Microbial transmission and ecology of human and environmental microbial communities in childcare centers

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Early-life microbial exposures profoundly impact individuals' lifelong health trajectories by shaping immune maturation and modulating disease risk, e.g. as typified by the "hygiene hypothesis." Childcare facilities represent a critical yet understudied source of microbial exposures where preschool-aged children spend 7-10 hours daily during key developmental periods. This study presents the first multi-omic and multi-kingdom investigation of microbial transmission and ecology across childcare environments, integrating microbiome samples from both high-touch and low-touch surfaces with children's nasal and oral microbiomes. We used full-length bacterial and fungal amplicons (16S and ITS) and paired SR and LR shotgun metagenomics, which in combination provide enhanced taxonomic resolution and the ability to assess functional elements such as genes, lateral transfers, and evolution. This work highlights previously understudied components of early-life microbial exposures in childcare environments, and it provides methods for identifying potential pathogen reservoirs, tracking transmission routes, and developing targeted interventions.



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Distinct distribution of 583 unique bacteria across environments



- Human-associated communities are more phylogenetically similar than environmental ones. man-associated communities.
- High-touch environments harbor a mix of shared human-associated and environmentally-derived microbes, mostly in Proteobacteria, Firmicutes, and Actinobacteria.

Bacterial transmission mainly driven by human shedding/behaviors



Species sharedness was quantified as the proportion of ASVs uniquely or jointly present | across human and environmental samples. Among the top prevalent and abundant species, those with high transmission included: • Human-associated taxa from the nasal, oral, and skin microbiomes; Lactic acid bacteria commonly found in fermented foods and dairy products; In contrast, species dominating low-touch environments were exclusively environmentally derived, with contribution from environmental ASVs only.



• Low-touch environments show a greater microbial diversity that differ substantially from hu-

Functional enrichment associated with lateral gene transfer

- variability;
- tive traits.

mobile elements **DNA** integration proteins





