Linking organic matter breakdown to abundance and community composition of denitrification and DNRA microorganisms in tidal wetlands

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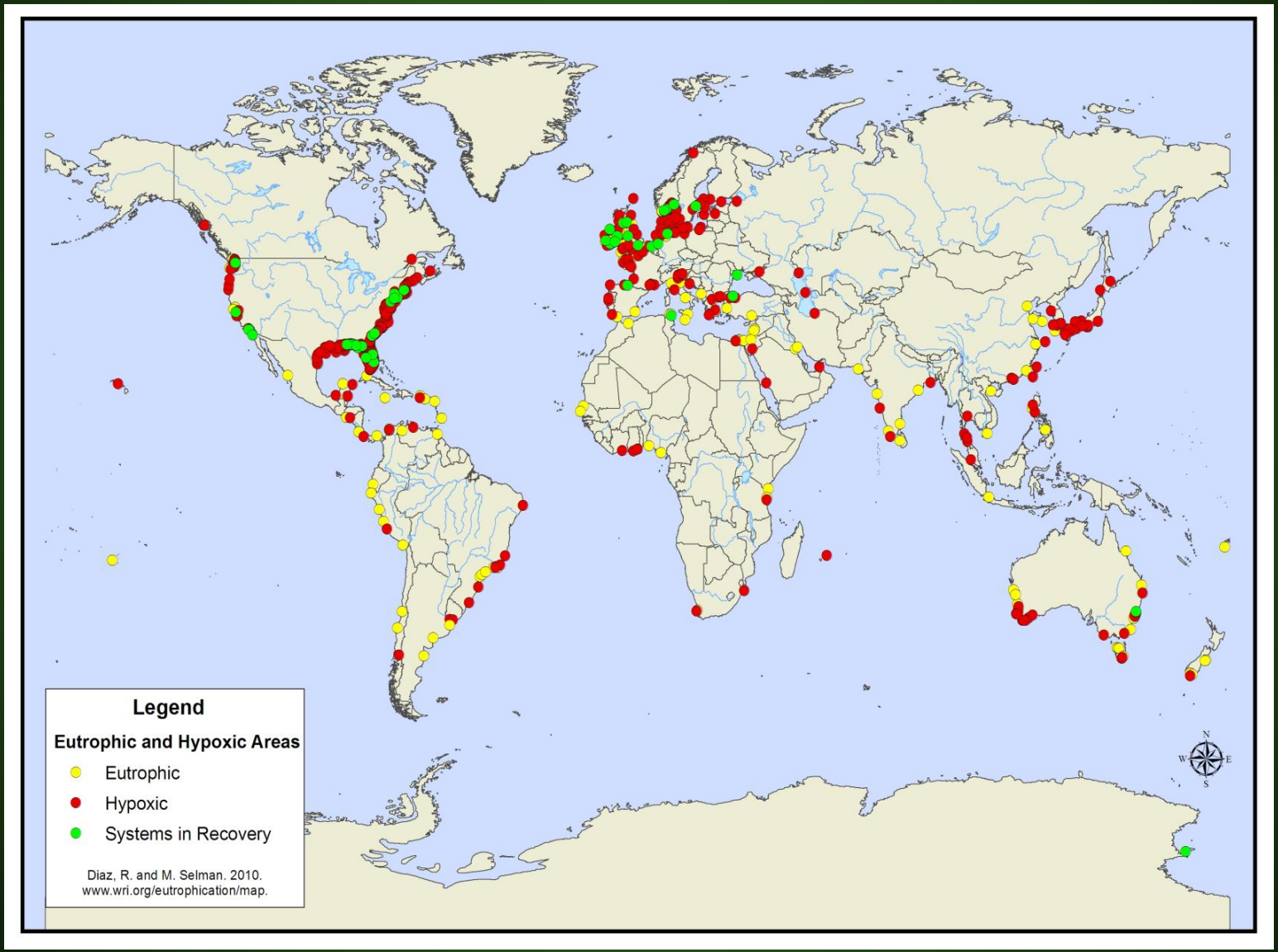
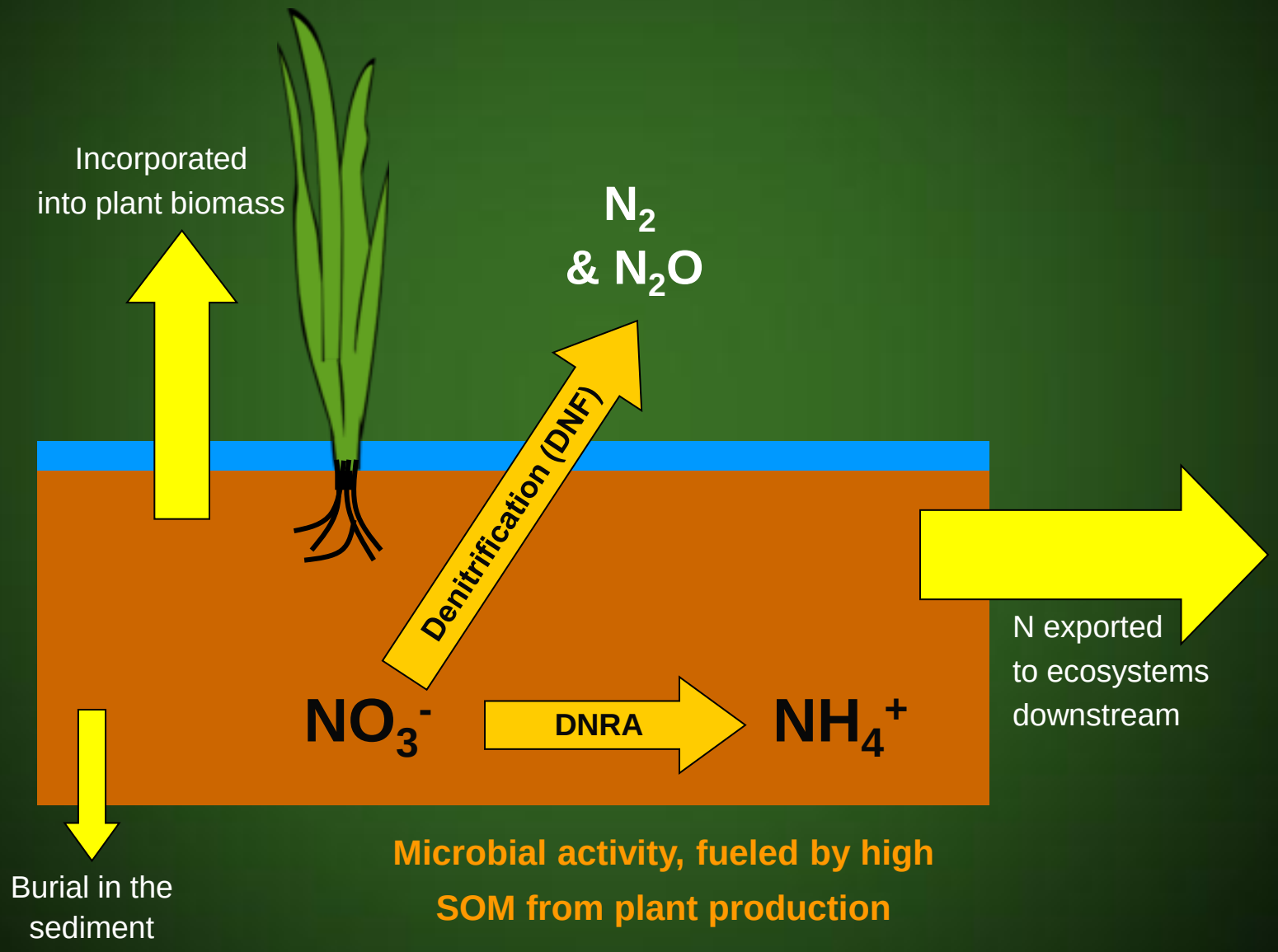
Anthropogenic Nitrogen



