

Linking biodiversity and ecological function through extensive microeukaryotic movement across different habitats in six urban parks

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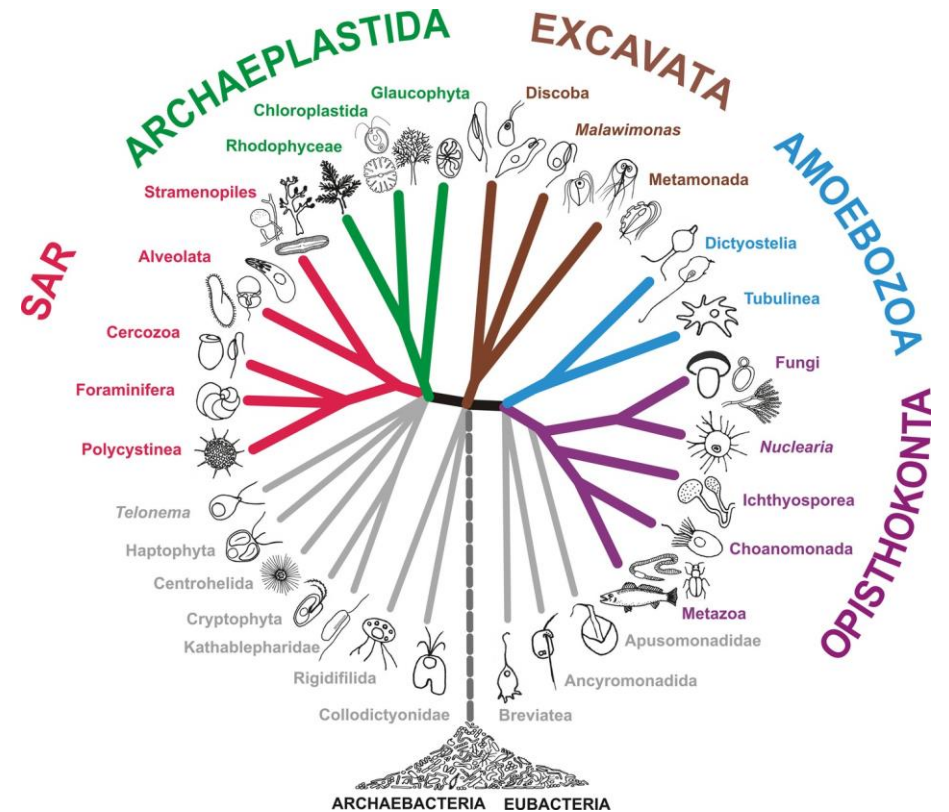
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Microeukaryotes in urban park ecosystems

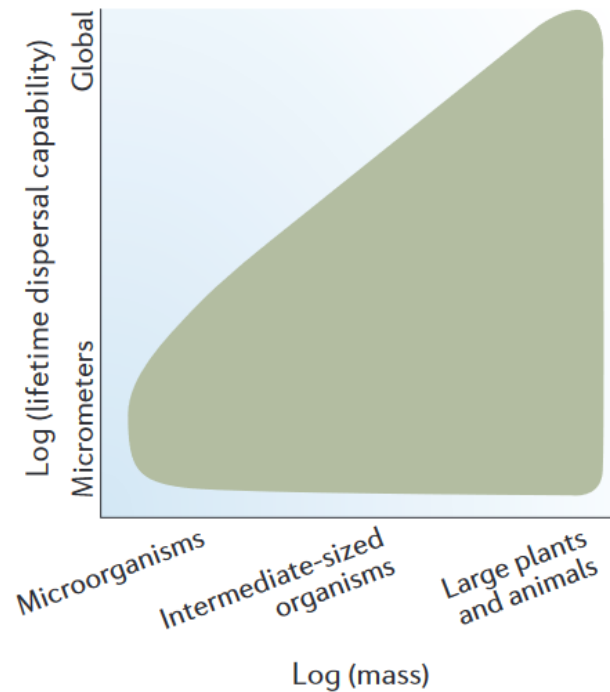
- Urban parks are important hot spots for human recreational activity and microeukaryotes.
- The biodiversity pattern of microeukaryotes in various habitats in urban parks remain uncovered.



