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Microbial and soil parameters in relation to N mineralization in soils of diverse genesis under differing management systems

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Abstract Oregon soils from various management and genetic histories were used in a greenhouse study to determine the relationships between soil chemical and biological parameters and the uptake of soil mineralized nitrogen (N) by ryegrass (*Lolium perenne* L.). The soils were tested for asparaginase, amidase, urease, β-glucosidase, and dipeptidase activities and fluorescein diacetate hydrolysis. Microbial biomass carbon (C) and N as well as metabolic diversity using Biolog GN plates were measured, as were total soil N and C, pH, and absorbance of soil extracts at 270 nm and 210 nm. Potentially mineralizable N (N_0) and the mineralization rate constant (k) were calculated using a first order nonlinear regression model and these coefficients were used to calculate the initial potential rate of N mineralization (N_0k). Except for Biolog GN plates, the other parameters were highly correlated to mineralized N uptake and each other. A model using total soil N and β-glucosidase as parameters provided the best predictor of mineralized N uptake by ryegrass ($R^2=0.83$). Chemical and biological parameters of soils with the same history of formation but under different management systems differed significantly from each other in most cases. The calculated values of the initial potential rate of mineralization in some cases revealed management differences within the same soil types. The results showed that management of soils is readily reflected in certain soil chemical and biological indicators and that some biological tests may be useful in predicting N mineralization in soils.

Key words Enzyme assays · N mineralization · Biolog · Functional diversity · Management systems

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Introduction

Chemical and biological tests have been used for many years in an attempt to predict the nitrogen (N) supplying capacity of soils (Keeney and Bremner 1966; Gasser and Kalembasa 1976; Stanford 1982) but a satisfactory method of predicting N mineralization continues to elude investigators. Better knowledge of the mechanisms and indicators of N mineralization in soils is essential to improve N-use efficiency and lessen environmental impacts from agricultural production on N contamination of surface and groundwater. Soil microbes are the engines of organic N transformations and information is needed on key characteristics of soil biological activity, microbial biomass, and functional diversity in relation to N cycling processes to better predict N mineralization in soils.

Enzymes are central to microbial activity and N transformations. Enzyme activities have been shown to be responsive to environmental conditions and agricultural management (Dick 1992, 1994). For example, Pancholy and Rice (1973) showed that enzymes involved in organic carbon (C) compound decomposition such as amylase, cellulase, and invertase decreased while dehydrogenase and N-releasing enzymes such as urease increased during plant succession in an abandoned field. In another study, protease, urease, and asparaginase had higher activities in fields with crop rotations than in fields with corn monocultures (Blagoveshchenskaya and Danchenko 1974). Sparling and Searle (1993) found that dimethyl sulfoxide (DMSO) reduction, microbial biomass C, total soil C and N, and anaerobically mineralized N were all highly correlated to each other in a wide range of New Zealand soils. Soil deaminase activity was higher in forest soils and in grass leys with more available N compared to soil in barley fields, suggesting that this enzyme activity may be useful in predicting N mineralization (Killham and Rashid 1986). Urease and phosphatase have been associated with net N immobilization, whereas protease has

been related to net N mineralization (Nannipieri et al. 1983).

Microbial biomass N is not only an important indicator of viable soil microbial populations but also is an important pool of readily mineralizable organic N in soils (Kai et al. 1973; Myrold 1987; Bonde et al. 1988). Since soil management has a strong influence on microbial biomass in both agricultural (McGill et al. 1986; Fauci and Dick 1994; Franzluebbers et al. 1995) and forest (Soderstrom et al. 1983) soils, it is a critical component for assessing potentially mineralizable N.

It seems reasonable that the degree of soil microbial biodiversity resulting from soil management and/or genesis should be important in controlling N transformations. Although genetic diversity measurements such as DNA characterization provide information on biodiversity, it cannot determine whether genes or functions are expressed. Another approach which may be more useful relative to N transformation is to challenge the microbial population with diverse C substrates to determine functional diversity (Zak et al. 1994). This approach has been used to distinguish differences: in soil moisture regimes and vegetation communities in the Chiuahuan Desert (Zak et al. 1994); among forest, meadow, and agricultural soils in Denmark (Torsvik et al. 1990); and among different C inputs and flooding of agricultural plots in California (Bossio and Scow 1995). There is no information available on the relationship of functional metabolic diversity and N mineralization.

Long-term management of soils, particularly C and N inputs, can have a significant effect on N mineralization (Burket and Dick 1997), but little is known about the relationship of soil management relative to soil biology and N mineralization. Therefore, the objective of this study was to examine the relationships between soil biological/chemical characteristics and soil N mineralization among soils with diverse histories of genesis and management.

