Background: Staphylococcus epidermidis is considered to be one of the main causes of nosocomial infection related to prosthetic joint infection (PJI). Biofilm formation is considered to be the major virulence factor of S. epidermidis. icaADBC expression via the ica operon mediates staphylococcal biofilm formation by encoding enzymes for polysaccharide intercellular adhesin (PIA) formation. Little is known of the molecular characteristics of S. epidermidis causing PJI. In this study, MLST was performed with clinical samples of S. epidermidis causing PJI to investigate the relationships amongst clinical features and phylogenetic characteristics of virulent S. epidermidis clones.

Materials/methods: Clinical isolates of S. epidermidis (n=37) obtained from patients with prosthetic joint infection presenting to the Royal National Orthopaedic Hospital, Stanmore, UK, between 2015 to 2017 were cultured overnight in L.B. broth and DNA extracted from bacterial pellets following centrifugation. PCR was performed using primers of the seven housekeeping genes of S. epidermidis: arcC, aroE, gtr, mutS, pyrR, tpiA and yqiL, and amplified DNA sequenced by Sanger sequencing. Sequences were analysed using BioNumerics software and submitted to the central MLST database, which allowed the identification of an MLST type of each S. epidermidis isolate.

Results: A total of 13 sequence types (ST) were obtained from 35 S. epidermidis sample isolates. 2 isolates did not amplify upon PCR. ST2 was the most commonly occurring sequence type (13, 37.1 %) followed by ST5 (6, 17.1%). When the clinical characteristics of patients were analysed, ST2 was dominant in knee (6, 60%) and hip infections (6, 37.5%).
Conclusions: ST2 and ST5 were identified as the major STs causing PJI in this cohort. This finding is consistent with other molecular epidemiological studies and in keeping with the observation that ST2 is the most prevalent ica operon-positive clone. Surveillance of the clinical characteristics and genetic features of *S. epidermidis* should be performed on a larger scale to better identify specific virulence factors related to pathogenesis.