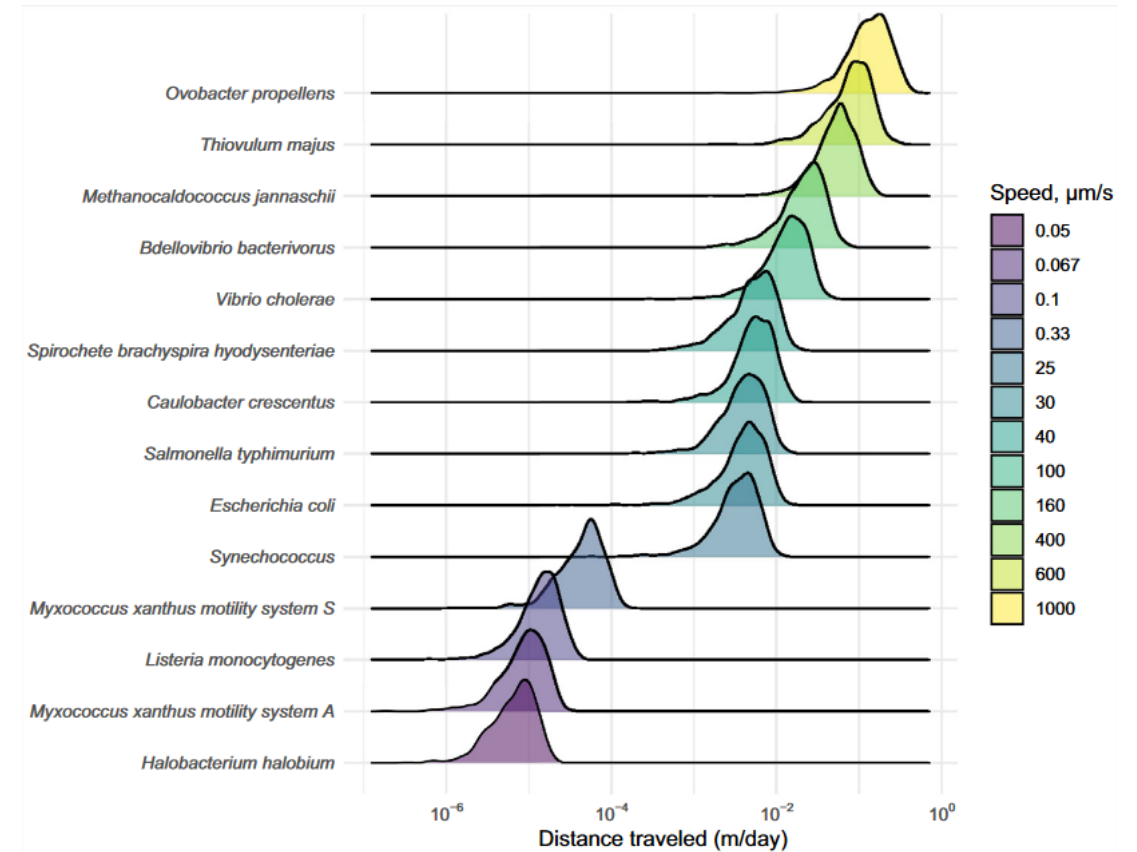
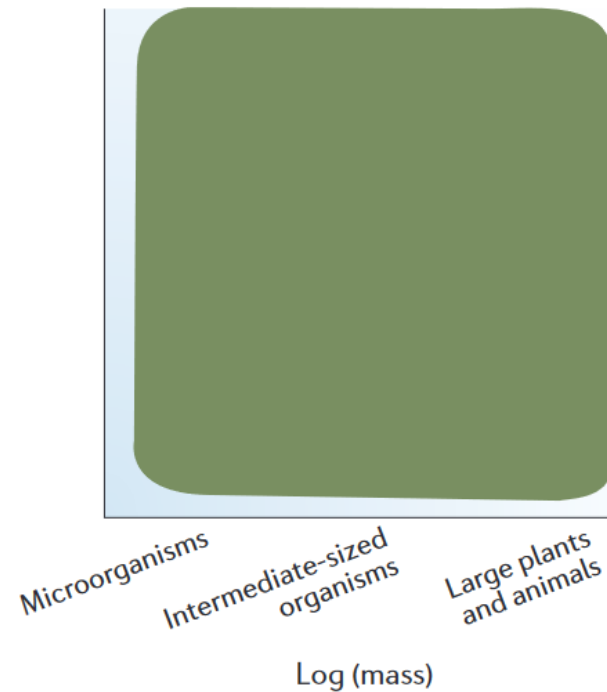
Impacts of microbial movement on communities and ecosystems

- Microbial movement across habitats plays important roles in determining microbial diversity and dynamic.
- Which microbes move and the ecological consequences of cross-habitat movements are poorly understood.

a Active dispersal



b Passive dispersal

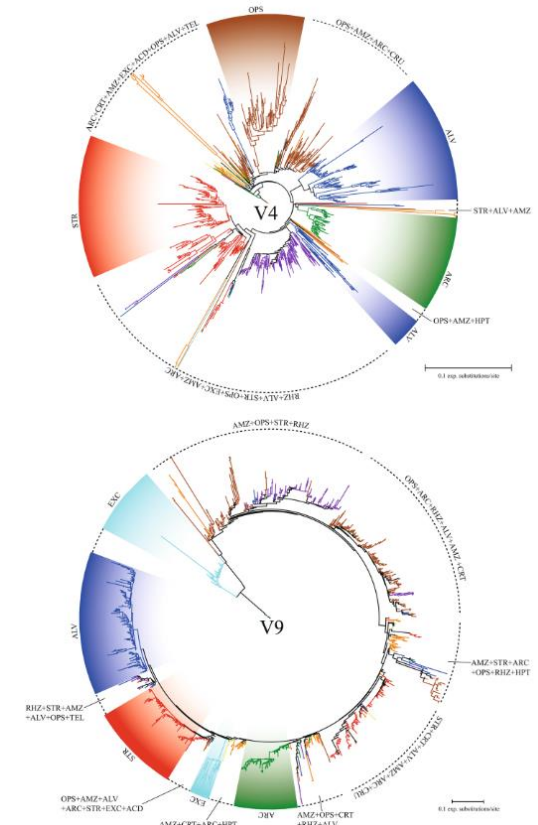
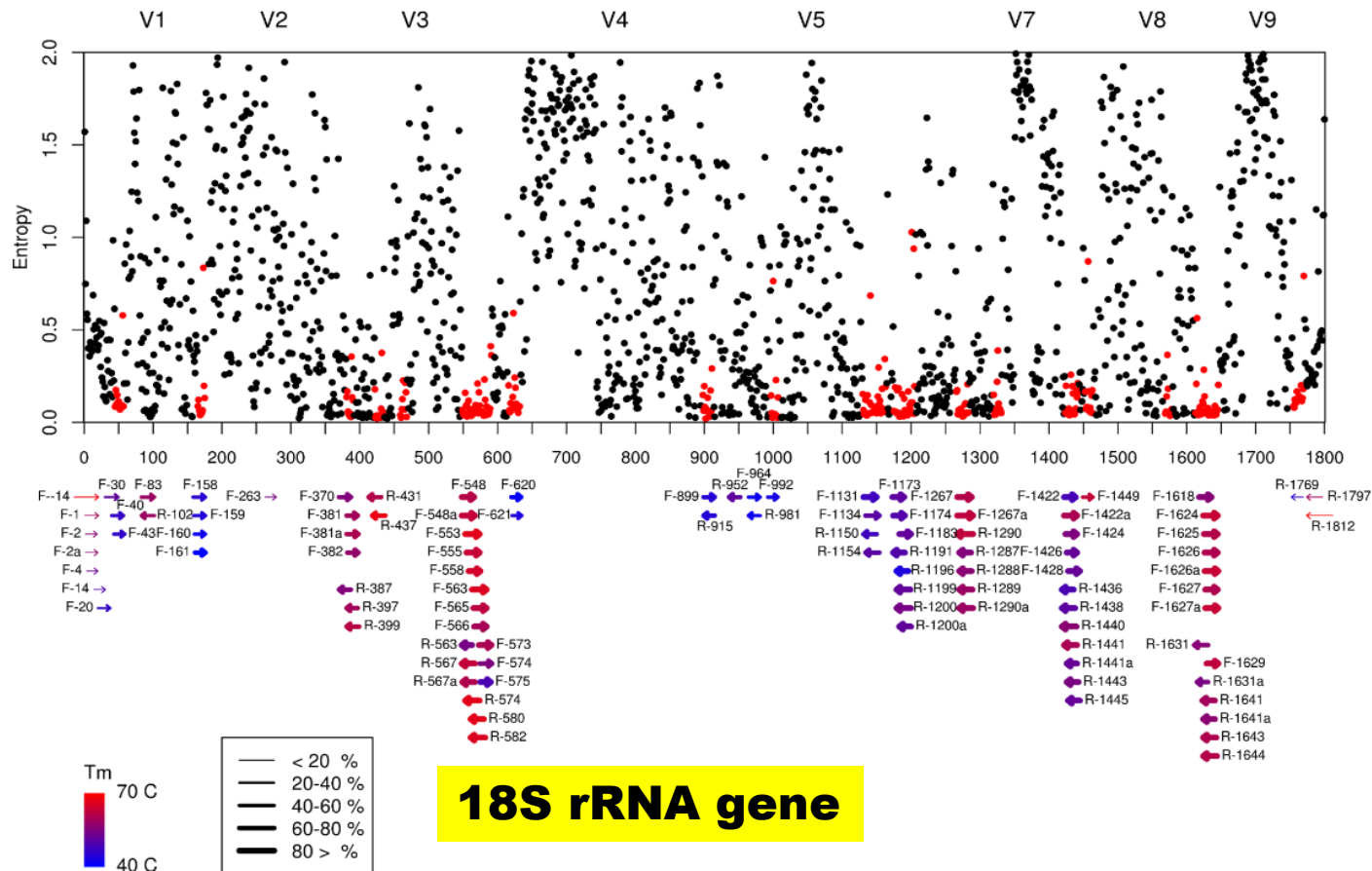


