

Farm-Scale Variation of Soil Quality Indices and Association with Edaphic Properties

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Farm-scale variation of soil quality indices and association with edaphic properties. Soil organisms can be used as indicators of dynamic soil quality because their community structure and population density are sensitive to management changes. However, edaphic properties can also affect soil organisms and spatial variability can confound their utility for soil evaluation. We evaluate the relationship between two important agronomic functions, N-mineralization potential and aggregate stability, and biological, chemical, and physical edaphic properties. Decomposers, nematodes, collembolans, total C, total N, pH, bulk density (D_b), and texture were evaluated at 81 sites across 25-ha of an organic farm in western Washington. We built regression trees with biological, chemical, physical, and management parameters to explain the farm-scale variation in microbial biomass ($r^2 = 0.74$), nematode density ($r^2 = 0.61$), collembolan density ($r^2 = 0.36$), nematode structure index (SI, $r^2 = 0.41$), nematode enrichment index (EI, $r^2 = 0.54$), proportion of soil as aggregates > 0.25 mm ($r^2 = 0.60$) and N-mineralization potential ($r^2 = 0.58$). Soils with microbial biomass > 597 $\mu\text{g C}_{\text{mic}} \text{g}^{-1}$ formed a homogeneous group with the greatest N-mineralization potential, and soils with >13.5% clay formed a homogeneous group with the greatest proportion of soil aggregates > 0.25 mm. Increased soil aggregation was associated with larger nematode SI, though much of the variability in SI remained unexplained by the data. Tillage had a strong effect on both decomposer and nematode populations; soils not tilled for 5 yr had the largest microbial biomass and soils not tilled 2 wk before sampling had the largest nematode populations. Comparisons of soil quality indicators across farms should be sensitive to the association of indicators with soil texture and recent management practices.

Abbreviations: D_b , bulk density; B/F, ratio of bacterial/fungal biomass; CI, nematode channel index; EI, nematode enrichment index; Log_{10} COLL, Log_{10} collembolans 100 cm^{-3} ; Log_{10} NEM, Log_{10} nematodes 100 cm^{-3} ; MI, nematode maturity index; N MIN POT, N-mineralized ($\text{mg kg}^{-1} \text{ d}^{-1}$); Nematodes, total nematodes 100 cm^{-3} ; NO_3 -10 cm, NO_3 (mg kg^{-1}) 0 to 10 cm; NO_3 -30 cm, NO_3 (mg kg^{-1}) 0 to 30 cm; Parasitic NEM, Parasitic nematodes 100 cm^{-3} ; PLFA-biomass, phospholipid fatty acid biomass ($\mu\text{g C}_{\text{mic}} \text{g}^{-1}$); PROP AGG, proportion aggregates > 0.25 mm; SI, nematode structure index; SIR-biomass, substrate-induced respiration biomass ($\mu\text{g C}_{\text{mic}} \text{g}^{-1}$).

Most soil properties exhibit high degrees of spatial structure; “hotspots” of biological activity ebb into areas of little or no activity often over predictable distances (Klironomos et al., 1999). While spatial heterogeneity has typically been viewed as a hindrance to understanding soil biogeochemical phenomena, Ettema and Wardle (2002) suggest “spatial variability may be the key, rather than the obstacle to understanding the structure and function of soil biodiversity.” Ignoring spatial variability compromises our ability to describe soil communities, as we are then limited to classical sampling plans. A spatially explicit research approach can strengthen our understanding of biological diversity and abundance and better connect those parameters to edaphic properties and biological processes.

Soil decomposer activity, collembolans, and nematodes have all been used as biological indicators of soil quality (Reganold et al., 1993; Fließbach et al., 2007; Ponge et al., 2003; Fountain and Hopkin, 2004; Ferris et al., 2001). Trasar-Cepeda et al. (1998) found microbial biomass was a strong predictor of available N in minimally disturbed soils. In addition to total biomass, the relative dominance of fungi versus

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bacteria in agronomic soil can affect soil physical and chemical properties. Increased fungal activity has been associated with increased aggregate stability and soil organic matter (Guggenberger et al., 1999; Denef et al., 2001; Bailey et al., 2002). Collembolans, the majority of which feed on fungi or decaying plant material, are among the most abundant soil microarthropods and are an important component of the detrital food web (Hopkin, 1997). They are also sensitive to agricultural disturbance and values of a collembolan-derived soil quality index were significantly correlated with the inverse of the number of years since the last tillage operation (Gardi et al., 2003). Nematodes are unique soil quality indicators because they are the most abundant of the mesofauna, occupy multiple functional groups representing most trophic levels, and occur in essentially all soil environments.

Bongers (1990) ranked nematode families based on their tendency to colonize or rapidly multiply in newly disturbed soil ecosystems or to persist in rarely disturbed, late-successional soil ecosystems. The index of maturity (MI) is derived from the relative abundance of early colonizers and late-successional nematode species (Bongers, 1990). The EI signifies the degree that nematode families indicating enrichment predominate; these enrichment opportunist nematodes are primarily bacterial-feeders that multiply rapidly in response to inputs of N-rich and easily decomposed organic matter. The SI signifies the degree that nematode families indicating ecosystem structure (numerous trophic linkages present) predominate (Ferris et al., 2001). Forge et al. (2003) correlated SI with mulch treatments that promote tree vigor and Berkelmans et al. (2003) suggested that a large SI is indicative of a well-regulated, healthy ecosystem that could, for example, regulate or suppress plant parasitic nematode species. The channel index (CI) is a measure of the relative preponderance of certain groups of fungal feeding nematodes relative to bacterivores, and was proposed to predict the degree of fungal participation in primary decomposition (Ferris et al., 2001).

Doran and Zeiss (2000) identified soil functions that can be influenced by management decisions as “dynamic soil quality” and those properties not easily changed or influenced by management decisions (e.g., clay mineralogy, texture, etc.) as “inherent soil quality”. The importance of soil texture and other edaphic properties on biological properties has been demonstrated in several studies. Franzluebbers et al. (1996) found increasing soil microbial activity in coarser textured soils. This finding is in agreement with the general recognition that organic matter decomposes more rapidly in sandy soils than in fine textured soils (Hassink, 1994). However, Thomsen et al. (1999) found more rapid turnover of organic matter in clay-amended soils when the soils were adjusted for soil water potential. Understanding how inherent soil properties affect potential biological indicators will help researchers in the development of feasible indicators and their interpretation so that these can be of use to growers in making site-specific management adjustments accordingly.

