Variability of nitrogen and carbon-cycle microbial communities determined by the age of restored wetlands

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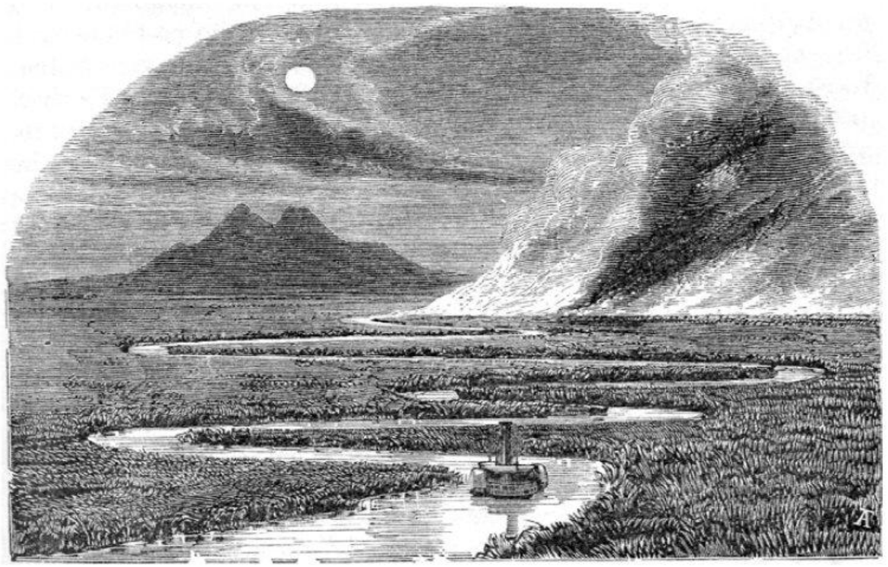
The Sacramento-San Joaquin Delta

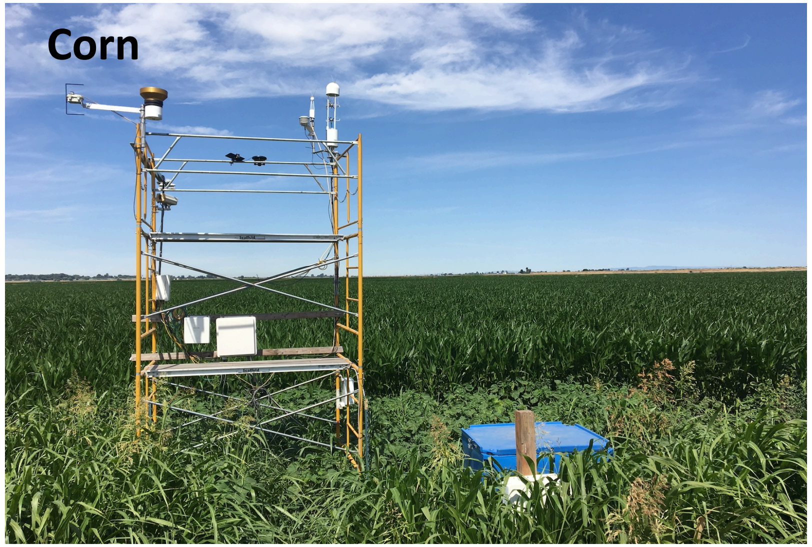
San Francisco Estuary Institute-Aquatic Science Center, 2012