Materials and methods

Soils and greenhouse experiment

Soils were collected at 0–20 cm depths from five different locations in Oregon and represented three soil orders and 19 different management histories (Table 1). The Walla Walla soils from the

Table 1 Description of the 19 Oregon soils used in the N mineralization greenhouse study (*WIL* North Willamette Research and Extension Center, *WW* Columbia Basin Research Center, Pendleton)

Soil name	Soil classification	Soil abbreviation	Management
Willamette silt loam	Mixed, mesic Pachic Ultic Argixeroll	WIL grass, burn	Tall fescue, 125 kg N ha^{-1} applied every year, seed harvested, straw removed
		WIL grass, no burn	Tall fescue, 125 kg N ha^{-1} applied every year, seed harvested, straw burned
		WIL fallow, no N	Alternate years of sweet corn and broccoli, no N, winter fallow
		WIL, fallow, high N	Alternate years of sweet corn and broccoli, 224 or 280 kg N ha^{-1}, winter fallow
		WIL clover, no N	Alternate years of sweet corn and broccoli, no N, red clover winter cover crop
		WIL clover, high N	Alternate years of sweet corn and broccoli, 224 or 280 kg N ha^{-1}, red clover winter cover crop
		WIL rye, no N	Alternate years of sweet corn and broccoli, no N, cereal rye winter cover crop
		WIL rye, high N	Alternate years of sweet corn and broccoli, 224 or 280 kg N ha^{-1}, cereal rye winter cover crop
Walla Walla silt loam	Coarse-silty, mixed, mesic Typic Haploxeroll	WW manure	Wheat, 22.4 Mg ha^{-1} beef manure incorporated every 2 years, straw incorporated
		WW pea vine	Wheat, 22.4 Mg ha^{-1} pea vine incorporated every 2 years, straw incorporated
		WW no N	Wheat, no organic inputs, no fertilizer N, straw incorporated
		WW high N	Wheat, 90 kg N ha^{-1} fertilizer applied every year, straw incorporated
		WW pasture	Mixed grass pasture
Newberg loam	Coarse-loamy, mixed mesic Fluventic Haploxeroll	NB sod	Unused area, no soil amendments for past 25 years
		NB corn, high N	Sweet corn past 3 years, 240 kg N ha^{-1}
Jory silty clay loam	Clayey, mixed, mesic Xeric Haplohumult	JY forest	Land in preserved forest for past 75 years
		JY orchard	Pear trees, soil under trees kept in bare fallow for past 30 years, no amendments
Bashaw clay	Very fine, montmorillonitic, mesic Typic Pelloxeret	BSHW wetland	Natural wetland area, minimal disturbance
		BSHW grass	Perennial ryegrass field past 4 years, 125 kg N ha^{-1} applied every year

long-term Residue Utilization Plots (initiated in 1931) at the Columbia Basin Research Center, Pendleton, Ore., USA, are located in a semi-arid Mediterranean climate region of eastern Oregon (400 mm rainfall $year^{-1}$). The other soils are from western Oregon which has a humid Mediterranean climate (1200 mm rainfall $year^{-1}$). The Willamette soils are from the long-term Vegetable Cover Crop Plots (initiated in 1989) located at the North Willamette Research and Extension Center, Aurora, Ore. After sampling, soils were stored at 4 °C prior to sieving through a 2-mm mesh screen, distributed into solid-bottom pots (three replications per soil sample) of approximately 2 l volume, and kept at 70–80% of field capacity, gravimetrically, with deionized water for 21 days to establish an equilibrium. Soil was collected from each replicate pot to perform enzyme, microbial biomass, and other measurements (i.e., all analyses replicated three times) and then the pots were adjusted to contain 1 kg dry soil.

All pots were sown with 1 g of perennial ryegrass (*Lolium perenne* L.) seed. Pots sown to ryegrass were fertilized at the beginning of the experiment and after 3 months with a liquid solution of K_2SO_4 and $Ca(H_2PO_4)$ such that each pot received 143 mg K, 60 mg S, 175 mg P, and 113 mg Ca at each application. All pots were maintained at 70–80% of field capacity, gravimetrically, throughout the experiment by weighing pots every 3 days and adjusting them to their appropriate weight with deionized water. Greenhouse temperature was kept between 25 °C and 20 °C, and day length was 14 h. Cuttings from the ryegrass plants were taken at a height of 1 cm every 30 days for 6 months, dried in a forced air oven at 65 °C, ground to pass a 0.37-mm sieve, and analyzed for total N (Bremner and Mulvaney 1982).

