

FIG S1 Example of a non-metric multidimensional scaling (NMDS) ordination based on Bray Curtis similarities for bacterial/archaeal community composition for the assimilatory nitrite to ammonia pathway. Sample collection date is represented by number. The symbols shapes represent plot treatment: ambient conditions (star), drought (triangle), or nitrogen addition (circle). The symbol color denotes winter-spring (blue) or summer-fall (orange) seasons.

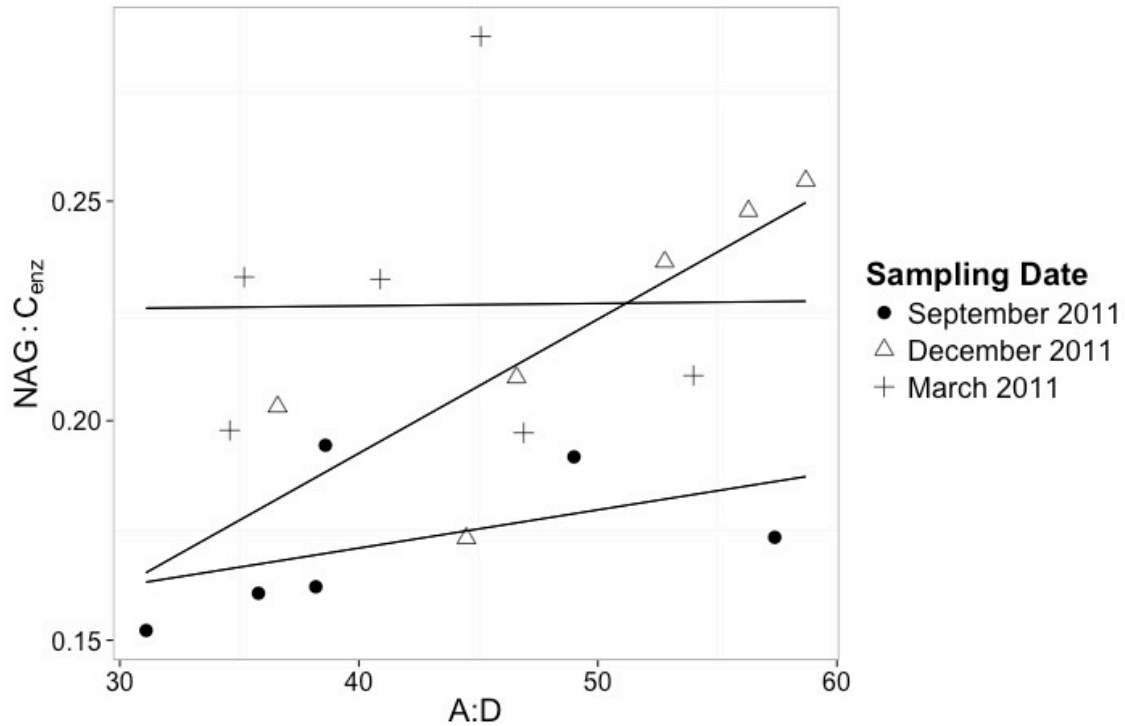


FIG S2 A:D ratio (x-axis) and NAG:Cenz ratio (y-axis). Symbols represent sampling date. The ratio of A:D abundance explained almost half the variation in NAG:Cenz (ANCOVA; $p=0.045$; adjusted $R^2=0.47$). The covariate time (sampling date), was also significant ($p=0.004$), but there was no A:D by time interaction ($p=0.88$).

TABLE S1 MG-RAST accession numbers for the plant litter metagenomes used in this study.

<u>Sampling Date</u>	<u>Treatment</u>		
	Control	Drought	Nitrogen Addition
April 2010	4511049	4511045	4511047
	4511050	4511046	4511048
August 2010	4511065	4511061	4511063
	4511060	4511062	4511064
December 2010	4511116	4511112	4511114
	4511111	4511113	4511115
February 2011	4511140	4511137	4511139
	4511141	4511134	4511135
June 2011	4511146	4511142	4511144
	4511147	4511143	4511145
September 2011	4511153	4511148	4511152
	4511151	4511149	4511150
December 2011	4511184	4511182	4511183
	4511185	4511179	4511180
March 2012	4511191	4511193	4511189
	4511192	4511188	4511190

TABLE S2 Nitrogen cycling pathways, number of genes, the genes searched in the pathways and KEGG identification. Denitrification and nitrogen fixation pathways are a combination SEED (1) and KEGG (2) database classifications. All other pathways were classified using the FOAM database (3).

N- cycle pathway	# of genes	genes	KEGG ID
Ammonia assimilation	10	glutamine synthase (ferredoxin), glutamate dehydrogenase (gdhA), glutamate synthase (NADPH/NADH) large chain (gltB), glutamate synthase (NADPH/NADH) small chain (gltD), glutamin asparaginase (aspQ), glutamine synthetase (glnA), glutamate synthase (GLT1), glutamate dehydrogenase (GLUDI_2), glutamate dehydrogenase (gudB, rocG), glutamate dehydrogenase (GDH2)	K00265 K01425 K00284 K01953 K00261 K15371 K00266 K00260 K00264 K05597 K00262 K01915
Nitrification	2	ammonia monooxygenase (amo), hydroxylamine oxidase (hoa)	K10945 K10944 K10535 K10946
Dissimilatory Nitrate to Nitrite	9	nitrate reductase delta subunit (narJ), nitrate reductase gamma subunit (narI), nitrate reductase alpha subunit (narG), nitrate reductase beta subunit (narH), periplasmic nitrate reductase (napA), rieske iron-sulfur protein (narB), nitrate reductase catalytic subunit (nasA), cytochrome b-561 (narC), cytochrome c-type protein (napB)	K00373 K08346 K00374 K00370 K08361 K00371 K08347 K02567 K15878 K00372 K08345 K15879 K02568
Dissimilatory Nitrite to Ammonia	4	nitrite reductase cytochrome c-552 (nrfA), protein nrfD (nrfD), nitrite reductase protein NrfC (nrfC), cytochrome c-type protein (NrfB)	K04014 K03385 K04013 K04015
Assimilatory Nitrate to Nitrite	2	assimilatory nitrate reductase electron transfer subunit (nasB), nitrate reductase (NAD(P)H) (NR)	K00360 K15875 K10534

