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Original Research

The Effect of Tillage System on Soil Microbiota in Relation to Soil Structure

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Abstract

Adoption of sustainable tillage can protect soils from biological degradation and maintain soil quality, as compared with conventional management. This paper presents findings from a long-term tillage experiment carried out in *Endocalcari-Endohypogleyic Cambisols* on a sandy loam soil in Lithuania. The tillage systems were: conventional (CT), moderate (MT), and no tillage (NT). Tillage intensity positively affected microbial substrate utilization and urease activity, as well as, negatively, dehydrogenase activity, bacteria and fungi amounts, and Shannon diversity index of microbiological community. Higher total porosity provoked higher enzyme activity; but, microbial activity correlated negatively with bulk density.

Keywords: tillage, soil structure, biological properties

Introduction

Soil quality (SQ) highly depends on its structure, natural productivity, and human influence. Tillage is one of the major management practices affecting soil physical parameters. Despite economical and environmental benefits from low-intensity tillage systems, its adoption is still low in Lithuania. The reason for this is that reduced tillage and, especially, no tillage (NT) often results in lower crop yields than the conventional tillage (CT) system [1, 2]. This often is caused by soil compaction, residue management, germination problems, and weed and pest incidence [1, 3]. Nevertheless, long-term NT application increases organic carbon content, positively effecting not only soil structure, but also microbiota activity [4]. The role of soil organisms is central to soil processes. The influence of tillage systems on the total soil organic matter (OM) content is detectable only after several years of its application. Microbial activity may respond to disturbances on a shorter period of time than those based on physical or chemical properties. As a consequence, microbiological properties such as soil enzyme activities have been suggested as potential indicators of SQ [5] because of their rapid response to changes in soil management [6]. The effect of tillage on soil microbial populations have generally been studied by comparing microbial numbers, the soil microbial community [7-9], enzyme activity (in particular dehydrogenase as a general measure of microbial activity), and microbial biomass [10]. In many cases, both bacteria and fungi were more abundant under no-tillage than conventional tillage [7, 11]. The main objective of this study was to explore the effect of tillage intensity on soil physical conditions in the arable layer and to determine its effect on soil biological activity.

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Materials and Methods

The experiment was established in autumn 2003 on a sandy loam, *Endocalcari-Epihypogleyic Cambisol*, in Dotnuva, Lithuania (55º23'50''N and 23º51'40''E). The experiment was a standard design of four replications. Tillage treatments: conventional – mouldboard ploughing 20-22 cm depth (CT), moderate – stubble cultivation to 10-12 cm depth (MT), and no tillage – direct drilling using disc

Table 1. Tillage effect on soil physical parameters, Dotnuva 2010.

Tillage systems	Bulk density $mg \cdot m^{-3}$		Water stable aggregates > 0.25 mm		Total porosity $m^3 \cdot m^{-3}$		Field capacity $m^3 \cdot m^{-3}$	
	5-10 cm	15-20 cm	0-10 cm	10-20 cm	5-10 cm	15-20 cm	10-15 cm	15-20 cm
Conventional tillage	ns	1.62*	ns	ns	ns	0.39*	ns	ns
Moderate tillage	ns	1.55	ns	ns	ns	0.41	ns	ns
No tillage	ns	1.53	ns	ns	ns	0.42	ns	ns

*significant at $p < 0.05$ (LSD test); ns – not significant

drill with seed bed preparation (NT). For CT and MT a traditional seed drill was used. The gross area of each plot was 10 × 20 m. Crop rotation was: winter wheat, spring wheat, spring wheat, pea, pea, winter wheat, and pea. Pea (*Pisum sativum*) variety 'Pinochio' was sown on 12 May 2010, 280 $kg \cdot ha^{-1}$.

Soil samples were collected in June 2010 at the beginning of the growing season for peas, when soil moisture was near field capacity (FC). Stainless steel cylinders (of 100 cm^2) were used to take undisturbed soil samples to determine FC, soil bulk density (BD), and total porosity (TP). Two soil cores were taken from each plot per two depth increments of 5-10 and 15-20 cm. We also collected disturbed soil samples from each plot at 0-10 and 10-20 cm depth to determine water stable soil aggregates (WSA) by Savinov method [12]. To determinate FC, undisturbed soil cores were adjusted to 100 hPa matric potential using tension tables at 20ºC. After the adjustment, soil cores were oven-dried at 105ºC for 24 h. Samples were weighed at field moisture, at 100 hPa matric potential, and after oven-drying.

