

**P0312**

**Paper Poster Session**  
**Bacterial strain typing**

**Identifying genetic determinants of persistent *Staphylococcus aureus* during bacteraemia and lower respiratory tract infections**

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**Background:** To identify genetic determinants or patterns thereof from *Staphylococcus aureus* that may be related to its persistence in blood of patients with bacteraemia and in tracheal aspirates of patients undergoing mechanical ventilation despite a treatment adjusted to susceptibility test results.

**Material/methods:** Patient populations included a cohort of patients with *S.aureus* bacteraemia and a cohort of ICU patients with bronchial colonization, tracheobronchitis and pneumonia from whom *S. aureus* was isolated in tracheal aspirates. Clinical and epidemiological variables were recorded and persistence was considered in cases of repeated isolation from blood cultures or tracheal aspirates, respectively, after 72 h of therapy adjusted to susceptibility test results. Based on the recovery of *S.aureus* after 72h, both cohorts were split in "persistently" and "transiently" infected subgroups. Isolates were genotypically characterized with a microarray based assay (*S. aureus* genotyping, Alere Technologies, Germany), which detects the presence or absence of specific resistance and virulence genes and their allelic variants. Genome-wide association tests were performed using a recently described statistical tool for mapping the genes that influence bacterial

phenotypes(<http://www.danielwilson.me.uk/virulogenomics.html>). The population structure was taken into account when testing for an association between the phenotype of interest and the genetic variants selected. The Bonferroni method was used to correct for multiple testing.

**Results:** A total of 82 bacteraemia strains (9 "persistent" and 73 "transient") and 81 respiratory strains (38 "persistent" and 43 "transient") were analysed. No significant association was found for any gene in the two study populations regarding persistence confirming previous results obtained by conventional univariate and multivariate analyses. Manhattan plots were used to summarise the results representing each individual gene and its association to the phenotype of interest (persistence).

**Conclusions:** Genome wide association studies are useful to analyse complex databases combined with multiplex genotyping, e.g., microarrays or next generation sequencing. No significant correlations were found between bacterial genetic variants and persistence of *S. aureus* suggesting that alternative factors such as host factors might be related. Another aspect to be considered is the role of bacterial gene expression regulation, protein translation and transport.