Patterns in soil ammonia-oxidizer responses to global change

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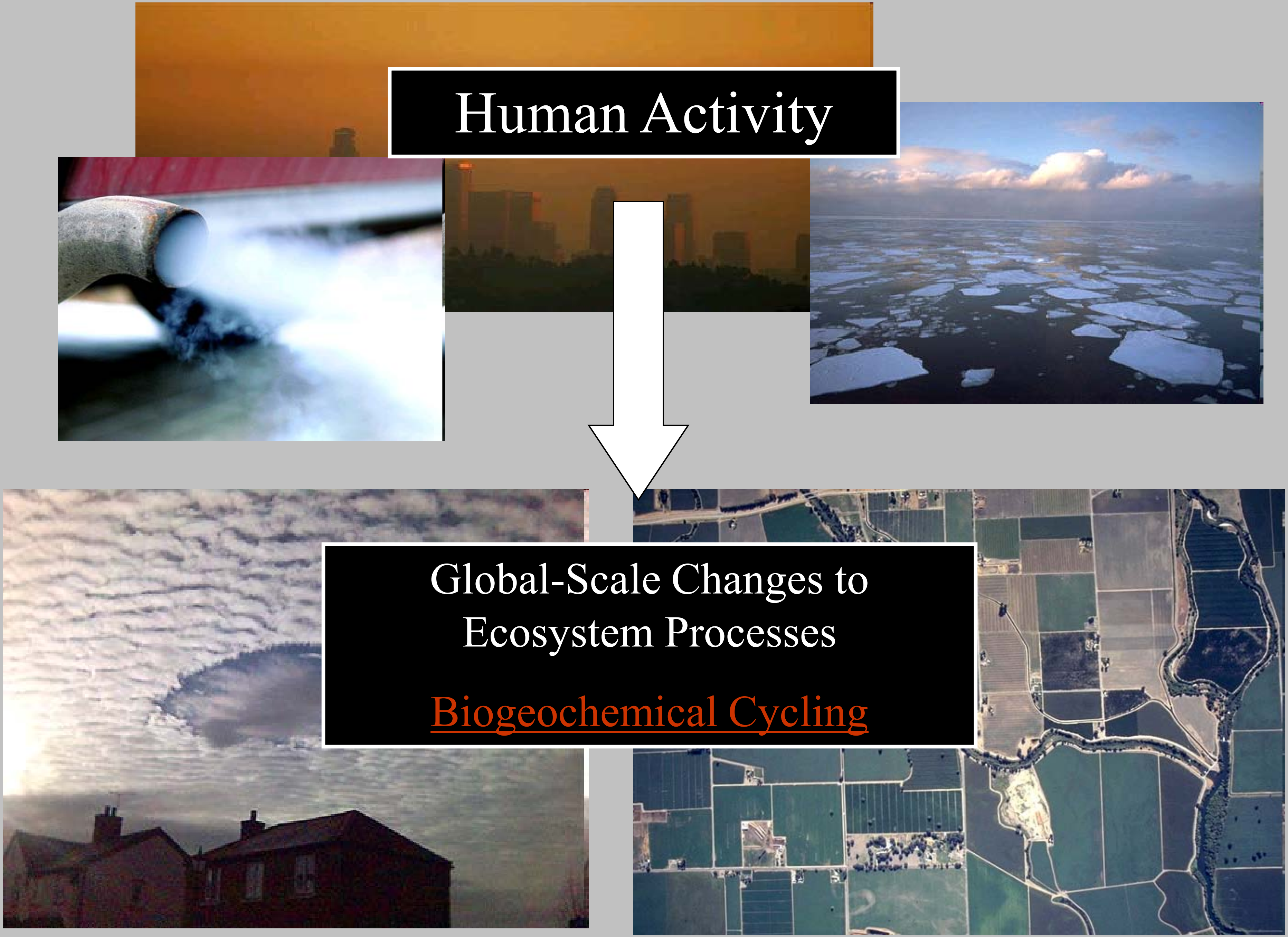


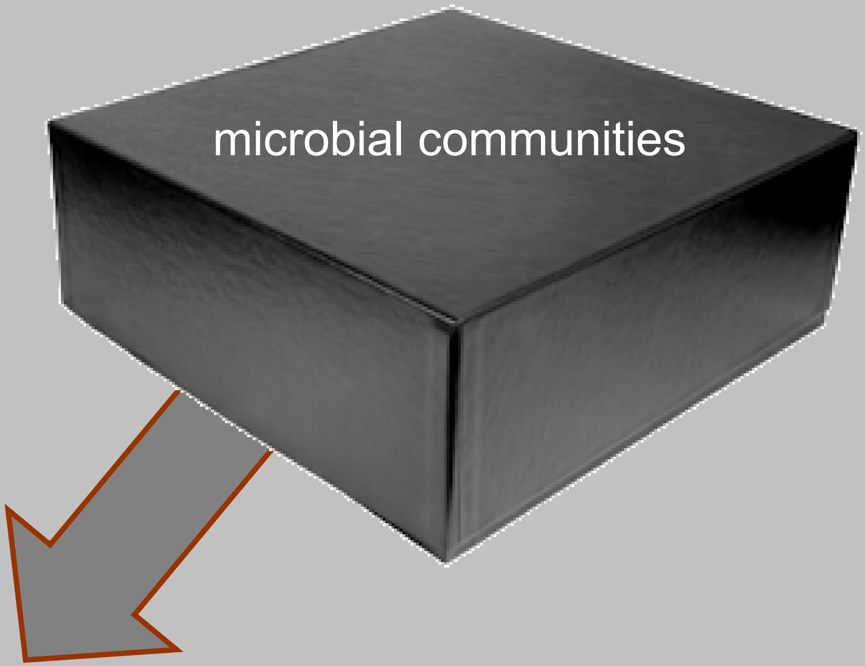
Human Activity

Global-Scale Changes to Ecosystem Processes

Biogeochemical Cycling

Amazing Abundance and Biodiversity.

Relatively Little Understanding.



microbial communities

Development of molecular techniques to examine microbial biodiversity

Amazing Abundance and Biodiversity.

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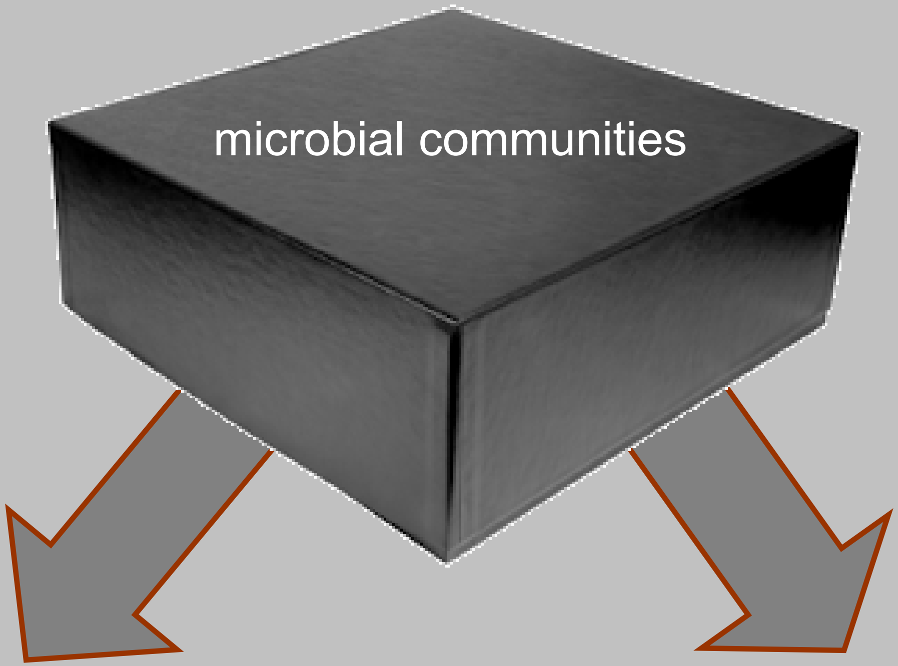