Nitrogen Cycling in Freshwater Wetlands



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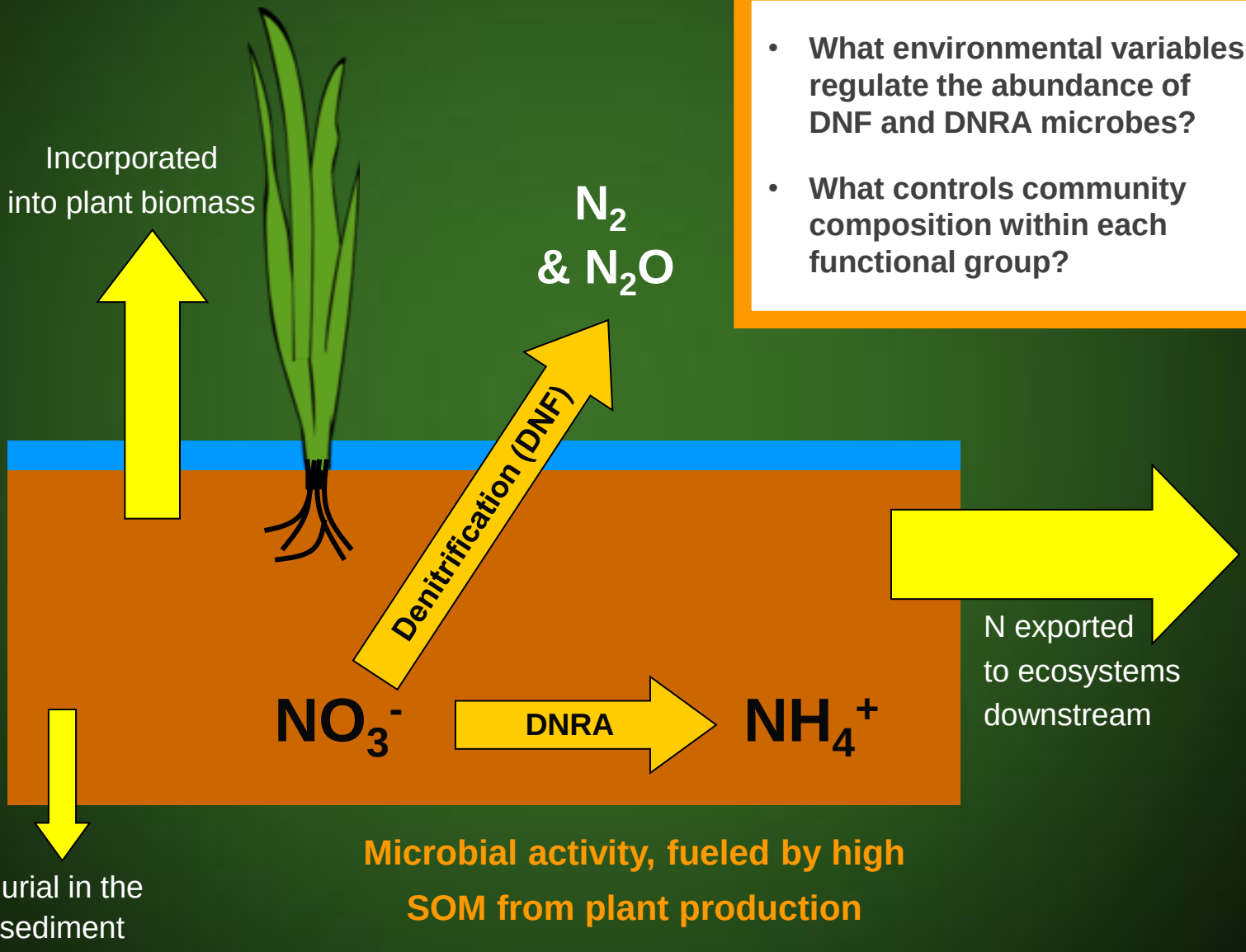
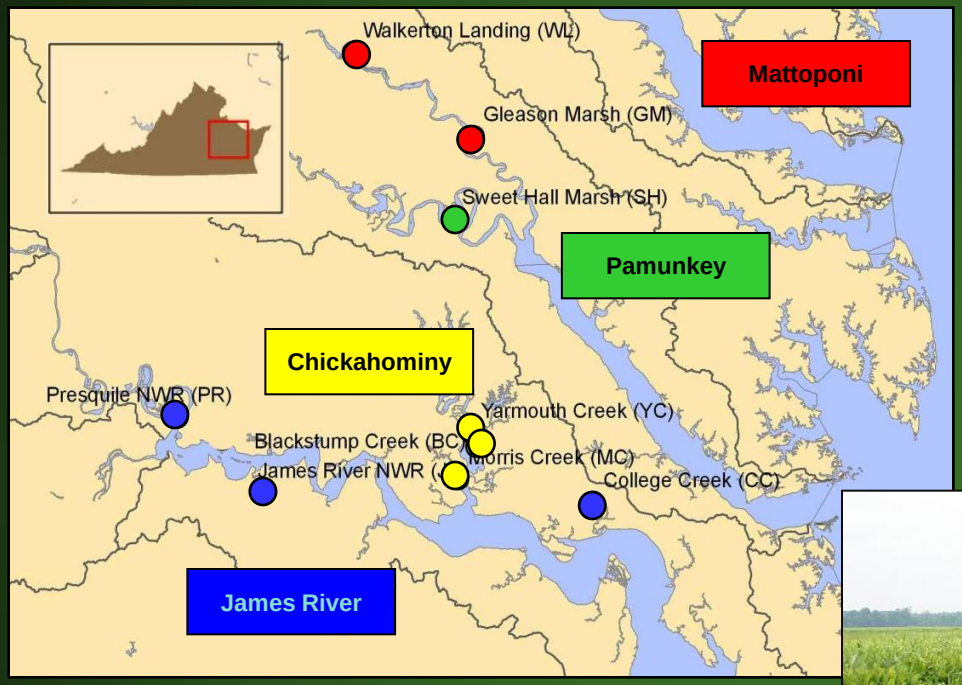


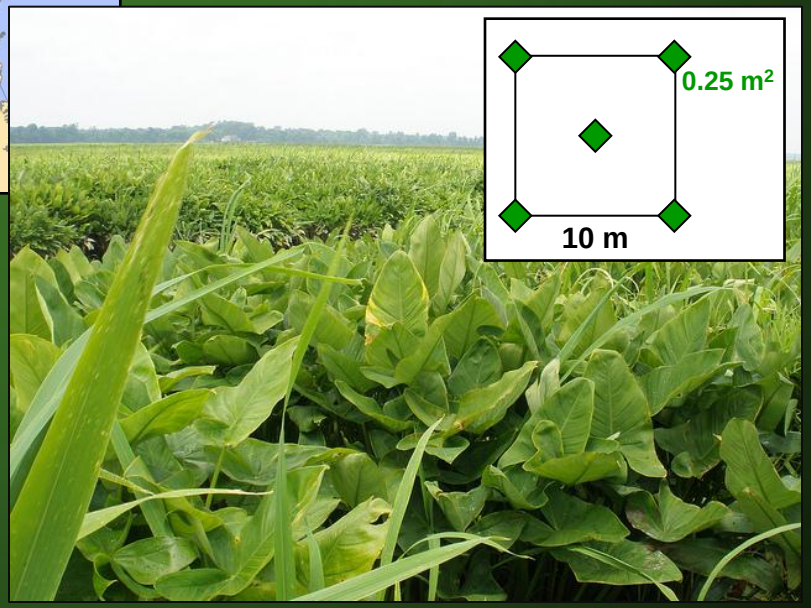
- **What environmental variables regulate the abundance of DNF and DNRA microbes?**
- **What controls community composition within each functional group?**

