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Soil Biology & Biochemistry 34 (2002) 1717–1725

Soil Biology & Biochemistry

www.elsevier.com/locate/soilbio

# Soil microbiological properties 20 years after surface mine reclamation: spatial analysis of reclaimed and undisturbed sites

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Received 14 December 2001; received in revised form 19 June 2002; accepted 6 August 2002

**Abstract**

Spatial characteristics of soil microbial community structure and selected soil chemical factors were analyzed in soil surrounding *Agropyron smithii* (Western wheatgrass) and *Artemisia tridentata* (Wyoming big sagebrush) plants in sites reclaimed after surface mining and adjacent undisturbed sites in Wyoming. Microbial biomass C (MBC) and fatty acid methyl ester (FAME) biomarkers for total biomass, bacteria, and fungi were used as indicators of soil microbial community abundance and structure. In soil 20 years after reclamation FAME total microbial biomass, bacterial and fungal biomarkers, MBC and soil organic matter (SOM) averaged only 20, 16, 28, 44 and 36% of values found in undisturbed soils. In contrast to undisturbed soils, FAME biomarkers and MBC of reclaimed soils exhibited spatial correlation up to 42 cm. Reclaimed soils also exhibited localized enrichment of bacterial, fungal, and total microbial biomass, as well as depletion of inorganic N concentrations, around plant bases ($<10$ cm), suggesting relatively poor soil exploration by roots and microorganisms compared to the undisturbed ecosystem. Strong spatial stratification of undisturbed SOM and soil $NH_4^+$ pools was found with highest concentrations on the leeward side of shrubs, likely due to localized changes in microclimate and plant litter deposition. This indicates that shrub cover plays a central role in the establishment of site heterogeneity and regulation of ecological processes, such as C and N mineralization and immobilization, which has important implications for reclamation. 

*Keywords:* Soil disturbance; Restoration; Spatial variability; Fatty acid methyl ester analysis; Shortgrass steppe

## 1. Introduction

The goal of surface mine reclamation is to restore the ecological integrity of these disturbed areas. Ecological integrity includes a critical range of variability in biodiversity, ecological processes, and structural relationships (Montalvo et al., 1997). Fundamental to assessment of ecological integrity in a given ecosystem are the spatial relationships of its biotic and abiotic components (White and Walker, 1997). Severe ecological disturbance, in addition to causing changes in plant species composition and abundance, disrupts spatial organization, and therefore functional relationships of ecosystem components.

Of critical importance to the ecological functioning of terrestrial ecosystems are soil microbial communities. Soil microorganisms are very sensitive to changes in their chemical and physical environment (Turco et al., 1994) and significant alteration of the microbial community can occur following drastic disturbance, both in terms of total microbial biomass and microbial species composition (Harris et al., 1993; Insam and Domsch, 1988; Stahl et al., 1988; Visser et al., 1983). Disturbance of soil ecosystems that impact normal functioning of microbial community structure is potentially detrimental to soil formation, energy transfers, nutrient cycling, plant reestablishment and long-term stability.

Spatial analysis of soil microbial community structure and chemical properties in undisturbed ecosystems may permit more complete understanding of the sources of variation in self-sustaining ecosystems, potentially providing insights into how best to reproduce patterns of natural variation in disturbed ecosystems. Restoration of natural variation is important to reestablishing controls on ecological processes critical to sustainable ecological function. Differences in spatial characteristics indicating disparate controls on populations and processes (Levin, 1992) could also be useful for evaluating reclamation success.

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0038-0717/02/$ - see front matter 
PII: S0038-0717(02)00158-X

The aim of this study was to examine spatial variation within microbial communities of disturbed and undisturbed ecosystems. We compared the spatial characteristics of fatty acid methyl ester (FAME) total biomass, bacterial, and fungal biomarkers, Microbial biomass C (MBC), and selected soil chemical properties around individuals of dominant plant species in an ecosystem reclaimed after surface mining and an adjacent undisturbed ecosystem representative of pre-disturbance conditions.

## 2. Methods

### 2.1. Study site and sample strategies

Research was conducted at the Pathfinder Uranium Mine in the Shirley Basin of southeastern Wyoming, USA. The landscape is a semi-arid, short-grass steppe with mean annual precipitation of 28 cm and persistent desiccating winds. The area has a rolling topography with a mean elevation of 2150 m. Average annual temperature is 3.5 °C, with the lowest average minimum temperatures occurring in January (−16 °C) and the highest average maximum temperatures in July (26.3 °C). Undisturbed soils in the area are classified as Ustic Haplargids.

Two sites, a reclamation site seeded with native and non-native grasses, forbs and shrubs in 1982, and an undisturbed site, dominated by *Artemisia tridentata* Nutt. ssp. *wyomingensis* (Wyoming big sagebrush) with an under story of small grasses and forbs, were chosen on the basis of similarity of slope and aspect as well as proximity to one another (<50 m). Treatment of soil on the reclaimed site followed standard practice on surface mine sites; topsoil was removed before mining and stockpiled until mining operations were completed, in this site for over 10 years. Stored soil was then spread on overburden materials to a depth of 20–30 cm and seeded with native plant species.

