

Spatial and Temporal Variability of Microbes in Selected Soils at the Nevada Test Site

J. P. Angerer
V. K. Winkel
W. K. Ostler
P. F. Hall

Abstract—Large land areas encompassing almost 700 hectares on the U.S. Department of Energy Nevada Test Site, Nellis Air Force Range and the Tonopah Test Range are contaminated with plutonium. Plutonium decontamination of these sites may involve removal of plants and almost 370,000 cubic meters of soil from the sites. The soil may be subjected to a series of plutonium removal processes. After decontamination, the soils may be returned to the site and revegetated. Because a paucity of information exists on the microbial components of the Mojave and Great Basin Deserts, especially how the components vary spatially and temporally, this study was initiated to determine baseline microbial activity and biomass in soils prior to decontamination. Information from this study will aid in determining the effects of plutonium decontamination on soil microorganisms, and what measures, if any, will be required to restore microbial populations upon subsequent revegetation of these sites. Soils were collected to a depth of 10 cm along each of five randomly located 30-m transects at each of four sites. In order to ascertain spatial differences, soils were collected from beneath major shrubs and from associated interspaces. Soils were collected at 3 to 4 month intervals to determine temporal (seasonal) differences in microbial parameters. Analysis showed that soils from beneath shrubs generally had greater active fungi and bacteria, and greater non-amended respiration than soils from interspaces. Temporal variability in the microbial components were found, with total and active fungi, and non-amended respiration being highly correlated to soil moisture at the time of sampling.

Large land areas on the Nevada Test Site, Tonopah Test Range (TTR), and the Nellis Air Force Range (NAFR) were contaminated with plutonium (Pu) during safety tests conducted in the late 1950's and early 1960's. The Resource Conservation and Recovery Act (RCRA), and the Comprehensive Environmental Response, Compensation and Liability

Act (CERCLA) may require that these sites be decontaminated. Plutonium decontamination of these areas will potentially involve the removal of the upper 5-10 cm of topsoil. Because of the large soil volume involved, an examination of alternatives for separating Pu from the soil prior to disposal is required to minimize the quantity of disposed soil. Many of the Pu separation processes will require destruction of soil structure and washing of the soil particles. The impact of these processes on the viability of soil organisms such as bacteria, fungi, algae, protozoa, and nematodes is not known. In order to ascertain how plutonium decontamination will affect the microbial population, an assessment of the spatial and temporal variability of microbes must be conducted to provide baseline information on how the decontamination processes will affect the soil microbial components. The baseline information will also provide guidelines for re-establishment of the microbial population during subsequent reclamation after decontamination of these sites.

In deserts, the topsoil is a valuable ecosystem component serving as a source of nutrients and water (Ostler and Allred 1987; Wallace 1980). The upper 5-10 cm of soil contains the majority of the seed bank and a large percentage of the living organisms associated with nutrient cycling (Foth and Turk 1972). The soil microbial population (bacteria, fungi, algae, etc.) plays an important role in ecosystem stability. Microbial processes essential to ecosystem stability include soil structure development, the synthesis of various plant nutrients through biogeochemical cycling, and the improvement of unfavorable physical and chemical conditions (Tate 1985). The productivity of any ecosystem, whether undisturbed or disturbed, is dependent on the resident microbial community. The availability of organic matter and soil water can have a great influence on microorganisms in desert soils (Dommergues and others 1978; Focht and Martin 1979). Microbial numbers are closely associated with the amount of organic material available for breakdown and uptake (Fuller 1974). Generally, microbial species diversity and biomass varies more in deserts than in other ecosystems (Kieft 1991).

A paucity of information exists on the microbial components of the Mojave and Great Basin Deserts, especially how the components vary spatially and temporally. In other arid and semi-arid ecosystems, spatial and temporal variability in soil microbial populations has been documented. Spatial variability exists within a site, with soils from beneath plants generally having greater microbial

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Jay Angerer, Von K. Winkel, and W. Kent Ostler are currently Scientist II, Scientist III, and Division Director, respectively at EG&G Energy Measurements, Environmental Sciences Division, P.O. Box 1912 MS/V-01, Las Vegas, NV 89125. Pam F. Hall is currently Student Trainee, National Biological Survey, National Wetlands Research Center, 700 Cajundome Blvd., Lafayette, LA 70506. Prepared for the Department of Energy under Contract No. DE-AC08-93NV11265.

