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Temporal airway microbiome changes related to ventilator-associated pneumonia in children

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In mechanically ventilated children, microbial factors were subtly different at intubation between those who did and did not develop VAP, and changes over time were marginally associated with VAP risk, suggesting other factors may contribute to VAP https://bit.ly/3ijsaTO

Cite this article as: Mourani PM, Sontag MK, Williamson KM, *et al*. Temporal airway microbiome changes related to ventilator-associated pneumonia in children. *Eur Respir J* 2021; 57: 2001829 [https://doi.org/10.1183/13993003.01829-2020].

ABSTRACT We sought to determine whether temporal changes in the lower airway microbiome are associated with ventilator-associated pneumonia (VAP) in children.

Using a multicentre prospective study of children aged 31 days to 18 years requiring mechanical ventilation support for >72 h, daily tracheal aspirates were collected and analysed by sequencing of the 16S rRNA gene. VAP was assessed using 2008 Centers for Disease Control and Prevention paediatric criteria.

The association between microbial factors and VAP was evaluated using joint longitudinal time-to-event modelling, matched case–control comparisons and unsupervised clustering.

Out of 366 eligible subjects, 66 (15%) developed VAP at a median of 5 (interquartile range 3–5) days post intubation. At intubation, there was no difference in total bacterial load (TBL), but Shannon diversity and the relative abundance of *Streptococcus*, Lactobacillales and *Prevotella* were lower for VAP subjects *versus* non-VAP subjects. However, higher TBL on each sequential day was associated with a lower hazard (hazard ratio 0.39, 95% CI 0.23–0.64) for developing VAP, but sequential values of diversity were not associated with VAP. Similar findings were observed from the matched analysis and unsupervised clustering. The most common dominant VAP pathogens included *Prevotella* species (19%), *Pseudomonas aeruginosa* (14%) and *Streptococcus mitis/pneumoniae* (10%). *Mycoplasma* and *Ureaplasma* were also identified as dominant organisms in several subjects.

In mechanically ventilated children, changes over time in microbial factors were marginally associated with VAP risk, although these changes were not suitable for predicting VAP in individual patients. These findings suggest that focusing exclusively on pathogen burden may not adequately inform VAP diagnosis.