To determine the small-scale spatial properties of microbial communities and soil characteristics, two sample plots were established on both the reclaimed and undisturbed sites. Twenty-nine soil samples were collected beneath the pebbly surface layers (5–10 cm depth) from grids centered on individual members of the dominant vegetation species of each site. Sample grids were designed to facilitate the use of geostatistical methods by maximizing the number of samples within each potential lag distance. Subsamples for FAME analysis were stored at −20 °C prior to analysis. Subsamples for all other analyses were stored at 4 °C prior to analysis (<2 weeks).

### 2.2. FAME analysis

Frozen soil samples were lyophilized and 1 g was placed in 50 ml glass centrifuge tubes with 10 ml 0.2 M KOH in methanol. Centrifuge tubes were then mixed and placed in a 37 °C water bath for 1 h with occasional shaking. One ml 1N acetic acid and 5 ml hexane were then added, followed by mixing and centrifugation at 2000 rpm for 10 min. The hexane layer was removed and extraction repeated twice more with 5 ml hexane. Hexane layers were combined, evaporated under nitrogen until dry, dissolved in 100 μl of 1:1 hexane/methyl *t*-butyl ether, and transferred to GC vials. Analysis was performed using a Hewlett–Packard 5890 gas chromatograph equipped with a flame ionization detector as described by Buyer et al. (1999). Fatty acid biomarkers for total biomass, fungi and eubacteria assayed in this study are listed in Table 1.

Table 1
Fatty acid biomarkers used for estimating relative total microbial biomass, fungi, and bacteria

| Group | Fatty acids[a] |
|---|---|
| Biomass | 14:0 |
| Fungi | 18:2 ω6c |
| Eubacteria | 15:0, 17:0 cyclo, 19:0 cyclo, 15:1 iso, 17:0 iso, 17:0 anteiso |

[a] See Cavigelli et al. (1995), Frostegård et al. (1993) and Zelles et al. (1994, 1995).

### 2.3. Microbial biomass

Microbial extractable C was measured using the chloroform ($CHCl_3$) fumigation–extraction technique (Vance et al., 1987). Briefly, 20 g field wet soil were $CHCl_3$ fumigated for 24 h at 25 °C. After removal of $CHCl_3$, soluble C was extracted from both fumigated and duplicate unfumigated samples with 0.5 M $K_2SO_4$ (1:5 soil to solution w/v) for 30 min on a reciprocating shaker. Total organic C in filtered extracts was analyzed using a Shimazu TOC 5000 soluble carbon analyzer. Microbial biomass was calculated from the difference between fumigated and unfumigated extractable C ($k_{EC} = 0.35$).

### 2.4. Inorganic nitrogen, organic matter, pH, and EC

Inorganic N contents were determined by extracting 10 g soil samples with 1 M KCl. Suspensions were filtered through Whatman No 42 filter paper and $NH_4^+$ and $NO_3^-$ concentrations determined colorimetrically using a Technicon 2 inorganic N analyzer. Soil organic matter (SOM) was quantified as the amount of soil carbon oxidized during reaction with $Cr_2O_7^{2-}$ and sulfuric acid using the method of Mebius (1960). Soil electrical conductivity (EC) and pH were determined using the saturation paste extract EC and saturation paste pH methods of Gavlak et al. (1994).

### 2.5. Plant canopy-coverage and species diversity

Canopy cover was estimated using the Daubenmire canopy-coverage method (Daubenmire, 1959). A metal frame ($30 \times 60$ cm$^2$) was placed at eight random locations within each site. Total number of species present within

frames was determined and percent coverage of grass, forb, and woody species visually estimated.

### 2.6. Data analyses

Data from 58 reclaimed and 58 undisturbed ecosystem soil samples were analyzed using univariate statistical analyses to determine mean, standard deviation, and frequency distributions for biological and chemical properties. Linear correlation analysis was performed to determine relationships between variables. Differences in overall average values between disturbed and native plots were determined using Student's *t*-test.

Geostatistical analysis methods were used to analyze spatial relationships of microbial biomarkers and biomass, as well as SOM, inorganic N pools, pH, and EC. The spatial relationship between samples is based on the distance between samples or lag. The autocorrelation function was used to determine lag correlation values, which were plotted against lag distance (correlogram) (Isaaks and Srivastava, 1989). Values at unsampled locations were interpolated using ordinary point kriging, which utilizes spatial relationships defined by the autocorrelation function and a weighted linear combination of surrounding sampled locations (Isaaks and Srivastava, 1989). Kriged estimates were plotted as contours in order to visualize spatial distributions of selected variables.

