SOIL MITES AND NEMATODES COMMUNITY STRUCTURE IN A CONVENTIONAL AND NO-TILLAGE CHRONOSEQUENCE, COMPARED TO GRASSLANDS

A Thesis Submitted to the College of Graduate and Postdoctoral Studies In Partial Fulfillment of the Requirements For the Degree of Master of Science In the Department of Soil Science University of Saskatchewan Saskatoon

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ABSTRACT

Understanding the impact of long-term conventional tillage and no-tillage practices on soil biota is useful for estimating the level of disturbance in agroecosystems. An investigation was conducted in a long-term field experiment under no-till and conventional tillage management with a wheat-fallow rotation and in undisturbed grasslands, in the southwestern Canadian Prairies of Saskatchewan, at two different locations: Swift Current and Central Butte. The primary goal of the research was to compare the soil community structure of the nematodes and mites between long-term agro-management regimes and between long-term agro-management regimes and the native prairie land. After over 35 years of conventional tillage practices, both nematode and mite communities were negatively impacted. Thus, the increased soil disturbance (CT, conventional tillage) led to lower diversity and weaker soil nematode community structure than reduced soil disturbance (NT, no-till). The nematode maturity index (MI) revealed a more stable environment in the NT system. Oribatid mites dominated the soil mite community's relative density and genera diversity, regardless of agricultural management. Overall our results showed a positive relationship between crop rotation, reduced soil disturbance, and soil Acari's diversity and maturity in long-term agro-management regimes. Also, long-term agricultural practices (CT, NT) significantly altered the community structures of nematodes and mites compared to those from undisturbed grasslands. Thus, the highest number of identified nematode genera (68) was under native prairie (NP) systems. Nematode diversity and maturity decreased with the intensity of land cultivation. Farming impacted the diversity and community structure of Acari as well. Thus, the highest number of identified mites genera (53) was observed in NP systems, and the most mature community structure was also found in the grasslands. Oribatid mites dominated the soil mite communities in terms of relative density and genera diversity in agricultural land and in terms of diversity in the native prairies. A significantly higher proportion of Prostigmata was observed in grasslands, and a significantly lower proportion of Mesostigmata was attested in the CT system. Overall, the nematode and mites communities analysis affirmed that the tillage system significantly decreased the diversity of nematodes and mites, favoring a weaker organization of their communities. Consequently, their functional metabolic footprint had been severely altered compared to communities in native grasslands.

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DEDICATION

DEDICATED TO MY DAUGHTERS

ANDREA & SOFIA

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LIST OF ABBREVIATIONS

ANOVA	Analysis of variance			
BF	Bacteria-feeder			
BI	Basal index			
CI	Channel index			
c-p	colonizer-persister			
DNA	Deoxyribonucleic acid			
EI	Enrichment index			
F/B	Fungivorous-bacterivorous ratio			
FF	Fungi feeder			
#G	Number of identified genera			
IDH	Intermediate disturbance hypothesis			
λ	Dominance			
LSD	Least significant difference			
Mac	Macrophytophag			
Mic	Microphytophag			
MI	Maturity index			
MMI	Modified maturity index			
0MCT	Zero-Minimum-Conventional Tillage			
OM	Omnivor			
OP	Omnivorous predator			
Pan	Panphytophag			
Phy	Phytophag			
PF	Plant feeder			
PP	Plant parasite			
PPI	Plant parasite index			
Pre	Predatory			
PR	Predator			
RA	Relative abundance			
RCBD	Randomized complete block design			
SD	Shannon diversity index			
SE	Species evenness			
SI	Structure index			
SID	Simpson's index of diversity			
SPARC	Semiarid Prairie Agricultural Research Centre			
SR	Richness			
TI	Trophic diversity index			
WI	Wasilewska index			

1. INTRODUCTION

1.1 Soil Food Web under Agro-management Regimes

The simplest definition of the soil food web is that it represents the community of organisms living whole or just a part of their lives in the soil and also describes the transfer of energy between species in an ecosystem. Therefore, studies focused on the structure and functions of soil food webs provide valuable information about soil fertility and ecosystem stability and help sustain high and long-term agricultural productivity. Bio-indicators based on species frequency and community structure are useful for monitoring soil management practices. Soil contains a high abundance and biodiversity of organisms (Table 1.1), which infers that an extensive sampling, extraction, and identification effort is required in order to have a complete soil food web picture:

	Agricultural Soils	Prairie Soils	Forest Soils			
Organisms per gram of soil						
Bacteria	$10^8 - 10^{10}$	$10^8 - 10^{10}$	$10^8 - 10^{10}$			
Fungi	2 - 6 m	10 - 100 m	1 - 60 km			
Protists	$10^3 - 10^7$	$10^4 - 10^8$	$10^{6} - 10^{8}$			
Nematodes	10 - 20	10 - 10 ²	102			
Organisms per square meter						
Arthropods	<10	45-200	900 - 2300			
Earthworms	4 - 25	8 - 42	8-42			

Table 1.1 The abundance of guilds of soil organisms in different ecosystems

*Information compiled from Blair et al., 1986; Coleman et al., 2004; Roesch et al., 2007; Mora et al., 2011; Lehman et al., 2015.

For a better understanding of ecosystem functioning, the studies of soil biodiversity are best to target the particular groups of soil organisms (Barrios, 2007) and focus on the measurement of their activity (Brussaard et al., 2004; Coleman et al., 2004) and their community structure, rather than having multiple studies on the soil food web assemblage of interacting organisms/populations occupying a given area. The last two decades of relatively intensive studies of the soil food web across the world have revealed a set of functional groups (Fig. 1) that play a key role in ecosystem processes (Wall and Moore, 1999; Hunt and Wall, 2002; Bloem et al., 2003; Swift et al., 2004; Barrios, 2007; Moore and De Ruiter, 2012). Among them, particular attention was given by soil ecologists to bacteria (Sun et al., 2004), fungi (Brodie et al., 2003; Porras-Alfaro et al., 2011) and nematodes (Bongers and Ferris, 1999; Ferris and Bongers, 2006; Ferris, 2010) assemblages as potential bio-indicators for estimating the functionality and stability of the soil food web under agricultural management (Fig. 2). The impact of tillage and fertilization regimes on the soil food web under agricultural land use is significant. Tillage will slow down the development of fungal hyphal networks, while fertilization will decrease the demands of plants to form symbiotic interactions with mycorrhiza (Morriën, 2016). Also, agricultural sites are monoculture-dominated, so a large spectrum of herbicides and pesticides are used to diminish yield loss, negatively affecting soil biota. There is evidence that bacterial and fungal community structures are influenced by the root exudates (Haichar et al., 2014; Kaiser et al., 2015); in turn, the composition of other functional groups of the soil food web, such as bacterivores and fungivores could be affected (Choi et al., 2017).



Fig. 1 The energy flux descriptions of the belowground food web (Adapted from Moore and de Ruiter, 2012). The different colors and thicknesses of arrows indicate the source and amount of the transferred material. The yellow ellipses indicate the groups that are investigated in the thesis.



Fig. 2 The functional groups of soil biota in agroecosystems: impact on soil processes and provided services.

The last two decades of soil ecology brought a new light to understanding soil food web biodiversity and function due to continuously improving access to next-generation sequencing (Popescu and Cao, 2018; Semenov, 2021) and stable isotope techniques (Staddon, 2004; Tiunov, 2007). Frequently, these techniques are used to direct attention to specific research questions that refer to tiny pieces of the big puzzle of the soil food web.

In general, crops dictate the type and intensity of agricultural practices, which in tum defines the disturbance level of the soil food web. How the interaction of crop rotation and tillage or no-till affects the soil biota is relatively known. Nevertheless, no-till and rotation are the leading agricultural practices that are usually applied together in the agricultural industry, not only in Canada and the USA but in many other countries of Europe, and is a relatively new approach in Asian countries, where rotation and tillage are still the two important agricultural practices. Therefore, studies focused on the interactive effect of no-till, tillage, and crop rotation on soil biota are imperatively needed. The information can develop a sustainable management and restoration program of soil biota of agricultural soils.

1.2 Justification of Research

There is a lack of data about the consequences of long-term agricultural management on soil biota community structure in Saskatchewan, the largest agricultural province of Canada. Many studies suggest that intensive agriculture leads to the loss of belowground species, which causes food web functional losses, affects nutrient availability and alters the ecosystem services (Hooper et al., 2005; Ma et al., 2014). Thus, understanding the sorting of traits in the soil food web of natural communities and applying those efficiently in managed ecosystems is a real challenge and a necessity. This information can guide management practice in sustaining and complementing soil fertility.

The primary goal of this research was to compare the soil community structure of the nematodes and mites between long-term agro-management regimes and/with native prairie land.

1.3 Hypotheses and Objectives

In light of the above information and gaps in knowledge mentioned above, the following hypothesis was proposed.

I did predict that the long-term agricultural management sites will be found with lower species diversity and functional groups of soil micro-fauna compared to undisturbed prairie sites as follows: conventional tillage (CT) < no-till (NT) < native prairie (NP).

To accomplish the purpose of this research, were set up the following objectives:

- To characterize and compare the community structure of identified functional groups of organisms under different agro-management practices such as no-till (NT), conventional tillage (CT), and native prairie (NP).
- To evaluate and compare the level of disturbance of soil nematodes and mites communities in agroecosystems to a natural prairie system.

1.4 Organization of Thesis

This thesis is presented as a collection of chapters. The first chapter introduces the topic of the thesis. Chapter 2, following the Introduction, is the Literature Review, which discusses the importance of soil biota and its biodiversity, especially referring to mesofauna and macrofauna. Chapter 3 is Materials and Methods, which presents the locations and treatments description and the nematode and mites extraction methods and formulae used to calculate the ecological indices to assess their communities' structure and composition. Chapter 4 presents the results of two related aspects of the research project: Soil community structures of nematodes and mites under long-term agro-management practices; and Soil community structures of nematodes and mites under under long-term agro-management practices compared to natural prairie systems. A synthesis of

the findings emphasizing relationships among assessed ecological indices and the agricultural impact on soil biota, along with an ample discussion and conclusions, are presented in Chapter 5. Finally, Chapter 6 summarizes the findings and points out possible future challenges and recommendations. References cited throughout the text are listed in Chapter 7. The Appendices contain supplemental data and details on the parameters determined over the research study period.

2. LITERATURE REVIEW

Agroecosystems are managed ecosystems (Bethwell et al., 2021), widely accepted to be called high or moderate disturbed ecosystems (Scow, 1997; Kandji et al., 2001; Daofeng et al., 2007; Power, 2010; Pulleman et al., 2022). Their internal biotic regulation is decreased or eventually eliminated (Gaba et al., 2014). Agricultural management leaves its direct and indirect mark on the physical and chemical proprieties of soil (Kaur et al., 2005; Wu et al., 2005; Karlen et al., 2006; Mendoza et al., 2008; Zhang et al., 2012; Golabi et al., 2014), but their measurement provides incomplete information about disturbance level of soil biota (Löbmann et al. 2016; Zhong et al., 2017; Choi et al., 2017). Usually, the type and intensity of agricultural practices define the disturbance level of the soil food web. Generally, the soil food web is a sophisticated community of organisms, but agricultural practices tend to make it simple by reducing its biodiversity (Kandji et al., 2001; Chen et al., 2014). Soil ecologists are still looking for an ideal group of organisms to be used as bioindicators of ecosystem conditions (Pulleman et al., 2022).

2.1 Protist Communities

Neher (1999) suggested that the high demand for food will keep agriculture for many years operating in the "paradigm of ignorance," thus, agricultural fields provide a considerable amount of data for comparison with natural sites. According to Adl and Gupta (2006), agricultural management is dominated by r-selected species of protists, which have short periods of activity, while k-selected species are commonly found in undisturbed sites. Therefore, the authors recommend that studies focus on the diversity of functional groups in soil rather than on the abundance and dynamics of soil protists. Foissner (1997) believes that among protists, the testate amoebae must be considered the most appropriate indicator group of agroecosystems since, in many studies, their species richness is sharply (\geq 50%) reduced under any soil disturbance. Heger et al. (2012) implied that testate amoebae are sensitive to agricultural practices. They found their abundance was five times higher in minimum tillage farming than in conventional tillage; however, no significant difference in their diversity was reported between agricultural fields. Lara and Acosta-Mercado (2012) reviewed the classical (morphological) and most recent molecular

approaches to estimate the diversity of ciliates in soils. They affirmed that a high abundance and diversity of Colpodea class indicates a highly disturbed soil. The rates of recovery of soil biota after disturbance have been a hot topic in the last decade, but more detailed studies are required in order to have a better understanding of soil food web resilience. Adl et al. (2006) found that in agricultural sites converted to no-tillage, the species diversity of protist increased slowly, with a significant shift only in 8-9 and 25-26 years sites. The community of testate amoebae was used by Fournier et al. (2012) as an indicator of floodplain restoration in Switzerland. The project results confirmed that the decrease in density and diversity of the testate amoebae community is the primary response to soil disturbance. The protist community is often used in biomonitoring, but functional groups and species are used differently considering the biogeographical location of the experimental site.

Until recently, in classical soil food web models, soil protists and nematodes were labeled as the primary controllers of the bacterial energy channel. In contrast, some arthropods and fungivores nematodes were considered to be the primary regulators of the fungal energy channels. In the last decade several studies (Böhme et al., 2009; Glücksman et al., 2010; Saleem et al., 2012; Geisen et al., 2015; Geisen, 2016) provided strong evidence that mycophagy among soil protists is much more common than was assumed. Protist functional groups, in general, are of considerable ecological importance in the soil food web as intermediaries between the microbial biomass turnover and higher trophic level consumers (Coleman, 1994) but, until now, insufficiently investigated. In fact, the primary consumers of soil protists are nematodes and colle mbola (de Castro et al., 2021; Geisen et al., 2018; Crotty et al., 2012)

2.2 Nematode communities

Members of the phylum Nematoda are one of the most diverse kinds of animals on earth (Wang et al. 1999). Their relatively simple anatomy, transparent bodies, and ecological diversity made them extremely useful as model organisms for biological research. Nematodes are multicellular animals containing not more than 1000 cells, found in marine and freshwater, in the soil as free-living nematodes, and parasites in other living creatures (plant, animal, and human bodies). Approximately 25,000 species have been described worldwide (Zhang, 2013). However, molecular data suggest a much higher diversity that remains unrecorded and may range from 40,000 to 50,000 species (Mora et al., 2011; Ramirez et al., 2015). In soil, the abundance of

nematodes is very high and can reach several millions per square meter. According to Sohlenius (1980), grasslands and forests are the ecosystems that have been found with the highest abundance and diversity of nematodes. Also, the highest abundance and diversity of nematodes are usually found within the soil's top 10-15 cm. The average length of soil nematodes is 1 mm, and being aquatic organisms, their movement depends on water films around soil particles.

Due to high diversity, abundance, and ubiquitousness, the nematode communities are considered by many soil ecologists a potential bioindicator for assessing the quality of the terrestrial ecosystem. Over two decades ago, Bongers (1990) claimed the maturity index (MI) as an ecological measure of environmental disturbance based on nematode community structure. The c-p values given to the nematode families according to their life strategies are the starting point for defining and estimating the maturity of a community. Thus, disturbed environments are represented by low MI values (<2), while more natural environments are indicated by higher MI values (>3). Generally, high values of MI are a result of the significantly increased density of Kstrategists nematodes or of taxa that are higher on the colonizer-persister (c-p) scale, which has a long life cycle, and are very sensitive to any soil disturbance (within 2-3 weeks). Many recent studies (Liang et al., 2001; DuPont et al., 2010; Zhang et al., 2012; Ito et al., 2014; Ito et al., 2015) have attested that agricultural fields are found with low diversity of nematodes. Usually, conventional tillage, no-till, and native grassland support different nematode assemblages and, accordingly, soil food webs. Thus, Sanchez-Moreno et al. (2009) found that indices of soil food web-based on the abundance of nematode functional groups produced the features of the mite community not only under conventional tillage plots but also under organic-no till sites. So, the authors observed that high values for enrichment and structure indices featured a higher abundance and diversity of predatory mites; in contrast, increased values of the channel and basal indices featured a higher abundance of algivorous mites. Also, it was assumed that the recovery of the invertebrate's community takes a longer time as the higher trophic level they occupy in the food web. Adl et al. (2006) concluded that the recovery of soil biodiversity, including nematodes, from agricultural tillage, was prolonged. Their abundance and diversity were highest in the 25-56 years field of no-till and lowest in the conventional tillage fields. Zhang et al. (2012) confirmed that four years of no-tillage practices did not improve the abundance either diversity of nematode communities after over 50 years of summer maize and winter wheat rotation under conventional tillage. Another recent study done by DuPont et al. (2010) focused on the no-tillage conversion of perennial grassland to annual cropland did confirm that the annual cropland, together with tillage, reduced the soil biota communities dramatically. Soil biota of 75 years of grassland was reduced to the minimum after three years of conventional agricultural management. Ito et al. (2015) also suggested that nine years of similar tillage did develop a low diversity community of nematodes, including certain genera adapted to agroperturbations. Similarly, Zhang et al. (2012) reported that the response of nematodes to tillage and applied residue were correlated to specific genera (i.e., *Acrobeles, Pratylenchus, Helicotylenchus*), which are typical for agroecosystems.

The trophic structure of the soil nematode community is essentially a functional classification that provides valuable information regarding how each functional group impacts the transfer of matter and energy in the soil food web (Yeates, 2003). Nematode genera/families are typically assigned to feeding groups (Yeates et al., 1993) with the purpose to follow a better understanding of the role of nematodes in the soil food web and how land use impacts the composition of the nematode community. Thus, based on the morphology of their mouthparts (<u>https://eorganic.org/node/4495</u>), their diet, genera/species morphology, and biological data, soil nematodes were allocated to the following trophic groups: (1) bacterivores; (2) fungivores; (3) herbivores; (4) predators; (5) omnivores (Yeates et al., 1993). Hitherto, feeding habits of many nematodes' genera have been assumed instead of being validated by defined conditions under laboratory observations. Due to the fact that feeding habit groupings are not clearly defined, the allocated names of trophic groups still generate disagreement among soil ecologists.

2.2.1 Bacterivorous nematodes

Indirectly, the nutrient cycling in a terrestrial ecosystem is greatly affected by bacterivorous nematodes. There is sufficient evidence to infer that they play a crucial role in soil nutrient cycling by intermediating and speeding up the decomposition processes in soil (Griffiths, 1990; Scheu et al., 2005; Zhao and Neher, 2013; Kudrin et al., 2015). Bacterial-feeding nematodes have a simple stoma (mouth) with no stylet. Nevertheless, they can have sophisticated lip structures (e.g., Acrobeles sp.) or just narrow, round mouths (e.g., Caenorhabditis sp.) that help nematodes prey on bacteria by filter-feeding them from soil suspension. Bacterivorous nematodes have no preferences regarding bacteria species; they are grazing randomly on beneficial, saprophytic, and plant-pathogenic bacteria (Ladygina et al., 2009). Therefore, bacterivorous nematodes were considered indicators of bacterial activity in the soil, especially in agricultural ones. Due to the

application of fertilizers, different kinds of amendments, or manure in agricultural soils, the bacterivores are at higher density than fungivores or even plant parasites nematodes. Frequently, due to the feeding habits, bacterivorous nematodes may shift and regulate the amount of mineral nitrogen available to the plants in agricultural soils. However, some nematodes can switch and prey on fungi (Gupta et al., 1979), which means bacterivores could compete with other functional groups of the soil food web not only for space but also for food in the rhizosphere zone.