Development of molecular techniques to examine microbial biodiversity

Rates of microbial processes are enough to understand how a system works

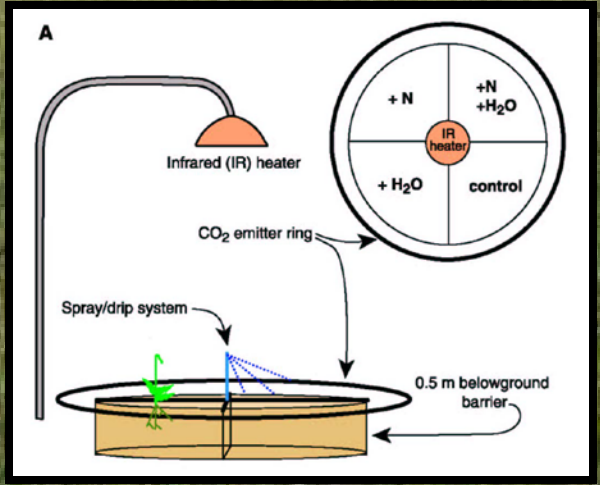
Does the microbial community matter to rates of soil nitrogen cycling?

- **What level of community resolution is important?**
    - Is knowing abundance enough?
    - Is information about specific community members important?

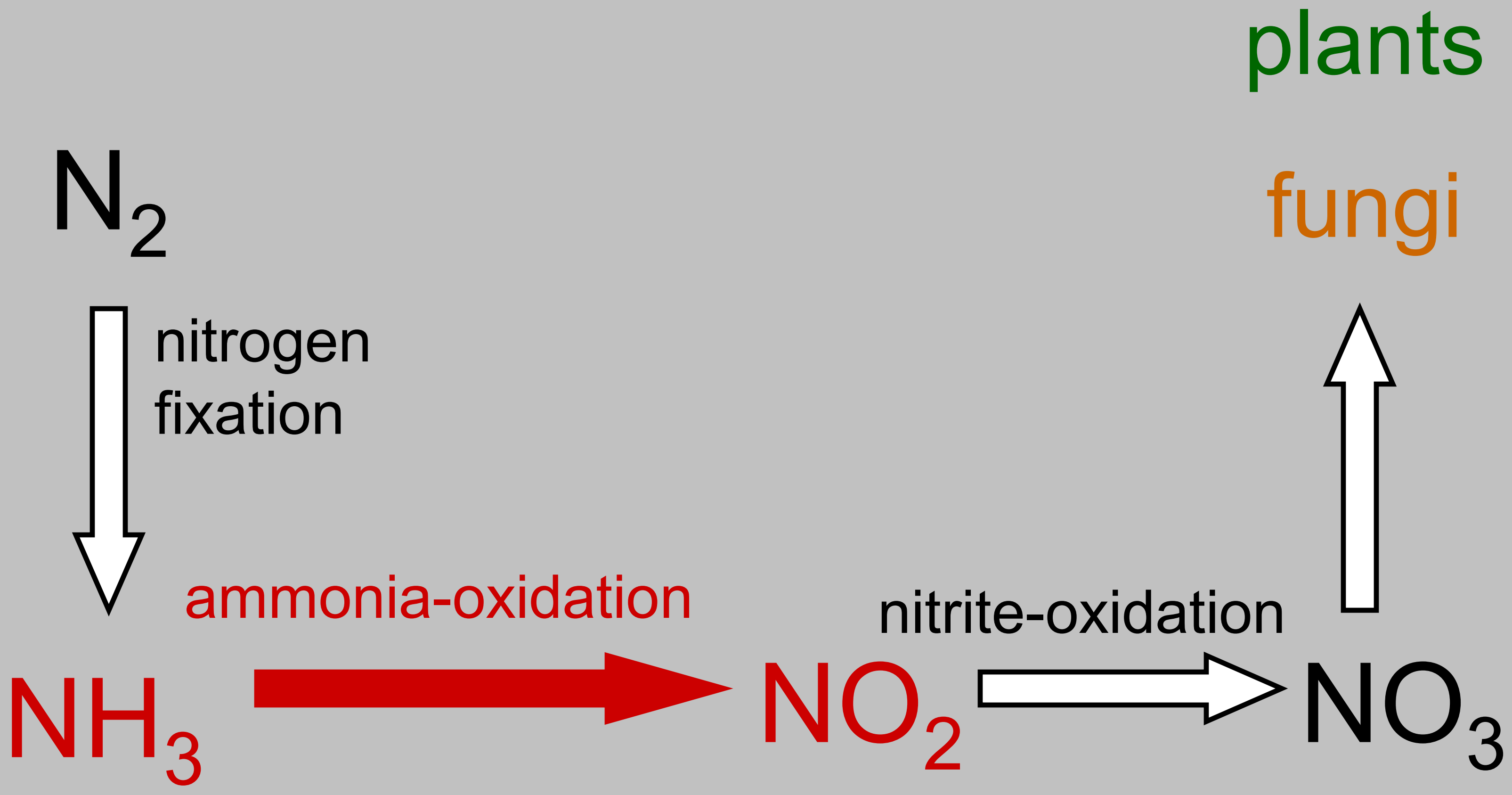
- **Are microbial communities impacted by global change?**
    - What are the implications for nutrient cycling?

Global Change is Multi-Factorial

- **CO_2*** (700 ppm)
- **Temperature*** (1.5-2°C)
- **Precipitation** (50% over ambient)
- **N-Deposition** (7 g NO_3 m^{-2} y^{-1})