Soil samples for microbial analysis were collected from each plot under peas 29 June, 2010 at 0-10 cm and 10-20 cm soil depth. Samples were pooled, sieved (<2 mm), and analyzed. Conventional dilution spread-plating was performed to assess the culturable bacterial and fungal colony forming units (CFU) on Soy Tryptic agar (TSA/10 agar, Biochemika) and malt extract agar (Liofilchem Diagnostici), respectively. The plates were incubated at 25ºC and bacterial and fungal counts were made after 4 and 7 days, respectively. Final counts were expressed as the number of CFU per 1 g of dry soil. Enzyme activities were assayed according to the procedure as described by Schinner et al. [13]. For the estimation of dehydrogenase activity a Perkin Elmer UV/VIS spectrometer with the wavelength of 485 nm, and 3% TTC (triphenyl-tetrazolium chloride) used as a substrate were applied to measure the activity of the studied enzyme. The urease activity was established using urea as the substrate, incubating the soil sample for 2 h at 37ºC and measuring the NH_3^+ released colorimetrically at 690 nm. To study the bacterial community composition we used Biolog EcoPlates (Biolog Inc., Hayward, CA, USA). The average well colour development (AWCD) in each Biolog plate was determined and was used to evaluate microbial functional diversity, the Shannon diversity index (H').

Data are reported as mean ± standard error of the mean and were examined using analysis of variance (ANOVA) procedures. Significant differences among treatment means were assessed by Fisher's least significant difference test (LSD, $P < 0.05$) and using an *F*-test. Statistical computations were performed using the statistical software package STATGRAPHICS PLUS 6.0 software.

Results and Discussions

Reduced tillage and especially direct drilling changes numerous soil properties compared to plowed soil, but often it has no deleterious effect on soil physical properties [14]. Bulk density (BD) is usually lower in conventional tillage (CT) than in no tillage (NT) for several weeks after drilling, but then it might not differ or even be higher compared to NT. Also, our experiment showed that BD of arable layer was critical under CT (Table 1). This might be influenced by a long last heavy rain before soil sampling (precipitation was 94.2 mm during May, while the perrenial mean was 52.3 mm); therefore, soil was compacted in all tillage treatments and especially in CT. The difference in BD was not statistically significant at the upper soil layer (5-10 cm depth) and BD was significantly higher under CT at the 15-20 cm depth compared to moderate tillage (MT) and NT. This also caused significantly lower total porosity (TP) under CT at the 15-20 cm depth. Different tillage practices did not have a significant influence on field capacity (FC). NT tended to increase the amount of water-stable aggregates (WSA) compared to CT and MT tillage systems. The increasing of WSA by reducing tillage intensity has also been found by other researchers [15]. It is known that WSA is an indicator of organic matter (OM) content, biological activity, and nutrient cycling in soil.

Tillage systems affect the soil physical and chemical environment in which soil organisms live, thereby affecting soil organisms in different ways [16]. Numerous studies in temperate regions have shown that decreasing tillage intensity results in higher organic C and N and improved soil quality (SQ) [17]. Conservation tillage practices (reduced or no-tillage) result in increasing enzyme activities [18], microbial biomass [19], and fungal and bacteria dominance under NT [7, 11]. However, our results demonstrate that overall amounts of bacteria and fungi decreased in NT system by 25.5 and 22.7%, respectively (Fig. 1). It can be con-

cluded that the CT system provides stimulating effects for microbial growth due to uniformly distributed residues in the arable layer [20] and increases the rate of supplied oxygen to soil microsites.

Though is indicated that NT increased soil microbial activity in the surface 5-7.5 cm, these differences in activity between high and low-intensity tillage treatments are commonly reversed at the 10-20 cm depth and those reports confirm our results. In our study we found decreasing bacteria and fungi by 3.49% and 11.83% at 10-20 cm to compare with that at 0-10 cm, respectively, also decreasing enzyme activity. However, in NT system the amount of bacteria dropped to about half at 10-20 cm. It is clearly evidence that in the upper soil layer in NT systems, which is relying within an environment where more OM exists and nutrients are readily available for microbial populations [21], is more intensive biological activity than at 10-20 cm. Hence, use of NT helped to improve SQ in this experiment only in the upper layer.

Biotic SQ factors in soil surface may be inversely related to tillage intensity [21]. We found increasing WSA in the NT system with a decreasing amount of fungi. Accordingly, in this study only a few significant correlations were found between soil properties and microbial activity (Table 2). Despite a negative effect of BD or less TP, compaction of soil from the tillage system had no consistent effects on microorganism amounts in CT and MT at 0-10 cm. At the 10-20 cm depth of soil in MT and NT, where lower BD was determined, the amount of bacteria and fungi were lower than in CT. More significant correlations were found in the deeper layer of the soil. On the other hand, CT often destroys soil structure, allowing for faster mineralization of soil OM [22], while NT can improve soil aggregation by the proliferation of fungal hyphae that contribute to macroaggregate formation [23]. The greatest enhancement of soil bacterial counts may occur due to the breaking up of aggregates by tillage, which leaves OM unprotected [24]. However, rarely are there studies that demonstrate the higher microbial activity in CT than NT [11]. WSA correlated with any microbial properties.