numbers and diversity than soils associated with bare areas (Fuller 1974). Litter accumulation, windblown soil and plant material, and greater root biomass beneath perennial plants leads to the creation of "fertile islands" (Garcia-Moya and McKell 1970), which tend to have greater microbial activity. In the Chihuahuan desert, microbial biomass was 3.6 times higher, and organic carbon was 2.6 times higher underneath canopies of *Larrea tridentata* when compared to associated bare areas (Kieft 1991). Bacterial numbers were greater in soil beneath *Prosopis glandulosa* than in soil in interspaces (Baker and Wright 1988). Spatial and temporal variability can be the result of variable soil moisture conditions (Skujins 1984), litter inputs, and physical stress (Kieft 1991). In the Chihuahuan desert, bacterial and fungal numbers did not fluctuate during repeated wetting and drying of the soil; in contrast, protozoan numbers fluctuated with the wetting and drying cycles (Parker and others 1984). The spatial and temporal variability in soil microbial components brought about by varying moisture, temperature, litter inputs and plant cover poses problems for a single point in time sampling of the microbial population. Therefore, sampling of microbial populations should be continued over a significant period of time to properly address microbial population variations (Parkinson 1978).

Objectives and Hypotheses

The principal objectives of this study were to: 1) determine the spatial variability in soil microbial components (bacteria, fungi, and respiring biomass) within and between selected sites and 2) determine the temporal (or seasonal) variation in soil microbial components within selected sites. The hypotheses of this study were: 1) soil microbial components would vary spatially within sites, with soils from beneath perennial shrub canopies having greater microbial activity and biomass than soils in associated interspaces (bare areas); 2) soil microbial components would vary over time because of seasonal differences in soil moisture; 3) soil microbial components would vary between sites due to differing soils and climatic patterns.

Study Area and Methods

Soil microbial samples were collected from soils adjacent to Pu-contaminated areas in Area 5 and Area 11 of the Nevada Test Site, Area 13 of the Nellis Air Force Range and Clean Slate 1 of the Tonopah Test Range (Figure 1). These sites follow a general south to north elevation and temperature gradient with Area 5 having the highest temperatures and lowest elevation and Clean Slate 1 having the lowest temperatures and highest elevation (Table 1). Average annual precipitation collected at nearby sites indicated that precipitation is lowest in Area 5 and highest in Area 13. Soils in Area 5 are gravelly, sandy loams and vegetation is typical of the lower Mojave Desert (Table 1). Area 11 has gravelly loam soil and is the most ecologically diverse, containing elements of both the Mojave and Great Basin Deserts. Area 13 and Clean Slate 1 have gravelly sandy loam soils and have vegetation that is typical of the Great Basin Desert.

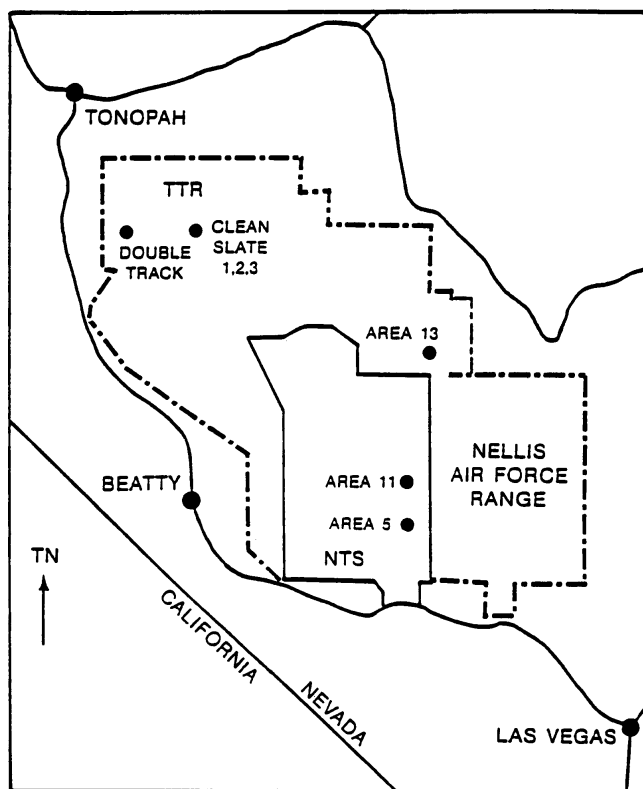


Figure 1—Location of plutonium contaminated sites where baseline microbial samples were collected. Tonopah Test Range = TTR. Nevada Test Site = NTS.