Biological measurements

Soils collected for chemical and biological assays were sieved to pass a 2-mm mesh screen and split so that half the sample was dried at room temperature for those analyses requiring air-dried soil. Both moist and dry subsamples were kept in the cooler at 4 C until analysis. Microbial properties were measured within 1 week after the ryegrass was planted in the pots.

Enzyme assays for asparaginase (L-asparagine amidohydolase, EC 3.5.1.1), amidase (acylamide amidohydolase, EC 3.5.1.4), urease (urea amidohydolase, EC 3.5.1.5), and β-glucosidase (β-D-glucopyranosidase, EC 3.2.1.21) followed the protocols of Tabatabai (1994) using air-dried soils. The dipeptidase assay was modified from Ladd and Butler (1972) as follows: 1 g moist soil was placed in a centrifuge tube; 1.8 ml of 0.1 M tris-sodium borate buffer and 2 ml of 0.002 M Z-phenylalanyl leucine substrate were added to non-controls and shaken to suspend the soil. The tubes were capped tightly, submerged in a 40 °C water bath, and shaken lengthwise for 30 min at 150 rpm. Tubes were removed and cooled rapidly to 20 °C in another water bath, followed by an addition and mixing of 0.2 ml of 5 N HCl to each tube. Substrate was then added to controls and all samples were centrifuged at 2000 *g* for 20 min. Two milliliters of supernatant was then placed in a small test tube, 1 ml ninhydrin reagent added, and the samples read at 570 nm. Absorbance of samples compared to prepared leucine standards determined the reported activities of dipeptidase.

The fluorescein diacetate (FDA) assay was modified from Schnürer and Rosswall (1982) as follows: 1 g air-dried soil was shaken with 20 ml of 60 mM sodium phosphate buffer in a 125 ml Erlenmeyer flask for 15 min. Then 100 µl of 2 mg ml^{-1} FDA stock solution (substrate) were added to non-controls and all samples were shaken for 2 h. After shaking, 20 ml acetone was added to all samples and 100 µl substrate was added to controls. The samples were transferred to centrifuge tubes and spun at 6000 rpm for 5 min. Samples were filtered through Whatman no. 4 filter paper and read at 499 nm. FDA activity was determined from absorbance of samples compared to a standard curve.

Microbial biomass C (MB_C) and N (MB_N) measurements were made according to the fumigation-incubation procedures of Jenkinson and Powlson (1976) with the following modifications. Fumigated and unfumigated samples in the tubes were incubated in the dark for 10 days at 24 °C. CO_2 produced after 10 days was analyzed with a thermal conductivity gas chromatograph. After CO_2 sampling, 50 ml of 2 M KCl was added to each tube and it was shaken lengthwise for 1 h and stored at 4 °C until analysis for NH_4^+ by steam distillation. Values for MB_c and MB_N were calculated with the following formulas:

$MB_C = (CO_2\text{–}C_f \text{ minus } CO_2\text{–}C_{uf}) / 0.41$ (Voroney and Paul 1984)

$MB_N = (NH_4^+\text{–}N_f \text{ minus } NH_4^+\text{–}N_{uf}) / 0.68$ (Shen et al. 1984)

The subscripts $_f$ and $_{uf}$ stand for fumigated and unfumigated, respectively.

To determine a measurement of metabolic diversity, 10^{-1} soil dilutions were made by dispersing 10 g moist soil in flasks containing 95 ml sterile physiological saline solution (0.15 M NaCl) and several sterile glass beads. The suspension was allowed to settle for 5 min and then wells of Biolog GN plates were inoculated with 150 µl aliquots taken from the top 10 cm of the flasks. The plates were covered, placed in containers on top of moist paper towels to limit desiccation, and incubated in the dark at 28 °C for 48 h.

Microplates were read at 590 nm on an automated microplate spectrophotometer. Positive wells were defined as those having an absorbance greater than 0.4 in order to avoid false positives.

Chemical measurements

Inorganic NO_3^- and NH_4^+ were determined by extraction with 2*M* KCl, steam distillation, and titration (Mulvaney 1996). Total soil N was determined by Kjeldahl digestion, followed by NaOH distillation, and measured by titration with 25 mM H_2SO_4 in boric acid indicator (Bremner 1996). Total soil C was measured by dry combustion on a Leco C analyzer. Soil pH was determined using a glass electrode on a pH meter with a soil:water ratio of 1:2.

For the ultraviolet absorption procedures, 2.5 g dry soil was extracted with 50 ml of 0.01 M $NaHCO_3$. The methods followed those of Fox and Piekielek (1978) except that the two wavelengths used for testing the extracts were 210 nm and 270 nm (Norman et al. 1985). The UV method was originally proposed to test for soil NO_3^- which absorbs at 200–210 nm (Cawse 1967).