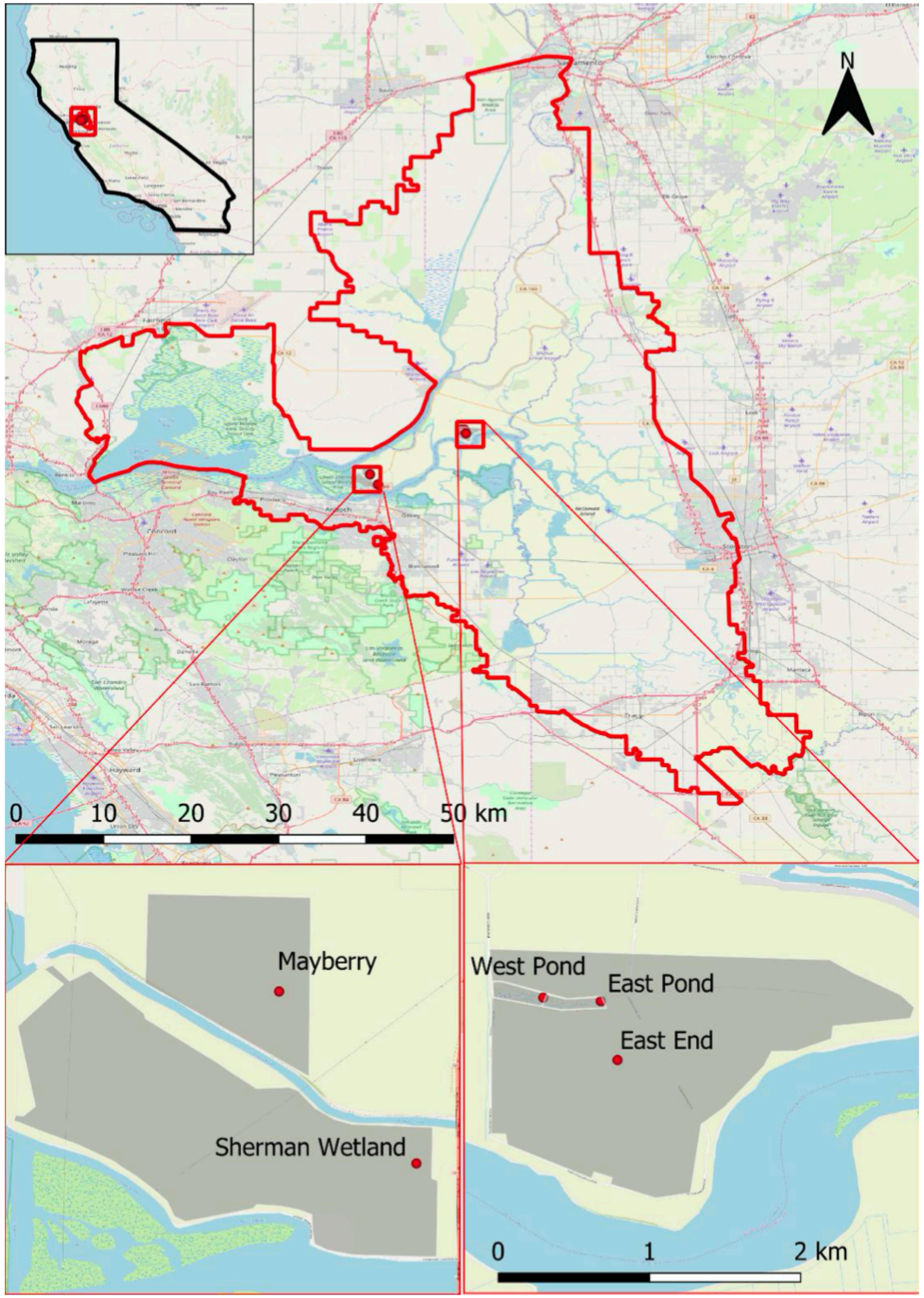


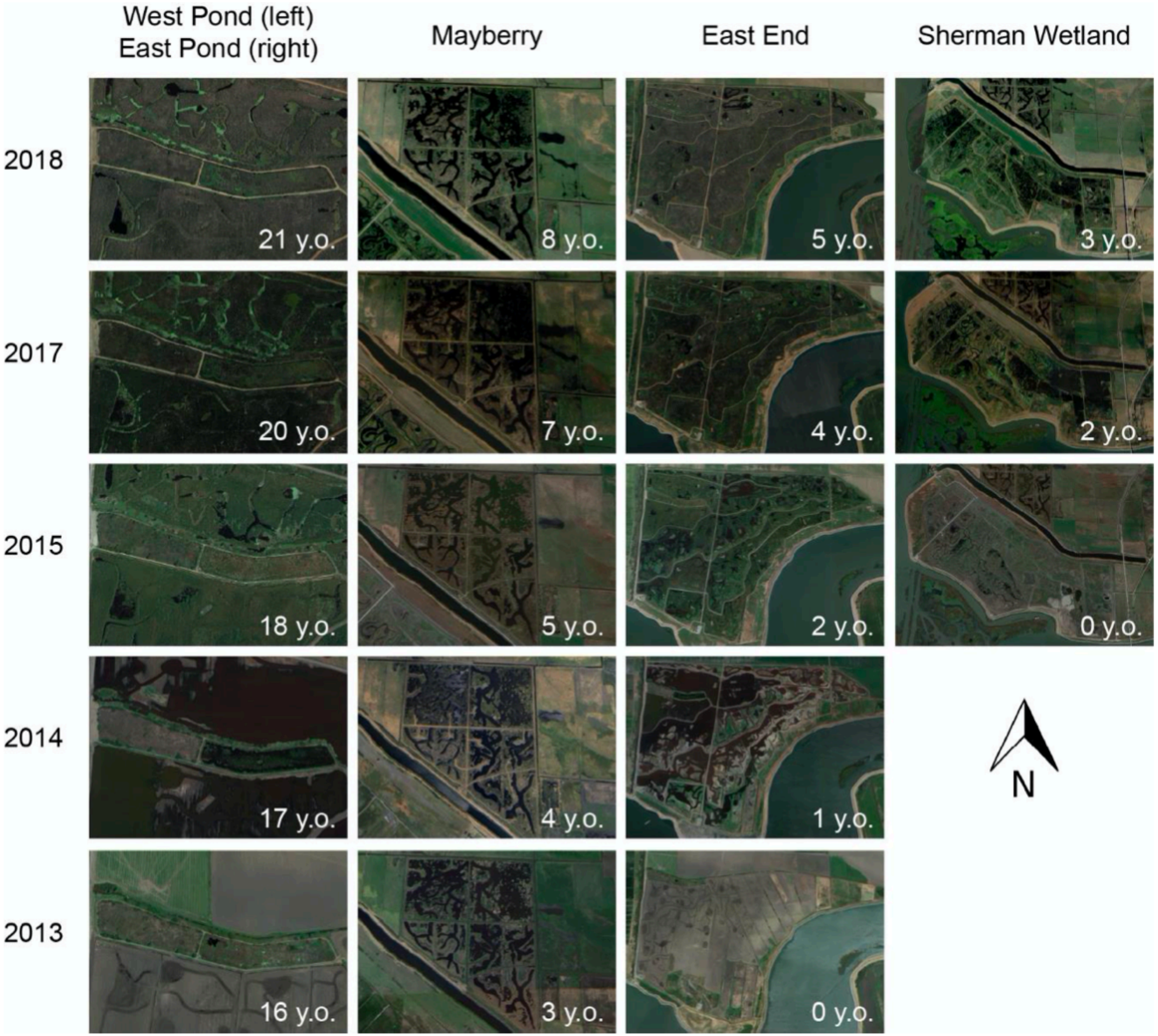
Carbon loss and subsidence

- Originally Delta had 15 m peat soil
- Drained mid to late 19th century for farming
- Up to 9m of subsidence
- Lost about 200 Tg C