Five random 30-m transects (replication) were established in uncontaminated areas at each site. In order to ascertain spatial variability, stratified sub-samples were collected at 20 locations along each transect; 10 beneath the canopy of the dominant shrub species (Table 1) and 10 in adjacent interspaces. Samples were collected with a 6-cm-diameter metal cylinder that was inserted into the soil to a depth of 10 cm. Each of the ten sub-samples from each zone were combined into one bulk sample. Samples were analyzed within 48 hours for microbial numbers and biomass. The bulk sample was treated as the experimental unit for each corresponding location, transect and site. Soil microbial samples were collected on three occasions: August 1992, December 1992, and April 1993.

The experimental design for this study was a split plot with five replications. The whole plot variables were site and date of collection, and the split plot variable was zone (beneath shrub or interspace). General linear model procedures (analysis of variance) (SAS 1984) were conducted on means for the variables being measured to test for the significance of variables and their associated interactions. Fischer's Least Significant Difference mean separation procedure was used to determine significant differences among means. T-tests were used to separate means for zone effects. Appropriate error terms (those used to test significance of the variable or interaction in the analysis of variance) were used as the variance in the mean separation procedures.

Table 1—Comparison of sites contaminated with plutonium at the Nevada Test Site, Nellis Air Force Range, and Tonopah Test Range used for determination of baseline spatial and temporal variability of soil microbial components.

Site	Elev- ation (m)	Soil type	Major perennial species	Latitude	Longitude	Annual rainfall (mm)	January max - min temperature (°C)	August max - min temperature (°C)
Area 5	997	Gravelly, sandy loam	<i>Larrea tridentata</i> <i>Ambrosia dumosa</i> <i>Acamptopappus schockleyi</i>	36° 50' 38"	115° 56' 07"	124 ¹	12, -3	34, 17
Area 11	1257	Very gravelly loam	<i>Menodora spinescens</i> <i>Atriplex confertifolia</i> <i>Chrysothamnus viscidiflorus</i>	36° 58' 32"	115° 57' 24"	170 ²	11, -6	34, 15
Area 13	1390	Gravelly, sandy loam	<i>Atriplex confertifolia</i> <i>Ceratoides lanata</i> <i>Kochia americana</i>	37° 19' 09"	115° 54' 20"	185 ³	8, -1	31, 19
Clean Slate 1	1644	Gravelly, sandy loam	<i>Hilaria jamesii</i> <i>Atriplex confertifolia</i> <i>Artemisia spinescens</i>	37° 42' 30"	116° 39' 25"	135 ⁴	3, -4	28, 16

¹Precipitation and temperature data are from long-term averages of the Area 5 - B National Weather Service weather collector (approx. 2 miles west of the site).

²Precipitation and temperature data are from long-term averages of the Yucca Lake National Weather Service weather collector (approx. 5 miles west of the site).

³Precipitation and temperature data are from long-term averages of the P-H Farm National Weather Service weather collector (approx. 14 miles southwest of the site).

⁴Precipitation and temperature data are from long-term averages of the Tonopah Airport National Weather Service weather collector (approx. 16 miles northwest of the site).

Microbial analyses were conducted by Microbial Biomass Services at Oregon State University in Corvallis, OR. Samples were analyzed to determine active and total fungal biomass, and active bacterial numbers and biomass by counting FDA (fluorescein diacetate) stained bacteria in agar-film soil suspensions (Lodge and Ingham 1991). The active component is important in determining the activity levels of the fungi or bacteria at different times of the year and how these relate to environmental conditions.

Non-amended soil respiration (Page 1982) and glucose-amended respiration were determined for samples. Determination of non-amended soil respiration is a useful tool in assessing the total respiring biomass of microbes in the soil. Increases in soil respiration over time indicates greater respiring microbial biomass. At times, respiration rates may be low due to limited degradable carbon sources. Glucose-amended respiration is a useful tool in determining if a soil is carbon-substrate limited. A comparison of the respiration rate of a non-amended soil to the respiration rate of the same soil that has had a glucose mixture (a readily degradable carbon substrate) added to it, can give an indication of the amounts of readily degradable substrates that are available to the respiring biomass (Parkinson and Coleman 1991). Increases in the respiration rate from the glucose-amended soil over that of the non-amended soil may indicate that the non-amended soil is carbon-substrate limited. Also, the amount of time it takes for a soil to reach maximum respiration after substrate addition can be indicative of the physical and chemical stresses to the soil, with stressed soils requiring more time to reach peak respiration (Visser et al. 1984; Visser and Parkinson 1989).

Soil moisture was measured gravimetrically at the time of respiration determination. Determination of soil moisture at the time of sampling allowed assessments of moisture stress, if any, during that sampling period. Because

soil moisture varies temporally, it can be used as a correlation variable to assess temporal differences in microbial components.

