Response of soil microbial communities during changes in land-management

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Background

An accelerated degradation of ecological environments has occurred over the last century. Natural revegetation has been regarded as the most effective restoration strategy. However, response of below-ground microbial communities to these successional processes is poorly understood.

Hypothesis

Microbial communities in restored soil would return to their native state with time. The structure & composition of stabilized state is dependent upon the nature of disturbance & the restoration regime used.

Study Site

W.K. Kellogg Biological Station, Michigan

- Never tilled cropland (NT)
- Moldboard plowed cropland (CT)
- Early-succession grassland restored in 1989 (ES)
- Mowed grassland (MG)
- Mid-successional forest restored in 1964 (SF)
- Native deciduous forest (DF)
- Coniferous forest planted with conifers in 1950 (CF)

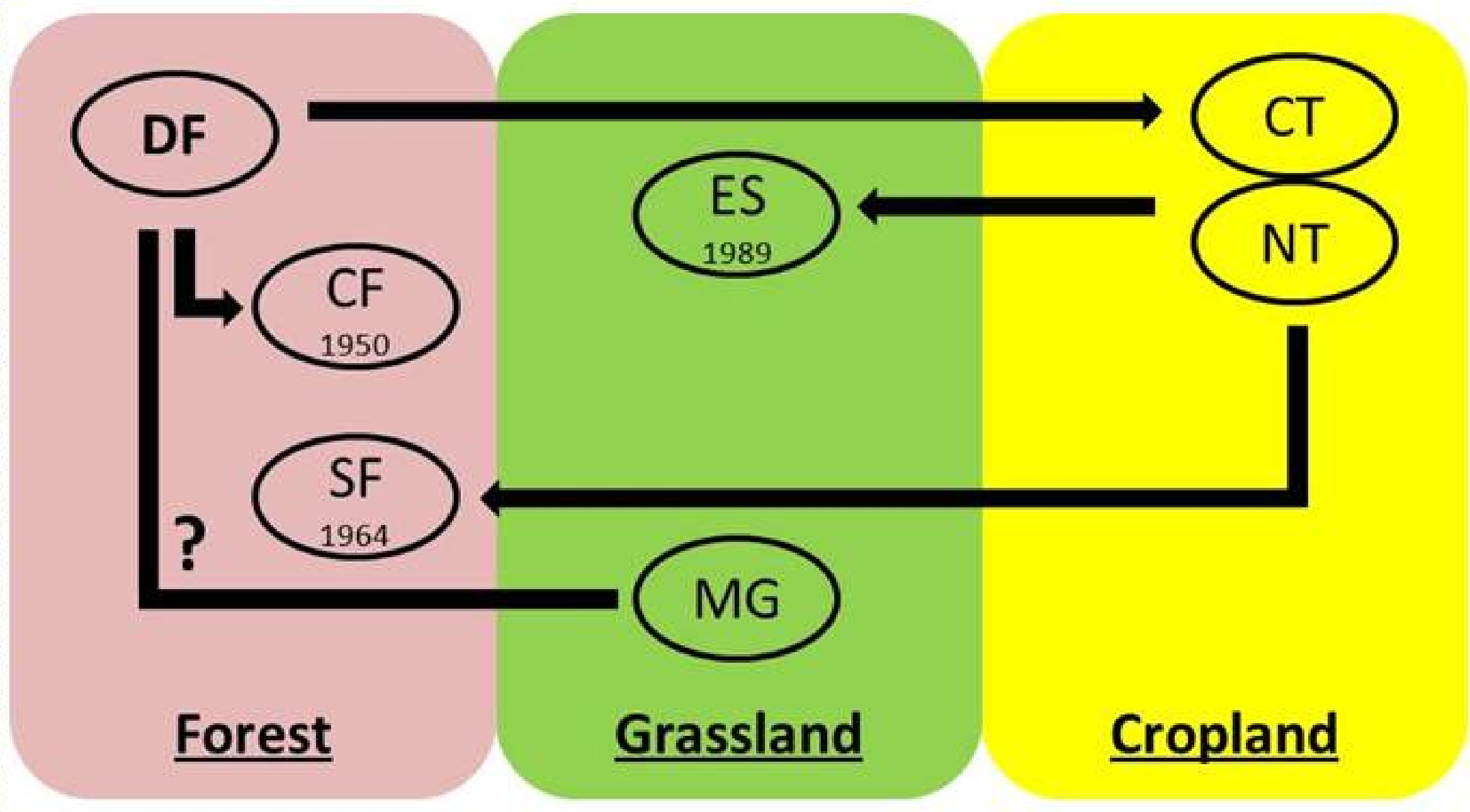
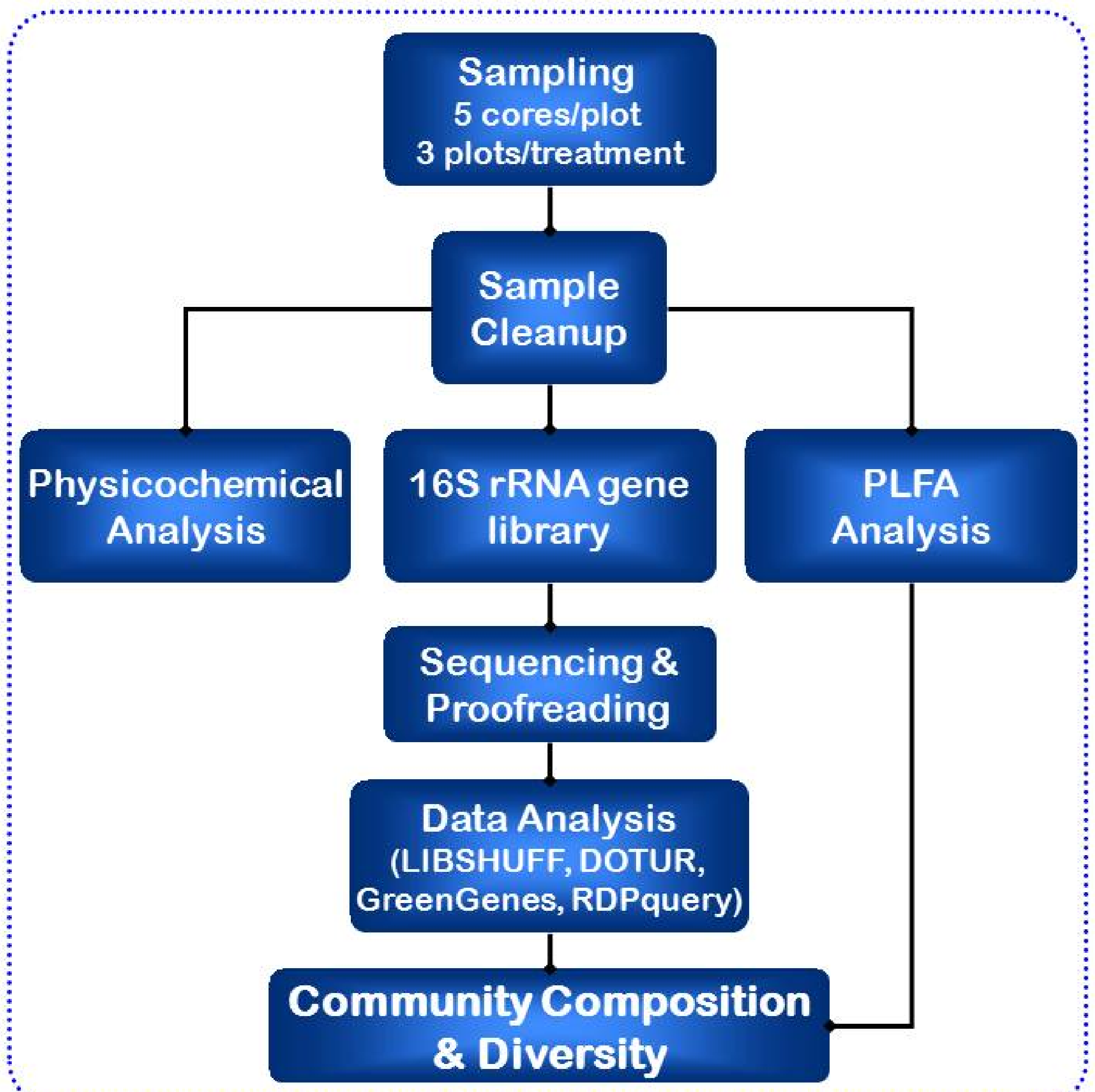


Fig. 1. Origins of various plots and their land management regimes studied at KBS, Michigan.