Knowledge of the spatial properties of parameters of interest as well as relationships to other spatially structured and predictable edaphic properties can be used to better represent

the variability of an area in sampling plans directed at improving management. Researchers have documented associations between specific pathogenic nematode species and soil texture (Avendaño et al., 2004), texture and organic matter (Wyse-Pester et al., 2002), and combinations of multiple chemical and physical soil properties (Noe and Barker, 1985) suggesting the potential for identifying infestations based on edaphic properties and areas to direct management tools.

The specific objectives of this project were to: (i) describe variability of selected indicators of soil community structure (collembolans, nematodes, microbial biomass) and their association with edaphic properties (soil texture, D_b , pH, soil C) and farm management, (ii) evaluate the ability of soil community attributes to predict important agronomic functions such as N-mineralization potential and aggregate stability.

MATERIALS AND METHODS

Study Site

Full Circle Farm (FCF), Carnation, WA is an approximately 40-ha organic vegetable farm located 30 km east of Seattle, WA (latitude 47°36'58.05"N, longitude 122°54'44.37"W). General farm operations are similar for all new vegetable plantings; beds are formed on 2.2-m centers with a bed shaper following primary tillage with a plow or spader, disking, and then rototilling as needed. A 4-3-3 chicken manure-based fertilizer is applied at 1.7 to 2.2 Mg ha⁻¹. Before conversion to a vegetable farm in 1998, the study site and adjacent buildings were used to raise dairy cows. From about 1940 to 1982 approximately 50 dairy cows grazed at the site and were milked and housed in the adjacent barn. From 1982 to 1998 the site was used to raise heifers with as many as 130 head on site at a time. There are three predominant soils mapped at the site (Soil Survey Staff, Natural Resources Conservation Service, United States Department of Agriculture, 2010): Edgewick silt loam (coarse-loamy, mixed, superactive, mesic fluventic Humic Dystrudepts), Puget silty clay loam (fine-silty, mixed, superactive, nonacid, mesic Fluvaquentic Endoaquepts) and Tukwila muck (diatomaceous, dysic, mesic Limnic Haplosaprists).

Farm-Scale Sampling and Analyses

The sampling plan covered a roughly rectangular 25-ha area of the farm while providing information about spatial variation at different scales. We collected 81 samples with a minimum distance between sample locations of 5 m (Fig. 1). Farm fields had been tilled from 1 to 30 wk before the time of sampling, which was between 12 and 20 Oct. 2006. Eleven of the sample locations were located in “meadow” areas, which had not been tilled for at least 5 yr (Fig. 1). Six meadow locations were within the area mapped as muck by the Natural Resource Conservation Service (Fig. 2).

At each location we delineated a 0.5-m² area to sample. We sampled from crop rows (unless no crop was planted) by taking three cores (5.6 cm diam., 5-cm depth) for collembolan analysis, five cores (2.5 cm diam., 15-cm depth) for nematode analysis, five cores (2.5 cm diam., 30-cm depth) for nitrate N, three cores (6 cm diam., 10-cm depth) for a composite sample used for microbial biomass, texture, N-mineralization potential, total C, total N, pH, ammonium N, and nitrate N, one core for D_b (5.4 cm diam., 6-cm depth) and two trowel samples for aggregate

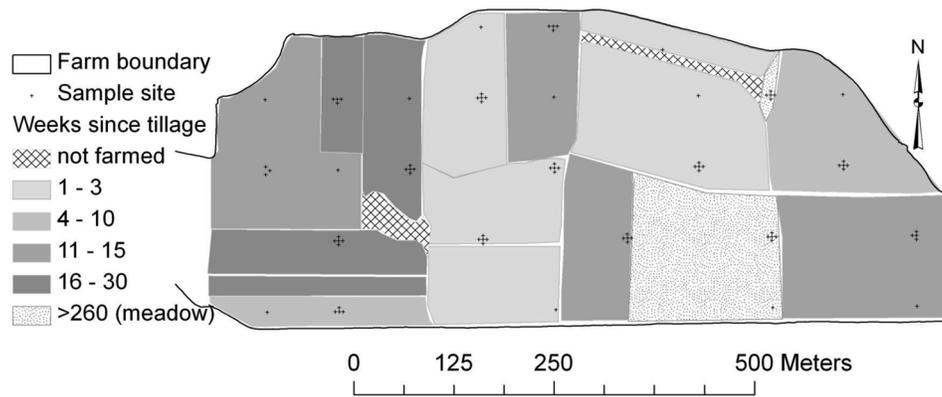


Fig. 1. Location of sample sites and tillage management at Full Circle Farm, Carnation WA in 2006 and 2007.

gate stability (10-cm depth). Sample number, depth, and total volume varied with the type of analyses. The sampling scheme reflected the fact that most Collembola are surface dwellers, while nematodes are found deeper in the profile. Other samples were taken at 10 cm to assess characteristics of surface soil. The volume of soil collected was optimized in preliminary studies (data not shown).

Collembola were isolated by inverting the three subsamples onto a piece of cheese cloth in one Burlese-Tullgren funnel (Moldenke, 1994). A 25-W bulb suspended above the sample was turned on for two 2-h periods each day for 7 d. Microarthropods were collected in 70% (v/v) isopropyl alcohol and collembolans were enumerated and identified to family level with a dissecting microscope. Nematodes were isolated from a 50-mL subsample by Baerman funnel modified with a wet-sieving step (Ingham, 1994). The soil sample was suspended in approximately 2 L of tap water, allowed to settle for 30 s, and then poured through a #18 (1 mm) sieve into another pitcher. The sample was then immediately collected onto a #400 sieve (38 μm), rinsed into a collection tube and allowed to settle for a minimum of 2 h before aspirating to a volume of 10 mL and then resuspended and pouring onto the Baerman funnel. Samples were collected after 48 h and stored at 4°C until they were enumerated at 25 \times magnification. A minimum of 100 individual nematodes were randomly selected from each sample and were then identified to genus or family level with the aid of an English translation of Bongers (1994) at 400 or 1000 \times , and community indices were computed (Bongers and Ferris, 1999; Forge et al., 2003).