Results and Discussion

Active and Total Fungal Biomass

Analysis of variance for active fungal biomass indicated a significant site-date of collection-zone interaction (Table 2). Site and zone were not significant main effects. Date of collection was highly significant, indicating that this variable had the greatest influence on the three-way interaction. Active fungal biomass means ranged from 0.0 to 4.6 µg/g soil dry weight with an overall average of 1.2 µg/g. The analysis of variance for total fungal biomass indicated a significant interaction between site, date of collection and zone (Table 2). In contrast to active fungal biomass, the main effects of date of collection and zone were reversed, with zone being a significant main effect and date of collection not significant. This may be an indication that total fungal biomass does not vary widely over time across sites, but the activity levels may vary widely.

Zone Influences—Mean active fungal biomass (µg/g soil dry weight) beneath perennial shrubs and in interspaces was not significantly different for each site and sampling date except for Area 5 during the December sampling (Figure 2). Total fungal biomass varied significantly between zones in Area 11 and 5 during the August 1992 sampling, Area 11 during the December 1992 sampling, and Area 13 during the April 1993 sampling. Area 5 had significantly greater active and total fungal biomass beneath shrubs. Area 11 exhibited significantly greater total fungal biomass beneath shrub canopies during August, but exhibited

Table 2—Analysis of variance levels of significance (p-values) for site, date of collection, zone (interspace or under canopy) and interactions of these variables for determining sources of variation in active fungal biomass, total fungal biomass, active bacterial numbers, non-amended respiration, glucose amended respiration and gravimetric soil moisture. Main effects and interactions were considered significant if the p-value was less than 0.05.

Variable	Active fungal biomass	Total fungal biomass	Active bacterial numbers	Non-amended respiration	Glucose amended respiration	Soil moisture
Site	0.8113	0.1490	0.3955	0.0753	0.0743	0.5146
Date (of collection)	0.0004	0.2747	0.0548	0.0002	0.0929	0.0004
Zone	0.8940	0.0065	0.0001	0.0001	0.0001	0.0004
Site*Date	0.3238	0.0134	0.0001	0.0091	0.0001	0.0001
Site*Zone	0.0034	0.1439	0.8863	0.0305	0.0001	0.3750
Date*Zone	0.3885	0.0233	0.0017	0.0001	0.0001	0.1633
Site*Date*Zone	0.0001	0.0002	0.1517	0.0006	0.0107	0.0002

greater active and total fungal biomass in the interspaces during the December sampling. Area 13 had greater total fungal biomass beneath shrub canopies during the April sampling.

Date of Collection Influences—Variability in active fungal biomass on a temporal scale was apparent and

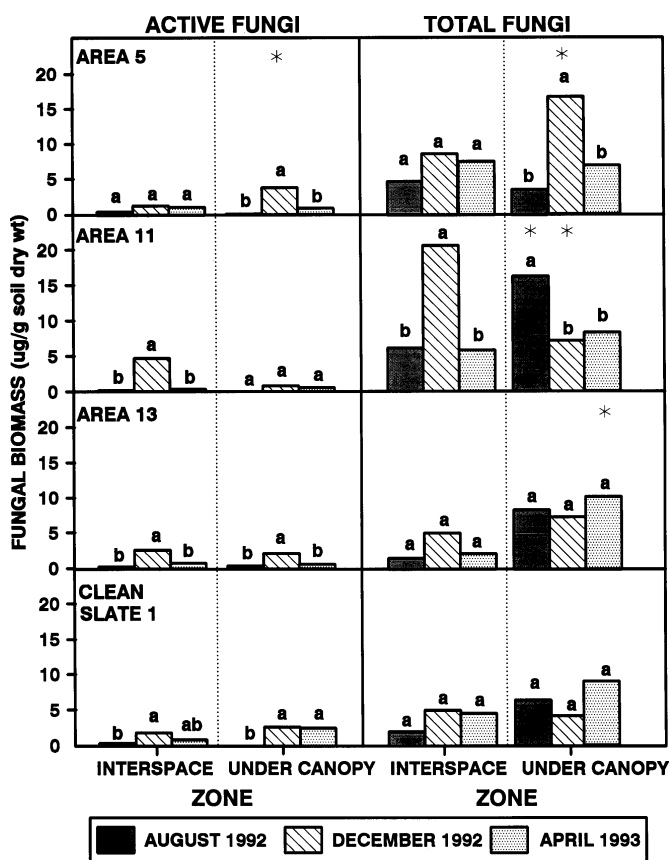


Figure 2—Mean active and total fungal biomass for soil beneath plant canopies and interspace zones for selected sites on three dates. Date mean values having the same letter within zones and sites were not significantly different. Means having a “*” indicate a significant difference in the interspace and under canopy means for that date and zone.