Nathan I. Wisnoski et al., 2022

Jennifer B. Hughes Martiny et al., 2006

Inconsistent results of different amplification regions

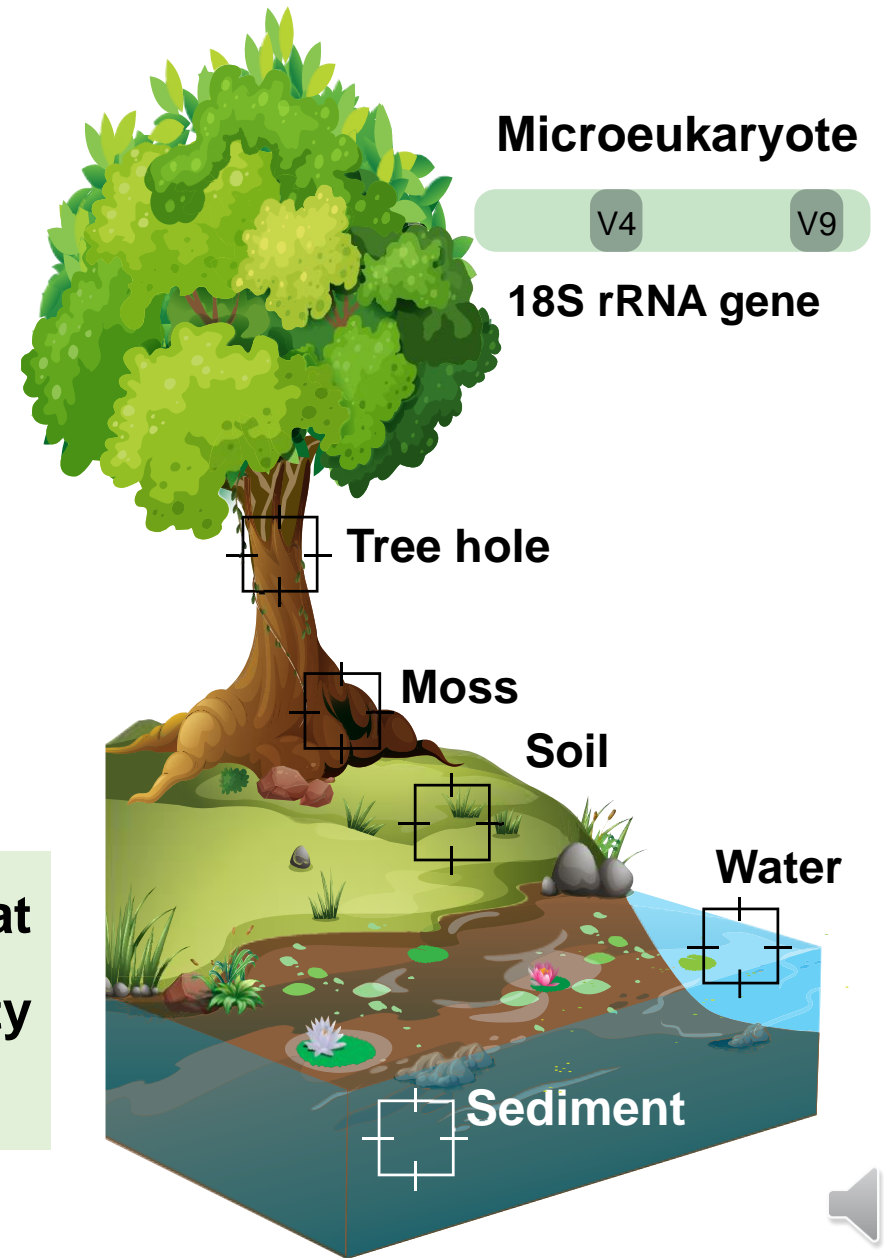
- V4 (~ 400 bp) and V9 (~ 150 bp) regions are most commonly used for microeukaryotic diversity assessments. However, there is no consensus on which region provides better recovery of the microeukaryotes.
- Previous comparisons have mainly focused on specific microeukaryotic groups or limited habitats, which may limit our understanding of the microeukaryotic diversity and movement profile.



