Wetlands Solutions *for the Future*

Learning from ALFAwetlands and REWET Projects

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rewet

Restoration for the future WETLANDS www.alfawetlands.eu

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HARNESSING MICROBIAL COMMUNITIES FOR SUCCESSFUL WETLAND RESTORATION

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Why wetlands matter?

Europe has lost 50–80% of historical **wetlands**

(Davidson, 2014; Verhoeven, 2014)

Consequences:

- reduced **carbon** and **nitrogen storage**
- more **greenhouse gases**
- poorer **water quality** and **regulation**
- reduced **biodiversity**

(Mander, Öpik, Espenberg, 2025)

What happens when wetlands are drained?

Dry soil → oxygen increases → decomposition → GHG emissions

Wet soil → low oxygen → carbon/nitrogen stored

Why microbes matter?

Microbes (bacteria, archaea, fungi) control how **carbon and nutrients** move through **wetlands**.

They determine whether **wetlands store carbon** or **release greenhouse gases**.

Different microbial groups produce or consume these greenhouse gase

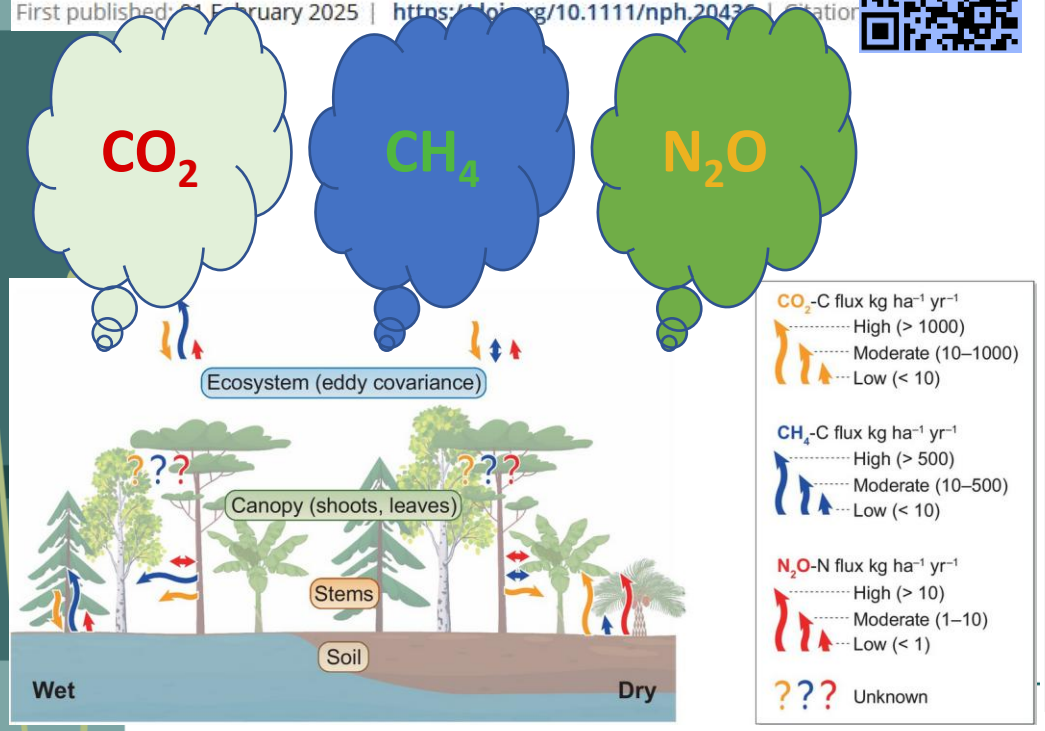
New Phytologist

Tansley insight | Open Access

Global peatland greenhouse gas dynamics: state of the art, processes, and perspectives