Wetland restoration in the Delta

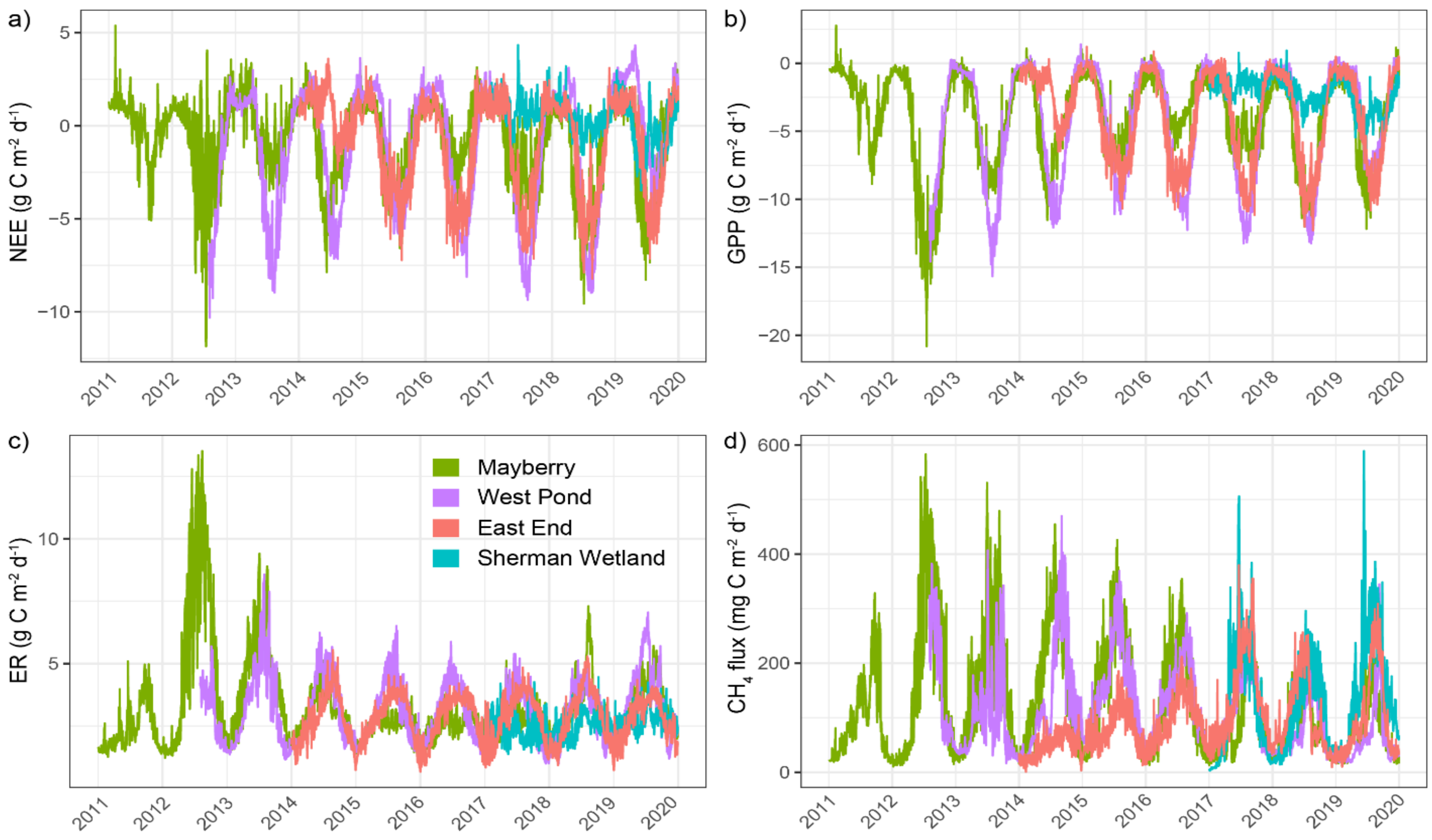






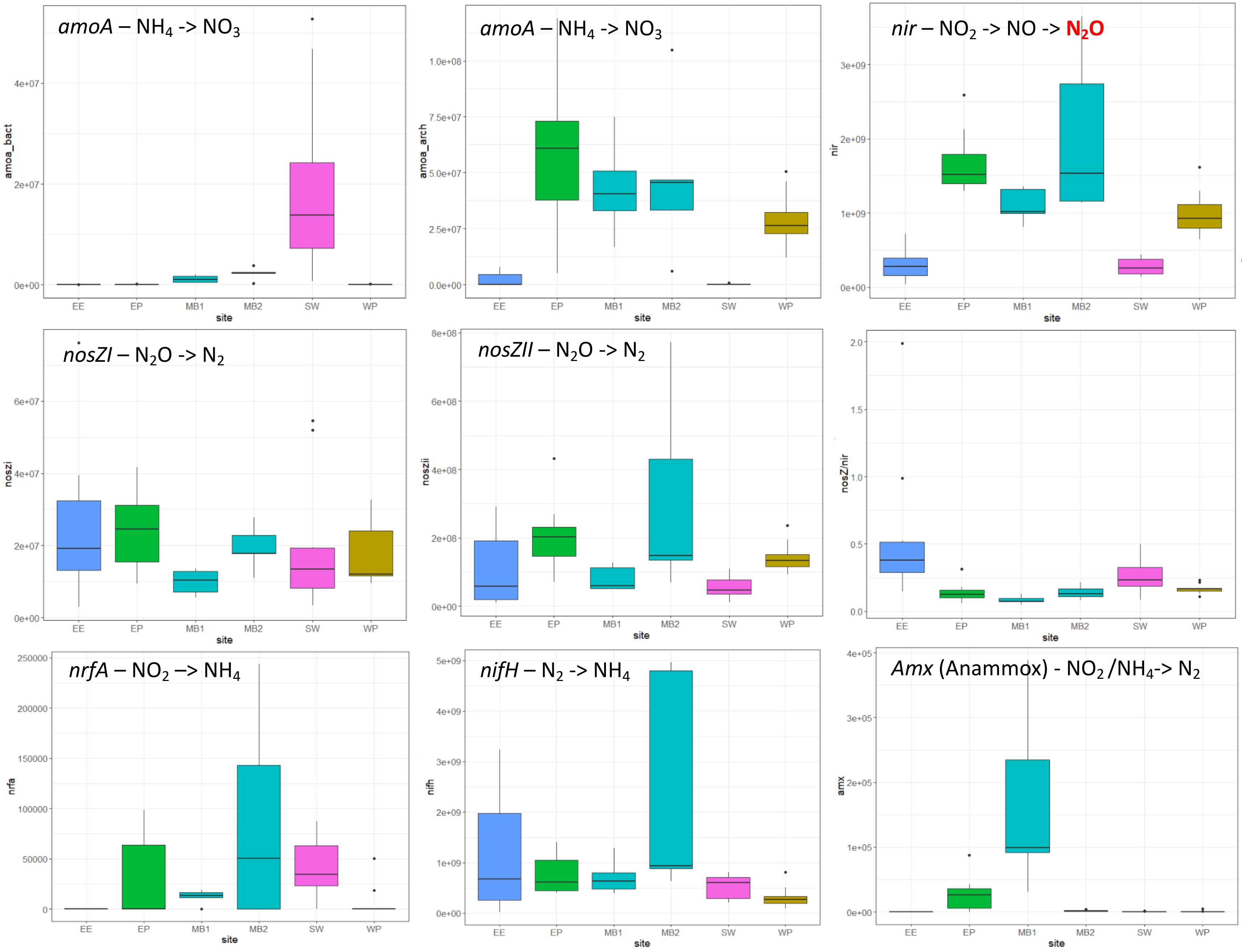
Valach et al. (submitted)