Spatial analysis was conducted using the Geostatistical Environment Assessment Software package (GEO-EAS) (EPA, 1988). All other statistical analyses were conducted using the SPSS for Windows software package (ver. 10.0.7).

## 3. Results

### 3.1. Vegetation cover and plant species diversity

Differences in total plant cover between reclaimed and undisturbed ecosystems were not significant (Fig. 1). Plant species diversity, however, was significantly less for the reclaimed ecosystem ($p \leq 0.001$), which averaged only two species per 0.18 $m^2$ compared to 6.2 species per 0.18 $m^2$ in the undisturbed ecosystem. Total cover and diversity of forbs and shrubs was more greatly reduced than for grasses (Fig. 1), although grass species composition differed greatly between the two ecosystems (data not shown). Forbs on the reclaimed site were mostly weedy species and no reestablishment of shrub species was observed.

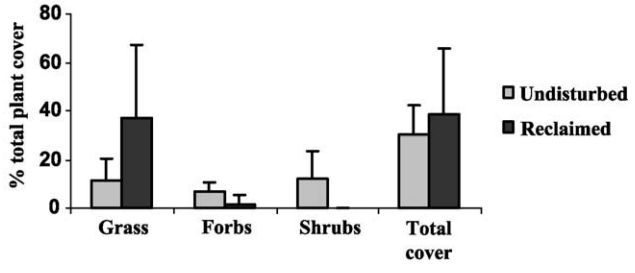


Fig. 1. Percent plant cover (mean, standard deviation) in undisturbed and reclaimed ecosystems as determined by the Daubenmire canopy-coverage method.

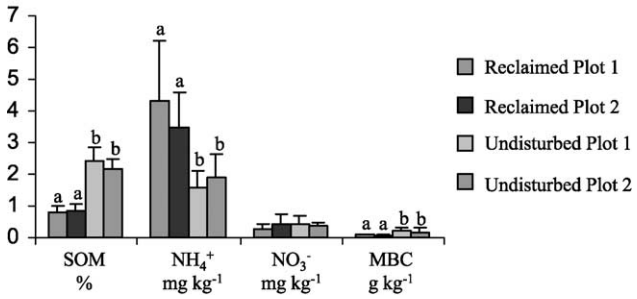


Fig. 2. Soil OM, $NH_4^+$, $NO_3^-$, and MBC content (mean and standard deviation) of reclaimed and undisturbed plots. Different letters indicate differences at $P \leq 0.05$ level of significance.

### 3.2. Soil physical, chemical and biological characteristics

Soil of the undisturbed site (5–10 cm depth) was found to have sandy loam texture, whereas soil of the reclaimed site is of gravelly clay loam texture. Water content at sampling time averaged 3.2 and 12.1% (w/w) for undisturbed and reclaimed soils, respectively, due to soil textural differences.

SOM contents of the reclaimed soil were significantly lower than those of undisturbed soil ($p \leq 0.001$) (Fig. 2). Reclaimed soil $NH_4^+$ concentration, pH, and EC were significantly greater in undisturbed soil (Fig. 2). No significant differences were found between reclaimed and undisturbed ecosystem soil $NO_3^-$ concentrations.

MBC and all FAME biomarkers (biomass, fungi, and bacteria) were significantly lower in reclaimed soil than in undisturbed soil ($p \leq 0.001$) (Fig. 3). The FAME biomass biomarker exhibited significant positive correlation with SOM and FAME bacterial and fungal biomarkers in both reclaimed and undisturbed ecosystems (Table 2). Unlike the reclaimed ecosystem, correlation between the FAME bacterial biomarker and SOM was positive and significant in the undisturbed ecosystem. Conversely, correlation between the FAME fungal biomarker and SOM was

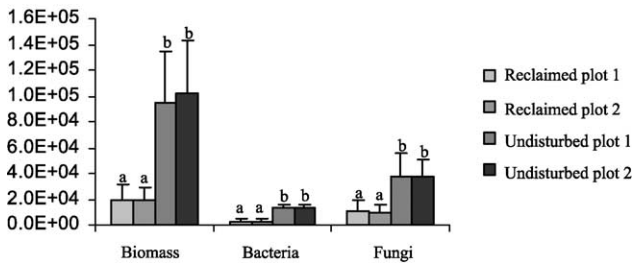


Fig. 3. Peak areas of FAME biomarkers (mean and standard deviation) for reclaimed and undisturbed plots. Different letters indicate differences at $P \leq 0.05$ level of significance.