In agricultural soils, bacterial-feeding nematodes are well represented by several families (e.g., *Rhabditidae*, *Cephalobidae*, *Prismatolaimidae*) in high densities. Usually, their density, but not diversity, are much lower in undisturbed sites, such as alpine meadows, grasslands or forest (Postma-Blaauw et al., 2010).

2.2.2 Fungivorous nematodes

The soil is home to an incredible variety of nematodes that are a part of several trophic levels of the soil food web. Fungivorous nematodes (12% of the described species) feed on fungal hyphae of many different species of fungi, including beneficial and pathogenic, saprophytic, and mycorrhizal fungi. They have small, narrow stylets, or spears, in their mouth (stoma), which are used to penetrate fungal cells and ingest cellular contents. Many fungivorous nematodes are not obligated fungivorous and are considered polyphagous, feeding on fungi, lichens, mosses, algae, and plant roots by piercing. The abundance of fungal-feeding nematodes in undisturbed systems (e.g., forest, native prairie, no-till systems) is higher than in disturbed systems (e.g., agricultural systems) where the different agricultural practices repress the conditions for fungal growth. There are several species of fungivorous nematodes, such as *Aphelenchus* spp., *Aphelenchoides* spp., Ditylenchus spp., Tylenchus spp., that are common to be found in agricultural soil. Multiple studies (Rhoades and Linford, 1959; Barnes et al., 1981; Gupta, 1986; Choi, 1994; Ishibashi et al., 2000; Jun and Kim, 2004; Friberg et al., 2007; Lagerlöf et al., 2011; Garcia de la Cruz et al., 2016) indicated that fungivorous nematodes diminish the pathogenic fungi population. Thus, several studies have used different species of soil nematodes such as Aphelenchoides besseyi (McGawley et al., 1984), Aphelenchus avenae (Ishibashi et al., 2000; Jun and Kim, 2004), Aphelenchoides saprophilus (Garcia De la Cruz et al., 2016), to assess their potential as biocontrol agents against soil-borne diseases caused by fungi. The research studies were conducted in laboratories, and the outcomes are difficult to extrapolate to open field conditions. However, nematodes were suggested

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to be used as natural enemies and biological control agents in organic farming systems (Briar et al., 2007).

In agricultural soils, fungal-feeding nematodes are well represented by several species (e.g., *Aphelenchus* spp., *Aphelencoides* spp., *Ditylenchus* spp., *Tylenchus* spp.) in low densities. However, the density and diversity are much higher in undisturbed sites (Postma-Blaauw et al., 2010).

2.2.3 Phytophagous nematodes

There are over 4200 species of plant-feeding nematodes described to date or about 15% of the worldwide described nematode species. Herbivorous nematodes exist in all sizes and shapes. Typically, their bodies' length ranges from 0.25 mm to 12 mm and about 0.025 mm to 1 mm in width. They can be recognized easily by the hollow mouth spear with big distinctive knobs at the end, known as stylet, located at the head and used to puncture plant cell walls to ingest the internal cell contents. Over the years, plant-feeding nematodes have been widely studied. Most studies were initiated due to the economic importance, with up to 12.3% of global crop yield losses (>150 billion dollars) caused by their damage (Singh et al., 2015). Plant-parasitic nematodes are classified into ectoparasites (e.g., Belonolaimus, Longidorus, Tylenchorhynchus, and Helicotylenchus) and endoparasites (e.g., Xiphinema, Rotylenchulus, Tylenchulus, Pratylenchus, Radopholus, Ditylenchus, and Hirschmanniella). Furthermore, they can feed on all plant parts (i.e., roots, stems, leaves, and seeds) and upon a relatively large range of plant species. Thus, due to these several adaptabilities and another crucial survival strategy which is cryptobiosis (i.e., the ability to dry out in extreme environmental conditions by suspending the metabolic activity), the plant-feeding nematodes can survive well and spread fast, making their extermination practically impossible in infected agricultural fields (Wharton, 1986; Viglierchio, 1991; Noel, 1992; Lambert and Bekal, 2002). Among plant parasites, the top five most damaging are the root-knot nematodes (Meloidogyne spp.), cyst lesion nematodes (Globodera and Heterodera spp.), root-lesion nematodes (*Pratylenchus* spp.), the rice root nematode (*Hirschmanniella* spp.) and the burrowing nematodes (Radopholus spp.), (Jones et al., 2013). In grassland ecosystems, the plant-feeding nematodes are numerically the most abundant group, making up approximately 50% of the total nematode community (Verschoor et al., 2002). Their abundance has been related to contribute to plant species replacements, especially under restoration management (Verschoor et al., 2002).

2.2.4 Omnivorous - Predatory nematodes

The omnivores and predatory nematodes are the less abundant broad groups of free-living nematodes that cohabit in soil. Some of them are known to prey on root-feeding nematodes, and these species would be the ones that would be the perfect bio-control agents (Gitanjali and Jisna, 2017) for organic agriculture in the greenhouse or open field. Depending on the environmental conditions and food availability, a few families of nematodes (e.g., Aporcelamidae, Dorylamidae, Nordiidae, Qudsianematidae, Thornematidae) are known to be feeding on more than one type of food (e.g., fungi, algae, bacteria, protist), and therefore are named omnivores. Their mouth has a big hollow tooth that can be used as a stylet to pierce their prey and suck out the contents. Frequently, omnivorous feeding habits may change not only by environmental conditions and food availability but also by the specific features/needs of nematode development (i.e., juvenile and adult stages).

All predaceous nematodes have large mouths. They often may have a stylet, denticles or teeth (from one to several), or various combinations of these. Their diet is quite diverse, from protists, tardigrades, and rotifers to nematodes. The nematodes, which have a stylet, feed on other microorganisms by piercing them and sucking out the internal contents. Those with teeth ingest their prey whole, using the tooth or teeth to remove the cuticula from the prey. Nygolaimidae and Mononchidae family species are the most common for agricultural soils (Keith et al., 2009), while in undisturbed ecosystems, the diversity and abundance of omnivores and predatory nematodes could be unexpectedly high.

Omnivores and predators are relatively large nematodes (1-3 mm long). They are sensitive to any kind of soil disturbance (e.g., tillage, grazing, salinity) and pollution (e.g., excess of fertilizers and pesticides; salinity) among soil nematodes (Yang et al., 2021). Furthermore, since it takes several months to complete their life cycles, then once lost from the soil community, it may take months or years for these species to return. Commonly, in agricultural soils, the relative abundance of omnivores plus carnivores rarely exceeds 6%, while their diversity may not cross even 3%.

2.3 Microarthropods communities

2.3.1 Acarine communities

Soil organisms were frequently classified according to body length. Thus, soil ecologists operate with one standard classification (Lavelle et al., 1997): microfauna (<100 µm, e.g., protist and nematodes), mesofauna (100 - 2000 µm, e.g., enchytraeids and microarthropods) and macrofauna (> 2000 µm, e.g., earthworms and arthropods). Among soil mesofauna, acarine communities have the highest taxonomic and ecological diversity. The phylogeny of the acarine is still "under the microscope." However, on the tree of life evolution, they are placed in the phylum Arthropoda, within the subphylum Chelicerata, class of Arachnida. The Arachnida is made up of 12 orders from which two, Acariformes and Parasitiformes, are mostly represented by the soil mites species. The Oribatida, Prostigmata, and Endostigmata suborders make up over 80% of species in Acariformes. With over 11,00 described species, the Mesostigmata suborder has the highest diversity among Parasitiformes. According to Meehan et al. (2018), more than 55,000 species of mites have been described to date, but the real richness is estimated to be up to 1 million (Walter and Proctor, 2013). Roughly 11,000 species were predicted to be found in Canada by Lindquist et al. (1979), 3000 of which have been described and with about 73% of Canada's mite fauna to be yet described (Beaulieu et al., 2019). Generally, mites have a morphological distinction from other arachnids in that they lack body segmentation. Their body is divided into gnathosoma (incorporated mouthparts) and idiosoma (incorporated eyes and brains). Adult mites have four pairs of legs and hair-like setae on the body that serve as sensory structures. Mites are relatively small (from 80 µm to 14 mm long). Although they might be tiny, they have a few well-developed systems such as nervous, digestive, reproductive, respiratory, and excretory (Halliday et al., 2000).

Soil health, which was defined by Lehmann et al. (2020) as "the continued capacity of soil to function as a vital living ecosystem that sustains plants, animals, and humans," nutrient cycling and decomposition are directly and indirectly dependent on the soil biodiversity of mites and their function maintenance. Natural and agricultural grasslands sustain a relatively stable diversity and abundance of micro-arthropods (Crotty et al., 2015), which are actively involved in carbon/nitrogen cycles and litter decomposition as well as improving soil aggregation (Sanchez-Moreno et al., 2009). Agricultural fields under conventional tillage are colonized by about 40% fewer mites than those under minimum or no-till management (Gupta, 1994). Koehler (1999) states that low species diversity of Uropodina and Gamasina predatory mites (Mesostigmata) indicates

soil compaction due to tillage practices, while a diversity of 25-30 species is the expected range in undisturbed grasslands. The effects of different intensity tillage practices on soil mites, evaluated by Hulsman and Wolters (1998), showed that mites diversity as well as their abundance depends on the type and the lengthened tillage time; yet, Oribatida fungivorous mites were particularly affected by tillage. The same study attested that the total abundance of soil mites was reduced by more than 50%, while the diversity by about 30% by tillage. A soil food web with a higher abundance and diversity of mites at higher trophic levels was found by Sanchez-Moreno et al. (2009) under 12 years of organic-no till plots. Also, the authors attested that the community structure of nematodes and mites in agricultural fields responds analogously to agricultural management and its duration. Recently, Crotty et al. (2015), by assuming that different crops can affect the diversity and abundance of soil biota differently, found that forage crops (which, in fact, are related to minimum tillage practices) did show trends towards a greater abundance of predatory mites, but were not significant after four years. However, other functional groups (i.e., nematodes and earthworms) of the soil food web were found to differ in response to different forage crops. Similar research was done by Wissuwa et al. (2012), and the results suggested that, particularly for mites, the quantity of food resources is more important than the quality of the resource. Also, mite population recovery was prolonged, did not respond to well-developed vegetation cover (forage: legume versus grass), but was found different mite species assemblages among three age classes (2-3, 6-8 and 12-15 years) as was earlier stated by Koehler (1998).

2.3.1.1 Overview of Oribatida

Oribatida, formerly Cryptostigmata, is included in the superorder Acariformes of the monophyletic group of Sarcoptiformes, along with the Astigmatina order. Oribatid mites range in size from <0.2 mm to 1.5 mm or more (Coddington and Colwell, 2001) and are the most abundant group of microarthropods in forest systems (Lindo and Visser, 2004) and worldwide, in the organic horizons of most soils (Behan-Pelletier, 2003). Also, oribatid mites have the highest diversity among soil mites and due to this fact, their community structure is a valuable bioindicator of soil conditions and level of ecological disturbance (Behan-Pelletier, 2003; Lindo and Visser, 2004; Cao et al., 2010). Oribatid mites have low metabolic rates, low fecundity, slow development (from several months to two years), and longer life cycles, which makes them part of "k-selected" organisms (Krantz and Walter, 2009; Walter and Proctor, 2013); thus, they have a low recovery

rate from any natural or anthropogenic disturbance (Norton, 1990; Behan-Pelletier, 1999). Oribatida has a considerable impact on litter decomposition (Lussenhop, 1992; Scheu et al., 2005;), soil formation, and its structure by feeding on fungi and dead plant material (Behan-Pelletier, 2003). Some species of Oribatida are predaceous, but none is parasitic. Nowadays, among soil mites, the suborder Oribatida has the most taxonomic, chorological, and ecological data available. Approximately 10,000 species have been described worldwide. In Canada, the described oribatid mites to date reached a total of 592 species from 84 families. However, molecular data suggest a much higher diversity that remains unrecorded and may range from 1800 to 3000 species (Beaulieu et al., 2019).

Astigmatina, with approximately 5,000 species worldwide recorded to date, is a cohort of mites within the suborder Oribatida, even though they are morphologically and ecologically different. Essentially, astigmatic mites are characterized by missing stigmata and peritremes. Therefore, the respiratory process occurs over the whole surface of their bodies. The Astigmata are relatively small, slow-moving, whitish, unsclerotized, and are the least common mites to be found in soil. However, they may develop an increased population in some agroecosystems after harvesting, when in soil persists high water content or after manure application (Coleman, 2004). The free-living soil Astigmata has a diversified diet, from dead organic materials and fungi to algae (Behan-Pelletier, 2003), but most of them are microbial feeders (Coleman, 2004). With high fecundity, high reproduction rate, fast development, and relatively short life spans (8 days to 3 weeks), the astigmatic mites are considered r-selected organisms (Behan-Pelletier, 2003), the colonizing mites of agroecosystems. In Canada, a total of 441 species from 43 families of Astigmata are recorded to date, but their diversity is estimated to be higher than 1600 species (Beaulieu et al., 2019).

2.3.1.2 Overview of Endostigmata

Endostigmata is included in the superorder Acariformes of the monophyletic group of Sarcoptiformes along with Oribatida and Astigmatina suborders. Currently, the Endostigmata suborder includes five superfamilies, and ten families, with 27 genera and over 110 species recorded worldwide. The adults of Endostigmata are soft-bodied or weakly sclerotized, with vermiform (e.g., Nematalycidae family), cylindrical or globular body shapes, white to yellowbrown or pale lilac to pink, and range in size from 0.2 to 1.0 mm. Most species are omnivores or predaceous on soft-bodied invertebrates (i.e., nematodes, tardigrades, and rotifers). However, some have piercing mouthparts, which would suggest a fungal diet and were mistakenly treated as Prostigmata for quite a long time by some authors (Bonkowski et al., 2011). The suborder Endostigmata is commonly accepted as an early derivative member of Acariformes (Norton et al., 1993; Dabert et al., 2010). They might be very ancient and relatively small taxon of mites but with a cosmopolitan distribution. Thereby, endostigmatids are found in extreme conditions, from hot deserts, sandy soils, seashores, and deep soil to cold deserts of the High Arctic tundra (Beaulieu et al., 2019). In Canada, a total of 168 species from eight families of Endostigmata have been recorded to date, but their diversity is estimated to be higher than 1000 species (Beaulieu et al., 2019).

2.3.1.3 Overview of Prostigmata

The Prostigmata suborder is included in the superorder Acariformes of the monophyletic group of Trombidiformes. Prostigmata is a large and extremely diverse suborder of sucking mites. The majority of prostigmatid mites have eyes, soft bodies, white to brightly colored or even colorless, and range in size from 100 µm to 10 mm. They have a distinctive characteristic regarding the diet; all prostigmatans are fluid feeders. Many large and medium soil-dwelling species of Prostigmata are preying on arthropods or their eggs and nematodes (e.g., Tydeidae, Bimichaelidae and Alicorhagiidae families), while smaller species, those with piercing stylet chelicerae (members of the Nanorchestidae and Nematalychidae families), are known to feed on fungal hyphae (Bonkowski et al., 2011). Some families are fungivorous, but they can switch to algae, nematodes, or even plants, making them omnivorous. Fungivorous species of Prostigmata (e.g., Eupodidae, Tarsonemidae, and Nanorchestidae families) are r-selected organisms, able to rapidly colonize the area following a disturbance or sudden shift in food resources (Coleman et al., 2004). In general, the abundance of prostigmatid mites is higher in the temperate zone than in tropical or subtropical zones (Coleman et al., 2004) and sometimes may exceed in number and diversity of the oribatid population (Norton, 1990). Prostigmata is the most abundant group of microarthropods in grassland systems (Behan-Pelletier and Kanashiro, 2010), especially dominant in shortgrass prairie (Leetham and Milchunas, 1985; Walter, 1987) and fescue prairie (Clapperton et al., 2002). A total of 1100 species from 86 families of Prostigmata are recorded to date in Canada, but their diversity

is estimated to be much higher. Thus, according to Beaulieu et al. (2019), the total diversity of the suborder can be over 3200 species, which means over 65% of which are yet to be described.

2.3.1.4 Overview of Mesostigmata

Mesostigmata (=Gamasina) is included in the superorder Parasitiformes. Many mesostigmatids are parasites of vertebrates and invertebrates, but most are free-living soil predators (Koehler, 1999; Khan et al., 2017). Approximately 25% of all recorded mites belong to the order Mesostigmata. Thus, over 110 families with 900 genera and more than 12,000 species have been recorded worldwide as being linked to the soil habitat. However, in temperate zones, the soil-dwelling gamasid mites have much lower species diversity and abundance than Prostigmata or Oribatida. For instance, in Canada, a total of 650 species from 46 families of Mesostigmata have been recorded to date, but their diversity is estimated to be much higher. Thus, according to Beaulieu et al. (2019), the total diversity of the suborder can be over 1600 species, which means over 65% of which are yet to be described.

Mesostigmatans have soft to well-sclerotized bodies, fast-moving, eyes absent, from the wide brown palette to cream-milk color, and range in size from 0.2 mm to 3 mm. With high fecundity, high rate of reproductivity, fast development, and relatively short developmental time 1 (i.e., egg to adult in 4 days to one week), the Gamasina mites are considered r-selected organisms (Behan-Pelletier, 2003) and the colonizing mites of forest ecosystems (Coleman et al., 2004). The inhabiting soil species are mostly predators. Usually, smaller species are mostly feeding on nematodes. There are species (e.g., in the family Ascidae, Uropodidae, Digamasellidae, and Laelapidae) that have been documented to be omnivorous by feeding on fungi, nematodes (3-8) nematodes/day), collembolans (3-4 indiv./day), small arthropods (5-7 mites/day) and their eggs and even on tiny insect larvae (Walter and Lindquist, 1989; Mueller et al., 1990; Behan-Pelletier, 2003; Freire and de Moraes, 2007; Gerson and Weintraub, 2012). There are some species of certain families that are widely and successfully used as standard organisms in ecotoxicological experiments (e.g., Laelapidae, Stratiolaelaps) (Bonkowski et al., 2011) or as biocontrol agents in the open field and greenhouses (Phytoseiidae, Phytoeiulsus) (Koehler, 1999; Gerson, 2014) and as bioindicators in soil remediation projects (Koehler, 1999; Koehler, 2000; Madej and Kozub, 2014; Meehan et al., 2019).

2.3.2 Collembola communities

Collembola, commonly known as springtails, are microarthropods that are found in most terrestrial ecosystems, from wet to arid ecosystems and from arctic to tropical rain forests. Thus, depending on the climate conditions, their densities may range from hundreds to several million individuals per m² and from two to 50 species in an ecosystem (Rusek, 1998). According to the most recent updates on Collembola taxonomy, there are over 8800 described species worldwide (Turnbull and Stebaeva, 2019; Bellinger et al., 2018), including 474 described species from Canada. However, due to the last decade's growing fast use of genetic biodiversity assessment methods, the total worldwide diversity of Collembola is expected to reach 10000, with approximately 675 species to be described in Canada (Turnbull and Stebaeva, 2019).

Along with mites, the springtails are the main actors of soil mesofauna, playing a significant role in plant litter decomposition processes and developing soil microstructure. The abundance of Collembola within meadows, prairies, and even agroecosystems is relatively high. Indirectly, by altering microbial activity and transporting the fungal spores, endospores, and microbial cysts (Moore, 1988; Lussenhop, 1992), they have a significant impact on N mineralization, soil respiration and rate of organic matter decomposition (Filser, 2002).

