

ABSTRACT

Cryptobiotic soil crusts in arid regions contribute to ecosystem stability through increased water infiltration, soil aggregate stability, and nutrient cycling between the soil community and vascular plants. These crusts are particularly sensitive to compaction/fracturing disturbances such as livestock grazing, off-road vehicle use, trampling by humans, and drilling and mining activities. Loss of soil crusts is believed to increase the rate of desertification, and recent findings indicate that crusts are extremely slow to recover, on the order of hundreds of years. However, post-disturbance recovery rates for soil bacterial and fungal populations is vastly understudied, and it is suggested that loss of soil crusts leads to decreased abundance and diversity of these non-crust soil biota. Soil microbial activity within and around two natural gas well pads embedded within a livestock grazing area were investigated. During the natural gas extraction process, the shallow surface soil is stockpiled near the well pad. Surface and subsurface soil samples were taken from the heavily compacted well pad, the surface soil stockpile (fallow 12 yr), the grazed area outside of the well pad, and a lightly grazed area with intact crusts. Microbial activity was measured using the MicroResp™ system, which measures respiration of microbes within whole soil samples supplemented with various carbon sources (simple and polymeric sugars, amino acids, carboxylic acids, and fatty acids). Preliminary results indicate slightly reduced activity in heavily disturbed well pad areas compared to grazed areas, although overall activity for all samples was not significantly different from controls. Activity was marginally higher in surface soils (top 5 cm) compared to subsurface soils (5-30 cm).

OBJECTIVES

The purpose of this study was to evaluate total-soil enzymatic activity profiles across three disturbance regimes on a Northern Chihuahuan desert grassland (Figure 1).

SIGNIFICANCE

Evaluation of soil microbial activity is an important tool in gauging soil health prior to plant restoration efforts. Functional diversity of the soil microbial community is commonly used in this assessment of soil health as it relates to the activity of soil microflora involved in carbon cycling. Functional diversity can be assessed through SIR (substrate induced respiration) utilizing certain carbon sources. Soil microbes in different microenvironments will have varying responses to different substrates, thus catabolic fingerprint information of each location specific community can be obtained. The impact on soil microbiology of differing approaches to plant reestablishment efforts can then be evaluated through the catabolic fingerprint of the soil community to illustrate the relationship between soil microbial diversity and plant restoration success.

METHODS

Triplicate soil cores were taken from each site and separated into surface (top 5 cm) and subsurface (5-30 cm) samples. Surface soils included disrupted or intact cryptobiotic crusts. At sampling, the soil water content of all samples was less than 3%.

Microbial activity of each sample was measured using the MicroResp™ system (Figure 1), which quantifies the CO₂ respired by microbes within whole soil samples supplemented with various carbon sources (list of substrates below) using water as a control. Respiration assays were carried out after the soil water content was corrected to the calculated equivalent of the soil's field water potential.

Simple Sugars	Amino Acids	Carboxylic Acids	Fatty Acid	Insolubles
arabinose	alanine	ascorbic acid	tween 80	xylan
glucose	cysteine	fumaric acid		
mannose	lysine	protocatechuic acid		
	phenylalanine	uric acid		



Figure 1. MicroResp™ assembly showing a deep well plate on the bottom which contains whole soil samples supplemented with various carbon sources. A detection plate (made with agar, sodium bicarbonate, potassium chloride, and cresol red) is placed on top, with a porous rubber seal sandwiched between the two plates. Typical reactions are left to incubate for 6h after which the detection plate is read in a spectrophotometer.

RESULTS

Average Activity Reading v. Substrate Type, Disturbance Regime

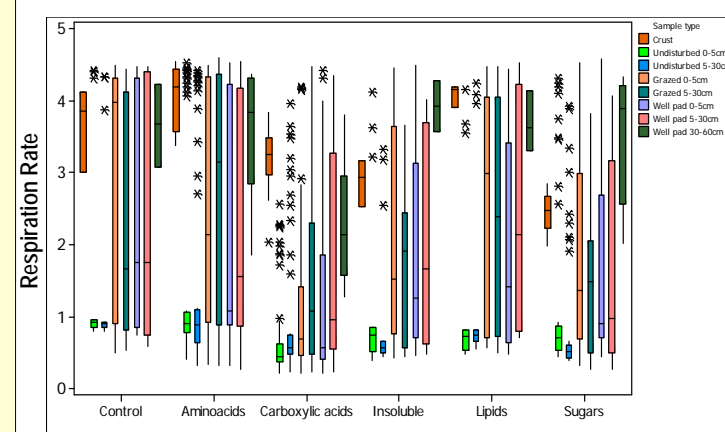


Figure 2. Box plot: Each box represents the 50th percentile of the data for microbial respiration rates in response to water (control), amino acids, carboxylic acids, insolubles, lipids and simple sugars, compared across disturbance regime and soil depth (n=3,28). Bars within each box indicate median. Whisker lines indicate the 75th percentile of all data points. Outliers and extreme outliers are represented by * and ** respectively. Respiration rate is inversely proportional to percent absorbance at 570 nm.