Total active fungal and bacterial biomasses were determined by both phospholipid fatty acid profile (PLFA; Ibekwe and Kennedy, 1998) and substrate induced respiration (SIR, Horwath and Paul, 1994). For SIR, the equivalent of 5 g oven dry, pre-incubated soil (adjusted to 40 to 50% water holding capacity and incubated at 25°C for 7 d) was dispersed to evenly cover the bottom of a half-pint canning jar (244 mL volume). Glucose solution was added with a syringe fitted with a 1.3-cm 27-gauge needle to bring the soil water content to between 75 and 80% water holding capacity and the glucose concentration to 20 $\mu\text{mol glucose g}^{-1}$ soil solution. Jars were closed with metal lids fitted with two air-tight septa and incubated at 25°C for 2 to 3 h. To determine initial and final CO_2 concentration we used an ADC 2250 IRGA (ADC BioScientific Ltd., Hoddesdon, UK; Collins, 2008a). A factor of 30 was used to convert SIR biomass from $\mu\text{L CO}_2 \text{ g}^{-1}$ soil h^{-1} to $\mu\text{g microbial C g}^{-1}$ soil (Kaiser et al., 1992). Phospholipid fatty acid methyl esters were prepared as described by Ibekwe and Kennedy (1998). Chain lengths were compared against a database of established microbial markers from the literature (Wortmann et al., 2008; Grigera et al., 2007; Hamman et al., 2007; Bååth, 2003; Madan et al., 2002; Olsson, 1999; Zelles, 1999; Sundh et al., 1997; Frostegård and Bååth, 1996). Bacterial and fungal biomass were calculated from mole response data using the relationship determined by Bailey et al. (2002). Components were summed individually and bacteria/fungi ratios (B/F) were calculated for each sample.

Wet aggregate stability was measured using a modified method of Nimmo and Perkins (2002). The sample was wetted and placed on a nest of sieves, with sizes of 4.75, 2, 1, and 0.250 mm. Sieves were placed in water and mechanically lowered and raised by 3.5 cm, 34 times per minute

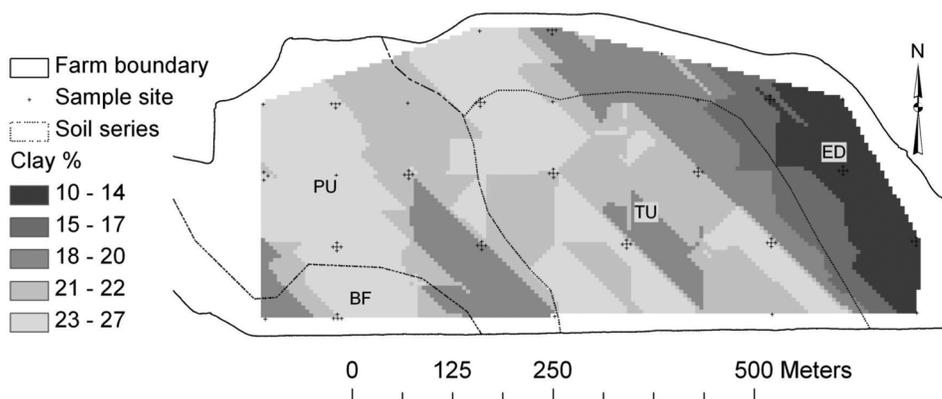


Fig. 2. Isoleth of clay content and soil series mapped by Natural Resources Conservation Service at Full Circle Farm, Carnation, WA in 2006. ED, Edgewick silt loam; TU, Tukwila muck; PU, Puget silty clay loam; BF, Belfast silt loam.

for 10 min. The soil remaining on each sieve was placed on preweighed filter paper, weighed and then dried at 105°C overnight. The soils from each size fraction were then dispersed using sodium hydroxide (2 g L⁻¹) and sieved through the appropriate sieve (4.75, 2, 1, or 0.250 mm) to determine the sand fraction. For this study, we determined the proportion of aggregates (proportion aggregates > 0.25 mm; PROP AGG) as the net weight of aggregates (after subtracting the sand) summed over all the sieves divided by the weight of the whole soil sample.

Ammonium N was determined in 2 M KCl extracts of the soil using a salicylate-nitroprusside method (Gavlak et al., 1994) and nitrate N was determined by a Cd reduction method (Gavlak et al., 1994). Total N and C were determined using a combustion analyzer equipped with an infrared detector (LECO Instruments Model CNS 2000, LECO Instruments, St. Joseph, MI). Nitrogen mineralization potential was determined using a 70-d, unleached aerobic incubation in 3.8-L polyethylene bags with repeated subsampling over time (Gale et al., 2006). Bulk density was determined on intact cores collected with a hammer-driven core sampler (Grossman and Reinsch, 2002), and texture determined with the hydrometer method of Gee and Or (2002). Organic matter was not removed before determining soil texture, based on a preliminary analysis of selected samples with and without organic matter removal.

Farm-Scale Texture and Total Carbon Mapping

We used kriging to generate total C, sand, silt and clay maps for the sampled area and this was done with GSLIB software (Deutsch and Journel, 1997). Semivariograms were produced for six directions at 30-degree intervals using a 120-m lag distance with 60 m tolerance. We displayed the kriged clay and total C maps with ArcMap 9.2 (ESRI Inc., Redland, CA) (Fig. 2 and 3).

Descriptive Statistics and Correlation Matrix

The distribution of each individual variable was analyzed with boxplots to check for normal distribution and the presence of outliers (points extending beyond 1.5× interquartile range) using the software package R (R Development Core Team, 2010). Summary statistics were calculated with the SUMMARY command in R and we calculated a correlation matrix for all of the continuous variables using PROC CORR with SAS software (SAS Institute, 2002).