Daily **(a)** ecosystem respiration (ER), **(b)** gross primary production (GPP), **(c)** net ecosystem exchange (NEE) and **(d)** methane flux (F_{CH4}) at the Mayberry, East End, West Pond and Sherman Wetland from Jan 2011 through Dec 2019

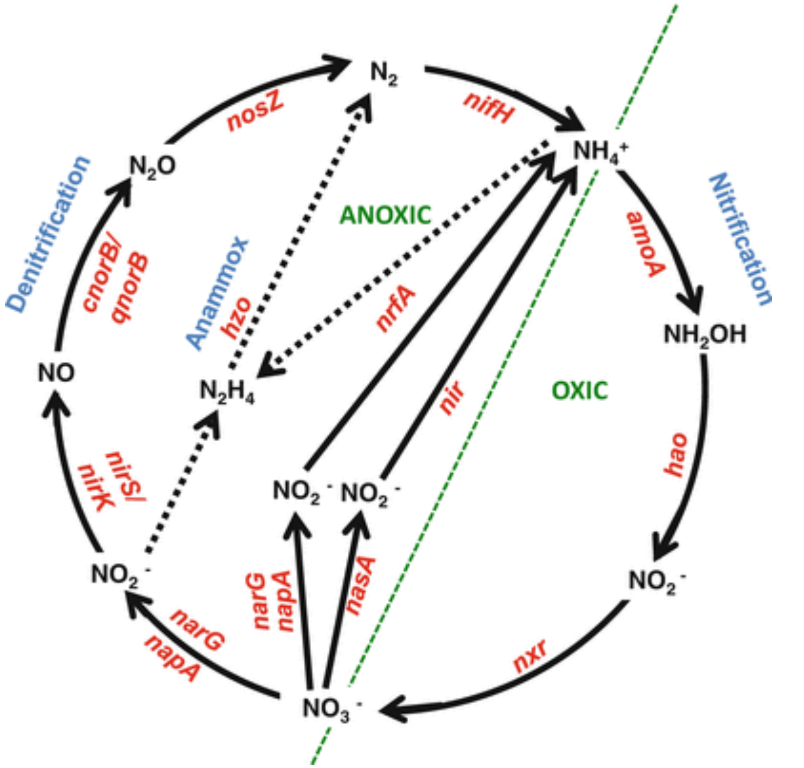


Valach et al. (submitted)

Delta microbiology (N-cycle)