Soils managed through reduced tillage generally have more surface plant residues, higher moisture content, and better structure and aggregation compared to soils managed under CT, and it impacts the higher activity of enzymes.

Several studies indicated that NT increases the activity of several enzymes [25, 26]. In our soils, increases in various soil enzyme activities also have been associated with decreases in tillage intensities (Fig. 1). Enzyme activity decreased with soil depth, especially for dehydrogenase activity by 26.7% and urease by 5.13%, respectively. According to Roldan et al. [27], dehydrogenase activity decreased particularly with intensive tillage. This finding is concomitant with strong correlation among the enzyme and soil BD (r=0.67*), being hydrolytic activity the most sensitive to tillage system at 0-10 cm soil depth. The results are in agreement with enzymatic activities playing an integrative role between physical and microbial soil properties.

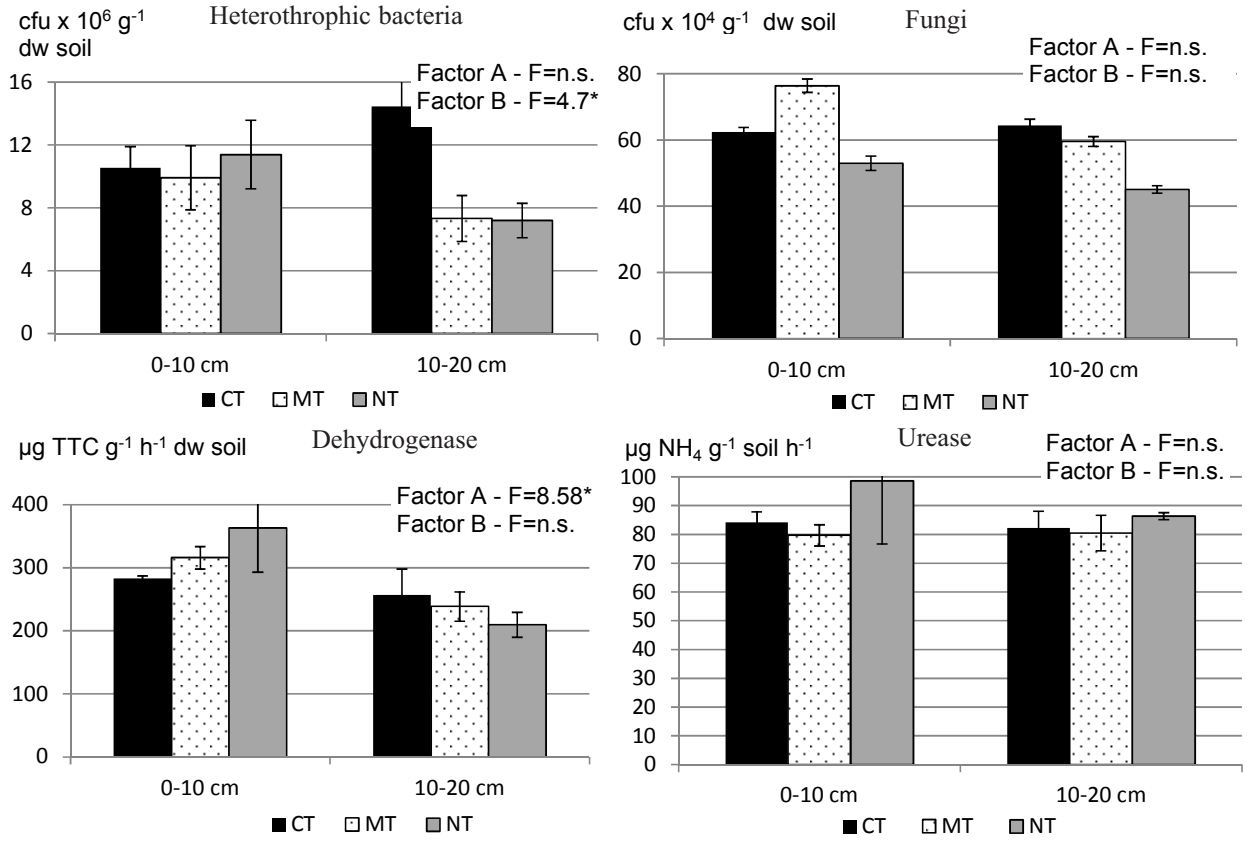

Fig. 1. The amount of soil microorganisms and enzyme activity affected by different tillage systems in columns representing means ± standard error (n=3). Factor A – tillage systems, factor B – soil depth.

Table 2. Pearson correlation analysis between biological, agrochemical, and physical properties of soil (Dotnuva, 2010).