Nitrogen Cycling and Global Change



plants

fungi

N_2

nitrogen fixation

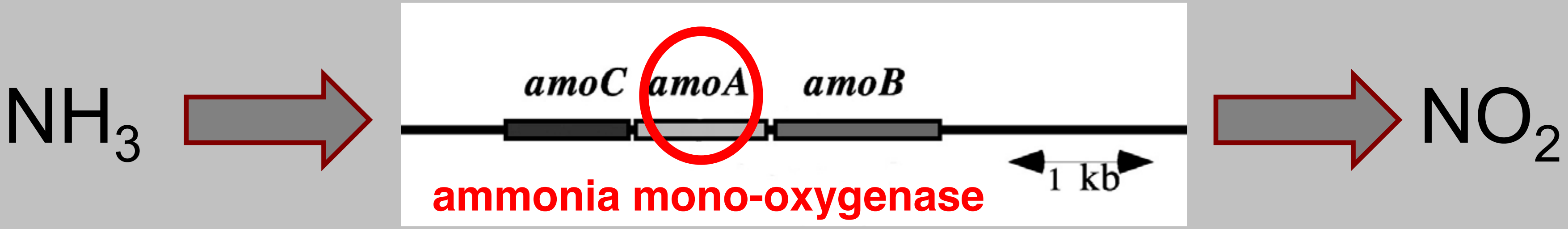
ammonia-oxidation

nitrite-oxidation

NH_3 NO_2 NO_3

NITRIFICATION

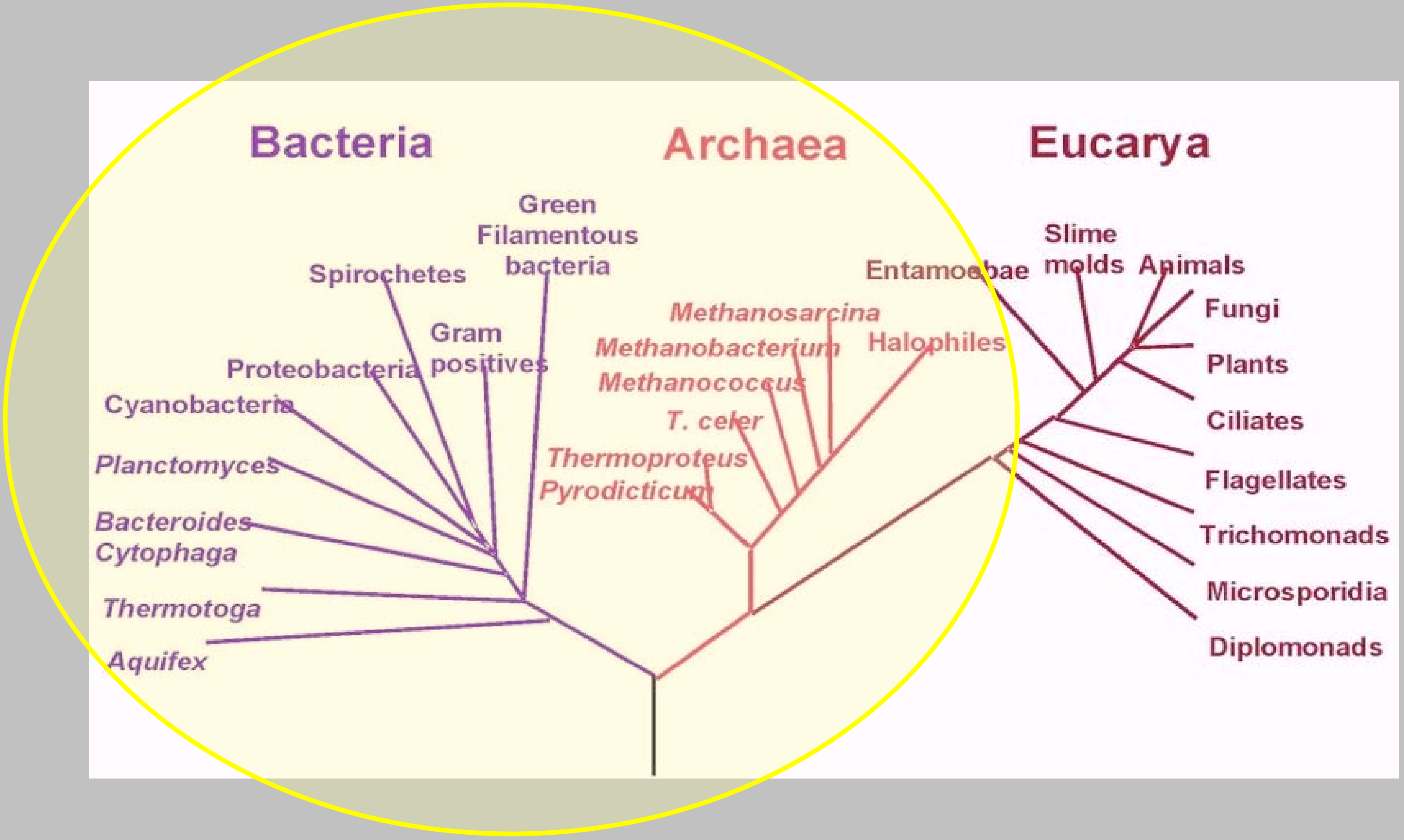
Functional Genes for Uncultured Microorganisms



