

# CORRELATION OF THE BACTERIAL COMMUNITIES WITH VEGETATION AND SOIL NUTRIENT STATUS IN A DEVELOPING ECOSYSTEM

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## Background

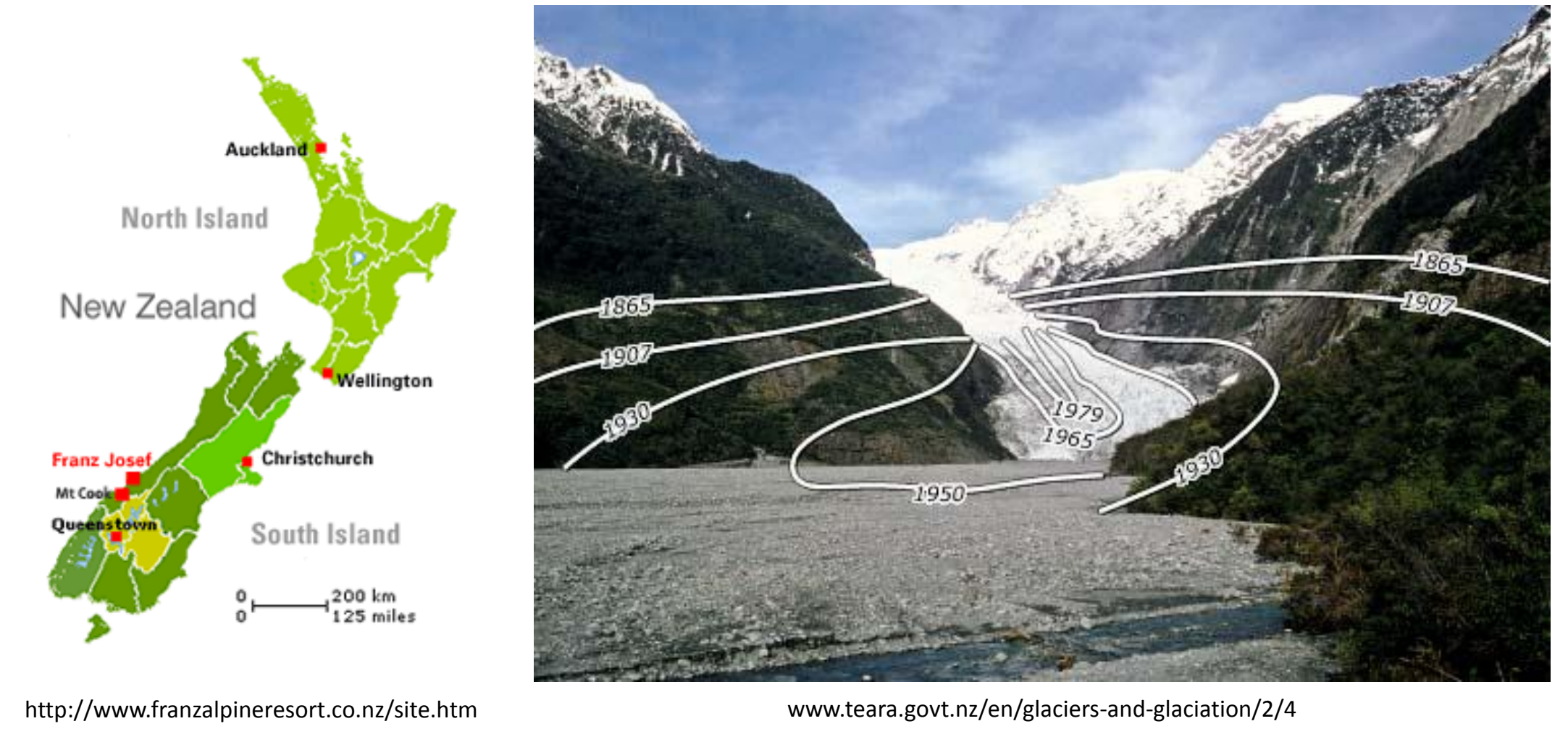
Microbial communities have previously been shown to assemble in patterns reminiscent of vegetative succession during soil and ecosystem development. However, recent studies link multiple environmental gradients with succession and soil development. An experiment across a gradient of ecosystem development was undertaken to further test the relationship between soil microbial community composition and their associated environmental habitat characteristics.