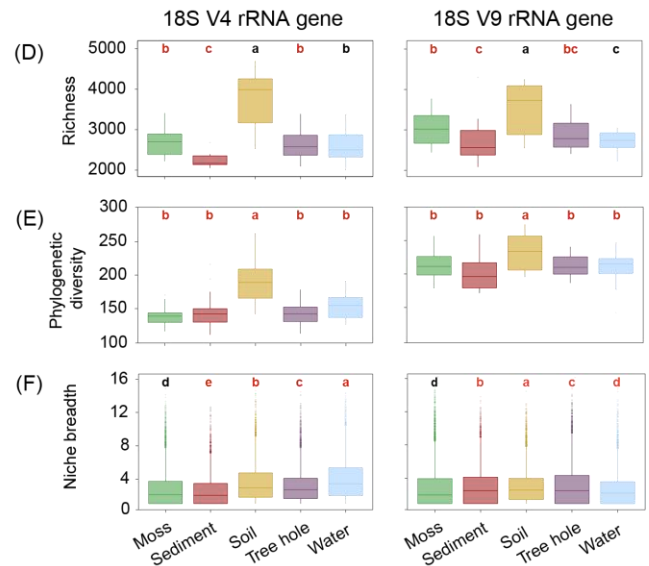
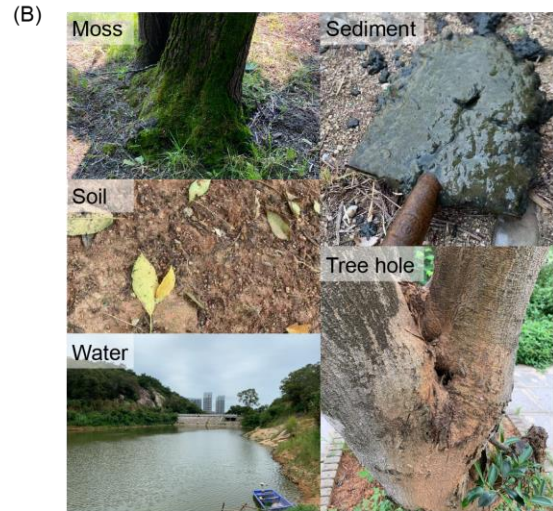
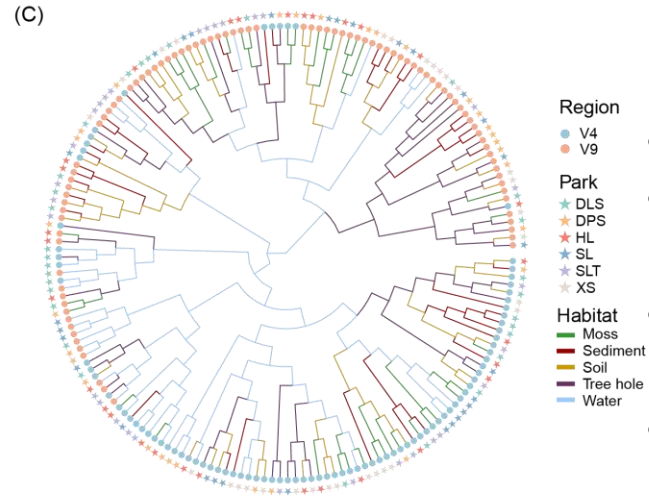
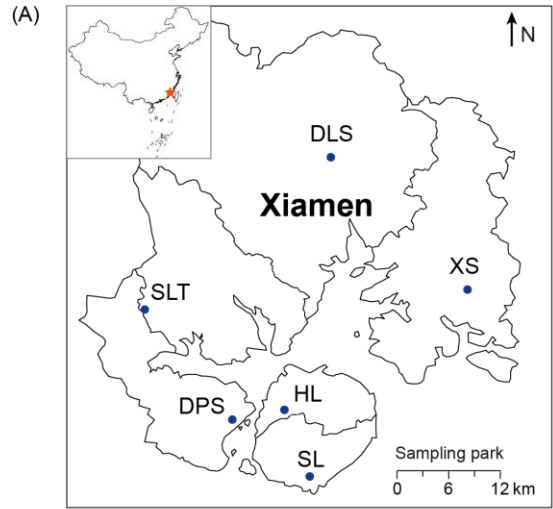
Key scientific questions and experimental design

- (1) What are the similarities and differences in biodiversity and community structure of microeukaryotes between habitats?
- (2) What are the community assembly driving force and migratory routes of microeukaryotes between habitats, and what are the effects of microbial movement on biodiversity and functions of specific groups?
- (3) Whether performing V4 and V9 region sequencing data will provide similar diversity patterns?

This is the first analysis focusing on the cross-habitat movement of microeukaryotes and its effect on biodiversity and ecosystem function in urban park ecosystems.