Table 2
Pearson correlation ($r$) matrices for reclaimed and undisturbed plots

| | Biomass[a] | Bacteria[a] | Fungi[a] | SOM | $NH_4^+$ | $NO_3^-$ |
|---|---|---|---|---|---|---|
| *Reclaimed plots* | | | | | | |
| Bacteria | 0.65** | | | | | |
| Fungi | 0.90** | 0.54** | | | | |
| SOM | 0.29* | 0.11 | 0.41** | | | |
| $NH_4^+$ | −0.11 | 0.08 | −0.08 | −0.20 | | |
| $NO_3^-$ | 0.11 | −0.02 | −0.03 | −0.04 | 0.07 | |
| MBC[b] | 0.24 | 0.19 | 0.42** | 0.39** | −0.04 | −0.32* |
| *Undistributed plots* | | | | | | |
| Bacteria | 0.48** | | | | | |
| Fungi | 0.46** | 0.30* | | | | |
| SOM | 0.63** | 0.27* | 0.18 | | | |
| $NH_4^+$ | 0.42** | −0.03 | 0.09 | 0.37** | | |
| $NO_3^-$ | 0.18 | 0.23 | −0.11 | 0.27* | −0.07 | |
| MBC | 0.00 | −0.09 | −0.03 | 0.17 | 0.05 | 0.04 |

(*) and (**) indicate significant correlation between the two variables at $P \leq 0.05$ and 0.001 level of significance, respectively.
[a] FAME biomass, bacterial, and fungal biomarkers (Table 1).
[b] Soil microbial biomass by the chloroform fumigation technique.

positive and significant for the reclaimed plots, but not for the undisturbed plots. Reclaimed soil MBC exhibited significant positive correlations with both the FAME fungal biomarker and SOM, and significant negative correlation with soil $NO_3^-$ concentration. No significant correlation was found between MBC and any other variable in undisturbed plots.

Although correlations between soil $NH_4^+$ concentration and both SOM and FAME biomass were positive and significant for the undisturbed site, significant correlation between these variables was not found for the reclaimed site (Table 2). EC and $NO_3^-$ concentration exhibited a significant positive correlation ($r^2 = 0.34$, $p = 0.01$) in the undisturbed soil, however, correlations between these variables were not significant for reclaimed soils.

### 3.3. Spatial analyses

Spatial autocorrelation graphs, which depict spatial autocorrelation with lag distance, for representative plots are shown in Fig. 4. Reclaimed plots exhibited spatial autocorrelation for MBC and all FAME biomarkers to a distance of at least 14 cm. No spatial autocorrelation was found in the undisturbed plots for MBC or FAME biomarkers, with the exception of plot 4, in which the bacterial biomarker exhibited spatial autocorrelation to a distance of 14 cm (Fig. 4).

SOM content exhibited spatial autocorrelation in only one of the reclaimed plots, while undisturbed plots 3 and 4 exhibited spatial autocorrelation to distances greater than 30 cm. All plots exhibited soil $NH_4^+$ concentration spatial autocorrelation, although the distances at which spatial autocorrelation approached zero were much shorter for reclaimed plots (16 and 10 cm for plots 1 and 2, respectively) than for undisturbed plots that exhibited