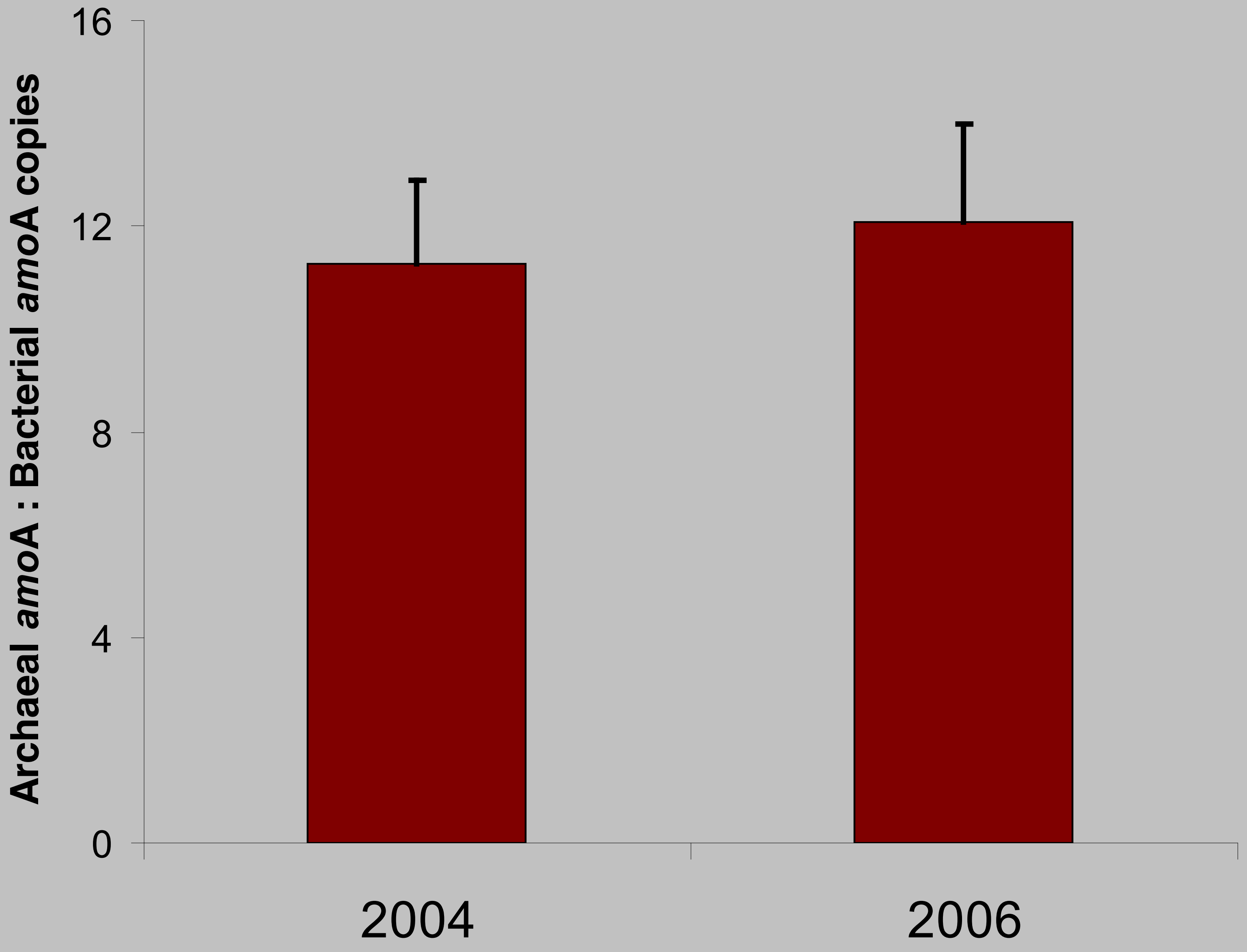
NH_3

ammonia mono-oxygenase

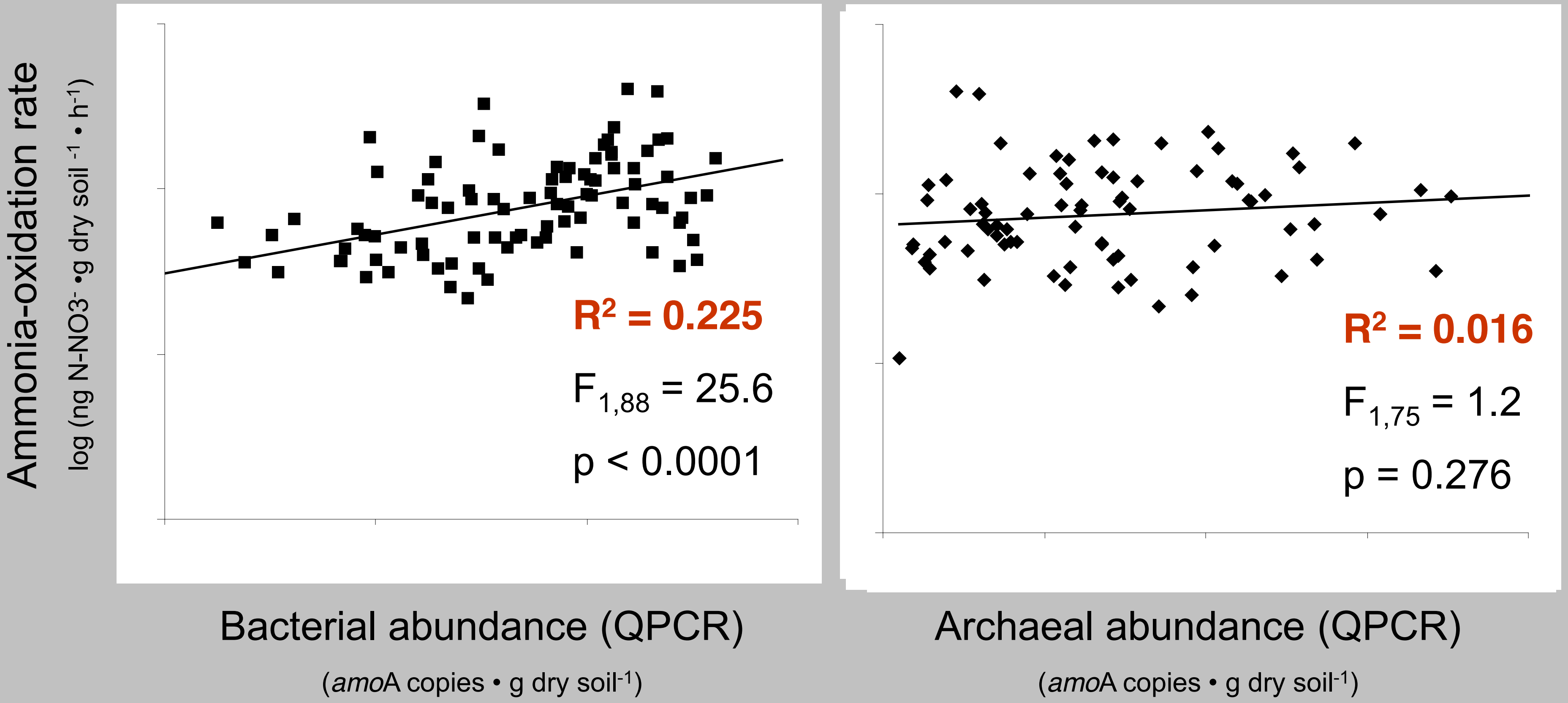
NO_2



Archaea are more abundant than Bacteria.



Does abundance of ammonia-oxidizers explain nitrification rate?



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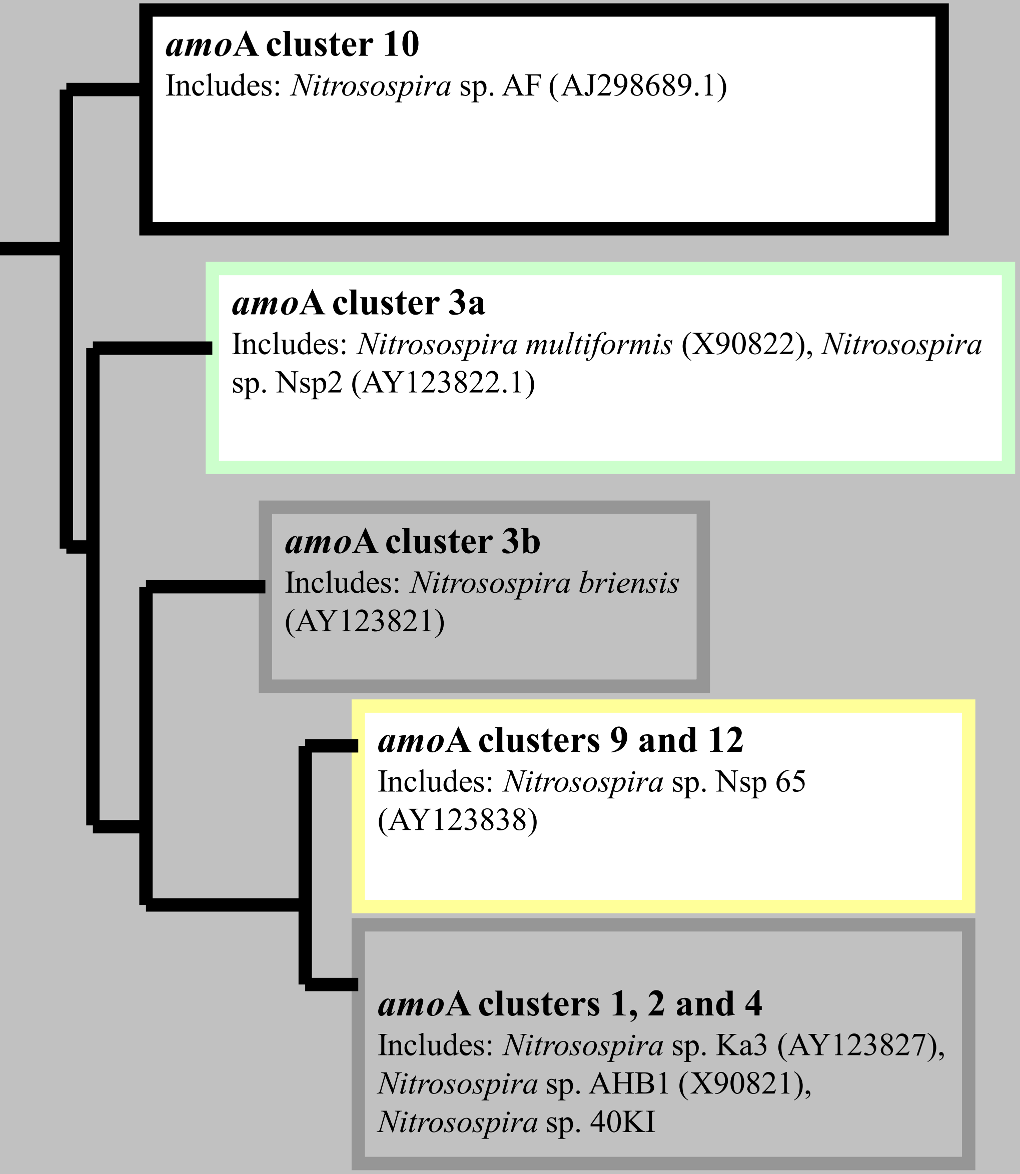
Ammonia-oxidizing Bacterial Community Structure



amo**A cluster 10**
Includes: *Nitrosospira* sp. AF (AJ298689.1)

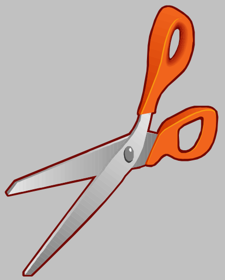
amo**A cluster 3a**
Includes: *Nitrosospira multiformis* (X90822), *Nitrosospira* sp. Nsp2 (AY123822.1)