Data analysis

Biological and chemical assay results were analyzed by ANOVA (SAS Institute 1990) and means separation by Fisher's protected LSD ($P < 0.05$). Preplant soil NO_3 levels (pre-plant soil NH_4 levels were negligible) were subtracted from total N uptake by ryegrass in order to calculate soil mineralized N uptake by ryegrass. N mineralization potential (N_0) and the mineralization rate constant (k) were calculated from the following exponential equation:

$$N_{min} = N_0[1-\exp(-kt)]$$

where N_{min} = cumulative amount of inorganic N at specific time (t).

The initial potential rate of mineralization was calculated as $N_0 \times k$ (Campbell et al. 1991a). Pearson correlation coefficients were generated among all assays and soil mineralized N uptake by ryegrass (SAS Institute 1990). Stepwise regression (SAS Institute 1990) was to find the best model for predicting N mineralization. The North Willamette (Willamette soil) winter fallow, no N vegetable treatment, and the Pendleton (Walla Walla soil) pea vine soil amendment were randomly chosen and left out of the original model development to provide two dissimilar soils for model testing. Collinearity diagnostics were performed to determine the degree of multicollinearity among the variables (Freund and Little 1986).

Results and discussion

Biological and chemical measurements

Biological and chemical measurements of the soils are shown in Tables 2 and 3. In general, soils with long-term additions of plant residues and organic matter had higher levels of the biological parameters (Table 2). Native soils or soils under management similar to native conditions (e.g., forests, pastures) showed much higher enzyme activities than more intensively managed soils (Table 2). An abundant supply of organic C to soils, either by natural seasonal dieback of vegetation or by addition within a cultural practice, is essential for maintaining biological activity in soils.

Overall, the C:N ratios of the whole soil and the microbial biomass were not significantly correlated to ryegrass N uptake (data not shown). However, the two least disturbed soils in the experiment (Jory forest and Bashaw wetland) had both the widest soil C:N ratio and the highest ryegrass N uptake (Tables 3, 4). Soil C:N ratios were similar across soil types and management systems (Table 3). Microbial biomass C:N, on the other hand, seems to be much more sensitive to management. Within all soil types, higher N or organic residue inputs and less disturbance resulted in narrower microbial biomass C:N ratios (Table 2). This observation emphasizes the responsiveness of soil microbial populations to management systems. One possible explanation for the lower ratios may be higher populations of soil bacteria in soils with residue and high N inputs. Bacteria have the lowest C:N ratio of all soil organisms (Paul and Clark 1989).

Within the same site, those soils which only received long-term N fertilizer additions (Willamette, Walla Walla, and Newberg) tended to reduce the activities of urease, FDA, and dipeptidase, as well as microbial biomass levels compared to native soils or soils with additional organic matter inputs (Table 2). Inorganic N fertilization without additional organic inputs could affect soil biology by several mechanisms. First, there can be a reduction of microbial biomass (Soderstrom et al. 1983) which might be due to a narrowing of C:N ratios in soils. This would likely cause more rapid decomposition of organic inputs, which in turn reduces stable C pools for maintaining microbial biomass. Without sufficient organic C inputs to the soil, the microbial biomass will be depressed regardless of the amount of available N present. A second factor is that N ions may have a direct effect on enzyme systems. Dick et al. (1988) showed a negative relationship between increasing rates of N fertilization and amidase and urease activities. They hypothesized that these enzymes were suppressed due to the long-term fertilizer application of the reaction product (NH_4) of these enzymes. This was later confirmed by McCarty et al. (1992), who showed that NH_4 repression of urease activity was real, but the NH_4 effect was indirect and due to by-products of NH_4