Experimental Strategy



Sampling
5 cores/plot
3 plots/treatment

Sample Cleanup

Physicochemical Analysis

16S rRNA gene library

PLFA Analysis

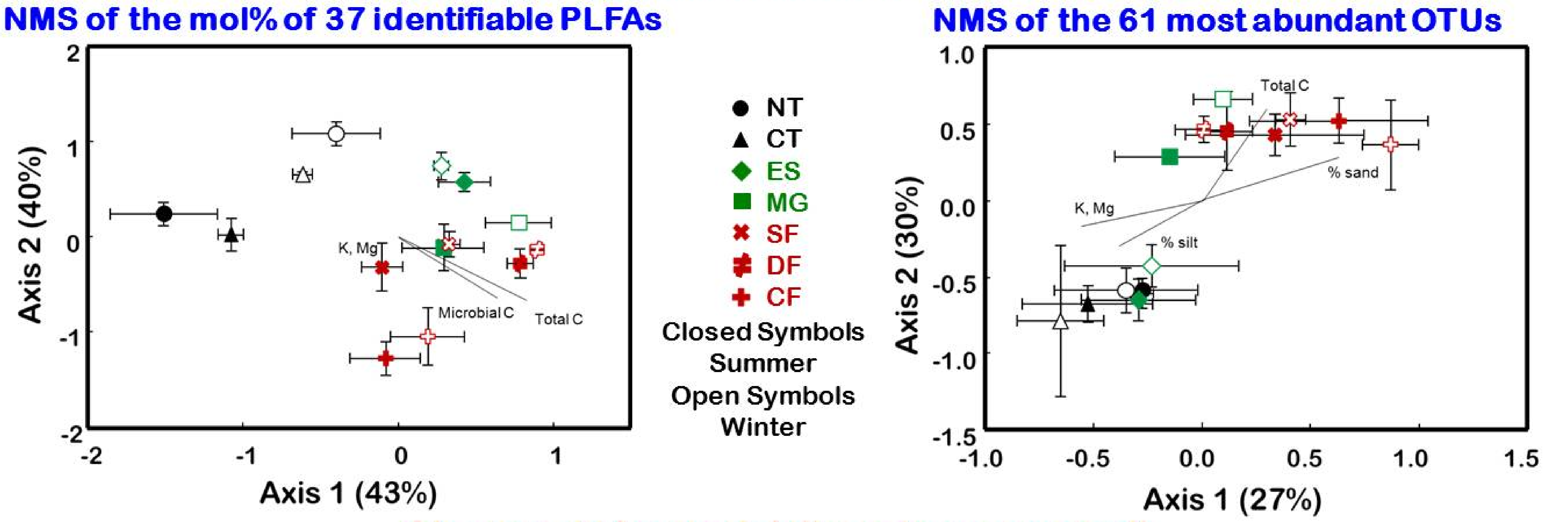
Sequencing & Proofreading

Data Analysis
(LIBSHUFF, DOTUR, GreenGenes, RDPquery)

Community Composition & Diversity

Results

Changes of community structure with restoration



NMS of the mol% of 37 identifiable PLFAs

NMS of the 61 most abundant OTUs

Changes in bacterial diversity were small

Diversity Index	NT	CT	ES	MG	SF	DF	CF
Number of clones, N	530	525	554	543	533	525	538
Number of OTUs, S	349	343	347	333	319	337	272
Shannon Index, $H = \Sigma[(n/N)\ln(n/N)]$	5.55	5.53	5.55	5.46	5.46	5.55	5.20
Reciprocal of Simpson's index, 1/D	211	197	236	193	221	256	146
Evenness= H/log(S)	2.18	2.18	2.18	2.17	2.18	2.20	2.14
H/H_{max}, at H_{max}, n= N; see above	0.89	0.88	0.88	0.87	0.87	0.89	0.83
Chao1= $S + n_1^2/2n_2$	1351	1248	1225	1152	1248	1099	803
95% lower confidence interval	1007	940	925	871	905	842	604
95% higher confidence interval	1787	1638	1606	1511	1690	1427	1066