appeared to be related to soil moisture conditions. The December sampling period generally had significantly higher fungal biomass followed by the April sampling date (Figure 2). The differences in biomass for these dates closely resembled the pattern of soil moisture (Figure 3) for these sites. Soil moisture was positively correlated to active fungal biomass ($r = 0.53$; Table 3) for all sites regardless of zone. However, correlation analysis on the means for each zone over time indicated that interspace active fungal biomass was strongly correlated to soil moisture ($r = 0.71$), whereas under canopy active fungal biomass had a low correlation ($r = 0.33$; Table 3). This may indicate that the activity of fungi under plant canopies is less dependent on soil moisture.

Total fungal biomass varied significantly over time within zones in Areas 5 and 11. Area 5 had significantly greater total fungal biomass beneath plant canopies during December (Figure 2). Area 11 had greater fungal biomass in interspaces during December and significantly higher total fungal biomass beneath shrubs during August. For Area 13 and Clean Slate 1, total fungal biomass apparently did not fluctuate greatly over time. There was a general tendency for total fungal biomass in interspaces (Figure 2) to follow soil moisture patterns (Figure 3). This trend was positively correlated with a significant r -value of 0.60 (Table 3). However, this trend was not apparent for under canopy total fungal biomass, which had low a low correlation with soil moisture ($r = 0.17$; Table 3).

Site Influences—Active and total fungi in interspace soils did not differ significantly between sites for each date of collection except for the Area 11 interspace soil during December, which had significantly greater active and total fungal biomass (Figure 2). Soil moisture at this site was significantly greater than at the other sites (Figure 3) and may have influenced this difference. Active and total fungal biomass under shrub canopies had significant differences between sites for the dates of collection. However, no consistent pattern was detected, with significant differences varying with each site and date of collection.

Numbers of Active Bacteria

Analysis of variance for numbers of active bacteria indicated a non-significant, site-date of collection-zone interaction (Table 2). Site and zone were not significant main

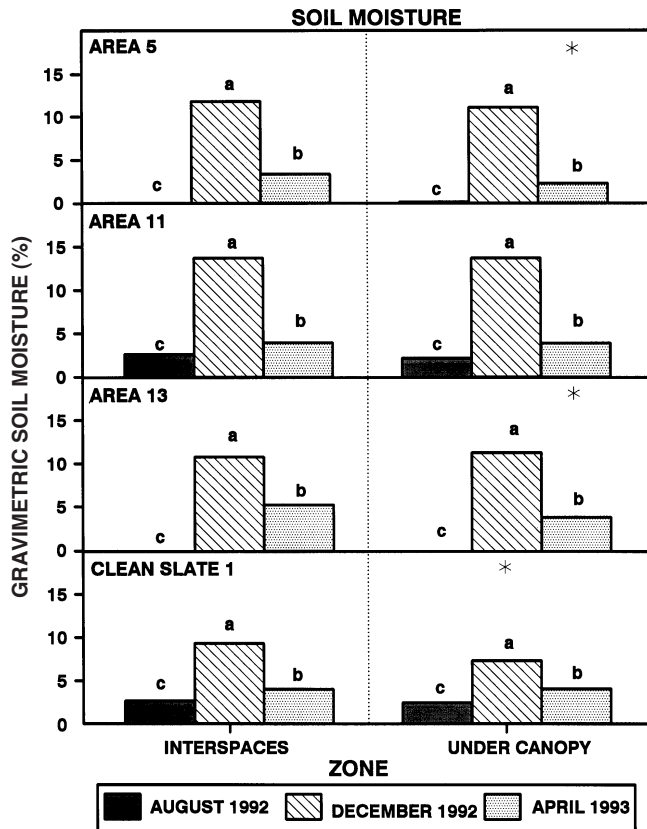


Figure 3—Mean gravimetric soil moisture for soil beneath plant canopies and interspace zones for selected sites on three dates. Date mean values having the same letter within zones and sites were not significantly different. Means having a “*” indicate a significant difference in the interspace and under canopy means for that date.

effects. However, date of collection was highly significant. Although the three-way interaction was not significant, mean separation procedures were conducted to determine if any consistent patterns in active bacterial numbers could be seen for the variables.