Ülo Mander, Maarja Öpik, Mikk Espenberg

First published: 01 February 2025 | https://doi.org/10.1111/nph.20436 | Citation



Key topics and research perspectives	Importance	References
Methanogenesis vs methanotrophy	Improved understanding of the processes regulating CH_4 balances, underpin strategies to reduce CH_4 emissions as well as fluvial C losses	Gios *et al*. (2024); Espenberg *et al*. (2024)
Denitrification vs nitrification vs DNRA	Improved understanding of the processes regulating N_2O balances, underpin strategies to reduce gaseous emissions as well as fluvial N losses	Bösch *et al*. (2023); Espenberg *et al*. (2024); Masta *et al*. (2024)
Impact of BVOCs on GHG fluxes in peatlands	Largely unknown, initial studies indicate impact on CH_4 fluxes	Junninen *et al*. (2022)
Integrated impact of soil moisture changes and microbiome dynamics on GHG fluxes in peatlands	Microbiome dynamics is a potential indicator for modelling of peatlands C and N	Bahram *et al*. (2022)
Impact of peat microbiome diversity and mycorrhiza on GHG fluxes in peatlands	Largely unknown, the impact on GHG fluxes yet to be fully analyzed	Storer *et al*. (2018); Wang *et al*. (2021); Page *et al*. (2022)

Microbial pathways controlling greenhouse gas fluxes are highly complex

Unraveling microbial processes involved in carbon and nitrogen cycling and greenhouse gas emissions in rewetted peatlands by molecular biology

Open access | Published: 16 March 2024
Volume 167, pages 609–629, (2024) Cite this article

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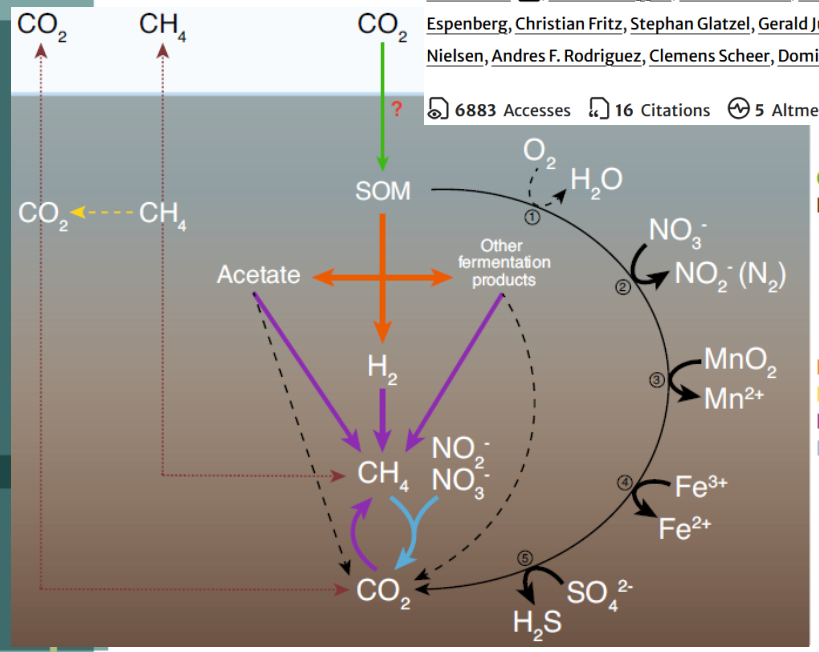
Emilie Gios, Erik Verbruggen, Joachim Audet, Rachel Burns, Klaus Butterbach-Bahl, Mikk Espenberg, Christian Fritz, Stephan Glatzel, Gerald Jurasinski, Tuula Larmola, Ülo Mander, Claudia Nielsen, Andres F. Rodriguez, Clemens Scheer, Dominik Zak & Hanna M. Silvennoinen

6883 Accesses | 16 Citations | 5 Altmetric | Explore all metrics →



Gios et al. 2024, *Biogeochemistry*

Structure and function of the soil microbiome underlying N_2O emissions from global wetlands