Regression Tree Analysis

Regression trees were used to examine associations and predictive capabilities among potential soil quality indices (substrate-induced respiration biomass [SIR-biomass], Log₁₀ collembolans 100 cm⁻³ [Log₁₀ COLL], Log₁₀ nematodes 100 cm⁻³ [Log₁₀ NEM], EI, SI, PROP AGG, and N-MIN POT) and edaphic properties and management systems in 2006. An advantage of regression trees compared to multiple linear regression models is that they can model variation using both categorical (e.g., soil texture class) and continuous variables (e.g., percentage of clay). With regression tree analysis there is no assumption that data conform to a particular distribution or that relationships are homogeneous throughout the data range (Breiman et al., 1984). For example, increasing clay content could produce a strong linear response in the number of nematodes at the low end of soil clay content, but have no effect on nematode density above a threshold. Regression trees also provide easy graphical interpretation of multidimensional data, provide for interactive exploration, and allow for models to be selected through cross-validation (De' Ath and Fabricius, 2000).

Trees were built with RPART in the R software package (Therneau and Atkinson, 2009; R Development Core Team, 2010). The procedure starts by splitting the entire population to produce two “daughter nodes” with maximum homogeneity of the chosen dependent variable, defined in this case as maximum reduction of the sums of squares around the node mean (a.k.a., “anova method”, Therneau and Atkinson, 1997). The population is split by ranking all observations based on the chosen dependent variable and then grouping to the left or right of the node depending on the value of the chosen dependent variable. Trees are grown by further splitting daughter nodes in a similar fashion, then pruned to a desired size.

Because each split produces more homogeneous groups than the unsplit group, the average relative error (1 - r²) tends to decrease with each split. If carried far enough the model will fit the data nearly perfectly, but will have little predictive value and will not perform well with new data (Torgo, 2003). The effectiveness of the model can be described with the cross-validation error as follows: 1. The whole data set is used to fit a model. 2. The data are split into groups (usually 10) and the first group is left out while a new model is formed from the remaining data. 3. The new model is then used to predict values for the remaining data and the error is calculated as the squared difference between observed and predicted. 4. The process is repeated with the remaining data sets to calculate an average cross-validated error and standard deviation. To prune the trees, we

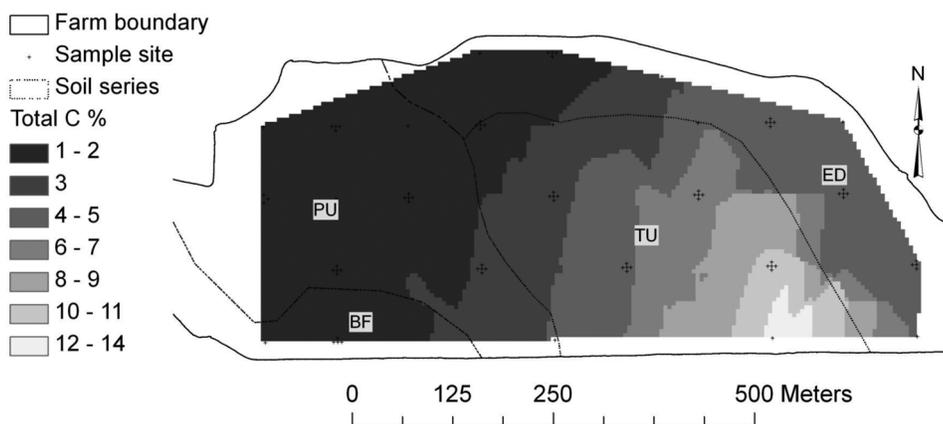


Fig. 3. Isopleth of total C content and soil series mapped by Natural Resources Conservation Service at Full Circle Farm, Carnation, WA in 2006. ED, Edgewick silt loam; TU, Tukwila muck; PU, Puget silty clay loam; BF, Belfast silt loam.

used the 1-standard deviation rule: choose the smallest tree whose cross-validated error is less than the minimum cross-validated error + 1 standard deviation (Maindonald and Braun, 2003). The shape of the tree does not change each time the model is computed. However, because the groups used for cross-validation are formed randomly, the cross-validated error does change. Because this can affect size of the pruned tree based on the 1 – standard deviation rule, we performed several cross-validation runs for each model, as recommended by Maindonald and Braun (2003).

For the regression tree models for biological communities (SIR-biomass, Log_{10} COLL and Log_{10} NEM) and indices derived from nematode community data (EI and SI) we used the following predictive variables: total C, total N, NO_3 –10 cm, NO_3 –30 cm, NH_4 –10 cm, NO_3 + NH_4 –10 cm, pH, percentage of sand, percentage of silt, percentage of clay, texture class, soil series, D_b , proportion of soil as aggregates > 0.25 mm (PROP AGG), nitrate mineralization potential (N MIN POT), and management system (time since tillage). To emphasize the contribution of physical and chemical parameters on biological communities we did not include nematode indices (EI, SI, MI, CI), nematode abundance, collembolan abundance, or SIR-biomass in these regression tree analyses. For modeling the influences on the physical and biological soil processes represented by the indicators PROP AGG and N MIN POT, we included the biological community parameters along with the aforementioned physical, chemical, and management parameters.

RESULTS

Farm-Scale Variation and Association of Edaphic Properties

There was a strong texture gradient across the sample area and the eastern part of the farm had less clay than the western

part (Fig. 2). Estimation of clay content across the farm with kriging predicted clay content <15% in the eastern quarter of the farm and a braided pattern of areas of clay >20% and areas of clay between 18 and 20% clay in the western part of the mapped area (Fig. 2). The clay mean and median were 19.6 and 21.0, respectively, with an interquartile range of 6.

A Total C gradient was also apparent, with the lowest Total C in the western part of the farm, intermediate C in the eastern part, and the highest in the meadow area in the southeastern part of the farm (Fig. 3). Although the areas with the higher C are mapped as Tukwila muck, little, if any of this area contains enough C to be a true muck. Clay and C maps are provided to demonstrate gradients across the farm and not for quantitative purposes, thus geostatistical parameters are not presented.

The mean, standard deviation, median, and interquartile range for all of the parameters measured in 2006 are shown in Table 1. Inspection of boxplots (data not shown) indicated strong lognormal distribution of nematode and collembolan densities, so these parameters were log transformed for further analyses.

Strong positive correlations were apparent among Total C, Total N, N MIN POT, SIR-biomass, and PLFA biomass (Table 2). Total C was less strongly correlated with B/F ($R = 0.34$), SI ($R = 0.25$), and MI ($R = 0.36$), and was negatively correlated with EI (-0.25), PROP AGG (proportion of aggregates > 0.25 mm, $R = -0.45$), D_b ($R = -0.79$), and pH ($R = -0.36$). Soil parameters that were significantly (although often weakly) correlated with sand content included PROP AGG ($R = -0.70$), Total C ($R = 0.28$), SIR-biomass ($R = 0.25$), \log_{10} nematodes ($R = 0.34$), \log_{10} collembolans ($R = -0.27$), CI ($R = 0.39$), and MI ($R = 0.30$).

