Evidence for the Functional Significance of Microbial Diversity among Free-living Diazotrophs in Soils of a Long Term Agricultural Site

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Introduction

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Biological N-Fixation by free-living diazotrophs is a globally important process with implications for agriculture. Kennedy & Islam (2001) found that N2 Fixation by free-living diazotrophs can theoretically account for 50-150 kg N/ha. In addition, Global N2 fixation by free-living diazotrophs is estimated at 100-290 Tg N/yr in terrestrial systems (Clevland et al. 1999).

Surveys of nifH diversity in soil commonly reveal sequence types that correspond to diverse unidentified diazotrophs. Evidence indicates that these non-cultivated diazotrophs, rather than their cultivated cousins, are the dominant N-fixing organisms in many soil systems.

Agricultural experiments provide an excellent opportunity to study the functional significance of microbial community composition in soil. Long term agricultural experiments are particularly useful for studying microbial community composition and activity with respect to changes in management practice. Both tillage and biomass managements are known to impact the composition and function of the diazotrophic community in soil.

To evaluate whether diazotrophic community composition has functional significance in an agronomic context, we examined the effects of tillage and biomass management on diazotroph community structure, N-fixation, and soil characteristics in a long-term (> 30 years) experimental site in Chazy, Clinton county, NY (44°53.13'N, 73°28.40')



Results from previous research (Hsu and Buckley, 2009) indicates that:

- Diazotoph diversity was reduced by the long term impacts of agricultural management.
- Within long term agricultural treatments, tillage effects were found to dominate most soil characteristics, but biomass management practices were found to have the largest impact on diazotrophic community composition and N-fixation rates: biomass retention depresses both diazotroph diversity and N-fixation rates.

- Results suggest an association between the diversity of diazotrophic community and N-fixation.

Goal:

Determine whether functional redundancy within the diazotrophic community serves as the mechanism linking changes in diazotroph diversity to changes in N-fixation rate that have been observed in our site.

Hypothesis:

Greater diversity in the diazotrophic community will lead to an increase in functional diversity which will buffer N-fixation rates against variation in environmental conditions.

Experimental Designs:

- A cultivation experiment was performed using a range of different N-free media to evaluate whether community diversity corresponds to the diversity of conditions that support the growth
- of diazotrophs.
- In addition, soil microcosms were exposed to a variety of conditions to determine whether increased diversity in the diazotrophic community is associated with resilience of soil Nfixation to changes in the environment.

Materials & Methods:

Experiment1

15 soil cores (top 0-5 cm) were taken from each of four field replicates and pooled to represent treatments T2, T4 and NC. N2 fixation was determined by assessing 15N2 incorporation into soil in relation to controls incubated with unlabeled N2.





14N₂ N gas incorporation

15N₂ N gas incorporation

Experiment 2

a) N-free media were used to enumerate different functional classes of diazotrophs by MPN. Growth conditions included differences in carbon sources (C1 malate, C2 cellobiose, C3 sucrose, C4 mannitol, C5 vanillin, and C6 acetate), pH (7.5, 5.5 and 3.5), oxygen levels (20%, 5% and 0%), trace metals (Mo, V and Fe), and temperatures (4, 22, 30, and 42 degree C). All inoculation tests were incubated in 96-wells plates and growth was detected by absorbance at 590 nm after 40 days of incubation. b) Bacteria were isolated and purified from different growth conditions and

characterized by analysis of their 16S rRNA gene sequences.

^{0.5} 1 1.5 2 2.5 3 3.5 **Evenness component of the Shannon index (J'=H'/H'max)** Fig 2 Diazotroph diversity plotted in relation to N-fixation rate and functional diversity

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Table 1 Number of conditions that supported growth of Nfixing bacteria compared across all MPN experiments (20,000 cells/g of soil as cut-off of growth) # of growth at

		C	A	C 4 J	Dent
	20000 cut off	Sum	Ave	Sta	U-test
T4r1	6				
T4r2	8				
T4r3	7				
T4r4	8	29	7.25	0.9574	ns*
T2r1	7				
T2r2	12				
T2r3	9				
T2r4	8	36	9	2.1602	ns
NCr1	12	화복공물			에서 독취 가슴 또한 동 이 속이 있는 것이 있는 것이
NCr2	14				
NCr3	13				
NCr4	11	50	12.5	1.2910	NC>T4
*ns: No si	enificant	바람 관계			



Fig 1 MPN results for growth in C2 cellobiose, C3 sucrose, C4 mannitol and C6 Acetate under 3 levels of oxygen.

Table 2 Numbers of conditions that support growth of Nfixers compared across different levels of oxygen. (20,000 cells/g of soil as cut-off of growth)

	aerobicr	nicroaerobi	c anoxic	sum
T 4		12	0	13
T2	3	12	5	20
NC	E -	12	10	27
r ovact tost	D nc*	12 hc		
No significant	115	115	110,12>14	(P=0.015)





Fig 6 Phylogenetic analyses of bacteria isolated from MPN experiments in different C sources and N-Free media under 30 degree C growth condition.

Conclusions:

- range of growth conditions
- environmental perturbation.
- Further directions:





	Table 4 ANOVA table for N-fixation rates under conditions								
b,c t	b,c → C ↓	within each to the second seco	treatment. F Sum of Sq Mean Sq 5 0.0151 0.0030 5 0.0028 0.0006 5 0.0142 0.0028	F-Value 8.8243 1.2897 2.6090	P-Value 0.0002 0.3116 0.0607				
s under 6 nificant p	different environmental ><0.05)	Table 3 ANOVA tal or 6 inocula Image: T2, T4, NC 6 conditions 5	ble for N-fixation rate ation conditions. Sum of S9 Mean S9 F- 0.0021 0.0011 10.2300 0.0046 6	under 3 Value P-4 .1418 0.1 .6677 <0.	treatments Jalue 3254 0001				
	Microbacterium sp. Microbacterium sp.	Actinobacteria	Sphingomonas sp. Sphingopyxis sp. 30T434 Sphingomonas oligophenolica 30T417 30T418 Comamonas sp. 30T422 AB291842						
eria		α-Proteobacteria	30T411 Bosea sp. 30T412 30T409 Afipia sp. 30T410 Agrobacterium sp. Rhizobium radiobacter						
pria	30T208 30T213 30T206 30T209 30T249 Bradyrhizobium sp. 30T224 30T223 30T233 30T219 30T251 30T246 Herbaspirillum huttiense Herbaspirillum putei 30T243 Variovorax paradoxus	β-Proteobacteria	Acidovorax sp. Antarctic bacterium 30T426 Polaromonas sp. 30T427 Pseudoxanthomonas sp.		β-Proteobacteria				
	- Seudoxaninomonas mexicana		X I		N_Protechacteria				

- The cultivation experiment showed that more diverse diazotrophic communities could respond to a greater - In soil microcosms no relationship was observed between diazotroph diversity and resiliance to

- Use nifH primers to evalute the isolates and compare to nifH clone libraries recovered directly from soil. - Evaluate the portion of the diazotrophic community that was recovered through cultivation. Acknowledgments: Funding provided by NSF Microbial Observatories Program and USDA-CSREES Soil Process Program