Table 2 Measured values of biological tests

Soil name	Asparaginase	Amidase	Urease	β-glucosidase	FDA	Dipeptidase	Biolog GN plates wells >0.4 absorbance	Microbial biomass C	Microbial biomass N	Microbial biomass C:N
	mg $NH_4-N \cdot kg\ soil^{-1} \cdot 2\ h^{-1}$			mg p-nitrophenol $kg\ soil^{-1} \cdot h^{-1}$	mg flourescein $kg\ soil^{-1} \cdot h^{-1}$	mg leucine kg $soil^{-1} \cdot h^{-1}$		mg C $kg\ soil^{-1}$	mg N $kg\ soil^{-1}$	
WIL[a] grass, burn	6.9	87.7	28.0	97.5	82.8	49.5	52.7	144.9	20.1	7.2
WIL grass, no burn	7.0	91.6	30.8	86.5	83.9	58.2	37.3	193.1	16.0	12.1
WIL fallow, no N	8.8	84.9	17.5	64.1	47.0	31.7	35.0	142.7	5.6	25.5
Wil fallow, high N	8.6	35.0	10.1	61.7	39.3	25.2	36.3	64.5	5.7	11.3
WIL clover, No N	9.1	51.1	15.5	95.1	59.1	51.3	57.7	182.5	8.7	21.0
WIL clover, high N	6.7	29.6	16.5	82.7	48.9	36.1	51.7	131.4	15.5	8.5
WIL rye, no N	7.2	40.5	24.5	70.7	51.8	32.9	53.3	168.4	16.3	10.3
WIL rye, high N	9.5	40.8	17.8	74.7	48.4	19.2	46.0	120.9	13.7	8.8
WW[b] manure	11.9	141.2	67.7	76.6	61.1	125.2	44.7	268.4	32.6	8.2
WW pea vine	8.2	130.7	44.6	84.0	51.7	65.8	56.7	171.1	20.7	8.3
WW no N	3.3	76.7	26.3	53.0	35.3	26.0	31.0	96.7	3.1	31.2
WW high N	3.8	89.8	18.3	67.8	34.4	9.3	47.7	38.2	5.8	6.6
WW pasture	43.3	213.3	161.2	115.6	124.7	237.2	51.7	502.3	80.2	6.3
NB[c] sod	135.3	430.3	111.6	49.7	182.4	314.1	34.7	1705.9	186.0	9.2
NB corn, high N	11.3	67.2	27.1	102.0	46.2	44.2	48.6	150.6	11.3	13.3
JY[d] forest	90.0	343.8	131.5	160.2	172.4	226.6	44.0	1352.0	154.0	8.8
JY orchard	3.8	59.2	13.0	36.0	64.6	11.2	11.7	74.3	4.4	16.9
BSHW[e] wetland	83.6	323.3	100.9	35.4	200.2	418.2	54.7	2577.5	300.0	8.6
BSHW grass	26.0	174.9	76.0	73.3	187.9	111.5	52.7	602.0	59.3	10.2
LSD, $P<0.05$	7.4	14.7	6.8	7.5	3.6	45.3	1.5	91.7	5.6	

[a] Willamette silt loam [b] Walla Walla silt loam [c] Newberg loam [d] Jory silty clay loam [e] Bashaw clay

Table 3 Measured values of chemical tests

Soil name	pH	Total soil C kg^{-1}	Total soil N kg^{-1}	Total C:N	UV 210 nm Absorbance	UV 270 nm Absorbance	Preplant soil ammonium mg kg^{-1}	Preplant soil nitrate mg kg^{-1}
WIL[a] grass, burn	5.4	16.12	1.16	13.9	0.676	0.209	0.9	8.0
WIL grass, no burn	5.6	16.20	1.08	14.9	0.586	0.202	1.3	4.4
WIL fallow, no N	5.6	15.33	1.11	13.7	2.719	0.172	2.4	91.3
WIL fallow, high N	5.3	16.07	0.98	16.4	2.317	0.170	1.1	74.7
WIL clover, no N	5.6	15.12	1.03	14.6	2.241	0.189	4.4	69.8
WIL clover, high N	5.3	15.64	1.13	13.8	3.378	0.188	5.7	119.1
WIL rye, no N	5.6	13.87	0.96	14.4	2.669	0.143	2.8	86.5
WIL rye, high N	5.5	14.32	1.07	13.3	3.426	0.165	4.6	114.8
WW[b] manure	7.1	14.00	1.13	12.3	0.780	0.156	0.9	21.3
WW pea vine	6.5	11.51	0.96	11.9	0.641	0.146	3.9	20.9
WW no N	6.3	9.29	0.71	13.0	0.393	0.114	1.7	15.9
WW high N	5.8	9.44	0.71	13.2	0.570	0.131	3.0	17.9
WW pasture	6.9	22.32	1.68	13.2	0.952	0.207	3.9	22.0
NB[c] sod	6.1	34.17	2.47	13.8	0.916	0.257	3.7	17.0
NB corn, high N	6.1	8.18	0.62	13.1	1.415	0.096	4.4	39.9
JY[d] forest	6.2	45.36	1.94	23.3	0.433	0.225	7.8	0.9
JY orchard	5.3	10.74	0.78	13.7	1.121	0.231	0.9	31.1
BSHW[e] wetland	5.5	91.66	4.79	19.1	3.415	0.511	5.4	81.3
BSHW grass	5.1	28.13	2.05	13.7	1.324	0.276	8.3	32.6
LSD, $P<0.05$	0.1	3.09	0.15		0.157	0.030	2.0	5.2