Table 1. Statistical summary of soil parameters for a farm-scale survey from Full Circle Farm, Carnation, WA in 2006.

Variable	Description	Mean	SD†	Median	IQR‡
Total C	Total carbon (%)	4.3	2.7	3.3	2.7
Total N	Total nitrogen (%)	0.36	0.17	0.3	0.19
NO_3 –10 cm	NO_3 (mg kg^{-1}) 0–10 cm	46.5	33.7	37.8	28.8
NO_3 –30 cm	NO_3 (mg kg^{-1}) 0–30 cm	17.8	14.9	13.3	19.3
N MIN POT	N- mineralized (mg kg^{-1} d^{-1})	0.57	0.3	0.5	0.3
pH	pH	5.7	0.4	5.7	0.4
Sand	Sand (%)	19.6	15.6	12.0	12.0
Silt	Silt (%)	60.8	11.7	66.0	11.0
Clay	Clay (%)	19.6	4.6	21.0	6.0
D_b	Bulk density	0.96	0.13	1.0	0.14
PROP AGG	Proportion aggregates > 0.25mm	0.86	0.10	0.9	0.07
SIR-biomass	Substrate-induced respiration biomass ($\mu\text{g C}_{\text{mic}} \text{g}^{-1}$)	522.6	398.6	390.0	195.0
PLFA-biomass	Phospholipid fatty acid biomass ($\mu\text{g C}_{\text{mic}} \text{g}^{-1}$)	199.1	135.3	156.2	133.9
B/F	Ratio of bacterial to fungal biomass	2.2	0.7	2.1	0.8
Nematodes	Total nematodes 100 cm^{-3}	913.8	832.1	567.0	942.0
Log_{10} NEM	Log_{10} nematodes 100 cm^{-3}	2.8	0.4	2.8	0.6
Collembola	Total collembolans 100 cm^{-3}	41.3	43.3	22.0	58.0
Log_{10} COLL	Log_{10} collembolans 100 cm^{-3}	1.4	0.5	1.3	0.8
Parasitic NEM	Parasitic nematodes 100 cm^{-3}	50.2	206.6	0.0	15.8
EI	Nematode enrichment index	74.3	15.2	75.5	22.2
SI	Nematode structure index	40.3	25.1	42.2	47.4
CI	Nematode channel index	17.8	19.4	11.5	24.05
MI	Nematode maturity index	1.8	0.4	1.8	0.5

†SD, standard deviation.

‡IQR, interquartile range.

Table 2. Coefficients of correlations between management and edaphic properties for Full Circle Farm, Carnation, WA in 2006.

	Tillage	Total C -10 cm	Total N -10 cm	NO ₃ 10 cm	NO ₃ 30 cm	N MIN POT	pH	Sand	Silt	Clay	D _B	PROP AGG
Tillage†	1.00											
Total C	0.52**	1.00										
Total N	0.54**	0.99**	1.00									
NO ₃ 10 cm	-0.21	0.17	0.16	1.00								
NO ₃ 30 cm	-0.27*	-0.01	0.00	0.69**	1.00							
N MIN POT	0.58**	0.79**	0.79**	0.09	-0.22	1.00						
pH	-0.02	-0.36**	-0.35**	-0.64**	-0.51**	-0.40**	1.00					
Sand	0.37**	0.28*	0.36**	-0.09	0.05	0.19	0.02	1.00				
Silt	-0.41**	-0.31**	-0.38**	0.08	-0.05	-0.19	-0.02	-0.98**	1.00			
Clay	-0.21	-0.19	-0.26*	0.09	-0.05	-0.18	0.01	-0.89**	0.79**	1.00		
D _B	-0.32**	-0.79**	-0.77**	-0.32**	-0.07	-0.65**	0.47**	0.06	-0.04	-0.05	1.00	
PROP AGG	-0.16	-0.45**	-0.48**	0.16	-0.03	-0.24*	-0.06	-0.70**	0.70**	0.61**	0.11	1.00
SIR-biomass	0.81**	0.77**	0.77**	-0.10	-0.31**	0.74**	-0.06	0.25*	-0.29**	-0.13	-0.53**	-0.21
PLFA-biomass	0.66**	0.85**	0.85**	-0.02	-0.25*	0.77**	-0.21	0.17	-0.20	-0.08	-0.71**	-0.20
B/F	0.03	0.34**	0.34**	0.39**	0.21	0.20	-0.36**	0.14	-0.13	-0.14	-0.39**	-0.08
Log ₁₀ NEM	0.18	-0.11	-0.07	-0.41**	-0.11	-0.15	0.47**	0.33**	-0.34**	-0.23*	0.36**	-0.33**
Log ₁₀ COLL	0.04	-0.03	-0.05	-0.03	-0.27*	0.09	0.15	-0.27*	0.29**	0.19	0.04	0.29**
Parasitic NEM	0.51**	0.31**	0.32**	-0.13	-0.16	0.38**	-0.05	0.10	-0.17	0.07	-0.21	-0.06
EI	-0.21	-0.25*	-0.22*	-0.13	0.06	-0.39**	0.37**	0.22	-0.26*	-0.06	0.34**	-0.16
SI	0.26*	0.25*	0.24*	0.23*	-0.13	0.42**	-0.40**	-0.09	0.06	0.13	-0.35**	0.25*
CI	-0.12	-0.09	-0.13	0.11	-0.02	-0.01	-0.12	-0.34**	0.39**	0.13	-0.14	0.22
MI	0.25*	0.36**	0.34**	0.30**	-0.08	0.57**	-0.58**	-0.29**	0.30**	0.21	-0.48**	0.29**
	SIR- biomass	PLFA- biomass	B/F	Log₁₀ NEM	Log₁₀ COLL	Parasitic NEM	EI	SI	CI	MI		
SIR-biomass	1.00											
PLFA-biomass	0.83**	1.00										
B/F	0.12	0.36	1.00									
Log ₁₀ NEM	0.08	-0.03	-0.13	1.00								
Log ₁₀ COLL	0.23*	0.04	-0.15	0.02	1.00							
Parasitic NEM	0.39**	0.47**	-0.02	0.24*	-0.06	1.00						
EI	-0.17	-0.24*	0.08	0.4**	-0.09	-0.06	1.00					
SI	0.34**	0.33**	0.29*	-0.22	0.15	0.26*	0.11	1.00				
CI	-0.17	-0.03	-0.14	-0.33**	0.00	-0.01	-0.72**	-0.28*	1.00			
MI	0.32**	0.38**	0.08	-0.53**	0.09	0.27*	-0.77**	0.44**	0.45**	1.00		

* Significant at $p < 0.05$.