Microbial activity, fueled by high SOM from plant production

Experimental Design

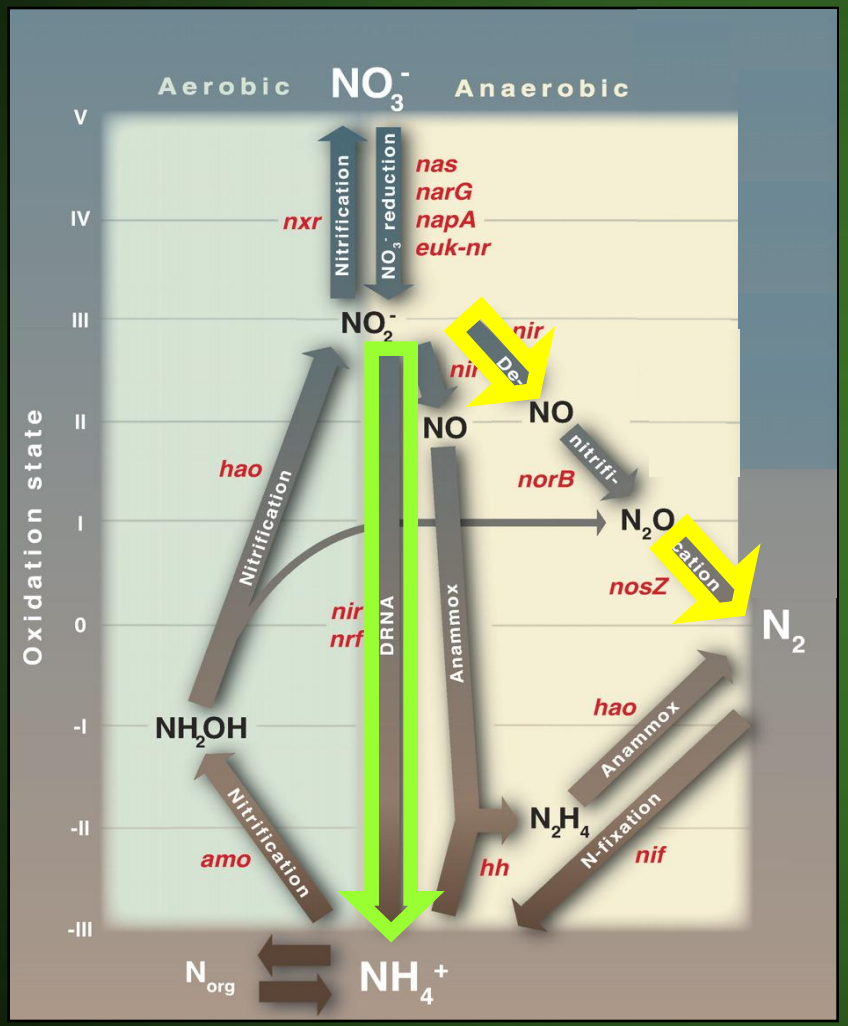


- June 2010
- Sampled 9 tidal freshwater wetlands in Virginia
- Selected for dominance of *Peltandra virginica* (> 50%)



- pH
- Redox
- % Moisture
- Plants (above ground biomass)
- Roots (below ground biomass)

Functional Gene Assays for DNF & DNRA



"The Evolution and Future of Earth's Nitrogen Cycle" – Canfield et al. *Science* (2010)

(1) Abundance of each group:

- quantitative PCR (qPCR) to determine the abundance of selected functional genes

(2) Composition:

- Terminal Restriction Fragment Length Polymorphism (T-RFLP)
- Fingerprinting technique to evaluate the presence and absence of different microbes
- Separate profiles for DNF- and DNRA-capable organisms

Characterizing Sediment Organic Matter

(1) Amount available as %OM

(2) C:N as traditional quality metric

- High C:N – recalcitrant OM
- Low C:N – labile OM

(3) Extracellular enzyme activity:

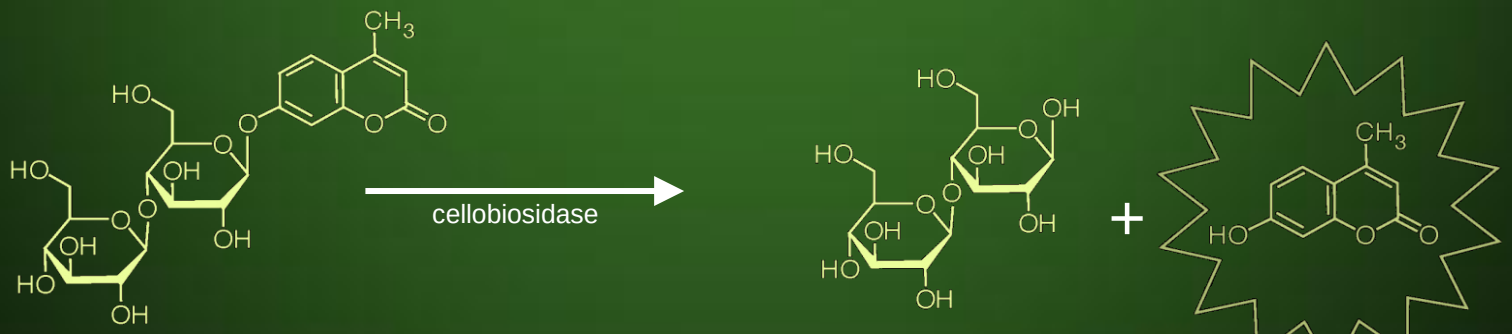
- Proxy for OM quality
- Microbes produce enzymes targeted to local substrate conditions

Enzymes for labile carbon substrates

- Cellulose → β-1,4-glucosidase (BG)
- Cellulose → 1,4- β cellubiosidase (CB)

Enzymes for recalcitrant substrates

- Lignins → Phenol Oxidase (PO)
- Hemicellulose → β-D-xylosidase (Xylo)