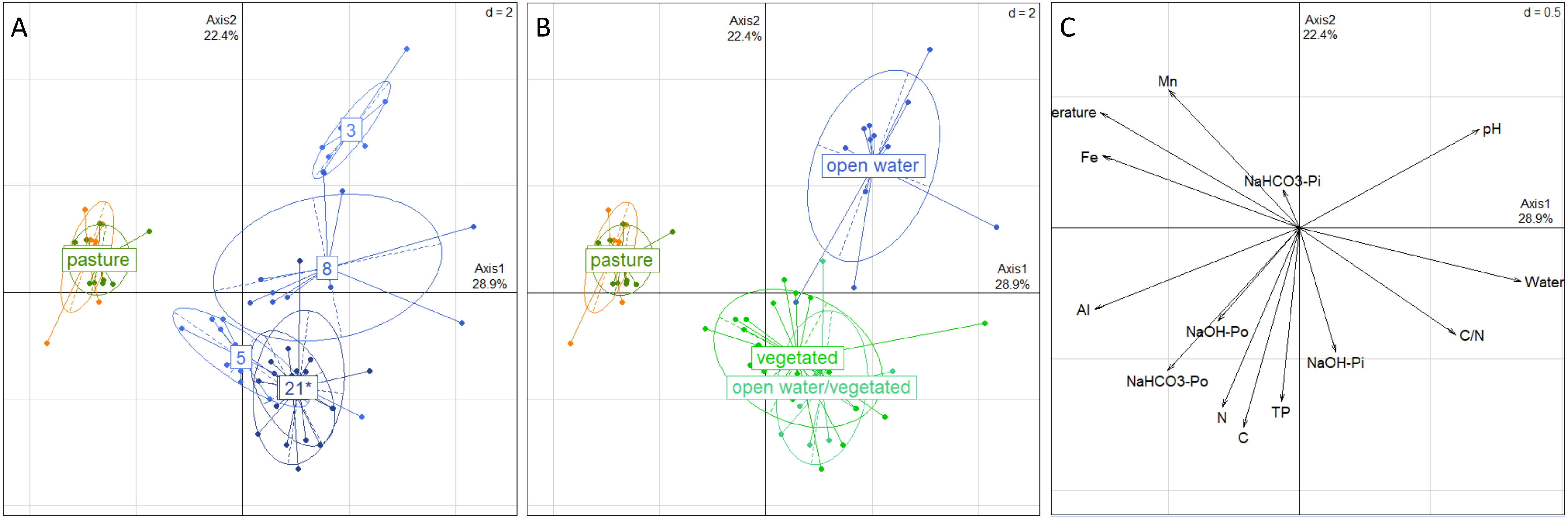


N transforming cycle in wetlands

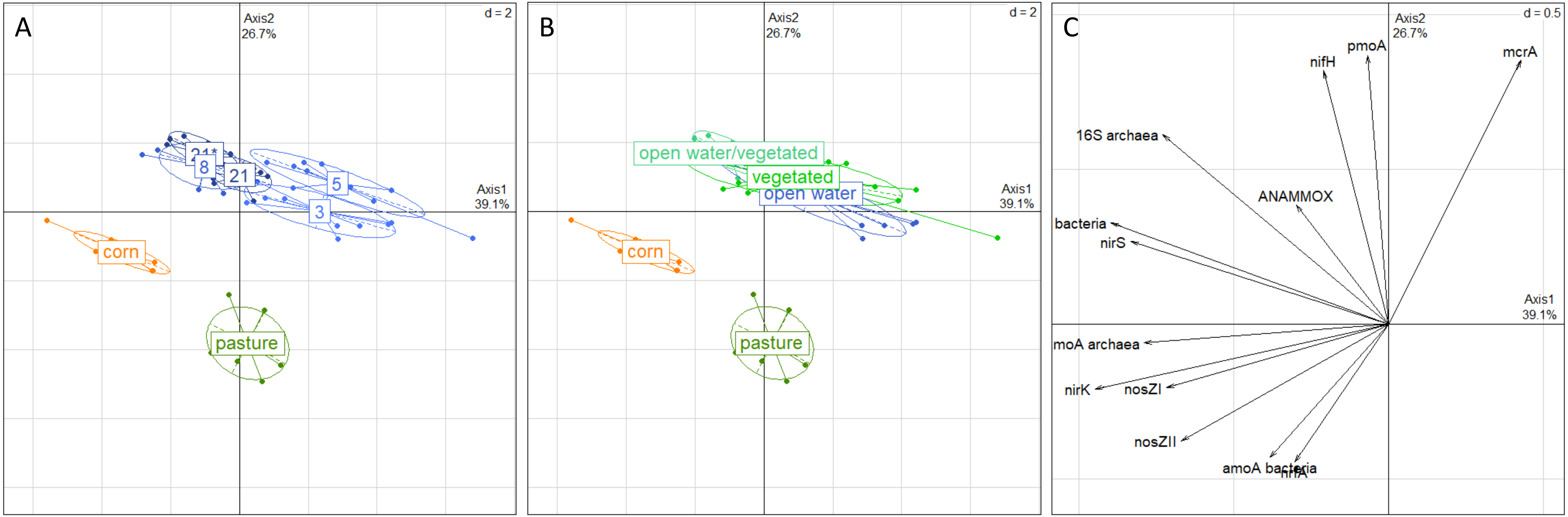


EE – East End wetland (5 y.o.)
EP – East Pond wetland (21* y.o.)
MB1 (vegetated) and **MB2** (open water channels) wetland (8 y.o.)
SW – Sherman wetland (3 y.o.)
WP – West Pond wetland (21 y.o.)

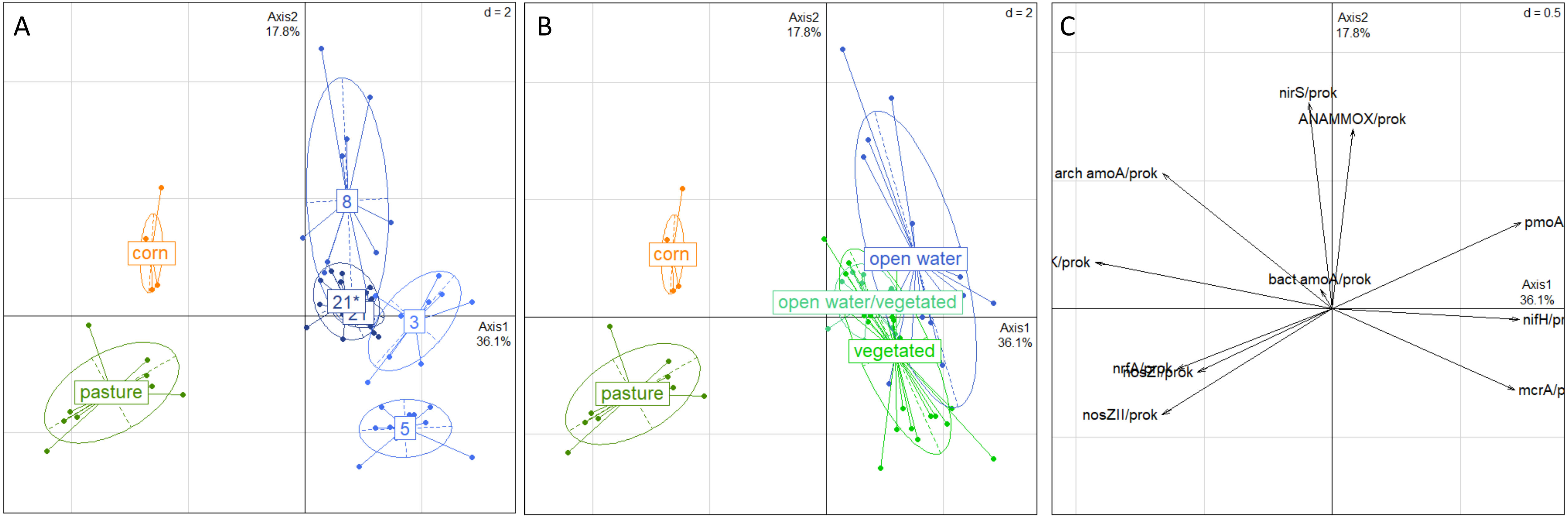
Clustering of the **wetland age after restoration (A)** and **the wetland type (open water or vegetated) (B)** compared to not restored sites of the Delta wetland (California), based on principal component analysis (PCA) of the **physicochemical characteristics (C)** (n = 70).