[a] Willamete silt loam
[b] Walla Walla silt loam
[c] Newberg loam
[d] Jory silty clay loam
[e] Bashaw clay

Table 4 Calculated values of rye N uptake minus preplant soil nitrate, N mineralization potential (N_0), mineralization rate constant (k), and initial potential mineralization rate ($N_0 \times k$)

Soil name	Rye N uptake mg kg^{-1}	N_0 mg kg^{-1}	(SE)	k week^{-1}	$N_0 \times k$
WIL[a] grass, burn	30.4	28.8	(4.1)	0.001432	0.583
WIL grass, no burn	36.8	27.6	(4.6)	0.016168	0.673
WIL fallow, no N	24.9	28.6	(17.2)	0.028223	3.213
WIL fallow, high N	11.3	58.5	(41.9)	0.024141	2.022
WIL clover, no N	35.0	38.5	(2.3)	0.022844	2.369
WIL clover, high N	43.0	34.1	(6.3)	0.028432	4.577
WIL rye, no N	36.4	36.2	(2.2)	0.026217	3.198
WIL rye, high N	20.6	28.5	(22.8)	0.028001	3.524
WW[b] manure	36.3	39.3	(2.4)	0.015799	0.918
WW pea vine	24.0	28.9	(4.6)	0.017037	0.768
WW no N	14.8	24.9	(6.4)	0.016364	0.505
WW high N	23.6	26.3	(7.7)	0.016045	0.639
WW pasture	56.5	93.9	(16.8)	0.010734	0.907
NB[c] sod	50.5	73.3	(35.1)	0.008589	0.662
NB corn, high N	18.2	20.1	(4.5)	0.022689	1.312
JY[d] forest	69.1	76.7	(8.8)	0.009289	0.753
JY orchard	19.7	38.1	(31.0)	0.020545	1.039
BSHW[e] wetland	105.1	279.9	(217.5)	0.012819	2.477
BSHW grass	61.9	63.5	(10.5)	0.016373	1.542

[a] Willamete silt loam
[b] Walla Walla silt loam
[c] Newberg loam
[d] Jory silty clay loam
[e] Barshaw clay

assimilation. Lastly, C may become less available with long-term N additions owing to condensation of N-rich compounds (Haider et al. 1975).

Within soil types, management regimes that minimize soil disturbance (such as pasture, sod, wetland, and forest) had significantly higher levels of enzyme activities, and microbial biomass (Table 2). This is consistent with findings in India on disturbed forest soils that had lower microbial populations and enzyme activities than undisturbed soils (Jha et al. 1992). Klein and Koths (1980) found the highest urease and protease activities in field soils with less disturbance (no-till) and higher crop residue inputs than in conventionally tilled soils with residues removed. Less disturbance of soils results

in greater aggregation (Gupta and Germida 1988), which in turn preserves soil organic matter and allows for a greater variety of microhabitats. Work in soil ecology has shown that the composition of organisms at all trophic levels in the soil is important to ecosystem stability and nutrient transformations (de Ruiter et al. 1995). Some of the differences observed in the N mineralization rates between relatively disturbed and undisturbed soils of the same soil genesis could be attributed to altered trophic structures above the bacteria level.

Biolog plate metabolic diversity was significantly higher in soils with less disturbance and higher organic matter inputs (Table 2) with the highest number of positive wells from the Willamette soil with clover and zero N and the lowest number from the Jory orchard site. The Willamette soil in this treatment was one in which yields of broccoli and sweet corn were comparable to other treatments that received over 200 kg ha^{-1} inorganic N fertilizer. The red clover winter cover crop contained about 1200 kg ha^{-1} dry weight and 43 kg N ha^{-1} above ground (Burket et al. 1997). In contrast, the Jory orchard soil was in bare fallow for over 15 years with no soil amendments applied. When the 29 Biolog wells containing amino acids, amides, and amines were examined separately from all 95 wells, results were similar and correlation between this subgroup and the whole plate was high (Pearson correlation coefficient = 0.87, $P < 0.0001$). These results are in agreement with Zak et al. (1994) who found that separating substrates into six guilds did not, with the exception of a slight change when looking at only the polymers, change the positional relationships among the environments when compared to overall substrate utilization.

Our method of Biolog analysis did not take into consideration the intensity of color development in the wells as an indication of abundance of any particular ability to metabolize a substrate. Using positive and negative responses for individual wells rather than absorbance numbers is a way to ameliorate possible sources of variability among replicates due to inoculum density differences or natural soil heterogeneity (Zak et al. 1994). The positive response threshold has been a standard method for other microplate methodologies in avoiding false positive results (Pscheidt et al. 1992). The presence or absence of a metabolic capability from a soil is the simplest measurement of metabolic diversity and is analogous to counting species from different environments to compare diversity (Magurran 1988).