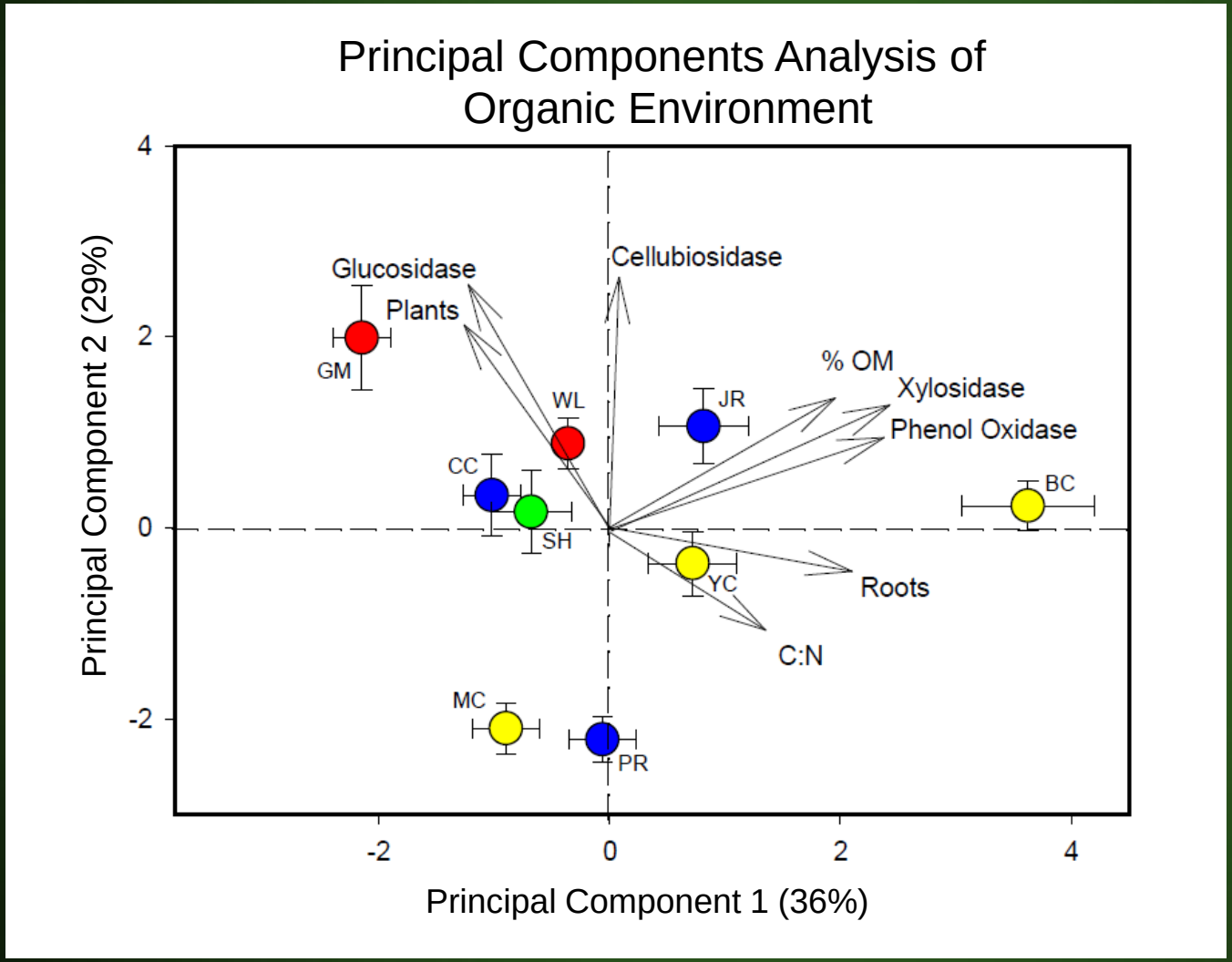


4-Methylumbelliferyl β-D-cellobioside
(proxy for cellulose)

β-D-cellobiose

Methylumbelliferone
+ fluorescence

Site Differences- Biotic Environments



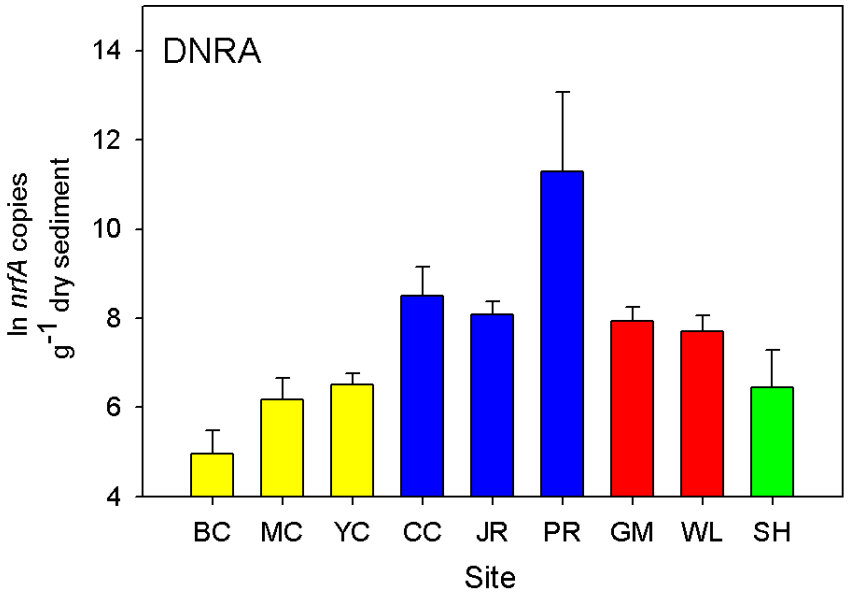
Mattoponi

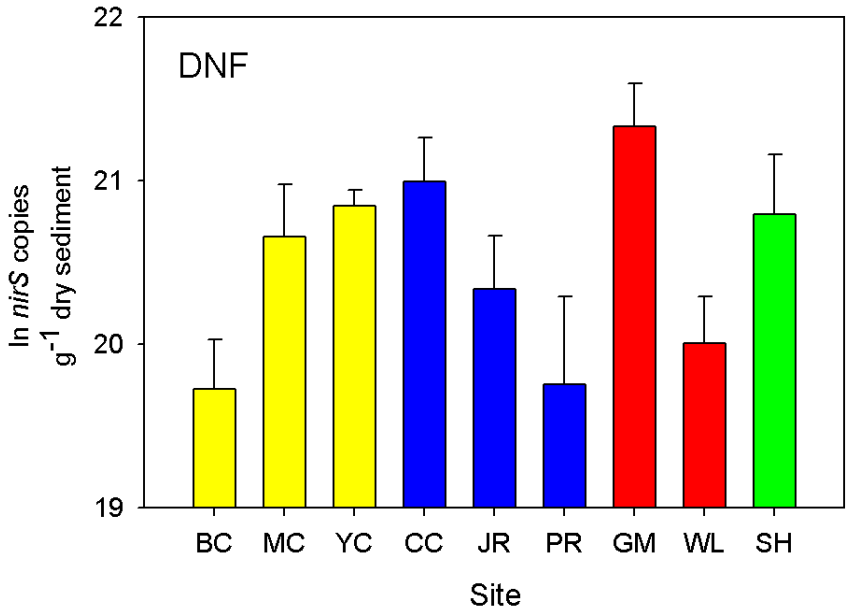
Pamunkey

Chickahominy

James River

Site Differences - DNF & DNRA abundance





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- No consistent trend within or between rivers
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Regression Analysis – Predictors of Functional Group Abundance

Mixed direction stepwise (inclusion α=0.05)

- Response - DNF or DNRA abundance (g^{-1} dry sediment)
- Predictors – pH, redox, plant biomass, %OM, C:N, enzyme activity