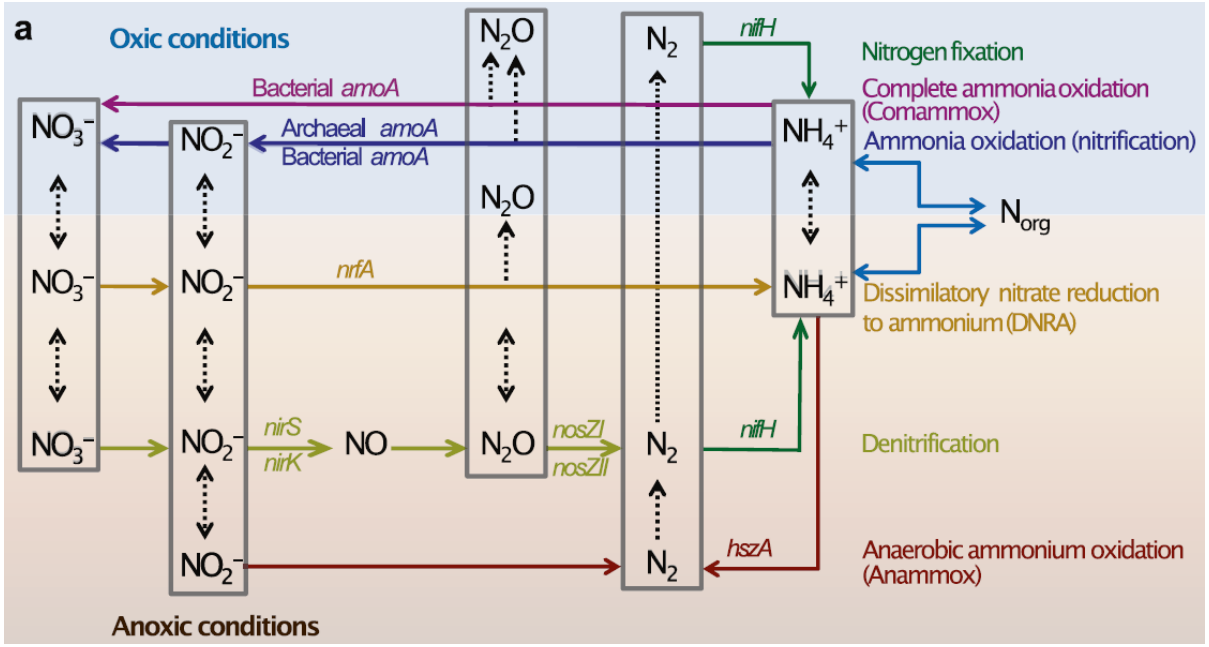
Article | Open access | Published: 17 March 2022

Mohammad Bahram, Mikk Espenberg, Jaan Pärn, Laura Lehtovirta-Morley, Sten Anslan, Kuno Kasak, Urmas Kõljalg, Jaan Liira, Martin Maddison, Mari Moora, Ülo Niinemets, Maarja Öpik, Meelis Pärtel, Kaido Soosaar, Martin Zobel, Falk Hildebrand, Leho Tedersoo & Ülo Mander

Nature Communications **13**, Article number: 1430 (2022) | Cite this article

37k Accesses | 227 Citations | 80 Altmetric

These authors contributed equally: Mohammad Bahram, Mikk Espenberg, Jaan Pärn, Leho Tedersoo, Ülo Mander.



Bahram et al. 2022, *Nature Communications*

One soil – many players – What do not we know yet?

1) Interactions. Are cycles and microbial domains interconnected?

Carbon, **nitrogen**, and **metals** cycles – **bacteria**, **archaea**, and **fungi**.

2) Restoration effects. Can restoration restore microbial processes?