** Significant at $p < 0.01$.

†Tillage, weeks since last tillage.

Nematode density was positively correlated with pH ($R = 0.47$) and sand ($R = 0.33$) indicating that nematode populations were greater in sandier, less acid areas of the farm. The total nematode count was negatively correlated with surface NO₃ ($R = -0.41$), but SI and MI were positively correlated with surface NO₃ ($R = 0.24, 0.34$). Fungal-feeding nematodes were more dominant in the silt-rich soils than sandy soils as evidenced by the correlation of CI with silt ($R = 0.39$) and sand ($R = -0.34$). Greater collembolan populations were also associated with silt-rich areas of the farm ($R = 0.29$).

Regression Tree Analysis of Soil Communities

The regression tree analysis for SIR-biomass across the whole farm showed that the 11 meadow sites (high-carbon soils that were untilled for more than 5 yr) formed a relatively cohesive group. Location in the meadow areas explained 74% of the variance in this parameter (Fig. 4a). We built a second tree,

without the meadow areas, and this model explained 60% of the variance of the remaining 70 sites (Fig. 4b). Areas with Total C > 5.7% had the greatest biomass, and in those areas with less C, no tillage for at least 16.5 wk promoted microbial biomass.

Time since tillage explained most of the variation in total nematodes; areas that had been tilled < 2 wk before sampling formed a cohesive group with the lowest nematode populations (Fig. 5a). Where tillage had not occurred recently, soils with pH above 6.11 had greater nematode populations. In the more acid soils (pH < 6.11) NO₃ content > 33.1 mg kg⁻¹ in the top 30 cm was associated with greater nematode populations. The combination of time since tillage, pH, and NO₃ explained 61% of the nematode population variance (Fig. 5a). The more structured nematode communities were associated with soils with greater aggregation (Fig. 5b). In the soils with a proportion of aggregates < 0.93, nematode communities with greater structure were associated with soils with N MIN POT > 0.69 mg N mineralized kg⁻¹ d⁻¹. This model explained 41% of

the variance in SI (Fig. 5b). The regression tree for EI (Fig. 5c) indicated that opportunistic microbivorous nematodes were associated with soils with N MIN POT < 0.62 mg N mineralized kg⁻¹ d⁻¹ and < 65.5% silt. In soils with lower N MIN POT and greater silt concentrations more opportunistic microbivorous nematodes were associated with NH₄ > 2.8 mg kg⁻¹ in the top 10 cm of soil (Fig. 5c). The model explained 54% of the variance in EI.

For collembolans, both the sandiest soil type (sandy loam) and the most clay-rich soil type (silty clay loam) in the study area were associated with the lowest populations. Within the other two soil types, loam and silt loam, soils from more recently tilled areas (<5 wk) had smaller collembolan populations. The regression tree model with these two parameters explained 36% of the variation in collembolans (Fig. 6). Only 20% of the cross-validation runs for this model suggested that a tree with two or three splits be built while the other runs suggested pruning the tree back to zero splits (i.e., not building a tree).

Regression Tree Analysis of Soil Processes

The variance in N mineralization potential was largely explained by microbial biomass; the greatest mineralization rates were associated with biomass >597 μg C_{mic} g⁻¹ (Fig. 7). Soil pH explained some of the variance in soils with microbial biomass < 597 μg C_{mic} g⁻¹, with pH values < 5.12 being associated with greater mineralization rates. The variation of a large portion of the population (n = 58) with microbial biomass < 597 μg C_{mic} g⁻¹ and pH ≥ 5.12 remained unexplained.

The regression tree model explained 58% of the variance, while soil C alone explained 62% of the variance (100× the square of the correlation, 0.79, between soil C and mineralization, Table 2). The output from RPART ranks the best five parameters for splitting the group at each node (data not shown). For the first node in the N MIN POT tree, SIR-Biomass provided only a slightly better split than the next best parameter, soil C (i.e., splitting with SIR-biomass at 597 μg C_{mic} g⁻¹ improved the homogeneity of the group by 0.45 and splitting with total C at 7.87% improved homogeneity by 0.43).

In a regression tree built for PROP AGG soil texture properties explained most of the variation in this parameter (r² =

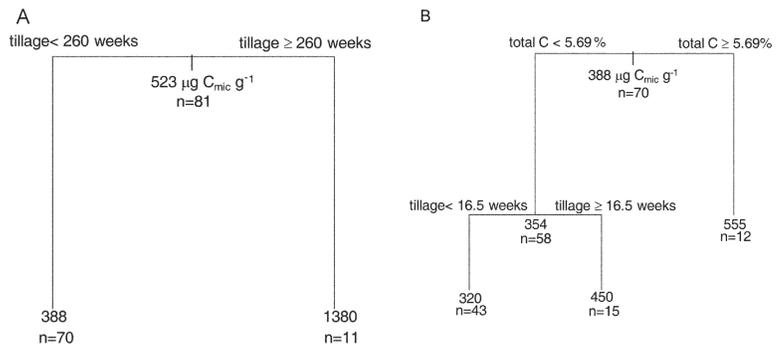


Fig. 4. Regression trees for substrate-induced respiration biomass, (a) SIR-biomass (μg C_{mic} g⁻¹ soil) using all 81 samples (r² = 0.74), (b) SIR-biomass using the 70 sites in cultivation (r² = 0.60) for soils from Full Circle Farm, Carnation WA in 2007. Tillage equals weeks since tillage.

0.60, Fig. 8). Soils with >13.5% clay (69 sites) had the greatest proportion of soil as aggregates > 0.25 mm.