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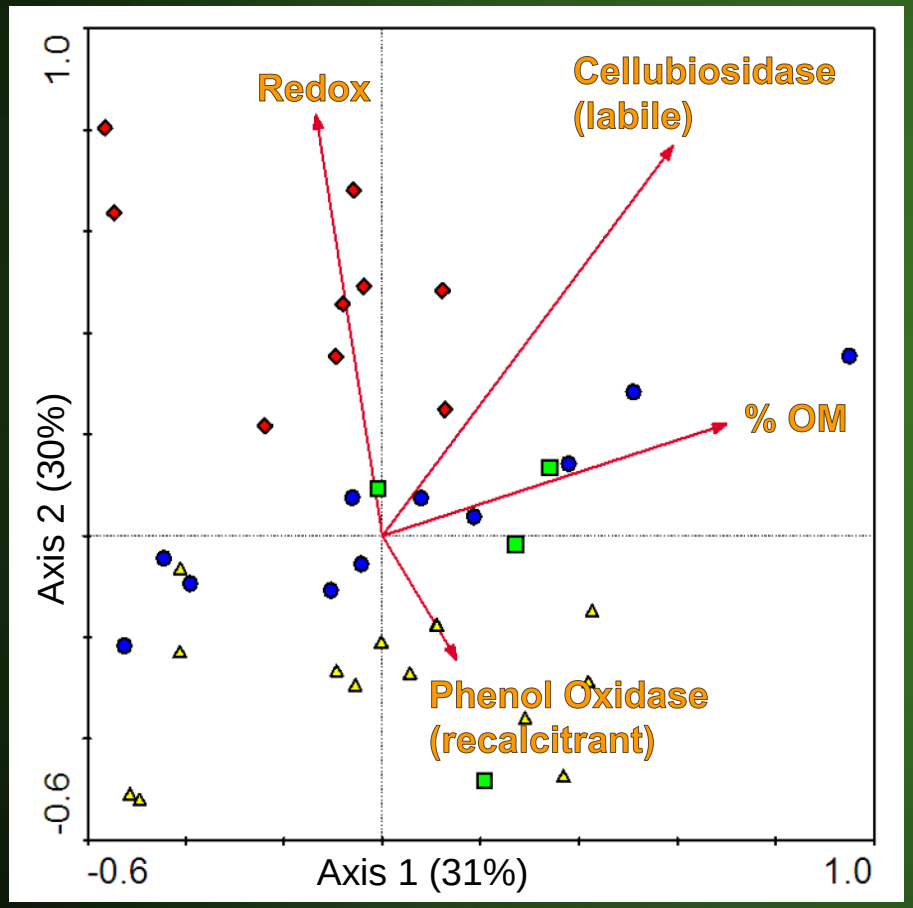
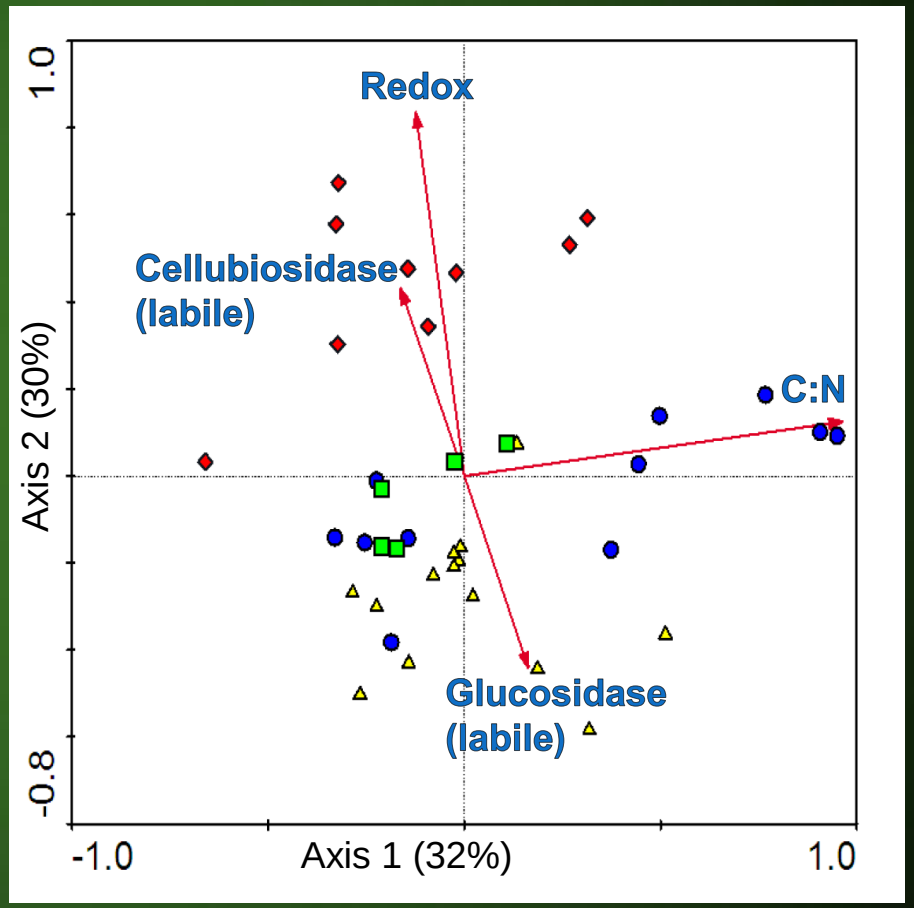
Well….
Yes and No!

Drivers of Community Composition

DNRA



DNF



Mattoponi | Pamunkey | Chickahominy | James River

So what do these relationships mean for biogeochemical activity ?

Roots

Recalcitrant EEA

% Organic Matter

Redox

Labile EEA

C:N Ratio

Plants

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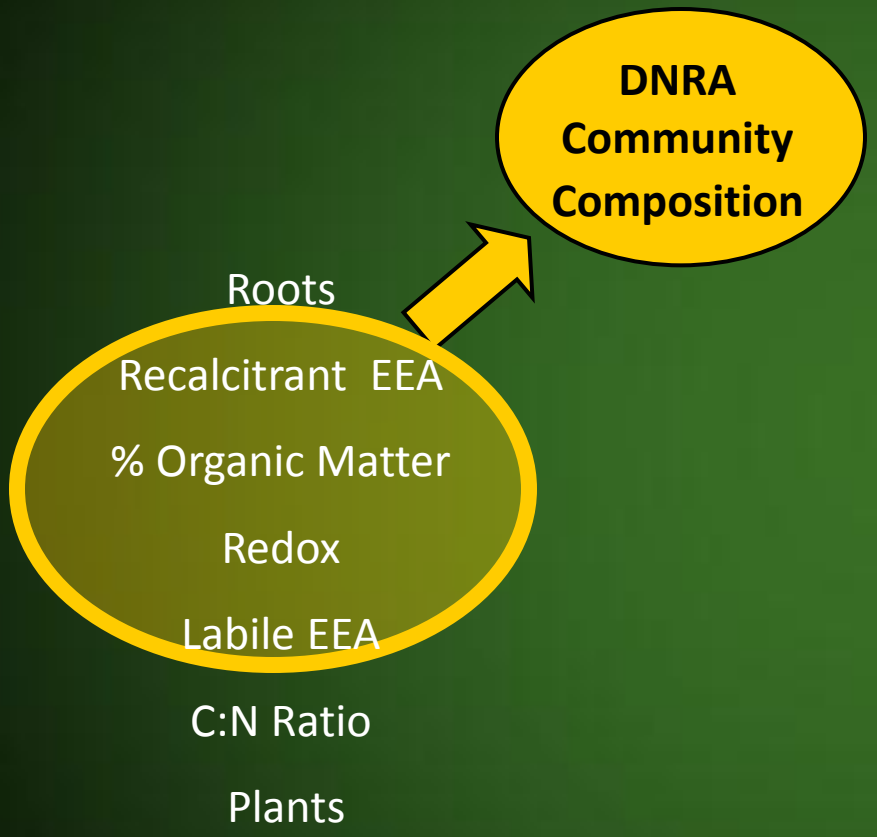

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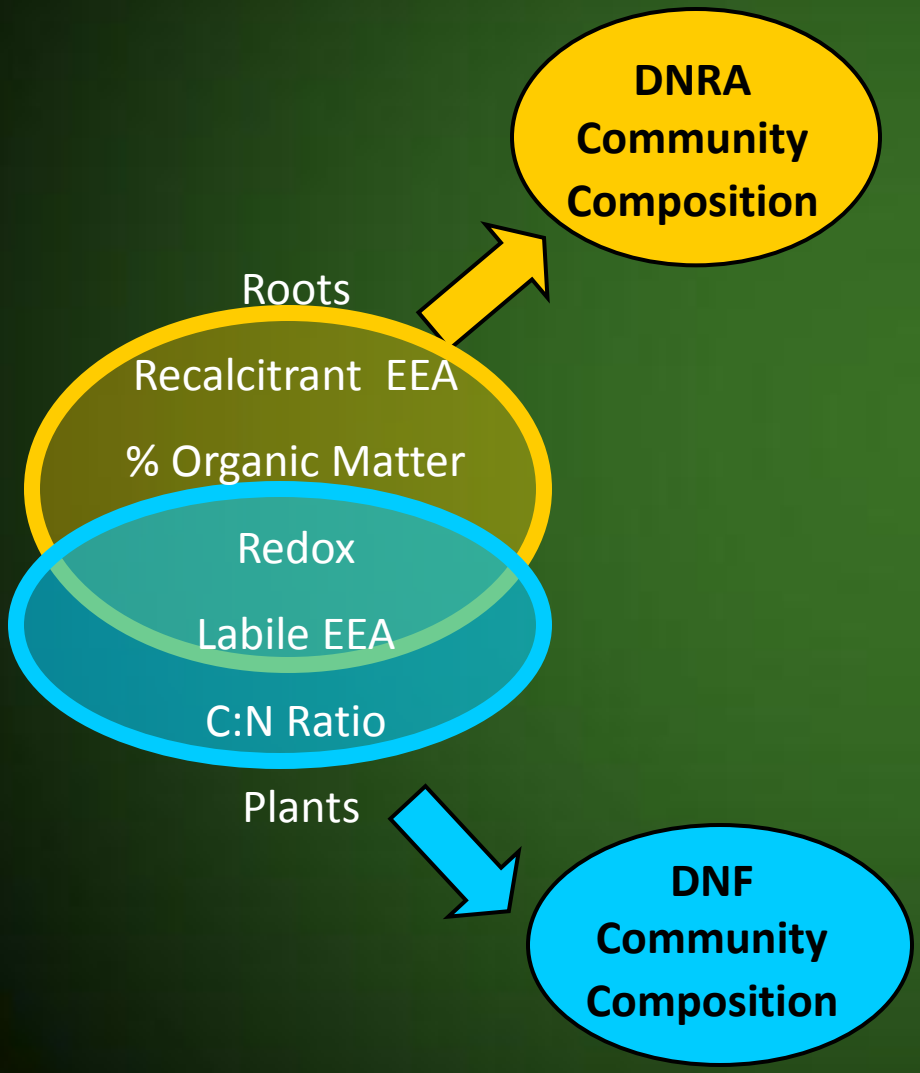