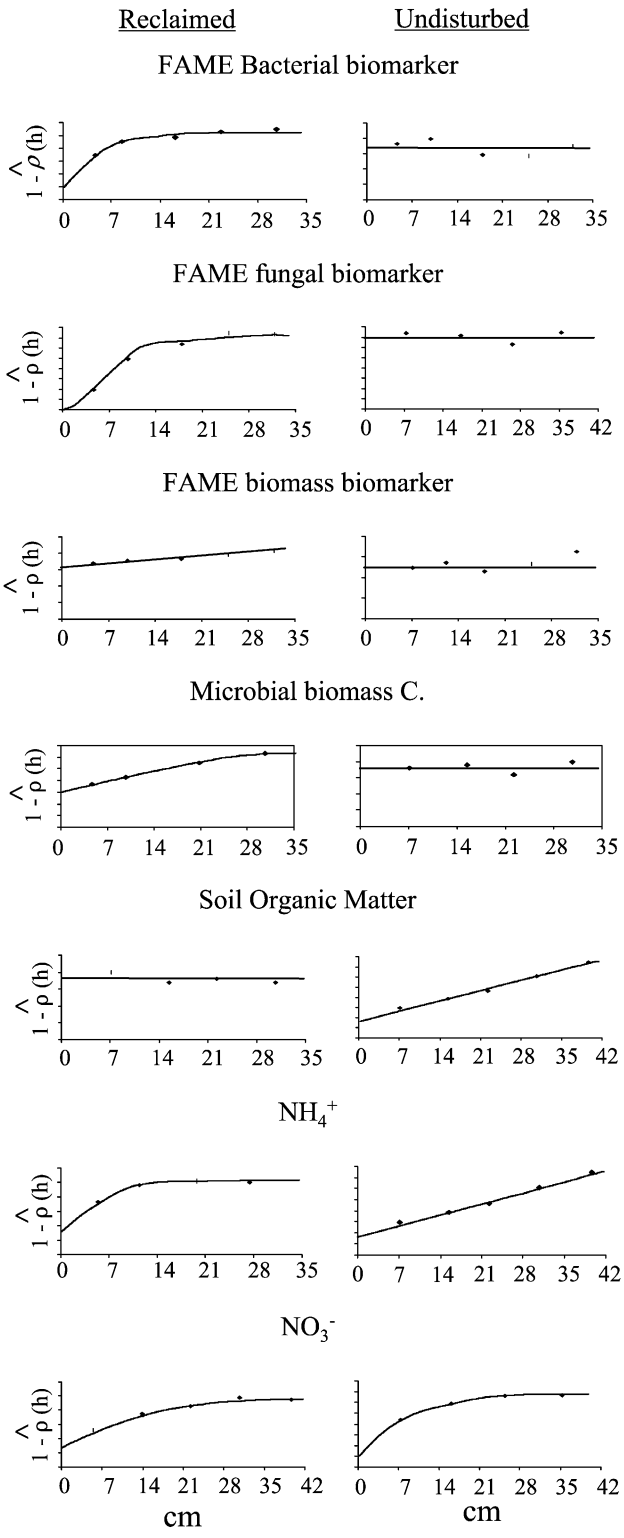


Fig. 4. Autocorrelograms for FAME biomarkers, MBC, SOM, and inorganic N species in representative reclaimed and undisturbed plots.

spatial autocorrelation to distances greater than 42 cm. Spatial autocorrelation of soil $NO_3^-$ content was found in both reclaimed plots but in only one of the undisturbed plots (Fig. 4).

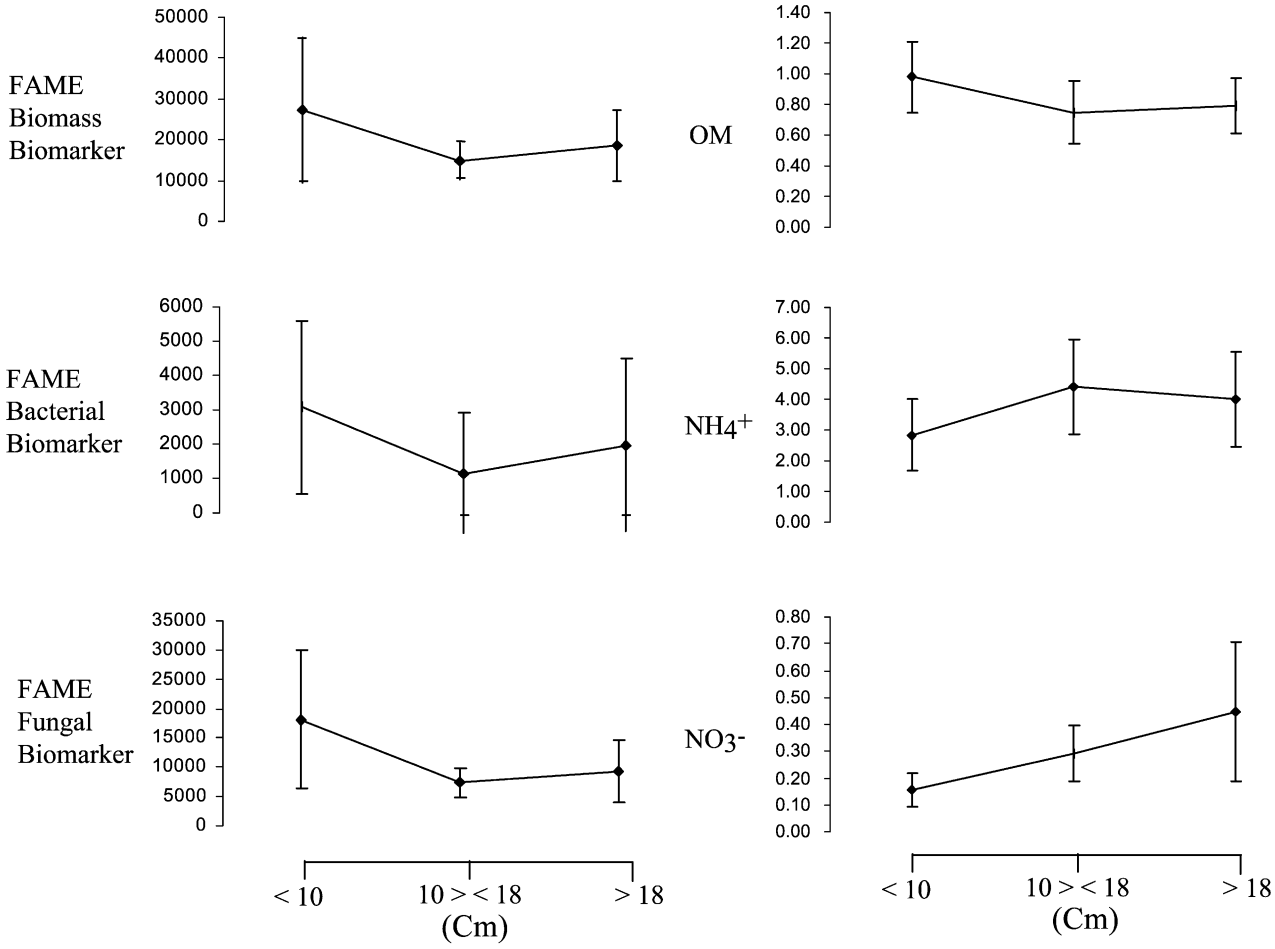


Fig. 5. Plots of kriged estimates for selected variables with distance from plant bases in reclaimed plots. Error bars represent standard deviation.