N mineralization parameters

Ryegrass N uptake, N mineralization potentials (N_0), and rate constants (k) data are shown in Table 4. Within the four cultivated plots of the Walla Walla soils (Table 4), the highest N_0 value is from the manure treatment and the lowest is from the zero N treatment. Janzen (1987) also found that soils from long-term rotations with the highest residue inputs had the highest N_0 values. Except for the winter fallow treatments, N_0 was consistently lower in the Willamette soil plots and the Newberg plots receiving high fertilizer N inputs compared to plots with no inorganic N inputs having the same cover crop and vegetable rotation (Table 4). Apparently, a winter cover crop of either rye or clover is more effective in increasing N_0 than fertilizer N inputs. The same relationship among these soils holds true when considering the initial potential mineralization rate (N_0k) with the fallow plots being exceptions (Table 4). These results are in contrast to that of Campbell et al. (1991a) where fertilizers were shown to be as effective as cover crop residues for increasing N_0k. This parameter, N_0k, was found by Campbell et al. (1991a) to be a better index than total N, N_0, or k for assessing the quality of the active fraction of soil organic matter. The cultivated Walla Walla plots, which are from a more arid climate, similar to the Saskatchewan site in the Campbell et al. (1991a) study, had results consistent with that study in which a higher fertilizer N input resulted in a higher N_0k value (Table 4). However, among all the five Walla Walla plots, the highest N_0k was from the pasture and is no more useful than N_0 in distinguishing among treatments.

The initial potential rate of mineralization, N_0k, appears to be useful in distinguishing management treatments within, but not between, soil type; for instance, the Willamette soil under fallow with zero N and high N, the Walla Walla soil under zero N, Jory orchard, and the Newberg corn with high N treatments all had similar values of N_0k (Table 4).

Campbell et al. (1991a) compared only soils from cultivated fertilized and unfertilized treatments that had similar organic matter C and N contents, unlike the work presented here which includes relatively undisturbed soils with high levels of soil organic C and N (Table 3). Normalizing N_0 by dividing it by total N creates a ratio that shows whether N_0 is in direct proportion to the soils' N content and is also an indication of the soil organic matter's "active fraction." Except for the Willamette fallow, high N soil, which had an especially high standard error for its N_0, this ratio is highest in the two soils that also had the highest N_0 (Bashaw wetland and the Walla Walla pasture soils) (Table 4). This ratio is also very high in the Jory orchard soil, which had a relatively low N_0. Within the Walla Walla soils, the only treatment that stands out in regard to this ratio is the pasture, which had twice the total C as any of the other four treatments (Tables 3, 4).

When native soils are compared for N_0 or N_0k, the quantity rather than the quality of the soil organic matter seems to become the dominant discriminator according to soil management. In addition, soils from western Oregon, where there is over twice the annual rainfall of eastern Oregon, appear to create more variability in the calculated parameters N_0 and N_0k and also result in patterns that do not distinguish among treatments very well (see Willamette soils in Table 4).

Campbell et al. (1991b) also reported differences in findings when comparing their results to similar treatments from more humid conditions.

Model for N mineralization

Highly significant correlations were found among total and microbial biomass N, UV 270, all enzymes (except β-glucosidase), and mineralized N uptake by ryegrass (Table 5). Measurements of microbial biomass would be expected to correlate highly with enzyme activities, since microbes are mainly responsible for production of soil enzymes. Schnürer and Rosswell (1982) found FDA activity to correlate well with soil respiration levels and many enzymes, but enzymes can persist in soils and also reflect past microbial population levels via extracellular enzymes stabilized in the soil matrix (Burns 1982). The calculated parameters k and N_0k had no significant correlations with any of the measured parameters. Mineralized N uptake by ryegrass and N_0 were highly correlated to each other ($r=0.97$) as would be expected.

Stepwise regression analysis showed that total soil N and β-glucosidase activity accounted for a significant proportion of the variation of N uptake by ryegrass in the 17 soils used for model development ($R^2=0.82$; $F=114$; $df=2, 48$; $P<0.0001$). The model equation is as follows:

Mineralized N uptake by ryegrass =
$-12.38+0.23$ (β-glucosidase activity, mg kg^{-1} h^{-1}) +
0.023 (total N, mg kg^{-1})

with standard errors of 5.1, 0.05, and 0.002 for y-intercept, β-glucosidase activity constant, and total N constant, respectively.