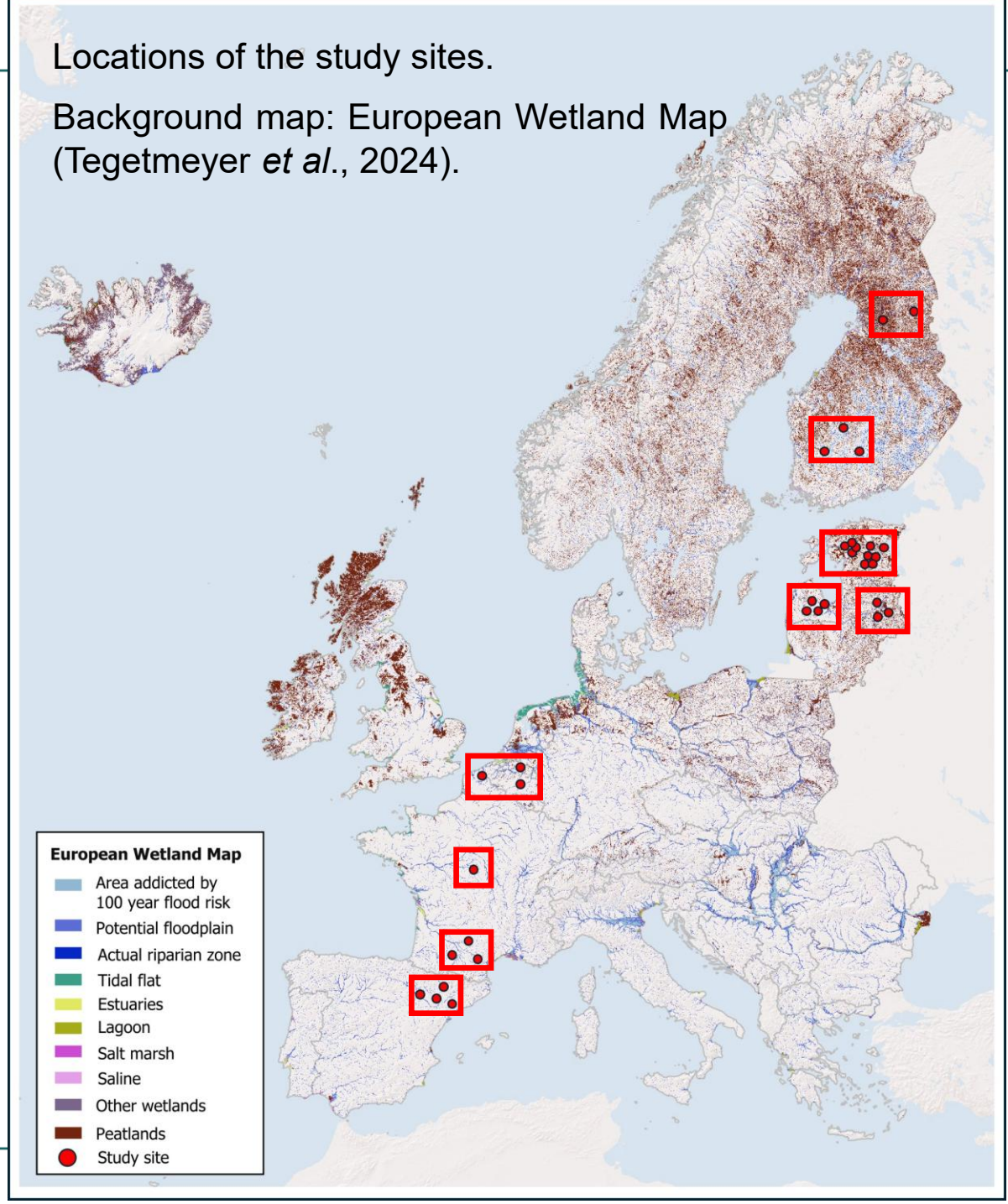
Rewetting changes soil conditions – and microbial communities respond.

3) European-scale patterns. Do responses differ across wetland types?

Most studies are site-specific, limiting **generalisation across climates and land-use types**.

Study sites

- **33 sites**
- **6 countries** (Spain, France, Belgium, Latvia, Estonia, Finland)
- **8 wetland ecosystem types**
  - Unmanaged wetlands
  - Rewetted wetlands
  - Former peat extraction areas
  - Grazed peatlands
  - Reforested peatlands
  - Continuous cover forestry
  - Drained peatland forests
  - Treatment wetlands
- **543 soil samples**



Locations of the study sites.

Background map: European Wetland Map (Tegetmeyer *et al.*, 2024).