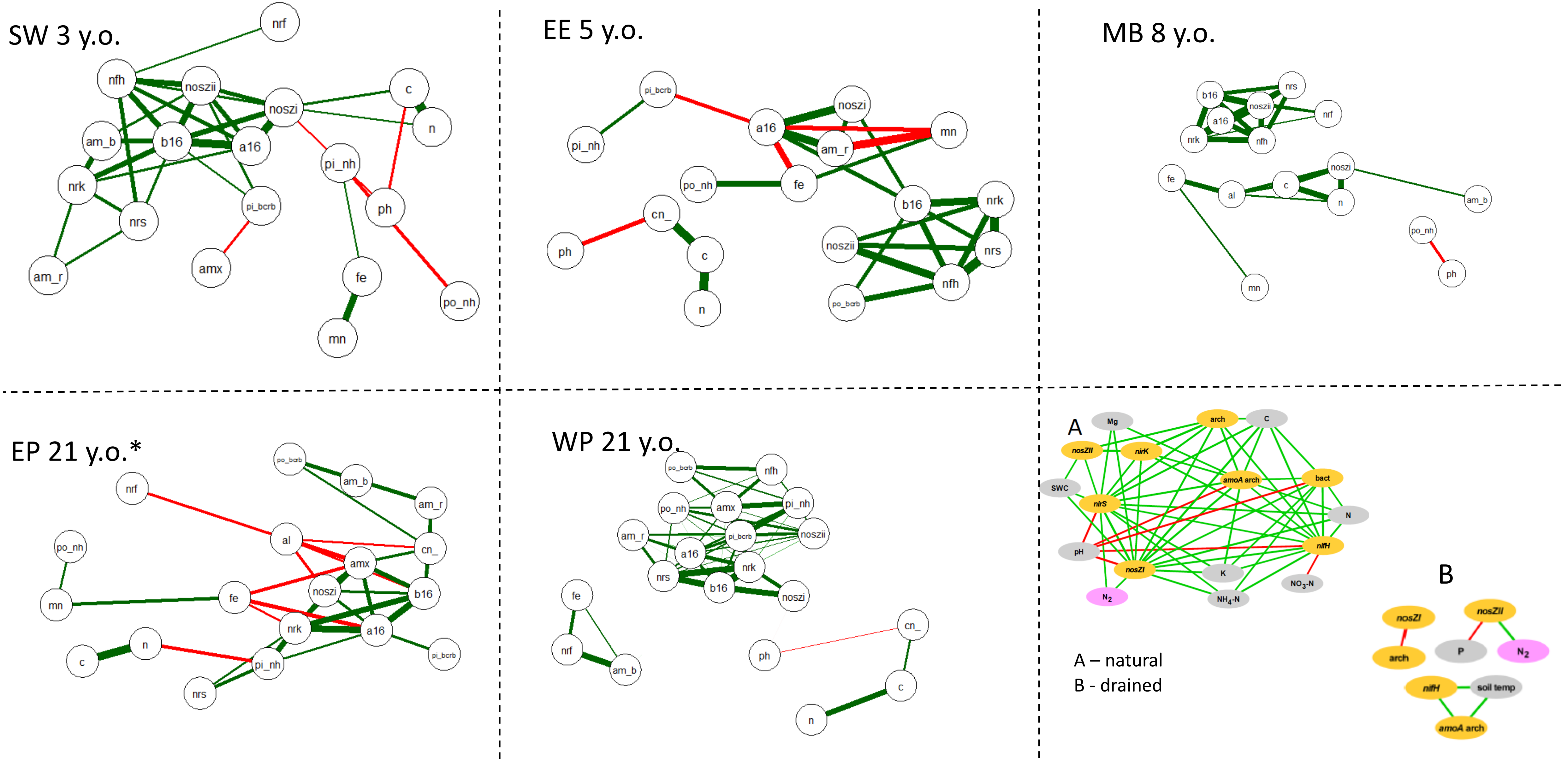
Clustering of the **wetland age after restoration (A)** and **the wetland type (open water or vegetated) (B)** compared to not restored sites of the Delta wetland (California), based on principal components analysis (PCA) of the **target gene abundances (C)** (n = 70).



Clustering of the **wetland restoration age (A)** and **the wetland type (B)** compared to not restored sites of the Delta wetland (California), based on principal components analysis (PCA) of the **target gene proportions in the prokaryotic community (C)** (n = 70).