Similarity Analysis of Chihuahuan Desert Grassland Soil Microbial Activity Profiles



Figure 3. Dendrogram with UPGMA Linkage & Manhattan Distance; Cluster dendrogram showing grouping of soils across three disturbance regimes (Undisturbed, Grazed, Well Pad) and two soil depths (0-5 cm, and 5-30 cm) according to soil microbial respiration against all carbon sources. Sites are labeled by disturbance regime, location point, and soil sample depth.

RESULTS (continued)

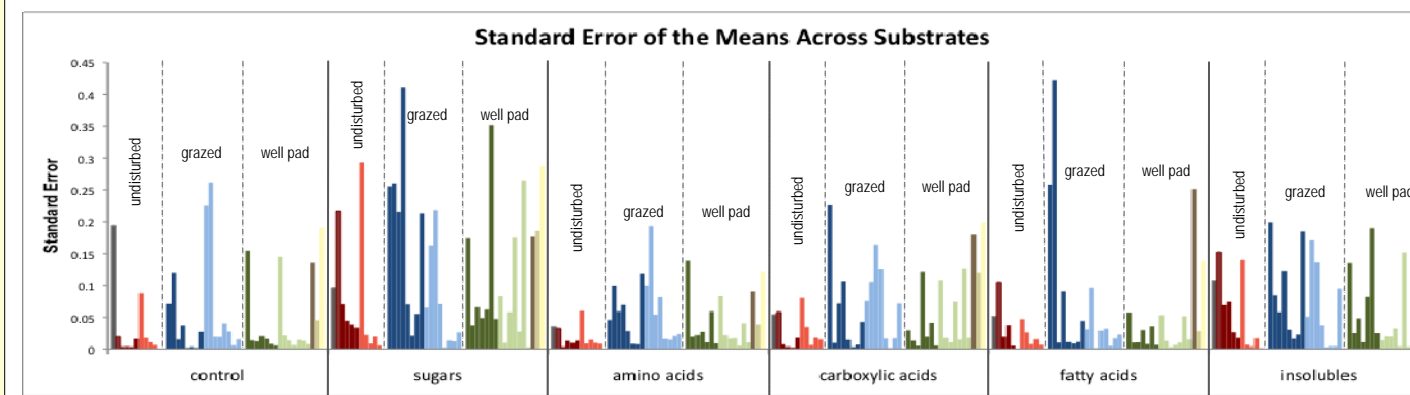


Figure 4. Histogram plotting the standard error of the means, grouped according to carbon source. Data are subdivided according to disturbance regime (undisturbed, grazed, and well pad), and soil sampling depth (darker colors representing surface 0-5 cm, lighter colors representing subsurface 5-30 cm and 30-60 cm). Grey bars in the "undisturbed" subdivisions represent soil crust alone; brown and yellow bars in the "well pad" subdivisions represent the topsoil stockpile samples.

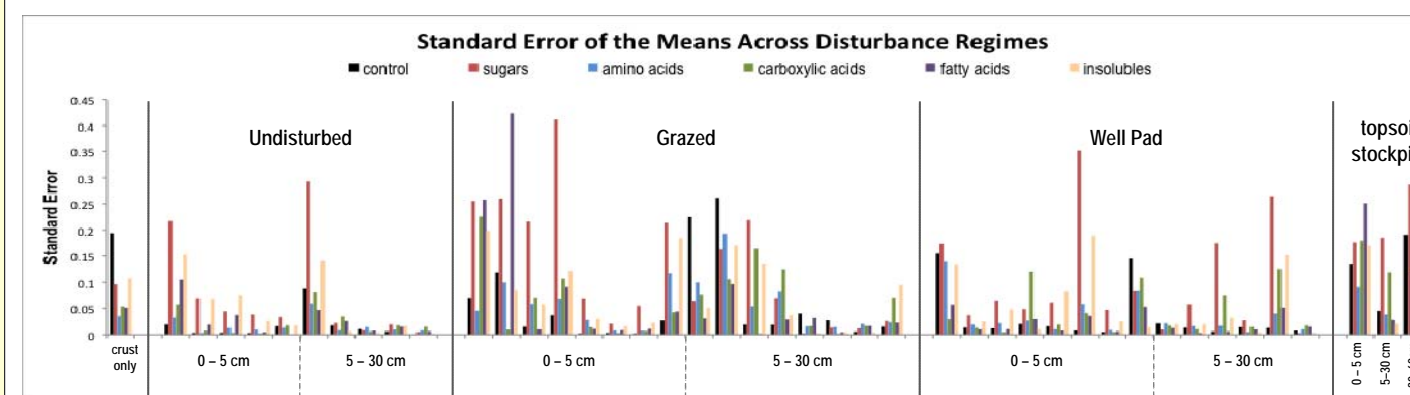


Figure 5. Histogram plotting the standard error of the means, grouped according to disturbance regime and sampling depth. Data for crust alone (on the undisturbed site) and the topsoil stockpile (on the well pad site) are represented separately.