Variable	Urease (μg ammonium·g^{-1} of soil for 1 h)		Dehydrogenase (μg triphenyl formazan·g^{-1} of soil for 24 h)		Bacteria (10^6 × CFU·g^{-1} soil)		Fungi (10^4 × CFU·g^{-1} soil)	
	0-10 cm	10-20 cm	0-10 cm	10-20 cm	0-10 cm	10-20 cm	0-10 cm	10-20 cm
Bulk density	n.s.	n.s.	0.67 (0.049)	0.63 (0.071)	n.s.	0.88 (0.003)	n.s.	0.72 (0.030)
Total porocity	n.s.	n.s.	-0.67 (0.049)	-0.63 (0.071)	n.s.	-0.93 (0.003)	n.s.	-0.72 (0.030)
Field capacity	n.s.	n.s.	0.64 (0.065)	n.s.	n.s.	n.s.	n.s.	n.s.
N-NO_3	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.
N-NH_4	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.
Ca	n.s.	n.s.	n.s.	0.64 (0.064)	n.s.	0.78 (0.014)	n.s.	n.s.
P_2O_5	n.s.	n.s.	n.s.	n.s.	n.s.	0.71 (0.031)	n.s.	n.s.
K	n.s.	n.s.	n.s.	0.64 (0.062)	-0.64 (0.063)	0.79 (0.011)	n.s.	n.s.
Water stable aggregates	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.

In parenthesis are highly significant with $p < 0.05$; ns – not significant

The influence of tillage on urease activity was less pronounced with depth.

The functional diversity as community level physiological profiles (CLPP) of the microbial communities was assessed using such indices as average well color development (AWCD) and the Shannon (H') diversity index of microbial communities, determined in soil samples from the 0-10 cm soil layer. A result reveals different physiological profiles in the microbial communities under tillage systems (Fig. 2). The Shannon diversity and AWCD were higher with CT than with NT, 2.67 and 2.76 for H'; and 0.1248 and 0.116 for AWCD, respectively. The same results were found by Govaerts et al. [7], showing a significantly higher overall AWCD value under CT. Higher availability of hydrocarbon sources in CT soil promote an increase of the microbial community's diversity. The higher microbial diversity also contributes to explaining the increased use of carbon sources used in Biolog with conventional tillage than with no-till. It also illustrated the large differences of microbial community at physiological level to soil of contrasting management practices by Chaer et al. [7, 28]. Other research showed significantly reducing the diversity of bacteria under CT [29].

Conclusions

1. Conventional tillage caused higher bulk density and lower total porosity compared to no tillage and moderate tillage systems.
2. Water stable aggregates tended to increase by decreasing tillage intensity.
3. Soils managed under no tillage contained approximately 22.7% lower fungi, 25.5% bacteria, and supported approximately 5.6% higher dehydrogenase activity, and 10.1% higher urease activity.
4. Soil urease and dehydrogenase activity were higher in no tillage than in conventional and moderate tillage systems in the upper layer.

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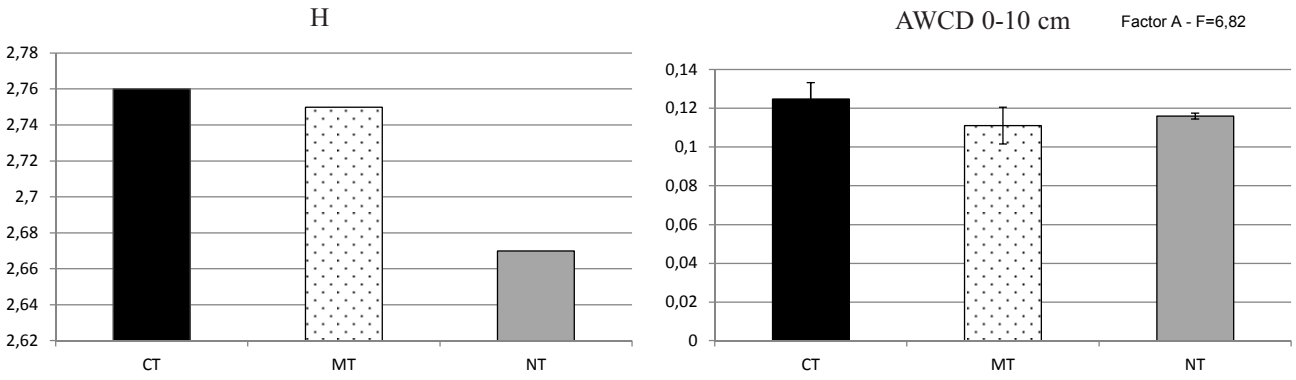

Fig. 2. Shannon (H') diversity index and metabolic potential of microbial community. Factor A – tillage systems.

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