α -diversity of microeukaryotic communities in urban parks

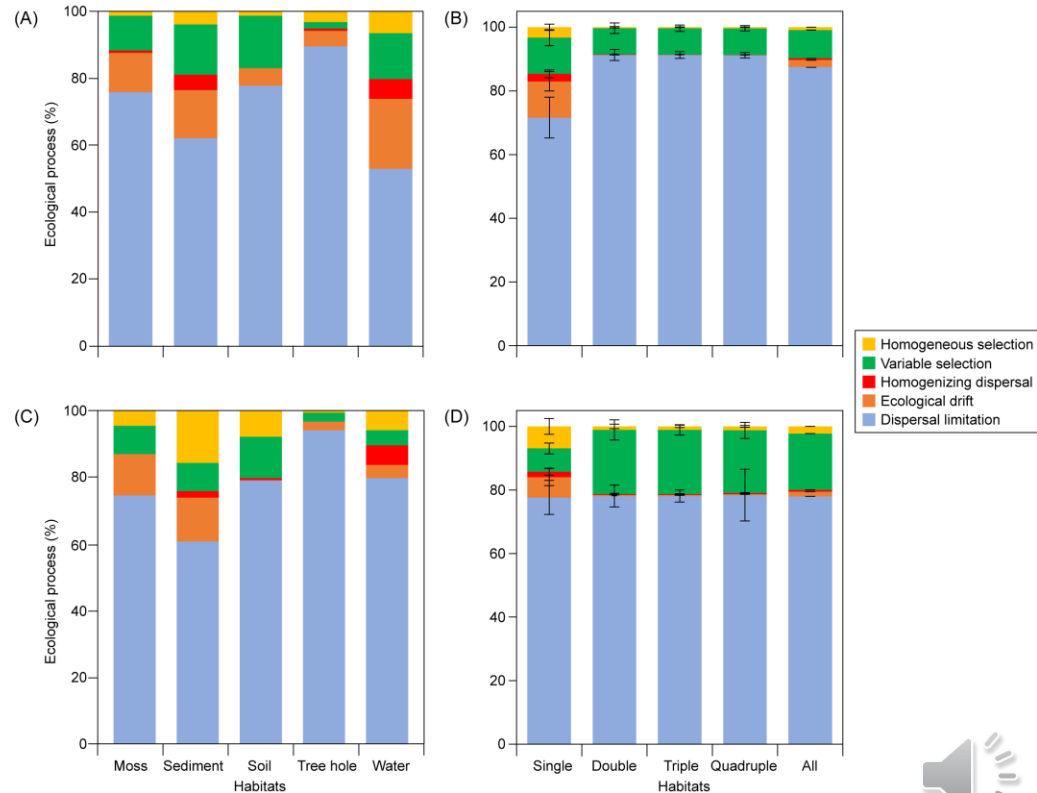
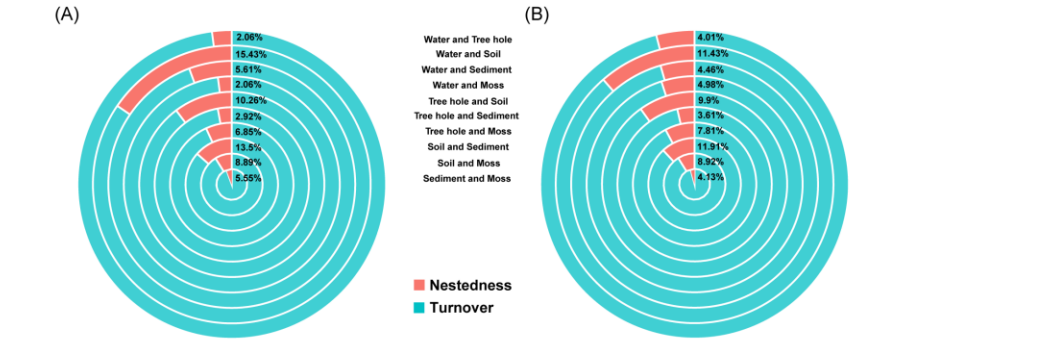
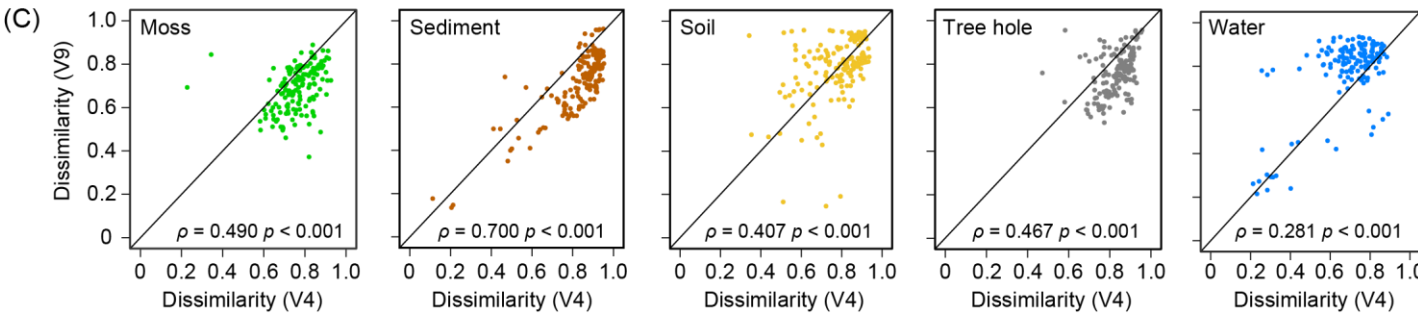
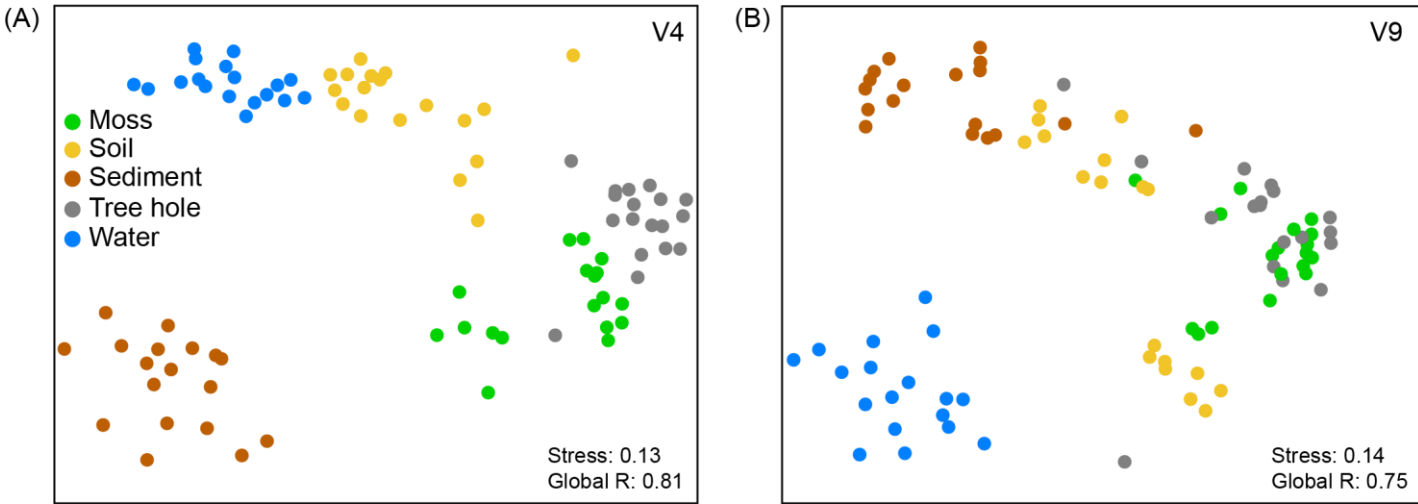


- **Amplicon region** contributed most of the community differences, followed by **habitat types (environment)**, and **different parks (distance)** had the least effect.
- **Soil** had the highest taxonomic and phylogenetic diversities.
- Microeukaryotes based on the V9 region were **more diverse** at both taxonomic and phylogenetic levels than the V4 region.
- Controversial results were observed in **aquatic environments** by different primers.
- V4 region was more accurate than the V9 region in some group (i.e., **testate amoebae**).