Collembola species are well assembled in three different ecomorphological life forms (euedaphic, hemiedaphic, euedaphic); consequently, they are related to three different life strategies and feeding guilds (Coulibaly et al., 2017). In general, they feed on a wide range of microorganisms (protists, nematodes, rotators, bacteria, fungi, algae) and plant litter (Rusek, 1998). Collembola was found to be one of the relevant prey groups for generalist arthropod predators, especially in agroecosystems (Bilde et al., 2001). With regards to organic agriculture, several studies suggested that springtails considerably shape soil microbial communities (Schneider and Maraun, 2009) and are one of the best biological control of crops diseases caused by soil-borne fungal pathogens (Nakamura et al., 1992; Lartey et al., 1994; Klironomos and Kendrick, 1995; Sabatini and Innocenti, 2000a, 2000b; Innocenti and Sabatini, 2018).

Despite their small size (0.25-6 mm), springtails are hosts of many pathogenic bacteria, parasitic protists, and even nematodes. Nevertheless, there was no evidence that the number of pathogens transported by springtails was sufficient to cause plant disease (Nakamura et al., 1992; Sabatini and Innocenti, 2001).

3. MATERIALS AND METHODS

3.1 Study Sites and Experimental Design

The research study was carried out in the Canadian Prairies of Saskatchewan at two different locations. Swift Current - the location of the study site under agricultural management was purposefully chosen to be in the most southern site among currently existing six long-term research studies in Saskatchewan province. Thus, the "Zero-Minimum-Conventional Tillage" (0MCT) experiment – established in 1981 at the South Farm of the Semiarid Prairie Agricultural Research Centre (SPARC) (latitude 50°18'N; longitude 107° 41'W), has been chosen for soil sampling collection, having the most appropriate experimental design for the research project purpose. The experiment was set up as a randomized complete block design consisting (RCBD) of four blocks for a total of 64 plots. Each block (consisting of 16 plots) was separated from other blocks by a distance/buffer area of 5 m in all directions. Currently, there are several main crop rotation types under no-till, minimum tillage, and conventional tillage management. The no-tillage plots were planted without preseeding tillage; during seeding the machinery carry out four tasks in one operation such as clean a narrow strip over the crop row, open the soil for seed insertion, place the seed and cover it properly, while for weed control only recommended cultivars using a commercial zero-till air hoe drill was used. The conventional tillage had three to five tillage operations from early May to late September: plow, pre-seeding, seeding and weed control operations. The research project was focused on first crop rotation (Wheat, $2015 \rightarrow$ Fallow, 2016), which had a total of 8 plots ($15 \text{ m} \times 30 \text{ m}$ each plot area) with no-till wheat and fallow (4 plots) and conventional tillage wheat and fallow (4 plots). At the same Agriculture and Agri-Food Canada Research Centre, just 2 km North of the 0MCT experiment site, was located one of two native prairie sites (Figure 3.3). The native prairie site (NP) has never been exposed to agricultural works, but cattle grazing did occur in the last ten years. A Commercial/Research farm near Central Butte, located approximately 200 km from Saskatoon and Swift Current, hosts the second native prairie site (Figure 3.4). The native prairie site (NP) has never been exposed to agricultural works and never burned, used only for grazing. However, in the last ten years, grazing did not occur. Vegetation cover at both NP sites is a mix of perennial native prairie grasses and perennial agronomic grasses: Western Wheatgrass (*Pascopyrum smithii*), Smooth Brome (*Bromus inermis*), Fescue grass (*Festuca pratensis*), Little bluestem (*Schizachyrium scoparium*), and Needle-andthread grass (*Hesperostipa comata*). Four plots with an approximate area comparable to those from the Swift Current agricultural site were established for soil sample collection. According to the Canadian System of Soil Classification, both the Swift Current and Central Butte sites are located in the Brown Soil Zone (Figure 3.1), having a loam to clay loam texture and classified as an Orthic Brown Chernozem (Soil Classification Working Group, 1998). The type of soil or cover crop was not a factor in the experiment.



Figure 3.1. Map of Southern Saskatchewan displaying the main soil zones and identifying the location of the study sites.

Adapted from: http://esask.uregina.ca/entry/agricultural regions.html



Figure 3.2. Swift Current agricultural site at the South Farm of the Semiarid Prairie Agricultural Research Centre: a) no-till wheat; b) no-till fallow.



b)

a)

Figure 3.3. Swift Current agricultural site at the South Farm of the Semiarid Prairie Agricultural Research Centre: a) conventional tillage wheat; b) conventional tillage fallow.



Figure 3.4. Swift Current native prairie site at the Semiarid Prairie Agricultural Research Centre.



Figure 3.5. Native prairie site at the commercial/research farm near Central Butte.
3.2 Soil Sampling, Biota Extraction, Identification, and Community Analysis

Soil samples were collected in July and October 2015; and in May and September 2016. Five soil subsamples were collected from each agricultural plot, while from native prairie plots, only three each. To avoid damage to soil biota (especially protist biota), soil samples were collected by removing with a hand-held shovel a 15 cm \times 15 cm \times 15 cm cube of soil, with an amount of approximately 500 g (wet weight) of soil. Samples were transported to the laboratory in insulated plastic bags, and mites were extracted immediately. The rest of the soil for nematodes and DNA extractions was stored at 4°C for no more than eight days before extractions. Soil samples were sieved through a 2-mm mesh screen to remove stones, shoot fragments, and other organic debris.

In parallel with the preparation of biota extractions, soil water content was determined in the lab gravimetrically by drying the soil samples at 105°C for 24h and expressed as a percent of dry weight.

Soil micro-arthropods (mites) were extracted from 300 g of soil/subsample, using the Tullgren funnel unit (Agronomic Division of Burkard Scientific Limited, UK) for 48 to 72 hours and preserved in 75% ethanol (Hu and Wang, 1992) for sorting and identification. All the subsamples have had a population under 100 individuals. After the mites were clarified in lactic acid, they were picked out under a stereoscopic zoom microscope (SMZ1000, Bioscience, Nikon Instruments INC, Tokyo, Japan) at low magnification. Further identification work has been done under inverted microscopes (Eclipse TS100 and Eclipse Ts2R, Nikon Instruments INC, Tokyo, Japan), at 100× and/or 400× magnification, into super-families/families, based mainly on Baker (1952), Balogh (1972) and two mites identification websites:

http://www.zoology.ubc.ca/~srivast/mites/alpha.html#top;

http://itp.lucidcentral.org/id/mites/invasive_mite/Invasive_Mite_Identification/key/Whole_site/H ome_whole_key.html. Soil mites were classified into broad taxonomic groupings following the procedure of Seastedt and Crossley (1981). Initially, the microarthropod soil community was aggregated and described in terms of functional groups, but only the dominant Acari groups like Oribatida, Prostigmata, and Mesostigmata were reported in the thesis.

Soil nematodes were extracted from 20 g fresh soil sample in water, using the Baermann funnel technique for 48 to 72 hours, killed by heating (60°C), fixed in 10% neutral buffered formalin (100 ml formalin; 900 ml distilled water; 4g/L NaH₂PO₄; 6.5g/L Na₂HPO₄) and were

stored for further enumeration and identification. A subsample of 100 individuals was selected randomly from each sample and identified under inverted microscopes (Eclipse TS100 and Eclipse Ts2R, Nikon Instruments INC, Tokyo, Japan), at 100× and 400× magnification, at the genera level. If the total number of nematodes was < 100, then all nematodes present in the sample were identified. Nematodes were identified based mainly on the nematode identification website: http://plpnemweb.ucdavis.edu/nemaplex/Uppermnus/Classifmnu.htm; http://nematode.unl.edu/; http://nematode.unl.edu/konzlistbutt.htm, Goodey (1963), Bongers (1988) and other taxonomic works as needed, and allocated to the following trophic groups according to Yeates et al. (1993): (1) herbivores (PP); (2) fungivores (FF); (3) bacteria-feeders (BF); (4) predators (PR); and (5) omnivores (OM). The final nematode populations abundance was expressed in 100 g dry mass. The total number of identified nematodes in every trophic group and the percentage of every trophic group within the nematode community were recorded. Each identified nematode was recorded as a juvenile or adult. The c-p values of 1-5 were given according to Bongers (1990) to classify nematode families according to their life strategies. As measures of functional diversity, the maturity index (MI= $\Sigma v(i)f(i)$), (without plant-feeding families), the plant parasite index, PPI, (only plant-feeding families) (Bongers, 1990; Bongers and Bongers, 1998), ΣMI(2-5) for all nematodes with c-p=2-5 (Bongers 1990; Neher and Campbell, 1996) and the sum of the maturity index, Σ MI (all families) (Yeates, 1994) were calculated.

For each subsample the nematode diversity was described using the measures calculated at the genus level (Magurran, 1988).

The Shannon-Wiener Diversity Index:

$$H' = -\Sigma[(p_i) \times \ln(p_i)], \tag{1}$$

where: H' – Shannon Diversity Index;

N – total number of individuals in a community;

 Σ – the sum symbol;

ln – the natural logarithm.

Pielou's Index of Evenness:

$$J' = H' / H'_{max},\tag{2}$$

where:

H′ - Shannon-Wiener Diversity Index;

$$H'_{max} = -\sum_{i=1}^{s} \frac{1}{s} \times ln \frac{1}{s} = ln S,$$

where: S – total number of genera in the sample

Margalef's Index of Richness:

$$SR = (S-1) / \ln N \tag{3}$$

where:

S – total number of genera;

N – total number of individuals in the sample;

ln – natural logarithm.

Genera Dominance:

$$D = \lambda = \Sigma p_i^2 \tag{4}$$

where: $p_{i=}n_i / N$

where: n_i – number of individuals of i, i_2 etc.;

N-total number of individuals.

Simpson's Index of Diversity:

$$SID = (1-D) \tag{5}$$

The trophic diversity index described trophic diversity (Heip et al., 1988).

$$T = 1 / D$$
 (6)

Following the weighted faunal analysis concept (Ferris et al., 2001), soil nematodes were classified into functional groups to calculate:

The enrichment index (EI):

$$(EI) = 100 \times (e/(e+b)),$$
 (7)

The basal index (BI):

$$(BI) = 100 \times (s / (s + e + b))$$
 (8)

The structure index (SI):

$$(SI) = 100 \times (s / (b + s)) \tag{9}$$

where: $b = (Ba_2 + Fu_2) W_2$

where: $W_2 = 0.8$

$$e = (Ba_1W_1) + (Fu_2W_2)$$

where: W₁= 3.2 and W₂= 0.8
$$s = (Ba_nW_n) + (Ca_nW_n) + (Fu_nW_n) + (Om_nW_n)$$

where:
$$n = 3-5$$
, $W_3 = 1.8$, $W_4 = 3.2$, $W_5 = 5.0$

The fungal to bacterial feeder ratio (FF/BF) = f/b (Hendrix et al. 1986, Wasilewska, 1997) and the channel index (CI) (Ferris et al., 2001) were calculated to indicate predominant decomposition pathways (bacterial or fungal) within the detritus food web (Hendrix et al. 1986, Ruess, 2003).

$$CI = 100 \times (Fu_2 W_2 / (Ba_1 W_1 + Fu_2 W_2))$$
(10)

Additionally, the Wasilewska index (WI = (FF + BF / PP)) was calculated to reflect differences in the mineralization of dead and live plant tissues, i.e., to indicate the dominant pathway of mineralization (Wasilewska, 1991a,b; 1994).

3.3 Statistical analyses

All data were subjected to statistical analysis of variance (ANOVA) using the IBM SPSS 24.0 statistical package for Windows 7 Home Premium and GLM randomized block design (General Linear Model Multivariate, SPSS). The research study to determine the nematodes and mites community structure was conducted as an RCBD with a total of four treatments in replicates of four; from each replicated plot, five soil subsamples (n=5) were collected. An ANOVA was conducted with treatments as a fixed effect and month as a random effect. Turkey's HSD multiple range tests evaluated differences between separated means. Differences at the p<0.05 level were considered statistically significant using the LSD (least significant difference) test. Species diversity was estimated with the Shannon-Wiener index. As measures of functional diversity, the maturity index (MI), richness (*SR*), dominance (λ), and the trophic diversity index (T) were calculated for the nematode community structure.

4. **RESULTS**

4.1 Soil community structures of nematode and mites under long-term agro-management practices

4.1.1 Nematode communities

4.1.1.1 Trophic Groups

Bacterial feeders (BF) were found to be the most abundant group under no-till management (NTW; NTF) throughout the study period (Figure 4.1), with a mean proportion of 44.6 % in 2015 under wheat and 49.3% in 2016 under fallow of the total nematode community. Fungal feeders (FF) were found to be the second most abundant trophic group with significantly higher values under conventional tillage management (36.7% under CTW; 38.3% under CTF). The highest and lowest proportion (%) of plant feeders (PF) nematodes for the study period were found to range from 19.3% to 10%, with both values recorded under no-till management. There was no significant difference for omnivorous-predators (OP) nematodes among treatments (Figure 4.1).

Table 4.1 F-values of ANOVA of trophic groups of the nematode communities composition underdifferent agricultural management during the study period (2015-2016)

		Bacterivorous	Fungivorous	Phytophagous	Omnivor.+Predators
	_				
Months ^a	F	9.474	5.699	21.614	37.046
	Р	< 0.001	NS^{b}	< 0.001	< 0.001
Agricultural	F	26.197	37.979	10.449	0.971
System ^c	Р	< 0.001	< 0.001	< 0.001	NS

^a Mean value of four sampling times (July & Sep., 2015 and May & Sep., 2016).

^b NS means no significant difference.

^c Mean value of five replicates (n=5).

Among treatments, a significant difference (p<0.001) was found between sampling months for all trophic groups except the fungal feeders (FF) nematodes (Table 4.1).



Figure 4.1 The proportion (%) of trophic groups (BF=Bacterial feeders; FF=Fungal Feeders; PF=Phytophagous; OP=Omnivorous-Predators) of the nematode community under different agricultural management (SE; n=5).

a,b,c, different letters within one index indicates a significant difference (ANOVA: Tukey's test; p<0.05); NTW, no-till wheat 2015; CTW, conventional tillage wheat 2015; NTF, no-till fallow 2016; CTF, conventional tillage fallow 2016.

4.1.1.2 Nematode diversity and relative abundance

During the present agricultural field investigation, a total of 65 nematode genera belonging to 31 families were identified (Tables 4.3; 4.4 & 4.5). The total number of identified nematode genera included 27 bacterivorous genera/ten families, ten fungivorous genera/six families, 15 phytophagous genera/eight families, nine omnivorous genera/four families, and four predatory genera/three families. Among identified genera *Prismatolaimus* (NTW, 13%), *Aphelenchoides* (CTW, 15,4% & CTF, 15%) and *Filenchus* (CTW, 10.7%) were found to be the only eudominant genera. *Acrolobus, Rhabdolaimus, Diphtherophora, Tylencholaimellus, Paratrophurus*, and *Basiria* genera were identified only under conventional tillage management (Tables 4.3 & 4.4), and *Metateratocephalus, Xiphinema*, and *Prionchulus* were identified only under no-till management (Tables 4.3; 4.4 & 4.5). Among treatments, no-till fallow plots were characterized with the highest diversity, while the lowest diversity was attested under conventional tillage wheat crop (Figure 4.2). Both managements, no-till and conventional tillage, were found with increased genera diversity of nematodes under fallow and less under wheat crop. During the study period,

among treatments, the no-till fallow plots were found with a significantly higher diversity of nematodes (Figure 4.2). Also, a significant difference (p<0.001) was found between sampling months for the number of identified genera (Table 4.5).

Bacterial feeders	Genera			Mea	ı n, %	
families ^a		c-p ^b				
		•	NTW ^c	CTW	NTF	CTF
Rhabditidae	Rhabditis	1	+	+		+
	Mesorhabditis	1	+	++	+	+
Panagrolaimidae	Panagrolaimus	1	+		+	+
	Panagrobellus	1	+	+	+	
Cephalobidae	Acrobeles	2	++++	++	+++	+
	Acrobeloides	2	+	+	+++	++
	Acrolobus	2				+
	Cephalobus	2	++++	+++	+++	+++
	Cervidellus	2	+++	++	+++	++
	Chiloplacus	2	++++	++++	++++	+++
	Eucephalobus	2	+++	+++	+++	+++
	Heterocephalobus	2	+	+		
	Panagrolobus	2	++	+	++	++
	Placodira	2	+	+	++	+
	Stegelleta	2	+	+	+	+
	Stegelletina	2			+	+
Plectidae	Plectus	2	+++	+++	+++	+++
	Chiloplectus	2			+	+
	Tylocephalus	2			+	+
	Wilsonema	2	+	+	+	+
Prismatolaimidae	Prismatolaimus	3	+++++	++++	++++	+++
Chronogasteridae	Chronogaster	3	++	+	++++	+++
Cylindrolaimidae	Cylindrolaimus	3			+++	+++
Rhabdolaimidae	Rhabdolaimus	3				+
Teratocephaloidea	Steratocephalus	3	+	+		
	Metateratocephalus	3			+	
Alaimidae	Alaimus	4	+	++	++	+

Table 4.2 Mean relative abundance (RA, %) of bacterivorous nematodes families/genera and their c-p value under different agricultural management during the study period (2015-2016)

^a Trophic groups according to Yeates et al. (1993a); +++++ Eudominant (>10%), ++++ Dominant (5-10%), +++ Subdominant (2-5%), ++ Resident (1-2%), + Subresident (<1%);

^b Coloniser-persister values according to Bongers (1990);

^c NTW, no-till wheat 2015; CTW, conventional tillage wheat 2015; NTF, no-till fallow 2016; CTF, conventional tillage fallow 2016.

Trophic groups ^a &				Mea	n, %	
Familia	Genera	c-p ^b				
Families			NTW ^c	CTW	NTF	CTF
Fungivorous ^a						
Aphelenchoidae	Aphelenchoides	2	++++	+++++	++++	+++++
Aphelenchidae	Aphelenchus	2	++++	++++	++++	++++
	Paraphilenchus	2			++	+
Neotylenchidae	Boleodorus	2	+++	+++	+++	++++
Anguinidae	Ditylenchus	2	++	++++	+++	++++
	Nothotylenchus	2			+	+
Diphtherophoridae	Diphtherophora	3				+
Leptonchidae	Dorylaimoides	4	+	+	+	+
	Tylencholaimus	4			+	+
	Tylencholaimellus	4				+
Phytophagous ^a						
Dolichodoridae	Paratrophurus	2				+
Tylenchidae	Tylenchus	2	+++	+	+	+
	Filenchus	2	++++	+++++	+++	++++
	Aglenchus	2	+		++	++
	Basiria	2		+		
Tylenchulidae	Trophotylenchulus	2	+	+		+
	Paratylenchus	2			+	+
	Gracilacus	2			+	+
Heteroderidae	Meloidogyne juv.	3	+	++	+	++
Hoplolaimidae	Hoplolaimus	3		+	+	+
	Helicotylenchus	3	+		+	+
	Pararotylenchus	3		+	+	+
Pratylenchidae	Pratylenchus	3	+	++	+	
Tylenchorhynchidae	Tylenchorhynchus	3	+++	++	+	+
Longidoridae	Xiphinema	5			+	

Table 4.3 Mean relative abundance (RA, %) of fungivorous and phytophagous nematodes families/genera and their c-p value under different agricultural management during the study period (2015-2016)

^a Trophic groups according to Yeates et al. (1993a); +++++ Eudominant (>10%), ++++ Dominant (5-10%), +++ Subdominant (2-5%), ++ Resident (1-2), + Subresident (<1%);

^b Coloniser-persister values according to Bongers (1990);

^c NTW, no-till wheat 2015; CTW, conventional tillage wheat 2015; NTF, no-till fallow 2016; CTF, conv. tillage fallow 2016.