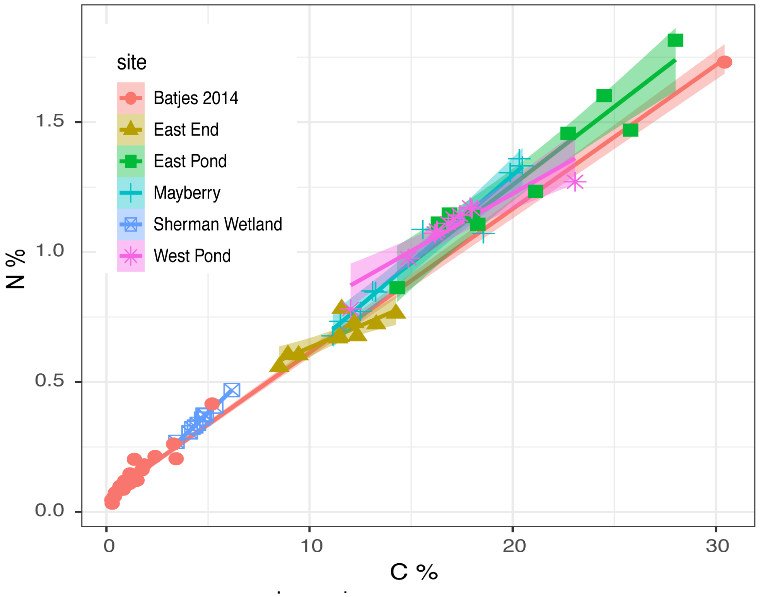


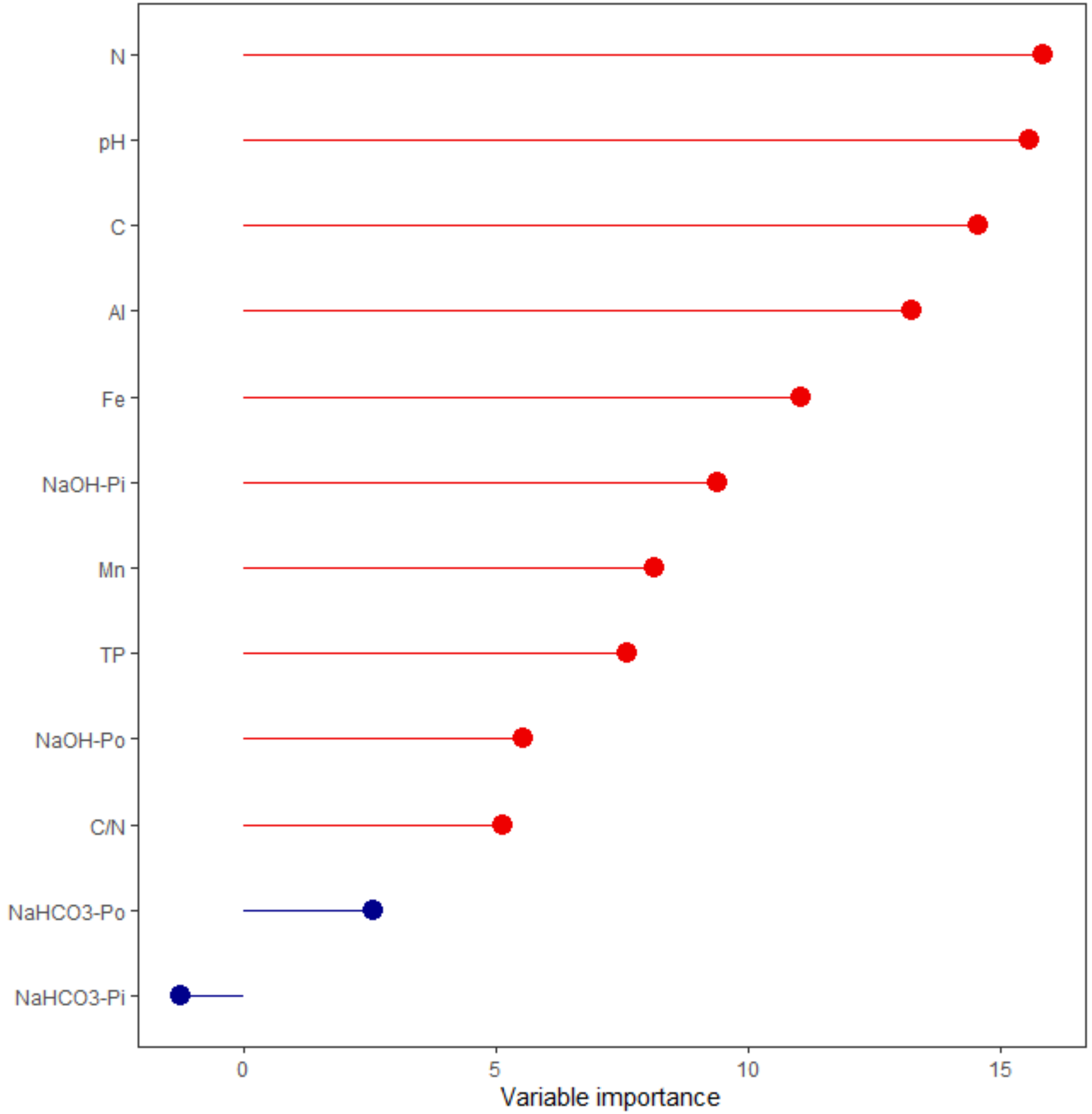
Delta microbiology & soil chemistry



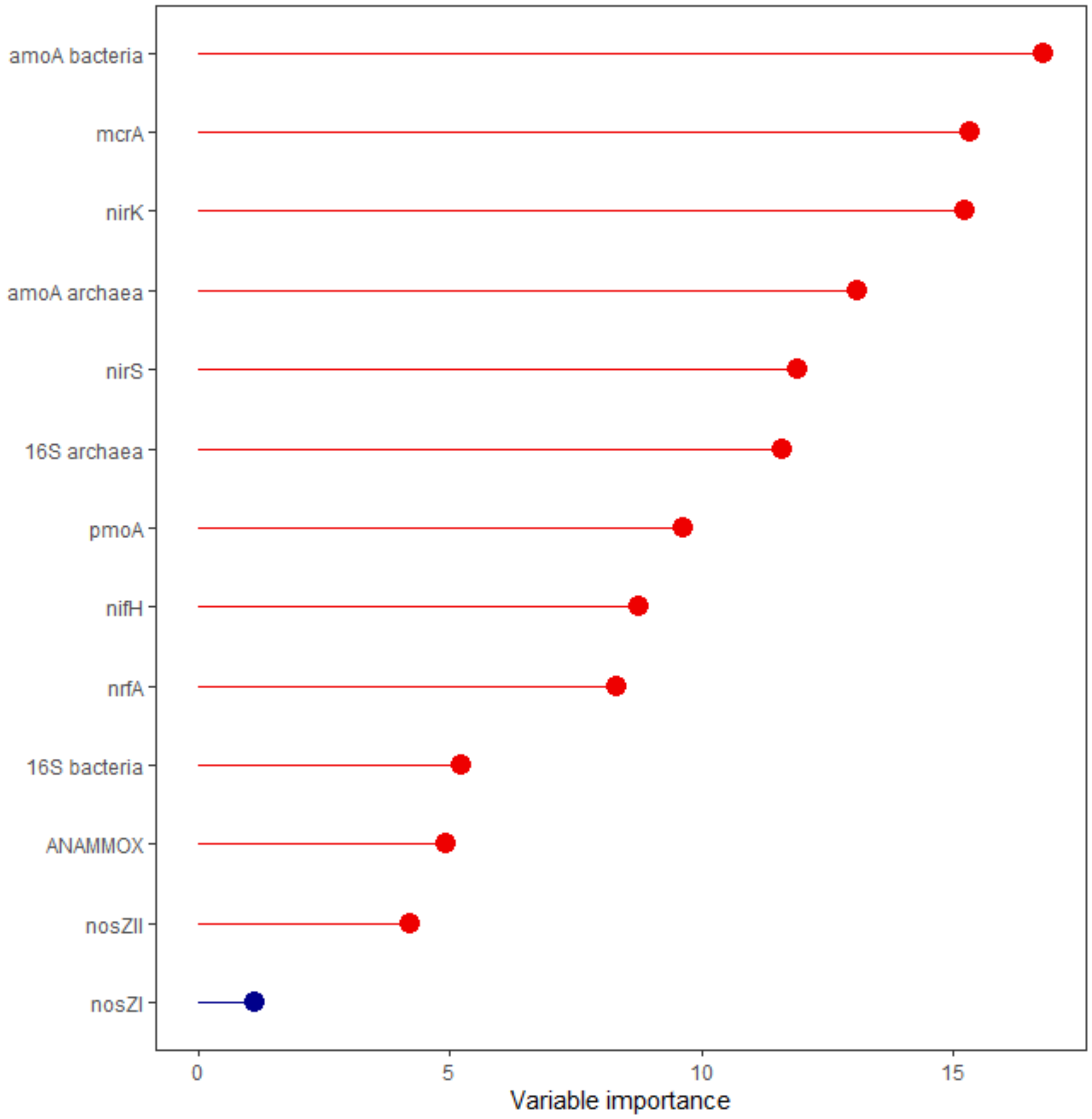
French Guiana (Espenberg et al., 2018)