Significant differences in bacterial community composition by LIBSHUFF[a]

Phylogenetic Group[b]	CT-SF-DF Gradient			CT-ES-MG Gradient			Tillage	Vegetation	Succession	Native
	CT vs SF	SF vs DF	CT vs DF	CT vs ES	ES vs MG	CT vs MG	CT vs NT	CF vs DF	ES vs SF[c]	MG vs DF
Acidobacteria	0.002	0.002	0.002	0.002	0.004	0.002	0.558	0.002	0.002	0.002
Bacteroidetes	0.008	0.032	0.002	0.382	0.227	0.006	0.165	0.006	0.143	0.010
Planctomycetes	0.550	0.407	0.832	0.621	0.004	0.765	0.937	0.664	0.148	0.510
Proteobacteria	0.002	0.016	0.002	0.002	0.002	0.002	0.358	0.012	0.032	0.002
α-Proteobacteria	0.018	0.314	0.002	0.873	0.583	0.194	0.399	0.143	0.063	0.120
β-Proteobacteria	0.055	0.150	0.002	0.002	0.002	0.002	0.407	0.047	0.206	0.002
Δ-Proteobacteria	0.433	0.567	0.168	0.047	0.636	0.040	0.724	0.888	0.449	0.443
γ-Proteobacteria	0.040	0.168	0.038	0.002	0.183	0.002	0.358	0.203	0.609	0.002

[a] Experimentwise p-value calculated after Bonferroni correction are reported. P-values ≤ 0.01 are in RED; ≤ 0.05 are in GREEN.

[b] Phylogenetic groups for which total number of sequences compared were >20 are not shown and included *Firmicutes* and *Gemmatimonadetes*. The composition of *Actinobacteria* did not differ significantly for any comparison.

[c] The composition of *Verrucomicrobia* differed significantly.

Distribution of most abundant operational taxonomic units (OTUs)[a]

Rep. OTU Clone ID	No. of Clones in Library							Total
	NT	CT	ES	MG	SF	DF	CF	
MA1S1_G01[b]	20	20	14	9	4	5	5	77
MA1S1_B02	9	4	9	18	11	10	12	73
MA1S3_E12	2	1	1	14	22	10	15	65
MA1S1_A06[b]	17	19	17	3	0	0	1	57
MA1S2_H11	10	4	10	8	6	5	1	44
MA1S3_H10	3	1	4	7	10	4	11	40
MA1S1_A08	6	7	3	1	5	14	2	38
MA1S3_B11	3	1	8	4	3	3	14	36
MA1S3_B12	2	2	1	4	8	2	15	34
MA1S1_B05	4	3	5	1	8	10	2	33
MA1S1_H08	10	7	6	2	1	4	2	32
MA1W3_A02	4	2	1	4	9	6	6	32
MA3W1_G10	0	0	0	3	10	5	11	29
MA2S1_B04	3	0	0	5	6	8	5	27
MA1S2_A11	1	2	3	10	4	5	0	25
MA1S1_A11[b]	8	6	8	0	1	0	1	24
MA1S1_D01	2	2	3	8	4	0	5	24
MA1S1_H09	4	5	5	3	2	2	3	24

[a] Only representative OTUs are presented. Distributions where $p \leq 0.05$ by the binomial test are in RED.

[b] Indicator species ($p < 0.01$) contributing to differences.

Conclusions

- Despite significantly different soil properties & vegetation, microbial communities in MG & DF are very similar, although some notable differences existed
- After 42 years, microbial communities in SF are very similar to those in DF
- ES & MG have similar vegetation but significantly different microbial communities due to history of land-management
- Even after 17 years, ES is more similar to CT than MG indicative of a slow response to restoration

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