

Supporting Information

TITLE: The role of denitrification in stormwater detention basin treatment of nitrogen

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Supporting Information. Table S1: Average measured N₂O fluxes for Dry Basin2 and Wet Basin1. Figure S1: Stormwater basin sampling scheme, Figure S2: Site location map. Figure S3: Normalized total denitrification reads vs soil water content at time of sample collection. S4: Individual denitrification gene reads normalized by total reads per sample.

5 pages in Supporting Information (S1-S5)

Table S1. Site average and standard error (se) of N₂O fluxes, n=3 per sample date.

Site	Date	N ₂ O Flux g N m ⁻² yr ⁻¹	se N ₂ O flux g N m ⁻² yr ⁻¹
Dry Basin2	4/20/2016	0.145	0.277
	4/27/2016	0.413	0.068
	5/11/2016	-0.183	0.058
	6/2/2016	0.307	0.151
	6/20/2016	-0.039	0.043
	6/27/2016	0.064	0.106
	7/8/2016	0.293	0.022
	7/13/2016	0.153	0.051
	7/22/2016	-2.617	0.560
	7/25/2016	0.436	0.394
	8/2/2016	0.258	0.185
	8/10/2016	0.107	0.202
	8/23/2016	0.709	0.288
	9/14/2016	0.216	0.065
	9/19/2016	0.195	0.127
	9/21/2016	-0.162	0.201
	10/8/2016	-0.105	0.291
	Site Average	0.011	0.173
Wet Basin1	4/20/2016	0.130	0.148
	4/27/2016	-0.214	0.154
	5/11/2016	-0.295	0.268
	6/2/2016	0.126	0.116
	6/20/2016	0.305	0.434
	6/27/2016	0.407	0.325
	7/8/2016	1.856	1.770
	7/13/2016	0.897	0.348
	7/22/2016	NA	NA
	7/25/2016	1.207	0.790
	8/2/2016	-0.096	0.155
	8/10/2016	0.185	0.305
	8/23/2016	-0.048	0.091
	9/14/2016	0.180	0.130
	9/19/2016	0.063	0.085
	9/21/2016	0.074	0.132
	10/8/2016	-0.035	0.187
	Site Average	0.296	0.142

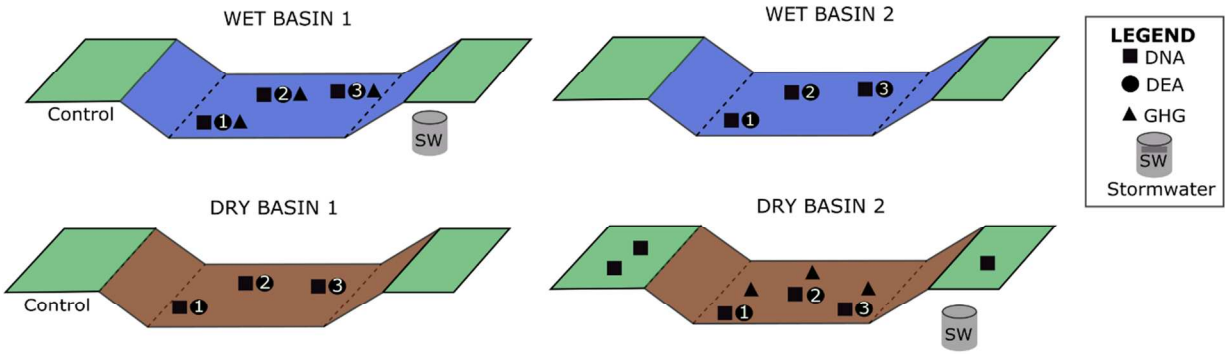


Figure S1. Stormwater basin sampling scheme. Each symbol denotes approximate location of sample collection point (not to scale). DNA = DNA metagenomics, DEA = potential denitrification enzyme assays, GHG = static chamber GHG sampling, SW = stormwater sampling at inflow and outflow of basin.