Trophic groups ^a &	Genera			Mear	ı, %	
Families		c-p ^b				
rannics			NTW ^c	CTW	NTF	CTF
<u>Omnivorous</u>						
Qudsianematidae	Eudorylaimus	4	+++	+	+++	+
	Labronema	4	+	+	++	++
	Microdorylaimus	4	+++	+++	+++	++
Nordiidae	Pungentus	4	+	+	+	+
Aporcelamidae	Aporcelaimus	5	+++	+++	+	+
	Aporcelaimellus	5	+	+	+	+
Dorylaimidae	Dorylaimus	5	++	+++	++	+++
	Laimydorus	5	+	++	+	+
	Mesodorylaimus	5	+++	+++	+++	++++
Predatory						
Mononchidae	Prionchulus	4	+			
Discolaimidae	Discolaimus	5	+		+	+
Nygolaimidae	Nygolaimus	5		+	+	+
	Paravulvus	5	+	+	+	+

Table 4.4 Mean relative abundance (RA, %) of omnivorous and predatory nematodes families/genera and their c-p value under different agricultural management during the study period (2015-2016)

^a Trophic groups according to Yeates et al. (1993a); +++++ Eudominant (>10%), ++++ Dominant (5-10%), +++ Subdominant (2-5%), ++ Resident (1-2), + Subresident (<1%);

^b Coloniser-persister values according to Bongers (1990);

^c NTW, no-till wheat 2015; CTW, conventional tillage wheat 2015; NTF, no-till fallow 2016; CTF, conv. tillage fallow 2016.

4.1.1.3 Faunal structure

The highest value of 23 for the number of identified genera (#G) was found for no-tillage fallow (NTF) treatment, while the lowest value of 18 was found for conventional tillage wheat (CTW) treatment (Figure 4.2). The same trend was observed for the species richness index (SR), with the highest value of 4.8 for NTF treatment and the lowest value of 3.8 for CTW treatment. The species diversity (SD) of the soil free-living nematode community found at the different treatments displayed a substantial similarity between the farming systems, with a significantly (p<0.05) lower diversity in the soil free-living nematode community, except at the NTF treatment. The soil free-living nematode community, except at the NTF treatment.

when comparing the species evenness (SE), dominance (λ), and Simpson's index of diversity (SID) values.



Figure 4.2 The nematode faunal structures under different agricultural management during the study period (SE; n=5)

NTW, no-till wheat 2015; CTW, conventional tillage wheat 2015; NTF, no-till fallow 2016; CTF, conventional tillage fallow 2016; #G, number of identified genera; SD, species diversity; SR, species richness; SE, species evenness; λ , dominance; SID, Simpson's index of diversity.

a,b,c different letters within one index indicate a significant difference (ANOVA: Tukey's test; p<0.05).

Table 4.5 F-values of ANOVA of the nematode faunal structures under different agricultural management during the study period (2015-2016).

		#G	SD	SR	SE	λ	SID	F/B	MI	PPI	MMI	WI
Month ^a	F	20.39	11.32	19.84	5.23	4.06	4.06	3.87	19.97	2.11	26.94	2.12
	P	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	NS ^b	<0.001	NS	<0.001	NS
Agric.	F	26.3	13.97	26.07	1.84	2.62	2.62	9.94	3.37	5.15	0.81	5.6
System ^c	P	<0.001	<0.001	<0.001	NS	NS	NS	<0.001	NS	<0.001	NS	<0.001

#G, number of identified genera; SD, species diversity; SR, species richness; SE, species evenness;

 λ , dominance; SID, Simpson's diversity index; F/B, fungivorous-bacterivorous ratio; MI, maturity index; PPI, plant parasite index; MMI, modified maturity index for all nematodes with c-p=2-5; WI, Wa silewska index.

^a Mean value of four sampling times;

^b NS means no significant difference;

^c Mean value of five replicates (n=5).

During the study period, the values of the F/B, MI, PPI, and WI indices were significantly different (p<0.05) between the soil samples collected from the no-tillage sites and those from the

conventional tillage (Figure 4.3). Thus, the no-tillage farming system was found with significantly (p<0.05) higher values of MI and WI indices. In comparison, conventional tillage farming was found with significantly (p<0.05) higher values of F/B and PPI indices. No significant (p<0.05) differences in the MMI index were found between treatments.

During the study period, a significant difference (p<0.001) was found between sampling months for all calculated faunal indices (Table 4.5), except for the fungivorous-bacterivorous ratio index (F/B), plant parasite index (PPI), and the Wasilewska index (WI).



Figure 4.3 The nematode community structure under different agricultural management during the study period (SE; n=5)

NTW, no-till wheat 2015; CTW, conventional tillage wheat 2015; NTF, no-till fallow 2016; CTF, conventional tillage fallow 2016; F/B, fungivorous-bacterivorous ratio; MI, maturity index; PPI, plant parasite index; MMI, modified maturity index for all nematodes with c-p=2-5; WI, Wasilewska index.

a,b,c different letters within one index indicate a significant difference (ANOVA: Tukey's test; p<0.05).

4.1.1.4 Ecological indices

Several ecological indices were calculated and graphically represented to evaluate the impact of agricultural management on nematode community structure (Figure 4.4). Thus, no-tillage plots were found with significantly (p<0.05) higher values of trophic diversity (TI) and basal indices (BI) and significantly (p<0.05) lower values of enrichment index (EI). On the other

hand, structure (SI) and channel (CI) indices did not allow us to differentiate clearly between the different agricultural management systems.



Figure 4.4 The impact of agricultural management practices on nematode ecological indices (SE; n=5).

NTW, no-till wheat 2015; CTW, conventional tillage wheat 2015; NTF, no-till fallow 2016; CTF, conventional tillage fallow 2016; TI, trophic diversity index; EI, enrichment index; BI, basal index; SI, structure index; CI, channel index; a,b, different letters within one index indicate a significant difference (ANOVA: Tukey's test; p<0.05).

During the study period, a significant difference (p<0.001) was found between sampling months for all calculated ecological indices (Table 4.6).

		TI	EI	BI	SI	CI
Month ^a	F	6.121	9.516	22.468	26.120	5.594
	P	<0.001	<0.001	<0.001	<0.001	<0.001
Agricultural	F	7.653	19.154	5.14	2.404	0.937
System ^b	P	<0.001	<0.001	<0.001	NS ^c	NS

Table 4.6 F-values of ANOVA of the nematode ecological indices under different agricultural management during the study period (2015-2016).

TI, trophic diversity index; EI, enrichment index; BI, basal index; SI, structure index; CI, channel index;

^a Mean value of four sampling times (July&Sep., 2015 and May&Sep., 2016; n=5).

^b Mean value of five replicates (n=5).

^c NS means no significant difference.

4.1.2 Soil mites communities

4.1.2.1 Community structure and diversity

The micro-arthropods data presented for the four orders (Oribatida, Prostigmata, Endostigmata, and Mesostigmata) include only adults and unidentified mites. All taxonomic genera were used for diversity and community analyses. Across all sampling dates and treatments, Oribatida mites had the highest abundance, followed by Prostigmata and Endostigmata, while Mesostigmata was the rare group. Oribatida was the most abundant group (65%) in the conventional tillage fallow (CTF) plots and was significantly (p<0.05) less abundant (40%) in the no-till wheat (NTW) treatment (Figure 4.5). Prostigmata and Endostigmata had a similar trend, with significantly (p<0.05) higher (32.1% and 20.8%, respectively) abundance in the NTW treatment and significantly (p<0.05) lower (15.2% and 13.8%, respectively) abundance in the CTF treatment. Mesostigmata was significantly (p<0.05) higher (11.4%) in the no-till fallow (NTF) than in the other three treatments.



Figure 4.5 Soil community structure of mites under different agricultural management during the study period (SE; n=5).

NTW, no-till wheat 2015; CTW, conv. tillage wheat 2015; NTF, no-till fallow 2016; CTF, conv. tillage fallow 2016; a,b,c,d, different letters within one index indicate a significant difference (ANOVA: Tukey's test; p < 0.05).

During the study period, in the present agricultural field investigation, a total of 53 mites genera belonging to 43 families were found in soil samples (Appendices: Tables A.4 & A.5). A

total of 21 families of Oribatida, which included 25 genera, ten families of Prostigmata with eleven genera, three families of Endostigmata with four genera, and nine families of Mesostigmata, which included 13 genera were identified. The most common oribatid genera found in all treatments were *Carabodes, Eremaeus, Eueremaeus, Oppiella, Oribatella, Nothrus,* and *Hypochthonius* (Appendices: Table A.4). The most common prostigmatid genera identified in all treatments were *Coccorhagidia, Tydeus, Siteroptinae, Pygmephorus,* and *Scutacarus.* The four genera of endostigmatid mites were found in all treatments, and only two genera (*Gamasellodes* and *Rhodacarellus*) of mesostigmatid mites were present in all treatments. Some genera were noted in only one of the treatments, e.g., *Bdella* and *Digamasellus* in the CTW, *Diapterobates, Scheloribates,* and *Cyta* in the NTW, *Oripoda, Veigaia,* and *Eniochthonius* in the NTF. Unexpectedly, in the CTF were noted ten genera that were not found in the rest three microhabitats (Appendices: Tables A.4 & A.5).

4.1.2.2 Faunal structure

The soil mite community exhibited significantly (p<0.05) higher values of diversity, richness, evenness, and maturity indices in both NTF and CTF treatments compared to the other two treatments (Table 4.9). Essentially, the significant differences in the calculated indices were found between the wheat crop year (NTW and CTW) and fallow year (NTF and CTF) management. A significant (p<0.05) difference in Simpson's dominance and diversity indices was found between CTF and other treatments.

During the study period, a significant difference (p<0.001) was found between sampling months for all calculated ecological indices (Table 4.9).

	Mo	nth ^a	Α	gricultur	al System	5 ^b
	F	Р	NTW	CTW	NTF	CTF
Nr. of Identified Genera	76.952	< 0.001	7.5b ^c	8.28b	12.47 a	13.23 a
Species Diversity	77.572	< 0.001	0.75b	0.93b	1.49 a	1.63 a
Species Richness	43.174	< 0.001	2.31b	2.28b	3.01 a	3.09 a
Species Evenness	74.480	< 0.001	0.34b	0.42b	0.58 a	0.62 a
Dominance	43.081	< 0.001	0.02b	0.02b	0.03b	0.06 a
Simpson's Index of Diversity	43.081	< 0.001	0.98 a	0.98 a	0.97 a	0.94b
Maturity Index ^d	6.389	< 0.001	0.49ab	0.3b	0.61 a	0.61 a

Table 4.7 Univariate analysis of variance (ANOVA) for the mite faunal structure under differentagricultural management during the study period (2015-2016)

^a Mean value of two sampling times (July & Sep., 2015 for NTW & CTW; May & Sep., 2016 for NTF & CTF; n=5);

^b NTW, no-till wheat 2015; CTW, conventional tillage wheat 2015; NTF, no-till fallow 2016; CTF, conventional tillage fallow 2016;

^c Values within a row sharing the same letter do not differ significantly (ANOVA: Tukey test; <0.05);

^d Maturity Index of Ruf (1998) calculated based on different life strategies "r" and "K" of Mesostigmata families.

4.2 Soil community structure of nematode and mites under long-term agro-management practices compared to natural prairie system

4.2.1 Nematode communities

4.2.1.1 Trophic Groups

Throughout the study period, among functional groups of nematodes, bacterial feeders (BF) were found to be the most abundant group under native prairies (NP-CB; NP-SC) and no-till (NT-SC) sites (Figure 4.6). Thus, the mean percentages of bacterial feeders of the total nematode community from the four sampling sites were NP-CB (72.7%)>NP-SC (56.3%)>NT-SC (48.6%) > CT-SC (27.3%). Fungal feeders (FF) were found to be the trophic group with significantly higher values under conventional tillage management (CT-SC), with a mean proportion of 40%. Native prairie and no-till Swift Current (NP-SC; NT-SC) sites had a similar proportion of FF nematodes (21.2% and 24.2%), while the native prairie Central Butte site was found with the lowest proportion of FF nematodes (10.5%). The highest and lowest proportion (%) of plant feeders (PF) nematodes for the study period were found to range from 10% to 16.8%. Thus, among sites, the CT-SC was found with a significantly higher proportion of PF nematodes, while the NP-CB and NT-SC sites



Figure 4.6 The proportion (%) of trophic groups of the nematode community at each site (SE; n=3).

NP-CB, native prairie – Central Butte; NP-SC, native prairie – Swift Current; NT-SC, no-till (fallow) – Swift Current; CT-SC, conventional tillage (fallow) – Swift Current.

BF, bacterial feeders; FF, fungal feeders; PF, phytophagous; OP, omnivorous-predators.

a,b,c,d, different letters within one index indicate a significant difference (ANOVA: Tukey's test; p<0.05).

were found with the lowest proportion of PF nematodes. Unexpectedly, the agricultural sites were found with a significantly higher proportion of omnivorous-predator (OP) nematodes (NT-SC 14.8% and CT-SC 16.8%), while native prairie sites were found with a lower proportion of OP nematodes (NP-CB 6.9% and NP-SC 7.7%).

Among sites, no significant difference (p<0.001) was found between sampling months for all trophic groups except the omnivorous-predator nematodes (Table 4.8).

		BF	FF	PF	OP	
Months ^a	F	1.731 NSb	0.013	2.899 NS	16.424	
Sites ^c	r F	93 878	68 886	6 4 9 5	<0.001	
Bites	P	<0.001	< 0.001	<0.001	<0.001	

Table 4.8 F-values of ANOVA of trophic groups of the nematode communities under different agricultural management and native prairie during the study period (2016)

BF, bacterial feeders; FF, fungal feeders; PF, phytophagous; OP, omnivorous-predators.

^a Mean value of two sampling times (May & September, 2016).

^b NS means no significant difference.

^c Mean value of three replicates (n=3).

4.2.1.2 Diversity and relative abundance

During the study period, in the present field investigation, a total of 73 nematode genera belonging to 35 families were identified (Tables 4.9; 4.10 & 4.11). The total number of identified nematode genera included 30 bacterivorous genera/11 families, 11 fungivorous genera/six families, 19 phytophagous genera/ten families, and nine omnivorous genera/five families, and four predatory genera/three families. Among identified genera, *Prismatolaimus* (NP-CB, 42.2% & NP-SC, 13.6%) and *Aphelenchoides* (CT-SC, 15%) were found to be the only eudominant genera. *Acrolobus* and *Paratrophurus* genera were identified only under conventional tillage management (Tables 4.9 & 4.10). *Osstella, Panagrocephalus, Psilenchus*, and *Longidorus* genera were found only at the native prairie Swift Current site (Tables 4.9 & 4.10). *Leptolaimus, Dorylaimellus*, and Prionchulus genera were identified only under no-till management (Tables 4.9; 4.10 & 4.11), and *Metateratocephalus* were identified only under no-till management (Tables 4.9). Both native prairie Swift Current and no-till sites were attested with a significantly higher number of

identified genera (Figure 4.7). However, no significant difference (p<0.001) was found between sampling months for the number of identified genera (Table 4.12).

Bacterial feeders				Mean	ı, %	
families ^a	Genera	c-p ^b	NP-CB ^c	NP-SC	NT-SC	CT-SC
Rhabditidae	Rhabditis	1	+			+
	Mesorhabditis	1	++		+	+
Panagrolaimidae	Panagrolaimus	1	+	+	+	+
	Panagrobellus	1	+	+	+	
Cephalobidae	Acrobeles	2	++	+++	+++	+
	Acrobeloides	2	+	+	+++	++
	Acrolobus	2				+
	Nothacrobeles	2	+	+		
	Cephalobus	2	++	+++	+++	+++
	Cervidellus	2	+++	++++	+++	++
	Chiloplacus	2	+++	++++	++++	+++
	Eucephalobus	2	++	++	+++	+++
	Panagrolobus	2	+	++	++	++
	Placodira	2	+	+	++	+
	Stegelleta	2	+	+	+	+
	Stegelletina	2			+	+
	Osstella	2		+		
	Panagrocephalus	2		+		
Plectidae	Plectus	2	+	+	+++	+++
	Chiloplectus	2			+	+
	Tylocephalus	2		+	+	+
	Wilsonema	2	+++	++	+	+
Prismatolaimidae	Prismatolaimus	3	+++++	+++++	++++	+++
Chronogasteridae	Chronogaster	3	++++	++++	++++	+++
Cylindrolaimidae	Cylindrolaimus	3	++++	+++	+++	+++
Rhabdolaimidae	Rhabdolaimus	3		++		+
Teratocephaloidea	Teratocephalus	3	++	+		
	Metateratocephalus	3			+	
Leptolaimidae	Leptolaimus	3	+			
Alaimidae	Alaimus	4	+	+	++	+

Table 4.9 Mean relative abundance (RA, %) of bacterivorous nematodes families/genera and their c-p value under different agricultural management and native prairies during the study period

^a Trophic groups according to Yeates et al. (1993a) :

+++++ Eudominant (>10%), ++++ Dominant (5-10%), +++ Subdominant (2-5%), ++ Resident (1-2), + Subresident (<1%). ^b Coloniser-persister values according to Bongers (1990).

^c NP-CB, native prairie – Central Butte; NP-SC, native prairie – Swift Current; NT-SC, no-till (fallow) – Swift Current; CT-SC, conventional tillage (fallow) – Swift Current.

Trophic groups ^a				Mea	n, %	
& Families	Genera	c-p ^b			,	
		-	NP-CB ^c	NP-SC	NT-SC	CT-SC
<u>Fungivorous^a</u>						
Aphelenchoidae	Aphelenchoides	2	+++	++++	++++	+++++
Aphelenchidae	Aphelenchus	2	++	+++	++++	++++
	Paraphilenchus	2	+	+	++	+
Neotylenchidae	Boleodorus	2	++	+++	+++	++++
Anguinidae	Ditylenchus	2	+	+++	+++	++++
	Nothotylenchus	2		+	+	+
Diphtherophoridae	Diphtherophora	3	+	+++		+
Leptonchidae	Leptonchus	4	+	+		
-	Dorylaimoides	4	++	+++	+	+
	Tylencholaimus	4	+	++	+	+
	Tylencholaimellus	4	++	+		+
<u>Phytophagous^a</u>						
Dolichodoridae	Paratrophurus	2				+
Tylenchidae	Tylenchus	2	++	+	+	+
	Filenchus	2	++	+++	+++	++++
	Aglenchus	2	+	++	++	++
	Psilenchus	2		+		
Tylenchulidae	Paratylenchus	2		+	+	+
	Gracilacus	2		+++	+	+
	Trophotylenchulus	2	++	+		+
Heteroderidae	Meloidogyne juv.	3	+	+	+	++
Hoplolaimidae	Hoplolaimus	3		+	+	+
	Helicotylenchus	3	+++	++	+	+
	Rotylenchus	3	+	+		
	Pararotylenchus	3	+	+	+	+
Pratylenchidae	Pratylenchus	3	+	+	+	
Tylenchorhynchidae	Tylenchorhynchus	3	+	+	+	+
Belondiridae	Axonchium	5	+	+		
Dorylaimellidae	Dorylaimellus	5	+			
Longidoridae	Longidorus	5		+		
	Xiphinema	5		++	+	

Table 4.10 Mean relative abundance (RA, %) of fungivorous and phytophagous nematodes families/genera and their c-p value under different agricultural management and native prairies during the study period (2016)

^a Trophic groups according to Yeates et al. (1993a):

+++++ Eudominant (>10%), ++++ Dominant (5-10%), +++ Subdominant (2-5%), ++ Resident (1-2), + Subresident (<1%). ^b Coloniser-persister values according to Bongers (1990).