DISCUSSION

Both surface geological processes and historical management have affected soil properties at Full Circle Farm. Yearly floods from the Snoqualmie River inundate 50% or more of the farm and have contributed to the present soil texture pattern. The eastern portion of the farm has higher elevation, has been less enriched with clay and silt deposited from flooding, typically remains dry throughout the year, and can be farmed earlier in the spring than the rest of the farm. Full Circle Farm was once a small dairy with the original barn at the eastern edge of the farm surrounded by manured, C-enriched soil. Manure was also spread in areas of higher elevation that were not flooded and were workable earlier in the spring. The result is a positive correlation between C and the percentage of sand and also a negative correlation with clay (Table 2). These results are counter to the more common trend of increasing C with increasing clay content (Burke et al., 1989; Buschiazzo et al., 2004; Schimel et al., 1994; Franzluebbers et al., 1996). Others have found exceptions to this latter trend, indicating that site-specific characteristics or management can overshadow the more generally observed trend of increasing organic matter persistence being associated with increasing clay content (Silver et al., 2000; Springob et al., 2001).

Total C was greatest in the meadow area (not annually cropped) that is mapped as Tukwila muck (Fig. 1 and 3). In addition to increased soil C, SIR-biomass was relatively high in these

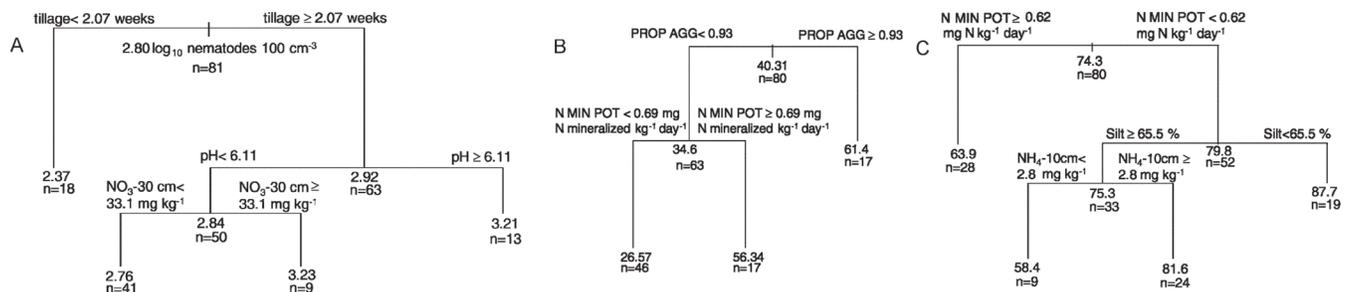


Fig. 5. Regression trees for total nematodes, nematode structure index, and nematode enrichment index (a) total nematodes (log₁₀ nematodes 100 cm⁻³) (r² = 0.61), (b) structure index (r² = 0.41), (c) enrichment index (r² = 0.54). PROP AGG, proportion of soil as aggregates > 0.25 mm; tillage = weeks since tillage; N MIN POT, N-mineralization potential (mg N kg⁻¹ soil d⁻¹).

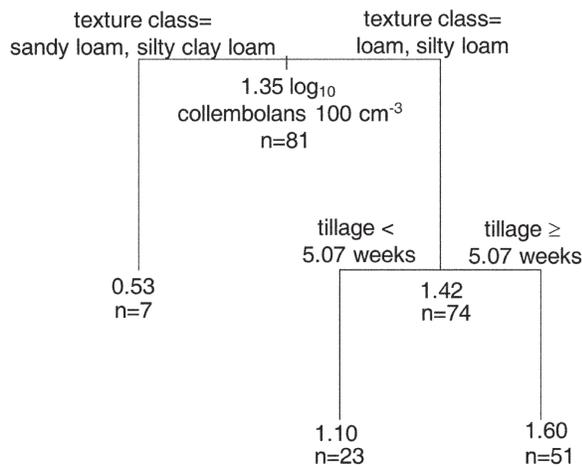


Fig. 6. Regression tree for collembolans (\log_{10} collembolans 100cm^{-3}) ($r^2 = 0.46$) for soils from Full Circle Farm, Carnation, WA in 2007. Tillage equals weeks since tillage.

areas (Fig. 4a). While lack of tillage is often associated with an increase in fungal biomass (Hedlund et al., 2004; Beare, 1997), no such trend appears to be present in these data. The mean B/F ratio for the meadow areas was identical to the overall mean. A regression tree built for B/F indicated that areas with high soil C ($>5.8\%$) had the largest bacterial biomass, and about half of the meadow sites were in this group (data not shown). Removing meadow sites from the analysis of SIR-biomass indicated that a model with soil C and weeks since tillage explained a significant amount of variation in the remaining group (Fig. 4b). While it is not surprising that the greatest microbial biomass was found in areas with greater soil C, it is interesting that the less recently tilled areas had increased biomass. Tillage can cause blooms in microbial biomass related to the incorporation of crop residues, that can last for two to 3 mo (Franzluebbers et al., 1995). In this farm survey, lack of recent tillage (<16.5 wk) explained the high microbial biomass in soils with moderate amounts of total C. Comparisons of microbial biomass across farms should be sensitive to the association of this parameter with both soil C and recent tillage.

The total nematode population was sensitive to recent tillage, and sites that had been tilled < 2 wk before sampling were associated with the lowest nematode populations. Tilling in

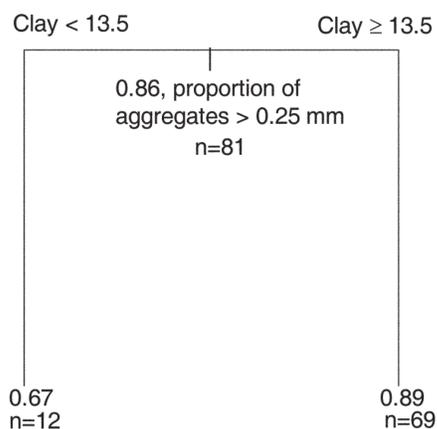


Fig. 8. Regression tree for proportion of aggregates > 0.25 mm (PROP AGG) ($r^2 = 0.60$) for soils from Full Circle Farm, Carnation, WA.