Physicochemical characteristics, which were changed the most with the **increasing wetland restoration age**, obtained by the random forest analysis.

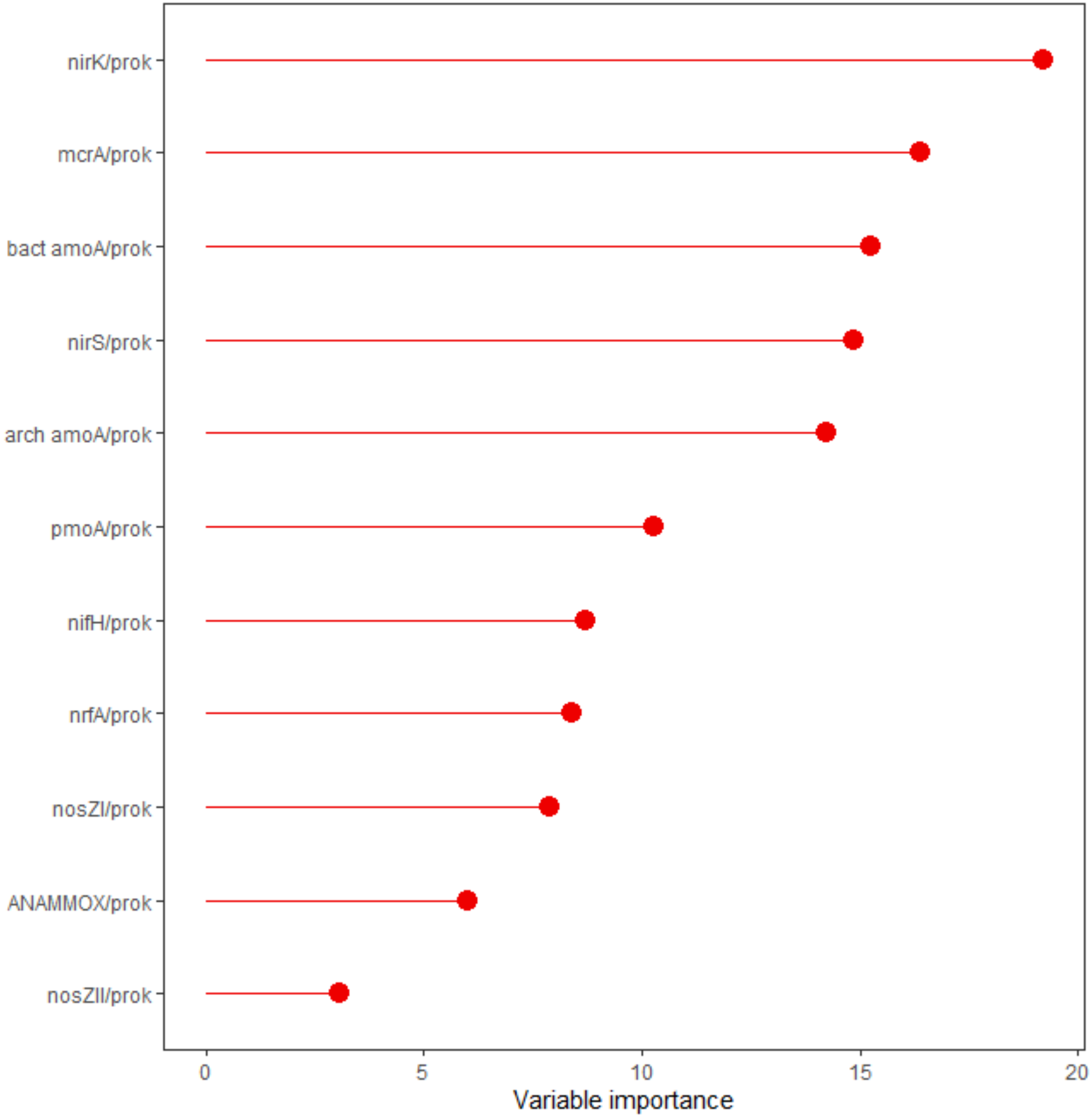




Target gene abundances, which were changed the most with the **increasing wetland restoration age**, obtained by the random forest analysis.



Target gene proportions in the prokaryotic community, which were changed the most with the **increasing wetland restoration age**, obtained by the random forest analysis.



Conclusions

- Both land management and wetland age has a clear impact to the soil physicochemical characteristics and to the abundance of target genes controlling the nitrogen transforming cycle.
- Previous land management and wetland design can affect the wetland restoration (and C uptake) efficiency.
- The interactions of N transforming genes and soil physicochemical parameters gets more complex in older wetlands.
- Soil phosphorus contents seems to be the limiting element for microbes in older wetland.

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