Reclaimed soil $NH_4^+$ and $NO_3^-$ concentrations were lowest for locations near plant bases (<10 cm) (Fig. 5). FAME biomarkers and SOM exhibited highest values near the plant base (<10 cm), lesser values found between 10 and 18 cm from the plant base, and intermediate values at greater distances (Fig. 5).

No significant differences were found between locations near and away from plant bases for any variable in the undisturbed plots. Soil OM and $NH_4^+$ contents, however, were found to be significantly greater ($p \leq 0.05$) on the eastern (leeward) side of the plants for both undisturbed plots and exhibited distinct spatial stratification with respect to the plant at the center of each plot (Fig. 6(a) and (b), respectively).

## 4. Discussion

Even with recovery of total plant cover to pre-disturbance levels 20 years after seeding (Fig. 1), all measures indicate that disturbance was highly detrimental to microbial populations and that all measured components of the microbial biomass remain greatly reduced from the undisturbed condition. Reclaimed soil FAME total biomass, bacterial, and fungal biomarkers averaged only 20, 16, and 28%, respectively, of amounts found in undisturbed soil (Fig. 3). Similarly, reclaimed soil MBC was estimated to average only 44% of amounts found for undisturbed soil (Fig. 2).

Our results also indicate that disturbance was highly detrimental to SOM pools. Reclaimed SOM averaged only 36% of amounts found for the undisturbed site. Although little information is available pertaining to SOM pools following disturbance associated with surface mine reclamation, SOM reductions found for disturbed soil are within the range associated with long-term cultivation in the Great Plains (Mann 1986; Robles and Burke, 1998). Effects of soil mixing and aeration, first when soil was removed in preparation for mining and again 10 or more years later when soil was respread prior to seeding, would be expected to enhance SOM decomposition in a manner similar to tillage. Further SOM losses were likely accrued from soil storage, which is known to be detrimental to SOM, primarily due to decreased plant organic matter inputs. Although we have no data pertaining to SOM content with depth in undisturbed soil of this ecosystem, low OM content of reclaimed soil may also be partially due to incorporation of high clay and potentially low OM subsurface horizons.