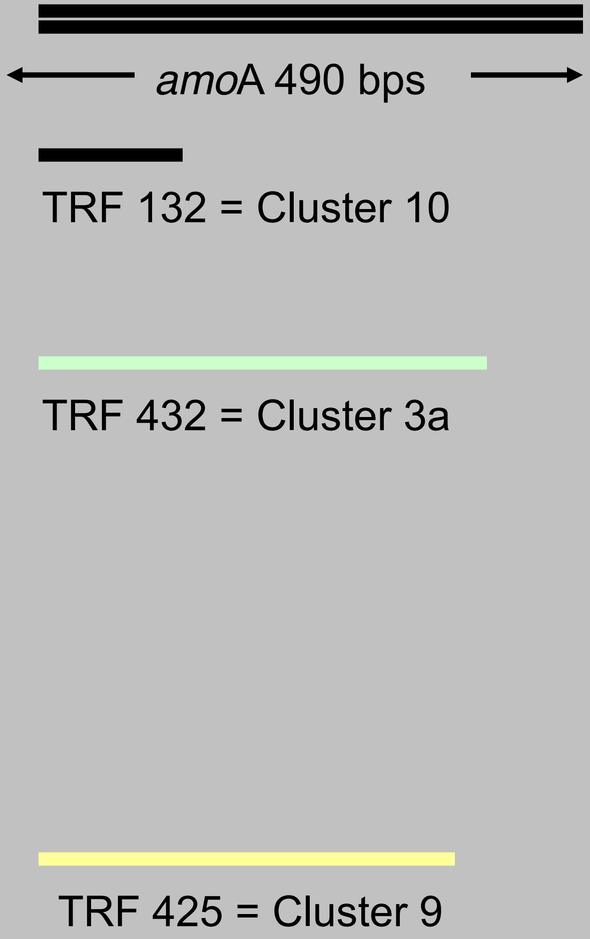
amo**A cluster 3b**
Includes: *Nitrosospira briensis* (AY123821)

amo**A clusters 9 and 12**
Includes: *Nitrosospira* sp. Nsp 65 (AY123838)

amo**A clusters 1, 2 and 4**
Includes: *Nitrosospira* sp. Ka3 (AY123827), *Nitrosospira* sp. AHB1 (X90821), *Nitrosospira* sp. 40KI

*Bsh*12362I





*amo*A 490 bps

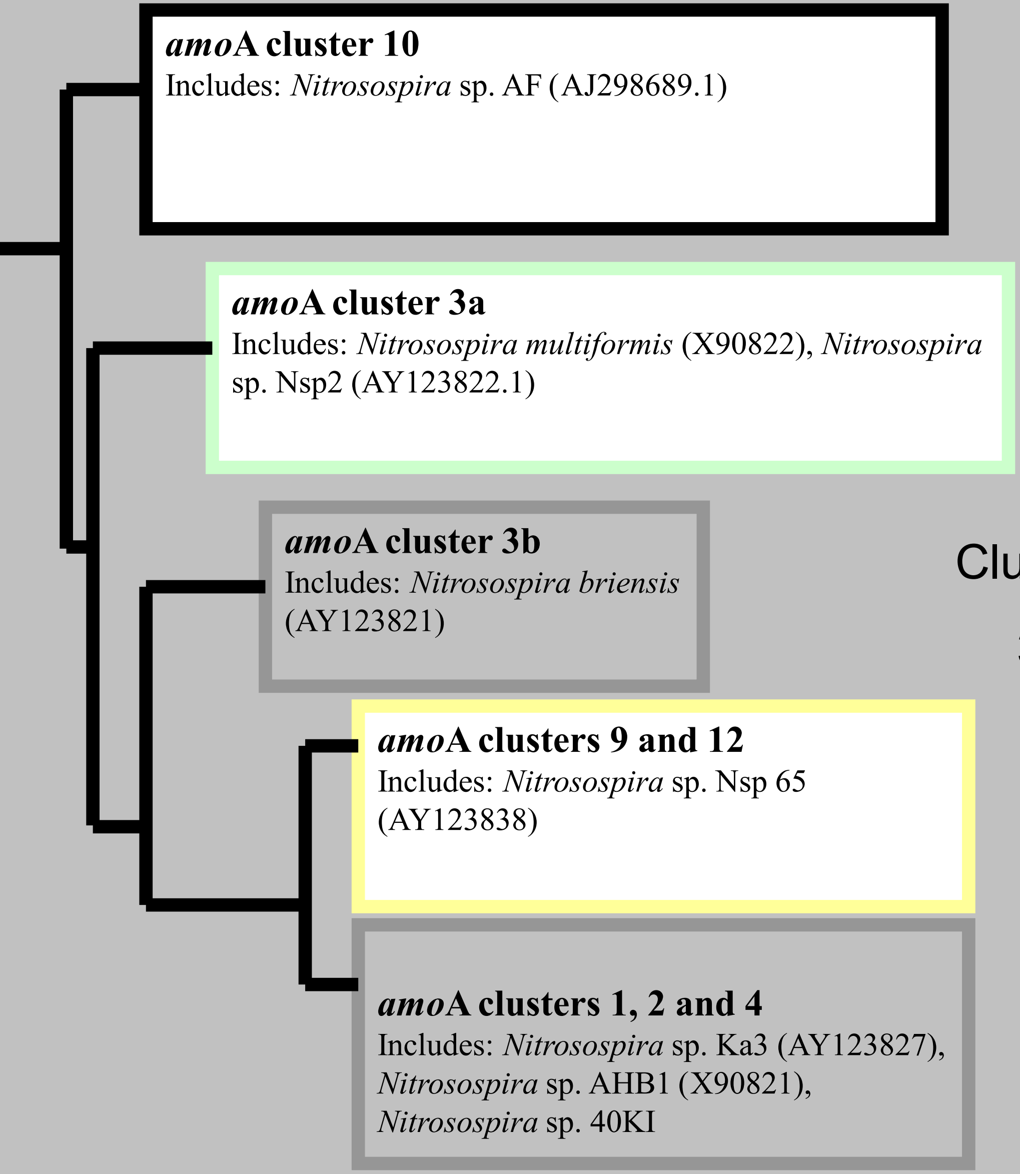
TRF 132 = Cluster 10

TRF 432 = Cluster 3a

TRF 425 = Cluster 9

from Horz et al. 2004, Avrahami and Conrad 2003

Ammonia-oxidizing Bacterial community



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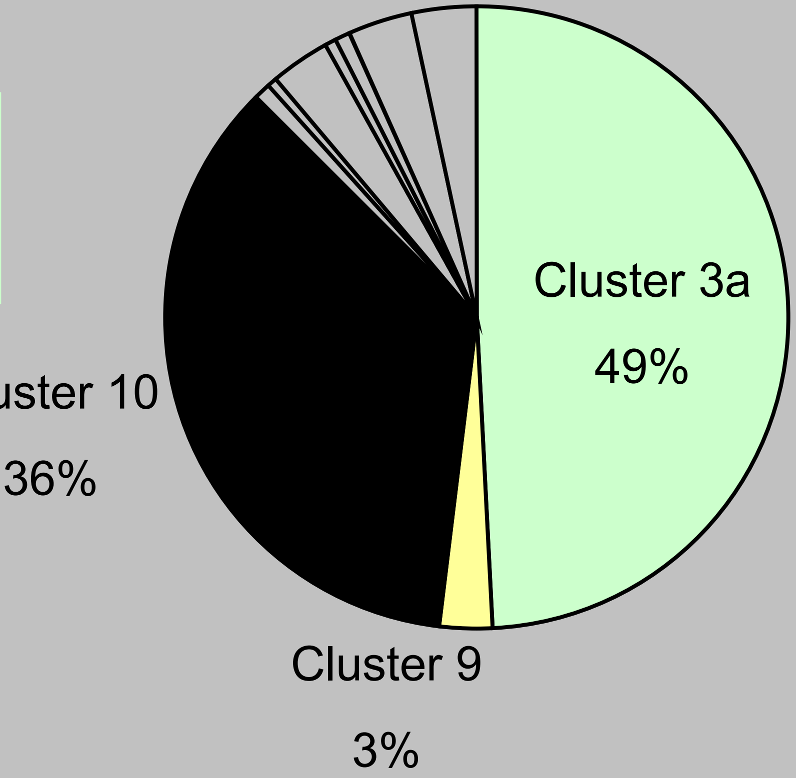
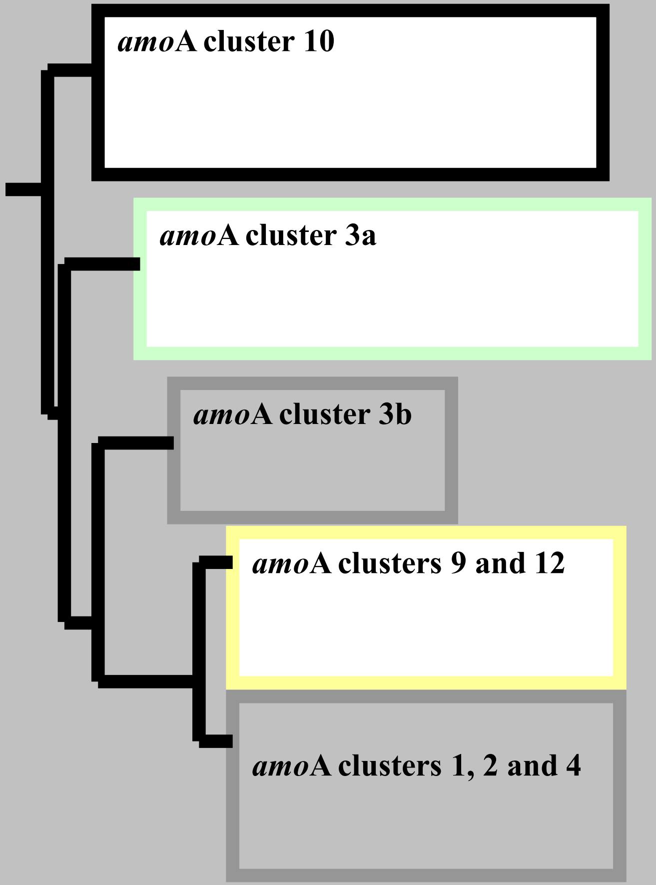