Genus	Microscope	V4 region		V9 region	
	Relative abundance (%)	Sequence	Relative abundance (%)	Sequence	Relative abundance (%)
<i>Euglypha</i>	16.6	54728	84.58	6818	100
<i>Cryptodiffugia</i>	0.3	218	0.34	0	0
<i>Pseudodiffugia</i>	3.7	426	0.66	0	0
<i>Tracheleuglypha</i>	0.2	28	0.04	0	0
<i>Trinema</i>	9.5	8057	12.45	0	0
<i>Corythion</i>	0.1	58	0.09	0	0
<i>Assulina</i>	2.4	1189	1.84	0	0
Pearson correlation (r)			0.908**		NA
Spearman correlation (r)			0.929**		NA



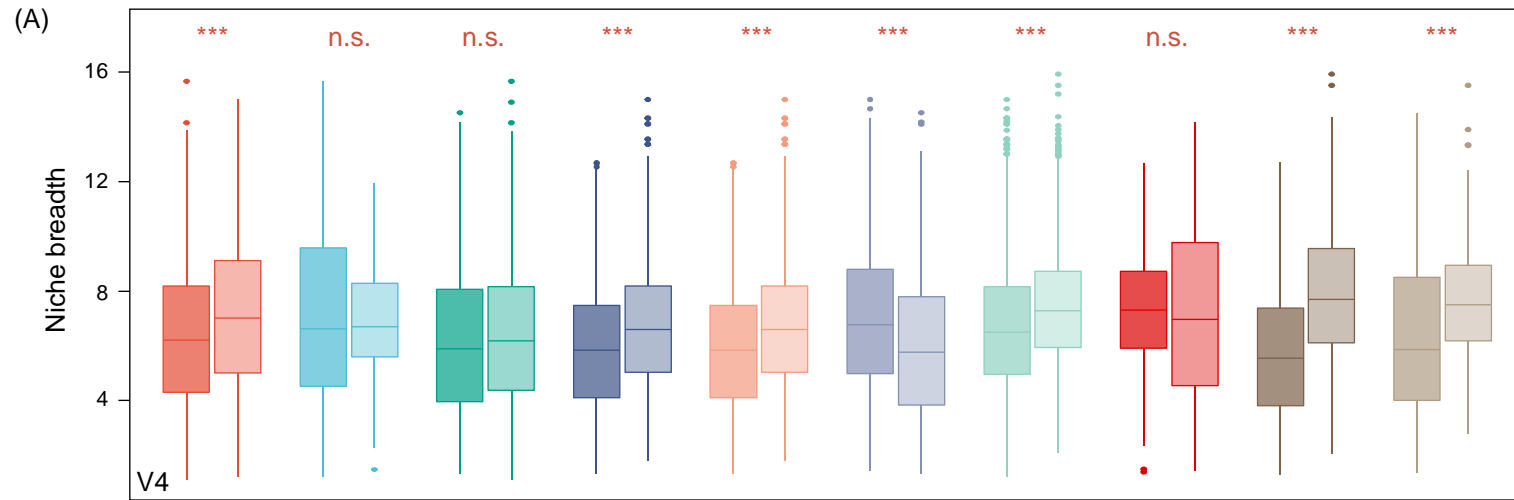
β -diversity and community assembly of microeukaryotes



- Communities were **significantly different** between habitats.
- Communities from V4 and V9 primers differ greatly in **water ecosystem**.
- **Turnover** was more important than nestedness in shaping communities.
- **Deterministic dispersal limitation** leads to community turnover.



Microeukaryotic movement/migration across habitats



Everything is everywhere, but different environments can select different species



Identifying shared species between habitat pair



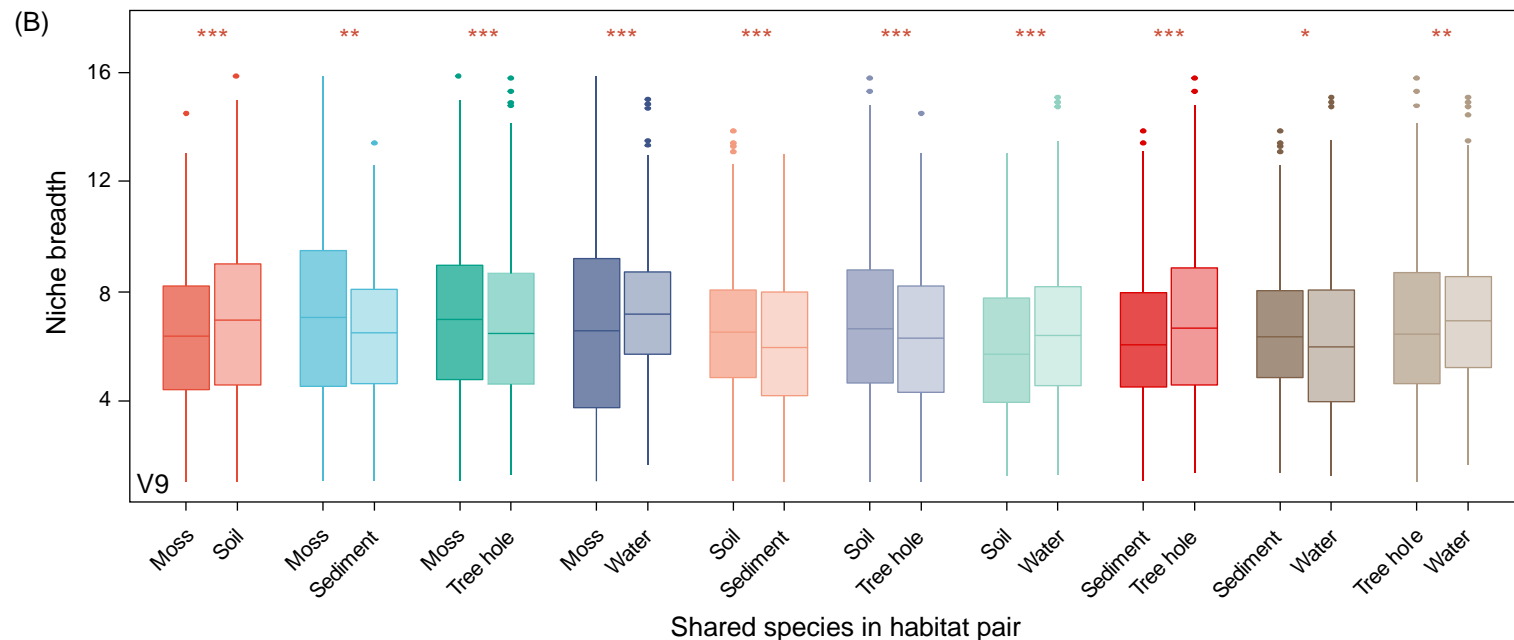
Niche breadth of the same species between habitat pair is significantly different