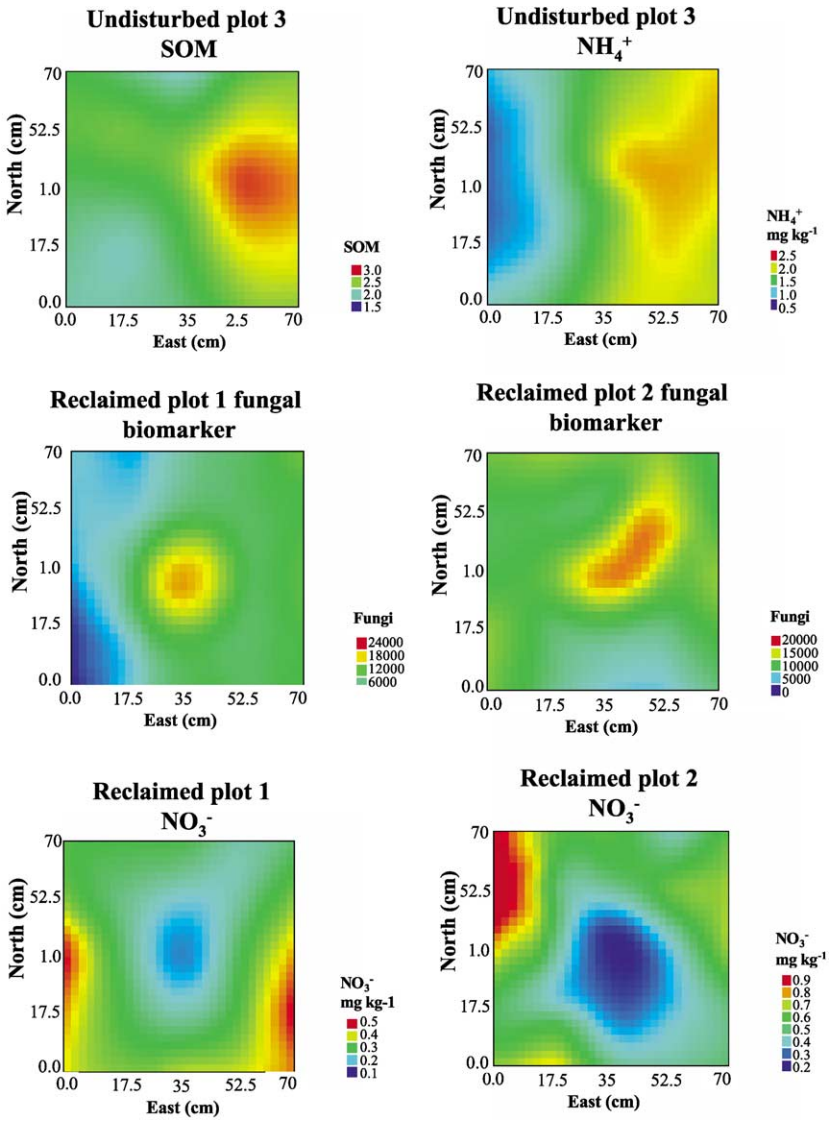


Fig. 6. Contour maps of selected variables (SOM, $NH_4^+$, $NO_3^-$, fungal biomarker) centered on members of the predominant plant species of reclaimed and undisturbed sites.

FAME fungal biomarkers for reclaimed spatial plots were highest under plant canopies (Fig. 5) and exhibited a significant positive correlation with SOM (Table 2). Conversely, undisturbed soil FAME fungal biomarkers were less spatially stratified (Fig. 4) and significant correlation with SOM was lacking (Table 2). Although we have no data pertaining to fungal species composition for these soils, a number of studies have shown that disturbance associated with surface mining is highly detrimental to arbuscular mycorrhizal (AM) fungal populations (Loree and Williams, 1987; Stahl et al., 1988). Soil storage is known to be especially detrimental to AM populations, in some cases to such an extent that the soil has little or no capacity to infect plants with fungal symbionts (Miller et al., 1985; Harris et al., 1989). Lack of FAME fungal biomarker spatial autocorrelation (Fig. 4) or significant correlation with SOM in undisturbed plots (Table 2), suggests that fungal biomass in undisturbed soil is dominated by AM. That is, AM fungi obtain energy from living host plants and their distribution in soil is less likely to be associated with SOM than non-mycorrhizal saprotrophic fungi, which oxidize SOM for energy.

Undisturbed plots exhibited SOM and $NH_4^+$ spatial autocorrelation to relatively long distances compared to reclaimed plots (Fig. 4). Moreover, SOM and $NH_4^+$ contents of undisturbed soil were significantly higher in the prevailing wind direction away from shrubs (Fig. 6(a) and (b)). The study site is subject to high winds accompanied by blowing snow for much of the year and much of the annual snowfall is lost from the system via sublimation (Tabler, 1973). Rigid woody species serve to disrupt wind flow, allowing snow to collect on the leeward side of plants, while unprotected areas, or areas containing only grass species, are often devoid of snow cover during winter months. Litter from

shrubs, and windblown soil particles, would also tend to be deposited in these areas. *A. tridentata* is a long-lived species and it is likely that the spatial patterns of SOM around shrubs at these sites are partially the result of many years of locally increased litter deposition.

Although the reclaimed site was seeded with *A. tridentata* and other shrub species, these species failed to establish. Shrub-facilitated OM, nutrient, and $H_2O$ concentration heterogeneity likely influences both macro- and micro biodiversity, by increasing seed bed and growth condition heterogeneity. Typically, soil of surface mine reclamation sites, including the site under study, is replaced to nearly uniform depth, yielding a smooth surface that supports little collection of snow. In ecosystems subject to high wind, inclusion of features to disrupt wind flow patterns may increase water capture and site heterogeneity, potentially increasing plant biodiversity and site stability.

Nitrogen, after water availability, is generally most limiting for plant growth in arid and semi-arid ecosystems (Bolton et al., 1993). In most natural ecosystems N inputs are minimal and N retention and efficient cycling are critical for maintenance of ecosystem productivity. Both $NH_4^+$ and $NO_3^-$ concentrations were found to be less for locations near plant bases in reclaimed plots (Fig. 5), with $NO_3^-$ concentrations exhibiting especially strong spatial stratification (Fig. 6(c)), suggesting localized patterns of increased N uptake. In addition, unlike undisturbed soil, reclaimed soil $NH_4^+$ and $NO_3^-$ concentrations were not correlated with SOM (Table 2). The higher inorganic N concentrations found in the reclaimed plots, as well as its spatial characteristics and lack of significant correlation with SOM, suggests that the N cycle of this system is less efficient, or less tightly coupled, than in the undisturbed ecosystem (DeLuca and Keeney, 1993; Smith 1993). Spatial analysis of biotic and abiotic characteristics suggest that root exploration is likely less in the reclaimed ecosystem, which may result in C limitations on microbial biomass and activity in areas away from plant bases. Subsequently, plant and microbial N uptake are likely less in these areas and mineralized N is not cycled as rapidly back into the organic pool. This may be important to long-term ecological stability because inorganic N is potentially subject to greater losses from leaching, volatilization, and conversion to gaseous forms than are organic forms of N. Additionally, high levels of ammonium are known to increase mineralization of the indigenous soil N, potentially resulting in N limitations in subsequent years. The underlying overburden of the reclaimed sites is at a shallow depth and very permeable. N leached into this medium may be carried below the root systems of grasses. Because deeper roots from forbs and shrubs are lacking, this N may not be cycled back into the system. Further research is required that measures organic-N pool sizes and N cycling rates, inputs, and outputs before the long-term sustainability of this ecosystem can be ascertained.