from Horz et al. 2004, Avrahami and Conrad 2003

Ammonia-oxidizing Bacterial community structure is more tightly linked to rate than abundance.



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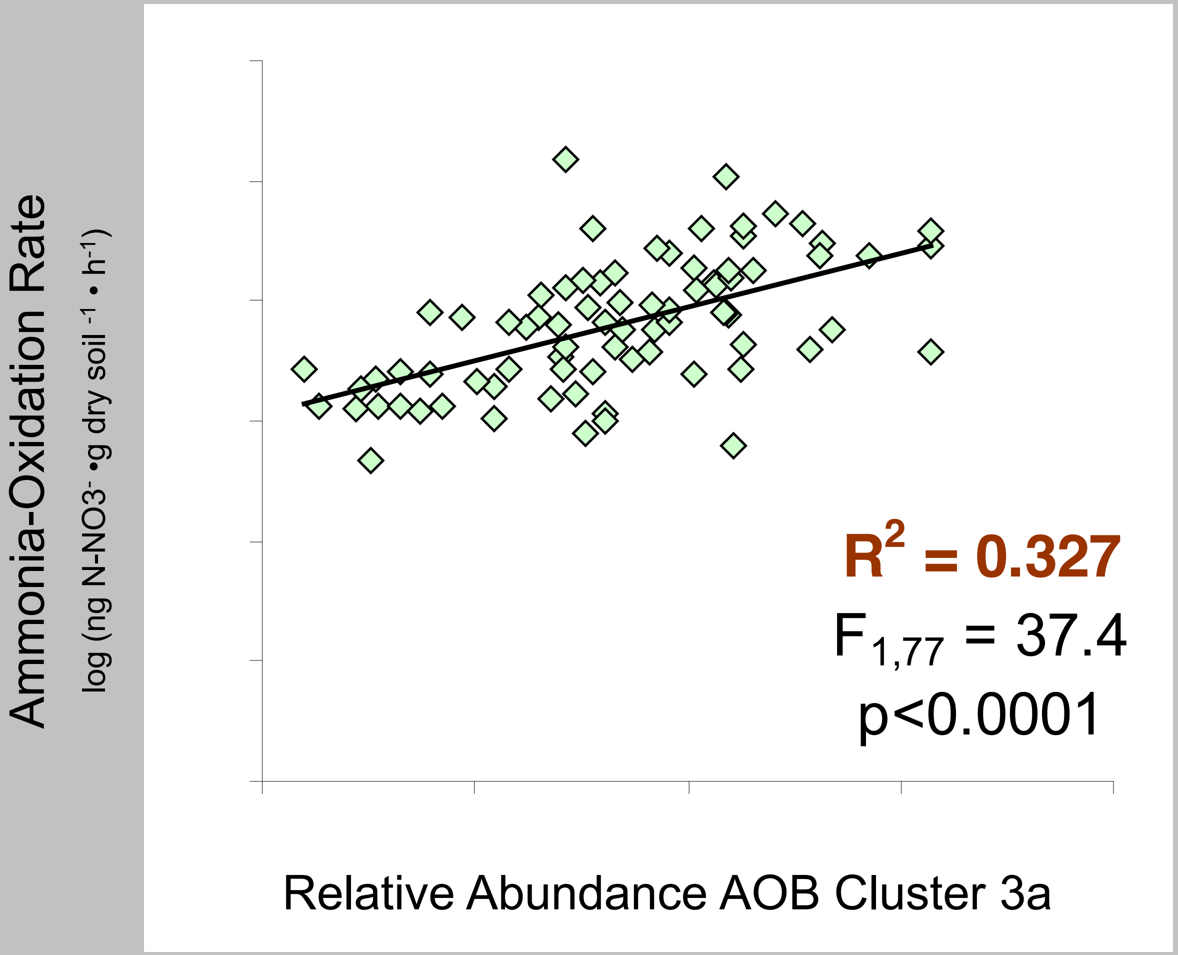
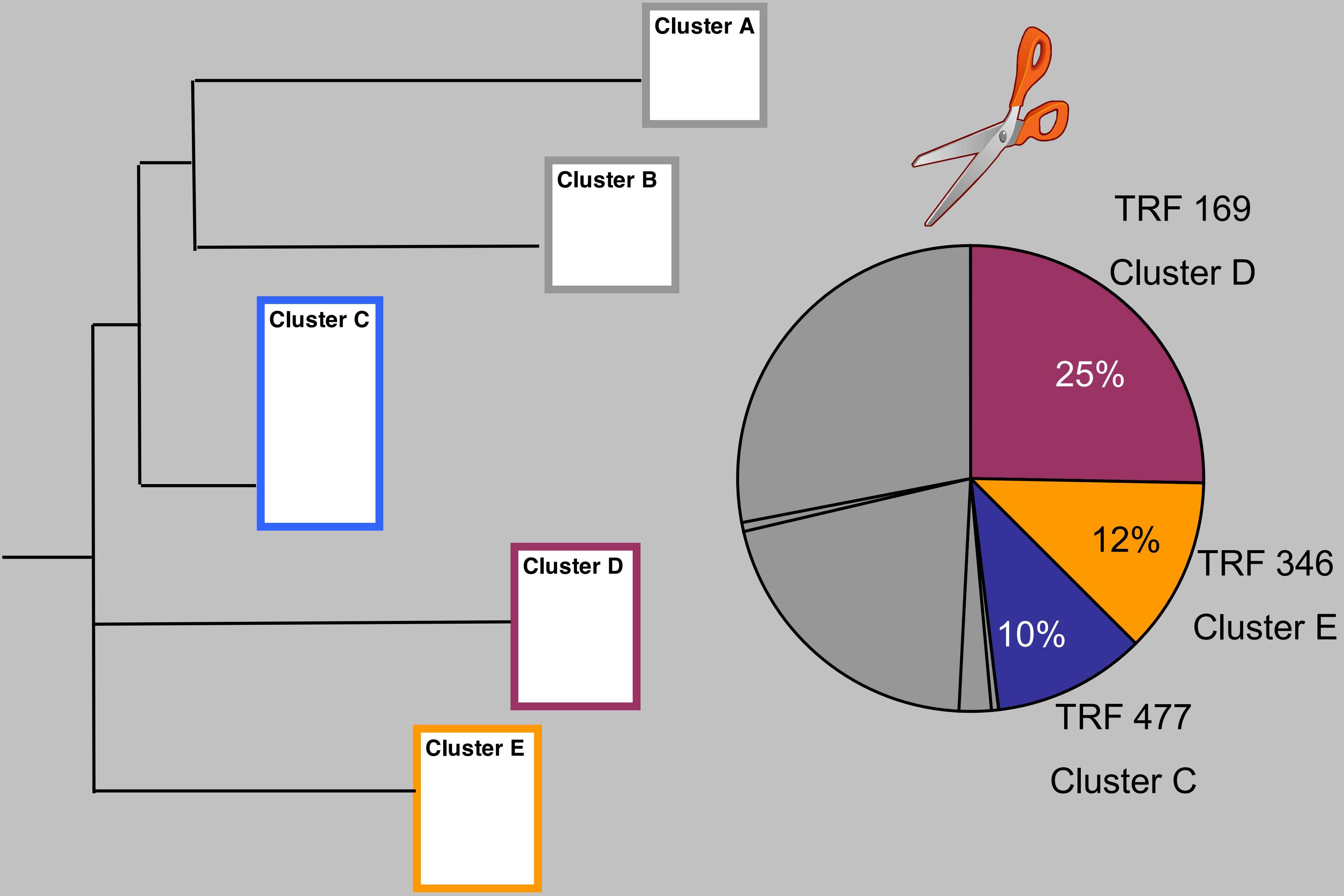