^c NP-CB, native prairie – Central Butte; NP-SC, native prairie – Swift Current; NT-SC, no-till (fallow) – Swift Current; CT-SC, conventional tillage (fallow) – Swift Current.

Trophic groups ^a &				Mea	n, %	
families	Genera	c-p ^b	NP-CB ^c	NP-SC	NT-SC	CT-SC
Omnivorous						
Qudsianematidae	Eudorylaimus	4	+	+	+++	+
	Labronema	4	+	++	++	++
	Microdorylaimus	4	+++	++	+++	++
Nordiidae	Pungentus	4	+	+	+	++
Aporcelamidae	Aporcelaimus	5	+	+	+	+
	Aporcelaimellus	5	+	+	+	+
Dorylaimidae	Dorylaimus	5	+	+++	++	+++
	Mesodorylaimus	5	+	+	+++	++++
Thornenematidae	Laimydorus	5	+		+	+
Predators						
Mononchidae	Prionchulus	4	+			
Discolaimidae	Discolaimus	5	+	+	+	+
Nygolaimidae	Nygolaimus	5	+	+	+	+
	Paravulvus	5	+	+	+	+

Table 4.11 Mean relative abundance (RA, %) of omnivorous and predatory nematodes families/genera and their c-p value under different agricultural management and native prairies during the study period (2016)

^a Trophic groups according to Yeates et al. (1993a) :

+++++ Eudominant (>10%), ++++ Dominant (5-10%), +++ Subdominant (2-5%), ++ Resident (1-2), + Subresident (<1%). ^b Coloniser-persister values according to Bongers (1990).

^c NP-CB, native prairie – Central Butte; NP-SC, native prairie – Swift Current; NT-SC, no-till (fallow) – Swift Current; CT-SC, conventional tillage (fallow) – Swift Current.

4.2.1.3 Faunal structure

The number of identified genera (#G), species diversity (SD), richness (SR), and evenness (SE) exhibited a similar trend, with significantly (p<0.05) high values for native prairie (NT-SC) and no-tillage (NT-SC) Swift Current sites, and low values for native prairie Central Bute (NP-CB) and conventional tillage Swift Current (CT-SC) sites (Figure 4.7). During the study period, the values of the dominance (λ), maturity (MI), modified maturity (MMI), and Simpson's diversity (SID) indices were able to significantly differentiate (p<0.05) between the soil samples collected from the agricultural sites and those from the native prairies (Figure 4.7). Thus, the agricultural sites were found with significantly (p<0.05) lower values of dominance, MI, and MMI indices and with significantly (p<0.05) higher values of SID. The fungivorous-bacterivorous (F/B) ratio and Wasilewska index (WI) displayed a substantial similarity between the native prairie sites and the

no-till farming system, with a significant (p<0.05) lower values of F/B ratio and higher values of WI (Figure 4.8).



Figure 4.7 The nematode faunal structures under different agricultural management and native prairie during the study period (SE; n=3)

NP-CB, native prairie – Central Butte; NP-SC, native prairie – Swift Current; NT-SC, no-till (fallow) – Swift Current; CT-SC, conventional tillage (fallow) – Swift Current; #G, number of identified genera; SD, species diversity; SR, species richness; SE, species evenness; λ , dominance; SID, Simpson's index of diversity.

a,b,c,d, different letters within one index indicate a significant difference (ANOVA: Tukey's test; p<0.05).

		#G	SD	SR	SE	λ	SID	F/B	MI	PPI	MMI	WI
Months ^a	F	0.14	1.25	0.14	1.88	1.27	1.27	3.24	15.61	8.11	7.82	0.26
	P	NS ^b	NS	NS	NS	NS	NS	NS	<0.001	<0.001	<0.001	NS
Sites ^c	F	16.63	22.86	16.47	14.71	106.5	106.5	12.53	85.82	4.27	172.34	4.25
	P	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001

Table 4.12 F-values of ANOVA of the nematode faunal structures under different agricultural management and native prairie during the study period (2016)

#G, number of identified genera; SD, species diversity; SR, species richness; SE, species evenness; λ , dominance; SID, Simpson's index of diversity; F/B, fungivorous-bacterivorous ratio; MI, maturity index; PPI, plant parasite index; MMI, modified maturity index for all nematodes with c-p=2-5; WI, Wasilewska index.

^a Mean value of two sampling times (May & September, 2016).

^b NS means no significant difference.

^c Mean value of three replicates (n=3).

During the study period, no significant difference (p<0.001) was found between sampling months for all calculated faunal indices (Table 4.5), except for the maturity index (MI), plant parasite index (PPI), and modified maturity index (MMI).



Figure 4.8 The nematode community structure under different agricultural management and native prairie during the study period (SE; n=3)

NP-CB, native prairie – Central Butte; NP-SC, native prairie – Swift Current; NT-SC, no-till (fallow) – Swift Current; CT-SC, conventional tillage (fallow) – Swift Current; F/B, fungivorous-bacterivorous ratio; MI, maturity index; PPI, plant parasite index; MMI, modified maturity index for all nematodes with c-p=2-5; WI, Wasilewska index. a,b,c,d, different letters within one index indicate a significant difference (ANOVA: Tukey's test; p < 0.05).

4.2.1.4 Ecological indices

Several ecological indices were calculated and graphically represented to evaluate the impact of agricultural management on soil free-living nematode community structure (Figure 4.9). Thus, conventional tillage plots were found with significantly (p<0.05) higher values of enrichment index (EI). The trophic diversity (TI) index values ranged from 3 to 13.6 and were highest (p<0.05) in agricultural plots. The calculated basal (BI) and structure (SI) indices exhibited a very similar trend, with significantly (p<0.05) higher values in prairie sites and lower in both agricultural sites. The channel (CI) index did not allow us to differentiate clearly between the different management systems.

During the study period, no significant difference (p<0.001) was found between sampling months for all calculated ecological indices (Table 4.13), except for the basal and structure indices.



Figure 4.9 The impact of different land use and management intensity on nematode ecological indices (SE; n=3).

NP-CB, native prairie – Central Butte; NP-SC, native prairie – Swift Current; NT-SC, no-till (fallow) – Swift Current; CT-SC, conventional tillage (fallow) – Swift Current.

TI, trophic diversity index; EI, enrichment index; BI, basal index; SI, structure index; CI, channel index.

a,b,c,d, different letters within one index indicate a significant difference (ANOVA: Tukey's test; p<0.05).

		TI	EI	BI	SI	CI
Month ^a	F	0.027	0.684	42.197	51.146	0.987
	P	NS ^c	NS	<0.001	<0.001	NS
Sites ^b	F	7.653	19.154	5.14	2.404	0.937
	P	<0.001	<0.001	<0.001	<0.001	<0.001

Table 4.13 F-values of ANOVA of the nematode ecological indices under different agricultural management and native prairie during the study period (2016).

TI, trophic diversity index; EI, enrichment index; BI, basal index; SI, structure index; CI, channel index.

^a Mean value of two sampling times (May & September, 2016).

^b NS means no significant difference.

^c Mean value of three replicates (n=3).

4.2.2 Soil mites communities

4.2.2.1 Community structure and diversity

The Acari data presented for the four orders (Oribatida, Prostigmata, Endostigmata, and Mesostigmata) include only adults and unidentified adult mites. All taxonomic groups (families and genera) were used for diversity and community analyses. Across all sampling dates and treatments, Oribatida mites had the highest abundance, followed by Prostigmata and Endostigmata, while Mesostigmata was the rare group (Figure 4.10). Oribatida was the most abundant group (67.5%) in the conventional tillage (CT-SC, fallow) plots and the less abundant group in the native prairie sites (NP-CB, 35.7%; NP-SC, 42.4%). The highest abundance of Prostigmata was found in soil samples from native prairie sites, accounting for 38.9% (NP-CB) and 36.5% (NP-SC) of the total mites, while the lowest abundance (13.5%) was found at conventional tillage site (CT-SC). No significant difference (p<0.05) between sampling sites was found for the abundance of the Endostigmata group. Among investigated sites, the conventional tillage site (CT-SC) was found with the lowest abundance of Mesostigmata, accounting for only 5.5% of the total mites.





NP-CB, native prairie – Central Butte; NP-SC, native prairie – Swift Current; NT-SC, no-till (fallow) – Swift Current; CT-SC, conventional tillage (fallow) – Swift Current.

a,b,c,d, different letters within one index indicate a significant difference (ANOVA: Tukey's test; p<0.05).

During the study period, no significant difference (p<0.001) was found between sampling months for the abundance of all four orders of micro-arthropods (Table 4.14), except for the Endostigmata.

		Oribatida	Prostigmata	Endostigmata	Mesostigmata
Months ^a	F	0.366	1.074	10.782	1.618
	Р	NS ^b	NS	< 0.001	NS
Sites ^c	F	36.973	28.269	2.007	4.334
	Р	< 0.001	< 0.001	NS	< 0.001

Table 4.14 F-values of ANOVA of the four orders of the soil mites community under different agricultural management and native prairie during the study period (2016).

^a Mean value of two sampling times (May & September, 2016).

^b NS means no significant difference.

^c Mean value of three replicates (n=3).

During the study period, in the present field investigation, a total of 68 mites genera belonging to 54 families were found in soil samples (Tables B.4 & B.5). A total of 26 families of Oribatida, which included 33 genera, 12 families of Prostigmata with 13 genera, four families of Endostigmata with five genera, and 12 families of Mesostigmata, which included 17 genera were identified. The most common oribatid genera found at all sites were Carabodes, Eremaeus, Eueremaeus, Oppiella, Oribatella, Tectocepheus, Trhypochthonius, Nothrus, Hypochthonius, and Eulohmannia (Table B.4). The most common prostigmatid genera identified at all treatments were Coccorhagidia, Tydeus, Siteroptinae, Pygmephorus, and Scutacarus (Table B.5). The four genera of endostigmatid mites, Alicorhagia, Nanorchestes, Speleorchestes, and Terpnacarus, and only two genera of mesostigmatid mites, Gamasellodes, Hypoaspis, and Rhodacarellus, were present at all sites (Table B.5). Some genera were noted only at one of the investigated locations, e.g., Banksinoma, Zygoribatula, Scheloribates, Nanhermannia, Anystis, Cyta, and Antennoseius only at the NP-CB site; Trychoribates, Liebstadia, Peloptulus, Bdella, Amblyseius, and Sejida at the NP-SC site; Veigaia only at the NT-SC. Unexpectedly, at the CT-SC were noted eleven genera (Synchthonius, Brachychthonius, Phthiracarus, Rhysotritia, Eupodes, Cunaxinae, Protogamasellus, Pergamasus, Lysigamasus, Alliphis, Macrocheles) that were not found at the other three microhabitats (Tables B.4 & B.5).

4.2.2.2 Faunal structure

The calculated number of identified genera, species diversity, richness, and evenness of the soil mite community did not allow us clearly differentiate between the different land management sites (Table 4.15). Simpson's index of diversity was significantly (p<0.05) higher under no-tillage management (NT-SC); correspondingly, the dominance index had the lowest value. Significant (p<0.05) differences in the maturity index were found between the native prairie Central Butte location and the other experimental plots located in Swift Current.

During the study period, a significant difference (p<0.001) was found between sampling months for all calculated ecological indices, except for the maturity index (Table 4.15).

	Month ^a		Sites ^b			
	F	Р	NP-CB	NP-SC	NT-SC	CT-SC
Nr. of Identified Genera	39 127	~0.001	13 879°	14 03a	12 639	13 839
Species Diversity	74.543	<0.001	1.81 a	14.05 a 1.7 a	1.52 a	1.73 a
Species Richness	6.033	< 0.001	3.1 a	3.23 a	3.03 a	3.17 a
Species Evenness	72.980	< 0.001	0.68 a	0.64 a	0.59 a	0.65 a
Dominance	86.251	< 0.001	0.08 a	0.08 a	0.04b	0.07 a
Simpson's Index of Diversity	86.251	< 0.001	0.92b	0.92b	0.96 a	0.93b
Maturity Index ^d	0.007	NS ^e	0.88 a	0.5b	0.63b	0.57b

Table 4.15 Univariate analysis of variance (ANOVA) for the mite faunal structure under agricultural management and native prairie during the study period (2016)

^a Mean value of two sampling times (May & September, 2016; n=3).

^b NP-CB, native prairie – Central Butte; NP-SC, native prairie – Swift Current; NT-SC, no-till (fallow) – Swift Current; CT-SC, conventional tillage (fallow) – Swift Current.

^c Values within a row sharing the same letter do not differ significantly (ANOVA: Tukey test; <0.05).

^d Maturity Index of Ruf (1998) calculated based on different life strategies "r" and "K" of Mesostigmata families.

^e NS means no significant difference.

5. DISCUSSION

5.1. Soil community structure of nematode and mites under long-term agro-management practices

In the recent decade, agricultural sites have been regarded as systems in which the longterm effect of the farming system negatively affects belowground biodiversity. However, the communities of soil biota are impacted differently, and therefore, their feedback effect on ecosystem services is diverse and idiosyncratic.

5.1.1 Nematode communities

Nowadays, three approaches are known and used to analyze soil nematode communities: through trophic groups, functional guilds, and nematode ecological indices. In this study, to compare the farming systems, the following indicators were chosen: nematode trophic groups and nematode food web indices (trophic diversity, enrichment, basal, structure, and channel indices). Since the assessment of nematode trophic groups provide valuable information about soil biological processes (Ritz and Trudgill, 1999; Bongers and Ferris, 1999; Ruess, 2003; Ito et al., 2014) and nematode food web indices provide a comprehensive evaluation of the belowground processes in cultivated fields (Bongers, 1990; Ferris et al., 1996; Ferris et al., 1999; Ferris et al., 2001; Dong et al., 2007), then it was expected that these indicators would fairly reflect the impact of long-term no-till and conventional tillage management practices on soil nematode community structure in our investigation.

The differences in soil management reasonably explain the shifting between the three nematode trophic groups (bacterivorous, fungivorous, and phytophagous). Tillage does reduce the quantity of soil organic carbon in soil (Dai et al., 2014; Arcand et al., 2016), which results in low abundance and diversity of the microbial community. Consequently, tillage management will be expected to be found with a lower proportion and diversity of bacterivorous communities than notill management. In our study, the results are consistent with the expectation. Further, the population of fungivorous nematodes was much higher under tillage treatment. Zhong et al. (2017) gained a similar observation in a tilled system. The cause of this difference in the proportion of the fungivorous trophic group is unknown. Still, there may have been significantly higher fungi biomass to support the higher abundance of some fungi feeding nematodes (particularly Aphelenchoides, Aphelenhus, and Ditylenchus) under conventionally-tilled plots. A similar pattern of increased abundance of the same fungal-feeder genera primarily associated with conventional tillage practices was reported by Sanchez-Moreno et al. (2009) and Treonis et al. (2018).

On the other hand, the phytophagous trophic group was found to be dominant only in the no-tilled crop plots, with the Tylenchidae and Tylenchorhynchidae families being the most abundant. According to previous studies (Briar et al., 2007; Liang et al., 2009; Zhang et al., 2012), nematode families such as Cephalobidae, Aphelenchoidae, Tylenchidae, Pratylenchidae, Hoplolaimidae, and Tylenchorhynchidae are common for agricultural fields, and the present research asserts this statement positively. However, the proportion of plant-feeding nematodes in the same no-tilled fallow plots declined sharply to 10.1% from 19.4%. Thus, the simple explanation given by other earlier researchers (Freckman and Ettema, 1993; Yeates, 1996; Dong et al., 2007; Viketoft et al., 2009) that high diversity of vegetation leads to a significant increase in phytophagous nematodes does not apply to our study. Earlier, Sohlenius et al. (2011) and recently, Dietrich et al. (2021) and Yan et al. (2021) found that low diversity plant communities support a higher abundance of plant-feeding nematodes. In contrast, the high diversity of vegetation positively affected the abundance and diversity of other nematode trophic groups, especially those that prey on bacteria and nematodes. Similar results were obtained in our study, suggesting a stronger top-down control by predators in the high plant diversity communities and weak top-down control of predators in low plant diversity communities such as agricultural.

Across all sampling dates and treatments, the number of nematode genera identified under no-till management (62) was surprisingly not much higher than those identified under conventional tillage (59). A similar investigation conducted by Zhong et al. (2017) revealed that a 12-year period of no-till management sustained the highest number of identified nematode genera (54) while conventional tillage management sustained the lowest (49). The species' evenness or dominance did not reveal the effects of agricultural management. However, despite differences in agricultural management, the treatments exhibited similar low dominance and high evenness values suggesting no absolutely dominant species in either of their faunal structures. After years of soil system investigations, soil ecologists generally accepted that disturbed systems are characterized by low diversity and richness. Thus, with significantly lower values for diversity and richness for conventional tillage management, our study does not make an exception. Furthermore, similar trends were found for agricultural land in many studies carried out in different countries on different continents (Yeates and Bongers, 1995; Liang et al., 2001; Dong et al., 2007; Kimenju et al., 2009; Culman et al., 2010; Zhang et al., 2012; Ito et al., 2014; Scharroba et al., 2016; Treonis et al., 2018; Bongiorno et al., 2019; Machado et al., 2020).

The maturity index (MI) is calculated as the weighted mean of the individual c-p values (Bongers, 1990) and has been a valuable tool to measure the agroecosystem level of disturbance and differentiate between the tillage practices (Bongers & Ferris, 1999). Thus, low values of MI (e.g., M < 2) suggest a highly disturbed system, whereas high values (e.g., >2) indicate better stable conditions. In this study, both the long-term no-till and conventional tillage systems have been found with MI values slightly over two (2.4 & 2.2, respectively). Nevertheless, there was room for significant differences between the two agricultural managements, thus, indicating a relatively stable environment in the no-till system. The effects of agricultural management were not revealed by the modified maturity index (MMI or Σ MI(2-5)). Along with the maturity index, the plant parasite index can mirror the impact of human activities due to tillage. Thus, PPI values (0.25 & 0.35) were low, with significantly higher values in the conventional system. According to Bongers et al. (1997) and Zheng et al. (2012), in most agroecosystems, the maturity and plant parasite index are found to be inversely related under nutrient enrichment conditions. The statement applies to our results, except there was no direct enrichment source apart from being under crop rotation that included a fallow every second year.

The ratio of bacterivores and fungivores to plant parasite nematodes (WI) indicates the dominant pathway of mineralization (Wasilewska, 1991; Ruess, 2002). In our investigation, disregarding crop rotation, significant-high values found in the no-till treatment implied domination of the detrital decomposition pathway in which bacterial and fungal grazers nematodes are vital intermediaries.