## Hypothesis

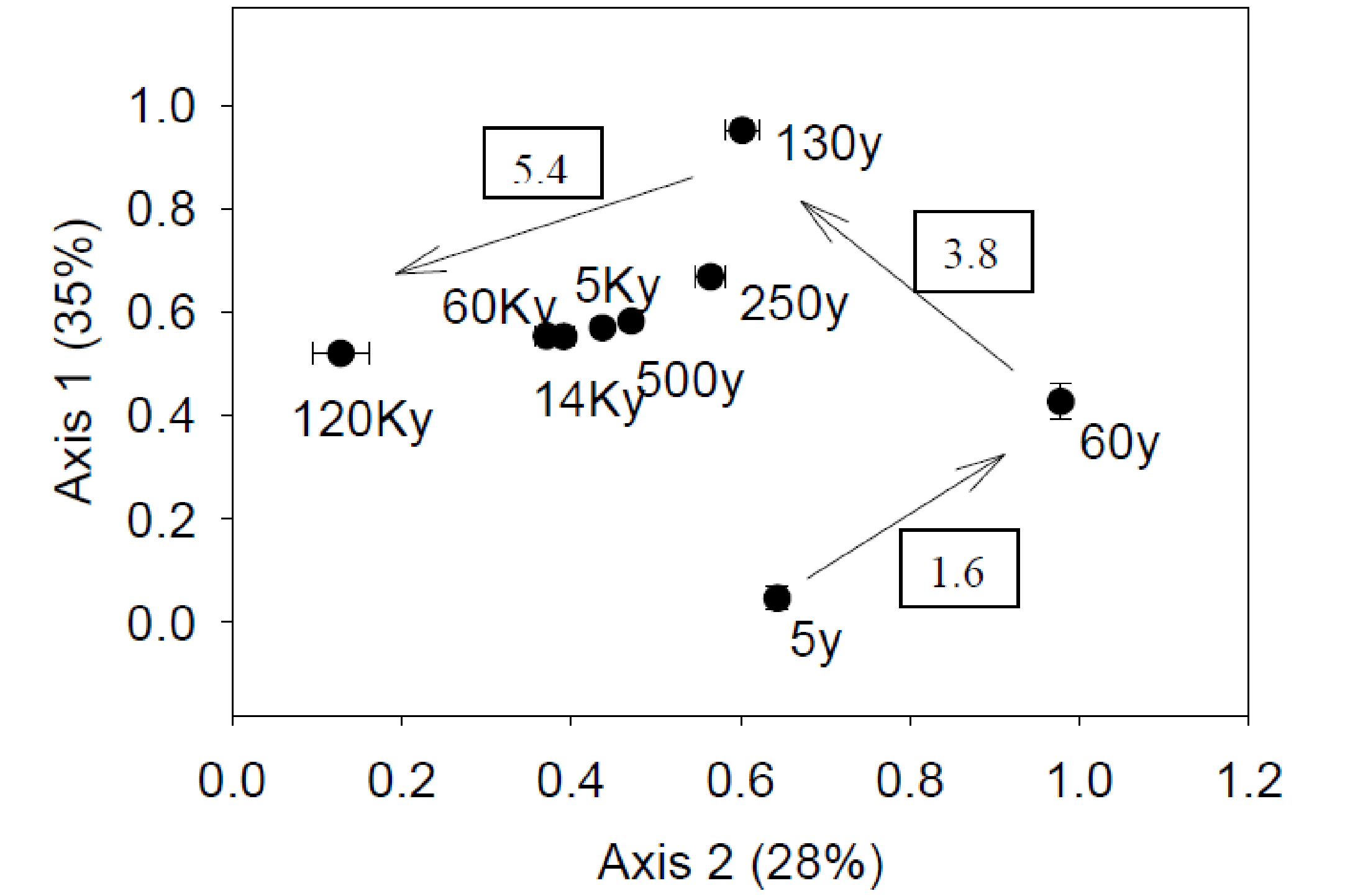
Changes in bacterial communities would closely follow the developing gradient of physiological and vegetative changes that define the soil habitat during ecosystem development.

