

Identification of a core microbiome of endotracheal tubes associated with *P. aeruginosa* and *S. epidermidis*

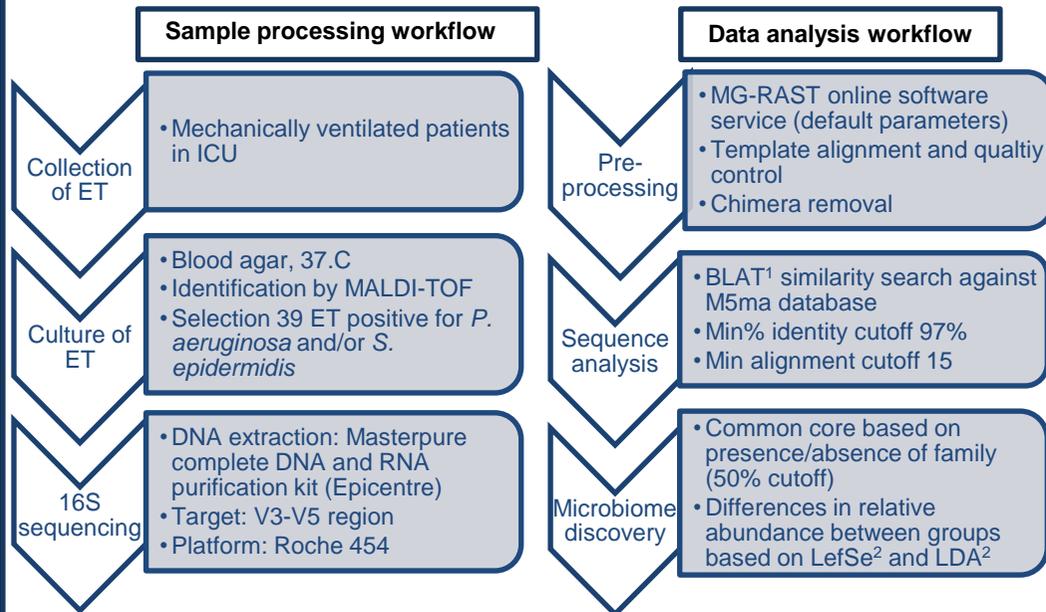
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Introduction

Pneumonia is a common complication in mechanically ventilated patients. The micro-organisms present on the endotracheal (ET) tube are thought to play a key role in the onset of ventilator associated pneumonia (VAP) but the exact mechanism is not yet understood. With the underlying hypothesis that microbial interactions might be important in the development of VAP, this study aimed to identify the core microbiomes present on ET tubes which were culture positive for the pathogens *Pseudomonas aeruginosa* and/or *Staphylococcus epidermidis* from mechanically ventilated patients.

Materials and Methods



Results (2) and Conclusion

Enterobacteriaceae and *Phylloacteriaceae* were found in almost all investigated ET tubes that showed presence of either *P. aeruginosa* or *S. epidermidis* (Figure 1, groups 1 and 2), and formed the core microbiome associated with these organisms. *Corynebacteriaceae* were more frequently associated with *S. epidermidis* (Figure 1 and 2), however, a clear association with a specific family was not noted for *P. aeruginosa*. In ET tubes that showed presence of both *P. aeruginosa* and *S. epidermidis* (group 3) showed a remarkably consistent presence of the *Lactobacillaceae* family (Figure 1 and 2). Further research on interactions between organisms identified in this study will elucidate the potential role of the ET tube microbiome in the development of VAP.

Results (1)

Figure 1: To distinguish the core microbiomes associated with the key pathogens *P. aeruginosa* and *S. epidermidis*, ET tubes with positive culture results for either one (group 1 and 2) or both (group 3) species were selected as shown in the figure above. Families present in more than 50% of the ET tubes in a certain group were assigned to the microbiome of that group.

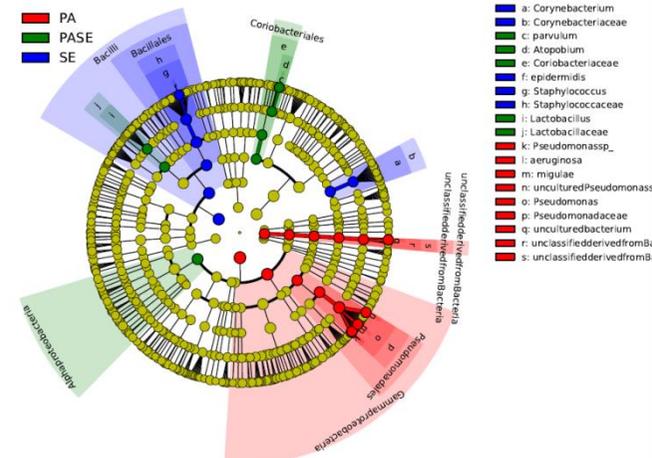
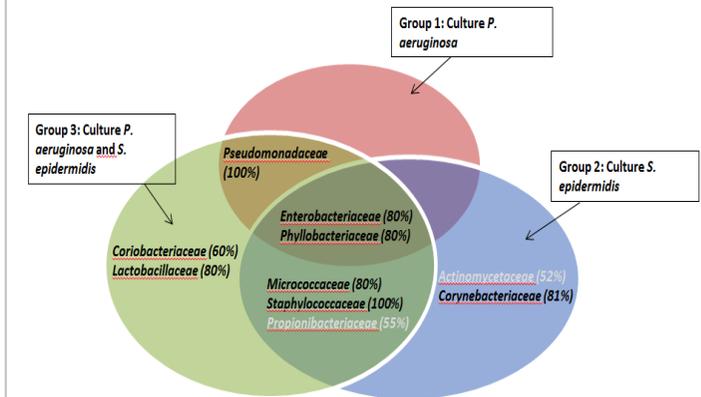


Figure 2: Cladogram generated using the LefSe² tool. The inner circles represent the highest taxonomic level and the colored bands contain the taxonomic levels which were significantly more associated with one group. The α -value for all statistical tests was 0.05 and the Linear discriminant analysis (LDA)² cutoff >2. Red: *P. aeruginosa*, Blue: *S. epidermidis*, Green: *P. aeruginosa* and *S. epidermidis*.

References

- Kent WJ (2002) Genome research 12:656-664
- Segata N (2011) Genome biology 12(6):R60