Evaluating soil biology: Where do we stand?

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Outline

Point #1: How has the state of the science changed related to measuring microorganisms in the environment?

Point #2: So what do we measure for biological soil health?

Point #3: What have we learned about soil health by using them?
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“We know more about the movement of celestial bodies than about the soil underfoot.”

-Leonardo Da Vinci, circa 1500’s
“Everything is everywhere, but the environment selects”

~Baas-Becking, 1936
FIG 2 Bacterial (a) and fungal (b) β-diversity. Microbial β-diversity was visualized with NMDS based on OTU abundance data. Environmental factors (Temp, moisture, available NH₄⁺, and NO₃⁻; gas fluxes of N₂O, CO₂, and CH₄; and TMB and SIR) are fit to the ordination with function envfit in R vegan package. Only significant factors are shown in the figure.
Sun and Badgley (2019)

Fig. 4. The variations of microbial functional groups, genera and functional genes involved in N cycle over chronosequence ages (chronosequence ages 6, 12, 22 and 31: years since reforestation when sampled; UM: nearby unmined sites as control). (a) AOB, NOB and major genera of AOB and NOB over chronosequence ages (relative abundance > 0.005%). (b) Major functional genes involved in N cycle over chronosequence ages (relative abundance > 0.001%). The heatmap shows the age variations. The key shows the z-scores of the relative abundances. The relative abundance, variance explained ($R^2$), regression slope and false discovery rate (FDR) of the linear regression with chronosequence age were shown in the table (* indicates FDR < 0.1, * indicates FDR < 0.05 and ** indicates FDR < 0.01).
Fig. 5. The variations of microbial genera and functional genes involved in greenhouse gas emission over chronosequence ages (chronosequence ages 6, 12, 22 and 31; years since reforestation when sampled; UM: nearby unmined sites as control). (a) Major methanotrophs and methanogens over chronosequence ages (relative abundance > 0.005%). (b) Major functional genes involved in methane and nitrous oxide production over chronosequence ages (relative abundance > 0.001%). The heatmap shows the age variations. The key shows the z-scores of the relative abundances. The relative abundance, variance explained ($R^2$), regression slope and false discovery rate (FDR) of the linear regression with chronosequence age were shown in the table (• indicates FDR < 0.1, * indicates FDR < 0.05 and ** indicates FDR < 0.01).

Sun and Badgley (2019)
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Comprehensive Assessment of Soil Health
The Cornell Framework

Soil Health
Technical Note No. 450-03

Recommended Soil Health Indicators and Associated Laboratory Procedures


Third Edition
Common Biological Indicators

“Food” Sources:

• Soil organic matter/carbon
• permanganate oxidizable carbon (readily available C)
• soil protein (readily available N)

General Microbial Activity:

• Carbon mineralization
• Nitrogen mineralization
• Respiration assays

Moebius-Clune et al. (2016), Stott et al. (2019)
Common Biological Indicators

Enzymatic assays:

- β-glucosidase: cellulose degradation
- N-acetyl-β-D-glucosaminidase: chitin degradation
- Phosphomonoesterases: P mineralization
- Arylsulfatase: S mineralization

Diversity:

- Phospholipid fatty acid analysis - recommended now
- DNA sequencing - recommended for archiving if possible

Moebius-Clune et al. (2016), Stott et al. (2019)
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Stewart et al. (2018)

(b) 1 year after cover crop

(c) 2 or 3 years after cover crop

Response indicators reported in the literature

Stewart et al. (2018)
*Neither total microbial biomass nor fungal:bacterial ratios were significantly different with and without cover crops*
What about water availability?

Varying clay content

Varying organic matter

Varying bulk density

Moyano et al. (2012)
What about water availability?

• Soil moisture availability is a key determinant of microbial activity
  • Too little = moisture stress
  • Too much = decreased oxygen availability

• Most microbial activity assays are determined at the bench scale on dried soils re-wetted to controlled moisture conditions
  • 50-60% of field capacity
  • Saturation for enzyme assays
Conclusions

Point #1: DNA sequencing has revolutionized soil microbiology but the information provided has not been linked to soil health metrics.

Point #2: Commonly recommended indicators are primarily related to SOM content and activity, but methods still vary.

Point #1: Biological indicators can certainly be responsive to soil management changes it’s generally assumed that “more is better”; but consistency and benchmarking is tricky across studies and regions.
References


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