Predicted values of mineralized N uptake by ryegrass and standard errors from the model equation for the two soils left out of the equation were 27.9 mg kg^{-1} (10.1 mg kg^{-1}) for the Willamette fallow/no N treated soil compared to 24.9 mg kg^{-1} (9.4 mg kg^{-1}) actual mineralized N (Table 4) and 28.6 mg kg^{-1} (17.2 mg kg^{-1}) calculated N mineralization potential (N_0 in Table 4). The predicted value for the Walla Walla pea vine soil was 29.1 mg kg^{-1} (10.7 mg kg^{-1}) compared to 24.0 mg kg^{-1} (0.6 mg kg^{-1}) actual mineralized N (Table 4) and 28.9 mg kg^{-1} (4.6 mg kg^{-1}) calculated N mineralization potential (N_0 in Table 4). The general agreement among the calculated and measured values for mineralized N for these two soils further confirms the potential usefulness of the model for predicting mineralized N availability. Total soil N and β-glucosidase activity are not correlated to each other (Table 5), which eliminates the problem of multicollinearity that is often severe among soil properties making them less useful for modeling soil processes because collinearity artificially increases R^2 values.

In agreement with other studies (Frankenberger and Dick 1983; Franzluebbers et al. 1995), measurements of organic matter such as MB_N, total N, total C, MB_C, and enzyme activities in soils are highly correlated to each other, so inclusion of anymore than one of these parameters in a model predicting mineralized N uptake would contribute to multicollinearity. This best fit mineralized N uptake model with the parameters total soil N and β-glucosidase activity are measurements that

Table 5 Matrix of Pearson correlation coefficients for 12 of the measured soil parameters ($P>0.0001$ are displayed in parentheses)

	UV 270	Asparaginase	Amidase	Urease	FDA	Dipeptidase	β-Glucosidase	Biolog	Total N	Microbial biomass N	Total C	Microbial biomass C
Mineralized N uptake	0.80	0.65	0.71	0.70	0.84	0.81	0.11 (0.41)	0.35 (0.01)	0.87	0.84	0.85	0.83
UV 270	–	0.58	0.60	0.47	0.78	0.75	−0.27 (0.04)	0.10 (0.46)	0.93	0.84	0.91	0.83
Asparaginase	–	–	0.95	0.77	0.83	0.87	0.07 (0.58)	0.01 (0.97)	0.77	0.87	0.71	0.88
Amidase	–	–	–	0.85	0.87	0.83	0.12 (0.39)	0.04 (0.77)	0.74	0.88	0.72	0.88
Urease	–	–	–	–	0.80	0.83	0.36 (0.01)	0.19 (0.16)	0.62	0.73	0.59	0.69
FDA	–	–	–	–	–	0.84	0.10 (0.46)	0.14 (0.29)	0.84	0.86	0.80	0.86
Dipeptidase	–	–	–	–	–	–	0.03 (0.85)	0.19 (0.15)	0.88	0.94	0.87	0.92
β-glucosidase	–	–	–	–	–	–	–	0.41 (0.00)	−0.18 (0.17)	−0.06 (0.67)	−0.09 (0.52)	−0.09 (0.49)
Biolog	–	–	–	–	–	–	–	–	0.23 (0.09)	0.16 (0.25)	0.21 (0.12)	0.12 (0.36)
Total N	–	–	–	–	–	–	–	–	–	0.95	0.96	0.95
Microbial biomass N	–	–	–	–	–	–	–	–	–	–	0.94	0.99
Total C	–	–	–	–	–	–	–	–	–	–	–	0.93

provide a relatively complete picture of readily mineralized soil organic matter that will yield plant available N. β-Glucosidase activity represents the soil's potential to hydrolyze low molecular weight carbohydrates (Eivazi and Tabatabai 1990) and release glucose, which is an important energy source for soil microbial populations. The combination of total N and β-glucosidase activity may best represent both the pool of mineralizable N in the soil and the potential to release C for energy available for microbes to carry out the mineralization.

Biolog metabolic diversity was significantly correlated with mineralized N uptake, but not with the other parameters except for β-glucosidase. Since the wells of Biolog GN plates contain C sources, correlation of Biolog metabolic diversity with β-glucosidase activity, an enzyme involved in C mineralization, is logical (Table 5). Clearly, many types of biological activity in soils are intimately associated with the process of N mineralization. In order to find a useful means of predicting N mineralization in the laboratory that will accurately reflect mineralized N that is also taken up by plants, the measurements should be both biologically relevant to the process of N mineralization and fairly easy to perform. Further work using measurements of total soil N and β-glucosidase activity on field soils to predict plant available mineralized N will determine if the model developed here from a variety of Oregon soils is more broadly applicable.

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