Active bacterial numbers ranged from 4.5 to 21.9×10^6 propagules/g dry soil. This range for active bacteria exceeded that found previously for total bacterial propagules of Mojave Desert soils in Nevada (Vollmer and others 1977). They reported total bacterial numbers ranging from 3 to 16×10^6 propagules per gram of soil. Their data represented total bacterial propagules, whereas the data reported in this study were for active bacterial propagules only. Total bacterial numbers for this study, although incomplete, indicate ranges of 11.9 to 73.0 total bacterial propagules per gram of dry soil for Area 5 and 11 which represent Mojave Desert habitats. Active bacterial numbers for Clean Slate 1 and Area 13, which have vegetation components like that of Great Basin Desert, were greater than total bacterial numbers reported for other Great Basin Deserts. Skujins (1984) reported that Great Basin soils had approximately 0.9×10^6 total bacterial propagules per gram of soil. As before, the

Table 3—Pearson’s correlation coefficients and associated p-values for correlation of mean values of active and total fungal biomass, active bacterial numbers, soil respiration, and glucose amended respiration to that of soil moisture at the time of sampling. Correlations were conducted by zone (interspace or under canopy) regardless of site, and for all sites and zones combined.

Variable	Soil moisture	
	Pearson’s correlation coefficient	p-value
Interspaces (n = 12)		
Active fungal biomass	0.71	0.0093
Total fungal biomass	0.60	0.0412
Active bacterial numbers	−0.44	0.1562
Respiration	0.76	0.0042
Glucose amended respiration	−0.11	0.7273
Under Canopy (n = 12)		
Active fungal biomass	0.33	0.2876
Total fungal biomass	0.17	0.5805
Active bacterial numbers	−0.28	0.3739
Respiration	0.92	0.0001
Glucose amended respiration	−0.48	0.1135
Zones and Sites Combined (n = 24)		
Active fungal biomass	0.53	0.0083
Total fungal biomass	0.37	0.0716
Active bacterial numbers	−0.36	0.0807
Respiration	0.73	0.0001
Glucose amended respiration	−0.28	0.1817

reported data for this Great Basin site was for total bacterial propagules only. Active bacterial propagules for Great Basin-type areas in this study ranged from 6.2 to 21.9×10^6 propagules and total bacterial numbers, although incomplete, ranged from 13.8 to 27.6×10^6 propagules.

Zone Influences—Numbers of active bacteria beneath shrubs were not significantly different from interspaces during the August sampling period (Figure 4). There was a general trend of greater numbers of active bacteria beneath shrubs during December and April. These differences were statistically significant for Areas 11 and 13 during December, and Areas 5 and 13 during April. Active bacteria numbers beneath shrubs and in interspaces had statistically insignificant correlations with soil moisture ($r = -0.44$ and -0.28 , respectively; Table 3).

Date of Collection Influences—Temporal variability in numbers of active bacteria was apparent for both collection zones in Areas 5, 11, and 13 with the August sampling date having significantly greater bacterial numbers (Figure 4). Soil moisture at all four of these sites was lowest during this collection date (Figure 3). Active bacterial numbers at Clean Slate 1 did not differ significantly over time for both interspaces and beneath shrub canopies.

Site Influences—Significant differences in active bacterial numbers for sites were variable across dates of collection and zones. There was a general trend for Area 13 to have greater active bacterial numbers, but this was generally not significant.