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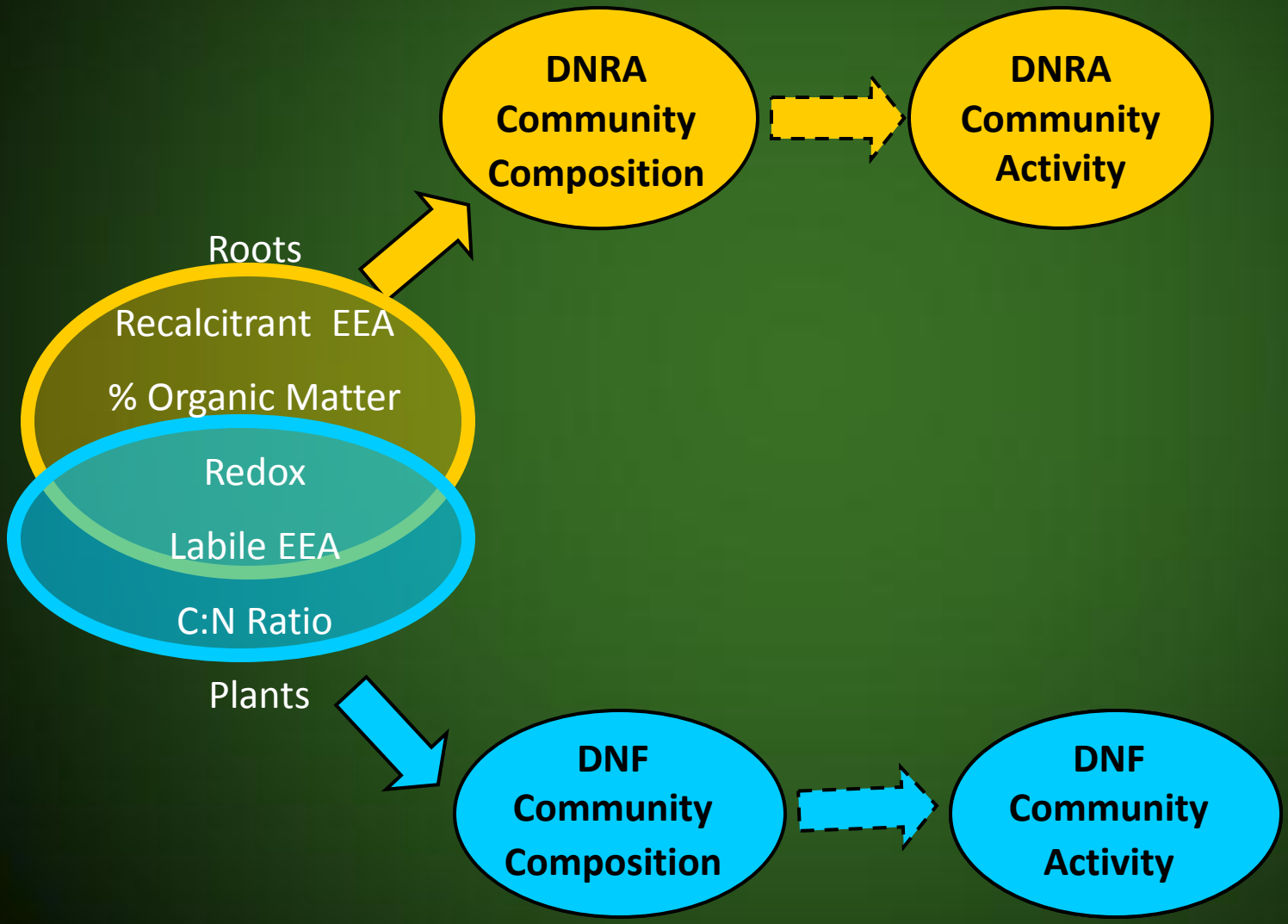

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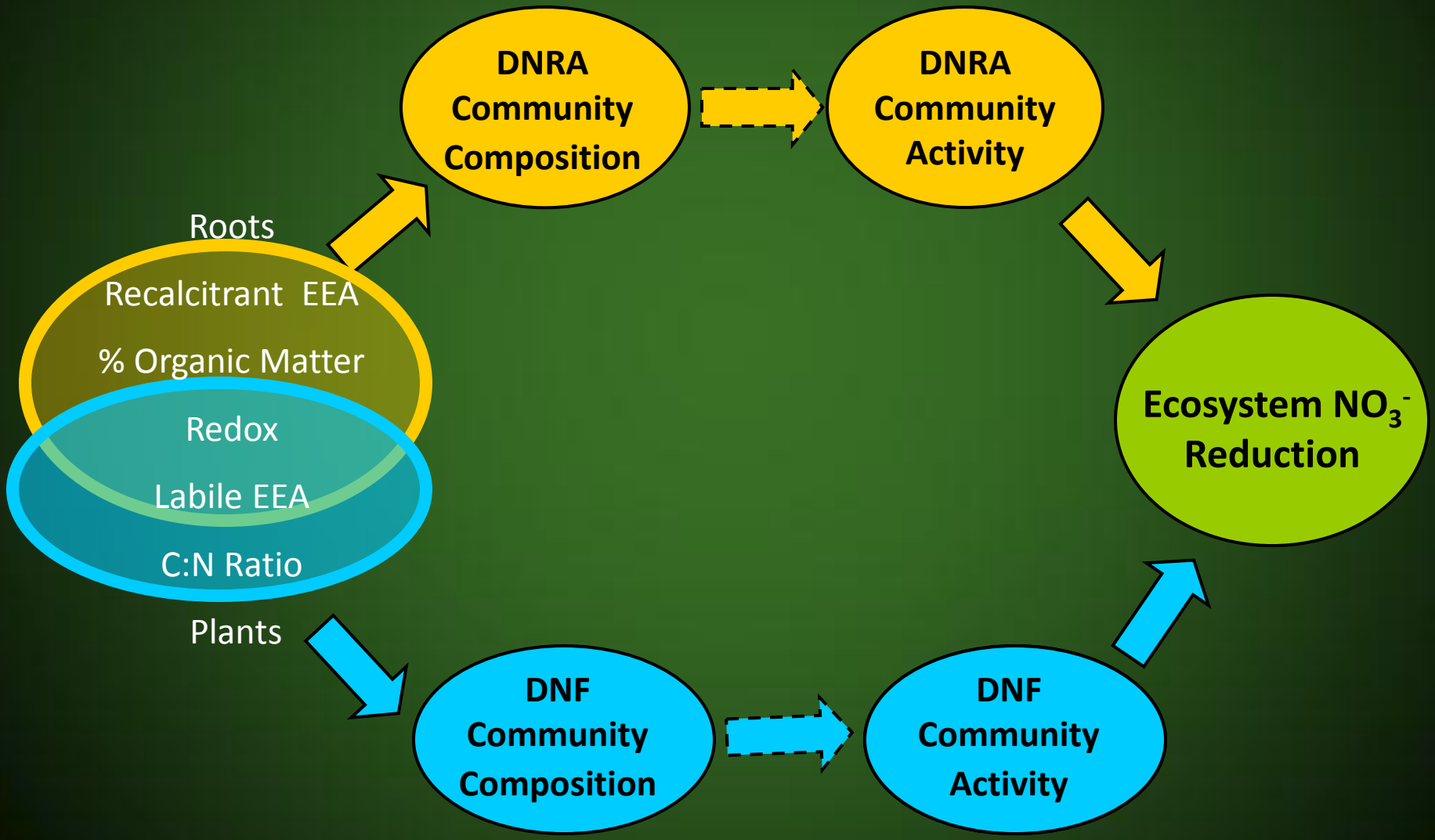