The relative abundance of certain soil nematodes guilds provides essential information regarding soil food web characteristics and soil conditions, such as disturbance level, enrichment, and complexity level of the investigated soil food web (Ferris et al., 2001; Ruess, 2003; Daofeng et al., 2007; Cesarz et al., 2015). Thus, the enrichment index (EI) estimates food web response to

available resources; the channel index (CI) reveals the dominating decomposition pathway; the basal index (BI) points out the basal characteristics of the soil food web, and the structure index (SI) indicates the number of trophic levels within the investigated soil food web. In our investigation, BI was relatively high for both treatments (>50), indicating a basal soil food web commonly found in agricultural soils with low or zero organic input (Ferris et al., 2001; Sanchez-Moreno et al., 2009). However, BI was unexpectedly lower under conventional tillage regardless of crop rotation. A reasonable explanation for it could be that basal bacterial feeders (e.g., *Cephalobidae* and *Panagrolaimidae*) were less abundant in the conventional tillage treatment and led to the high values of the EI and the low values of BI. A similar trend for both treatments, lower EI, and higher SI values indicate a relatively infertile and structured food web. Our observ ations were consistent with Dong et al. (2007) findings for fallows.

Overall, structure (SI) and channel (CI) indices did not allow us to differentiate clearly between the different agricultural management systems. Similarly, Minoshima et al. (2007) did not find a significant difference in SI values between no-till and standard tillage, probably due to the impact of long-term agro-management practices on the higher trophic levels represented by sensitive species of soil nematodes (Sanchez-Moreno et al., 2009). However, the high CI values in both no-till and conventional tillage management indicated a fungal-dominated decomposition pathway. Furthermore, the same readings were for the fungal to bacterial feeder ratio index (F/B), except that under conventional tillage management, F/B values were significantly higher than under no-till management. Thus, the higher F/B ratio points to a lower decomposition and nutrient turnover rate under the conventional tillage system. According to several long-term studies (Adl et al., 2006; de Vries et al., 2012; Liiri et al., 2012; Zhang et al., 2015), a fungal-dominated food web is likely to be less resilient and to have lower rates of recovery after any natural or human-kind disturbance.

5.1.2 Soil mites communities

In the present study, Oribatida mites had the highest abundance and diversity across all sampling dates and treatments, followed by Prostigmata and Endostigmata, while Mesostigmata was the rare group. Gulvik (2007) acknowledged the fact that Oribatida (including the Astigmata clade) is a very diverse suborder and affirmed that in "any given soil patch," its genera will make up 60-90% of the arthropods community. Our observations are partially consistent with her

affirmation. With a range of 40% to 64%, Oribatida mites were the most abundant among other suborders in our study.

Being one of the most abundant and frequent, the community structure of oribatid mites has been investigated at different sites and in different ecosystems around the world over the last three decades (Skubala, 1995; Siepel, 1996; Behan-Pelletier, 1999; Osler and Beattie. 1999; Maraun and Scheu, 2000; Ivan and Vasiliu, 2009; Gan et al., 2014; Meehan et al., 2019; Roy et al., 2021). Most studies aimed to determine their capacity to survive different ecosystem disturbances and be used as soil quality indicators. Thus, it is known that different species could be used as indicators of different kinds of disturbance to date. Still, there is a lack of information regarding specific keystone species in the infinite possible existing species assemblages. However, several studies (Maraun and Scheu, 2000; Maraun et al., 2003; Farska et al., 2014) concluded that among abiotic and biotic factors structuring soil oribatid mite communities (i.e., soil acidity, humidity, temperature, ecosystem type, plant species and soil biota diversity), the disturbance factor seems to have the most direct impact. Nevertheless, sensitivity to disturbance varies notably among oribatid mite suborders, families and even genera, generating a rank from high (Enarthronata suborder) to low (Tectocepheus and Oppiella genera) sensitivity. A very different pattern was found in our study, with the highest oribatid abundance and genera diversity under conventional tillage fallow. Although some oribatid families (e.g., Oppiidae, Hypochthoniidae, Nothridae, Brachychthonidae) were reported to be disturbance-sensitive (Maraun et al., 2003; Farska et al., 2014), we detected their genera in all four agricultural treatments. These contradictory results could be explained by the fact that even though oribatid mites are considered a K-selected group (Norton, 1994), meaning their diversity declines rapidly when there is any disturbance; still, we assume a certain degree of resilience in the long-term alterations (>35 yrs), and even more, partially, our data support the intermediate disturbance hypothesis (IDH) proposed by Connell (1978) and the pattern of resilience after press disturbance suggested by Bengtsson (2002). A similar resilience pattern of soil oribatid mite communities after fire disturbance in a temperate pine forest was reported by Kim and Jung (2013) in Korea and by Hasegawa et al. (2013) after the clear-cutting and replanting of broadleaved forest in Japan.

In our study, combined Prostigmata and Endostigmata groups had the highest proportion in no-till wheat treatment and the lowest in conventional tillage fallow. Since they are considered

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an r-selected group (Walter and Proctor, 1999; Behan-Pelletier and Kanashiro, 2010), which implies a rapid response to any disturbance, especially that involves the nutrient supply, then it is fair to assume that prostigmatid and endostigmatans individuals were significantly more distressed in conventional tillage treatment than no-till treatment. Similar results were reported recently by Khan et al. (2021) from different agroecological zones of Punjab, Pakistan. Also, Coleman et al. (2004) mentioned that, in general, the prostigmatid and endeostigmatid fungal feeder species are opportunistic and often found in high diversity and abundance in the agroecosystems of the temperate zone. Indeed, in our study, all six fungal feeding genera (except *Eupodes*) were detected in all treatments regardless of agricultural practices. An additional observation from data analysis is that the abundance of prostigmatid and endostigmatan populations significantly decreased in the second year of crop rotation (i.e., fallow). We assume this could be a consequence of a lack of crop cover, which might have created a more significant soil temperature fluctuation during the day (Miyazawa et al., 2002; Manu et al., 2016) along with lower water content (Huhta and Hanninen, 2001); respectively, soil mites (especially larva mites) have migrated deeper to meet the optimum temperature range and humidity for their development.

In our study, Mesostigmata was the rare group. According to Coleman et al. (2004), mesostigmatic mites are cosmopolitan predators; therefore, it is expected to occur in low abundance because they may be top-level predators for the soil food web. Study results contradict Behan-Pelletier's affirmation (2003) that mesostigmatan mites are highly abundant predators in Canadian agroecosystems. Our results showed a significantly lower relative abundance of mesostigmatid mites under the conventional tillage system. A similar pattern was found by Walter and Stirling (2018) in sugarcane soil in Australia. According to a recent study (Amani et al., 2020), the diversity of Mesostigmata in agroecosystems significantly declined with an increase in land management intensity. Unexpectedly, our results indicated a significant decline in their relative abundance while their diversity remained the same over the two years of soil sampling. There should be a reasonable explanation for the outcome apart from being a consequence of a long-term agro-management regime (conventional tillage & crop rotation) when a particular microarthropod community structure has been established. A bigger picture of soil food web structure and better expertise could provide a reliable explanation.

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Previous studies reported significant soil mite faunal structure variation among natural and agricultural ecosystems (McLaughlin and Mineau, 1995; Arroyo and Iturrondobeitia, 2006: Bedano et al., 2006; Maribie et al., 2011; Ponge et al., 2013; Leslie et al. 2017; Khan et al., 2021). However, in the present study, species diversity, richness, evenness and maturity indices did not allow us to differentiate clearly between the different agricultural management systems but only between crop rotation. Also, the maturity index (MI) values ranged from 0.3 to 0.61 and increased for both agricultural systems when fallow. The conventional tillage wheat treatment had the lowest MI value, suggesting a highly disturbed soil mite community due to tillage and monoculture practices.

5.1.3 Conclusions

The results of our investigation support our assumption that the increased soil disturbance (CT, conventional tillage) does lead to lower diversity and weaker soil nematode community structure compared to reduced soil disturbance (NT, no-till). Among indicators chosen to compare the farming systems, the most useful for our research objective were SR, F/B, WI, PPI, MI, EI, and BI. Thus, the monoculture in agroecosystems supports a higher abundance of plant-feeding nematodes in no-tillage and a higher abundance of fungi-feeding nematodes in the conventional tillage system. In addition, the MI revealed a more stable environment in the no-till system. At the same time, the F/B ratio suggested a fungal-dominated food web in a conventional tillage system that is likely to be less resilient and to have lower restoration rates after any natural or human-kind disturbance.

Oribatid mites dominated the soil mite communities in terms of frequency and species diversity, regardless of agricultural management. Among calculated indices to estimate the soil mite faunal structure, the maturity index was the only one to reveal the difference between treatments. Our results revealed a positive relationship between crop rotation, reduced soil disturbance, and soil Acari's diversity and maturity.

5.2 Soil community structure of micro-fauna under long-term agro-management practices compared to natural prairie system

Over the last six decades, agriculture has adopted two farming approaches (1) conventional farming, which implies important inputs of fertilizers, pesticides, herbicides, and different soil management practices such as tillage, crop rotation and irrigation; and (2) organic farming, which implies essential inputs of animal and green manure, crop rotation, no-tillage and often does rely on irrigation too. Just recently, for over a decade, farmers have embraced the idea of having no-tillage practices due to high cost and time consumption. However, regardless of the farming method, the process of farming means human intervention in a pristine soil ecosystem. Unfortunately, in most cases, the outcome of this human interference has never been beneficial for soil biodiversity.

5.2.1 Nematode communities

After four decades of intensive studies, soil nematodes are still one of the top groups of multicellular organisms most studied among soil fauna. Their functional diversity keeps them literally under the microscope in most soil food web studies. Directly or indirectly, soil nematodes regulate many vital processes in soil; therefore, their apport to the well-being of soil ecosystems cannot be overlooked. Thereby, many studies have documented soil nematode communities as bioindicators for different ecosystems. However, nematode populations from non-agricultural systems have been less investigated than those from agricultural areas. Our study tried to assess the disturbance level in agroecosystems with native grassland prairies as a reference. Thus, in this study, the treatments included two agricultural management practices (conventional tillage and no-till) that are known to impact soil biodiversity (Freekmann and Ettema, 1993) and undisturbed grassland.

As was stated earlier, prairies support the highest nematode diversity among other terrestrial ecosystems (Todd et al., 2006; Briar et al., 2012). Indeed, in our study, across sampling dates and treatments, the highest number of identified nematode genera (68) was under native prairie systems. Furthermore, Popovici and Ciobanu (2000) found similar diversity (65-67) in two grasslands developed on brown chernozem, the highest among 36 grassland ecosystems investigated in East Europe. Surprisingly, the number of nematode genera identified under no-till

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management (54) was lower than those identified under conventional tillage (57) and could be explained by the higher diversity of opportunistic families.

It was expected that the results of our study would indicate noticeable changes in the occurrence of nematode trophic groups. Indifferent of treatment or sampling month, nematode community composition included all five trophic groups (i.e., bacterivorous, fungivorous, phytophagous, omnivorous, predatory). However, the distribution and structure of trophic groups differed. The differences in land management reasonably explained the shifting between nematode trophic groups. Tillage does reduce the quantity of soil organic carbon in soil (Dai et al., 2014; Arcand et al., 2016), which results in low abundance and diversity of the microbial community. Consequently, tillage management will be expected to be found with a lower proportion and diversity of bacterivorous communities than prairie and no-till systems. In our study, the results are consistent with the expectation; thus, bacteria feeders had the most significant range across all four treatments, with the highest percentage in the grassland (>72%) and lowest in conventional tillage fallow (29%). Our study results contrast with other studies where native prairie lands were defined by relatively low abundance and diversity of bacteria feeders being correlated with low nutrient enrichment (Todd, 1996; Todd et al., 1999; Todd et al., 2006; Briar et al., 2012).

Further, the highest proportion of the fungivorous (FF) nematode population was found in the tillage treatment, which doubled and tripled those observed in native prairie treatments. Similarly, Fu et al. (2000), Liphadzi et al. (2005), and Zhang et al. (2015) also found a higher relative abundance of FF in conventional tillage. The cause of this difference in the proportion of the fungivorous trophic group is unknown. Still, there may have been significantly higher fungi biomass to support the higher abundance of some fungi feeding nematodes (particularly *Aphelenchoides, Aphelenhus, Boleodorus* and *Ditylenchus*) under conventionally-tilled plots. A similar pattern of increased abundance of the same fungal-feeder genera primarily associated with conventional tillage practices was reported by Sanchez-Moreno et al. (2009), Zhao and Neher (2013), Zhong et al. (2017), and Treonis et al. (2018). Despite the fact that conventional agricultural practices have a negative impact on fungi, the response of different fungal genera to tillage might vary (Calderon et al., 2001); so, according to van Groenigen et al. (2010), saprophytic fungi are less impacted by conventional tillage than arbuscular mycorrhizal fungi, which may explain the highest proportion of fungivorous nematodes population found in tillage treatment. Furthermore, the proportion of the phytophagous trophic group was significantly increased in the conventional tillage treatment, with the Tylenchidae family being the most abundant, which according to previous studies (Briar et al., 2007; Liang et al., 2009; Zhang et al., 2012), is a common family for agricultural fields. Earlier, Sohlenius et al. (2011) and recently, Dietrich et al. (2021) and Yan et al. (2021) concluded that monoculture and low diversity (i.e., 2-4 species) plant communities support a higher abundance of plant-feeding nematodes. The results of our study support their statement.

Unexpectedly, in agricultural land, omnivorous predators (OP) had a significantly higher representation (15.8-16.5%) as compared to the prairies (6.9-7.7%). Our results are contrary to the evidence found by Dietrich et al. (2021) that the prey quantity impacts OP abundance and diversity; therefore, the proportion of OP will be higher in high-diversity plant communities such as grasslands. Also, our results did not reveal the effects of agricultural management and contrast with the findings of Zhang et al. (2015) and Zhong et al. (2017), which showed a much higher abundance of OP in reduced till and no-till systems compared to conventional tillage. The relatively higher abundance of specific omnivorous nematode genera suggested less sensitivity to cultivation, such as *Mesodorylaimus* and *Dorylaimus* (Zhao and Neher, 2013), which might explain our results. Also, the OP group was represented by thirteen genera common for each treatment except *Prionchulus*, found only at the prairie sites. According to Freekman and Caswell (1985), the large *Mononchids* are the natural predators of ectoparasites such as *Xiphinema* and *Longidorus* and occur only in undisturbed ecosystems, an affirmation that translates in the results of our study.

Over the years of multiple studies, soil ecologists suggested that specific species/genera of nematodes are sensitive to different kinds of perturbations. For instance, our results are in agreement with previous studies (Sanches-Moreno et al., 2006, 2009; Fiscus and Neher, 2002; Todd et al., 2006; Zhao and Neher, 2013), which indicated that bacterivorous *Prismatolaimus* and *Teratocephalus* and the fungivorous *Diphtherophora* and *Leptonchus* are less abundant or even absent in agroecosystems. Also, most of the phytophagous K-strategists (c-p 5), according to Ferris et al. (2001) and Zhang et al. (2012), belong to the higher trophic level of the soil food web, such as *Axonchium, Dorylaimellus, Longidorus* and *Xiphinema* were absent in the agroecosystems suggesting high sensitivity to any agricultural management.

The nematode faunal structure revealed an unexpected pattern. On the one hand, the number of identified genera, species diversity, species richness and evenness for the native prairie
(Swift Current) and no-till treatments exhibited similar significant high values, suggesting that long term no-till management brought the nematode community composition to a state of restoration. On the other hand, despite differences in agricultural management, the treatments exhibited similar low dominance and high Simpson's index of diversity values suggesting no absolutely dominant species in either of their faunal structures.

The maturity index (MI) is calculated as the weighted mean of the individual c-p values (Bongers, 1990) and has been a valuable tool to measure the agroecosystem level of disturbance and differentiate between the tillage practices (Bongers & Ferris, 1999). Thus, low values of MI (e.g., M < 2) suggest a highly disturbed system, whereas a high value (e.g., >2) indicates better stable conditions. In this study, the differences in agricultural management were not revealed by either the maturity index (MI) or by the modified maturity index (MMI or Σ MI(2-5)). Thus, both treatments, no-till and conventional tillage, exhibited significantly lower values than native prairies, which according to Bongers et al. (1997), indicates a weak organization of nematode communities. In fact, the results confirmed our initial hypothesis and were endorsed by similar studies (Yeates et al., 1997; Kimenju et al., 2009; Zhong et al., 2017), where nematode diversity and maturity decreased with the intensity of land cultivation.

The ratio of bacterivores and fungivores to plant parasites nematodes (WI) indicates the dominant pathway of mineralization (Wasilewska, 1991; Ruess, 2002). In our investigation, disregarding crop rotation, significant-high values found in the no-till treatment and prairies implied domination of the detrital decomposition pathway in which bacterial and fungal grazers nematodes are vital intermediaries. Furthermore, the fungal to bacterial feeders ratio (F/B) reveals the decomposition pathway of organic matter in detrital food webs (Ruess, 2003). Thus, the comparison of systems showed a significant difference in the F/B ratio between conventional tillage and the rest of the treatments. The higher F/B feeders ratio points to a lower decomposition and nutrient turnover rate under the conventional tillage system. Our findings align with Yeates and Bird (1994), who detected F/B values up to 4.2 in agricultural soils. Also, other studies indicated high F/B values (>1.1) in conventionally managed agrosystems (Yeates, 2003; Briar et al., 2007; Heijden et al., 2008).

The relative abundance of certain soil nematodes guilds provides essential information regarding soil food web characteristics and soil conditions, such as disturbance level, enrichment, and complexity level of the investigated soil food web (Ferris et al., 2001; Ruess, 2003; Daofeng

et al., 2007; Cesarz et al., 2015; Gupta et al., 2019). Thus, the enrichment index (EI) estimates food web response to available resources; the channel index (CI) reveals the dominating decomposition pathway; the basal index (BI) points out the basal characteristics of the soil food web, and the structure index (SI) indicates the number of trophic levels within the investigated soil food web.

Our investigation observed that treatment had a significant impact on BI and SI. Both indices have shown a very similar pattern, with the highest values in native prairies and the lowest in conventional tillage, leaving no-till treatment as a transition in between. The relatively low SI values in conventional tillage suggest the presence of a less complex and shorter soil food web, a common feature for intensive agricultural management attested by multiple previous studies (Berkelmans et al., 2003; van Diepeningen et al., 2006; Minoshima et al., 2007; Dong et al., 2007; Sanches-Moreno et al., 2009; Zhang et al., 2012; Zhang et al., 2015); while native prairies and no-till treatments tend to have a more stable, infertile and basal structured soil food webs common found in soils with extreme low organic input as stated by Ferris et al. (2001), Dong et al., 2007, and Sanchez-Moreno et al. (2009). However, BI was unexpectedly lower under conventional tillage regardless of the crop rotation. A reasonable explanation for it could be that basal bacterial feeders (e.g., Cephalobidae and Panagrolaimidae families) were less abundant in the conventional tillage treatment and led to the high values of the EI and the low values of BI.

Overall, CI did not allow us to differentiate clearly between the different agricultural management systems. However, the high CI values in both no-till and conventional tillage management indicate a fungal-dominated decomposition pathway. According to several long-term studies (Adl et al., 2006; de Vries et al., 2012; Liiri et al., 2012; Zhang et al., 2015), a fungal-dominated food web is likely to be less resilient and to have lower rates of restoration after any natural or human-kind disturbance. Furthermore, the relatively highest CI and lowest EI in the native prairie (Swift Current site) implies that the decomposition of organic matter was also realized via a fungal energy channel (Sanchez-Moreno et al., 2010; Mills and Adl, 2011; Zhang et al., 2012).