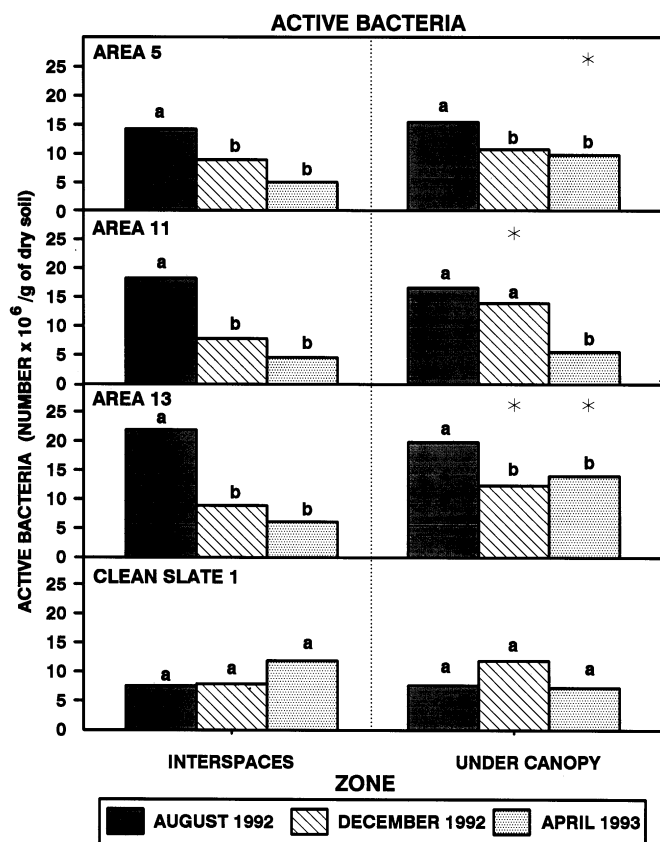


Figure 4—Mean active bacterial numbers for soil beneath plant canopies and interspace zones for selected sites on three dates. Date mean values having the same letter within zones and sites were not significantly different. Means having a “*” indicate a significant difference in the interspace and under canopy means for that date.

Soil Respiration

Analysis of variance for non-amended soil respiration indicated a significant site-date-of collection-zone interaction (Table 2). Date of collection and zone were significant main effects whereas site was not significant (Table 2). Non-amended soil respiration means ranged from 0.0139 to 0.798 with an overall mean of 0.241 $\mu\text{g C/g}$ of dry soil/hr. In contrast to non-amended respiration, date of collection and site main effects for glucose-amended respiration were not significant; however, as with the non-amended respiration, the zone main effect and the three way interaction between site, date of collection and zone was significant. Glucose-amended respiration means ranged from 0.057 to 1.474 with an overall mean of 0.505 $\mu\text{g C/g}$ dry soil/hr.

Zone Influences—Differences in non-amended soil respiration between interspaces and shrub canopies (Figure 5) existed on several dates with soil from beneath shrub canopies in Areas 5 and 13 exhibiting greater non-amended respiration during both December and April, and soils from beneath shrubs in Area 11 having greater non-amended respiration in December (Figure 5). Clean Slate 1 exhibited no significant differences in interspace and under canopy non-amended respiration for any of the dates sampled.

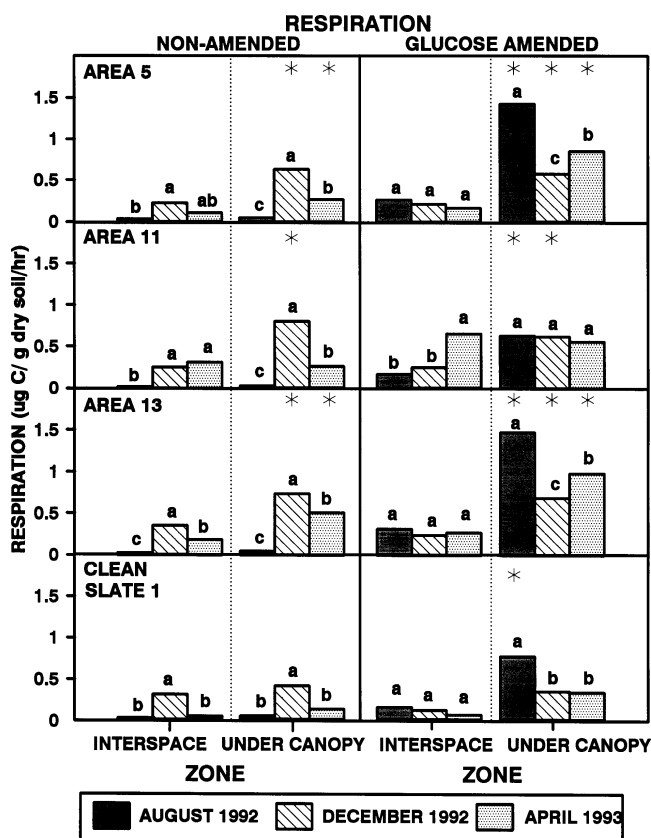


Figure 5—Mean non-amended and glucose amended respiration for soils beneath plant canopies and interspace zones for selected sites on three dates. Date mean values having the same letter within zones and sites were not significantly different. Means having a “*” indicate a significant difference in the interspace and under canopy means for that date.

Glucose-amended soils from beneath plant canopies generally had greater respiration rates than that of interspace soils (Figure 5). Glucose-amended soil respiration averaged across sites and dates indicated that respiration beneath shrub canopies was 4 times greater than that in interspaces. This may be an indication that the respiring microbial biomass was greater in soils beneath shrub canopies.

