



# Characterization of *Acidobacteriota* Communities in Finnish Soils

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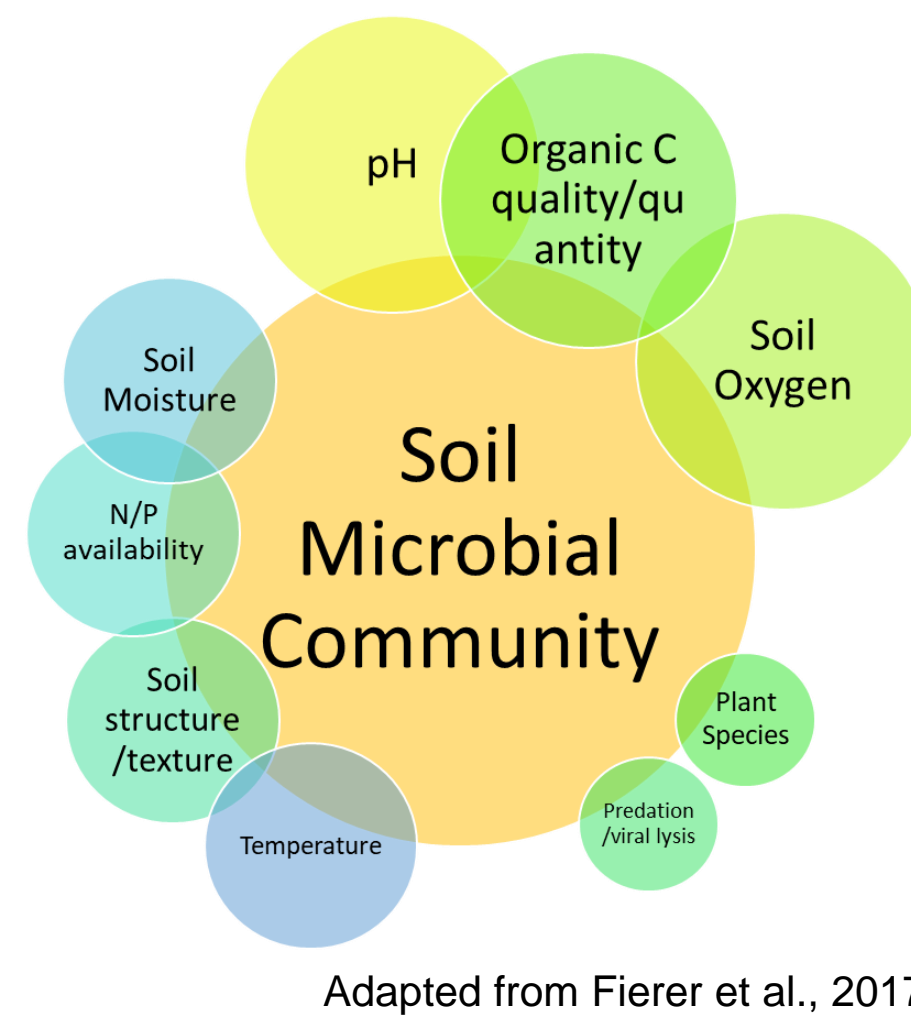