Although water contents of reclaimed soil were higher than the undisturbed site (12.1 vs. 3.2, respectively), water availability at the time of sampling was likely similar in the two systems due to higher matric potentials associated with the gravelly clay loam texture of reclaimed soil. However, in arid regions fine textured surface soils are generally associated with greater evaporative losses due to decreased infiltration into subsurface horizons (Sabey et al., 1987). Therefore, soil texture may limit plant diversity on this site, especially for deep-rooted species such as shrubs (Jones, 1991). The effect of soil texture on microbial reestablishment, especially mycorrhizal reestablishment, has received little attention but may be important to successful reclamation of arid and semi-arid ecosystems.

EC was low for soil of both systems (averaging 0.51 and 0.39 dS/m for reclaimed and undisturbed soils, respectively), although significantly higher ($p \leq 0.01$) for reclaimed soils. A relatively high correlation ($r^2 = 0.34$, $p = 0.01$) was found between soil $NO_3^-$ concentration and EC values in the undisturbed ecosystem, suggesting that soil $NO_3^-$ contributes substantially to soil EC in this ecosystem (Smith and Doran, 1996). Although no significant differences in soil $NO_3^-$ content were found for the two ecosystems (Fig. 2), reclaimed soil EC was not significantly correlated with $NO_3^-$, suggesting that other salts may be responsible for the greater soil EC of this site. Incorporation of subsurface horizons, containing elevated salt concentrations, into topsoil may be responsible for elevated soil EC. However, salts migrating upward from overburden materials is problematic for many surface mine reclamations (Jurinak et al., 1987) and may be partially responsible for higher EC values of the reclaimed soils, potentially compromising future ecosystem stability.

Reclaimed soil had significantly higher pH values than undisturbed soil ($p < 0.01$) (7.8 and 7 for reclaimed and undisturbed soils, respectively). This may also be due to the incorporation of subsurface horizons when soil was initially removed prior to commencement of mining operations, resulting in differences in buffering capacities between reclaimed and undisturbed soils. However, pH exhibited spatial stratification in both reclaimed and, to a lesser extent, undisturbed ecosystems, with high values under plant canopies. Low pH values found away from plants may be due to release of $H^+$ ions during conversion of $NH_4^+$ to $NO_3^-$ by nitrifying bacteria. When plants take up $NO_3^-$, $OH^-$ is released into the soil, thereby neutralizing the acidity produced during formation of $NO_3^-$ and resulting in the spatial stratification of pH around plants.

This study illustrates the importance of spatial analysis for evaluation of both reclaimed and undisturbed ecosystems. For example, our results suggest that soil exploitation by roots and microorganisms in the reclaimed ecosystem is relatively low 20 years after seeding. This is likely due to low plant diversity but may also reflect soil textural differences. Our results also suggest ways to increase site

heterogeneity and, hence, plant biodiversity. The importance of shrub cover and its effect on site heterogeneity strongly suggests that failure of shrub reestablishment may result in significant biotic and abiotic differences between reclaimed and undisturbed sites. For example, reclaimed sites without shrubs would differ from sites with shrubs in plant litter quality (Rickard and Vaughan, 1988), root distributions, water use and distribution (West, 1992), nutrient use and distributions, surface temperature (Hinds and Rickard, 1968), fire ecology (Halvorson et al., 1997), and in habitat suitability for wildlife (Urness, 1989). Inclusion of barriers to wind flow on windy sites in which shrub cover has failed to reestablish could partially mimic the ecological function of shrubs, locally increasing plant available soil moisture and, hence, seed bed heterogeneity. We suggest that partial stone cover would not only serve to increase snow capture, but lessen evaporative losses and locally increase water availability via runoff from stone surfaces (Munn et al., 1987). In addition, because rock cover increases the rate of heat transfer to the soil (Mehuys et al., 1975), the growing season may be locally increased, which could be advantageous for some species in this cold environment.

Full understanding of how soil microbial community abundance and functional relationships are regulated will ultimately require analysis at a multitude of spatial and temporal scales. Understanding of microbial community spatial reorganization after severe disturbance will also require analysis of reclamation sites of different ages. In addition, spatial relationships of soil biotic and abiotic components in arid soils can change rapidly over time (Mummey et al., 1997), therefore analysis at no single time point can be expected to fully elucidate these relationships.

## Acknowledgements

This research was partially supported by a grant from NSF-EPSCoR (EPS-9983278).

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