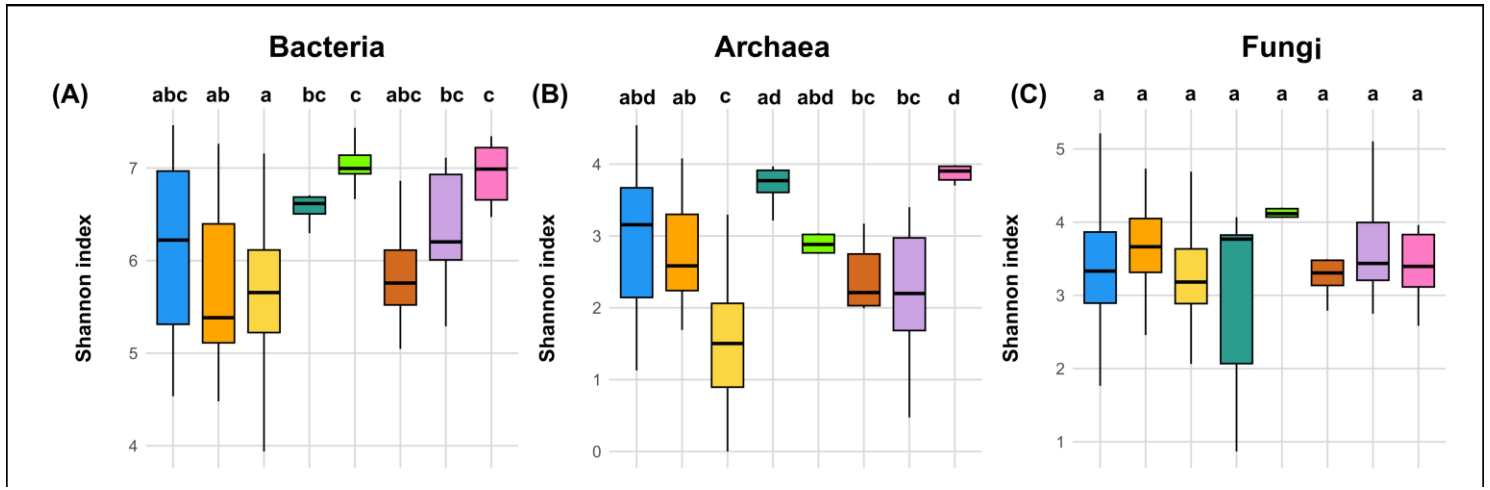
Methods: One of the largest wetland microbial studies across Europe

- **Soil sampling from three depths:**
  - 0-10 cm
  - 10-20 cm
  - 20-40 cm
- **Soil physicochemical parameters:**
  - Soil pH, TC, TN, NH_4, NO_3
  - Soil water content (SWC)
  - K, Ca, Mg, Zn, Fe, Cr, Cd, Mn, Ni, P, Cu, Pb, Co, B, Al, Na, S
- **Microbial communities:** DNA extraction; sequencing of bacterial, archaeal, and fungal communities
- **GHG measurements:** CO_2, CH_4, N_2O

Soil sampling.

Microbial community diversity in Europe

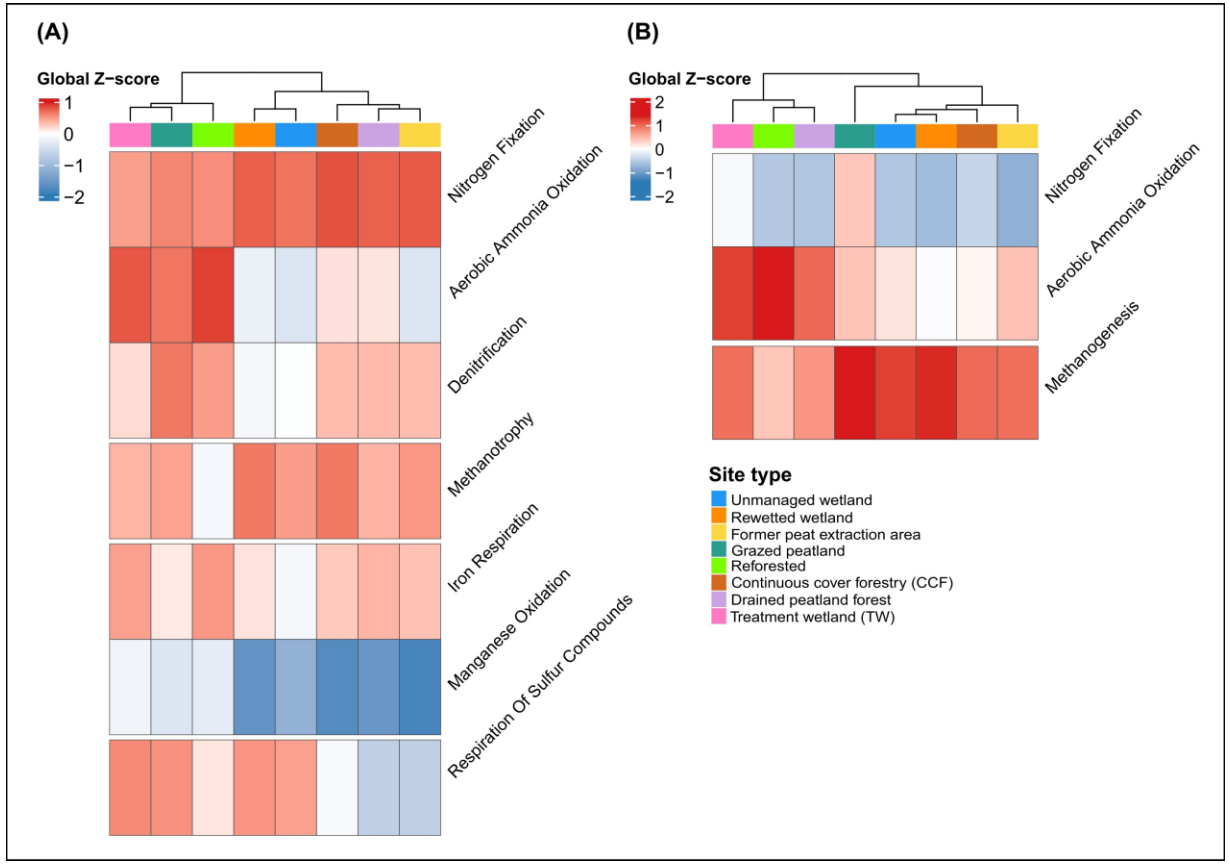
- Peat extraction reduces diversity.
- Rewetting partially restores diversity.
- Diversity alone is not enough.