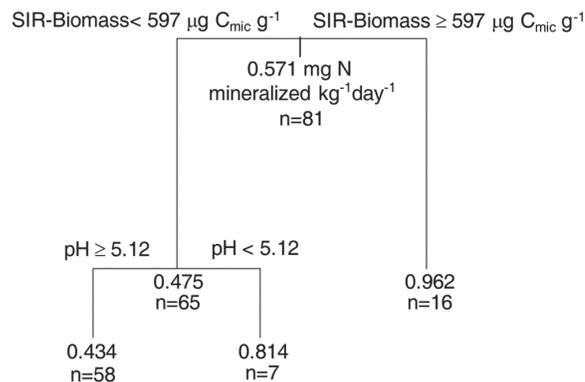


Fig. 7. Regression tree for N-mineralization potential ($\text{mg N kg}^{-1} \text{soil d}^{-1}$) ($r^2 = 0.58$) for soils from Full Circle Farm, Carnation, WA in 2007. SIR-Biomass, substrate-induced respiration biomass ($\mu\text{g C}_{\text{mic}} \text{g}^{-1}$).

crop residues can lead to blooms in microbial biomass followed by blooms in microbial-feeding nematodes. The sampling in this study followed fall tillage. The grower did not till in a cover crop, and this may explain why no bloom in nematode populations was observed.

The variation in the nematode SI and EI was explained by different soil parameters. Soils with the largest proportion of aggregates were associated with the most highly structured nematode communities (Fig. 5b). Variation in EI was explained more by N MIN POT than any other parameter, with soils with less N MIN POT associated with larger EI (Fig. 5c). The larger EI in sandier soils (less silt) could be associated with historic organic matter addition. Within the more silty soils, greater NH_4 was associated with larger EI. Opportunistic, bacterial-feeding nematodes are often associated with application of manures and fertilizers so their association with larger NH_4 concentration is expected (Ferris et al., 2001).

Collembolan populations were lowest in the sandiest and most clay rich soils. The important influence of tillage on collembolan population density in the other two soil types is not surprising as their sensitivity to tillage has been previously demonstrated (Collins, 2008b; Hedlund et al., 2004).

There was a large amount of variation in collembolan populations and in the nematode indices that was not explained by the parameters measured. Sources for this unexplained variability could include site-specific management that we were not able to accurately record and include in the model. Being a working farm, the soils are subjected to disturbance from harvesting and weeding. Aboveground biomass (weed and crop density) was also variable and was not recorded. Other edaphic properties such as compaction and soil mineralogy were not recorded and could also influence collembolan and nematode populations.

Reliability of Bio-Indicators to Predict Soil Processes

Likely because the microbial community mineralizes nutrients from organic matter, N MIN POT was highly correlated with microbial biomass and soil C (Table 2). Regression tree analysis showed that greatest reduction in variance for all N MIN POT data was achieved by grouping locations with the largest microbial biomass

(Fig. 7). Most of these sites were in the C-rich, undisturbed meadow areas (Fig. 1). The N-mineralization procedure requires soil sampling and sieving, which likely exposed organic matter from these C-rich soils and yielded high mineralization rates (Hassink, 1992). Though pH explained some of the variability in the remaining data, the tree shown here was pruned via the 1-standard deviation rule and yielded a terminal node with 58 observations, indicating that a more complex tree built with the available parameters would have little predictive value (Therneau and Atkinson, 1997).

The EI is sensitive to opportunistic, bacterial-feeding nematodes and increases when these nematodes become more prevalent. Because of the cycling activity of these opportunistic nematodes, we expected to see strong positive correlation between nematode EI and N MIN POT, but this was not the case. Instead, these parameters were negatively correlated (Table 2) and N MIN POT explained most of the variability in EI, with lower EI being associated with higher N MIN POT. The dynamic nature of nematode communities may compromise their reliability to predict N MIN POT. Though cumulative N mineralization has been correlated with EI in microplots (Ferris and Matute, 2003) population densities of enrichment opportunist nematodes can change rapidly over the time-frame of days to weeks, and population densities at a single point in time may have not been an accurate representation of their overall contribution to N mineralization.

The formation of aggregates is influenced by soil fauna, microorganisms, roots, inorganic compounds, and physical processes (Six et al., 2004). We found that PROP AGG was best predicted by soil texture, not biological indices; positive correlation was observed between PROP AGG and silt and clay content (Table 2) and locations with <13.5% clay formed a cohesive grouping with the smallest PROP AGG in regression tree analysis (Fig. 8). Others have also demonstrated the importance of clay content in forming and maintaining aggregates. Kemper et al. (1987) found a positive correlation between aggregate formation and increasing clay content in soils that were previously dispersed, while Gollany et al. (1991) demonstrated that clay content was important in maintaining aggregate stability, especially as soil moisture increased at the time of sampling.

Though biological indices were not the best predictors of PROP AGG, regression tree analysis of the nematode structure index indicated that areas with PROP AGG > 0.93 were associated with the greatest nematode SI (Fig. 5b). PROP AGG was strongly associated with soil texture (Fig. 8) and this soil physical property may also be affecting farm management and in turn SI. For example, the eastern, sandier area of the farm is more intensively farmed and has received more historical manure application and cultivation than the more clay-rich areas to the west. Both of these forms of agricultural intensification can negatively affect nematode taxa that are indicators of community structure. These nematodes are omnivores and predators that have larger body sizes and longer life cycles than the bacterivore and fungivore nematodes that are favored by physical disturbance and nutrient enrichment.

CONCLUSIONS

Nitrogen-mineralization potential and aggregate stability are two important agronomic functions that both affect and are affected by soil communities. Biologically based indicators have the potential to reflect changes in these functions, but across the range of edaphic conditions common at a typical farm, other chemical and physical properties may have a disproportionately strong influence. Our site-specific sampling method coupled with regression tree analysis identified that microbial biomass and clay content were the factors most likely to predict N MIN POT and PROP AGG, respectively, across a farm with diverse edaphic properties. However, microbial biomass was strongly influenced by recent tillage.

These results illustrate the importance of noting variation in physical and chemical parameters across an area when characterizing the biology. Mapping inherent soil quality parameters and management differences should be the first step in monitoring soil biological populations. Comparisons of soil quality indicators across farms should also be sensitive to soil texture, and past and recent management practices.

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