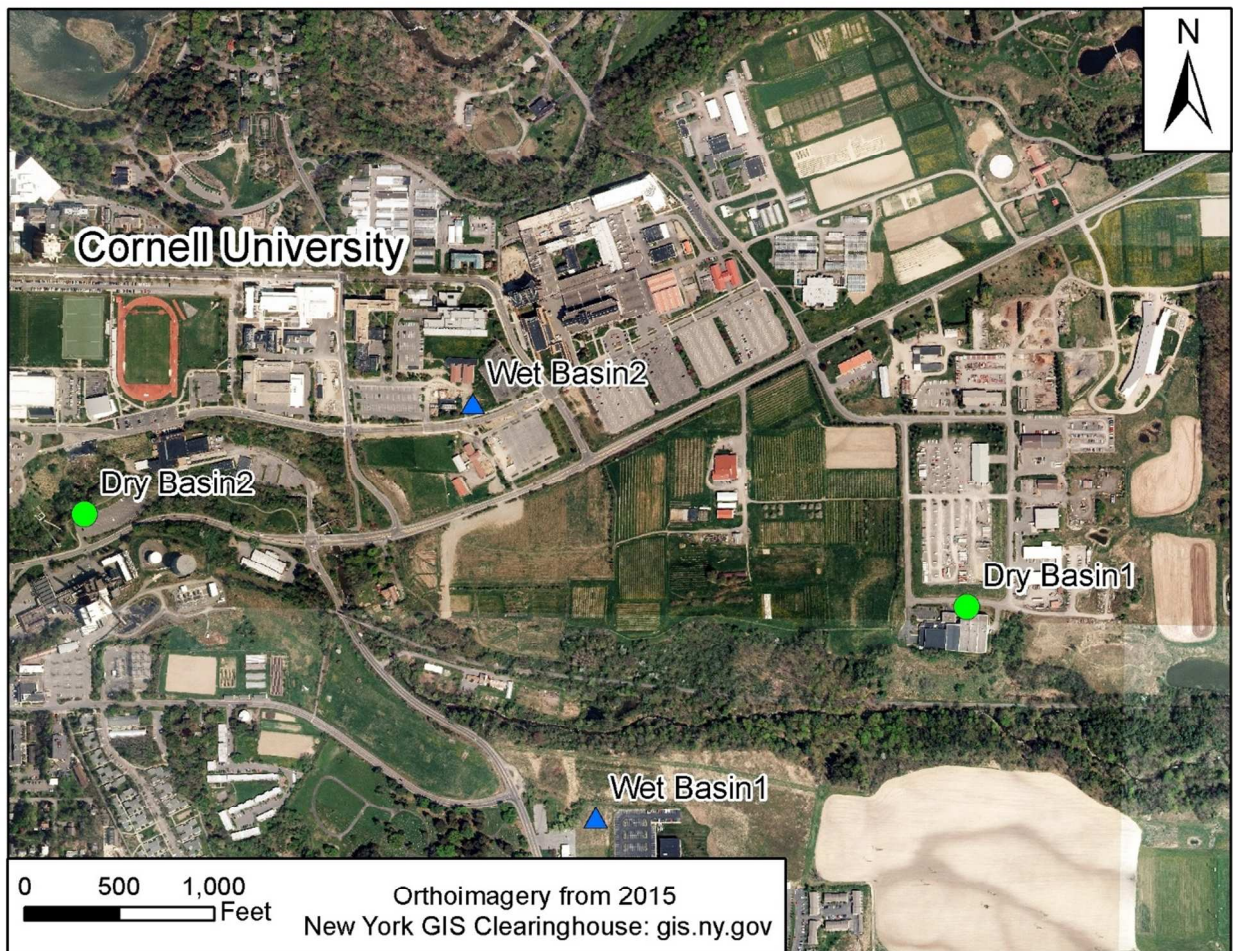


Figure S2. Site location map

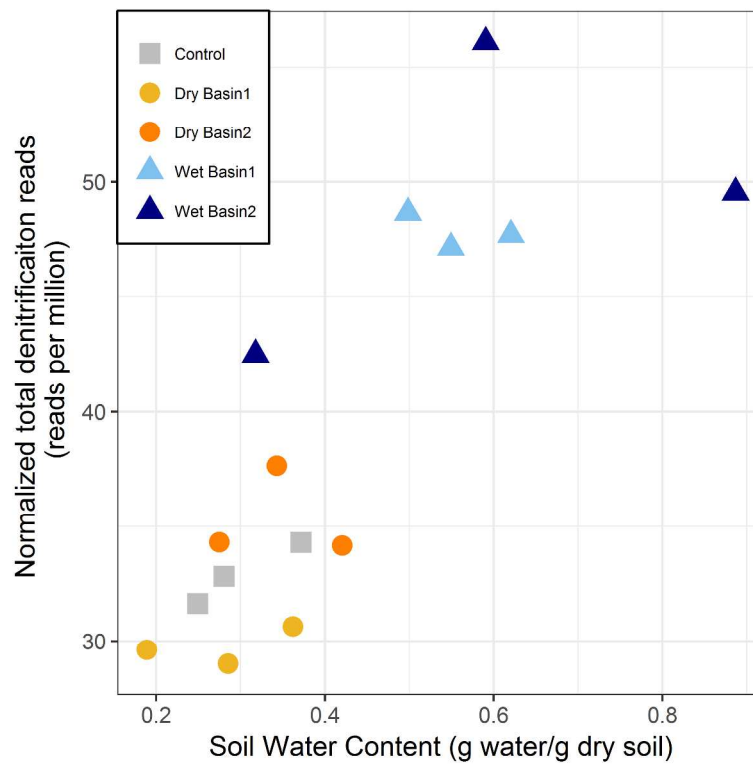


Figure S3. Normalized total denitrification gene reads vs soil water content at time of sample collection.

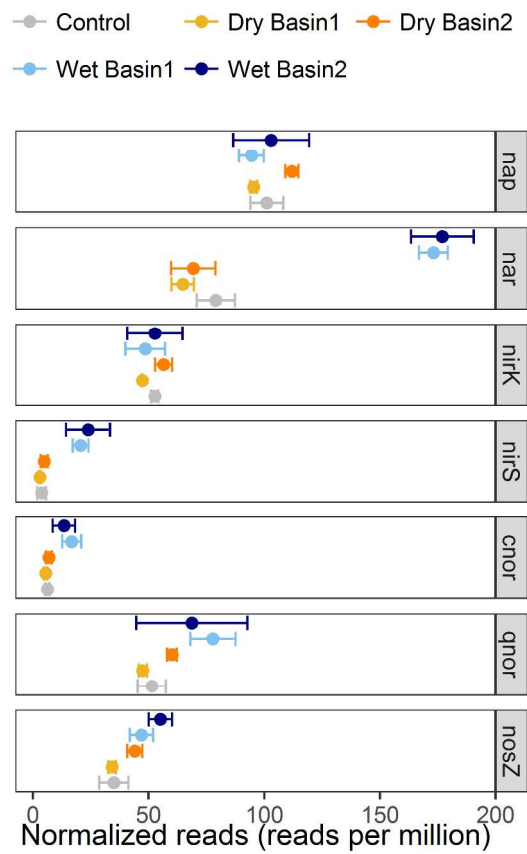


Figure S4. Individual denitrification gene reads normalized by total reads per sample. Error bars are 1 SD.