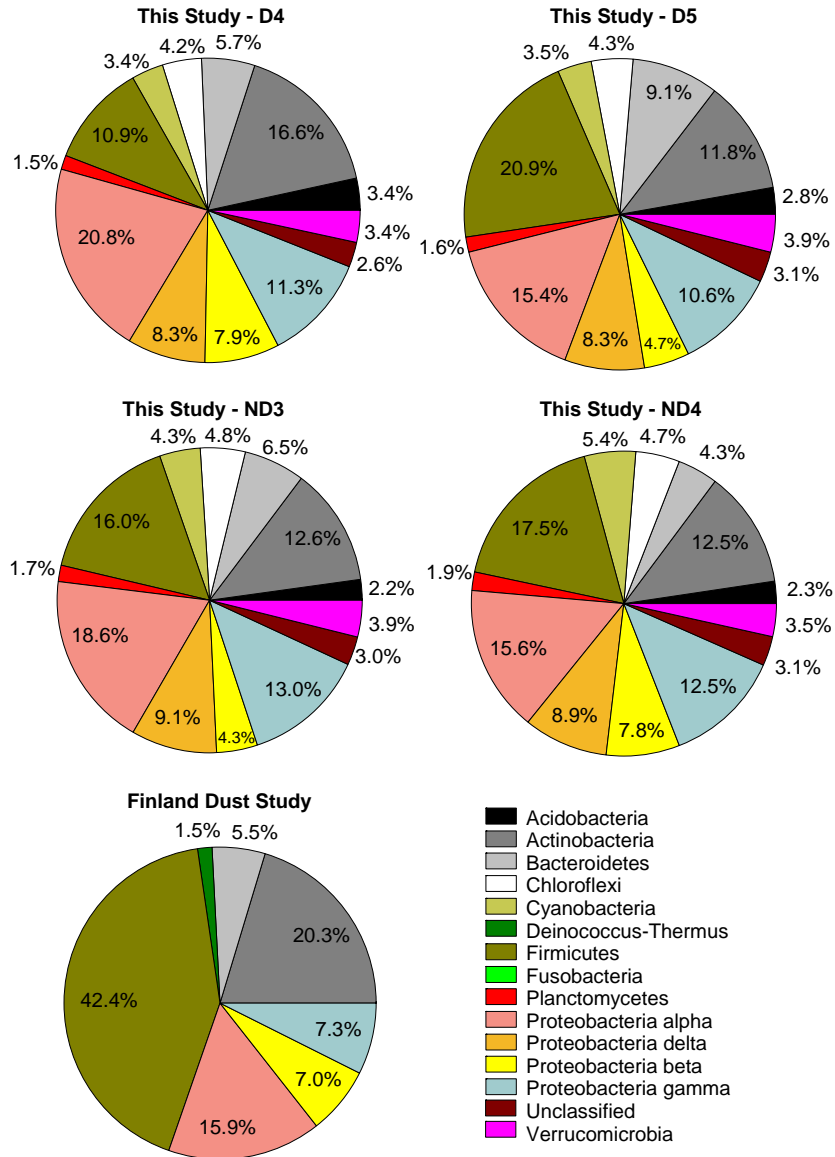


Supplementary Information

The Bacterial Community in Household Dust: Environmental Determinants and Impact on Childhood Asthma

Supplementary Figure and Legend



Supplementary Figure 1. PhyloChip analysis of dust microbial community structure including a comparison to a recent study from Finland.

The top four pie charts represent the distribution of OTUs identified by 16S rRNA PhyloChip microarray from four Tucson, AZ household dust samples (D4 and D5 from homes with dogs; ND3 and ND4 from homes without dogs). Each bacterial division shown accounts for >1% of all OTUs identified for a total of 85% of the total number of OTUs. The remaining 15% of the OTUs belonged to an additional 33 bacterial divisions but at <1% each. There is currently very little data regarding the microbial community in household dust but for comparison, the bottom pie chart represents the clone library results of dust samples from two buildings in Finland from Rintala et al. (1). Each bacterial division represents >1% of all OTUs identified for a total of 97% of the total number of OTUs. A total of 893 clones were analyzed resulting in 283 unique operational taxonomic units (OTUs). It appears that the bacterial diversity in the Tucson, AZ dust samples is similar to that found in Finland dust, but the gram-negative *Proteobacteria* were much more prevalent (45%) in Arizona samples, whereas the gram-positive *Firmicutes* and *Actinobacteria* (29%) predominated in Finland. Interestingly, the Finnish study showed a seasonal fluctuation in the dust bacterial communities with *Proteobacteria* increasing in summer samples (with a concomitant decrease in *Firmicutes*) and decreasing in winter samples. This suggests that the difference in the Arizona and Finland results may be climate related.

1. **Rintala, H., M. Pitkaranta, M. Toivola, L. Paulin, and A. Nevalainen.** 2008. Diversity and seasonal dynamics of bacterial community in indoor environment. *BMC Microbiol* **8**:56.