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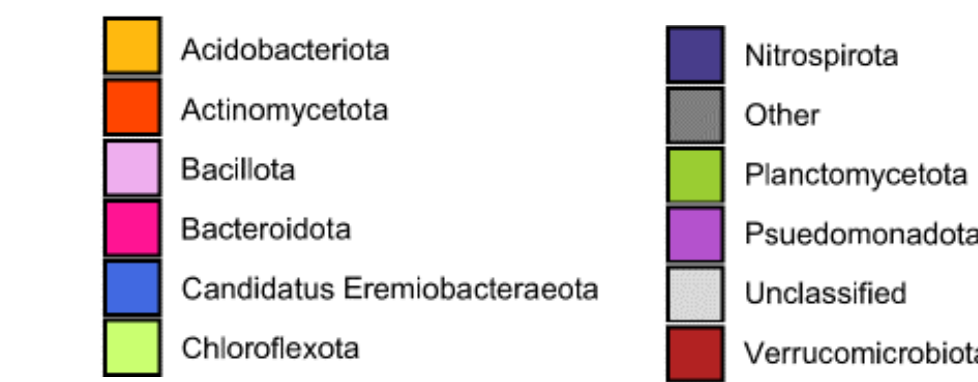
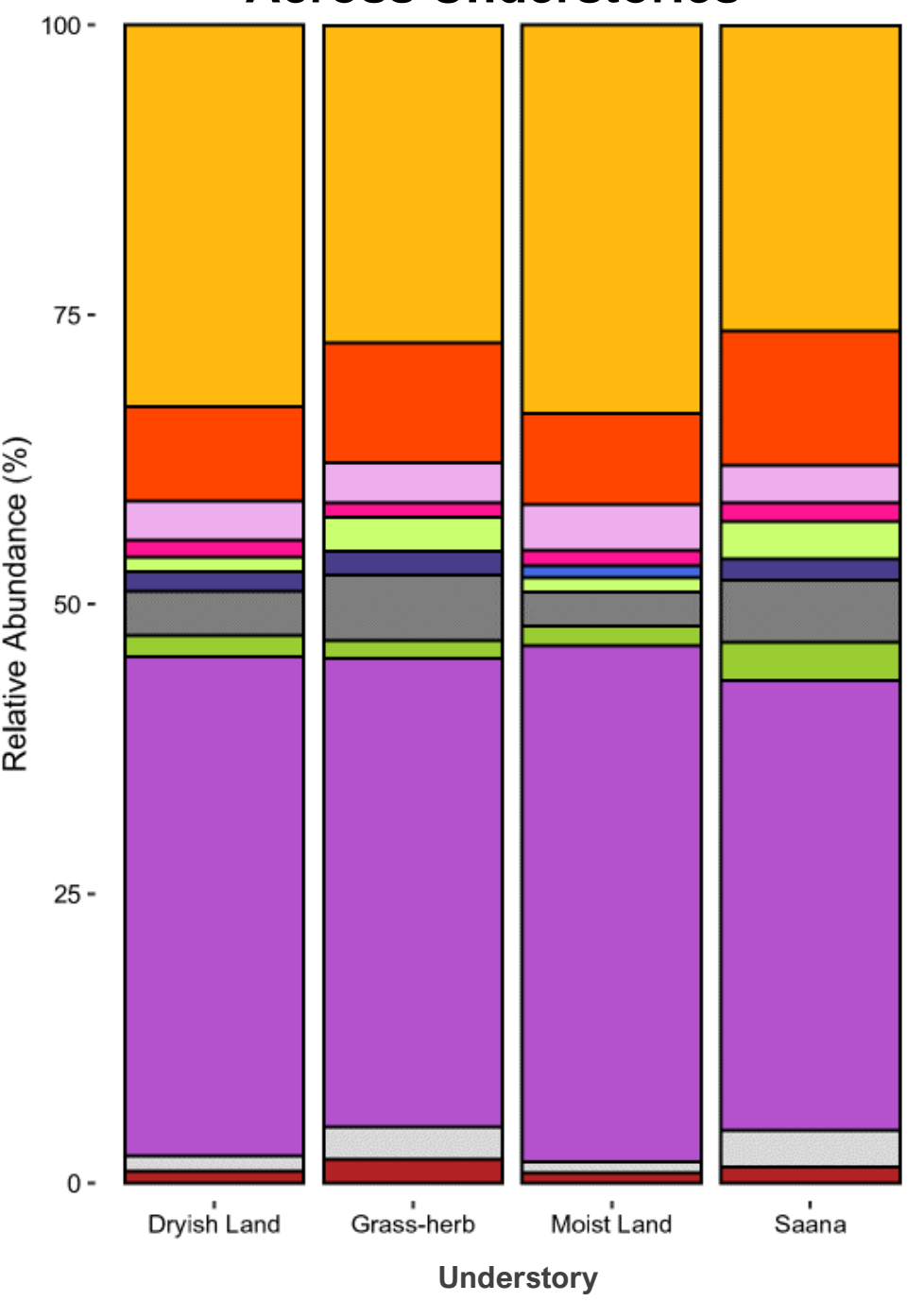
## Background

