

INDOOR MICROBIOME DIVERSITY AMONG ASTHMATIC AND HEALTHY CHILDREN – HIDDEN LIFE IN BED DUST

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Background: Indoor dust is an important reservoir of bacterial and fungal communities that may influence children's respiratory health.

Objective: The aim of this research was to compare microbiome diversity and abundance in bed dust samples from children with asthma and healthy children and to explore associations with household and environmental factors.

Subjects and methods: Bed dust samples from 150 children (69 with asthma, 81 controls) were analyzed using 16S rRNA and ITS sequencing. Microbial diversity and community composition were assessed and related to asthma status, socioeconomic factors, household characteristics, pet ownership, cleaning practices, and ventilation.

Results: Asthma status was not significantly associated with bacterial or fungal beta or alpha diversity, although a trend was observed for bacterial beta diversity between asthmatic and healthy children ($p = 0.065$). In contrast, several household and environmental variables were significantly associated with microbiome composition. For the bacterial microbiome, beta diversity was significantly associated with gender, parental education, household income, number of children and siblings, rural or urban living environment, pets' ownership, ventilation, dusting and cleaning practices. Alpha diversity was associated with gender, parental education and pets ownership. In addition to the finding that living environment and cleaning was significantly associated with fungal beta diversity, having cat showed strong associations with both bacterial and fungal alpha diversity measures (all p values < 0.05).

Conclusion: Bed dust microbiome diversity did not differ significantly between children with asthma and healthy controls, but household environment, pet exposure and cleaning practices were strongly associated with household microbiome, suggesting that environmental factors may influence indoor microbiome, relevant to childhood respiratory health.

Keywords: Dust microbiome; Bacterial and fungal communities; Asthma; Respiratory health; Illumina sequencing.

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