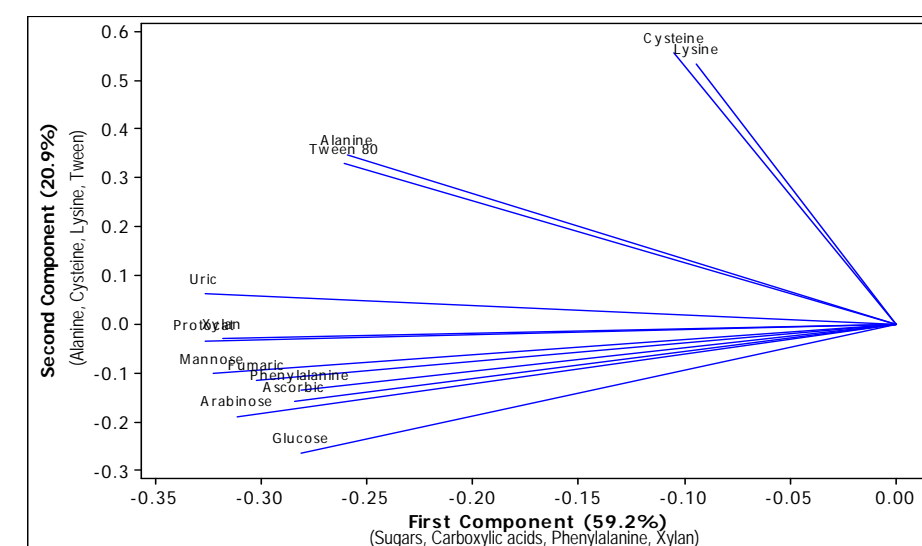


Figure 6. Principal Components Analysis vectorgram for the average readings for each carbon substrate across all samples. Eigenanalysis indicates that the first component representing mainly sugars and carboxylic acids accounted for 59.2% of the variability across samples. Adding the second component (aminoacids and lipids) accounted for a cumulative 80.1% of the variability across all samples.

CONCLUSIONS

Soil crusts had high, but consistent average respiration rates when supplemented with various carbon sources compared to other soil samples (Figure 2). Soil samples from undisturbed sites were unexpectedly low in their respiration response to carbon substrates compared to grazed and heavily-disturbed well pad sites. The extreme outliers within these samples may be a result of small sample size (n=15). Respiration readings (CO₂ production) for the carboxylic acids had extremely high variability for all soil samples except for the crust alone (Figure 2). The increased variability and high number of outliers for subsurface samples (5-30 cm depth) against the acids suggests CaCO₃ degradation may be responsible for inconsistencies. Further analyses will be conducted to separate CO₂ off gassing due to microbial respiration from that produced by CaCO₃ degradation in the presence of acids.

Samples clustering did not produce any noticeable patterns for soil depths or locations (Figure 3). Omitting the highly variable carboxylic acids do not improve grouping linkages (data not shown). However, plotting the standard errors of all samples showed some patterns between carbon sources (Figure 4) and disturbance regime (Figure 5). Highest variability in respiration rates across all soils samples was seen for sugars and carboxylic acids (Figure 4). This indicates that the use of simple sugars as carbon sources may not be optimal for gauging functional diversity of soil microbial communities at microscale in extremely heterogeneous environments. Variability in respiration rates was greatest for the disturbed sites (grazed and well pad) compared to relatively low variability for undisturbed sites (Figures 2 & 5). This may be an indication of microbial ecosystem stability in the undisturbed sites; the introduction of disturbance, and therefore enhanced heterogeneity, may drive changes in soils to have higher functional diversity to adapt to the disturbance. Disturbance may also introduce new microbial species into the soil system.

Principal components analysis indicated that nearly 60% of the variability seen across all soil sample averages is due to the sugars and carboxylic acids (Figure 6). Analyses that excluded the carboxylic acids showed little change in the overall principal component analyses (data not shown) suggesting that sugars are the most significantly used substrates by soil microbes. Separation of soils in relation to disturbance regime and depth could not be determined using amino acids or lipids. These carbon sources may be of less relevance for discrimination of soil biological activity in arid desert soils.

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