## Study Site

**Franz Josef Glacier, New Zealand**  
■ Chronosequence of nine sites dating ~5 to 120,000 y since glacial retreats.

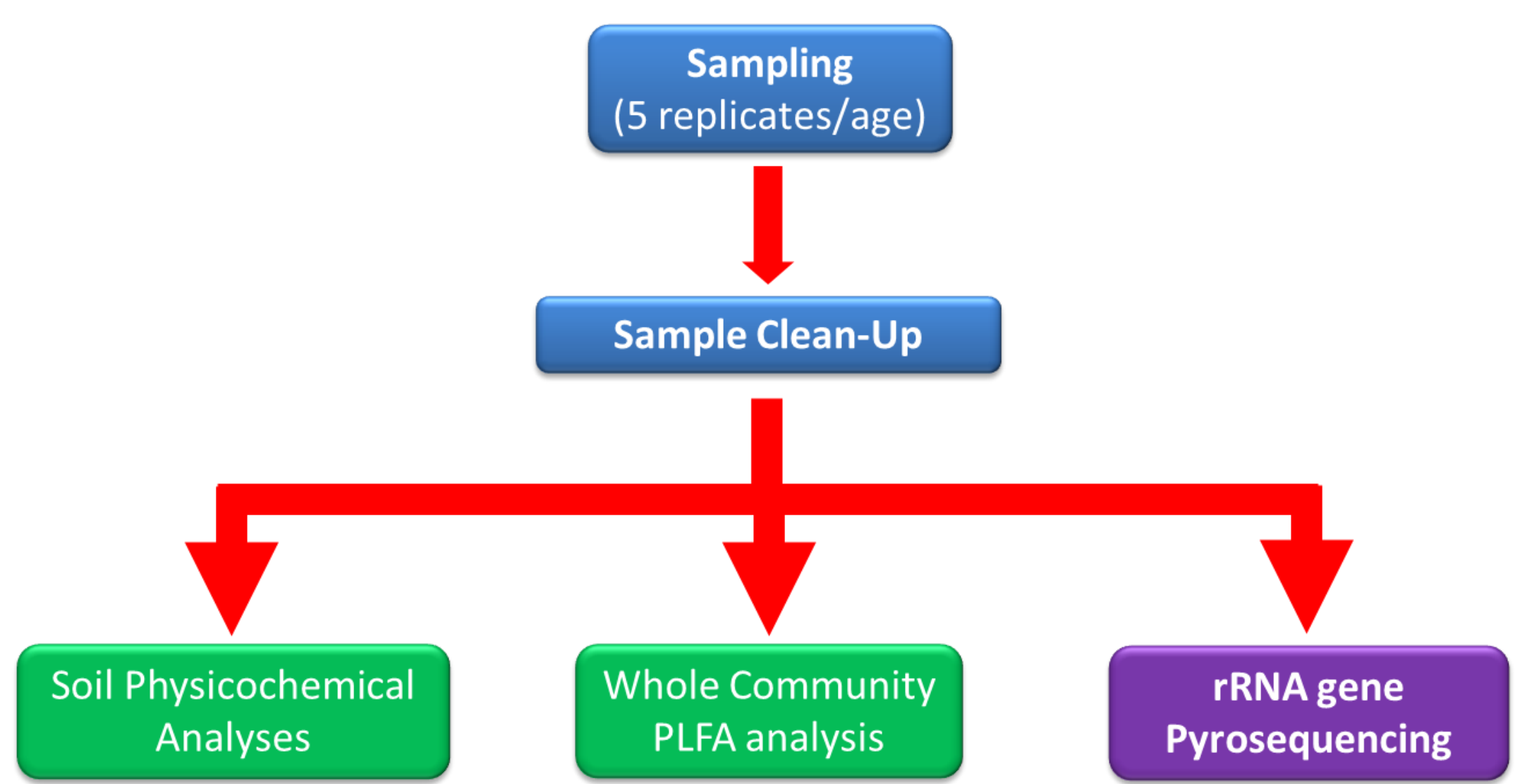


■ Significant change in plant community throughout the ecosystem.



Bray-Curtis ordination plot of the change in percent cover of 47 woody plant species. Numbers outside of boxes indicate time in years (y) or thousands of years (Ky) since deglaciation and those inside boxes indicate significant changes in plant species richness (1/D) along the chronosequence.