- Forests are major carbon sinks (45% of C in terrestrial ecosystem), but vegetation can be altered by global climate change, thereby changing microbial communities in associated soils (Baldrian et al., 2023).
- Nutrient gradients within macro- and micro-environments support diverse microbes in soil. Microbiome composition affects ecosystem processes; identifying organisms with high resolution is essential for determining their activities and functions (Sokol et al., 2022).
- Microbial survival and growth depends on biotic and abiotic factors, including resource availability, competition, and predation (Fierer, 2017).
- The *Acidobacteriota* phylum accounts for up to 60% of some soil communities. A few cultured representatives from 5 of 26 subdivisions reveal their success in oligotrophic environments and their ability to break down complex carbon, including various carbohydrates (Eichorst et al., 2018; Messyasz et al., 2024).
- We aim to determine drivers of *Acidobacteriota* diversity by analysing communities from Finnish soil samples across different forests. Previous studies suggest community composition is largely determined by dominant trees that influence turnover of organic matter.
- We hypothesize that communities will differ between organic and mineral layers of a single site and between locations due to environmental filtering.**

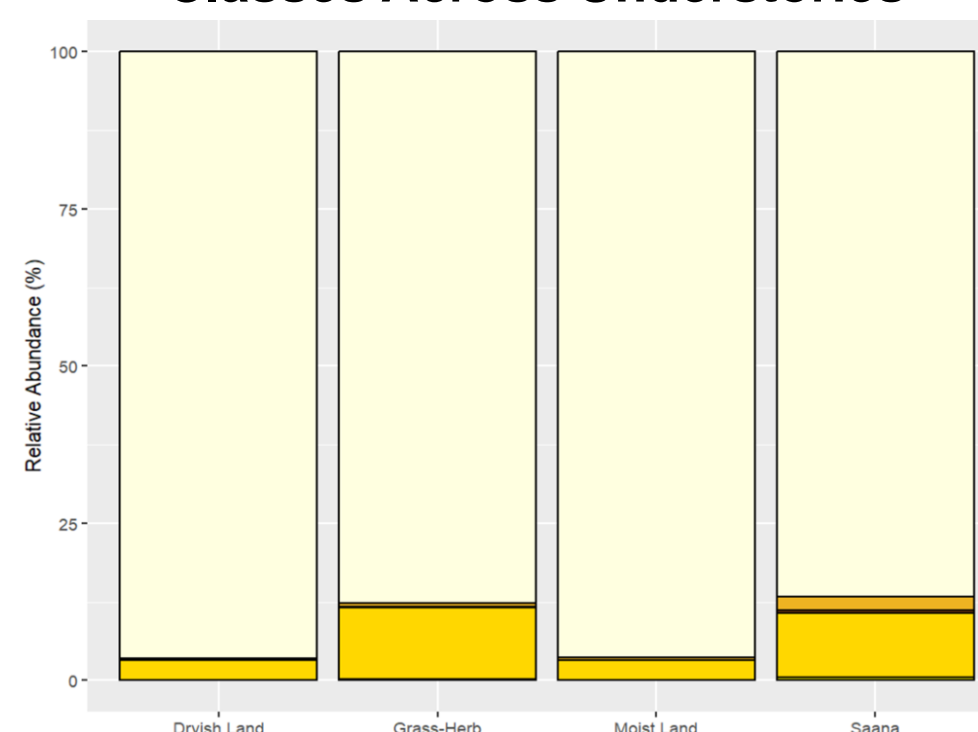


## Most Abundant *Acidobacteriota* Strains Among Forest and Tundra Soil

### Relative Abundance of Top 10 Phyla Across Understories

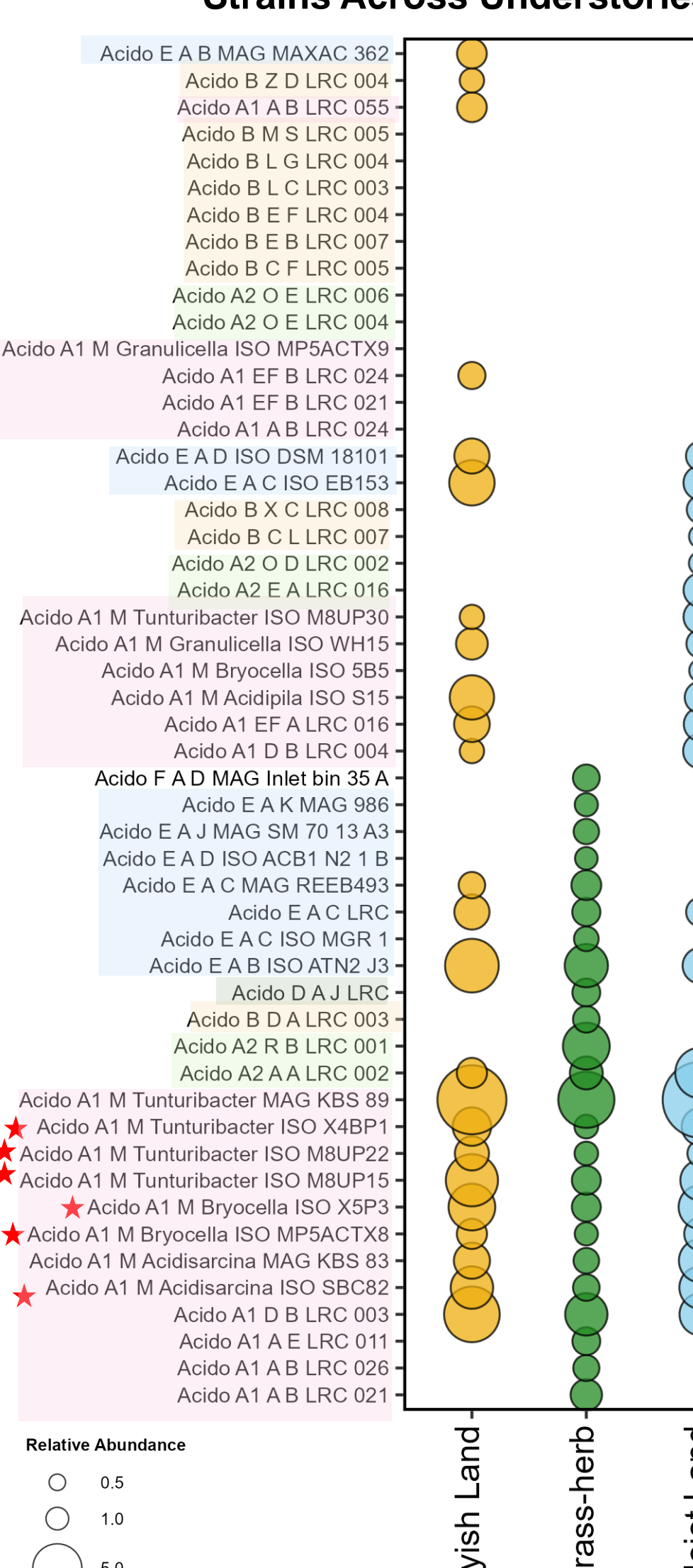


### Relative Abundance of *Acidobacteriota* Classes Across Understories



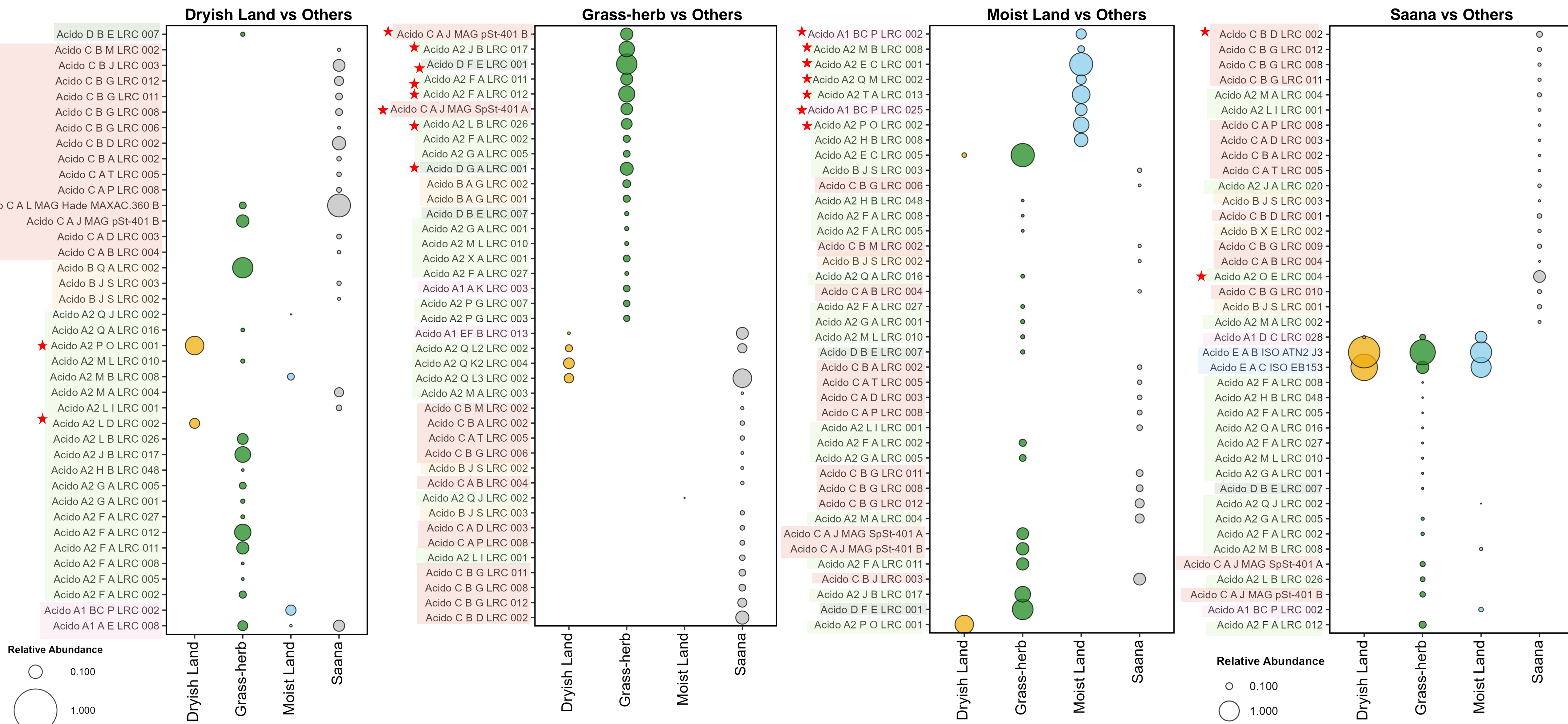
*Pseudomonadota*, *Acidobacteriota*, and *Actinomycetota* were most prevalent across forest types and tundra sites. The majority of *Acidobacteriota* were part of the class *Terriglobia*.