Ammonia-oxidizing Archaeal Community Structure



Cluster A

Cluster B

Cluster C

Cluster D

Cluster E

TRF 169

Cluster D

25%

12%

TRF 346

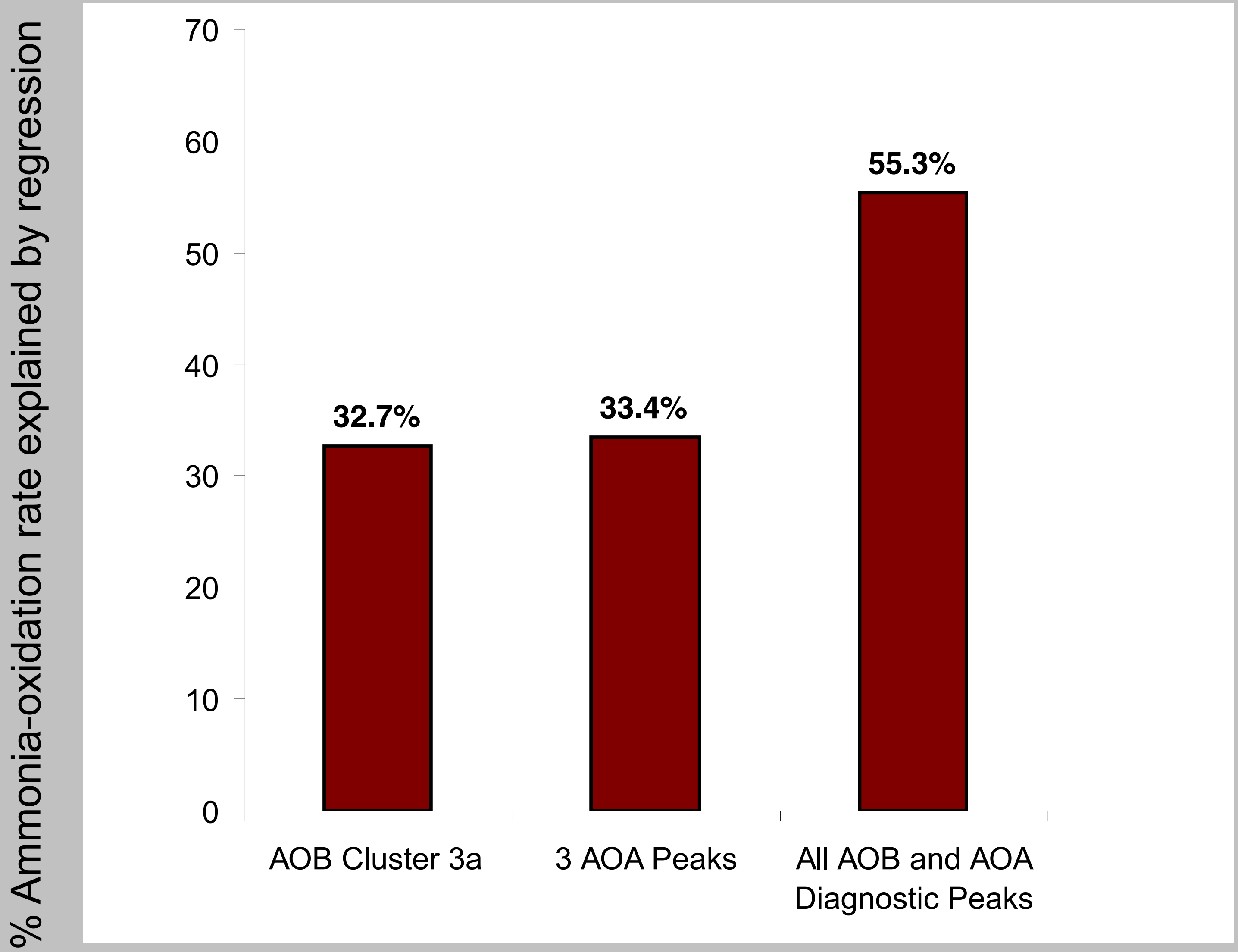
Cluster E

10%

TRF 477

Cluster C

Including Ammonia-oxidizing Archaeal community structure increases explanation of variation in rate



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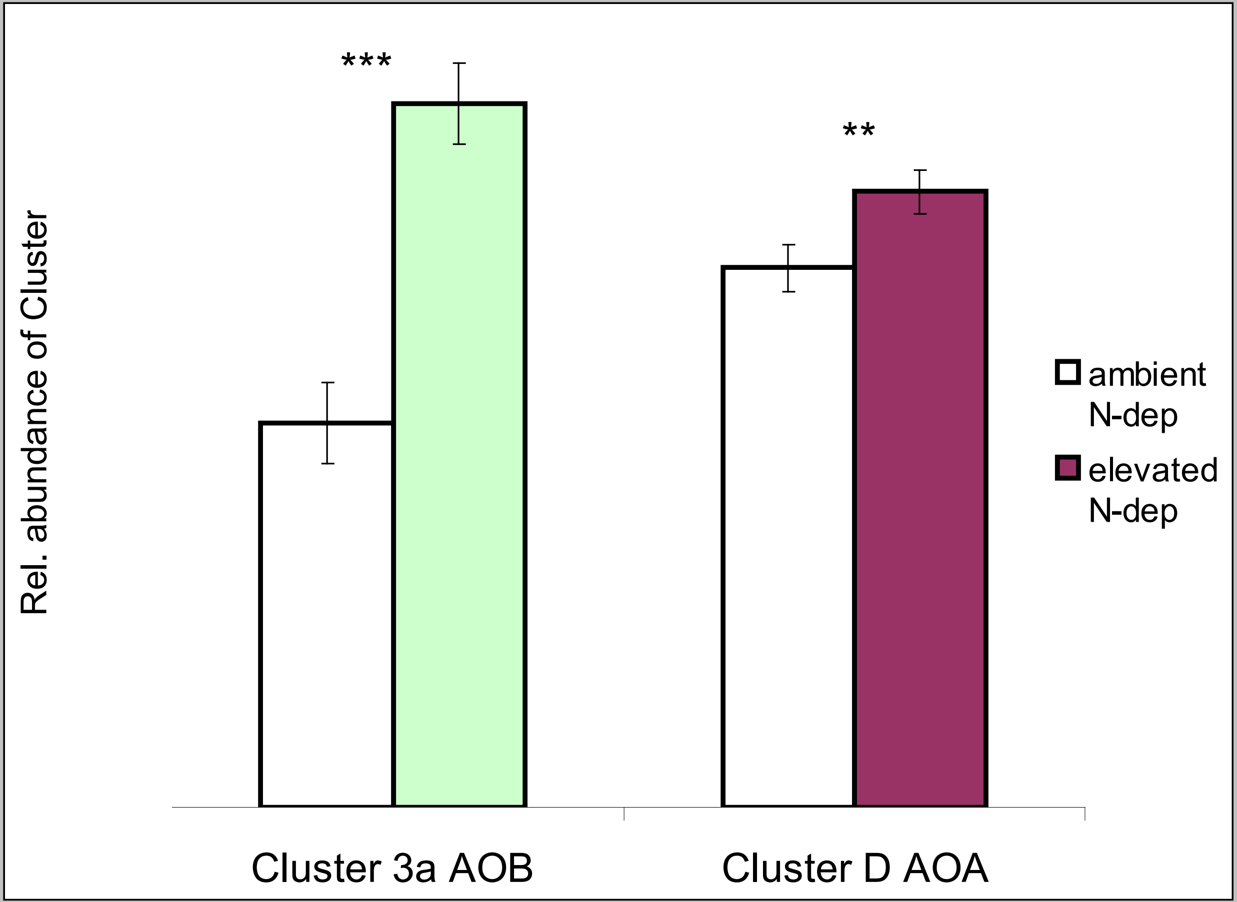
Nitrogen Deposition Influences Ammonia-Oxidizer Communities