Panels show: **(A)** bacterial, **(B)** archaeal, **(C)** fungal Shannon diversity.

Different management practices support different prokaryotic (bacteria, archaea) functions

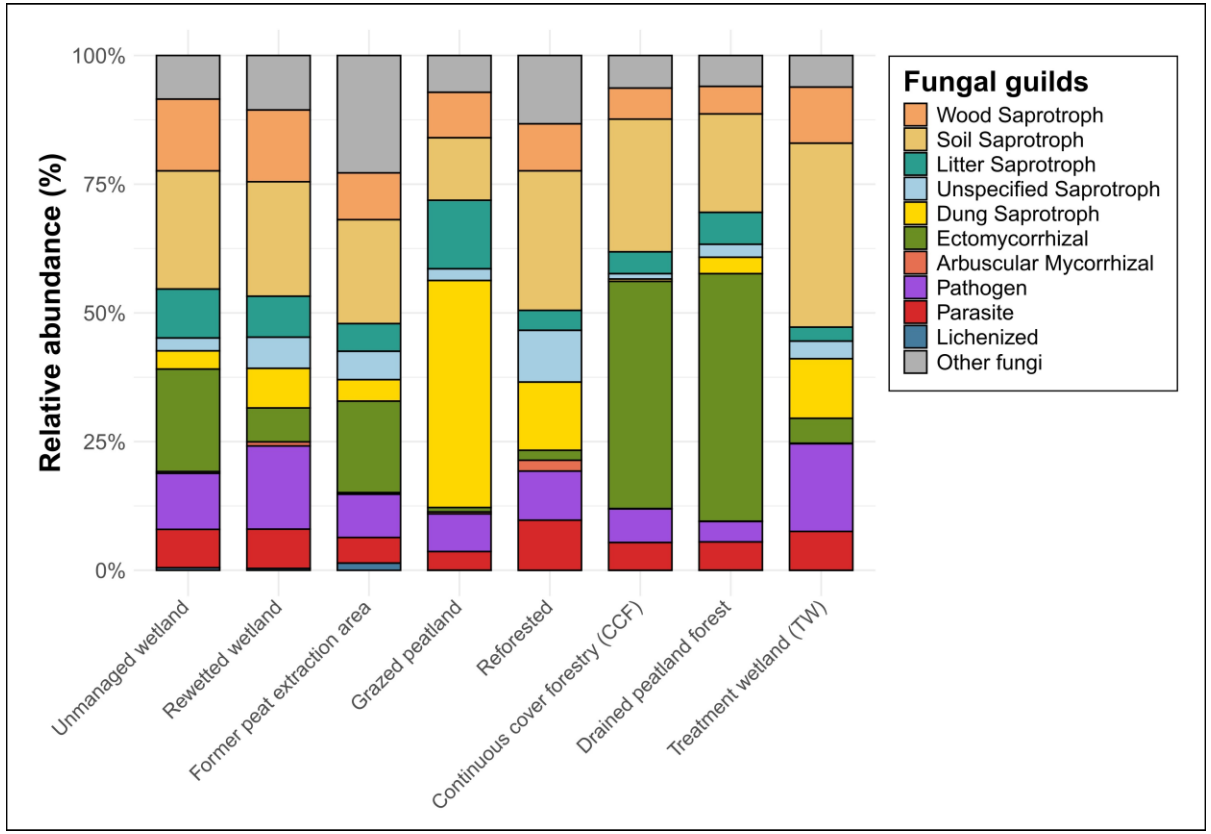
- **Natural and rewetted wetlands** support methane cycling → indicating **recovery of ecosystem functions**
- **Grazed peatlands** stimulate nutrient cycling → **driven by dung inputs**.
- **Treatment wetlands and reforested** sites → aligns with **high microbial diversity.**