### Relative Abundance of Top 25 *Acidobacteriota* Strains Across Understories

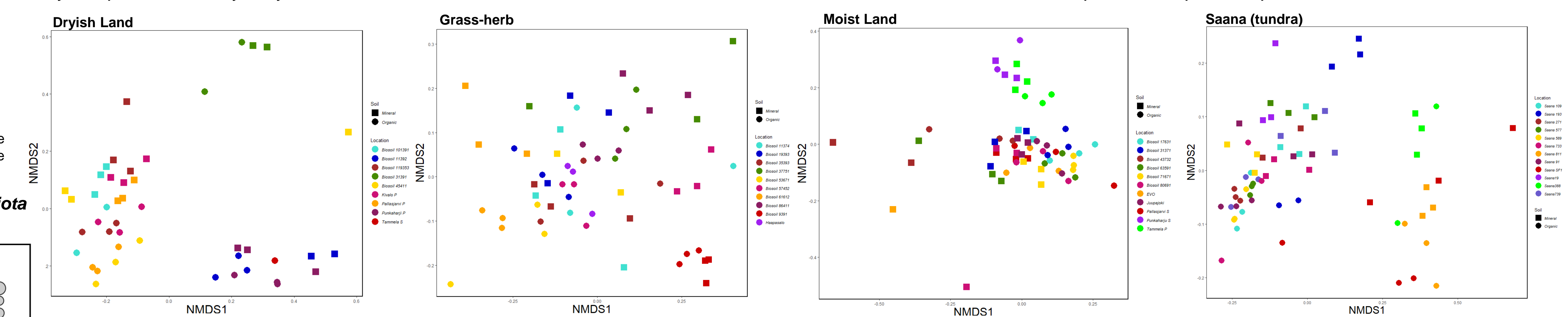


Most abundant *Acidobacteriota* strains across understory type. Relative abundances of the top 25 strains were calculated (~0.5% to 6%). Isolates and MAGs from *Tunturi*, *Bryocella*, and *Acidiasarcina* were seen in large percentages across all understories.

### Differential Abundance of Strains Across Understories:



DESeq2 was used to determine which strains were significantly (p-value <0.05) enriched or depleted when comparing one understory to all others. Results were sorted by log2Fold Change. Bubble plots represent the 20 strains with the greatest log2Fold increase and the 20 strains with the greatest log2Fold decrease. Samples analysed per understory: Dryish Land n= 50, Grass-herb n= 56, Moist Land n= 65, Saana n= 71. Stars indicate unique strains per comparison.



Bray-Cutis Dissimilarity of *Acidobacteriota* strains. NMDS plots were generated based on relative abundances. Beta diversity was calculated. Among Dryish Land sites, there were 3 distinct groups, indicating differences in communities between locations (e.g., Biosoil 11392 and Punkaharju P different from Biosoil 31391). Among Moist Land sites, Tammela P and Punkaharju S separated from the rest. From Saana sites, Saana 811, Saana SF1, and Saana 388 grouped away from the others. No clear patterns were observed for Grass-herb sites. Organic and mineral layers appeared distinct in some forest types.

	Average Enriched (log2Fold Change)	Average Depleted (log2Fold Change)	Total Strains
Dryish Land	19.2	-10.1	844,397
Grass-herb	11.3	-8.4	97,9492
Moist Land	19.9	-8.7	1,076,897
Saana	9.8	-7.9	722,197

## Conclusions/Future Directions

- NMDS plot comparing all understory types showed clear separation among Saana tundra heaths and forests. Grove and Dry Land (1 site each) grouped with Saana. Dryish Land formed a tighter cluster while still grouping with Moist Land and Grass-herb.
- Soil pH and carbon content key influencers of bacterial community composition, whereas plant and soil type have been less studied.
- Our data suggests that there is some difference in *Acidobacteriota* communities between mineral and organic layers at a given site and that microbial communities at different locations within the same forest type can be distinct. Certain species/strains were found in both mineral/organic layers while others were more restricted.
- Factors specific to these locations will be analysed (e.g., C/N content, moisture etc.). Stable isotope probing experiments on different carbon sources are also planned to determine active members of the community.