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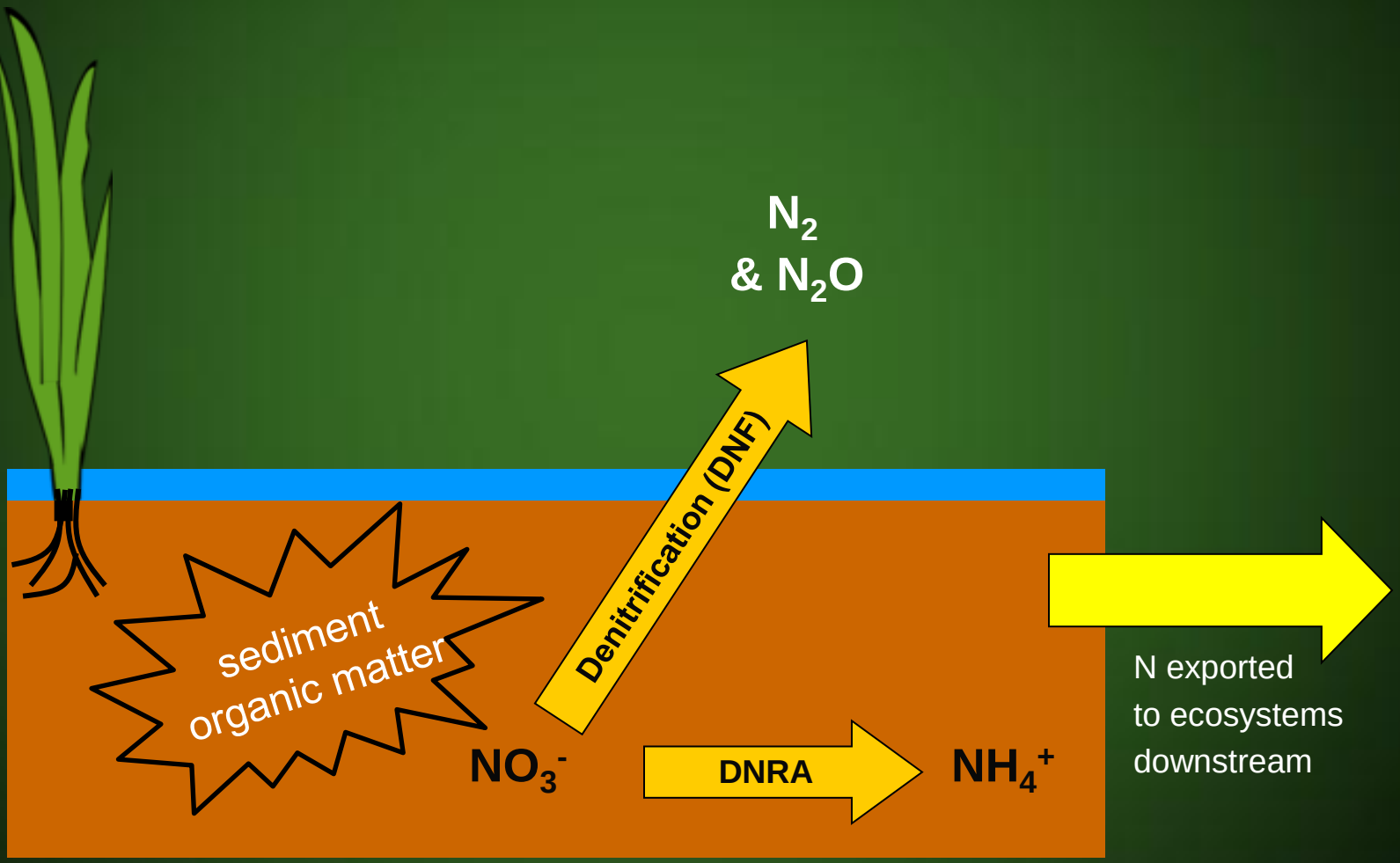

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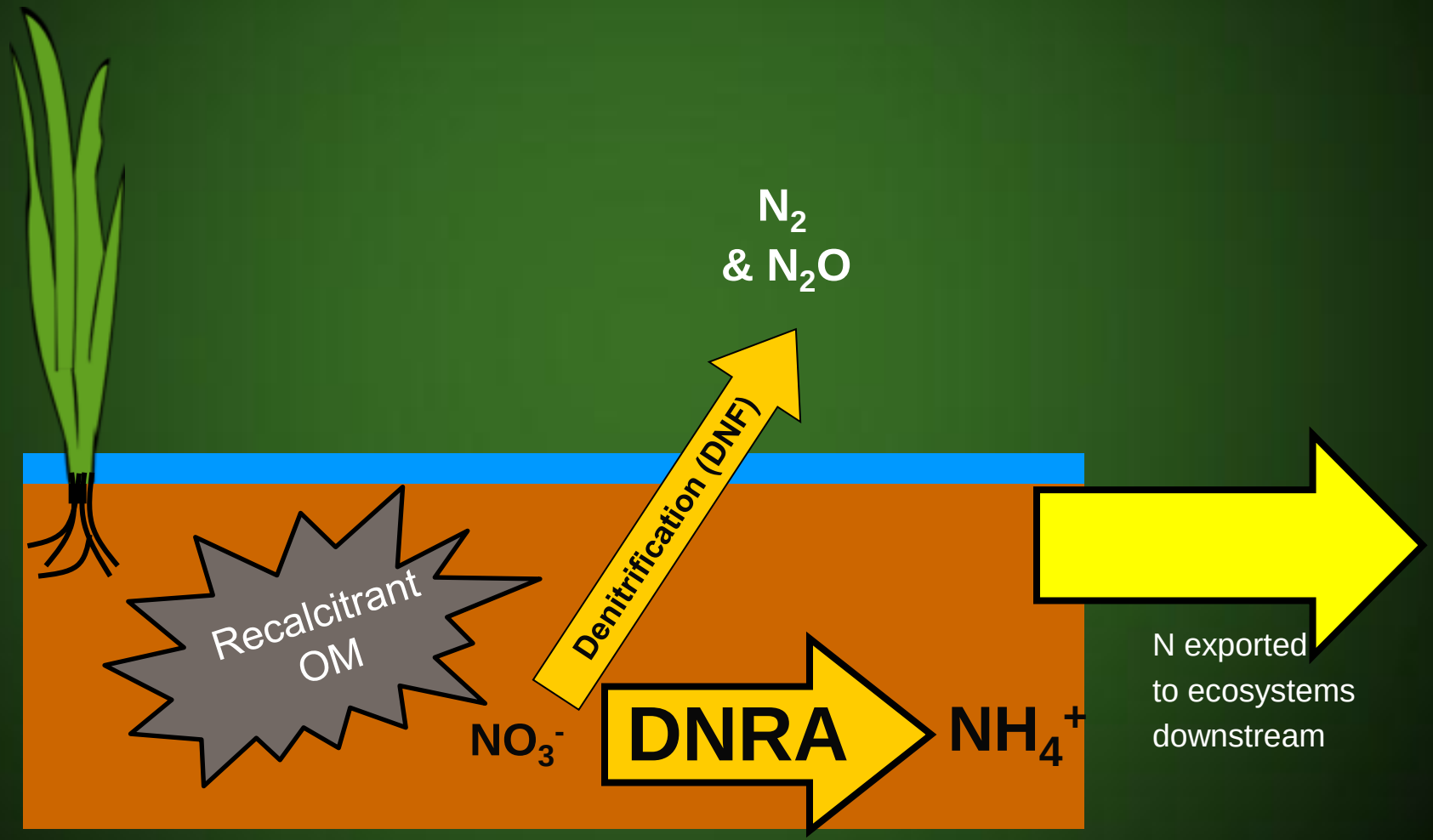

