HGTector.

**Results:** All 10 *S. haemolyticus* isolates recovered from high-frequency hand-touched areas in public settings were *mecA* positive. The isolates were phylogenetically related to those previously recovered from clinical blood cultures and eye infection, dog and kefir grains. 306 unique genes were identified in isolates recovered from general public settings in London. 34% of these unique genes were involved in replication, recombination and repair. 15-21% of all the genes identified in samples recovered from public setting in London predicted to be a result of HGT. 17 to 29 of these HGT genes were predicted to originate from the *Bacillus* genus.

**Conclusions:** The genetic diversity of *mecA* positive *S. haemolyticus* recovered from high-frequency hand-touched surfaces were phylogenetically related to those recovered from different sources. In this study, we demonstrate that *S. haemolyticus* have acquired a number of genes from other species of bacteria associated mainly with the environment.