## References

Baldrian P, López-Mondéjar R, Kohout P (2023) Forest microbiome and global change. *Nat Rev Microbiol* 21: 487–501.  
 Eichorst SA, Trojén D, Roux S, Herbold C, Rattier T, Woebken D (2018) Genomic insights into the Acidobacteria reveal strategies for their success in terrestrial environments. *Environ Microbiol* 20: 1041–1063.  
 Kerkhof LJ, Roth PA, Deshpande SV, Bernhards CR, Liem AT, Hill JM, Häggblom MM, Webster NS, Ibrankovic M, Mirzayan S, Polashock JJ, Sullivan RF (2022) A ribosomal operon database and MegaBLAST settings for strain level resolution of microbiomes. *FEMS Microbes* 3: xtac002.  
 Lee S, Cho J (2011) Group-specific PCR primers for the phylum Acidobacteria designed based on the comparative analysis of 16S rRNA gene sequences. *J Microbiol Methods* 86: 195–203.  
 Messyasz A, Männistö MK, Kerkhof LJ, Häggblom MM (2024) Genome analysis and description of *Tunturi* bacterium gen. nov. expands the diversity of Terriglobia in tundra soils. *Environmental Microbiology* 26: e116640.  
 Sokol NW, Slessarev E, Marschmann GL et al. (2022) Life and death in the soil microbiome: how ecological processes influence biogeochemistry. *Nat Rev Microbiol* 20: 415–430.

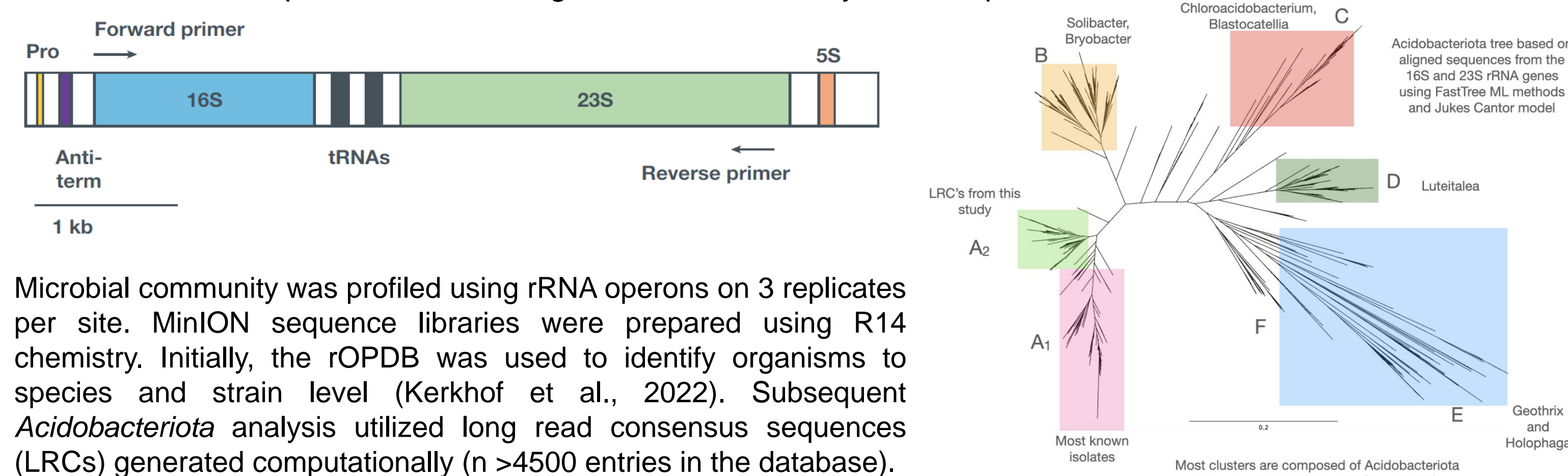
## Materials and Methods

Sample Collection July 2022:

Colour	Forest Understory	Dominant Tree Species
Yellow	Dryish Land	Pine
Green	Grass Herb	Spruce/Birch
Blue	Moist Land	Pine/Spruce
Pink	Grove	Spruce
Orange	Dry Land	Pine

\*Saana site – mainly tree-less

~230 soil cores were collected from the north to south of Finland. 4 replicates (A, B, C, D) were taken from each site, separated into the organic and mineral layers, and preserved in DESS.



Microbial community was profiled using rRNA operons on 3 replicates per site. MinION sequence libraries were prepared using R14 chemistry. Initially, the rOPDB was used to identify organisms to species and strain level (Kerkhof et al., 2022). Subsequent *Acidobacteriota* analysis utilized long read consensus sequences (LRCs) generated computationally (n >4500 entries in the database).