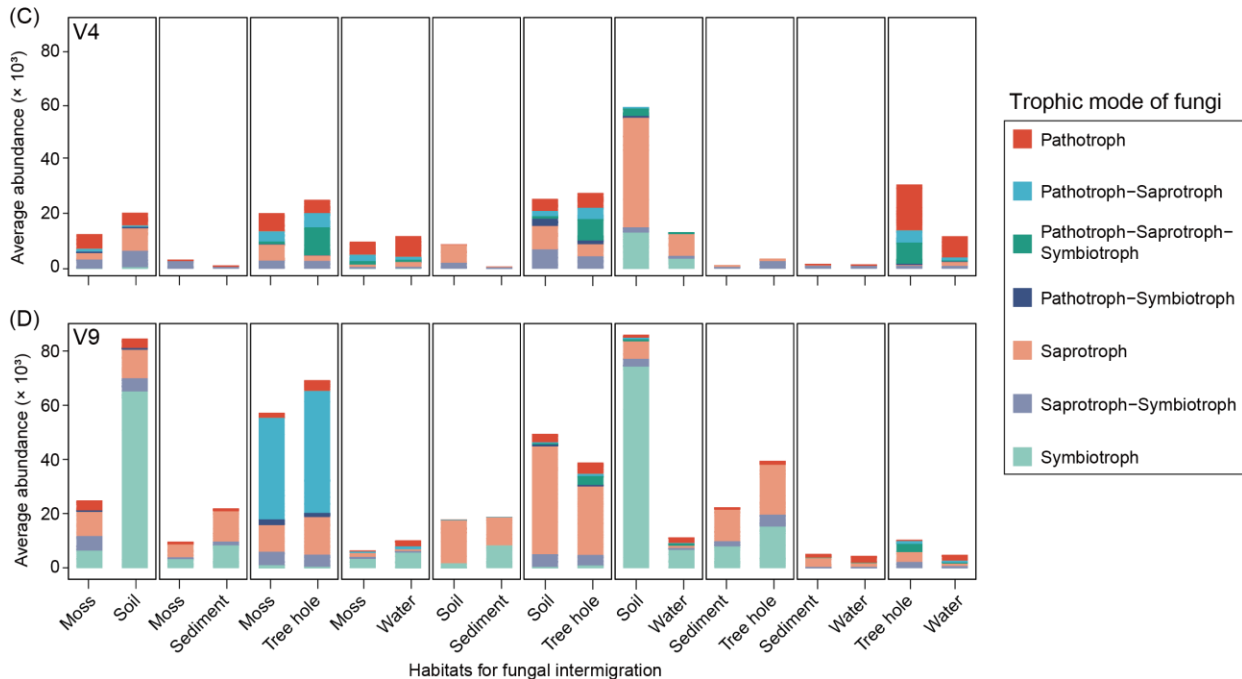
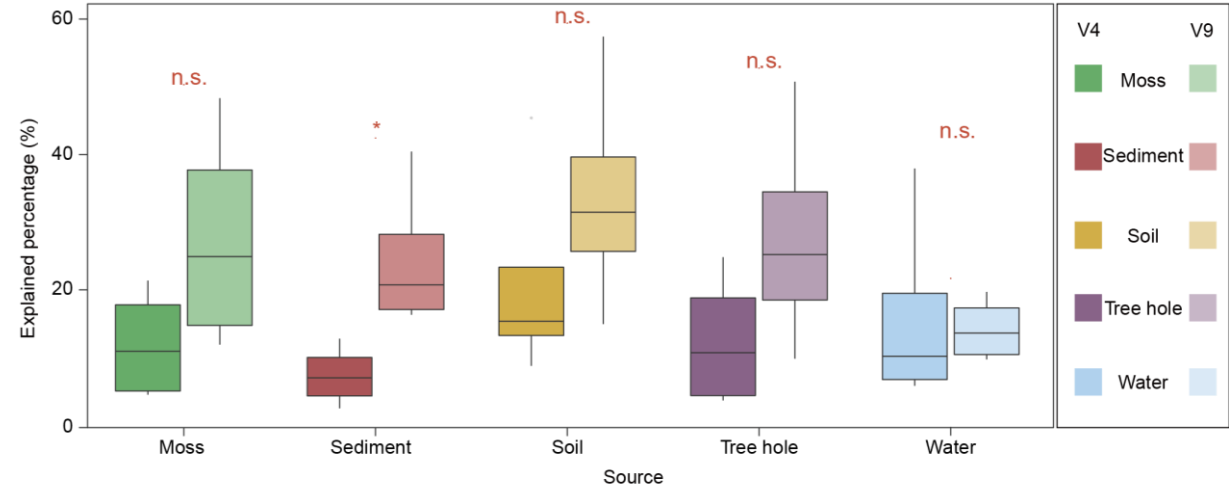
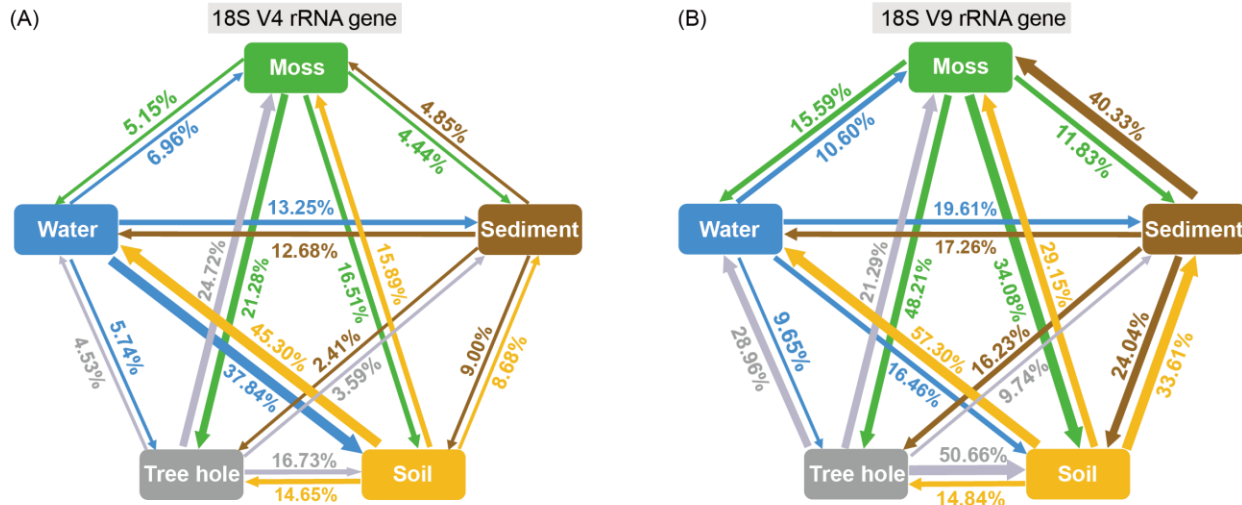
Different environments can hold different individual numbers for a species