Date of Collection Influences—Temporal variability in non-amended respiration was apparent among sites and zones with December generally having greater non-amended respiration than other collection dates (Figure 5). The pattern of non-amended respiration over time closely resembled that of soil moisture during sampling (Figure 3). Non-amended respiration rates of soils from interspaces and beneath shrub canopies were highly correlated to soil moisture ($r = 0.76$ and 0.92 , respectively; Table 3). This may be an indication that the activity levels of the microbial population as a whole are closely tied to soil moisture levels. The high correlation of non-amended respiration to soil moisture status is consistent with that reported in other desert climates. Knight and Skujins (1981) reported an exponential decrease in non-amended respiration with decreasing water potentials for two desert soils. Generally,

respiration rates are greatest when soils are at field capacity (Sommers and others 1981).

Glucose-amended respiration exhibited temporal patterns. The August 1992 sampling period exhibited significantly greater respiration than that of other collection dates (Figure 5) and did not appear to be related to soil moisture conditions at the time of sampling (Figure 3). Glucose-amended respiration from interspace soils had a low correlation with soil moisture ($r = -0.11$; Table 3). Glucose-amended respiration from under shrub canopy soils had a slightly higher correlation value and was negative ($r = -0.48$; Table 3). The negative correlation coefficient may indicate that there is a slight tendency for an increased moisture status beneath shrubs which leads to a decrease in the response of the microbial biomass to glucose substrate addition. Therefore, during periods of low soil moisture beneath shrubs, the microbial biomass may be carbon-substrate limited rather than water limited.

The increased respiration response after glucose addition of both interspace and under canopy soils over that of non-amended soils may partially be due to the fact that water was used to solubilize the glucose amendment. Non-amended soil respiration rates were highly correlated to soil water, especially for soils from under shrub canopies. The addition of water during the glucose amendment does not fully explain why the glucose amendment had a much greater response from under canopy soils as compared to interspace soils, when the non-amended respiration rates for each of these zones were not significantly different across sites. A partial explanation for this may be the influence of active bacteria. Glucose-amended respiration from soils beneath shrubs was positively correlated to active bacterial numbers ($r = 0.62$, $p = 0.03$), but was not correlated to active bacteria from interspaces ($r = -0.10$, $p = .76$). However, active bacterial numbers did not vary significantly between interspace and under canopy soil during the August sampling period (Figure 4). This may indicate that active bacteria and other microbial components beneath shrubs were water and carbon substrate limited whereas the components in interspaces were only water limited.

Site Influences—Significant differences in non-amended respiration rates were not consistent between sites when compared across sampling dates and zones of collection. However, when respiration from glucose-amended soils was compared between sites, Area 13 exhibited a general trend of having greater respiration than that of the other sites (overall mean of 0.66 for Area 13 as compared to 0.58, 0.47, and 0.29 for Area 5, Area 11 and Clean Slate 1, respectively). Although this greater respiration was not always significantly different across sampling dates and zones, it may indicate that Area 13 has a greater microbial biomass than the other sites.

Conclusions

Zone Influences

The differences in interspace and under canopy microbial components measured in this study (active and total fungi, active bacteria and soil respiration) were statistically

inconsistent among sites and dates of sampling. However, when significant differences between interspace and under canopy microbial components were observed, there was a general tendency for under canopy soils to have higher values for the microbial components.

Date of Collection Influences

Temporal variability existed for total and active fungi in interspace soils and appeared to be related to soil moisture. Soil moisture was positively correlated to interspace active and total fungal biomass indicating the dependence of these components on soil moisture in this zone. Active and total fungal biomass for soils from beneath shrub canopies was not correlated to moisture status, and therefore may be carbon substrate dependent rather than moisture dependent. Active bacterial numbers varied with dates of collection but were generally not correlated to soil moisture. The negative correlation of active bacteria with soil moisture may indicate that bacterial numbers are uncoupled from soil moisture conditions and may be coupled to amount of available carbon substrates. The greater number of bacteria during the summer months may allow a competitive advantage over the more moisture dependent fungi.

The temporal variability in non-amended respiration is an indication that the activity levels of the total microbial population varies over time. The high correlation of non-amended respiration for soils beneath shrubs and interspaces indicates that soil moisture plays an important role in maintaining soil microbial activity and biomass. The greater respiration after glucose amendment exhibited by soils underneath plant canopies indicates that these soils may be carbon substrate limited at certain times of the year.

Site Influences

The dominance of a microbial component varied across sites, dates of collection and zones. No consistent pattern was detected among sites for each of the microbial parameters measured. Apparently, the soils, elevation and temperatures at these sites do not greatly influence the soil microbial parameters as much as the temporal variability in soil moisture.

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