Assimilatory Nitrite to Ammonia	3	ferredoxin-nitrite reductase(nirA), nitrite reductase (NADH) large subunit (nirB), nitrite reductase (NADH) small subunit (nirD)	K00366 K00362 K00363
Denitrification	20	Cytochrome cd1 nitrite reductase (nirS), Copper-containing nitrite reductase (nirK), Nitrite reductase accessory protein (NirV), Nitric-oxide reductase quinol-dependent (qNor), Nitric-oxide reductase subunit B (cNor-B), Nitric-oxide reductase subunit C (cNor-C), Nitric oxide reductase activation protein (NorE), Nitric oxide reductase activation protein (NorD), Nitric oxide reductase activation protein (NorQ), Nitrous-oxide reductase (nosZ), Nitrous oxide reductase maturation protein (NosD), Nitrous oxide reductase maturation protein-ATPase (NosF), Nitrous oxide reductase maturation transmembrane protein (NosY), Nitrous oxide reductase maturation protein, outer-membrane lipoprotein (NosL), Nitrous oxide reductase maturation periplasmic protein (NosX), Nitrous oxide reductase maturation protein (NosR), NnrS protein involved in response to NO (NnrS), Nitric oxide-responding transcriptional regulator-Crp/Fnr family (NnrR), Nitric oxide-responding transcriptional regulator Dnr-Crp/Fnr family (DNR), fungal nitric oxide reductase (CYP55)	K00376 K04561 K02305 K15864 K00368
Nitrogen Fixation	20	nitrogenase reductase (nifH), nitrogenase molybdenum-iron protein subunit alpha (nifD), nitrogenase molybdenum-iron protein subunit beta (nifK),nitrogenase vanadium-iron protein delta chain (vnfG), oxidoreductase/nitrogenase- component 1, vanadium nitrogenase beta subunit (vnfK), vanadium nitrogenase, alpha subunit (vnfD), Fe-only nitrogenase- beta subunit (anfK), Fe-only nitrogenase- delta subunit (anfG), nitrogenase iron-iron protein- alpha chain (anfD), nitrogenase molybdenum-iron cofactor biosynthesis protein (nifN), nitrogenase iron protein 2 (nifH2), nitrogenase molybdenum-cofactor biosynthesis protein (nifE), two-component regulatory system (ntrX), two-component regulatory system (ntrY), homocitrate synthase (nifV), cysteine	K02591 K02595 K00531 K02588 K02586

desulfurase (nifS), regulatory protein
 (fixJ), nitrogen regulation protein NR(I
)(ntrC), regulatory protein (nifN/fixK)

Table S3 Effect of treatment, time, and their interaction on bacterial composition (order level) for each N cycle pathway. Values are p values. NS is not significant.

N Cycle Pathway	Treatment	Time	Treatment x Time
Dissimilatory Nitrate to Nitrite	P<0.01	P<0.001	P<0.01
Dissimilatory Nitrite to Ammonia	NS	NS	NS
Denitrification	NS	P<0.01	P<0.05
Nitrification	NS	NS	NS
Assimilatory Nitrate to Nitrite	NS	P<0.05	NS
Assimilatory Nitrite to Ammonia	P<0.05	P<.001	p=0.065
Ammonia Assimilation	NS	P<.001	NS
Nitrogen Fixation	NS	NS	NS

Table S4 Results of SIMPER analysis displaying the top five orders that contributed most to changes in composition for each pathway. The + sign indicates a higher relative abundance. Percent contribution is based on bray-curtis similarity.

Assimilatory Nitrite to Ammonia			
Order	Winter-Spring	Summer-Fall	% Contribution
Actinomycetales	+		20.4
Enterobacteriales		+	17.7
Burkholderiales	+		11.3
Sphingomonadales	+		10.16
Rhizobiales	+		8.63
Dissimilatory Nitrate to Nitrite			
Order	Winter-Spring	Summer-Fall	% Contribution
Enterobacteriales		+	30.86
Burkholderiales	+		14.32
Sphingomonadales	+		14.09
Actinomycetales		+	10.92
Rhizobiales	+		9.77
Denitrification			
Order	Winter-Spring	Summer-Fall	% Contribution
Rhizobiales		+	15.34
Burkholderiales	+		12.39
Rhodobacteriales		+	10.92
Flavobacteriales	+		8.72
Rhodospirales		+	5.87
Ammonia Assimilation			
Order	Winter-Spring	Summer-Fall	% Contribution
Actinomycetales		+	25.48
Rhizobiales	+		9.46
Enterobacteriales		+	9.15
Sphingomonadales	+		8.98
Caulobacteriales		+	7.89

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