Species may have migrated between the two habitats if species abundance has no significant difference in these two habitats

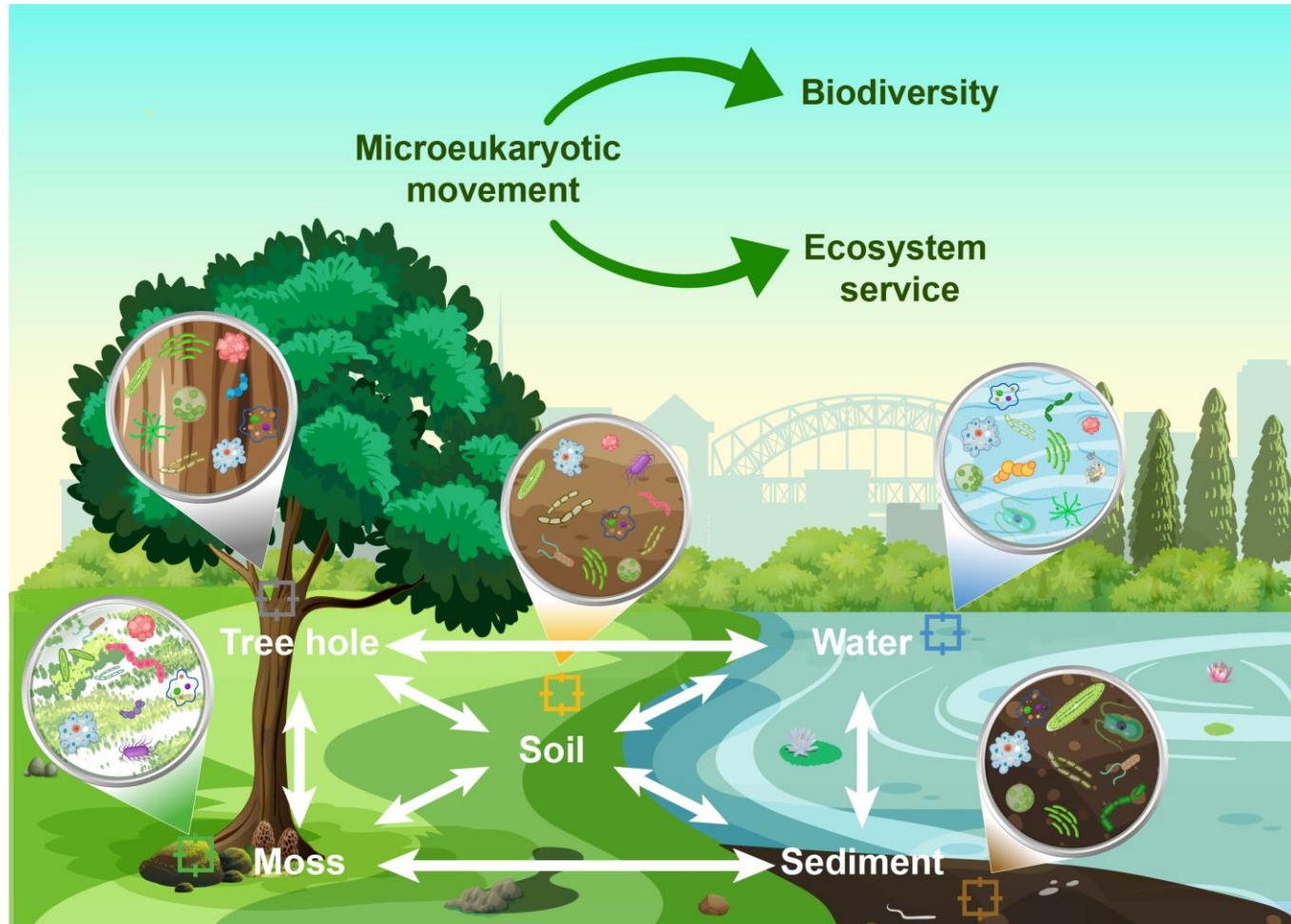


Microeukaryotic movement/migration across habitats



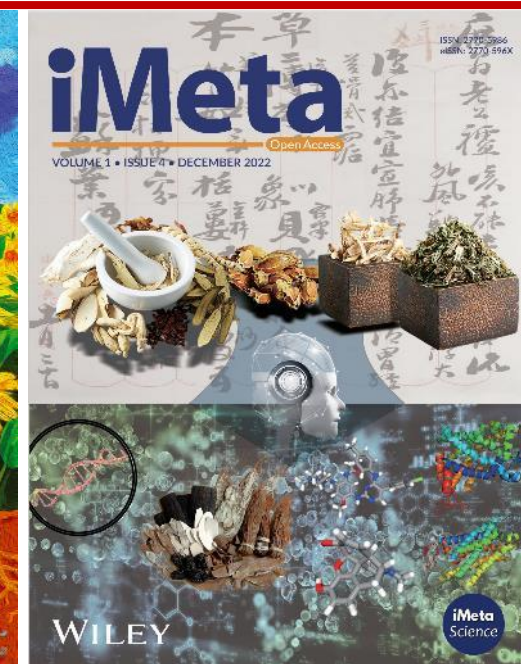
- **Soil** had the highest contribution to water, and had highest proportion of source microorganisms to its surroundings.
- V9 region identified a **significantly higher** percentage of clear sources than the V4 region.
- **Opisthokonta** was most likely to travel between habitats and accounted for half migrated taxa.
- **Pathotrophs** were more prone to migrate between moss and tree hole, and tree hole and water.
- Many **saprotrophs** and **symbiotrophs** moving from soil to water were detected by V4 and V9 regions, respectively.

Summary



- Microeukaryotic movement contributes to biodiversity maintenance through population exchange across habitats in urban park ecosystems.
- Microeukaryotic movement plays important roles in urban ecological functions indicated by the migration of different trophic fungi.
- Primers targeting the V4 region are more accurate than those targeting the V9 region in specific groups (e.g., testate amoeba). Microeukaryotic communities in aquatic habitats (water and sediment) showed greater differences than those in terrestrial habitats (moss, soil, and tree hole).

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