5.2.2 Soil mites communities

In the present study, Oribatida mites had the highest relative abundance and diversity across all sampling dates and treatments at the Swift Current location, followed by Prostigmata and Endostigmata, while Mesostigmata was the rare group. While at the Central Bute location, the relative abundance but diversity of Prostigmata was the highest, followed by Oribatida, Endostigmata and Mesostigmata. Remarkably, compared to agricultural sites, there is no significant difference between native prairie sites among soil mites orders (i.e., relative abundance or diversity) that form the community. Meanwhile, except for Endostigmata, the rest three mites orders exhibited significantly different soil mites community structures under both no-till and conventional tillage agricultural management.

Overall, among mites, oribatids could be recognized as bioindicators of soil health (Behan-Pelletier, 1999) in terms of species abundance but not in terms of community composition (Lindo and Visser, 2003). The impact of agricultural practices on cryptostigmatic mites has been proven by many studies to be negative, meaning their diversity declines rapidly when there is any disturbance (Seastedt and Crossley, 1981; Blair and Crossley, 1988). Nevertheless, sensitivity to disturbance varies notably among oribatid mite suborders, families and even genera, generating a rank from high (Enarthronata suborder) to low (Tectocepheus and *Oppiella* genera) sensitivity. However, our study found a very different pattern. Thus, Oribatida was the most relative abundant suborder among other mites suborders in the agroecosystems, with 50.4% in no-till and 67.5% in conventional tillage. Similar results (>50%) were reported by Gormsen et al. (2006), Gulvik (2007) and Cao et al. (2011) for arable lands. Also, the Matador Project carried out in southwestern Saskatchewan reported that Oribatida dominated the soil mite community with 55% in prairies and between 45% to 76% in wheat cultivated land (Willard, 1973). In our study, these contradictory results could also be explained by the dominance of several families such as Oppiidae, Hypochthoniidae, Nothridae and Brachychthonidae. Although these oribatid families were reported to be disturbance-sensitive (Maraun et al., 2003; Farska et al., 2014), we detected their genera in both agricultural treatments. Behan-Pelletier (2002) stated that Oribatida has the potential to be the most diverse mite suborder in Canadian prairies; however, our investigation did not reveal a significant difference in their diversity compared to cultivated soil.

Being one of the most abundant, diverse and cosmopolitan, the community structure of oribatid mites has been investigated at different sites and in different ecosystems around the world over the last several decades (Skubala, 1995; Siepel, 1996; Behan-Pelletier, 1999; Osler and Beattie, 1999; Maraun and Scheu, 2000; Ivan and Vasiliu, 2009; Cao et al., 2011; Gan et al., 2014; Meehan et al., 2019; Roy et al., 2021). The purpose of these studies was to determine their capacity to survive ecosystem disturbances and aimed to be used as soil quality indicators. Many studies, above mentioned, have concluded that oribatid communities respond to agricultural practices such as tillage and no-tillage practices, crop rotation, fertilizers and pesticides applications in a predictable manner. According to Behan-Pelletier (1999), the community structure of oribatid mites in agricultural soils usually is almost identical to those found in natural or anthropogenically disturbed ecosystems. Thus, the low presence of individuals from Oppiidae, Brachychthoniidae, Tectocepheidae (Norton and Sillman, 1985; Behan-Pelletier, 1999; Maraun et al., 2003), Oribatulidae (Aoki and Kuriki, 1980) and Trhypochthoniidae (Norton, 1994; Skubala 1995) families, that are considered as slow developing K-strategists sensitive to disturbance indicate medium to heavily disturbed habitats. Our observations are consistent with the above affirmation. According to Farska et al. (2014), there are genera within the reported Kstrategist family that are not affected by the intensity of agricultural management. And indeed, in our study, the oribatid population under agricultural management was partly dominated by the several genera "colonizers" (Tectocepheus, Hypochthonius, Eueremaeus, Carabodes and Oppiella), known to recover quickly and tolerate well agricultural practices (Behan-Pelletier, 1999; Maraun, 2000). It should be noted that the same genera, except Brachychthonius, Synchthonius and Oribatula, were found at the native prairie sites as well. These results suggest that there might take place some disturbance due to wild animal grazing.

Prostigmatid and endostigmatid mites occur in nearly all terrestrial habitats. However, they occur in higher numbers and diversity in the temperate zone than in tropical or subtropical (Behan-Pelletier, 1999; Coleman et al., 2004; Skvarla et al., 2014). The suborders include many predators, but some families (e.g., Eupodidae, Nanorchestidae and Terpnacaridae) feed on algae or fungi and are considered opportunistic; their population can grow fast and become dominant among other suborders that form the soil mites community (Crossley et al., 1992; Tian et al., 1997; Khan et al., 2021). In our investigation, the Prostigmata population had significantly higher representation at both native prairies sites, followed by 23% in no-till and with the lowest

of only 13.5% in conventional tillage. The Matador International Research Project reported a similar pattern carried out in southwestern Saskatchewan from 1967 to 1972, where the Prostigmata soil mite community was represented by 23-25% in prairies and only 3% in wheatcultivated grasslands (Willard, 1973). Our results contradict the statement of Crossley et al. (1992) that in agricultural soils, the abundance of oribatid mites drops while prostigmatid rises due to the dominance of some families (Tydeidae and Tarsonemidae) associated with disturbed soil habitats. We did not encounter any genera of the Tarsonemidae family. According to previous studies (Leetham and Milchunas, 1985; Walter, 1987; Kethley, 1990; Clapperton et al., 2002), Prostigmata were the most abundant Acari (35-80%) in North American prairie ecosystems. A similar trend was observed in our investigation. Also, the abundance of Prostigmata and Endostigmata populations was significantly higher in no-till treatment than in conventional tillage, implying that conventional tillage was the most disturbed habitat among treatments. Similar results were reported recently by Khan et al. (2021) from different agroecological zones of Punjab, Pakistan. Though the Acari diversity index did not show any significant difference between treatments, some predatory genera/families (Anystidae, Bdeliidae, Cheyletidae and Alycidae) were found in prairie sites that were absent from agricultural areas. We assume these large body size families must be susceptible to disturbance.

Overall, the mesostigmatans were rare among soil mites, with the lowest abundance of only 5.5% of the mite population in conventional tillage and double proportion (11%) in notillage. There was no significant difference between native prairie and no-till treatment. Most representants of the Mesostigmata suborder are predators; therefore, their population is expected to have a smaller proportion of soil mites community, but this does not diminish their importance in the soil food web structure. Walter and Ikonen (1989) concluded that even though the floors of western prairies of North America have low litter accumulation, the Mesostigmata mites play an imperative role in balancing the energy channel of the soil food web by praying on nematodes. There are few species (Uropodidae fam.) that are polyphagous (Gerson et al., 2003; Gerson, 2014), and these may become dominant in some undisturbed land (Coleman et al., 2004). Indeed, in our investigation, the Uropodidae genera were absent in agricultural land, being collected only from prairie areas. According to a recent investigation (Amani et al., 2020), the diversity of Mesostigmata in agroecosystems significantly declined with an increase in land management intensity. Our results indicated a significant decline in mesostigmata abundance in conventional

tillage compared to the rest of the treatments. At the same time, their diversity (i.e., number of observed genera) did not show a significant drop. Thus, five of the 17 genera were restricted to conventional tillage plots, five genera to native prairies, only one to no-tillage, and five partly occurred in all treatments. Among treatments, the most representative observed family was Ascidae, with five identified genera. Only two (Arctoseius and Protogamasellus) were collected in agricultural land, and only one (Gamasellodes) was observed at all treatments. There are records (Walter & Kaplan, 1990; Walter et al., 1993; de Castro et al., 2021) of Protogamasellus to tolerate relatively well the impact of conventional agriculture, along with a high tolerance for drought. In contrast, *Protogamasellus* has not been observed as dominant in Canadian prairies. However, numerically, the most predominant family in all four treatments was Rhodacaridae. For the first time in the southwestern Brazilian Amazon, de Castro et al. (2021) found a similar pattern for agricultural areas. In several studies (Castilho et al., 2015; Sourassou et al., 2015; Moreira and Moraes, 2015), it was suggested that Rhodocaridae species, along with Laelapidae, have strong potential as biocontrol agents not only in natural ecosystems but in agroecosystems as well. In our investigation, Hypoaspis genera (Laelapidae) was recorded in all four treatments but was not a dominant top predator as it was recorded by Walter (1987) in the shortgrass prairies of Colorado as an opportunistic genus. Behan-Pelletier and Kanashiro (2010) suggested that rhodacarid Rhodacarellus and representatives of Digamasellidae are anticipated to be common in Canadian prairies even though there are no published data yet. And indeed, we did observe Cornodendrolaelaps genera (Digamasellidae fam.) in all three sites at the Swift Current location, but only after harvest (September).

Previous studies reported significant soil mite faunal structure variation among natural and agricultural ecosystems (McLaughlin and Mineau, 1995; Arroyo and Iturrondobeitia, 2006: Bedano et al., 2006; Maribie et al., 2011; Ponge et al., 2013; Leslie et al. 2017; Khan et al., 2021). However, in the present study, species diversity, richness and evenness indices did not allow us to differentiate clearly between the different agricultural management systems and natural ecosystems. The no-tillage treatment exhibited a significantly low dominance value, suggesting no dominant genera in its mite faunal structure. According to the other treatments' relatively high dominance values, we can assume there is a moderate to high genera domination in their mite communities.

The Maturity Index (MI) proposed over two decades ago (1998) by Ruf, based on the life strategy (r-to-K) of mesostigmatan mites, can be a helpful instrument in soil quality evaluation. Thus, a high value of MI indicates high maturity and a well-structured organization of the mites community and, consequently, a low degree of environmental disturbance of the soil. In our investigation, as was anticipated, native prairie (NT-CB) displayed the highest MI value (0.88). However, the value of MI for another native prairie site located in Swift Current did not bring to light any significant difference compared to cultivated soil. Although the plots were not in approximate area, there was a similarity of mesostigmatan diversity (i.e., genus maturity) between prairie and two agricultural treatments at the Swift Current location, which could explain the low value of MI.

5.2.3 Conclusions

The results of our study indicate noticeable changes in the occurrence of nematode trophic groups in native prairies and agricultural land. Thus, the representation and structure of trophic groups in natural and cultivated land revealed an unexpected pattern as follows: BF > FF > PF > OP in native prairies, and BF < FF > PF \leq OP in agricultural land.

The highest number of identified nematode genera (68) was under native prairie systems.

Among indicators chosen to compare the farming systems with prairies, the most useful for our research objective were F/B, WI, MI, EI, BI and SI. Accordingly, nematode diversity and maturity decreased with the intensity of land cultivation resulting in a weak organization of their communities. The high F/B feeders ratio points to a lower decomposition and nutrient turnover rate under the conventional tillage system, followed by the no-till system. Thus, the fungal-dominated food web is likely to be less resilient and to have lower rates of restoration after any natural or human-kind disturbance. The relatively low SI values in conventional tillage suggest the presence of a less complex and shorter soil food web, a common feature for intensive agricultural management attested by multiple previous studies. Overall, the long-term no-till fields reflected an intermediate disturbance level.

Our investigation revealed the negative impact of agricultural management on mite diversity. Thus, the highest number of identified mites genera (53) was observed in native prairie systems, and the most mature community structure was also found in the grasslands. The above

being said, among calculated indices to estimate the soil mite faunal structure, the maturity index was the only one to reveal the difference between treatments.

Oribatid mites dominated the soil mite communities in terms of densities and genera diversity regardless of agricultural management. Oribatid mites dominated the native prairies mite communities but only in terms of diversity. A significantly higher proportion of Prostigmata (including Endostigmata) was observed in prairie ecosystems. The abundance of Mesostigmata in the conventional tillage system was significantly lower than in the other treatments.

6. SUMMARY

6.1 Future challenges and prospects

The results of our investigation support our prediction that long-term agricultural management sites will be found with lower species diversity and functional groups of soil micro-fauna compared to undisturbed prairie sites as follows: conventional tillage (CT) < no-till (NT) < native prairie (NP).

Regardless of the type of management practices, physicochemical properties of soil are significantly impacted (i.e., loss of organic matter, change in soil pH, an increase of soil density, a decrease in soil porosity and soil water holding capacity) (Six et al., 2000; Kushwaha et al., 2001; Moura and Franzener, 2017) and with that comes the loss of soil biodiversity (Timper, 2014; Bongiorno et al., 2019), which leads to an imbalance of functional groups of the soil food web, consequently disruption of ecosystem functions and services.

In Canada, the agricultural expansion had a negative impact on soil biota. The converted grasslands into cultivated and grazing lands in the prairie provinces (Alberta, Monitoba and Saskatchewan) resulted in <18% of pristine grasslands remaining in the Canadian Prairies ((cpaws-sask.org)). Despite this, only 1% of the pristine grasslands in Saskatchewan and Alberta are protected (Herriot, T., 2017). Also, only a few studies have been published regarding soil biodiversity to compare soil biota in agroecosystems to unaltered or even altered grasslands in Prairies Ecozone. Moreover, except for soil microbial ecology, there has been 50 years of silence in soil ecology since the Matador Project. There are no recent studies on soil mesofauna and macrofauna diversity in Saskatchewan.

In summary, agricultural management significantly altered the nematode and mites communities' composition, maturity, and diversity. Therefore, our results undeniably, indicated that mite and nematode ecological indices have the potential to provide valuable information about the status of the agroecosystems. However, as stated by other researchers (Yeates and Bongers; 1999; Majka et al., 2007; Behan-Pelletier and Kanashiro, 2010; Vankosky et al., 2017), concerning soil biota community, grasslands are patchy and dry. Therefore, a higher number of soil samples and at least three times collection over the growing period are recommended to better represent

the nematode and microarthropods community compositions. Also, investigating physical and chemical properties of soil, looking at more functional groups and taxa along with soil DNA extractions should cover the knowledge gaps that occur in the domain of provincial Soil Ecology. Looking on the bright side, the results of our investigation bring to the table promising data about soil biodiversity reservoirs that still remain in that 3% to 30 % of pristine grasslands in the Saskatchewan Prairies. Is it enough? We cannot say, but we believe it is worth continuing to investigate.

7. **REFERENCES**

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APPENDICES

A. Additional Statistical Information to:

4.1. Soil community structure of nematode and mites under long-term agro-management practices: Mean Relative Abundance of Soil Nematodes and Soil Mites Identification

Table A.1 Mean relative abundance (RA, %) of bacterivorous nematodes families/genera and their c-p value under different agricultural management during the study period (2015-2016). Identification were done at the microscope, without permanent slide preparation.

Bacterial feeders			Mean, %				
families ^a	Genera	c-p ^b					
		-	NTW ^c	CTW	NTF	CTF	
Rhabditidae	Rhabditis	1	0.2	0.275		0.025	
	Mesorhabditis	1	0.925	1.025	0.625	0.975	
Panagrolaimidae	Panagrolaimus	1	0.1		0.35	0.3	
	Panagrobellus	1	0.1	0.4	0.25		
Cephalobidae	Acrobeles	2	5.675	1.15	4.775	0.85	
	Acrobeloides	2	0.825	0.725	2.675	1.75	
	Acrolobus	2				0.05	
	Cephalobus	2	5.225	4.6	3.75	3.65	
	Cervidellus	2	4.05	1.85	2.5	1.55	
	Chiloplacus	2	8.125	6.95	5.525	4.575	
	Eucephalobus	2	3.025	2.475	3.075	2.025	
	Heterocephalobus	2	0.4	0.25			
	Panagrolobus	2	1.175	0.45	1.7	1.225	
	Placodira	2	0.2	0.175	1.05	0.175	
	Stegelleta	2	0.625	0.4	0.575	0.025	
	Stegelletina	2			0.125	0.05	
Plectidae	Plectus	2	3.675	3.6	2.25	2.45	
	Chiloplectus	2			0.625	0.375	
	Tylocephalus	2			0.025	0.125	
	Wilsonema	2	0.075	0.125	0.3	0.425	
Prismatolaimidae	Prismatolaimus	3	12.95	6.375	7.725	2.825	
Chronogasteridae	Chronogaster	3	1.275	0.25	7.225	2.05	
Cylindrolaimidae	Cylindrolaimus	3			2.175	2.875	
Rhabdolaimidae	Rhabdolaimus	3				0.05	
Teratocephaloidea	Steratocephalus	3	0.025	0.1			
	Metateratocephalus	3			0.025		
Alaimidae	Alaimus	4	0.6	1.15	1.45	0.75	

^a Trophic groups according to Yeates et al. (1993a); +++++ Eudominant (>10%), ++++ Dominant (5-10%), +++ Subdominant (2-5%), ++ Resident (1-2%), + Subresident (<1%);

^b Coloniser-persister values according to Bongers (1990);

° NTW, no-till wheat 2015; CTW, conventional tillage wheat 2015; NTF, no-till fallow 2016; CTF, conv. tillage fallow 2016.

Trophic groups &		Mean, %					
Families	Genera	c-p ^b					
			NTW ^c	CTW	NTF	CTF	
Fungivorous ^a							
Aphelenchoidae	Aphelenchoides	2	9.625	15.35	7.65	15.025	
Aphelenchidae	Aphelenchus	2	7.2	9.85	8.35	6.15	
	Paraphilenchus	2			1.2	0.775	
Neotylenchidae	Boleodorus	2	2.625	3.95	2.975	6.1	
Anguinidae	Ditylenchus	2	1.55	6.1	4	8.475	
	Nothotylenchus	2			0.25	0.825	
Diphtherophoridae	Diphtherophora	3				0.075	
Leptonchidae	Dorylaimoides	4	0.7	0.975	0.2	0.4	
	Tylencholaimus	4			0.25	0.025	
	Tylencholaimellus	4				0.475	
Phytophagous ^a							
Dolichodoridae	Paratrophurus	2				0.075	
Tylenchidae	Tylenchus	2	1.3	0.7	0.8	0.425	
-	Filenchus	2	5.3	10.725	4.25	9.45	
	Aglenchus	2	0.875		1.75	1.75	
	Basiria	2		0.325			
Tylenchulidae	Trophotylenchulus	2	0.625	0.025		0.2	
	Paratylenchus	2			0.175	0.125	
	Gracilacus	2			0.45	0.6	
Heteroderidae	Meloidogyne juv.	3	0.275	1.55	0.15	1.95	
Hoplolaimidae	Hoplolaimus	3		0.05	0.05	0.025	
*	Helicotylenchus	3	0.15		0.125	0.075	
	Pararotylenchus	3		0.025	0.5	0.875	
Pratylenchidae	Pratylenchus	3	0.45	1	0.575		
Tylenchorhynchidae	Tylenchorhynchus	3	2.125	1.15	0.3	0.5	
Longidoridae	Xiphinema	5			0.175		

Table A.2 Mean relative abundance (RA, %) of fungivorous and phytophagous nematodes families/genera and their c-p value under different agricultural management during the study period (2015-2016). Identification were done at the microscope, without permanent slide preparation.

^a Trophic groups according to Yeates et al. (1993a); +++++ Eudominant (>10%), ++++ Dominant (5-10%), +++ Subdominant (2-5%), ++ Resident (1-2), + Subresident (<1%);

^b Coloniser-persister values according to Bongers (1990);

^e NTW, no-till wheat 2015; CTW, conventional tillage wheat 2015; NTF, no-till fallow 2016; CTF, conv. tillage fallow 2016.