## Experimental Strategy



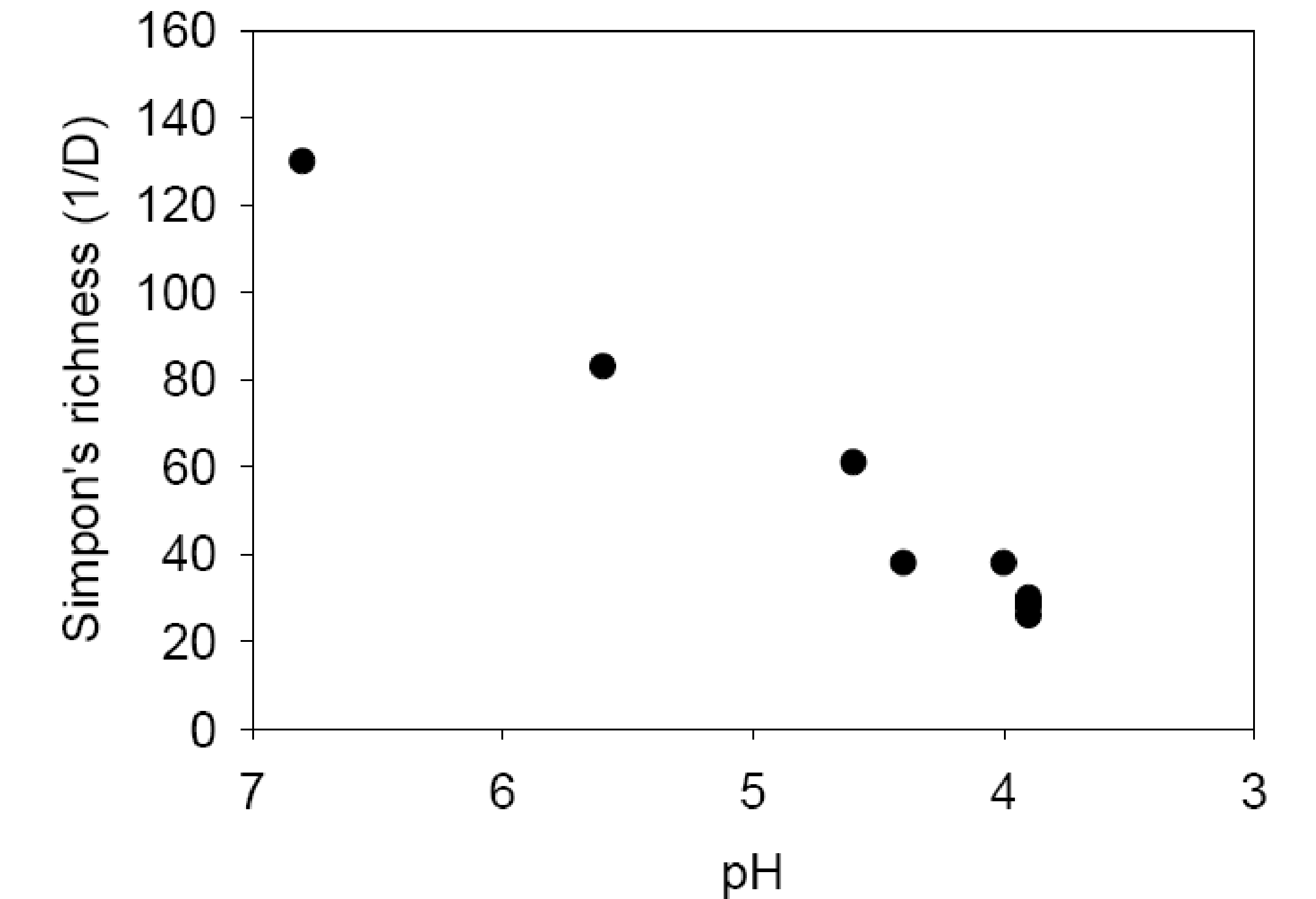
## Results

### Decrease in bacterial diversity along the chronosequence

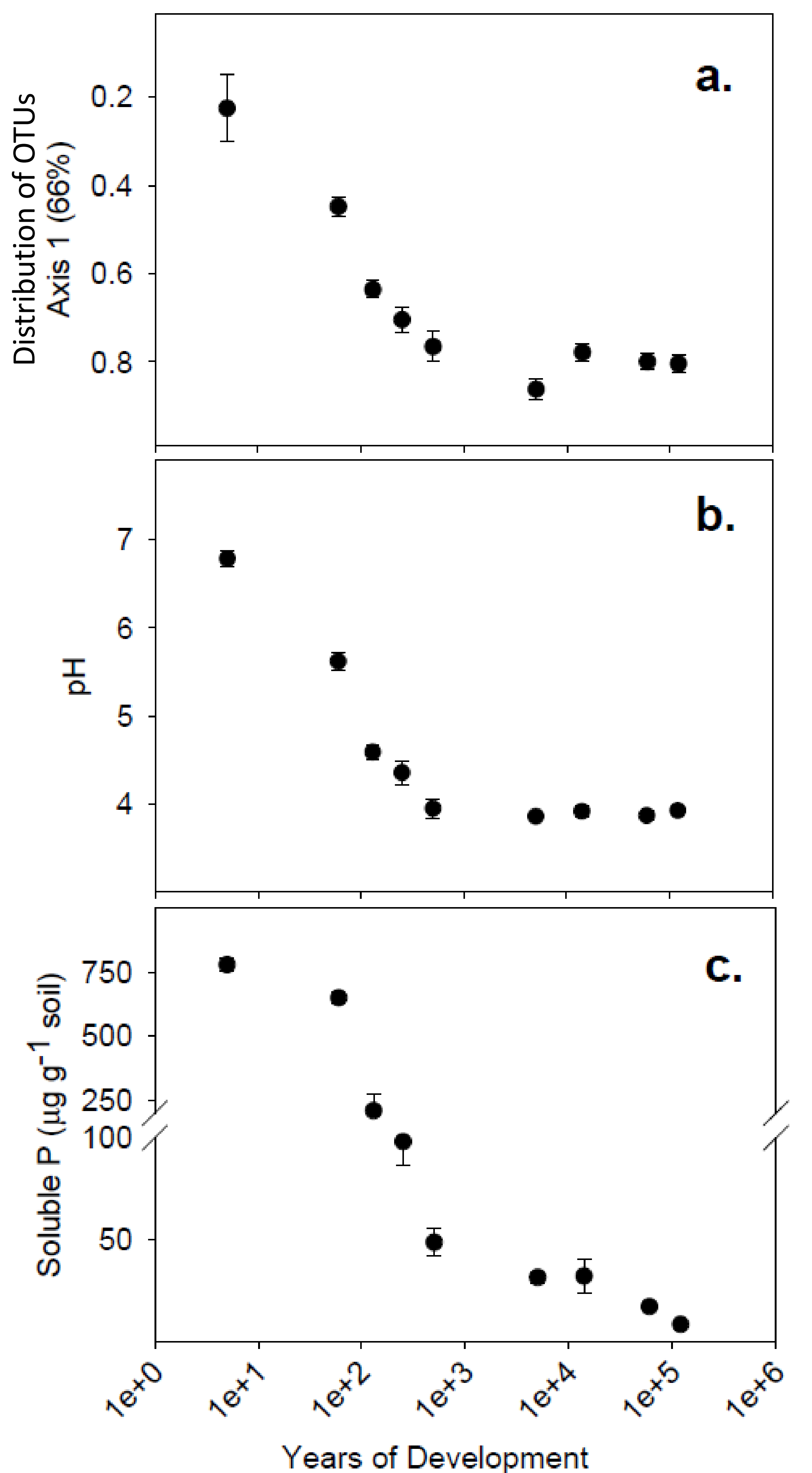
Diversity Index	5 y	60 y	130 y	250 y	500 y	5K y	14K y	60K y	120K y
# Sequences (N)	7155	8579	7779	7961	11284	8311	8826	7480	9180
# OTUs (S)*	1377	1420	978	953	1035	625	764	488	668
Goods Coverage	0.90	0.91	0.93	0.94	0.95	0.96	0.96	0.96	0.96
Ace Richness	3364	3871	2614	2502	2866	1483	1821	1431	2320
Shannon (H=Σ[(n/N)ln(n/N)])	5.99	5.72	5.20	4.99	4.77	4.42	4.46	4.09	4.27
Simpson (1/D)	130	83	61	38	38	30	28	26	29
Chao1=S + n <sub>1</sub> <sup>2</sup> /2n <sub>2</sub>	2508	2686	1851	1709	1998	1090	1411	1031	1414

\* Operational taxonomic units (OTUs) were formed using the average neighbor algorithm in MOTHUR at a distance of 0.03.