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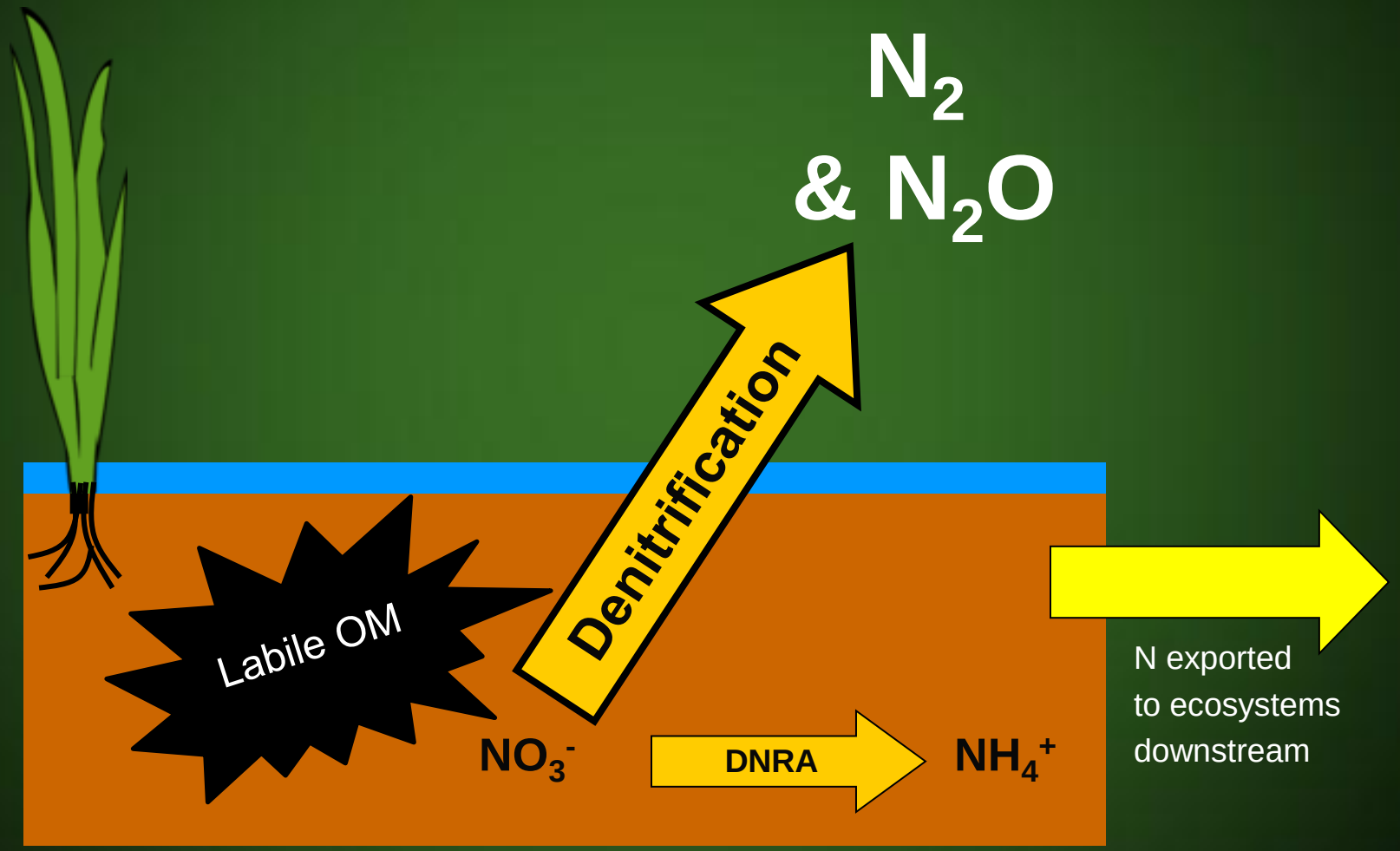

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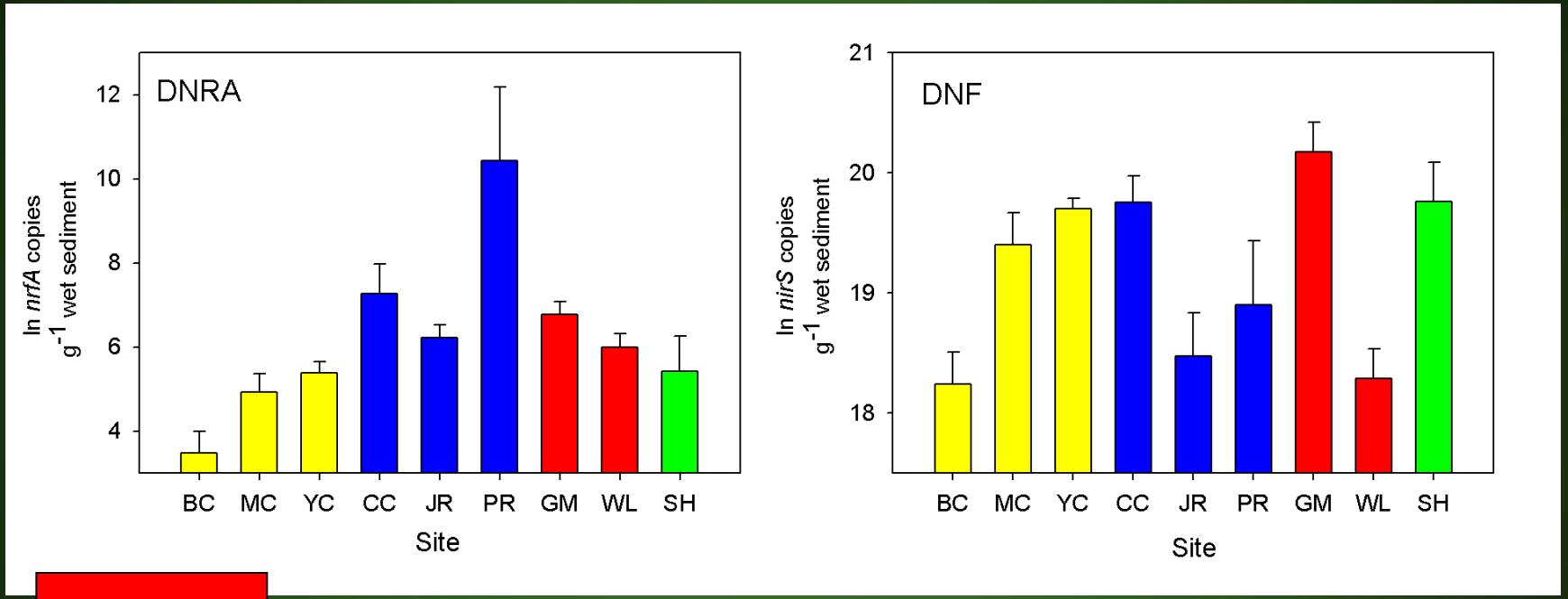

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	Predictors:	**Adj R^2 (p-value)**
DNRA	C:N (+) % OM (-) Roots (-)	0.33 (<0.001)
DNF	C:N (-) % OM (-) Plants (+) pH (+)	0.45 (<0.001)