Table A.3 Mean relative abundance (RA, %) of omnivorous and predatory nematodes families/genera and their c-p value under different agricultural management during the study period (2015-2016). Identification were done at the microscope, without permanent slide preparation.

Trophic groups ^a &			Mean, %					
formilian	Genera	c-p ^b						
<u>tamines</u>			NTW ^c	CTW	NTF	CTF		
<u>Omnivorous</u>								
Qudsianematidae	Eudorylaimus	4	2.65	0.15	3.05	0.35		
	Labronema	4	0.95	0.775	1.075	1.3		
	Microdorylaimus	4	4.5	3.45	3.85	1.925		
Nordiidae	Pungentus	4	0.1	0.175	0.95	1.3		
Aporcelamidae	Aporcelaimus	5	3.325	3.675	0.475	0.25		
	Aporcelaimellus	5	0.075	0.15	0.5	0.9		
Dorylaimidae	Dorylaimus	5	1.575	2.525	1.025	2.15		
	Laimydorus	5	0.475	1.45	0.125	0.35		
	Mesodorylaimus	5	3.25	4.025	4.55	7.725		
Predators								
Mononchidae	Prionchulus	4	0.025					
Discolaimidae	Discolaimus	5	0.05		0.175	0.075		
Nygolaimidae	Nygolaimus	5		0.05	0.075	0.05		
	Paravulvus	5	0.15	0.075	0.175	0.1		

^a Trophic groups according to Yeates et al. (1993a); +++++ Eudominant (>10%), ++++ Dominant (5-10%), +++ Subdominant (2-5%), ++ Resident (1-2), + Subresident (<1%);

^b Coloniser-persister values according to Bongers (1990);

^c NTW, no-till wheat 2015; CTW, conventional tillage wheat 2015; NTF, no-till fallow 2016; CTF, conv. tillage fallow 2016.

			Treatment			³ p	
Families	Genera	Feeding ^a					
			NTW	CTW	NTF	CTF	
<u>Oribatida</u>							
Acaridae	Tyrophagus	Pan		+		+	
Brachychthoniidae	Brachychthonius	Mic				+	
	Synchthonius	Mic	+			+	
Carabodidae	Carabodes	Pan, Phy	+	+	+	+	
	Diapterobates	Pan, Phy	+				
Certozetidae	Ceratozetes	Mic, Pan				+	
Eremaeidae	Eremaeus	Mic	+	+	+	+	
	Eueremaeus	Mic	+	+	+	+	
Galumnidae	Galumna	Pan				+	
Oppiidaae	Oppiella	Mic	+	+	+	+	
Oribatellidae	Oribatella	Mic	+	+	+	+	
Oripodidae	Oripoda	Pan			+		
Scheloribatidae	Scheloribates	Pan	+				
Phenopelopidae	Eupelops	Pan				+	
Phthiracaridae	Phthiracarus	Mac, Pan	+			+	
Tectocepheidae	Tectocepheus	Mic		+	+	+	
Trhypochthoniidae	Trhypochthonius	Mic	+		+	+	
	Mucronothrus	Mic	+	+		+	
Nothridae	Nothrus	Pan	+	+	+	+	
Crotonoidae	Camisia	Pan	+	+	+		
Oribatulidae	Oribatula	Mic			+	+	
Hypochthoniidae	Hypochthonius	Mic, Pan	+	+	+	+	
Eulohmanniidae	Eulohmannia	Unknown	+	+		+	
Eniochthoniidae	Eniochthonius	Mic			+		
Euphthiracaridae	Rhysotritia	Mac				+	

Table A.4 The oribatid mite genera identified in the soil of investigated agroecosystems during the study period (2015-2016). Identification were done at the microscope, without permanent slide preparation.

^a Mac = macrophytophages; Mic = microphytophages; Pan = panphytophages; Phy = phytophages; Pre = predatory (Siepel and de Ruiter-Dukman, 1993).

^b NTW, no-till wheat 2015; CTW, conv. tillage wheat 2015; NTF, no-till fallow 2016; CTF, conv. tillage fallow 2016

			Treatment		ments ^b	b	
Families	Genera	Feeding ^a					
			NTW	CTW	NTF	CTF	
<u>Prostigmata</u>							
Eupodidae	Eupodes	Mic				+	
Rhagidiidae	Coccorhagidia	Pre	+	+	+	+	
Cunaxidae	Cunaxinae	Pre				+	
Bdellidae	Bdella	Pre		+			
	Cyta	Pre	+				
Tydeidae	Tydeus	Pre	+	+	+	+	
Ereynetidae	Unidentified genera	Unknown			+	+	
Pyemotidae	Pyemotes	Pre			+	+	
Siteroptidae	Siteroptinae	Mic	+	+	+	+	
Pygmephoridae	Pygmephorus	Mic	+	+	+	+	
Scutacaridae	Scutacarus	Mic	+	+	+	+	
<u>Endostigmata</u>							
Alicorhagiidae	Alicorhagia	Pre	+	+	+	+	
Nanorchestidae	Nanorchestes	Mic	+	+	+	+	
	Speleorchestes	Mic	+	+	+	+	
Terpnacaridae	Terpnacarus	Mic	+	+	+	+	
<u>Mesostigmata</u>							
Ascidae	Arctoseius	Pre	+		+		
	Gamasellodes	Pre	+	+	+	+	
	Protogamasellus	Pre				+	
Laelapidae	Hypoaspis	Pre		+	+	+	
Parasitidae	Pergamasus	Pre	+	+		+	
	Lysigamasus	Pre	+	+		+	
Rhodacaridae	Rhodacarellus	Pre	+	+	+	+	
Digamasellidae	Digamasellus	Pre		+			
	Cornodendrolaelaps	Pre			+	+	
Zerconidae	Zercon	Pre				+	
Eviphididae	Alliphis	Pre				+	
Macrochelidae	Macrocheles	Pre		+		+	
Veigaiidae	Veigaia	Pre			+		

Table A.5 Prostigmata, Endostigmata and Mesostigmata mite genera identified in the soil of investigated agroecosystems during the study period (2015-2016). Identification were done at the microscope, without permanent slide preparation.

^a Mac = macrophytophages; Mic = microphytophages; Pan = panphytophages; Phy = phytophages; Pre = predatory (Behan-Pelletier and Kanashiro, 2010).

^b NTW, no-till wheat 2015; CTW, conv. tillage wheat 2015; NTF, no-till fallow 2016; CTF, conv. tillage fallow 2016.

Additional Statistical Information to:

4.2 Soil community structure of micro-fauna under long-term agro-management practices compared to natural prairie system: Mean Relative Abundance of Soil Nematodes and Soil Mites Identification

Table B.1. Mean relative abundance (RA, %) of bacterivorous nematodes families/genera and their c-p value under agricultural management and native prairie during the study period (2016). Identification were done at the microscope, without permanent slide preparation.

Bacterial feeders			Mean, %			
families ^a	Genera	с-р ^ь				
		_	NP-CB ^c	NP-SC	NT-SC	CT-SC
Rhabditidae	Rhabditis	1	0.167			0.025
	Mesorhabditis	1	1.167		0.625	0.975
Panagrolaimidae	Panagrolaimus	1	0.667	0.167	0.35	0.3
	Panagrobellus	1	0.033	0.1	0.25	
Cephalobidae	Acrobeles	2	1.767	2.7	4.775	0.85
	Acrobeloides	2	0.5	0.333	2.675	1.75
	Acrolobus	2				0.05
	Nothacrobeles	2	0.033	0.033		
	Cephalobus	2	1.533	3.833	3.75	3.65
	Cervidellus	2	2.267	5.1	2.5	1.55
	Chiloplacus	2	3.533	5.733	5.525	4.575
	Eucephalobus	2	1.467	2	3.075	2.025
	Panagrolobus	2	0.633	1.733	1.7	1.225
	Placodira	2	0.233	0.7	1.05	0.175
	Stegelleta	2	0.133	0.933	0.575	0.025
	Stegelletina	2			0.125	0.05
	Osstella	2		0.1		
	Panagrocephalus	2		0.133		
Plectidae	Plectus	2	0.933	0.167	2.25	2.45
	Chiloplectus	2			0.625	0.375
	Tylocephalus	2		0.4	0.025	0.125
	Wilsonema	2	2.133	1.767	0.3	0.425
Prismatolaimidae	Prismatolaimus	3	42.233	13.6	7.725	2.825
Chronogasteridae	Chronogaster	3	5.5	9.7	7.225	2.05
Cylindrolaimidae	Cylindrolaimus	3	5.5	4.5	2.175	2.875
Rhabdolaimidae	Rhabdolaimus	3		1.833		0.05
Teratocephaloidea	Teratocephalus	3	1.633	0.033		
-	Metateratocephalus	3			0.025	
Leptolaimidae	Leptolaimus	3	0.1			
Alaimidae	Alaimus	4	0.5	0.7	1.45	0.75

^a Trophic groups according to Yeates et al. (1993a) :

+++++ Eudominant (>10%), ++++ Dominant (5-10%), +++ Subdominant (2-5%), ++ Resident (1-2), + Subresident (<1%).

^b Coloniser-persister values according to Bongers (1990).

^c NP-CB, native prairie – Central Butte; NP-SC, native prairie – Swift Current; NT-SC, no-till (fallow) – Swift Current; CT-SC, conventional tillage (fallow) – Swift Current.

Trophic groups ^a			Mean, %				
&	Genera	c-p ^b					
families ^a		-	NP-CB ^c	NP-SC	NT-SC	CT-SC	
Fungivorous ^a							
Aphelenchoidae	Aphelenchoides	2	2.533	6.233	7.65	15.025	
Aphelenchidae	Aphelenchus	2	2	2.9	8.35	6.15	
	Paraphilenchus	2	0.1	0.267	1.2	0.775	
Neotylenchidae	Boleodorus	2	1.5	3	2.975	6.1	
Anguinidae	Ditylenchus	2	0.9	2.2	4	8.475	
	Nothotylenchus	2		0.133	0.25	0.825	
Diphtherophoridae	Diphtherophora	3	0.633	2.167		0.075	
Leptonchidae	Leptonchus	4	0.233	0.233			
	Dorylaimoides	4	1.333	2.6	0.2	0.4	
	Tylencholaimus	4	0.3	1.267	0.25	0.025	
	Tylencholaimellus	4	1	0.233		0.475	
Phytophagous ^a	-						
Dolichodoridae	Paratrophurus	2				0.075	
Tylenchidae	Tylenchus	2	0.133	0.433	0.8	0.425	
-	Filenchus	2	2.2	4.733	4.25	9.45	
	Aglenchus	2	0.5	1.867	1.75	1.75	
	Psilenchus	2		0.067			
Tylenchulidae	Paratylenchus	2		0.7	0.175	0.125	
	Gracilacus	2		2.033	0.45	0.6	
	Trophotylenchulus	2	1.067	0.1		0.2	
Heteroderidae	Meloidogyne juv.	3	0.133	0.667	0.15	1.95	
Hoplolaimidae	Hoplolaimus	3		0.133	0.05	0.025	
	Helicotylenchus	3	3.4	1.633	0.125	0.075	
	Rotylenchus	3	0.3	0.1			
	Pararotylenchus	3	0.2	0.2	0.5	0.875	
Pratylenchidae	Pratylenchus	3	0.067	0.3	0.575		
Tylenchorhynchidae	Tylenchorhynchus	3	0.7	0.467	0.3	0.5	
Belondiridae	Axonchium	5	0.033	0.1			
Dorylaimellidae	Dorylaimellus	5	0.133				
Longidoridae	Longidorus	5		0.033			
	Xiphinema	5		1.2	0.175		

Table B.2. Mean relative abundance (RA, %) of fungivorous nematodes families/genera and their c-p value under agricultural management and native prairie during the study period (2016). Identification were done at the microscope, without permanent slide preparation.

^a Trophic groups according to Yeates et al. (1993a) :

+++++ Eudominant (>10%), ++++ Dominant (5-10%), +++ Subdominant (2-5%), ++ Resident (1-2), + Subresident (<1%).

^b Coloniser-persister values according to Bongers (1990).

^e NP-CB, native prairie – Central Butte; NP-SC, native prairie – Swift Current; NT-SC, no-till (fallow) – Swift Current; CT-SC, conventional tillage (fallow) – Swift Current.

Trophic groups ^a &			_	Mear	n, %	
families	Genera	c-p ^b	NP-CB ^c	NP-SC	NT-SC	CT-SC
<u>Omnivorous</u>						
Qudsianematidae	Eudorylaimus	4	0.5	0.4	3.05	0.35
	Labronema	4	0.767	1.467	1.075	1.3
	Microdorylaimus	4	2.433	1.7	3.85	1.925
Nordiidae	Pungentus	4	0.333	0.233	0.95	1.3
Aporcelamidae	Aporcelaimus	5	0.4	0.333	0.475	0.25
	Aporcelaimellus	5	0.767	0.633	0.5	0.9
Dorylaimidae	Dorylaimus	5	0.9	2	1.025	2.15
	Mesodorylaimus	5	0.367	0.1	4.55	7.725
Thornenematidae	Laimydorus	5	0.033		0.125	0.35
Predators						
Mononchidae	Prionchulus	4	0.133			
Discolaimidae	Discolaimus	5	0.167	0.433	0.175	0.075
Nygolaimidae	Nygolaimus	5	0.033	0.133	0.075	0.05
	Paravulvus	5	0.1	0.267	0.175	0.1

Table B.3. Mean relative abundance (RA, %) of omnivorous and predatory nematodes families/genera and their c-p value under agricultural management and native prairie during the study period (2016). Identification were done at the microscope, without permanent slide preparation.

^a Trophic groups according to Yeates et al. (1993a) :

+++++ Eudominant (>10%), ++++ Dominant (5-10%), +++ Subdominant (2-5%), ++ Resident (1-2), + Subresident (<1%). ^b Coloniser-persister values according to Bongers (1990).

^c NP-CB, native prairie – Central Butte; NP-SC, native prairie – Swift Current; NT-SC, no-till (fallow) – Swift Current; CT-SC, conventional tillage (fallow) - Swift Current.

			Treatments ^b				
Families	Genera	Feeding ^a					
			NP-CB	NP-SC	NT-SC	CT-SC	
Oribatida							
Acaridae	Tyrophagus	Pan	+	+		+	
Brachychthoniidae	Brachychthonius	Mic				+	
	Synchthonius	Mic				+	
Carabodidae	Carabodes	Pan, Phy	+	+	+	+	
	Diapterobates	Pan, Phy	+	+			
Certozetidae	Ceratozetes	Mic, Pan		+		+	
Eremaeidae	Eremaeus	Mic	+	+	+	+	
	Eueremaeus	Mic	+	+	+	+	
Galumnidae	Galumna	Mic, Pan		+		+	
Oppiidae	Oppiella	Mic	+	+	+	+	
Suctobelbidae	Suctobelbella	Mic	+	+			
Thyrisomidae	Banksinoma	Mic	+				
Oribatellidae	Oribatella	Mic	+	+	+	+	
Oripodidae	Oripoda	Pan		+	+		
Scheloribatidae	Liebstadia	Pan		+			
Scheloribatidae	Scheloribates	Pan	+				
Haplozetidae	Peloribates	Pan	+	+			
r	Rostrozetes	Mic. Pan		+			
Phenopelopidae	Eupelops	Pan		+		+	
	Peloptulus	Pan		+			
Phthiracaridae	Phthiracarus	Mac, Pan				+	
Tectocepheidae	Tectocepheus	Mic	+	+	+	+	
Trhypochthoniidae	Trhypochthonius	Mic	+	+	+	+	
J 1	Mucronothrus	Mic	+	+		+	
Nothridae	Nothrus	Pan	+	+	+	+	
Crotonoidae	Camisia	Pan	+	+	+		
Nanhermanniidae	Nanhermannia	Pan	+				
Oribatulidae	Oribatula	Mic			+	+	
	Zygoribatula	Mic, Pan	+				
Hypochthoniidae	Hypochthonius	Mic, Pan	+	+	+	+	
Eulohmanniidae	Eulohmannia	Unknown	+	+	+	+	
Eniochthoniidae	Eniochthonius	Mic	+	+	+		
Euphthiracaridae	Rhysotritia	Mac				+	

Table B.4 The oribatid mite genera identified at each site during the study period (2016). Identification were done at the microscope, without permanent slide preparation.

^a Mac = macrophytophages; Mic = microphytophages; Pan = panphytophages; Phy = phytophages; Pre = predatory (Siepel and de Ruiter-Dukman, 1993).

^b NP-CB, native prairie – Central Butte; NP-SC, native prairie – Swift Current; NT-SC, no-till (fallow) – Swift Current; CT-SC, conventional tillage (fallow) – Swift Current.
Families	Genera	Feeding ^a	Treatments ^b			
					NT CC	CT SC
			NP-CB	NP-SC	NI-5C	CI-5C
<u>Prostigmata</u>						
Anystidae	Anystis	Pre	+			
Eupodidae	Eupodes	Mic				+
Rhagidiidae	Coccorhagidia	Pre	+	+	+	+
Cunaxidae	Cunaxinae	Pre				+
Bdellidae	Bdella	Pre		+		
	Cyta	Pre	+			
Tydeidae	Tydeus	Pre	+	+	+	+
Ereynetidae	Unidentified genera	Pre			+	+
Pyemotidae	Pyemotes	Pre			+	+
Siteroptidae	Siteroptinae	Mic	+	+	+	+
Pygmephoridae	Pygmephorus	Mic	+	+	+	+
Scutacaridae	Scutacarus	Mic	+	+	+	+
Cheyletidae	Unidentified genera	Unknown		+		
Endostigmata	-					
Alicorhagiidae	Alicorhagia	Pre	+	+	+	+
Nanorchestidae	Nanorchestes	Mic	+	+	+	+
	Speleorchestes	Mic	+	+	+	+
Terpnacaridae	<i>Îerpnacarus</i>	Mic	+	+	+	+
Alycidae	Bimichaelia	Mic	+	+		
<u>Mesostigmata</u>						
Ascidae	Asca	Pre	+	+		
	Arctoseius	Pre		+	+	
	Antennoseius	Pre	+			
	Gamasellodes	Pre	+	+	+	+
	Protogamasellus	Pre				+
Laelapidae	Hypoaspis	Pre	+	+	+	+
Phytoseiidae	Amblyseius	Pre		+		
Parasitidae	Pergamasus	Pre				+
	Lysigamasus	Pre				+
Rhodacaridae	Rhodacarellus	Pre	+	+	+	+
Digamasellidae	Cornodendrolaelaps	Pre		+	+	+
Zerconidae	Zercon	Pre	+	+		+
Eviphididae	Alliphis	Pre				+
Macrochelidae	Macrocheles	Pre				+
Veigaiidae	Veigaia	Pre			+	
Sejidae	Sejida	Pre		+		
Uropodidae	Unidentified genera	Pre, Pan	+	+		

Table B.5 The Prostigmata, Endostigmata and Mesostigmata mite genera identified at each site during the study period (2016). Identification were done at the microscope, without permanent slide preparation.

^a Mac = macrophytophages; Mic = microphytophages; Pan = panphytophages; Phy = phytophages; Pre = predatory. ^b NP-CB, native prairie – Central Butte; NP-SC, native prairie – Swift Current; NT-SC, no-till (fallow) – Swift Current; CT-SC, conventional tillage (fallow) – Swift Current.