### Decline in bacterial community richness associated with pH & soluble phosphorus

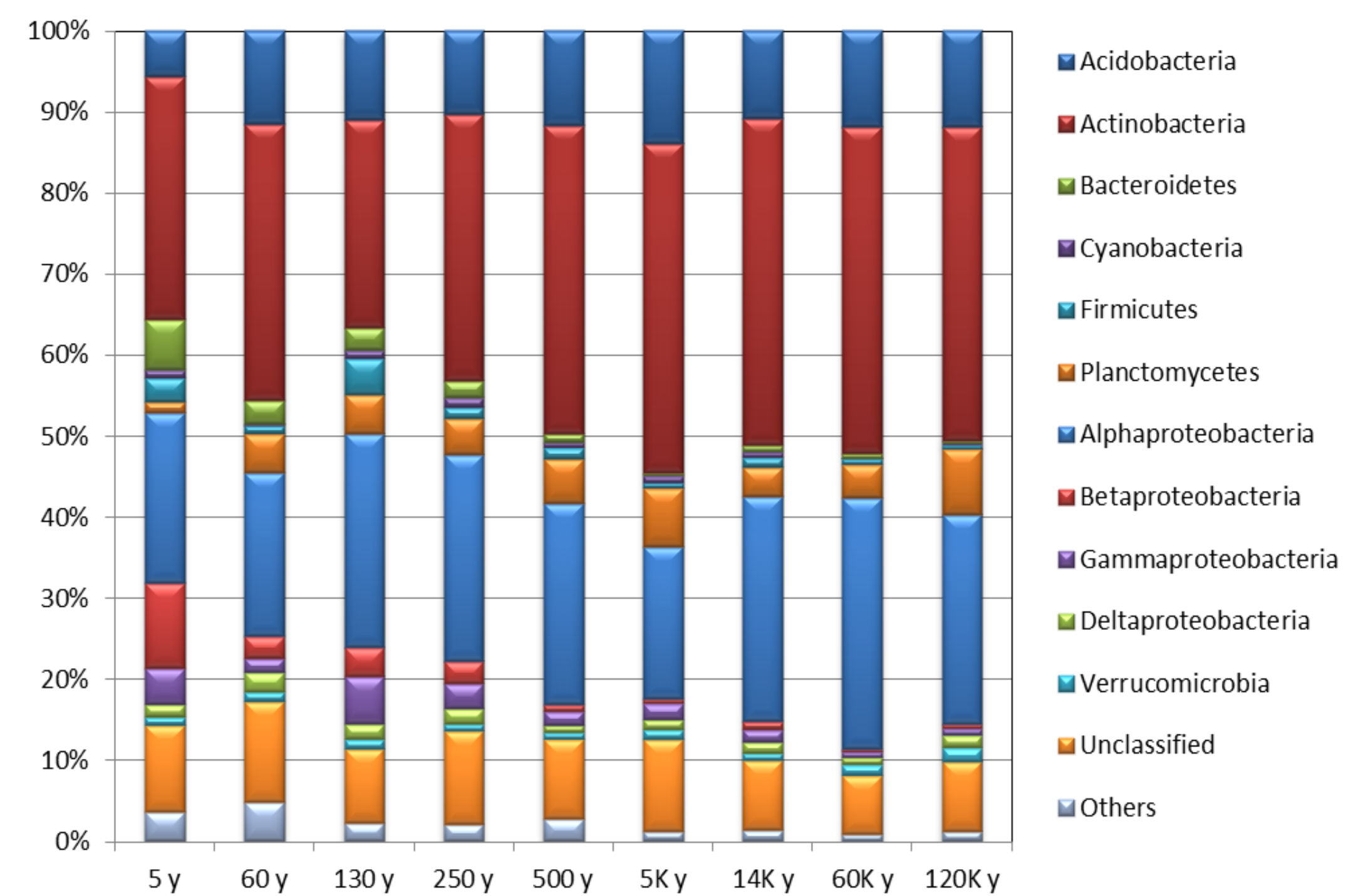


### Relationship between bacterial community structure and soil properties

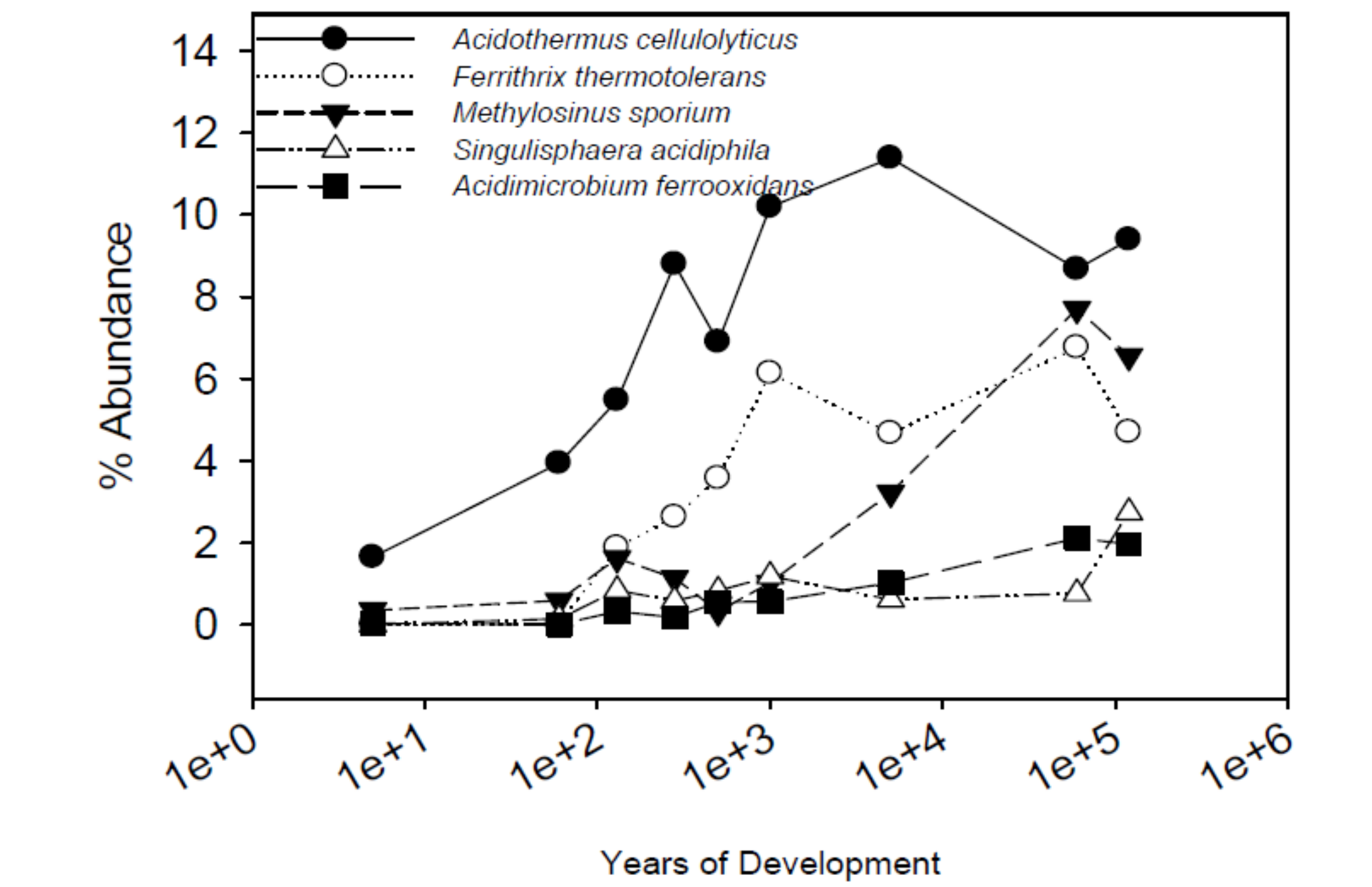


Relationship between soil ecosystem development and (a) bacterial community composition and structure, (b) pH, and (c) acid soluble phosphorus. Bray-Curtis ordination was used to analyze bacterial community structure in (a) based on the relative proportion of each of the 250 most abundant OTUs.

### Change in bacterial community composition along the chronosequence



### Changes in OTU abundance



The 5 most abundant OTUs that increased log-linearly as the ecosystem developed. OTUs are identified by their closest cultured representatives in RDP agent with a sequence similarity between 92-95%. Abundance was calculated based on the number of sequences found in each OTU relative to the total number of sequences collected.

## Conclusions

- Strong association between bacterial communities with soil and ecosystem habitat factors.
- Greatest community change occurred during the first several hundred years of soil and ecosystem development.
- Changes were closely related to soil chemical properties, especially pH, soluble phosphorus, and nutrient content across the gradient.
- Direct effect of plant species on soil bacterial community assemblage is relatively small.

## Acknowledgements

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