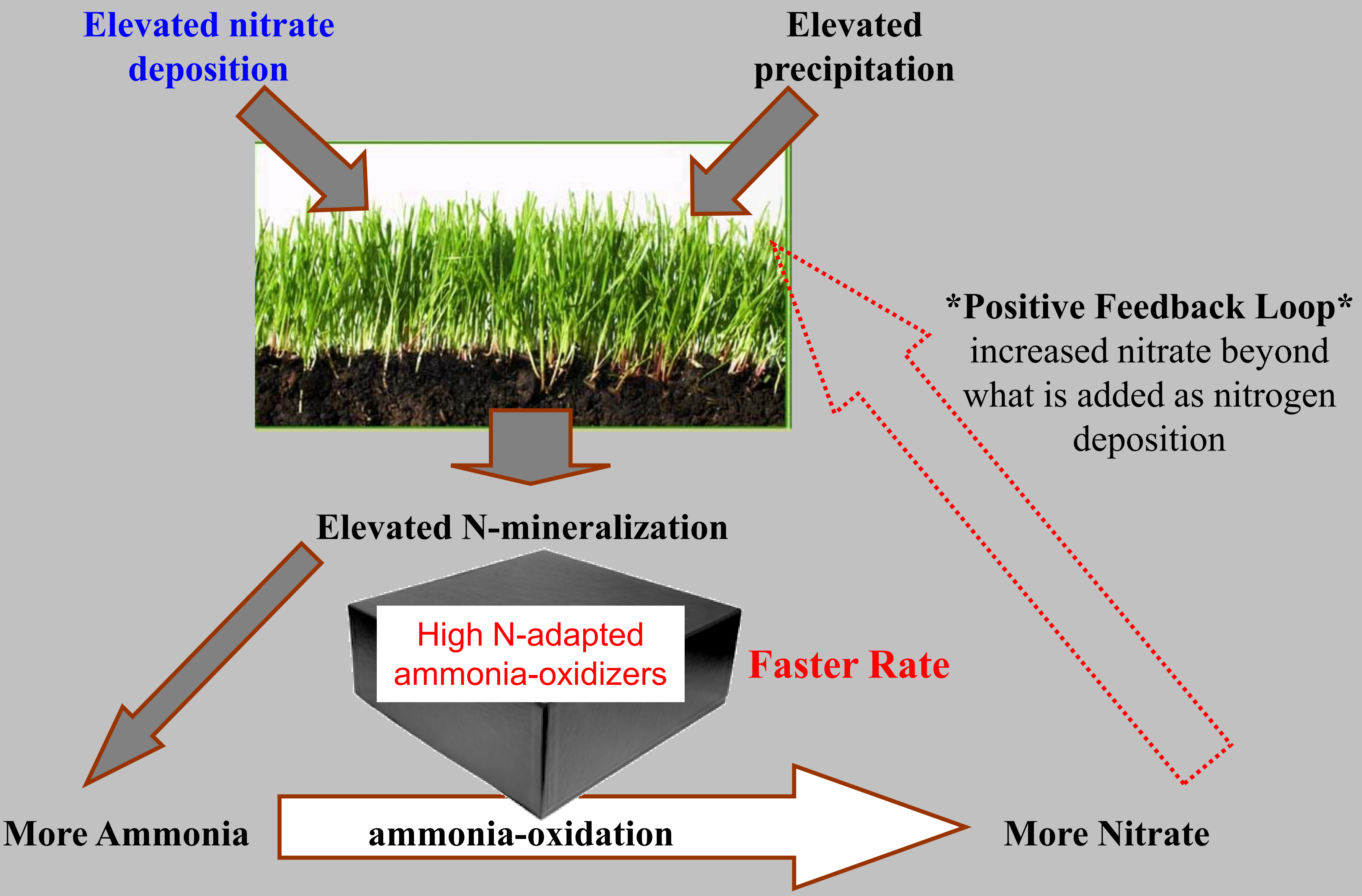
Bacteria

- N-deposition as a single factor is the only significant effect

Archaea

- N-deposition increases TRF166 and decreases TRF 474
- Precipitation increases TRF 345
- Heat x Nitrogen alters non-diagnostic peaks

Increased Consequences of Nitrogen Deposition



Elevated nitrate deposition

Elevated precipitation

Elevated N-mineralization

High N-adapted ammonia-oxidizers

Faster Rate

Positive Feedback Loop
increased nitrate beyond what is added as nitrogen deposition

More Ammonia

ammonia-oxidation

More Nitrate

Take home points

Abundance

- Bacterial abundance, but not Archaeal abundance, is related to ammonia-oxidation rate

Community Structure

- Bacterial Cluster 3a explains more variation in ammonia-oxidation rate than any other single community member
- Archaeal community structure + Bacterial Cluster 3a explains over 50% in ammonia-oxidation rate

Global Change

- Nitrogen deposition as a single factor significantly alters Bacterial and Archaeal communities
- Archaeal communities respond to multiple global change factors

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SYMP 13-5: Patterns in soil ammonia-oxidizer response to global change

Kathryn M. Docherty, University of Oregon and Brendan Bohannan, University of Oregon.

Background/Question/Methods

The Domains Archaea and Bacteria contain the vast majority of Earth's biodiversity and biomass, and their members play critical, often exclusive, roles in many biogeochemical cycles and ecosystem services. Human-induced global change, particularly with respect to increased nitrogen deposition, has the potential to drastically alter how soil nitrifying communities perform their biogeochemical function. Additionally, multi-factor global change can alter how microbial communities interact with each other and with the associated plant communities. This study, performed in the context of the long-term Jasper Ridge Global Change Experiment (JRGCE) in a California grassland ecosystem, examines how ammonia-oxidizing Archaea and Bacteria (AOA and AOB, respectively) respond to multi-factor global change. Manipulations at the JRGCE include simultaneous increases in CO_2, warming, precipitation and nitrogen deposition. Past studies have utilized DNA-fingerprinting methods to assess ammonia-oxidizer response to multi-factor global change. This study compares how seed bank (DNA-based) versus metabolically active (RNA-based) ammonia-oxidizing communities respond to global change manipulations over several seasons. We have employed ultra-deep 454-pyrosequencing techniques to examine these communities using the ammonia mono-oxygenase (*amo*A) functional gene marker. Effects of global change have been examined at several phylogenetic levels and linked this community information to gross rates of nitrification using ^{15}N stable isotopic methods. Ammonia-oxidizer and plant communities have been compared using multivariate statistical methods.

Results/Conclusions

Our results show that both AOB and AOA communities are highly influenced by nitrogen deposition in both their abundance and community structure. These changes are linked to increased nitrification rate in the elevated nitrogen deposition plots. Our results further show that the relationship between the AOB and plant communities fundamentally changes under long-term nitrogen deposition manipulation. This positive feedback loop may enhance the rate of change in ammonia-oxidizer communities, which may further elevate nitrification rates. This study provides strong evidence that incorporating microbial community and abundance information into global change predictions is crucial for understanding how ecosystem-level nutrient cycling rates may change.