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The respiratory microbiota during and following mechanical ventilation for respiratory infections in children

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During mechanical ventilation for an LRTI in children, the respiratory microbiota shifted from *Haemophilus*- and *Moraxella*-dominated profiles to profiles dominated by antibiotic-resistant *Enterobacteriaceae,* and *Staphylococcus* and *Streptococcus* species. https://bit.ly/3pGfvhQ

Cite this article as: de Koff EM, Man WH, van Houten MA, *et al*. The respiratory microbiota during and following mechanical ventilation for respiratory infections in children. *Eur Respir J* 2021; 57: 2002652 [https://doi.org/10.1183/13993003.02652-2020].

To the Editor:

The lower respiratory tract (LRT) harbours distinct, dynamic low-density microbial communities, established through micro-aspiration from the upper respiratory tract (URT) [1–3]. However, during intubation and mechanical ventilation, the endotracheal tube temporarily alters the anatomical continuity between URT and LRT, and may provide a bridge for airborne microbes and a barrier for micro-aspiration. Shortly after intubation for a severe LRT infection (LRTI) in children, the microbiota of the nasopharynx and LRT were shown to be very similar [4]. However, it remains unknown how the respiratory microbial community develops while the child recovers from the infection under treatment with mechanical ventilation and antibiotics. We therefore analysed respiratory microbiota changes in children participating in our study on acute LRTIs and who were admitted to the paediatric intensive care unit (PICU) for mechanical ventilation [4].