Heatmap of predicted functional profiles for bacterial **(A)** and archaeal **(B)** communities based on functional annotation of prokaryotic taxa (FAPROTAX).

Plant communities strongly influence fungal communities and ecosystem functioning

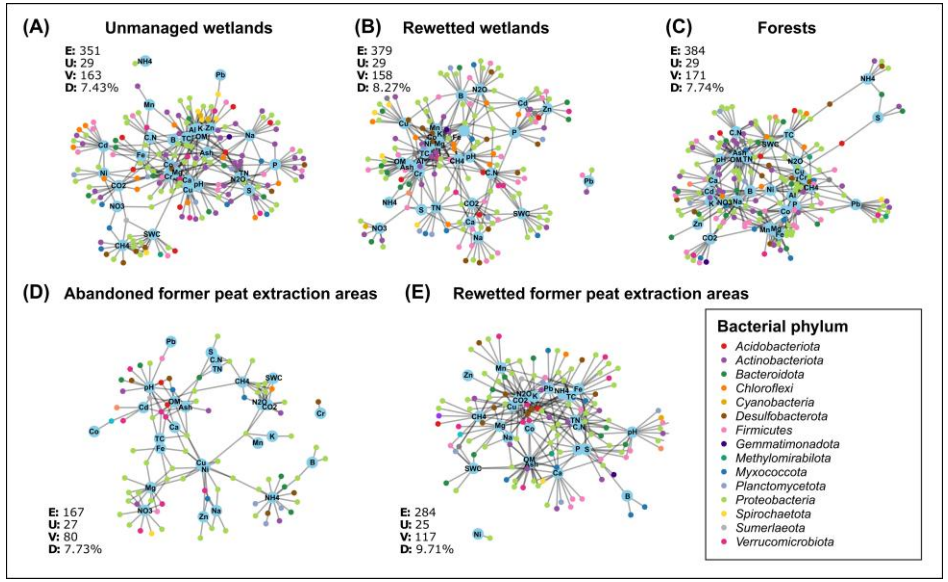
- **Highest decomposition** in **open** and **grazed wetlands**.
- **Forested** sites are **mycorrhizal-dominated** → stronger plant–fungal coupling.
- **Grazed** peatlands show **dung saprotroph dominance** & high methanogenesis → dung inputs can boost CH_4 production.



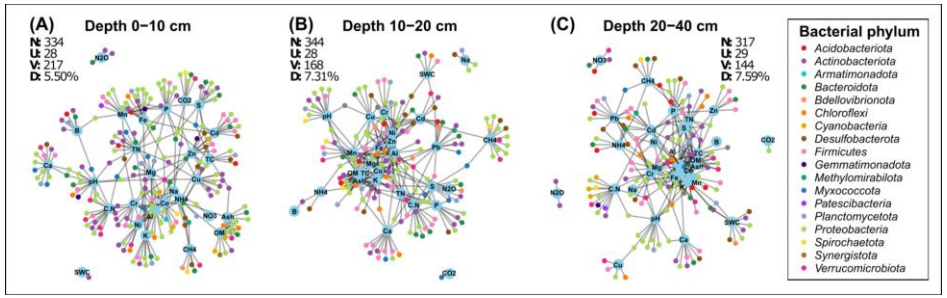
Relative abundance (%) of fungal trophic guilds assigned using the FungalTraits database across the studied ecosystem types.

Microbial networks reveal restoration success

- Rewetted wetlands resemble natural wetlands
  - Network structure recovers after rewetting
  - Key microbial groups are linked with GHG fluxes
- Microbial groups linked with methane, nitrous oxide and carbon dioxide fluxes.



Networks of bacterial genera, soil properties, and GHG emissions across site types.

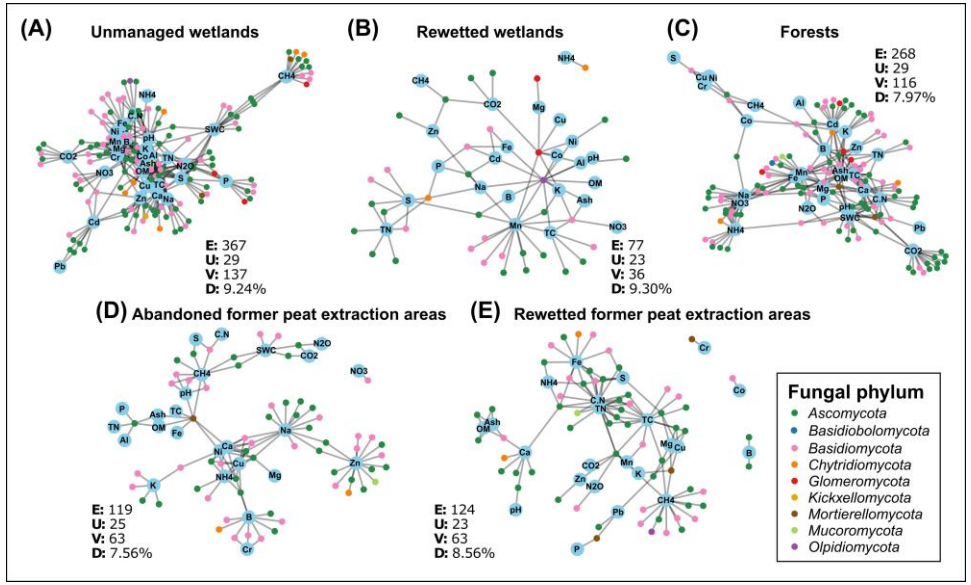


Networks of bacterial genera, soil properties, and GHG emissions across soil depths.

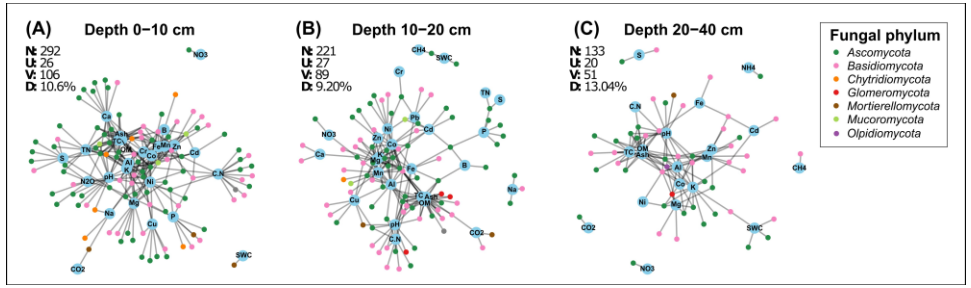
Metal availability strongly influences microbial communities and greenhouse gas processes

- **Iron (Fe)**, **magnesium (Mg)**, and **potassium (K)** are the strongest metal predictors of microbial taxa → have broad, cross-domain influences on wetland soil microbial communities.

- **Copper (Cu)**, **nickel (Ni)**, and **manganese (Mn)** show stronger domain-specific associations with bacterial, archaeal, and fungal communities, respectively.



Networks of fungal genera, soil properties, and GHG emissions across site types.



Networks of fungal genera, soil properties, and GHG emissions across soil depths.

Take-home message

- Rewetting restores microbial functioning
- Microbial networks indicate restoration success
- Metal availability influences greenhouse gas processes

What does this mean for wetland restoration?

- Rewetting restores key ecosystem processes
- Monitoring microbial networks can improve restoration assessment

THANK YOU

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